Supplementary Appendix

This appendix has been provided by the authors to give readers additional information about their work.

Supplement to: Zaretsky JM, Garcia-Diaz A, Shin DS, et al. Mutations associated with acquired resistance to PD-1 blockade in melanoma. N Engl J Med. DOI: 10.1056/NEJMoa1604958

Supplemental Appendix

Acquired resistance to PD-1 blockade through interferon pathway mutations

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Supplementary Methods

Tumour samples and cell lines

Patients underwent baseline biopsies before starting on therapy, early on therapy biopsies[1-3] (in some patients), and upon progression. When feasible, biopsy samples were split into three with one aliquot immediately fixed in formalin followed by paraffin embedding for pathological analyses, a second aliquot snap frozen by immediate immersion in liquid nitrogen for genetic analyses, and if there was residual tissue it was sterily processed in the laboratory to establish a cell line as previously described[4,5] . Cell lines were periodically authenticated using GenePrint® 10 System (Promega, Madison, WI), and were matched with the earliest passage cell lines. Tumour biopsy and peripheral blood cell collection and analyses were approved by UCLA IRBs 11-001918 and 11-003066. Snap frozen samples were disrupted in lysis buffer by BeadBug microtube homogenizer (Benchmark Scientific, Edison, NJ) using disposable stainless steel beads. DNA and RNA from snap frozen samples and cell lines were extracted concurrently using the Qiagen All-Prep kit (Qiagen, , Benelux B.V., Venlo, The Netherlands) and mirVana miRNA isolation kit (ThermoFisher, Canoga Park, CA). Ambion RecoverAll kit (also ThermoFisher) was used for DNA extraction from FFPE slides.

Immunohistochemistry and Immunofluorescence

Slides were stained for immunohistochemistry with S100 (Dako, Carpinteria, CA, CD8 (Dako), PD-L1 (all clone SP142, Spring Bio, Pleasanton, CA, except the PD-L1 in Figs S1B, S2B, and S2C which were previously stained[3] with clone 22C3, Merck). Staining was performed at the UCLA Anatomic Pathology IHC Laboratory. Immunostaining was performed on Leica Bond III autostainers using Leica Bond ancillary reagents and REFINE polymer DAB detection system as previously described[3]. Staining for MHC Class I (clone HC 10, Saphirre NA, Ann Arbor, MI) and MHC Class II (HLA-DR, sc-53319, Santa Cruz

Biotechnology, Santa Cruz, CA) was performed by the UCLA Translational Pathology Core Laboratory. Slides were scanned at 40X on an Aperio ScanScope AT (Leica Biosystems, Buffalo Grove, IL) and analyzed on the Halo Platform (Indica Labs, Corrales, NM). Immnofluoresecnce was performed with OPAL-5-plex reagents, imaged at 20X on the Vectra Automated Quantitative Pathology Imaging System, and analyzed using inForm software (all from Perkin-Elmer, Waltham, MA). Staining used the following antibodies: S100 (DAKO), CD8 (DAKO), PD-L1 (all clone SP142, Spring Bio), and Sox10 (Biocare Medical, Concord, CA).

Genetic analyses

Exon capture and library preparation were performed at the UCLA Clinical Microarray Core using the Roche Nimblegen SeqCap EZ Human Exome Library v3.0 targeting 64 Mb of genome. 2x100bp paired-end sequencing was carried out on the HiSeq 2000 platform (Illumina, San Diego, CA) and sequences were aligned to the UCSC hg19 reference using BWA-mem (v0.7.9). Sequencing for tumors and matched normal DNA from peripheral blood mononuclear cells was performed to a target depth of 150X (actual: minimum 90X, maximum 348X, median 143X). Pre-processing followed the Genome Analysis Toolkit (GATK) Best Practices Workflow v3, including duplicate removal, indel realignment, and base quality score recalibration.

Somatic mutations were called against a paired normal sample with methods as previously reported[6]. In brief, high-confidence mutations were retained if identified by at least two out of three programs between: MuTect (v1.1.7)[7], Varscan2 Somatic (v2.3.6)[8], and a one-sided Fisher's Exact Test (P value cut-off ≤ 0.01) for GATK-HaplotypeCaller (HC) calls between tumour/normal pairs for single nucleotide variants. Insertions/deletions were included if called by both Varscan2 and the GATK-HC. Variants were annotated by a stand-alone version of Oncotator[9] using the Dec112014 datasource. Non-synonymous mutations were those classified as nonsense, missense, splice_site, or nonstop mutations, frame_shift,

in_frame_, or start_codon altering insertions/deletions. Purity, ploidy, and allele-specific copy number status was determined by Sequenza[10] with default settings. Adjusted variant allele frequency was calculated according to the following equation to adjust for stromal content and copy number, with tumor/stromal fractions and local copy number from Sequenza output.

$VAFadjusted$=$VAFobserved*$[1+(2$*Stromal\ Fraction$)/(*Tumor Fraction*Local Copy Number*)]

Sanger validation of JAK and B2M mutations and Targeted Amplicon Re-Sequencing

The following primers pairs were used for PCR amplification of the mutation-containing region of JAK1, JAK2 and B2M from cases #1, #2, and #3 respectively.

JAK1 296bp: 5' caatgccttctcctggacctt 3' and 5' ccgaaccgtgcagactgtag 3'

JAk2 241bp: 5' acctcaccaacattacagaggc 3' and 5' acatctaacacaaggttggca 3'

B2M 257bp: 5' cttgtcctgattggctgggc 3' and 5' acttggagaagggaagtcacg 3'

PCR was performed with 250ng input genomic DNA using the AccuPrime Taq DNA Polymerase System (ThermoFisher, Canoga Park, CA) and cycling protocol 94^{o}C 2 min, [94^{o}C 30 sec, 52^{o}C 1min, 68^{o}C 1min] X 35 cycles , 68^{o}C 10min, 4^{o}C hold.

Products were purified by agarose gel elecrtophoresis and submitted for either Sanger sequencing (Laragen, Culver City, CA) or Illumina deep sequencing with the UCLA Clinical Microarray Core. Library prep of PCR products was performed without fragmentation using the KAPA Hyper Prep kit (Kapa Biosystems, Wilmington, MA), and sequenced on an Illumina Miseq 2x150bp or NextSeq 1x75bp. All sequencing reactions produced >1 million mapped reads per locus.

Western blot and flow cytometry analyses

Melanoma cell lines were maintained in 10 cm culture dishes and analyzed when approximately 70% confluent. Western blot and flow cytometry was performed as previously described[11-12] upon exposure to interferon alpha, beta or gamma (BD Bioscience, San Jose, CA) for 30 minutes or 18 hours. Experiments were performed at least twice for each cell line.

Primary antibodies included JAK1, JAK2, pSTAT1 (Tyr701), pSTAT3 (Tyr705), STAT1 and STAT3 total protein; IRF-1, PD-L1, TAP1 and GAPDH (all from Cell Signaling Technology, Danvers, MA) as well as MHC class I heavy chain clones HCA2 for HLA-A and clone HC10 for HLA-B/C (both from Sapphire NA, Ann Arbor, MI). Immuno-reactivity was revealed with an ECL-Plus kit (Amersham Biosciences Co, Piscataway, NJ), using the ChemiDoc MP system (Bio-Rad Laboratories, Hercules, CA).

Transcriptional Profiling Analysis

Total RNA was extracted from human melanoma cell lines in the absence or presence of interferon-gamma (100 IU/ml) at 3 hours according to the manufacturer's protocol (Qiagen, Benelux B.V., Venlo, The Netherlands). nCounter (NanoString Technologies, Seattle, WA) analysis was performed at the Center for Systems Biomedicine, a part of the Integrated Molecular Technologies Core (IMTC) at UCLA using the nCounter PanCancer immune profiling panel, including 769 genes to which we added 21 custom genes to capture the known interferon response genes. Through the use of color-coded probe pairs, mRNA transcripts of specific cellular genes, including housekeeping genes for normalization, were quantified in untreated M420 and M464 cells and after 3 hours of interferon gamma exposure. The list of genes included in the analysis appears in Table S4.

For RNA-seq analysis of JAK2 splicing in M420 and M464, paired-end transcriptome reads were mapped to the UCSC hg19 reference genome using Tophat2[13].

JAK CRISPR/Cas9-mediated Knockout

M407 with CRISPR/Cas9 mediated JAK1 and JAK2 knock-outs were generated by lentiviral transduction using particles encoding guide RNAs, a fully functional CAS9 cassette, green fluorescent protein, and puromycin as selectable markers (Sigma-Aldrich, St. Louis, MI). Two guide sequences were used per gene, targeting exon 4 (ccaagctctggtatgctccaaa) and

exon 5 (ccaattggcatggaaccaacga) for JAK1, and exon 1 (cctgccttacgatgacagaaat) and 2 (ccaggcataatgtactctacag) for JAK2. GFP positive single cell clones were isolated using a FACSARIA sorter (Becton-Dickinson, Franklin Lakes, NJ). Clones were screened by PCR with the following primers, and reading-frame disruption was confirmed by Sanger sequencing with TIDE analysis (Tracking of Indels by Decomposition, NKI, The Netherlands, https://tide.nki.nl).

JAK1 Exon4 : 5' agtcctttctcacatcaagca 3' and 5' gccaggaatttgtttgcatgt 3'

JAK1 Exon 5: 5' cagggttgtctgcctgcttc 3' and 5' gaagctggagtttgtgggat 3'

JAK2 Exon 1: 5' acttctgggctcaagctatctg 3' and 5' cttgggaaatctgaggcaga 3'

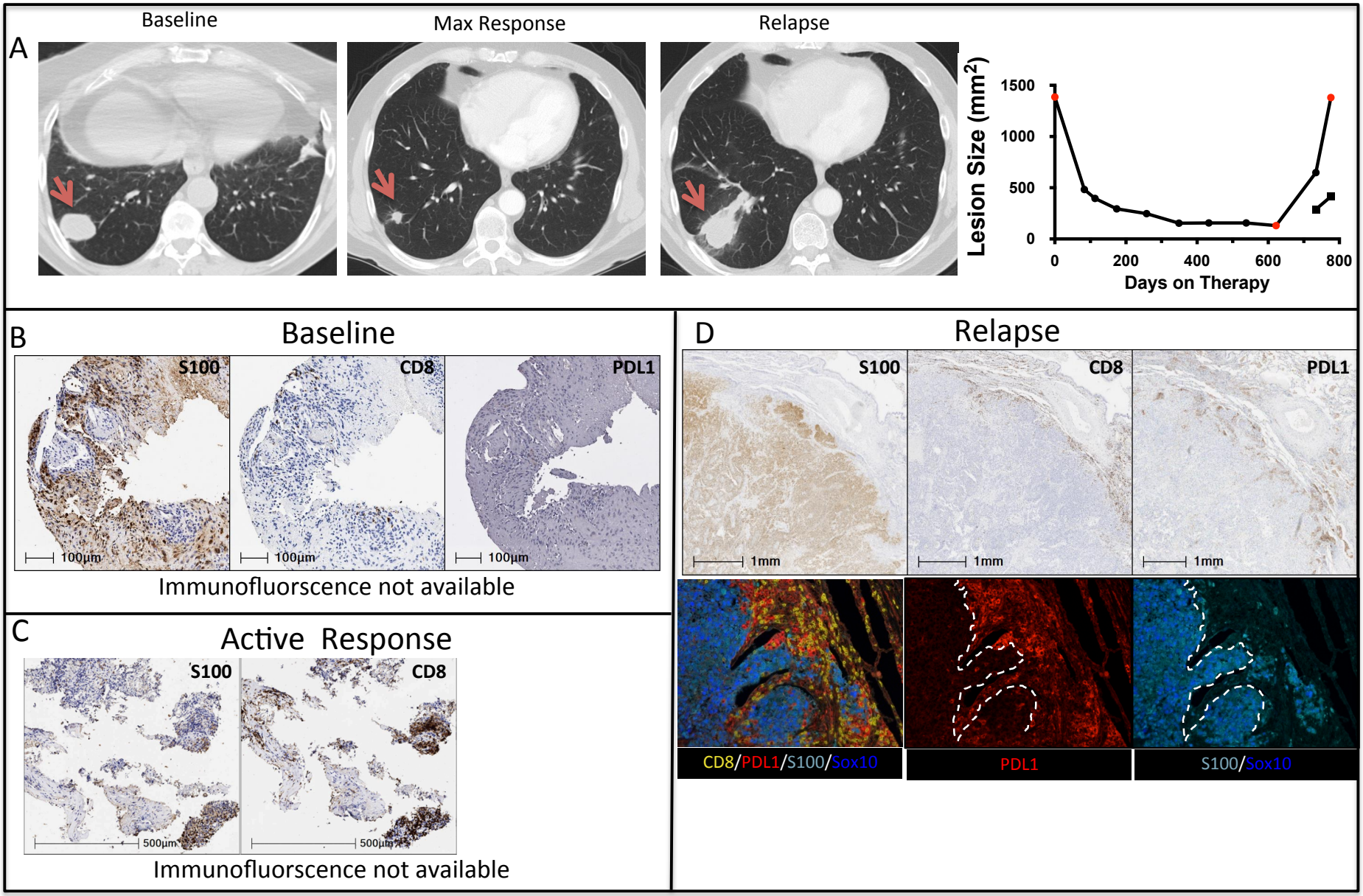
JAK2 Exon2: 5' ggtgctgacagacttactagattc 3' and 5' gatattgctggtttgtgcagcg 3'

Finally, knockout was confirmed by Western blot.

JAK Functional Studies with T-cell Co-culture and Interferon Treatment

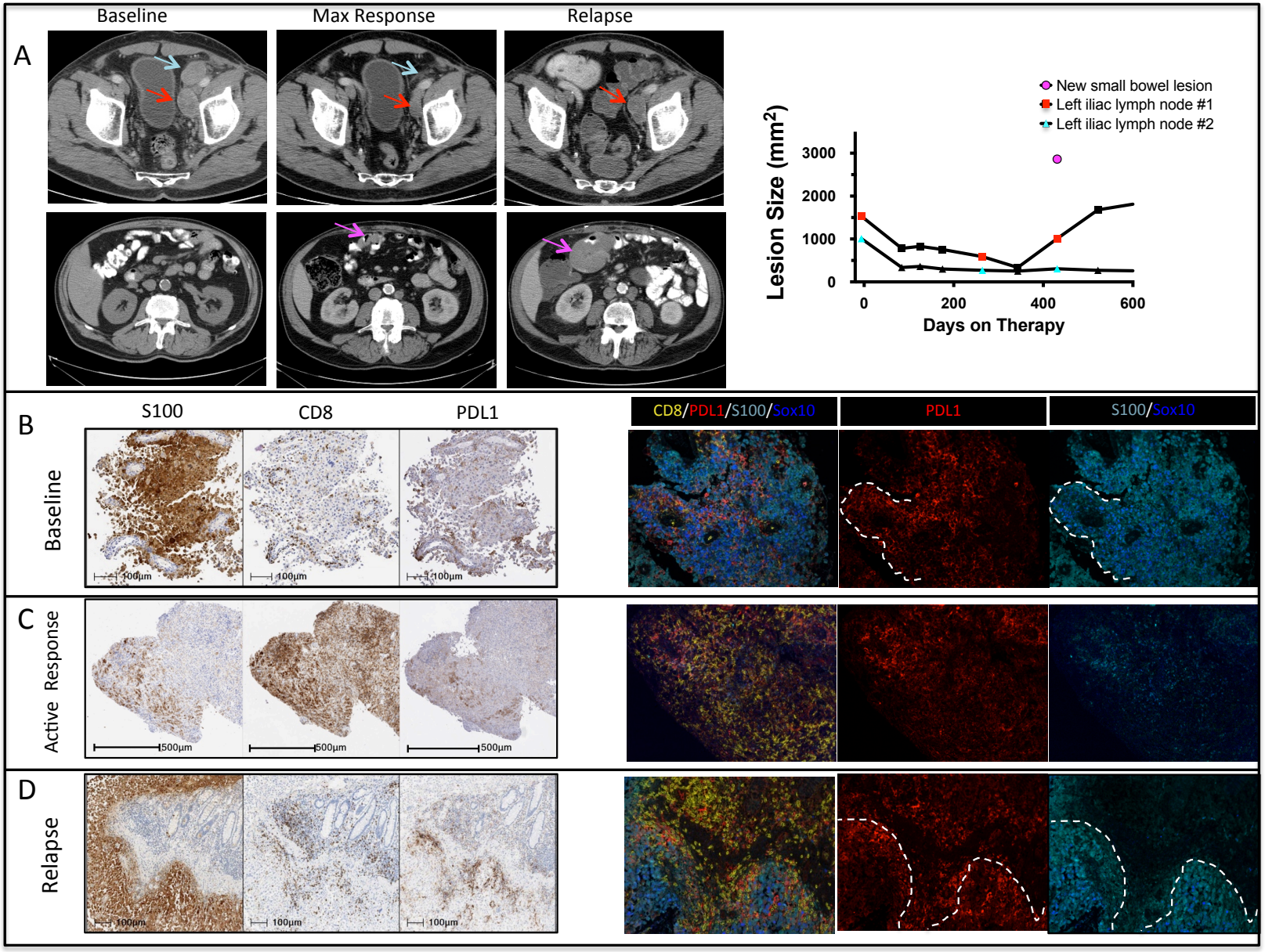
Parental and M407 JAK2 knock-out cells were co-cultured with human peripheral blood mononuclear cells transduced with an NY-ESO1 specific TCR[14]. Interferon-gamma release was measured in supernatant at 24 hours by ELISA (eBioscience, San Diego, CA). Proliferation assays were conducted by real-time live cell imaging in an IncuCyte ZOOM (Essen Biosciences, Ann Arbor, MI). Cell lines were stably transfected with a nuclear-localizing RFP (NucLight Red Lentivirus EF1a Reagent, Essen Biosceinces) to facilitate cell counts. Recombinant human interferon gamma (BD Bioscience, San Jose, CA), human interferon alpha and beta (EMD Millipore, Temecula, CA), and 2'3'-cGAMP (IngivoGen, San Diego, CA) were applied once to approx. 5000 cells per well seeded the previous day in a 96-well plate plate. Cells were maintained without media change for the duration of the experiments. 2'3'-cGAMP was complexed with Lipofectamine 2000 (1:500 dilution, Invitrogen, Carlsbad, CA) for cytosolic exposure. All experiments were performed with wells in triplicate at in a minimum of three independent runs. Graph production and statistical data were analyzed via Prism software (Graphpad, La Jolla, CA).

Figure S1. Clinical pattern of acquired resistance to anti-PD-1 therapy in case #2.



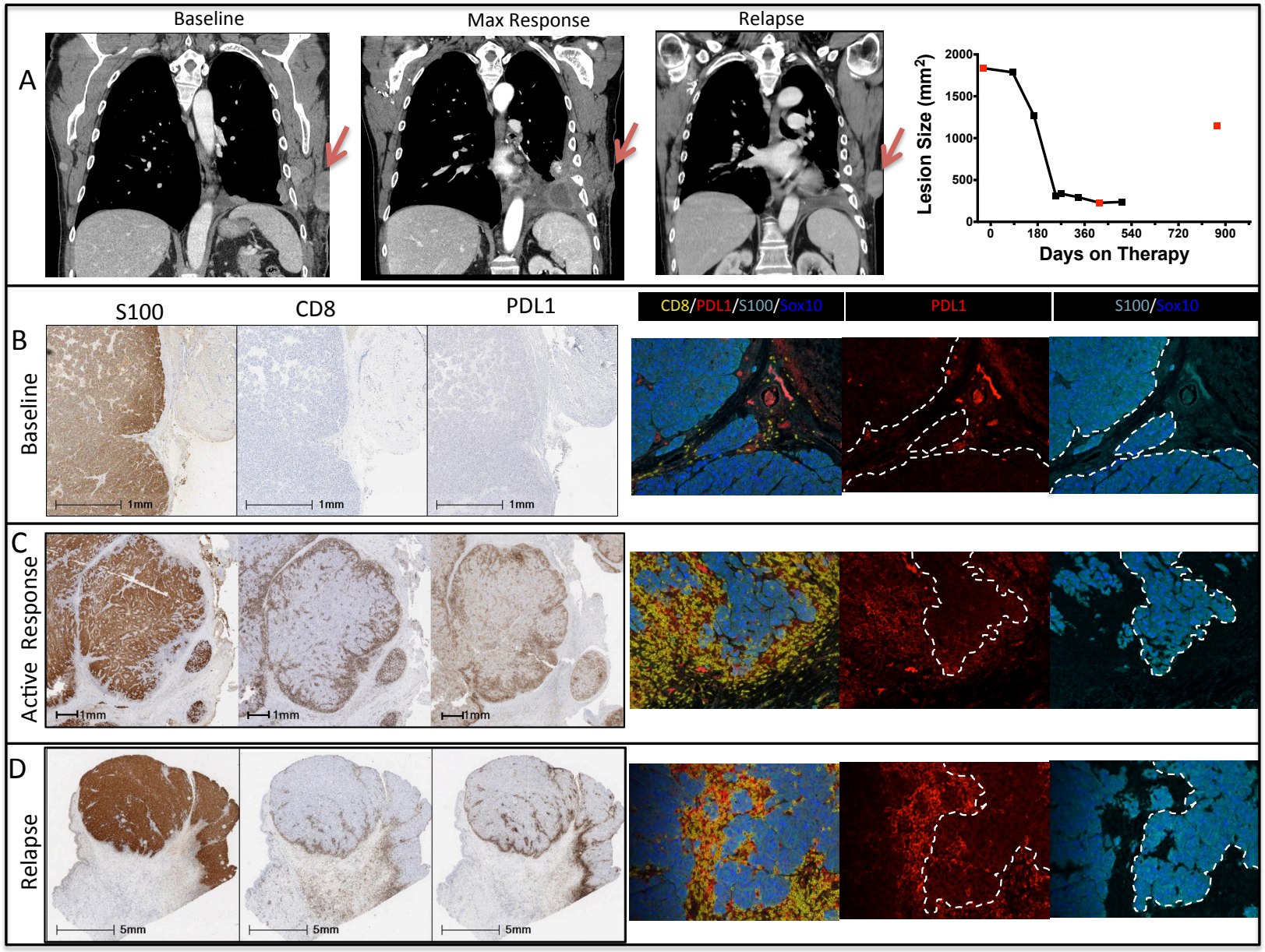
Patient #2 exhibited a 90% response in a solitary lung metastasis, followed by relapse in-situ after almost two years of minimal residual disease. Panel A shows CT images from time-points indicated by colored dots on the graph at right. Panels B-D show immunohistochemical staining of S100, CD8, and PDL1. CD8 T-cells were present at baseline (B), increased at relapse (C), and were abundant but primarily found at the tumor margin at relapse (D). At relapse, PD-L1 was not expressed on the cancer cells (Panel D). In the immunofluorescence images, red shows PD-L1, yellow shows CD8 T cells, while light blue (cytoplasmic) and dark blue (nuclear) indicate tumor markers S100 and SOX10, respectively.

Figure S2. Clinical pattern of acquired resistance to anti-PD-1 therapy in case #3.



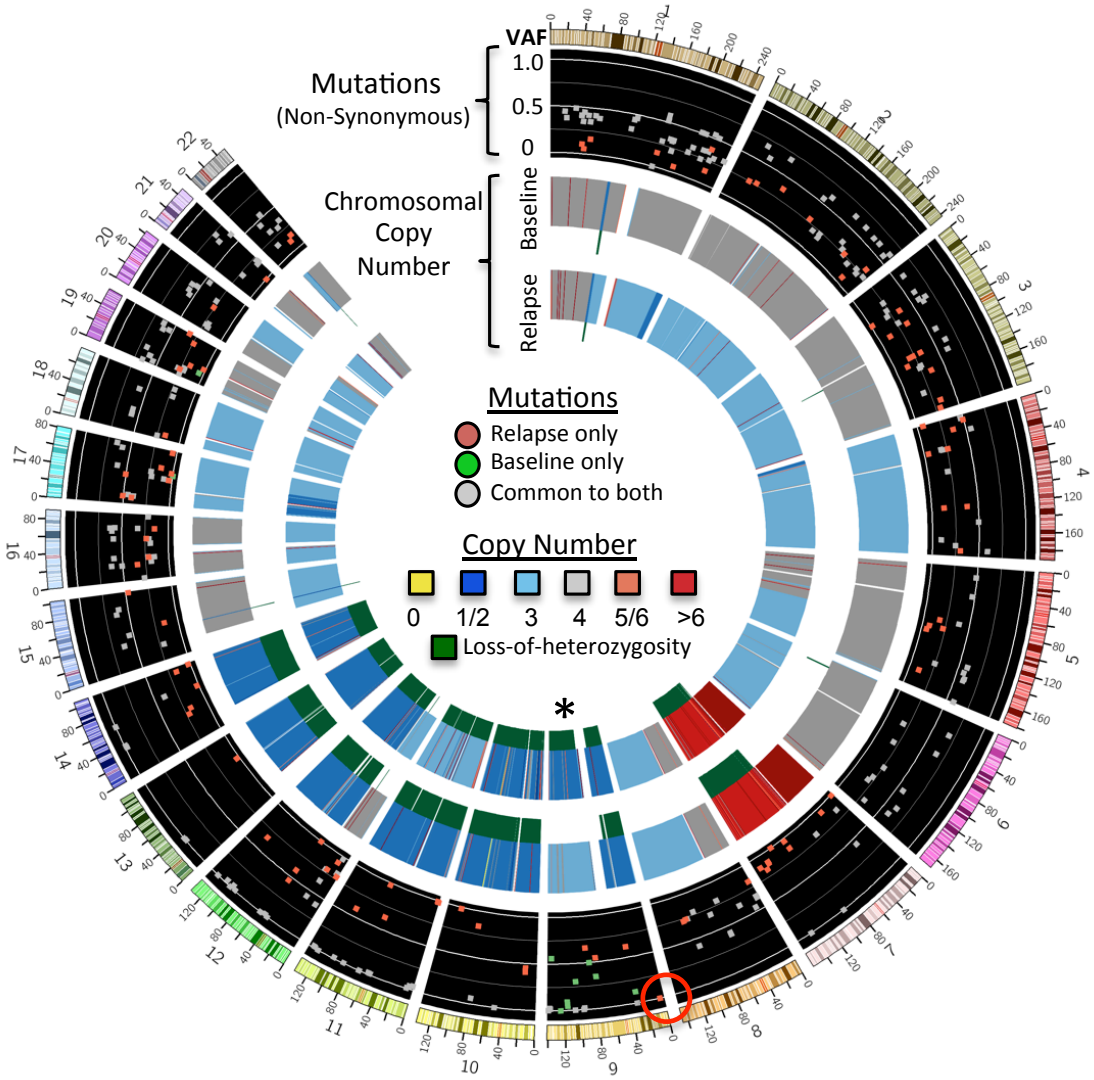
In Panel A, CT images correspond time-points indicated by colored dots on the graph at right. Inguinal lesions from baseline showed partial (red arrow) or complete (cyan arrow) regression. The relapse biopsy comes from a small bowel lesion first visualized at 264 days, with clear progression 453 days from therapy start. Panels B-D show immunohistochemical staining of S100, CD8, and PDL1 at baseline (B), during active response (day 39, C) and relapse (D), with massive CD8 infiltration during response. In the immunofluorescence images, red shows PD-L1, yellow shows CD8 T cells, while light blue (cytoplasmic) and dark blue (nuclear) indicate tumor markers S100 and SOX10, respectively.

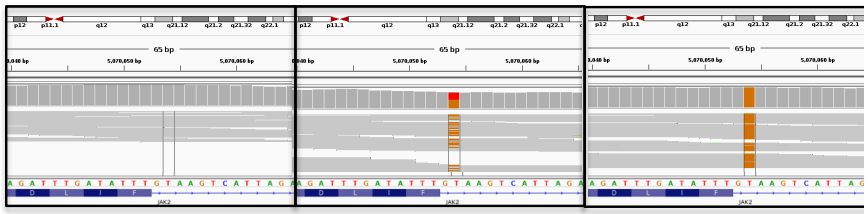
Figure S3. Clinical pattern of acquired resistance to anti-PD-1 therapy in case #4.

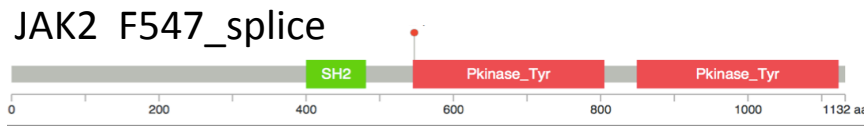


In Panel A, CT images corresponds to time-points indicated by colored dots on the graph at right. Panels B-D show immunohistochemical staining of S100, CD8, and PDL1 at baseline (B), during active response (day 187, C) and relapse (D). Case #4 had a very small pre-existing T-cell infiltrate which increased over time, corresponding to an initial pseudoprogression followed by a tumor response, as previously described[3]. The progressing tumor at relapse shows equally strong CD8 infiltration and local PD-L1 expression as active response, though PD-L1 is not expressed on the cancer cells at either timepoint. In the immunofluorescence images, red shows PD-L1, yellow shows CD8 T cells, while light blue (cytoplasmic) and dark blue (nuclear) indicate tumor markers S100 and SOX10, respectively.

Figure S4. Acquired *JAK2* loss of function mutation in case #2 with accompanying loss-of-heterozygosity.

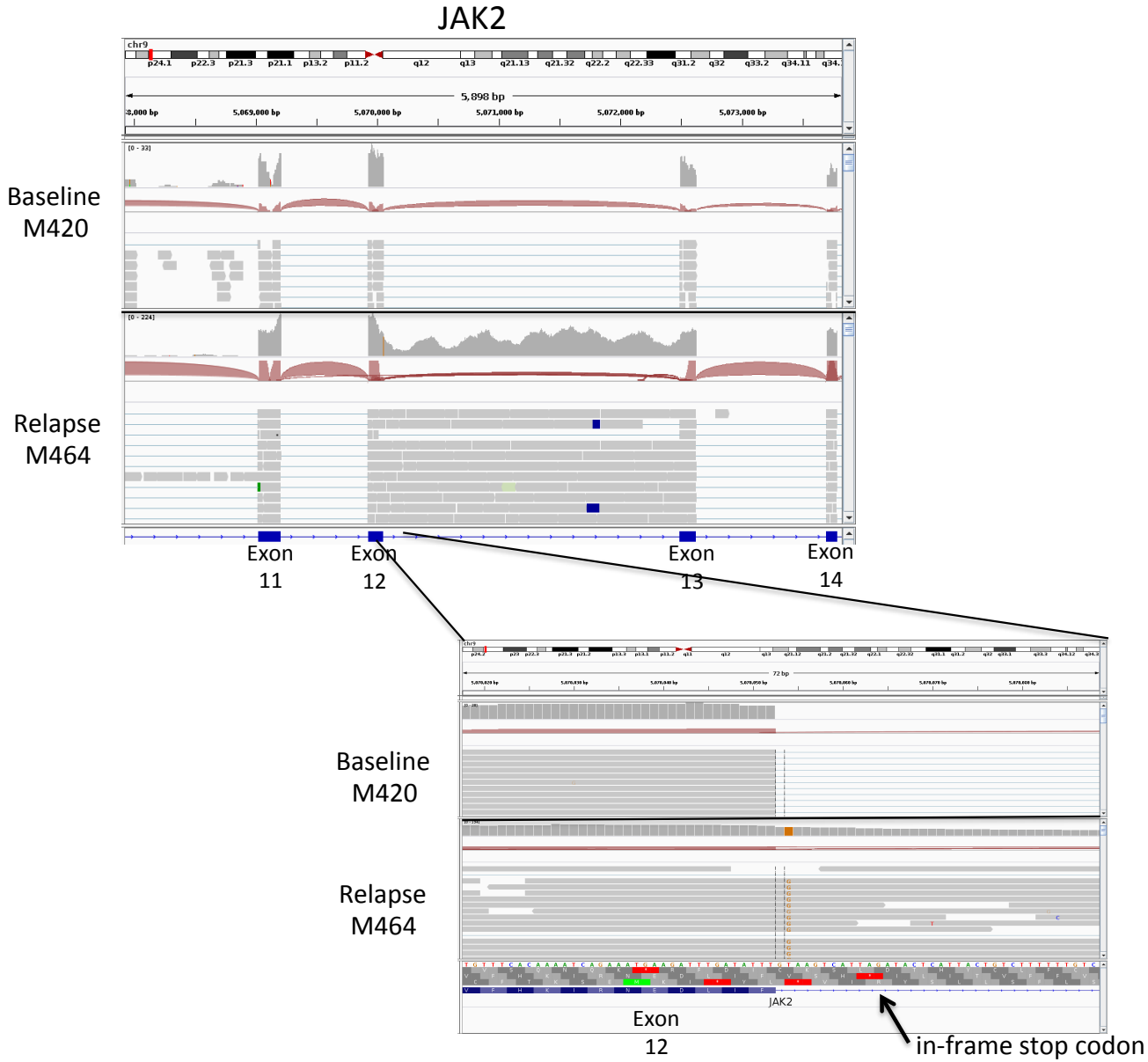






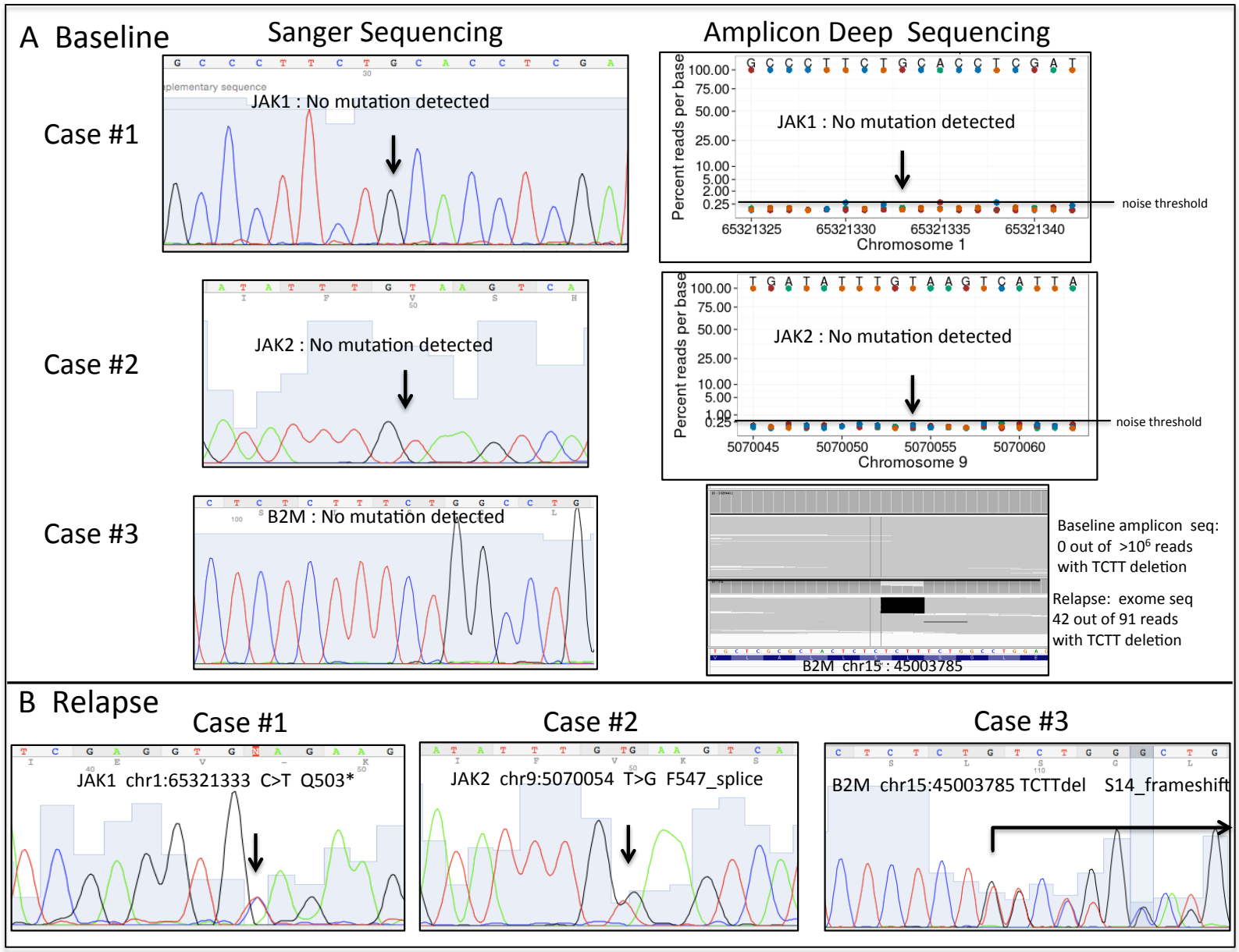
Circos plots (left) of whole exome sequencing changes between pre-pembrolizumab and post-relapse biopsies in case #2. The red circle highlights a new, high allele-frequency relapse-specific *JAK2* mutation in the setting of chromosomal loss of heterozygosity (asterisk). In the outer track (black background), each point represents a non-synonymous mutation, either shared in common (grey), or detected only at relapse (red) or baseline (green). Y-axis represents variant allele frequency (VAF) at relapse, unless baseline-specific. The middle and inner tracks show copy number status for the baseline and relapse biopsy, respectively, while dark green in the subtrack indicates loss-of-heterozygosity. Integrated genomics viewer (IGV) plots (right) show the *JAK2* F547 splice-site mutation is relapse-specific, while cBioPortal diagram revelas the JAK mutation is upstream of the kinase domains.

Figure S5. Relapse-specific JAK2 splice site mutation causes near universal intron inclusion.



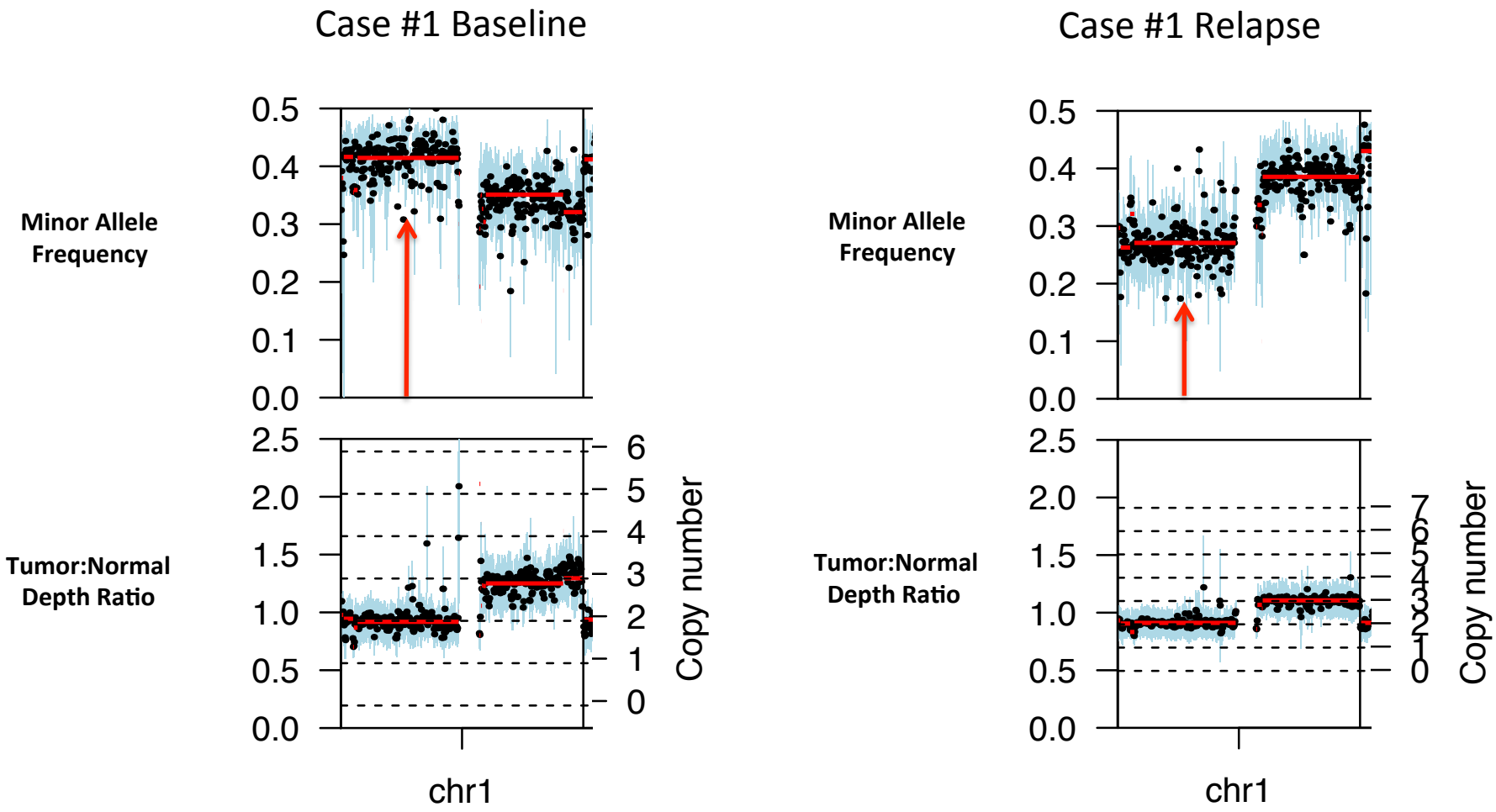
IGV plot of RNA-Seq reads for JAK2 exons 11-14 from the baseline and relapse cell lines from case #2. Intron-inclusion is only seen at relapse. Magnified locus shows RNA reads containing the splice site mutations continuing through the exon 12 exon/intron junction in the relapse cell line, compared to those at baseline that span the exon 12/13 splice junction (Reads with abrupt end at exon 12 with blue line indicating continuation of the RNA read at exon13). Intron inclusion introduces an in-frame stop codon within 10 base pairs of intron (arrow).

Figure S6. Relapse-specific JAK1, JAK2, and B2M mutations are not found at baseline by Sanger or Illumina deep amplicon sequencing



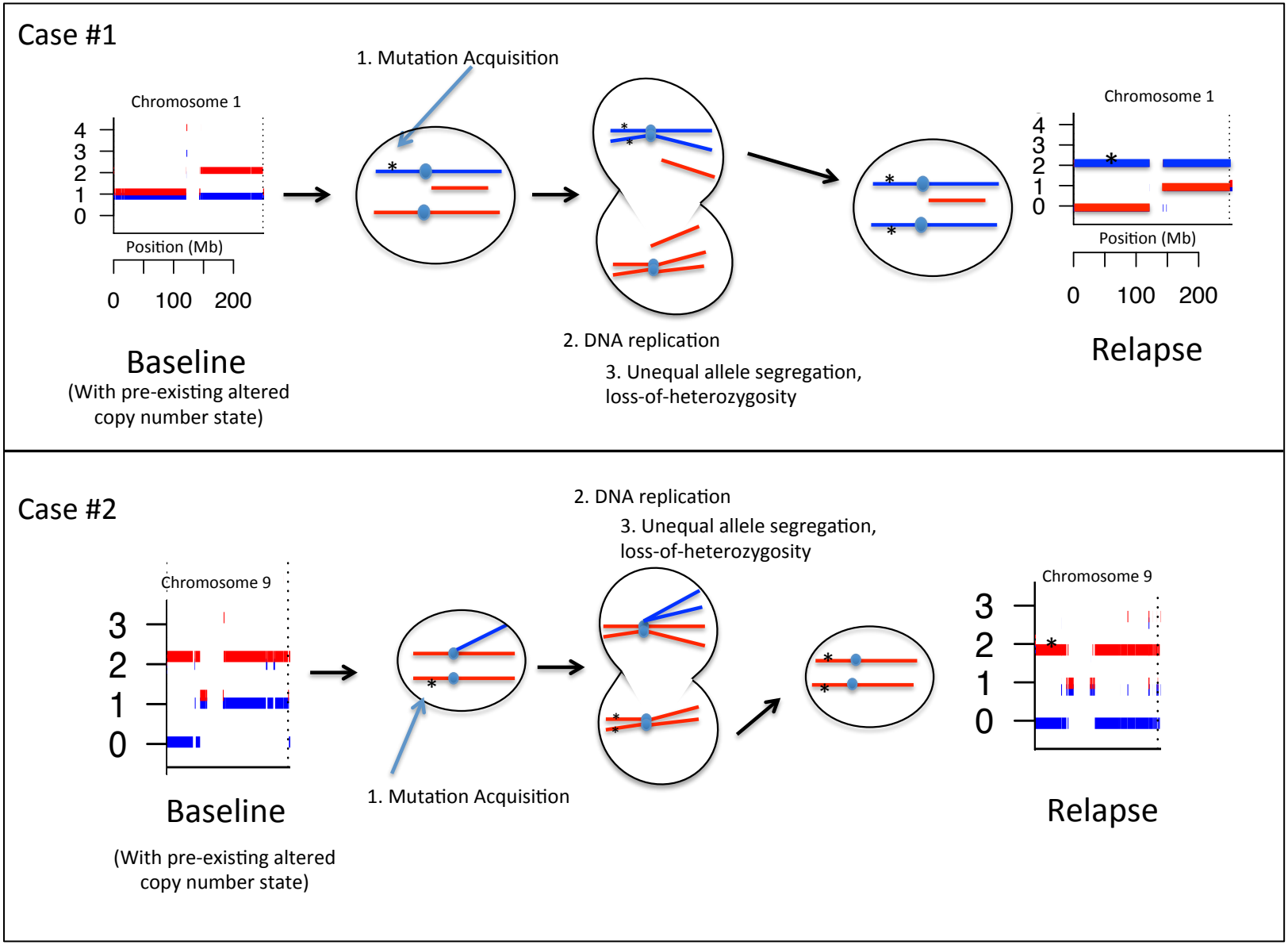
Panel A shows the JAK1, JAK2 and B2M mutations identified at relapse were not observed in PCR amplified genomic DNA from the baseline samples for case #1, #2, and #3 respectively, either by Sanger sequencing (left) or Illumina amplicon re-sequencing (right). For case #1 and #2, graphs show the percentage of each base per position out of 1 million mapped reads. No mutations were observed above the background error rate of ~0.25%. The case #3 baseline sample also had 0 detectable reads with the 4 basepair B2M deletion out of 1.6 million mapped reads examined. IGV plot shows representative sampling, with the relapse mutation for reference. In Panel B, Sanger sequencing of PCR products from genomic DNA of the relapse biopsies confirms the presence of the indicated mutations.

Figure S7. Changes in germline SNP allele frequency shows loss-of-heterozygosity upon relapse on chromosome 1p.



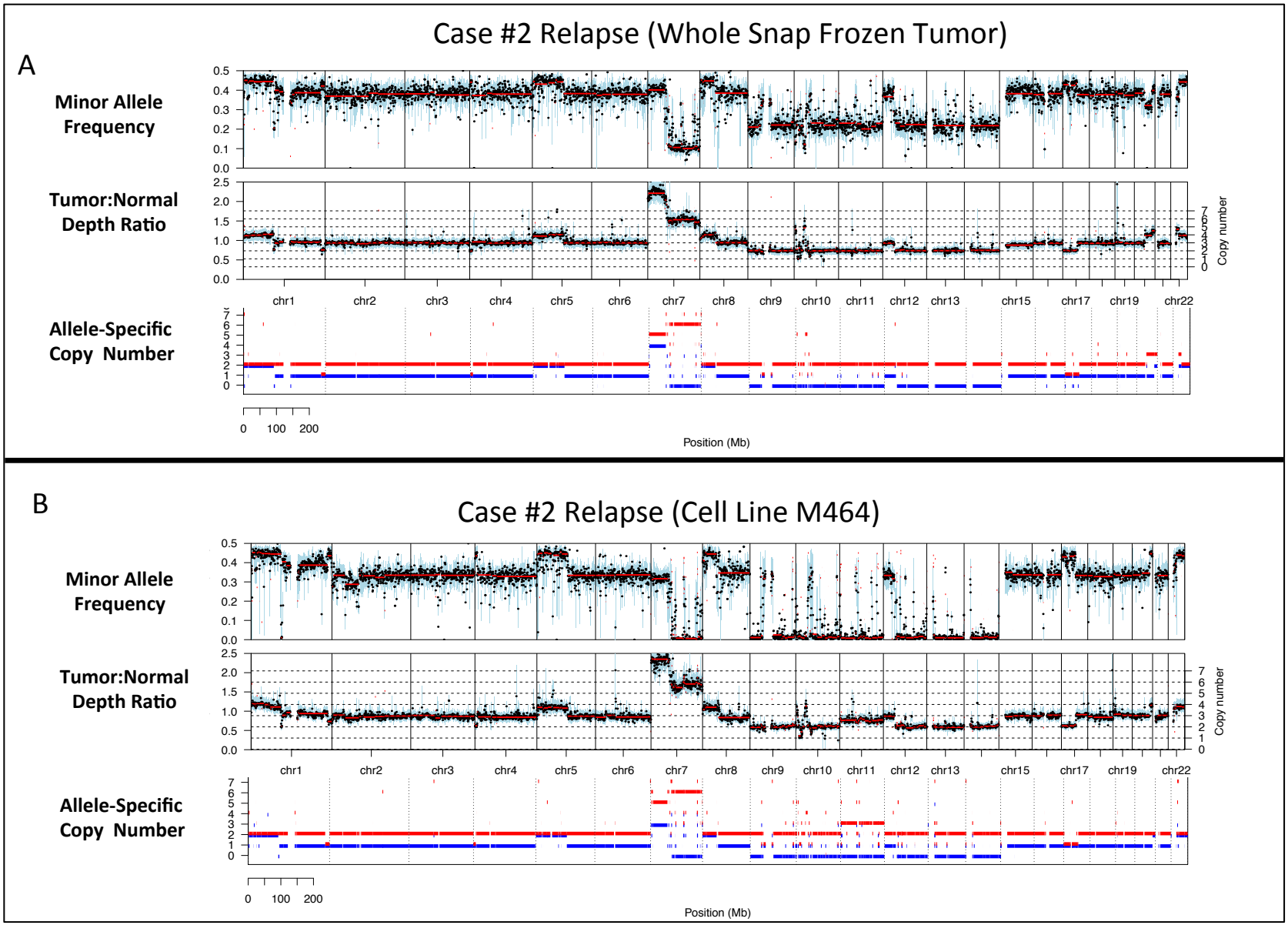
Sequenza output with upper plot showing the minor allele frequencies for germline single nucleotide polymorphisms (SNPs) on chromosome 1, and the lower plot showing the read depth ratio and stroma-adjusted copy number estimate. There is a decrease in SNP frequency for chromosome 1p upon relapse, yet there is no change in relative depth ratio (bottom panel), indicating stable overall copy number. Together, they suggest a copy-number neutral loss of heterozygosity event.

Figure S8. Model schematic of JAK mutation acquisition in the setting of copy-number neutral loss-of-heterozygosity events.



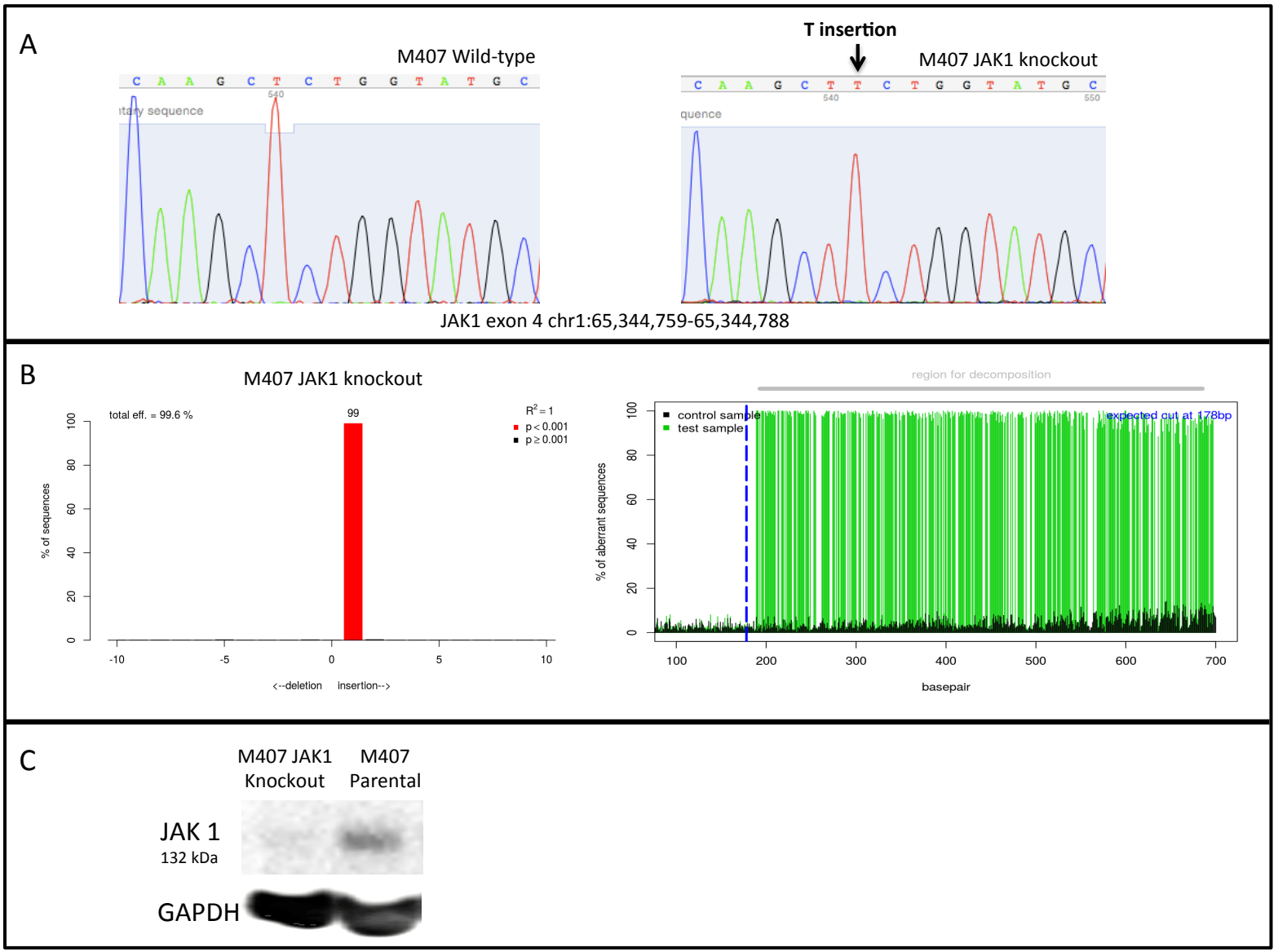
The JAK mutations in case #1 and case #2 were not observed at baseline, but were seen at homozygous allele frequency at relapse. We suggest the mutations were likely first acquired, then later followed by DNA replication and unequal allele segregation, resulting in loss of heterozygosity (and loss of the wild-type allele) without overall copy number change. This is modeled in the top panel for chromosome 1 in case #1, and in the bottom panel for chromosome 9 in case #2. Red and blue represent the maternal and paternal alleles, with arbitrary coloring.

Figure S9. Cell line M464 derived from case #2 relapse is almost identical to the snap-frozen tumor.



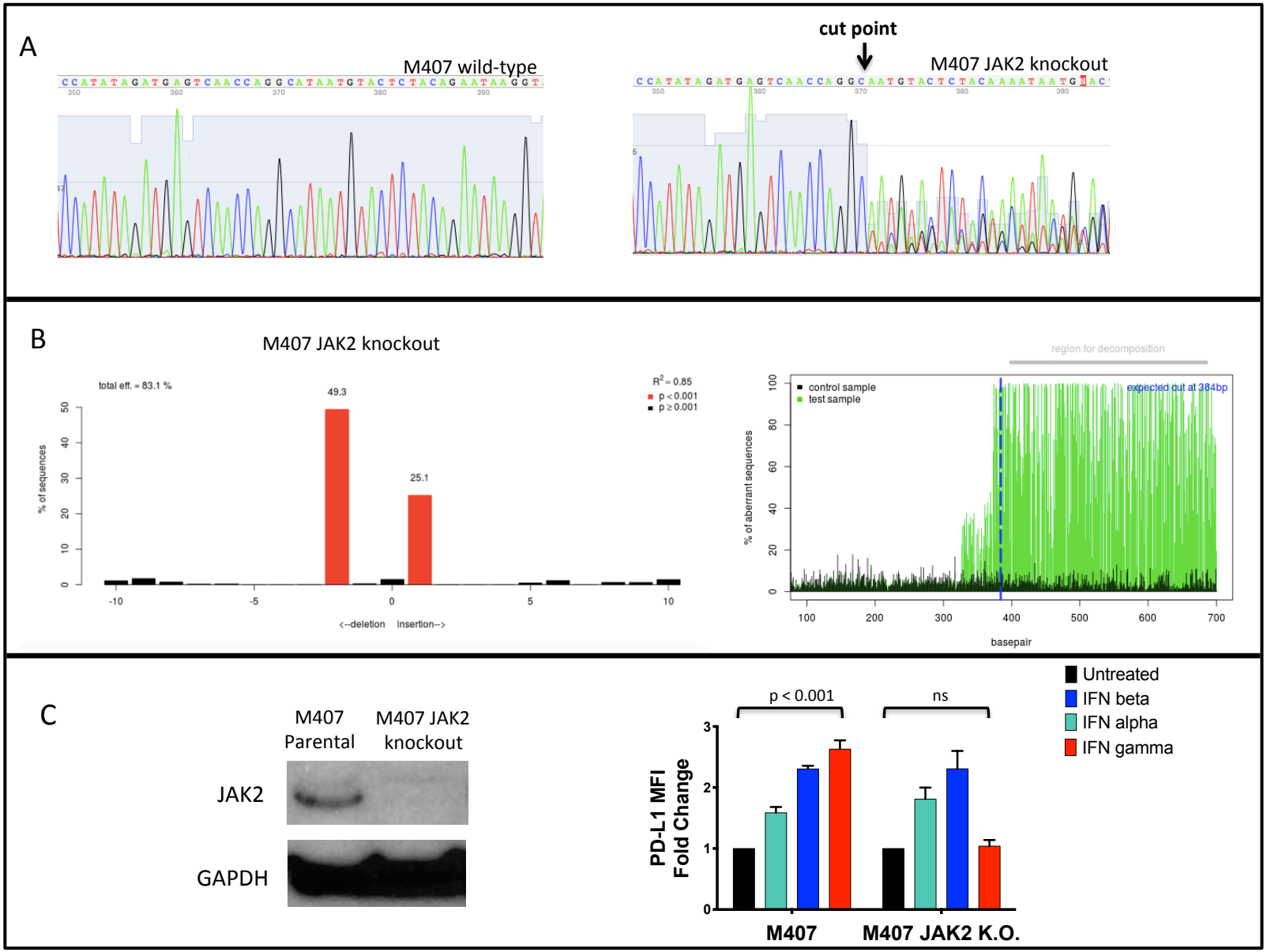
Genome-wide Sequenza plots show the minor-allele frequency, depth ratio, and allele-specific copy number from sequencing of both the snap-frozen whole tumor (Panel A) and the cell line (M464, Panel B) derived from the relapse biopsy in case #2. After model-fit adjustment for the 44% contaminating normal DNA in the bulk tumor (from lung stroma, immune infiltrates, etc), the allele-specific copy number estimates (bottom red/blue track) are nearly identical across most chromosomes between the bulk tumor and cell line.

Figure S10 CRISPR/Cas-9 knockout of JAK1 in M407.



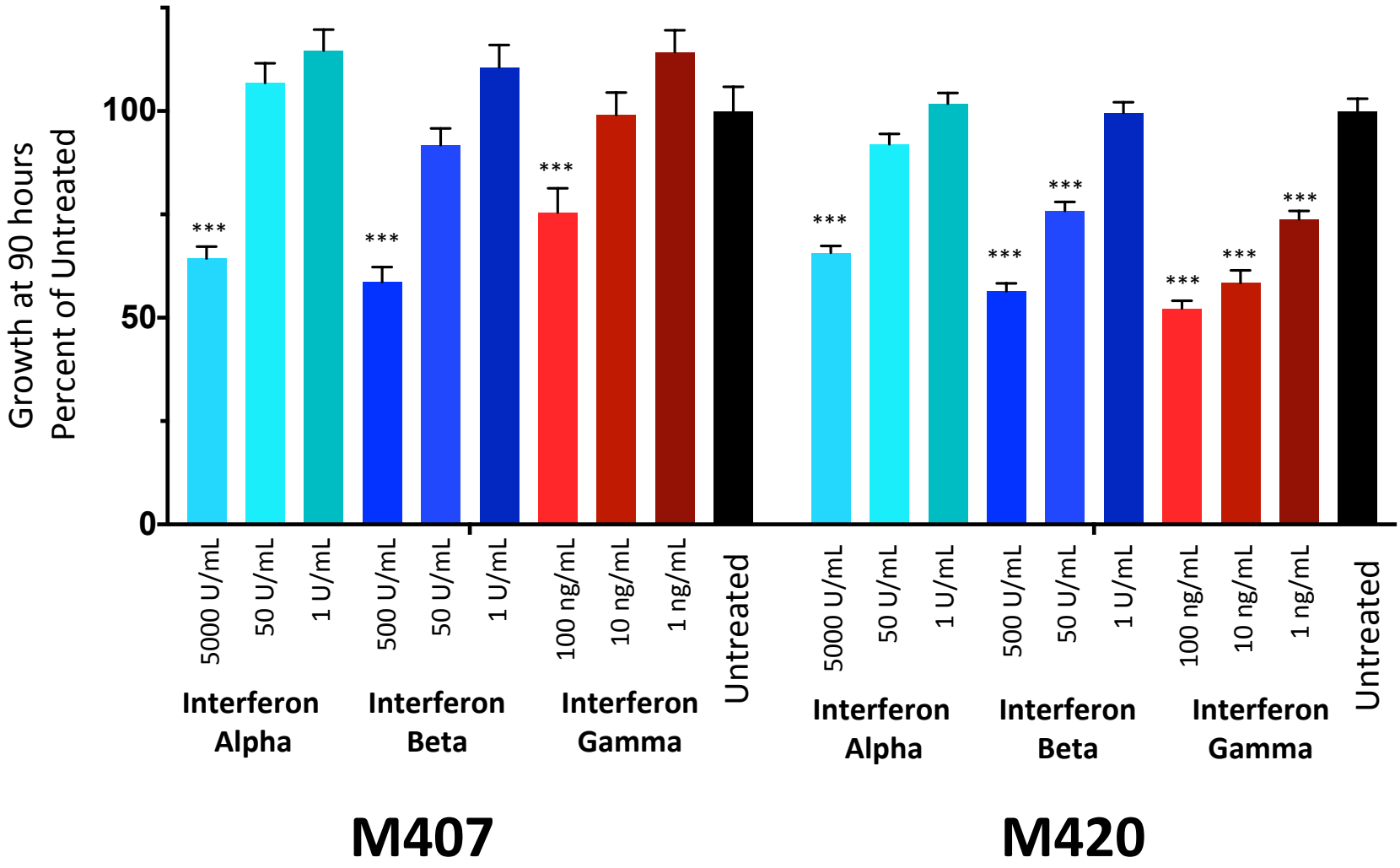
Panel A shows Sanger sequence of JAK1 exon 4 in the M407 parental cell line (left) versus the CRISPR/Cas9 edited subline (right.) showing insertion of a single thymine at the cutpoint. Panel B shows trace decomposition analysis of the JAK1 mutation by TIDE[15], showing 99% of alleles of sequences contain the one basepair insertion. Panel C shows total loss of JAK1 protein by western blot in this cell line.

Figure S11 CRISPR/Cas-9 knockout of JAK2 in M407.



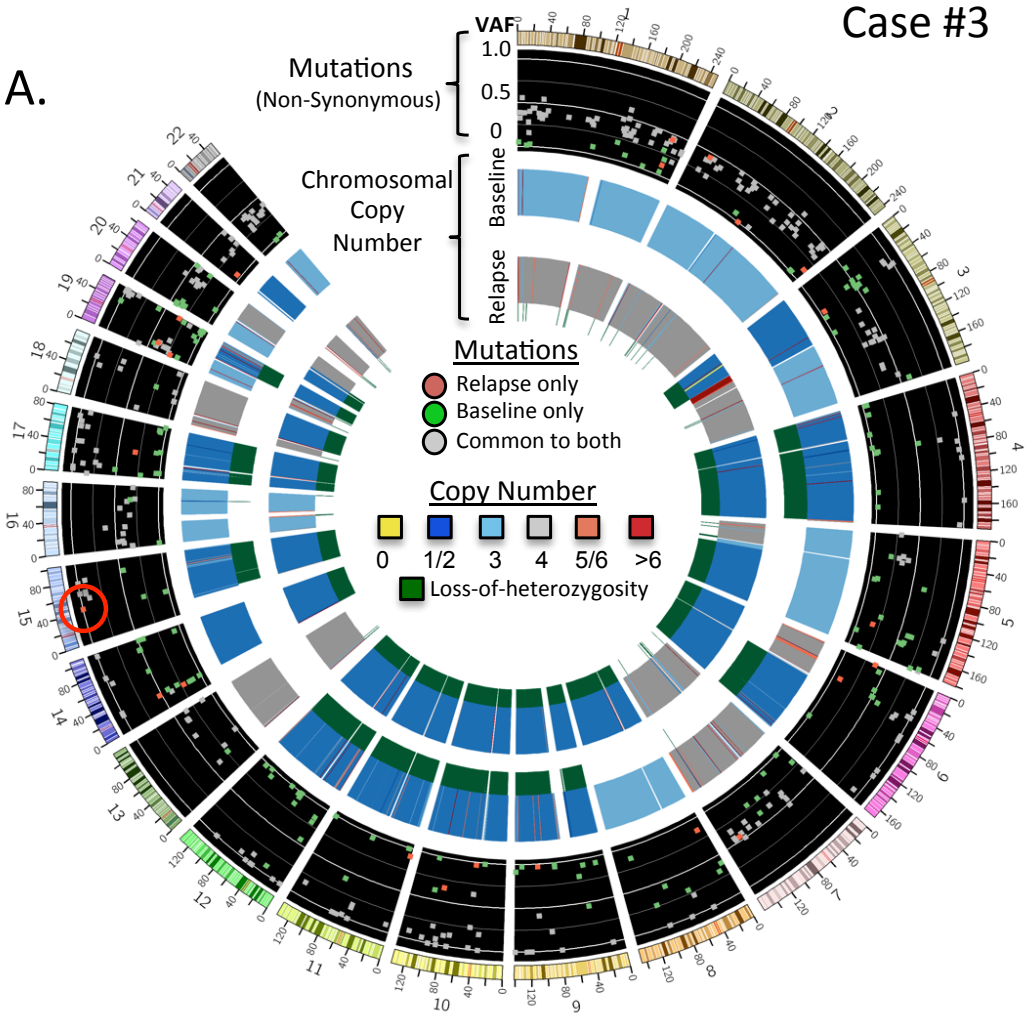
Panel A shows Sanger sequence of JAK2 exon 2 in the M407 parental cell line (left) versus the CRISPR/Cas9 edited subline (right.) Arrow shows the main breakpoint. Panel B shows trace decomposition analysis of the JAK2 mutation by TIDE[15]. Panel C shows total loss of JAK2 protein by western blot, and lack of PD-L1 upregulation in response interferon-gamma compared to parental cell line, with no change in response to interferon alpha or beta.

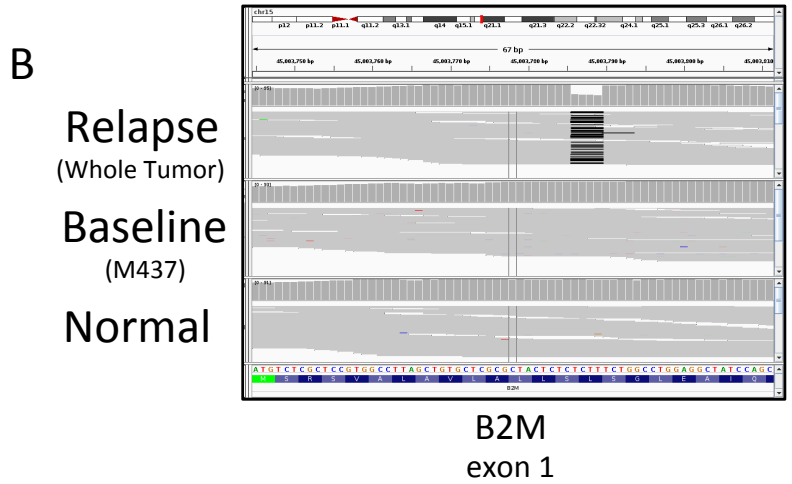
Figure S12. Dose-dependent growth inhibition of M420 and M407 by interferon alpha, beta, and gamma



Cell lines M420 and M407 were cultured in-vitro with recombinant human interferon alpha, beta, or gamma. Both cell lines showed significant (~50%) decrease in growth at the 90hr endpoint compared to untreated cells at the highest doses. M420 showed significant dose-sensitive inhibition at lower concentrations for beta and gamma, though there was a dose-sensitive trend for all interferons in both cell lines. Results are shown for a single representative experiment, three replicate wells per condition. Error bars show standard error of the mean. *** = p-value < 0.001 with Dunnett's multiple comparison correction. All others not significant.

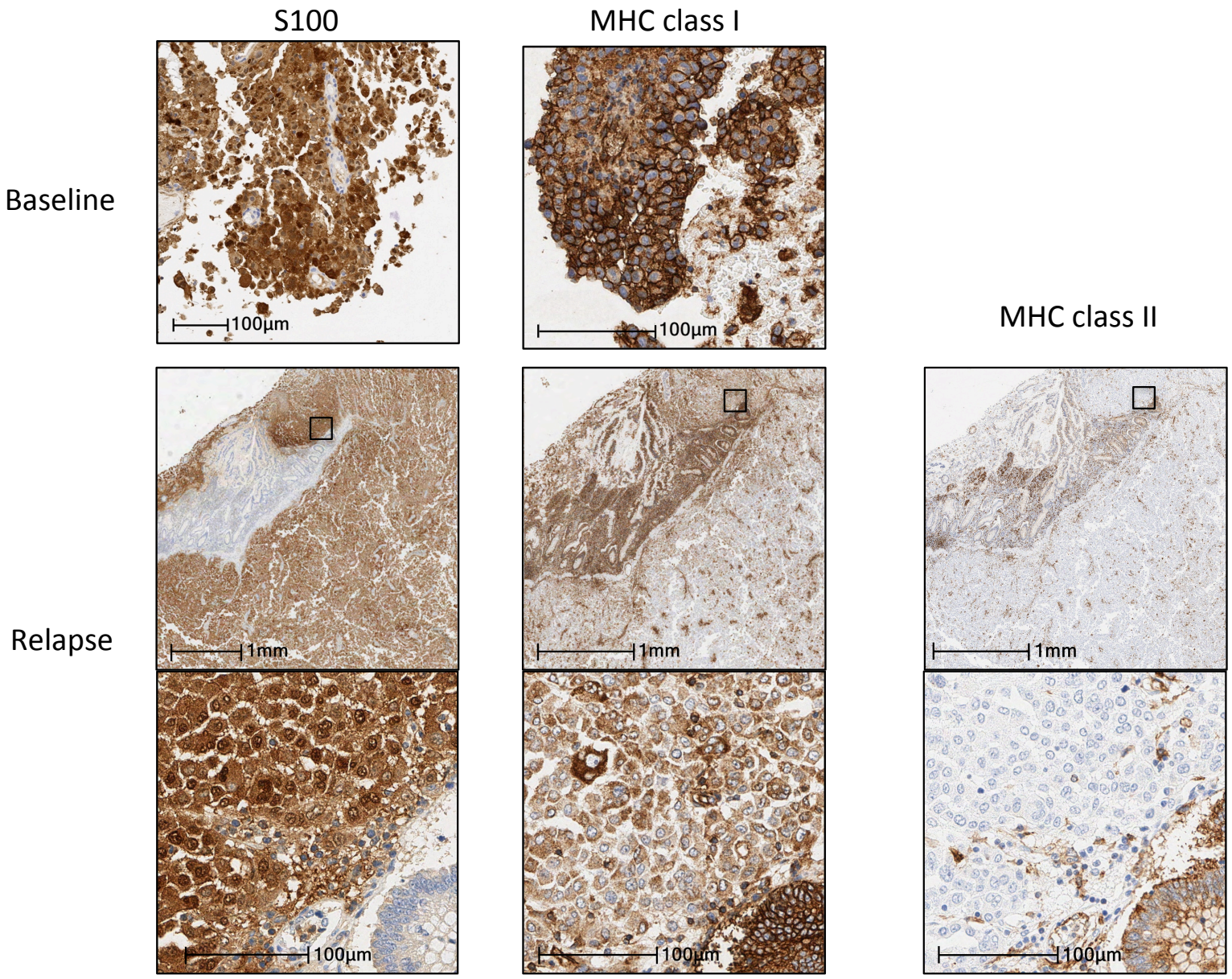
Figure 13 Genomic alterations in case #3 reveal Beta-2-microglobulin (B2M) mutation





Panel A shows a Circos plot as in Figure 2. A cell line (M437) derived from the baseline biopsy is compared to the progressing tumor. Both lesions shared a core of 304 non-synonymous mutations and a similar copy number profile with mostly shallow gains/losses. Most baseline-specific mutations were subclonal (62% of 149 mutations with allele frequency <0.35), while others were eliminated in loss-of-heterozygosity events on chromosomes 3p, 5q, 6p, 8, 14, and 20. Relapse was notable for a strong amplification of the microphthalmia-associated transcription factor (MITF) locus on chromosome 3 (asterisk), and a four basepair S14fs frameshift deletion in the MHC class I component *B2M* (red circle), shown in integrated genomics viewer (IGV) plot in Panel B. Normal reads in the relapse come from stromal components.

Figure S14. Class II MHC immunohistochemistry and additional example of loss of Class I MHC membrane localization in Case #3 relapse biopsy with B2M mutation.



Immunohistochemical staining of MHC class I (clone HC10, specific for some HLA-A, and all HLA-B/C heavy chains) shows lack of localization to the outer cell membrane of S100-positive tumor cells at relapse, in contrast to baseline tumor or adjacent normal bowel tissue. By contrast, the tumor appears negative for MHC class II. Lower panel for relapse samples represent boxed insets from upper panel.

Supplementary Table S1: Demographic and baseline patient clinical characteristics.

	Case #1	Case # 2	Case #3	Case #4
irRECIST	Partial Response	Partial Response	Partial Response	Partial Response
Study	Merck MK3475-006	Merck MK-3475-001	Merck MK-3475-001	Merck MK-3475-001
Progression Free Survival (Days)	419	734	453	888
Overall Survival (Days) ***ongoing at census**	691	945	974	1262*
Age at Tx start	58	60	70	61
Sex	M	M	M	M
ECOG Status at Baseline	0	0	0	0
Disease Status at Baseline	M1c	M1b	M1c	M1c
Baseline LDH **(ULN 223)**	358	83	263	222
BRAF/NRAS	BRAF V600E	BRAF L597S	NRAS Q61K	BRAF V600E
Melanoma Type	Cutaenous	Cutaneous	Cutaneous	Cutaneous
# Prior Systemic Therapies	2	0	0	4
Prior Immunotherapy?	Interferon-alpha	0	0	IL-2, Ipilimumab, TIL adoptive cell transfer
Prior BRAF/MEK inhibitor?	Vemurafenib	0	0	Vemurafenib
Prior Chemotherapy?	0	0	0	0

Supplementary Table S2: Sample list and whole exome sequencing metrics

Case	Timepoint (Days from C1D1)	Anatomic Location	Clinical Scenario	Sequenced Sample Type	Exome Seq Sample Name	Non-synonymous Mutation Count	% Tumor Cellularity (Sequenza)	Ploidy (Sequenza)	Total Reads	Mean Coverage	%_bases_above_15X
Case #1	-233	Small Bowel	Baseline, pre-response	Bulk tumor - FFPE	Case#1-Baseline	1173	0.79	2.2	5869797548	91.44	96.6
Case #1	425	Sigmoid Colon	In-situ Relapse	Bulk tumor - Snap Frozen	Case#1-Relapse	1140	0.45	2.5	8122321016	126.53	97
Case #1	NA	Normal (PBMC)	N/A	PBMC	N/A		NA	NA	5810616299	90.52	96.2
Case #2	-5	Lung	Baseline, pre-response	Cell Line (M420)	Case#2-Baseline-M420	240	0.95	3.8	9198284962	143.3	97.1
Case #2	788	Lung	In-situ Relapse	Bulk tumor - Snap Frozen	Case#2-Relapse-WholeTumor	305	0.56	3.3	11499597416	179.15	97.7
Case #2	788	Lung	In-situ Relapse	Cell Line (M464)	Case#2-Relapse-M464	333	0.98	3.5	13430534410	209.23	97.9
Case #2	NA	Normal (PBMC)	N/A	PBMC	N/A		NA	NA	9109279242	141.91	97.3
Case #3	-8	Inguinal lymph node	Baseline, pre-response	Cell Line (M437)	Case#3-Baseline-M437	453	0.95	2.9	7667504038	119.45	96.8
Case #3	453	Small Bowel	Relapse; New lesion	Bulk tumor - Snap Frozen	Case#3-Relapse	328	0.4	2.9	11983298763	186.68	97.2
Case #3	NA	Normal (PBMC)	N/A	PBMC	N/A		NA	NA	9572406229	149.12	97.5
Case #4	-28	Left chestwall	Baseline, pre-response	Bulk tumor - Snap Frozen	Case#4-Baseline	347	0.89	3.4	11619208625	181.01	97.5
Case #4	898	Left chestwall	Relapse; New lesion	Bulk tumor - Snap Frozen	Case#4-Relapse	406	0.74	3.4	10358188486	161.37	97.1
Case #4	NA	Normal (PBMC)	N/A	PBMC	N/A		NA	NA	7196761543	112.12	95.9

Supplementary Table S3: Quantification of immunohistochemistry for CD8 infiltration and PD-L1 expression.

		CD8								PD-L1							
		Invasive Margin				Intra-tumoral Area				Invasive Margin				Intra-tumoral Area			
Case	Timepoint	% CD8	Total Nuclei Count	Tissue Area (mm^2)	CD8 Density cells/mm^2	% CD8	Total Nuclei Count	Tissue Area (mm^2)	CD8 Density cells/mm^2	% PD-L1	Total Nuclei Count	Tissue Area (mm^2)	PD-L1 Density cells/mm^2	% PD-L1	Total Nuclei Count	Tissue Area (mm^2)	PD-L1 Density cells/mm^2
Case #1	Baseline	38	242766	42	2196.5	13	791627	163	631.4	49	206074	26	3883.7	17.5	898011	162	970.1
Case #1	Relapse	16.5	35447	7.3	799.6	1.65	115919.5	26.1	73.3	53.9	41978.66667	7.03	3217.0	22.05	110552.5	24.4	999.1
Case #2	Baseline *+	NA	NA	NA	NA	3	4309	0.663	195.1	NA	NA	NA	NA	9.4	4799	0.713	632.6
Case #2	On-treatment+	NA	NA	NA	NA	84	604	0.059925	8466.6	NA	NA	NA	NA	72	623	0.048498	9249.0
Case #2	Relapse	26	31086	5.3	1525.0	2.5	255321	35	182.4	38	30483	4.8	2413.2	6	213040	37.7	339.1
Case #3	Baseline*^	58	2023	0.293	4009.4	23	5653	0.921	1411.8	NA	NA	NA	NA	40	3933	0.360	4374.2
Case #3	On-treatment^+	NA	NA	NA	NA	90	5557	6	833.6	NA	NA	NA	NA	31	50244	6	2595.9
Case #3	Relapse	18	27463	4	1235.8	8.9	678132	135	447.1	25	28784	4.4	1635.5	20	1460378	212	1377.7
Case #4	Baseline	24	9003	1.7	1271.0	0.3	225012	41	16.5	2.9	12404	1.7	211.6	0.14	194354	37.7	7.2
Case #4	On-treatment	62.5	90954	14.7	3867.1	39	199070	36.6	2121.2	76.6	129461	14.1	7033.1	60	237179	31	4590.6
Case #4	Relapse	60	53901	7.6	4255.3	15.6	322322	60	838.0	72.5	70934	7.6	6766.7	30	364649	60	1823.2

*Poor quality tissue/staining

^Lymph node biopsy

+ Unable to delineate invasive margin

Supplementary Table S4: List of non-synonymous somatic mutations from all whole exome sequencing samples

Sample	Hugo_Symbol	Chromosome	Start_position	Variant_Classification	Reference Allele	Mutant Allele	Protein Change	Tumor Coverage	Mutant Read Count	VAF	Adjusted_VAF	CopyNumber Total	CN_A	CN_B	Normal Coverage	Description	Annotation_Transcript
Case#1-Relapse-WholeTumor	MIIP	1	12090096	Missense_Mutation	C	A	p.P286Q	102	6	0.059	0.131	2	2	0	94	migration and invasion inhibitory protein	ENST00000235332.4
Case#1-Relapse-WholeTumor	PRAMEF22	1	13036403	Missense_Mutation	G	A	p.E159K	571	129	0.226	0.502	2	2	0	441	PRAME family member 22	ENST00000376187.1
Case#1-Relapse-WholeTumor	UBR4	1	19411143	Nonsense_Mutation	G	A	p.Q4955*	117	54	0.462	1.026	2	2	0	94	ubiquitin protein ligase E3 component n-recognin 4	ENST00000375254.3
Case#1-Relapse-WholeTumor	HSPG2	1	22170753	Missense_Mutation	G	A	p.S2835F	76	24	0.316	0.702	2	2	0	72	heparan sulfate proteoglycan 2	ENST00000374695.3
Case#1-Relapse-WholeTumor	LACTBL1	1	23285254	Missense_Mutation	C	T	p.M159I	61	22	0.361	0.801	2	2	0	55	lactamase, beta-like 1	ENST00000426928.2
Case#1-Relapse-WholeTumor	YTHDF2	1	29070382	Missense_Mutation	C	G	p.L534V	192	85	0.443	0.984	2	2	0	112	YTH domain family, member 2	ENST00000373812.3
Case#1-Relapse-WholeTumor	CSMD2	1	34128655	Missense_Mutation	C	T	p.D237N	56	24	0.429	0.952	2	2	0	37	CUB and Sushi multiple domains 2	ENST00000373380.1
Case#1-Relapse-WholeTumor	ZMYM4	1	35885142	Missense_Mutation	C	T	p.P1504L	122	50	0.410	0.911	2	2	0	125	zinc finger, MYM-type 4	ENST00000314607.6
Case#1-Relapse-WholeTumor	MACF1	1	39823309	Missense_Mutation	C	T	p.S3901F	77	33	0.429	0.952	2	2	0	67	microtubule-actin crosslinking factor 1	ENST00000372915.3
Case#1-Relapse-WholeTumor	C1orf50	1	43240949	Missense_Mutation	C	T	p.P162S	80	40	0.500	1.111	2	2	0	74	chromosome 1 open reading frame 50	ENST00000372525.5
Case#1-Relapse-WholeTumor	SLC5A9	1	48694988	Missense_Mutation	C	T	p.L121F	102	47	0.461	1.024	2	2	0	67	solute carrier family 5 (sodium/sugar cotransporter), member 9	ENST00000438567.2
Case#1-Relapse-WholeTumor	PODN	1	53543414	Missense_Mutation	G	A	p.E314K	59	26	0.441	0.979	2	2	0	66	podocan	ENST00000312553.5
Case#1-Relapse-WholeTumor	FAM151A	1	55088975	Missense_Mutation	G	A	p.L32F	176	93	0.528	1.174	2	2	0	153	family with sequence similarity 151, member A	ENST00000302250.2
Case#1-Relapse-WholeTumor	TTC22	1	55266809	Missense_Mutation	C	T	p.D10N	35	13	0.371	0.825	2	2	0	40	tetratricopeptide repeat domain 22	ENST00000371276.4
Case#1-Relapse-WholeTumor	C1orf168	1	57219580	Missense_Mutation	C	T	p.E387K	166	81	0.488	1.084	2	2	0	124	chromosome 1 open reading frame 168	ENST00000343433.6
Case#1-Relapse-WholeTumor	C1orf168	1	57257903	Missense_Mutation	G	A	p.P195S	93	45	0.484	1.075	2	2	0	69	chromosome 1 open reading frame 168	ENST00000343433.6
Case#1-Relapse-WholeTumor	FGGY	1	60139762	Missense_Mutation	C	T	p.A490V	152	73	0.480	1.067	2	2	0	117	FGGY carbohydrate kinase domain containing	ENST00000303721.7
Case#1-Relapse-WholeTumor	JAK1	1	65321333	Nonsense_Mutation	G	A	p.Q503*	83	44	0.530	1.178	2	2	0	58	Janus kinase 1	ENST00000342505.4
Case#1-Relapse-WholeTumor	DEPDC1	1	68944934	Missense_Mutation	C	T	p.G669R	74	31	0.419	0.931	2	2	0	66	DEP domain containing 1	ENST00000456315.2
Case#1-Relapse-WholeTumor	LRRC7	1	70504734	Missense_Mutation	G	A	p.G1038E	78	27	0.346	0.769	2	2	0	47	leucine rich repeat containing 7	ENST00000035383.5
Case#1-Relapse-WholeTumor	SLC44A5	1	75708615	Missense_Mutation	C	T	p.E143K	102	41	0.402	0.893	2	2	0	73	solute carrier family 44, member 5	ENST00000370855.5
Case#1-Relapse-WholeTumor	AK5	1	77752704	Missense_Mutation	G	A	p.E47K	104	40	0.385	0.855	2	2	0	103	adenylate kinase 5	ENST00000354567.2
Case#1-Relapse-WholeTumor	GIPC2	1	78560732	Missense_Mutation	C	T	p.H175Y	146	68	0.466	1.035	2	2	0	104	GIPC PDZ domain containing family, member 2	ENST00000370759.3
Case#1-Relapse-WholeTumor	OLFM3	1	102270241	Nonsense_Mutation	A	C	p.Y330*	111	43	0.387	0.861	2	2	0	84	olfactomedin 3	ENST00000338858.5
Case#1-Relapse-WholeTumor	MYBPHL	1	109839414	Nonsense_Mutation	G	A	p.Q241*	158	68	0.430	0.956	2	2	0	121	myosin binding protein H-like	ENST00000357155.1
Case#1-Relapse-WholeTumor	LRIG2	1	113666581	Missense_Mutation	C	T	p.S1019L	106	44	0.415	0.922	2	2	0	84	leucine-rich repeats and immunoglobulin-like domains 2	ENST00000361127.5
Case#1-Relapse-WholeTumor	SYCP1	1	115487554	Missense_Mutation	G	A	p.R702Q	118	60	0.508	1.130	2	2	0	96	synaptonemal complex protein 1	ENST00000369522.3
Case#1-Relapse-WholeTumor	NGF	1	115829131	Missense_Mutation	C	T	p.E96K	59	24	0.407	0.904	2	2	0	61	nerve growth factor (beta polypeptide)	ENST00000369512.2
Case#1-Relapse-WholeTumor	HSD3B2	1	119964548	Missense_Mutation	G	A	p.E142K	145	72	0.497	1.103	2	2	0	104	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2	ENST00000543831.1
Case#1-Relapse-WholeTumor	HSD3B2	1	119965208	Missense_Mutation	C	T	p.R362W	149	74	0.497	1.104	2	2	0	112	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2	ENST00000543831.1
Case#1-Relapse-WholeTumor	ANKRD35	1	145561858	Missense_Mutation	CC	TT	p.P516L	102	24	0.235	0.427	3	2	1	66	ankyrin repeat domain 35	ENST00000355594.4
Case#1-Relapse-WholeTumor	FCGR1A	1	149759943	Missense_Mutation	C	T	p.S110F	436	167	0.383	0.695	3	2	1	242	Fc fragment of IgG, high affinity Ia, receptor (CD64)	ENST00000369168.4
Case#1-Relapse-WholeTumor	SEMA6C	1	151109476	Missense_Mutation	C	G	p.W277C	190	19	0.100	0.181	3	2	1	115	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C	ENST00000341697.3
Case#1-Relapse-WholeTumor	TCHH	1	152080664	Nonsense_Mutation	G	A	p.Q1677*	130	24	0.185	0.335	3	2	1	82	trichohyalin	ENST00000368804.1
Case#1-Relapse-WholeTumor	TCHH	1	152082830	Missense_Mutation	C	T	p.E955K	93	9	0.097	0.176	3	2	1	72	trichohyalin	ENST00000368804.1
Case#1-Relapse-WholeTumor	HRNR	1	152190971	Missense_Mutation	C	T	p.G1045D	419	55	0.131	0.238	3	2	1	246	hornerin	ENST00000368801.2
Case#1-Relapse-WholeTumor	FLG	1	152280808	Missense_Mutation	C	T	p.G2185E	547	88	0.161	0.292	3	2	1	335	filaggrin	ENST00000368799.1
Case#1-Relapse-WholeTumor	FLG	1	152283826	Missense_Mutation	G	A	p.S1179F	535	109	0.204	0.370	3	2	1	338	filaggrin	ENST00000368799.1
Case#1-Relapse-WholeTumor	FLG	1	152284345	Missense_Mutation	C	T	p.G1006E	409	60	0.147	0.266	3	2	1	225	filaggrin	ENST00000368799.1
Case#1-Relapse-WholeTumor	FLG2	1	152325229	Missense_Mutation	C	T	p.G1678E	466	77	0.165	0.300	3	2	1	315	filaggrin family member 2	ENST00000388718.5
Case#1-Relapse-WholeTumor	FLG2	1	152329859	Missense_Mutation	T	A	p.S135C	323	18	0.056	0.101	3	2	1	209	filaggrin family member 2	ENST00000388718.5
Case#1-Relapse-WholeTumor	CRNN	1	152383101	Nonsense_Mutation	G	A	p.Q153*	61	13	0.213	0.387	3	2	1	53	cornulin	ENST00000271835.3
Case#1-Relapse-WholeTumor	S100A3	1	153520165	Missense_Mutation	G	A	p.S100F	195	28	0.144	0.261	3	2	1	128	S100 calcium binding protein A3	ENST00000368713.3
Case#1-Relapse-WholeTumor	SNAPIN	1	153633746	Missense_Mutation	G	A	p.G127E	113	22	0.195	0.353	3	2	1	79	SNAP-associated protein	ENST00000368685.5
Case#1-Relapse-WholeTumor	NUP210L	1	154062058	Nonsense_Mutation	G	A	p.R734*	95	11	0.116	0.210	3	2	1	50	nucleoporin 210kDa-like	ENST00000368559.3
Case#1-Relapse-WholeTumor	UBAP2L	1	154228226	Missense_Mutation	C	T	p.L718F	161	29	0.180	0.327	3	2	1	73	ubiquitin associated protein 2-like	ENST00000361546.2
Case#1-Relapse-WholeTumor	BCAN	1	156622520	Missense_Mutation	C	T	p.S593F	44	8	0.182	0.330	3	2	1	34	brevican	ENST00000329117.5
Case#1-Relapse-WholeTumor	PRCC	1	156756716	Missense_Mutation	C	T	p.S278F	95	18	0.189	0.344	3	2	1	72	papillary renal cell carcinoma (translocation-associated)	ENST00000271526.4
Case#1-Relapse-WholeTumor	FCRL2	1	157737021	Splice_Site	C	A	p.G388*	58	9	0.155	0.282	3	2	1	46	Fc receptor-like 2	ENST00000361516.3
Case#1-Relapse-WholeTumor	OR10T2	1	158368898	Missense_Mutation	C	T	p.G120E	80	13	0.163	0.295	3	2	1	39	olfactory receptor, family 10, subfamily T, member 2	ENST00000334438.1
Case#1-Relapse-WholeTumor	OR10X1	1	158548760	Missense_Mutation	C	T	p.M310I	175	35	0.200	0.363	3	2	1	104	olfactory receptor, family 10, subfamily X, member 1 (gene/pseudogene)	ENST00000368150.1
Case#1-Relapse-WholeTumor	SPTA1	1	158585076	Nonsense_Mutation	G	A	p.Q2240*	163	30	0.184	0.334	3	2	1	86	spectrin, alpha, erythrocytic 1	ENST00000368147.4
Case#1-Relapse-WholeTumor	OR6K3	1	158687250	Missense_Mutation	C	T	p.R235K	120	14	0.117	0.212	3	2	1	63	olfactory receptor, family 6, subfamily K, member 3	ENST00000368146.1
Case#1-Relapse-WholeTumor	OR6N1	1	158736124	Missense_Mutation	C	T	p.A117T	112	43	0.384	0.697	3	2	1	72	olfactory receptor, family 6, subfamily N, member 1	ENST00000335094.2
Case#1-Relapse-WholeTumor	OR10J1	1	159410110	Missense_Mutation	T	G	p.F188V	130	27	0.208	0.377	3	2	1	98	olfactory receptor, family 10, subfamily J, member 1	ENST00000423932.3
Case#1-Relapse-WholeTumor	CRP	1	159683805	Missense_Mutation	G	A	p.S62F	79	30	0.380	0.689	3	2	1	51	C-reactive protein, pentraxin-related	ENST00000255030.5
Case#1-Relapse-WholeTumor	SLAMF8	1	159799815	Missense_Mutation	C	T	p.S67F	71	22	0.310	0.562	3	2	1	30	SLAM family member 8	ENST00000289707.5
Case#1-Relapse-WholeTumor	CD48	1	160650992	Splice_Site	C	T	p.A218T	152	11	0.072	0.131	3	2	1	113	CD48 molecule	ENST00000368046.3
Case#1-Relapse-WholeTumor	LY9	1	160783554	Missense_Mutation	G	A	p.E195K	178	32	0.180	0.326	3	2	1	110	lymphocyte antigen 9	ENST00000263285.6
Case#1-Relapse-WholeTumor	ITLN1	1	160851081	Nonsense_Mutation	G	A	p.Q143*	178	34	0.191	0.347	3	2	1	110	intelectin 1 (galactofuranose binding)	ENST00000326245.3
Case#1-Relapse-WholeTumor	FCGR3A	1	161518217	Missense_Mutation	G	A	p.H105Y	466	51	0.109	0.199	3	2	1	244	Fc fragment of IgG, low affinity IIIa, receptor (CD16a)	ENST00000436743.1
Case#1-Relapse-WholeTumor	UHMK1	1	162487933	Missense_Mutation	C	T	p.P356S	202	40	0.198	0.359	3	2	1	133	U2AF homology motif (UHM) kinase 1	ENST00000489294.1
Case#1-Relapse-WholeTumor	RGS5	1	163122504	Missense_Mutation	C	T	p.G74R	102	39	0.382	0.694	3	2	1	63	regulator of G-protein signaling 5	ENST00000313961.5
Case#1-Relapse-WholeTumor	MAEL	1	166960705	Missense_Mutation	GG	AA	p.G106N	153	19	0.124	0.225	3	2	1	104	maelstrom spermatogenic transposon silencer	ENST00000367872.4
Case#1-Relapse-WholeTumor	CD247	1	167402275	Missense_Mutation	C	T	p.D139N	72	22	0.306	0.555	3	2	1	48	CD247 molecule	ENST00000362089.5
Case#1-Relapse-WholeTumor	ADCY10	1	167871277	Missense_Mutation	C	T	p.G90E	135	22	0.163	0.296	3	2	1	80	adenylate cyclase 10 (soluble)	ENST00000367851.4
Case#1-Relapse-WholeTumor	NME7	1	169292461	Missense_Mutation	C	T	p.E58K	82	7	0.085	0.155	3	2	1	55	NME/NM23 family member 7	ENST00000367811.3
Case#1-Relapse-WholeTumor	CCDC181	1	169391259	Missense_Mutation	A	T	p.L137H	40	7	0.175	0.318	3	2	1	29	coiled-coil domain containing 181	ENST00000367806.3
Case#1-Relapse-WholeTumor	FMO4	1	171292331	Splice_Site	G	A	p.K107K	124	21	0.169	0.307	3	2	1	97	flavin containing monooxygenase 4	ENST00000367749.3
Case#1-Relapse-WholeTumor	SLC9C2	1	173545816	Missense_Mutation	C	T	p.E296K	67	16	0.239	0.433	3	2	1	32	solute carrier family 9, member C2 (putative)	ENST00000367714.3
Case#1-Relapse-WholeTumor	SLC9C2	1	173567152	Missense_Mutation	G	A	p.P83L	111	21	0.189	0.343	3	2	1	43	solute carrier family 9, member C2 (putative)	ENST00000367714.3
Case#1-Relapse-WholeTumor	TNN	1	175046583	Missense_Mutation	C	T	p.P10L	51	12	0.235	0.427	3	2	1	25	tenascin N	ENST00000239462.4
Case#1-Relapse-WholeTumor	TNR	1	175293631	Missense_Mutation	C	T	p.G1273E	163	26	0.160	0.289	3	2	1	93	tenascin R	ENST00000367674.2
Case#1-Relapse-WholeTumor	TNR	1	175324709	Missense_Mutation	G	A	p.S1060F	123	25	0.203	0.369	3	2	1	85	tenascin R	ENST00000367674.2

Case#1-Relapse-WholeTumor	TNR	1	175325572	Missense_Mutation	C	T	p.G1001R	221	46	0.208	0.378	3	2	1	124	tenascin R	ENST00000367674.2
Case#1-Relapse-WholeTumor	TNR	1	175331865	Missense_Mutation	C	T	p.E930K	350	118	0.337	0.612	3	2	1	226	tenascin R	ENST00000367674.2
Case#1-Relapse-WholeTumor	PAPPA2	1	176525628	Missense_Mutation	G	A	p.R57Q	143	22	0.154	0.279	3	2	1	106	pappalysin 2	ENST00000367662.3
Case#1-Relapse-WholeTumor	PAPPA2	1	176709218	Missense_Mutation	C	T	p.S1346L	123	29	0.236	0.428	3	2	1	85	pappalysin 2	ENST00000367662.3
Case#1-Relapse-WholeTumor	ASTN1	1	176926845	Missense_Mutation	G	A	p.S627L	146	29	0.199	0.360	3	2	1	106	astrotactin 1	ENST00000367654.3
Case#1-Relapse-WholeTumor	ASTN1	1	177133719	Missense_Mutation	C	T	p.E32K	47	6	0.128	0.232	3	2	1	31	astrotactin 1	ENST00000367654.3
Case#1-Relapse-WholeTumor	RASAL2	1	178423643	Missense_Mutation	G	A	p.G543R	116	16	0.138	0.250	3	2	1	74	RAS protein activator like 2	ENST00000462775.1
Case#1-Relapse-WholeTumor	QSOX1	1	180158768	Missense_Mutation	C	T	p.P367S	86	10	0.116	0.211	3	2	1	79	quiescin Q6 sulfhydryl oxidase 1	ENST00000367602.3
Case#1-Relapse-WholeTumor	CACNA1E	1	181695231	Nonsense_Mutation	C	T	p.Q725*	122	26	0.213	0.387	3	2	1	79	calcium channel, voltage-dependent, R type, alpha 1E subunit	ENST00000367573.2
Case#1-Relapse-WholeTumor	RGSL1	1	182443171	Missense_Mutation	G	A	p.E309K	75	14	0.187	0.339	3	2	1	50	regulator of G-protein signaling like 1	ENST00000294854.8
Case#1-Relapse-WholeTumor	NMNAT2	1	183261971	Missense_Mutation	G	C	p.R66G	95	20	0.211	0.382	3	2	1	63	nicotinamide nucleotide adenylyltransferase 2	ENST00000287713.6
Case#1-Relapse-WholeTumor	SMG7	1	183498642	Nonsense_Mutation	C	T	p.R273*	168	27	0.161	0.292	3	2	1	87	SMG7 nonsense mediated mRNA decay factor	ENST00000347615.2
Case#1-Relapse-WholeTumor	FAM129A	1	184764464	Missense_Mutation	C	T	p.E812K	95	18	0.189	0.344	3	2	1	50	family with sequence similarity 129, member A	ENST00000367511.3
Case#1-Relapse-WholeTumor	HMCN1	1	186059892	Missense_Mutation	C	T	p.P3244S	121	25	0.207	0.375	3	2	1	70	hemicentin 1	ENST00000271588.4
Case#1-Relapse-WholeTumor	HMCN1	1	186084051	Missense_Mutation	C	T	p.R3793C	143	23	0.161	0.292	3	2	1	98	hemicentin 1	ENST00000271588.4
Case#1-Relapse-WholeTumor	PRG4	1	186276622	Missense_Mutation	G	A	p.E591K	98	6	0.061	0.111	3	2	1	76	proteoglycan 4	ENST00000445192.2
Case#1-Relapse-WholeTumor	PDC	1	186413125	Missense_Mutation	C	T	p.E243K	145	19	0.131	0.238	3	2	1	97	phosducin	ENST00000391997.2
Case#1-Relapse-WholeTumor	UCHL5	1	192993057	Nonsense_Mutation	G	A	p.R217*	69	11	0.159	0.289	3	2	1	52	ubiquitin carboxyl-terminal hydrolase L5	ENST00000367455.4
Case#1-Relapse-WholeTumor	PTPRC	1	198718604	Missense_Mutation	G	A	p.D998N	120	41	0.342	0.620	3	2	1	51	protein tyrosine phosphatase, receptor type, C	ENST00000367376.2
Case#1-Relapse-WholeTumor	CACNA1S	1	201039480	Missense_Mutation	GG	AA	p.P760L	79	27	0.342	0.620	3	2	1	27	calcium channel, voltage-dependent, L type, alpha 1S subunit	ENST00000362061.3
Case#1-Relapse-WholeTumor	PKP1	1	201294101	Missense_Mutation	C	T	p.L644F	82	17	0.207	0.376	3	2	1	78	plakophilin 1	ENST00000352845.3
Case#1-Relapse-WholeTumor	LGR6	1	202287440	Missense_Mutation	C	T	p.S670F	111	15	0.135	0.245	3	2	1	59	leucine-rich repeat containing G protein-coupled receptor 6	ENST00000367278.3
Case#1-Relapse-WholeTumor	FMOD	1	203317046	Missense_Mutation	G	A	p.T118I	168	34	0.202	0.367	3	2	1	97	fibromodulin	ENST00000354955.4
Case#1-Relapse-WholeTumor	NFASC	1	204949527	Missense_Mutation	G	A	p.G736R	149	17	0.114	0.207	3	2	1	83	neurofascin	ENST00000401399.1
Case#1-Relapse-WholeTumor	CR1	1	207751155	Missense_Mutation	C	T	p.P1515S	389	124	0.319	0.579	3	2	1	276	complement component (3b/4b) receptor 1 (Knops blood group)	ENST00000367049.4
Case#1-Relapse-WholeTumor	C1orf74	1	209956207	Missense_Mutation	G	A	p.S258F	91	16	0.176	0.319	3	2	1	61	chromosome 1 open reading frame 74	ENST00000294811.1
Case#1-Relapse-WholeTumor	KCNH1	1	211263988	Missense_Mutation	C	T	p.E119K	150	27	0.180	0.327	3	2	1	95	potassium voltage-gated channel, subfamily H (eag-related), member 1	ENST00000271751.4
Case#1-Relapse-WholeTumor	USH2A	1	216498829	Missense_Mutation	G	A	p.P321S	155	52	0.335	0.609	3	2	1	89	Usher syndrome 2A (autosomal recessive, mild)	ENST00000307340.3
Case#1-Relapse-WholeTumor	C1orf65	1	223568085	Missense_Mutation	A	G	p.N423S	46	7	0.152	0.276	3	2	1	21		ENST00000366875.3
Case#1-Relapse-WholeTumor	DNAH14	1	225380471	Missense_Mutation	G	A	p.G1488E	93	21	0.226	0.410	3	2	1	53	dynein, axonemal, heavy chain 14	ENST00000445597.2
Case#1-Relapse-WholeTumor	IBA57	1	228362852	Missense_Mutation	C	T	p.P237S	200	65	0.325	0.590	3	2	1	150	IBA57, iron-sulfur cluster assembly homolog (S. cerevisiae)	ENST00000366711.3
Case#1-Relapse-WholeTumor	OBSCN	1	228444456	Missense_Mutation	G	A	p.E1472K	289	39	0.135	0.245	3	2	1	190	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	ENST00000422127.1
Case#1-Relapse-WholeTumor	OBSCN	1	228467086	Missense_Mutation	C	T	p.T2446I	183	33	0.180	0.327	3	2	1	124	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	ENST00000422127.1
Case#1-Relapse-WholeTumor	OBSCN	1	228480416	Missense_Mutation	C	T	p.A3599V	281	57	0.203	0.368	3	2	1	164	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	ENST00000422127.1
Case#1-Relapse-WholeTumor	OBSCN	1	228563861	Missense_Mutation	GG	AA	p.G7647K	152	21	0.138	0.251	3	2	1	91	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	ENST00000422127.1
Case#1-Relapse-WholeTumor	PCNXL2	1	233388499	Missense_Mutation	C	T	p.E624K	85	11	0.129	0.235	3	2	1	57	pecanex-like 2 (Drosophila)	ENST00000258229.9
Case#1-Relapse-WholeTumor	TARBP1	1	234565167	Missense_Mutation	G	A	p.P956S	90	14	0.156	0.282	3	2	1	69	TAR (HIV-1) RNA binding protein 1	ENST00000040877.1
Case#1-Relapse-WholeTumor	B3GALNT2	1	235658121	Missense_Mutation	G	A	p.P44S	140	31	0.221	0.402	3	2	1	80	beta-1,3-N-acetylgalactosaminyltransferase 2	ENST00000366600.3
Case#1-Relapse-WholeTumor	LYST	1	235926080	Missense_Mutation	GG	AA	p.L2065F	112	14	0.125	0.227	3	2	1	60	lysosomal trafficking regulator	ENST00000389794.3
Case#1-Relapse-WholeTumor	NID1	1	236175223	Missense_Mutation	C	T	p.G842E	130	18	0.138	0.251	3	2	1	104	nidogen 1	ENST00000264187.6
Case#1-Relapse-WholeTumor	RYR2	1	237675076	Missense_Mutation	C	T	p.S936L	92	14	0.152	0.276	3	2	1	57	ryanodine receptor 2 (cardiac)	ENST00000366574.2
Case#1-Relapse-WholeTumor	RYR2	1	237948261	Missense_Mutation	G	A	p.E4417K	78	23	0.295	0.535	3	2	1	44	ryanodine receptor 2 (cardiac)	ENST00000366574.2
Case#1-Relapse-WholeTumor	RYR2	1	237965216	Splice_Site	C	T	p.N4717N	187	26	0.139	0.252	3	2	1	112	ryanodine receptor 2 (cardiac)	ENST00000366574.2
Case#1-Relapse-WholeTumor	RGS7	1	241262011	Missense_Mutation	G	A	p.R44C	131	19	0.145	0.263	3	2	1	107	regulator of G-protein signaling 7	ENST00000407727.1
Case#1-Relapse-WholeTumor	AKT3	1	243736329	Missense_Mutation	C	T	p.E240K	89	17	0.191	0.347	3	2	1	85	v-akt murine thymoma viral oncogene homolog 3	ENST00000366539.1
Case#1-Relapse-WholeTumor	NLRP3	1	247586553	Missense_Mutation	CG	TA	p.S102L	315	49	0.156	0.282	3	2	1	180	NLR family, pyrin domain containing 3	ENST00000336119.3
Case#1-Relapse-WholeTumor	OR2G3	1	247769009	Missense_Mutation	G	A	p.G41E	179	31	0.173	0.314	3	2	1	105	olfactory receptor, family 2, subfamily G, member 3	ENST00000320002.2
Case#1-Relapse-WholeTumor	OR13G1	1	247836148	Missense_Mutation	C	T	p.V66M	130	16	0.123	0.223	3	2	1	99	olfactory receptor, family 13, subfamily G, member 1	ENST00000359688.2
Case#1-Relapse-WholeTumor	OR6F1	1	247875661	Missense_Mutation	C	T	p.G133R	60	7	0.117	0.212	3	2	1	55	olfactory receptor, family 6, subfamily F, member 1	ENST00000302084.2
Case#1-Relapse-WholeTumor	OR2L3	1	248224777	Missense_Mutation	G	A	p.R265Q	340	47	0.138	0.251	3	2	1	251	olfactory receptor, family 2, subfamily L, member 3	ENST00000359959.3
Case#1-Relapse-WholeTumor	OR2M3	1	248366400	Missense_Mutation	G	A	p.D11N	289	57	0.197	0.358	3	2	1	200	olfactory receptor, family 2, subfamily M, member 3	ENST00000456743.1
Case#1-Relapse-WholeTumor	OR2M3	1	248366416	Missense_Mutation	G	A	p.G16E	308	48	0.156	0.283	3	2	1	199	olfactory receptor, family 2, subfamily M, member 3	ENST00000456743.1
Case#1-Relapse-WholeTumor	OR2T7	1	248604980	Missense_Mutation	C	T	p.P158L	305	39	0.128	0.232	3	2	1	183	olfactory receptor, family 2, subfamily T, member 7	ENST00000460972.3
Case#1-Relapse-WholeTumor	OR2T27	1	248813686	Missense_Mutation	G	A	p.P167L	114	32	0.281	0.509	3	2	1	82	olfactory receptor, family 2, subfamily T, member 27	ENST00000344889.3
Case#1-Relapse-WholeTumor	ADARB2	10	1779337	Missense_Mutation	G	A	p.S3L	119	34	0.286	0.635	2	1	1	77	adenosine deaminase, RNA-specific, B2 (non-functional)	ENST00000381312.1
Case#1-Relapse-WholeTumor	IL15RA	10	6008182	Missense_Mutation	G	A	p.S70F	130	35	0.269	0.598	2	1	1	91	interleukin 15 receptor, alpha	ENST00000379977.3
Case#1-Relapse-WholeTumor	ITIH5	10	7611648	Missense_Mutation	G	A	p.S711F	118	34	0.288	0.640	2	1	1	90	inter-alpha-trypsin inhibitor heavy chain family, member 5	ENST00000256861.6
Case#1-Relapse-WholeTumor	GATA3	10	8115931	Missense_Mutation	C	T	p.S426F	61	11	0.180	0.401	2	1	1	52	GATA binding protein 3	ENST00000346208.3
Case#1-Relapse-WholeTumor	CAMK1D	10	12856222	Missense_Mutation	G	A	p.E224K	146	23	0.158	0.350	2	1	1	123	calcium/calmodulin-dependent protein kinase ID	ENST00000378847.3
Case#1-Relapse-WholeTumor	FAM171A1	10	15256377	Missense_Mutation	G	A	p.P404S	84	12	0.143	0.317	2	1	1	65	family with sequence similarity 171, member A1	ENST00000378116.4
Case#1-Relapse-WholeTumor	VIM	10	17271596	Missense_Mutation	GG	AA	p.G59N	27	10	0.370	0.823	2	1	1	14	vimentin	ENST00000224237.5
Case#1-Relapse-WholeTumor	C10orf112	10	19498265	Missense_Mutation	G	A	p.D179N	70	16	0.229	0.508	2	1	1	41		ENST00000454679.2
Case#1-Relapse-WholeTumor	C10orf112	10	19636906	Missense_Mutation	A	T	p.I666F	76	16	0.211	0.468	2	1	1	50		ENST00000454679.2
Case#1-Relapse-WholeTumor	C10orf112	10	19787440	Missense_Mutation	T	G	p.C1095G	127	22	0.173	0.385	2	1	1	104		ENST00000454679.2
Case#1-Relapse-WholeTumor	PLXDC2	10	20335803	Missense_Mutation	T	A	p.D110E	145	33	0.228	0.506	2	1	1	104	plexin domain containing 2	ENST00000377252.4
Case#1-Relapse-WholeTumor	THNSL1	10	25313606	Missense_Mutation	C	T	p.S485F	70	10	0.143	0.317	2	1	1	72	threonine synthase-like 1 (S. cerevisiae)	ENST00000524413.1
Case#1-Relapse-WholeTumor	SVIL	10	29840084	Missense_Mutation	G	A	p.S90L	90	24	0.267	0.593	2	1	1	89	supervillin	ENST00000355867.4
Case#1-Relapse-WholeTumor	RET	10	43609005	Splice_Site	G	A	p.R587R	45	15	0.333	0.741	2	1	1	41	ret proto-oncogene	ENST00000355710.3
Case#1-Relapse-WholeTumor	GPRIN2	10	46999649	Missense_Mutation	G	A	p.A257T	49	8	0.163	0.363	2	1	1	47	G protein regulated inducer of neurite outgrowth 2	ENST00000374317.1
Case#1-Relapse-WholeTumor	ZNF488	10	48370630	Missense_Mutation	G	A	p.R33K	200	42	0.210	0.467	2	1	1	154	zinc finger protein 488	ENST00000395702.2
Case#1-Relapse-WholeTumor	WDFY4	10	50028286	Missense_Mutation	G	A	p.G1838E	43	16	0.372	0.827	2	1	1	38	WDFY family member 4	ENST00000325239.5
Case#1-Relapse-WholeTumor	C10orf128	10	50374999	Missense_Mutation	G	T	p.F51L	37	8	0.216	0.480	2	1	1	56	chromosome 10 open reading frame 128	ENST00000474718.1
Case#1-Relapse-WholeTumor	OGDHL	10	50943359	Missense_Mutation	C	T	p.G983E	80	26	0.325	0.722	2	1	1	110	oxoglutarate dehydrogenase-like	ENST00000374103.4
Case#1-Relapse-WholeTumor	SGMS1	10	52103527	Missense_Mutation	T	C	p.I116M	102	18	0.176	0.392	2	1	1	78	sphingomyelin synthase 1	ENST00000361781.2
Case#1-Relapse-WholeTumor	A1CF	10	52595855	Missense_Mutation	C	T	p.A195T	119	27	0.227	0.504	2	1	1	89	APOBEC1 complementation factor	ENST00000373993.1
Case#1-Relapse-WholeTumor	MBL2	10	54531257	Missense_Mutation	G	A	p.P47S	89	16	0.180	0.400	2	1	1	67	mannose-binding lectin (protein C) 2, soluble	ENST00000373968.3
Case#1-Relapse-WholeTumor	PCDH15	10	55569228	Missense_Mutation	C	T	p.E1528K	127	24	0.189	0.420	2	1	1	119	protocadherin-related 15	ENST00000395445.1
Case#1-Relapse-WholeTumor	PCDH15	10	55582867	Missense_Mutation	G	A	p.S1540L	143	33	0.231	0.513	2	1	1	112	protocadherin-related 15	ENST00000320301.6
Case#1-Relapse-WholeTumor	PCDH15	10	55945022	Missense_Mutation	C	T	p.D438N	105	14	0.133	0.296	2	1	1	92	protocadherin-related 15	ENST00000320301.6
Case#1-Relapse-WholeTumor	FAM13C	10	61112097	Missense_Mutation	T	G	p.N86T	93	17	0.183	0.406	2	1	1	97	family with sequence similarity 13, member C	ENST00000373868.2
Case#1-Relapse-WholeTumor	ANK3	10	61824037	Missense_Mutation	C	T	p.R4110K	41	7	0.171	0.379	2	1	1	35	ankyrin 3, node of Ranvier (ankyrin G)	ENST00000280772.2
Case#1-Relapse-WholeTumor	ANK3	10	61830674	Missense_Mutation	G	A	p.S3322F	49	10	0.204	0.454	2	1	1	25	ankyrin 3, node of Ranvier (ankyrin G)	ENST00000280772.2
Case#1-Relapse-WholeTumor	JMJD1C	10	64960426	Missense_Mutation	G	A	p.R1696C	165	45	0.273	0.606	2	1	1	127	jumonji domain containing 1C	ENST00000399262.2
Case#1-Relapse-WholeTumor	CCAR1	10	70508974	Missense_Mutation	G	A	p.G303E	180	34	0.189	0.420	2	1	1	119	cell division cycle and apoptosis regulator 1	ENST00000265872.6

Case#1-Relapse-WholeTumor	PALD1	10	72300880	Missense_Mutation	C	T	p.A644V	84	25	0.298	0.661	2	1	1	50	phosphatase domain containing, paladin 1	ENST00000263563.6
Case#1-Relapse-WholeTumor	PRF1	10	72358636	Missense_Mutation	C	T	p.E281K	111	28	0.252	0.561	2	1	1	78	perforin 1 (pore forming protein)	ENST00000441259.1
Case#1-Relapse-WholeTumor	CDH23	10	73500633	Missense_Mutation	G	A	p.V1520M	124	23	0.185	0.412	2	1	1	86	cadherin-related 23	ENST00000224721.6
Case#1-Relapse-WholeTumor	P4HA1	10	74806804	Missense_Mutation	G	A	p.P319L	128	33	0.258	0.573	2	1	1	100	prolyl 4-hydroxylase, alpha polypeptide I	ENST00000307116.2
Case#1-Relapse-WholeTumor	TTC18	10	75034301	Missense_Mutation	G	A	p.H979Y	113	28	0.248	0.551	2	1	1	87		ENST00000310715.3
Case#1-Relapse-WholeTumor	PTEN	10	89720808	Missense_Mutation	T	C	p.L320S	89	35	0.393	0.874	2	2	0	49	phosphatase and tensin homolog	ENST00000371953.3
Case#1-Relapse-WholeTumor	BTAF1	10	93719750	Missense_Mutation	C	T	p.R368C	129	61	0.473	1.051	2	2	0	94	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa	ENST00000265990.6
Case#1-Relapse-WholeTumor	PLCE1	10	95791077	Missense_Mutation	G	A	p.E92K	52	22	0.423	0.940	2	2	0	56	phospholipase C, epsilon 1	ENST00000371380.3
Case#1-Relapse-WholeTumor	TCTN3	10	97440329	Missense_Mutation	G	A	p.S497F	100	41	0.410	0.911	2	2	0	95	tectonic family member 3	ENST00000371217.5
Case#1-Relapse-WholeTumor	SEC31B	10	102269137	Missense_Mutation	G	A	p.P112L	52	31	0.596	1.325	2	2	0	38	SEC31 homolog B (S. cerevisiae)	ENST00000370345.3
Case#1-Relapse-WholeTumor	SORCS3	10	106918686	Missense_Mutation	G	A	p.E556K	56	33	0.589	1.310	2	2	0	76	sortilin-related VPS10 domain containing receptor 3	ENST00000369701.3
Case#1-Relapse-WholeTumor	PNLIPRP3	10	118203946	Missense_Mutation	G	A	p.G126D	81	31	0.383	0.850	2	2	0	72	pancreatic lipase-related protein 3	ENST00000369230.3
Case#1-Relapse-WholeTumor	TACC2	10	123847216	Missense_Mutation	C	T	p.S1734F	103	51	0.495	1.100	2	2	0	94	transforming, acidic coiled-coil containing protein 2	ENST00000369005.1
Case#1-Relapse-WholeTumor	DOCK1	10	129207624	Missense_Mutation	T	G	p.F1417V	109	9	0.083	0.183	2	2	0	108	dedicator of cytokinesis 1	ENST00000280333.6
Case#1-Relapse-WholeTumor	NPS	10	129350899	Missense_Mutation	C	T	p.S89L	53	20	0.377	0.839	2	2	0	58	neuropeptide S	ENST00000398023.1
Case#1-Relapse-WholeTumor	MKI67	10	129914052	Missense_Mutation	G	A	p.S207F	66	36	0.545	1.212	2	2	0	51	marker of proliferation Ki-67	ENST00000368654.3
Case#1-Relapse-WholeTumor	AL450307.1	10	133608090	Missense_Mutation	G	A	p.P96S	63	34	0.540	1.199	2	2	0	43		ENST00000341866.3
Case#1-Relapse-WholeTumor	TTC40	10	134699335	Missense_Mutation	C	T	p.A1145T	32	13	0.406	0.903	2	2	0	39		ENST00000368586.5
Case#1-Relapse-WholeTumor	MUC6	11	1016547	Missense_Mutation	G	A	p.S2085F	214	34	0.159	0.353	2	1	1	179	mucin 6, oligomeric mucus/gel-forming	ENST00000421673.2
Case#1-Relapse-WholeTumor	MUC5B	11	1270408	Missense_Mutation	G	A	p.A4100T	261	40	0.153	0.341	2	1	1	211	mucin 5B, oligomeric mucus/gel-forming	ENST00000529681.1
Case#1-Relapse-WholeTumor	OR52R1	11	4825594	Missense_Mutation	C	T	p.G6E	124	26	0.210	0.466	2	1	1	89	olfactory receptor, family 52, subfamily R, member 1	ENST00000356069.2
Case#1-Relapse-WholeTumor	OR51S1	11	4870024	Missense_Mutation	G	A	p.H139Y	115	34	0.296	0.657	2	1	1	88	olfactory receptor, family 51, subfamily S, member 1	ENST00000322101.2
Case#1-Relapse-WholeTumor	OR51G1	11	4945500	Missense_Mutation	C	T	p.G24S	157	33	0.210	0.467	2	1	1	117	olfactory receptor, family 51, subfamily G, member 1	ENST00000321961.2
Case#1-Relapse-WholeTumor	MMP26	11	5013192	Splice_Site	A	C		16	4	0.250	0.556	2	1	1	21	matrix metallopeptidase 26	ENST00000380390.1
Case#1-Relapse-WholeTumor	OR52J3	11	5068546	Missense_Mutation	G	A	p.R264Q	99	24	0.242	0.539	2	1	1	100	olfactory receptor, family 52, subfamily J, member 3	ENST00000380370.1
Case#1-Relapse-WholeTumor	OR52E2	11	5079909	Missense_Mutation	C	T	p.E317K	114	15	0.132	0.292	2	1	1	86	olfactory receptor, family 52, subfamily E, member 2	ENST00000321522.2
Case#1-Relapse-WholeTumor	OR51B2	11	5345263	Missense_Mutation	C	T	p.E89K	47	13	0.277	0.615	2	1	1	40	olfactory receptor, family 51, subfamily B, member 2	ENST00000328813.2
Case#1-Relapse-WholeTumor	OR51I2	11	5475346	Missense_Mutation	G	A	p.D210N	228	34	0.149	0.331	2	1	1	190	olfactory receptor, family 51, subfamily I, member 2	ENST00000341449.2
Case#1-Relapse-WholeTumor	UBQLN3	11	5529629	Missense_Mutation	G	A	p.S387F	134	38	0.284	0.630	2	1	1	77	ubiquilin 3	ENST00000311659.4
Case#1-Relapse-WholeTumor	TRIM22	11	5730807	Nonsense_Mutation	C	T	p.R476*	108	19	0.176	0.391	2	1	1	76	tripartite motif containing 22	ENST00000379965.3
Case#1-Relapse-WholeTumor	OR56B4	11	6129543	Missense_Mutation	G	A	p.E179K	77	19	0.247	0.548	2	1	1	50	olfactory receptor, family 56, subfamily B, member 4	ENST00000316529.3
Case#1-Relapse-WholeTumor	NLRP10	11	7981652	Missense_Mutation	C	T	p.E503K	96	18	0.188	0.417	2	1	1	57	NLR family, pyrin domain containing 10	ENST00000328600.2
Case#1-Relapse-WholeTumor	KCNC1	11	17793758	Missense_Mutation	C	T	p.P373S	37	10	0.270	0.601	2	1	1	35	potassium voltage-gated channel, Shaw-related subfamily, member 1	ENST00000379472.3
Case#1-Relapse-WholeTumor	SPTY2D1	11	18633868	Nonsense_Mutation	G	A	p.R627*	120	22	0.183	0.407	2	1	1	69	SPT2, Suppressor of Ty, domain containing 1 (S. cerevisiae)	ENST00000336349.5
Case#1-Relapse-WholeTumor	NAV2	11	20099567	Missense_Mutation	C	T	p.T1755I	74	16	0.216	0.480	2	1	1	43	neuron navigator 2	ENST00000396087.3
Case#1-Relapse-WholeTumor	NELL1	11	21581750	Missense_Mutation	C	T	p.A601V	77	11	0.143	0.317	2	1	1	82	NEL-like 1 (chicken)	ENST00000357134.5
Case#1-Relapse-WholeTumor	CREB3L1	11	46334162	Splice_Site	G	A		171	29	0.170	0.377	2	1	1	96	cAMP responsive element binding protein 3-like 1	ENST00000529193.1
Case#1-Relapse-WholeTumor	PTPRJ	11	48157838	Nonsense_Mutation	AC	TT	p.Q622*	62	7	0.113	0.251	2	1	1	72	protein tyrosine phosphatase, receptor type, J	ENST00000418331.2
Case#1-Relapse-WholeTumor	OR4A47	11	48510661	Missense_Mutation	G	A	p.G106D	104	29	0.279	0.620	2	2	0	81	olfactory receptor, family 4, subfamily A, member 47	ENST00000446524.1
Case#1-Relapse-WholeTumor	OR5D14	11	55563272	Missense_Mutation	C	T	p.P81S	211	49	0.232	0.516	2	1	1	181	olfactory receptor, family 5, subfamily D, member 14	ENST00000335605.1
Case#1-Relapse-WholeTumor	OR5M9	11	56230749	Missense_Mutation	C	T	p.M43I	61	7	0.115	0.255	2	1	1	54	olfactory receptor, family 5, subfamily M, member 9	ENST00000279791.1
Case#1-Relapse-WholeTumor	OR5M8	11	56258275	Missense_Mutation	G	A	p.T191I	273	67	0.245	0.545	2	1	1	241	olfactory receptor, family 5, subfamily M, member 8	ENST00000327216.2
Case#1-Relapse-WholeTumor	OR5AP2	11	56408980	Nonsense_Mutation	C	T	p.W312*	99	27	0.273	0.606	2	1	1	88	olfactory receptor, family 5, subfamily AP, member 2	ENST00000302981.1
Case#1-Relapse-WholeTumor	OR5AK2	11	56756827	Missense_Mutation	G	A	p.G147S	173	54	0.312	0.694	2	1	1	125	olfactory receptor, family 5, subfamily AK, member 2	ENST00000326855.2
Case#1-Relapse-WholeTumor	OR5AK2	11	56756984	Missense_Mutation	T	G	p.L199R	340	28	0.082	0.183	2	1	1	286	olfactory receptor, family 5, subfamily AK, member 2	ENST00000326855.2
Case#1-Relapse-WholeTumor	OR4D6	11	59224841	Missense_Mutation	G	A	p.M136I	140	31	0.221	0.492	2	1	1	102	olfactory receptor, family 4, subfamily D, member 6	ENST00000300127.2
Case#1-Relapse-WholeTumor	TUT1	11	62348929	Missense_Mutation	G	C	p.S173C	116	20	0.172	0.383	2	1	1	82	terminal uridylyl transferase 1, U6 snRNA-specific	ENST00000476907.1
Case#1-Relapse-WholeTumor	SLC22A9	11	63141402	Missense_Mutation	G	A	p.G233E	129	28	0.217	0.482	2	1	1	87	solute carrier family 22 (organic anion transporter), member 9	ENST00000279178.3
Case#1-Relapse-WholeTumor	PLCB3	11	64028965	Nonsense_Mutation	C	T	p.R609*	111	30	0.270	0.601	2	1	1	89	phospholipase C, beta 3 (phosphatidylinositol-specific)	ENST00000540288.1
Case#1-Relapse-WholeTumor	RPS6KA4	11	64129178	Missense_Mutation	C	T	p.T239I	103	31	0.301	0.669	2	1	1	64	ribosomal protein S6 kinase, 90kDa, polypeptide 4	ENST00000334205.4
Case#1-Relapse-WholeTumor	ATG2A	11	64664948	Missense_Mutation	GG	AA	p.L1696F	130	37	0.285	0.632	2	1	1	113	autophagy related 2A	ENST00000377264.3
Case#1-Relapse-WholeTumor	CTSW	11	65649988	Missense_Mutation	T	C	p.S177P	98	26	0.265	0.590	2	1	1	69	cathepsin W	ENST00000307886.3
Case#1-Relapse-WholeTumor	CD248	11	66082544	Missense_Mutation	C	T	p.S652N	57	11	0.193	0.429	2	1	1	48	CD248 molecule, endosialin	ENST00000311330.3
Case#1-Relapse-WholeTumor	SPTBN2	11	66455082	Missense_Mutation	C	T	p.G2180R	49	7	0.143	0.317	2	1	1	33	spectrin, beta, non-erythrocytic 2	ENST00000533211.1
Case#1-Relapse-WholeTumor	TBX10	11	67402378	Missense_Mutation	G	A	p.P96S	110	25	0.227	0.505	2	1	1	72	T-box 10	ENST00000335385.3
Case#1-Relapse-WholeTumor	FGF3	11	69625429	Missense_Mutation	G	A	p.H122Y	137	39	0.285	0.633	2	1	1	116	fibroblast growth factor 3	ENST00000334134.2
Case#1-Relapse-WholeTumor	INPPL1	11	71944487	Missense_Mutation	CC	TT	p.R682W	64	15	0.234	0.521	2	1	1	53	inositol polyphosphate phosphatase-like 1	ENST00000298229.2
Case#1-Relapse-WholeTumor	GDPD4	11	76944167	Missense_Mutation	G	A	p.P431L	180	43	0.239	0.531	2	1	1	146	glycerophosphodiester phosphodiesterase domain containing 4	ENST00000376217.2
Case#1-Relapse-WholeTumor	NARS2	11	78277192	Missense_Mutation	G	A	p.H167Y	88	17	0.193	0.429	2	1	1	65	asparaginyl-tRNA synthetase 2, mitochondrial (putative)	ENST00000281038.5
Case#1-Relapse-WholeTumor	EED	11	85988157	Missense_Mutation	T	C	p.F368L	176	40	0.227	0.505	2	1	1	114	embryonic ectoderm development	ENST00000263360.6
Case#1-Relapse-WholeTumor	TRIM77	11	89450921	Missense_Mutation	G	A	p.D412N	191	41	0.215	0.477	2	1	1	154	tripartite motif containing 77	ENST00000398290.3
Case#1-Relapse-WholeTumor	FAT3	11	92085636	Missense_Mutation	G	A	p.E120K	91	18	0.198	0.440	2	1	1	95	FAT atypical cadherin 3	ENST00000298047.6
Case#1-Relapse-WholeTumor	CCDC67	11	93127766	Missense_Mutation	G	A	p.E395K	82	16	0.195	0.434	2	1	1	56	coiled-coil domain containing 67	ENST00000298050.3
Case#1-Relapse-WholeTumor	HEPHL1	11	93839165	Missense_Mutation	G	A	p.G972R	121	22	0.182	0.404	2	1	1	89	hephaestin-like 1	ENST00000315765.9
Case#1-Relapse-WholeTumor	CNTN5	11	99872774	Missense_Mutation	G	A	p.G296R	125	29	0.232	0.516	2	1	1	118	contactin 5	ENST00000524871.1
Case#1-Relapse-WholeTumor	CNTN5	11	99872807	Missense_Mutation	C	T	p.P307S	144	34	0.236	0.525	2	1	1	135	contactin 5	ENST00000524871.1
Case#1-Relapse-WholeTumor	CNTN5	11	100061937	Missense_Mutation	G	A	p.E554K	219	41	0.187	0.416	2	1	1	166	contactin 5	ENST00000524871.1
Case#1-Relapse-WholeTumor	CNTN5	11	100168399	Missense_Mutation	GA	AT	p.R786N	227	50	0.220	0.489	2	1	1	186	contactin 5	ENST00000524871.1
Case#1-Relapse-WholeTumor	MMP8	11	102589181	Missense_Mutation	G	A	p.P250S	147	34	0.231	0.514	2	1	1	124	matrix metallopeptidase 8 (neutrophil collagenase)	ENST00000236826.3
Case#1-Relapse-WholeTumor	DYNC2H1	11	103092818	Missense_Mutation	C	T	p.S3056L	138	19	0.138	0.306	2	1	1	86	dynein, cytoplasmic 2, heavy chain 1	ENST00000375735.2
Case#1-Relapse-WholeTumor	NCAM1	11	113076767	Nonsense_Mutation	C	T	p.R47*	119	26	0.218	0.486	2	1	1	67	neural cell adhesion molecule 1	ENST00000533760.1
Case#1-Relapse-WholeTumor	ZW10	11	113629345	Missense_Mutation	G	A	p.P222S	134	36	0.269	0.597	2	1	1	122	zw10 kinetochore protein	ENST00000200135.3
Case#1-Relapse-WholeTumor	HTR3B	11	113803745	Missense_Mutation	T	C	p.L209P	163	22	0.135	0.300	2	1	1	96	5-hydroxytryptamine (serotonin) receptor 3B, ionotropic	ENST00000260191.2
Case#1-Relapse-WholeTumor	NXPE2	11	114577134	Missense_Mutation	C	T	p.H388Y	61	9	0.148	0.328	2	1	1	61	neurexophilin and PC-esterase domain family, member 2	ENST00000389586.4
Case#1-Relapse-WholeTumor	PAFAH1B2	11	117038213	Missense_Mutation	C	T	p.S163L	94	22	0.234	0.520	2	1	1	65	platelet-activating factor acetylhydrolase 1b, catalytic subunit 2 (30kDa)	ENST00000527958.1
Case#1-Relapse-WholeTumor	KMT2A	11	118362000	Missense_Mutation	C	T	p.H1596Y	121	26	0.215	0.478	2	1	1	102	lysine (K)-specific methyltransferase 2A	ENST00000389506.5
Case#1-Relapse-WholeTumor	PDZD3	11	119057283	Missense_Mutation	G	A	p.G138R	48	14	0.292	0.648	2	1	1	51	PDZ domain containing 3	ENST00000531114.1
Case#1-Relapse-WholeTumor	CBL	11	119169212	Missense_Mutation	C	T	p.S799F	170	39	0.229	0.510	2	1	1	131	Cbl proto-oncogene, E3 ubiquitin protein ligase	ENST00000264033.4
Case#1-Relapse-WholeTumor	SORL1	11	121367627	Missense_Mutation	G	A	p.E270K	118	18	0.153	0.339	2	1	1	96	sortilin-related receptor, L(DLR class) A repeats containing	ENST00000260197.7
Case#1-Relapse-WholeTumor	OR8D4	11	123777185	Missense_Mutation	G	A	p.G16E	102	17	0.167	0.370	2	1	1	68	olfactory receptor, family 8, subfamily D, member 4	ENST00000321355.2
Case#1-Relapse-WholeTumor	OR8D4	11	123778058	Missense_Mutation	G	A	p.R307K	66	19	0.288	0.640	2	1	1	48	olfactory receptor, family 8, subfamily D, member 4	ENST00000321355.2
Case#1-Relapse-WholeTumor	OR10S1	11	123848326	Missense_Mutation	A	G	p.F25L	125	26	0.208	0.462	2	1	1	114	olfactory receptor, family 10, subfamily S, member 1	ENST00000531945.1

Case#1-Relapse-WholeTumor	SRPR	11	126136477	Missense_Mutation	GG	AA	p.P245F	122	24	0.197	0.437	2	1	1	91	signal recognition particle receptor (docking protein)	ENST00000332118.6
Case#1-Relapse-WholeTumor	SRPR	11	126138630	Missense_Mutation	A	G	p.S24P	109	25	0.229	0.510	2	1	1	93	signal recognition particle receptor (docking protein)	ENST00000332118.6
Case#1-Relapse-WholeTumor	ARHGAP32	11	128840469	Missense_Mutation	G	A	p.R1533C	212	34	0.160	0.356	2	1	1	175	Rho GTPase activating protein 32	ENST00000310343.9
Case#1-Relapse-WholeTumor	ADAMTS8	11	130286943	Missense_Mutation	C	T	p.D330N	110	23	0.209	0.465	2	1	1	85	ADAM metallopeptidase with thrombospondin type 1 motif, 8	ENST00000257359.6
Case#1-Relapse-WholeTumor	NCAPD3	11	134080186	Missense_Mutation	GG	AA	p.P182L	130	14	0.108	0.239	2	1	1	114	non-SMC condensin II complex, subunit D3	ENST00000534548.2
Case#1-Relapse-WholeTumor	DCP1B	12	2061631	Missense_Mutation	G	A	p.S492F	132	35	0.265	0.589	2	1	1	114	decapping mRNA 1B	ENST00000280665.6
Case#1-Relapse-WholeTumor	AC005841.1	12	2966135	Missense_Mutation	C	T	p.E27K	128	19	0.148	0.330	2	1	1	111		ENST00000382678.3
Case#1-Relapse-WholeTumor	GALNT8	12	4870294	Nonsense_Mutation	G	A	p.W448*	66	13	0.197	0.438	2	1	1	58	polypeptide N-acetylgalactosaminyltransferase 8	ENST00000252318.2
Case#1-Relapse-WholeTumor	KCNA5	12	5154520	Missense_Mutation	C	T	p.R403C	54	18	0.333	0.741	2	1	1	56	potassium voltage-gated channel, shaker-related subfamily, member 5	ENST00000252321.3
Case#1-Relapse-WholeTumor	CD163	12	7637740	Missense_Mutation	C	T	p.E911K	80	22	0.275	0.611	2	1	1	54	CD163 molecule	ENST00000359156.4
Case#1-Relapse-WholeTumor	PRB2	12	11546665	Missense_Mutation	C	T	p.G116E	405	52	0.128	0.285	2	1	1	359	proline-rich protein BstNI subfamily 2	ENST00000389362.4
Case#1-Relapse-WholeTumor	GRIN2B	12	13906630	Missense_Mutation	C	T	p.D211N	78	14	0.179	0.399	2	1	1	62	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	ENST00000609686.1
Case#1-Relapse-WholeTumor	PIK3C2G	12	18658227	Splice_Site	C	T	p.A1011V	116	28	0.241	0.536	2	1	1	93	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 gamma	ENST00000266497.5
Case#1-Relapse-WholeTumor	SLCO1B1	12	21329769	Missense_Mutation	C	T	p.S140F	72	15	0.208	0.463	2	1	1	69	solute carrier organic anion transporter family, member 1B1	ENST00000256958.2
Case#1-Relapse-WholeTumor	SOX5	12	23687236	Missense_Mutation	C	T	p.D737N	246	64	0.260	0.578	2	1	1	154	SRY (sex determining region Y)-box 5	ENST00000451604.2
Case#1-Relapse-WholeTumor	BCAT1	12	24970979	Missense_Mutation	C	T	p.G375E	110	24	0.218	0.485	2	1	1	107	branched chain amino-acid transaminase 1, cytosolic	ENST00000261192.7
Case#1-Relapse-WholeTumor	C12orf40	12	40114658	Missense_Mutation	G	A	p.E522K	80	8	0.100	0.222	2	1	1	63	chromosome 12 open reading frame 40	ENST00000324616.5
Case#1-Relapse-WholeTumor	MUC19	12	40832004	Missense_Mutation	G	A	p.E515K	89	20	0.225	NA	NA	NA	NA	68	mucin 19, oligomeric	ENST00000454784.4
Case#1-Relapse-WholeTumor	ARID2	12	46287234	Missense_Mutation	C	T	p.P1727S	77	18	0.234	0.519	2	1	1	63	AT rich interactive domain 2 (ARID, RFX-like)	ENST00000334344.6
Case#1-Relapse-WholeTumor	PCED1B	12	47629420	Missense_Mutation	G	A	p.E192K	174	37	0.213	0.473	2	1	1	135	PC-esterase domain containing 1B	ENST00000546455.1
Case#1-Relapse-WholeTumor	SENP1	12	48439118	Missense_Mutation	C	T	p.R641Q	170	36	0.212	0.471	2	1	1	127	SUMO1/sentrin specific peptidase 1	ENST00000004980.5
Case#1-Relapse-WholeTumor	RND1	12	49254905	Missense_Mutation	C	T	p.E110K	33	13	0.394	0.875	2	1	1	30	Rho family GTPase 1	ENST00000309739.5
Case#1-Relapse-WholeTumor	TFCP2	12	51510103	Missense_Mutation	T	C	p.D151G	66	13	0.197	0.438	2	1	1	57	transcription factor CP2	ENST00000257915.5
Case#1-Relapse-WholeTumor	SCN8A	12	52184276	Missense_Mutation	C	T	p.P1505L	80	20	0.250	0.556	2	1	1	79	sodium channel, voltage gated, type VIII, alpha subunit	ENST00000354534.6
Case#1-Relapse-WholeTumor	KRT71	12	52943113	Missense_Mutation	CC	AT	p.R227H	106	22	0.208	0.461	2	1	1	64	keratin 71	ENST00000267119.5
Case#1-Relapse-WholeTumor	SOAT2	12	53512909	Splice_Site	C	T	p.A304V	70	14	0.200	0.444	2	1	1	47	sterol O-acyltransferase 2	ENST00000301466.3
Case#1-Relapse-WholeTumor	ITGB7	12	53590388	Missense_Mutation	G	A	p.A264V	82	18	0.220	0.488	2	1	1	60	integrin, beta 7	ENST00000267082.5
Case#1-Relapse-WholeTumor	GPR84	12	54757016	Missense_Mutation	C	T	p.R207Q	148	25	0.169	0.375	2	1	1	96	G protein-coupled receptor 84	ENST00000551809.1
Case#1-Relapse-WholeTumor	OR6C74	12	55641512	Nonsense_Mutation	G	A	p.W147*	102	19	0.186	0.414	2	1	1	82	olfactory receptor, family 6, subfamily C, member 74	ENST00000343870.4
Case#1-Relapse-WholeTumor	OR6C75	12	55759151	Missense_Mutation	G	A	p.G86E	94	23	0.245	0.544	2	1	1	60	olfactory receptor, family 6, subfamily C, member 75	ENST00000343399.3
Case#1-Relapse-WholeTumor	OR6C65	12	55795213	Missense_Mutation	G	A	p.E301K	65	14	0.215	0.479	2	1	1	59	olfactory receptor, family 6, subfamily C, member 65	ENST00000379665.2
Case#1-Relapse-WholeTumor	PMEL	12	56359790	Missense_Mutation	A	T	p.D2E	70	17	0.243	0.540	2	1	1	57	premelanosome protein	ENST00000548747.1
Case#1-Relapse-WholeTumor	SMARCC2	12	56565658	Missense_Mutation	C	T	p.D633N	73	21	0.288	0.639	2	1	1	63	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	ENST00000267064.4
Case#1-Relapse-WholeTumor	PAN2	12	56718253	Missense_Mutation	G	A	p.R585C	119	28	0.235	0.523	2	1	1	79	PAN2 poly(A) specific ribonuclease subunit	ENST00000425394.2
Case#1-Relapse-WholeTumor	HSD17B6	12	57167760	Missense_Mutation	G	A	p.G42R	73	18	0.247	0.548	2	1	1	83	hydroxysteroid (17-beta) dehydrogenase 6	ENST00000554643.1
Case#1-Relapse-WholeTumor	B4GALNT1	12	58025711	Missense_Mutation	C	T	p.E69K	58	13	0.224	0.498	2	1	1	48	beta-1,4-N-acetyl-galactosaminyl transferase 1	ENST00000341156.4
Case#1-Relapse-WholeTumor	AGAP2	12	58125350	Missense_Mutation	G	A	p.P677S	170	50	0.294	0.654	2	1	1	122	ArfGAP with GTPase domain, ankyrin repeat and PH domain 2	ENST00000547588.1
Case#1-Relapse-WholeTumor	OTOGL	12	80704481	Missense_Mutation	G	A	p.D1133N	103	32	0.311	0.690	2	1	1	66	otogelin-like	ENST00000547103.1
Case#1-Relapse-WholeTumor	PTPRQ	12	81062909	Missense_Mutation	G	A	p.E2102K	213	41	0.192	0.428	2	1	1	194	protein tyrosine phosphatase, receptor type, Q	ENST00000266688.5
Case#1-Relapse-WholeTumor	METTL25	12	82796892	Missense_Mutation	T	A	p.F421Y	142	29	0.204	0.454	2	1	1	87	methyltransferase like 25	ENST00000248306.3
Case#1-Relapse-WholeTumor	METTL25	12	82871108	Nonsense_Mutation	C	T	p.R566*	171	27	0.158	0.351	2	1	1	133	methyltransferase like 25	ENST00000248306.3
Case#1-Relapse-WholeTumor	NUAK1	12	106461083	Missense_Mutation	C	T	p.D495N	62	11	0.177	0.394	2	1	1	55	NUAK family, SNF1-like kinase, 1	ENST00000261402.2
Case#1-Relapse-WholeTumor	NUAK1	12	106500267	Missense_Mutation	C	T	p.D93N	133	39	0.293	0.652	2	1	1	126	NUAK family, SNF1-like kinase, 1	ENST00000261402.2
Case#1-Relapse-WholeTumor	CMKLR1	12	108686645	Missense_Mutation	G	A	p.S32F	73	18	0.247	0.548	2	1	1	79	chemokine-like receptor 1	ENST00000312143.7
Case#1-Relapse-WholeTumor	ATXN2	12	111951289	Missense_Mutation	G	A	p.S637F	110	20	0.182	0.404	2	1	1	74	ataxin 2	ENST00000377617.3
Case#1-Relapse-WholeTumor	NOS1	12	117728218	Missense_Mutation	C	T	p.G289E	57	13	0.228	0.507	2	1	1	56	nitric oxide synthase 1 (neuronal)	ENST00000338101.4
Case#1-Relapse-WholeTumor	KSR2	12	117993071	Missense_Mutation	G	A	p.S474F	215	53	0.247	0.548	2	1	1	143	kinase suppressor of ras 2	ENST00000339824.5
Case#1-Relapse-WholeTumor	SRRM4	12	119592176	Missense_Mutation	G	A	p.R507Q	139	40	0.288	0.639	2	1	1	131	serine/arginine repetitive matrix 4	ENST00000267260.4
Case#1-Relapse-WholeTumor	TMEM132B	12	126138174	Missense_Mutation	G	A	p.D719N	128	20	0.156	0.347	2	1	1	108	transmembrane protein 132B	ENST00000299308.3
Case#1-Relapse-WholeTumor	TMEM132C	12	129178431	Missense_Mutation	G	A	p.D503N	89	17	0.191	0.424	2	1	1	91	transmembrane protein 132C	ENST00000435159.2
Case#1-Relapse-WholeTumor	TMEM132C	12	129180403	Missense_Mutation	G	A	p.E562K	101	15	0.149	0.330	2	1	1	84	transmembrane protein 132C	ENST00000435159.2
Case#1-Relapse-WholeTumor	ANKLE2	12	133313612	Missense_Mutation	G	A	p.S487F	45	6	0.133	0.296	2	1	1	36	ankyrin repeat and LEM domain containing 2	ENST00000357997.5
Case#1-Relapse-WholeTumor	TUBA3C	13	19751150	Missense_Mutation	G	A	p.P325S	416	65	0.156	0.252	4	3	1	195	tubulin, alpha 3c	ENST00000400113.3
Case#1-Relapse-WholeTumor	TUBA3C	13	19751338	Missense_Mutation	T	C	p.Y262C	373	59	0.158	0.255	4	3	1	234	tubulin, alpha 3c	ENST00000400113.3
Case#1-Relapse-WholeTumor	USP12	13	27669805	Missense_Mutation	G	A	p.P169L	199	78	0.392	0.631	4	3	1	108	ubiquitin specific peptidase 12	ENST00000282344.6
Case#1-Relapse-WholeTumor	MTUS2	13	29599268	Missense_Mutation	G	A	p.D155N	144	23	0.160	0.257	4	3	1	81	microtubule associated tumor suppressor candidate 2	ENST00000431530.3
Case#1-Relapse-WholeTumor	TEX26	13	31513914	Splice_Site	C	T	p.R49C	145	59	0.407	0.656	4	3	1	90	testis expressed 26	ENST00000380473.3
Case#1-Relapse-WholeTumor	FRY	13	32776086	Missense_Mutation	C	T	p.P1252L	102	54	0.529	0.853	4	3	1	87	furry homolog (Drosophila)	ENST00000380250.3
Case#1-Relapse-WholeTumor	BRCA2	13	32930694	Missense_Mutation	C	T	p.S2522F	107	55	0.514	0.828	4	3	1	50	breast cancer 2, early onset	ENST00000380152.3
Case#1-Relapse-WholeTumor	KL	13	33629411	Missense_Mutation	C	T	p.P520S	134	20	0.149	0.240	4	3	1	82	klotho	ENST00000380099.3
Case#1-Relapse-WholeTumor	NBEA	13	36141110	Missense_Mutation	G	A	p.E2331K	108	55	0.509	0.820	4	3	1	59	neurobeachin	ENST00000400445.3
Case#1-Relapse-WholeTumor	POSTN	13	38156628	Missense_Mutation	G	A	p.R423C	136	54	0.397	0.640	4	3	1	97	periostin, osteoblast specific factor	ENST00000379747.4
Case#1-Relapse-WholeTumor	FREM2	13	39261986	Missense_Mutation	G	A	p.V169I	189	26	0.138	0.222	4	3	1	94	FRAS1 related extracellular matrix protein 2	ENST00000280481.7
Case#1-Relapse-WholeTumor	PROSER1	13	39585573	Missense_Mutation	G	A	p.P922S	109	17	0.156	0.251	4	3	1	76	proline and serine rich 1	ENST00000352251.3
Case#1-Relapse-WholeTumor	COG3	13	46090309	Missense_Mutation	A	G	p.K614R	117	48	0.410	0.661	4	3	1	66	component of oligomeric golgi complex 3	ENST00000349995.5
Case#1-Relapse-WholeTumor	LRCH1	13	47315930	Missense_Mutation	C	T	p.L712F	232	103	0.444	0.715	4	3	1	145	leucine-rich repeats and calponin homology (CH) domain containing 1	ENST00000389798.3
Case#1-Relapse-WholeTumor	DACH1	13	72049903	Missense_Mutation	C	T	p.R704Q	200	74	0.370	0.596	4	3	1	110	dachshund family transcription factor 1	ENST00000359684.2
Case#1-Relapse-WholeTumor	LMO7	13	76287325	Missense_Mutation	C	G	p.T78R	437	48	0.110	0.177	4	3	1	262	LIM domain 7	ENST00000341547.4
Case#1-Relapse-WholeTumor	MYCBP2	13	77642818	Missense_Mutation	G	A	p.S3980F	189	75	0.397	0.639	4	3	1	125	MYC binding protein 2, E3 ubiquitin protein ligase	ENST00000544440.2
Case#1-Relapse-WholeTumor	DNAJC3	13	96412327	Nonsense_Mutation	C	T	p.R194*	128	16	0.125	0.201	4	3	1	88	DnaJ (Hsp40) homolog, subfamily C, member 3	ENST00000602402.1
Case#1-Relapse-WholeTumor	CCDC168	13	103386677	Missense_Mutation	G	A	p.S828F	183	21	0.115	0.185	4	3	1	115	coiled-coil domain containing 168	ENST00000322527.2
Case#1-Relapse-WholeTumor	CCDC168	13	103387112	Missense_Mutation	G	A	p.S683F	135	47	0.348	0.561	4	3	1	51	coiled-coil domain containing 168	ENST00000322527.2
Case#1-Relapse-WholeTumor	CCDC168	13	103387773	Missense_Mutation	C	T	p.E463K	210	78	0.371	0.598	4	3	1	131	coiled-coil domain containing 168	ENST00000322527.2
Case#1-Relapse-WholeTumor	BIVM	13	103474115	Missense_Mutation	G	A	p.E242K	184	25	0.136	0.219	4	3	1	94	basic, immunoglobulin-like variable motif containing	ENST00000257336.1
Case#1-Relapse-WholeTumor	SLC10A2	13	103718383	Missense_Mutation	G	A	p.L73F	131	15	0.115	0.184	4	3	1	61	solute carrier family 10 (sodium/bile acid cotransporter), member 2	ENST00000245312.3
Case#1-Relapse-WholeTumor	DAOA	13	106124931	Missense_Mutation	G	A	p.G60R	216	80	0.370	0.597	4	3	1	156	D-amino acid oxidase activator	ENST00000375936.3
Case#1-Relapse-WholeTumor	TUBGCP3	13	113210479	Missense_Mutation	A	C	p.L203R	264	27	0.102	0.165	4	3	1	173	tubulin, gamma complex associated protein 3	ENST00000261965.3
Case#1-Relapse-WholeTumor	MCF2L	13	113744025	Missense_Mutation	C	T	p.P1009L	101	46	0.455	0.734	4	3	1	50	MCF.2 cell line derived transforming sequence-like	ENST00000375608.3
Case#1-Relapse-WholeTumor	OR4K15	14	20444378	Missense_Mutation	C	T	p.S234F	218	45	0.206	0.459	2	1	1	217	olfactory receptor, family 4, subfamily K, member 15	ENST00000305051.5
Case#1-Relapse-WholeTumor	OR4L1	14	20529068	Missense_Mutation	C	A	p.L289M	36	6	0.167	0.370	2	1	1	39	olfactory receptor, family 4, subfamily L, member 1	ENST00000315683.1

Case#1-Relapse-WholeTumor	OR4K17	14	20585661	Missense_Mutation	G	A	p.M32I	150	25	0.167	0.370	2	1	1	106	olfactory receptor, family 4, subfamily K, member 17	ENST00000315543.4
Case#1-Relapse-WholeTumor	OR4K17	14	20586032	Missense_Mutation	C	T	p.A156V	107	21	0.196	0.436	2	1	1	78	olfactory receptor, family 4, subfamily K, member 17	ENST00000315543.4
Case#1-Relapse-WholeTumor	OR11H6	14	20692146	Missense_Mutation	C	T	p.S93F	49	12	0.245	0.544	2	1	1	38	olfactory receptor, family 11, subfamily H, member 6	ENST00000315519.2
Case#1-Relapse-WholeTumor	TOX4	14	21955823	Missense_Mutation	G	A	p.G97R	55	17	0.309	0.687	2	1	1	48	TOX high mobility group box family member 4	ENST00000405508.1
Case#1-Relapse-WholeTumor	ACIN1	14	23562690	Nonsense_Mutation	G	A	p.Q126*	198	41	0.207	0.460	2	1	1	142	apoptotic chromatin condensation inducer 1	ENST00000262710.1
Case#1-Relapse-WholeTumor	MYH6	14	23858841	Missense_Mutation	C	T	p.D1274N	154	30	0.195	0.433	2	1	1	96	myosin, heavy chain 6, cardiac muscle, alpha	ENST00000356287.3
Case#1-Relapse-WholeTumor	MYH6	14	23862245	Missense_Mutation	C	T	p.E1043K	86	16	0.186	0.413	2	1	1	81	myosin, heavy chain 6, cardiac muscle, alpha	ENST00000356287.3
Case#1-Relapse-WholeTumor	MYH7	14	23902319	Missense_Mutation	C	T	p.D107N	151	27	0.179	0.397	2	1	1	122	myosin, heavy chain 7, cardiac muscle, beta	ENST00000355349.3
Case#1-Relapse-WholeTumor	NGDN	14	23946546	Missense_Mutation	G	T	p.G284V	293	53	0.181	0.402	2	1	1	262	neuroguidin, EIF4E binding protein	ENST00000408901.3
Case#1-Relapse-WholeTumor	IRF9	14	24633109	Missense_Mutation	G	A	p.G173E	37	12	0.324	0.721	2	1	1	17	interferon regulatory factor 9	ENST00000396864.3
Case#1-Relapse-WholeTumor	HECTD1	14	31598018	Missense_Mutation	G	A	p.S1520F	70	16	0.229	0.508	2	1	1	41	HECT domain containing E3 ubiquitin protein ligase 1	ENST00000399332.1
Case#1-Relapse-WholeTumor	NPAS3	14	33684576	Missense_Mutation	G	A	p.G110E	114	25	0.219	0.487	2	1	1	98	neuronal PAS domain protein 3	ENST00000356141.4
Case#1-Relapse-WholeTumor	TTC6	14	38218445	Missense_Mutation	G	C	p.D889H	57	13	0.228	0.507	2	1	1	28	tetratricopeptide repeat domain 6	ENST00000553443.1
Case#1-Relapse-WholeTumor	TTC6	14	38311413	Missense_Mutation	C	T	p.R494C	93	14	0.151	0.335	2	1	1	75	tetratricopeptide repeat domain 6	ENST00000476979.1
Case#1-Relapse-WholeTumor	MIA2	14	39717294	Missense_Mutation	C	T	p.P506S	42	11	0.262	0.582	2	1	1	32	melanoma inhibitory activity 2	ENST00000280082.3
Case#1-Relapse-WholeTumor	SOS2	14	50585402	Missense_Mutation	G	A	p.P1220L	164	37	0.226	0.501	2	1	1	130	son of sevenless homolog 2 (Drosophila)	ENST00000216373.5
Case#1-Relapse-WholeTumor	PYGL	14	51379841	Missense_Mutation	C	T	p.G509E	52	18	0.346	0.769	2	1	1	34	phosphorylase, glycogen, liver	ENST00000216392.7
Case#1-Relapse-WholeTumor	PTGDR	14	52734740	Missense_Mutation	G	A	p.V70I	48	10	0.208	0.463	2	1	1	47	prostaglandin D2 receptor (DP)	ENST00000306051.2
Case#1-Relapse-WholeTumor	ERO1L	14	53119962	Missense_Mutation	C	T	p.E294K	106	18	0.170	0.377	2	1	1	82	ERO1-like (S. cerevisiae)	ENST00000395686.3
Case#1-Relapse-WholeTumor	C14orf37	14	58605950	Missense_Mutation	C	T	p.E43K	204	43	0.211	0.468	2	1	1	173	chromosome 14 open reading frame 37	ENST00000267485.7
Case#1-Relapse-WholeTumor	DACT1	14	59113232	Missense_Mutation	G	A	p.G631R	105	23	0.219	0.487	2	1	1	81	dishevelled-binding antagonist of beta-catenin 1	ENST00000335867.4
Case#1-Relapse-WholeTumor	CCDC175	14	60005543	Nonsense_Mutation	C	T	p.W457*	47	10	0.213	0.473	2	1	1	32	coiled-coil domain containing 175	ENST00000537690.2
Case#1-Relapse-WholeTumor	C14orf39	14	60935167	Missense_Mutation	C	T	p.E255K	69	13	0.188	0.419	2	2	0	39	chromosome 14 open reading frame 39	ENST00000321731.3
Case#1-Relapse-WholeTumor	KCNH5	14	63174459	Missense_Mutation	C	T	p.E912K	115	26	0.226	0.502	2	1	1	68	potassium voltage-gated channel, subfamily H (eag-related), member 5	ENST00000322893.7
Case#1-Relapse-WholeTumor	SMOC1	14	70480115	Missense_Mutation	G	A	p.G318E	106	23	0.217	0.482	2	1	1	66	SPARC related modular calcium binding 1	ENST00000381280.4
Case#1-Relapse-WholeTumor	SLC8A3	14	70527657	Splice_Site	C	T		51	12	0.235	0.523	2	1	1	41	solute carrier family 8 (sodium/calcium exchanger), member 3	ENST00000381269.2
Case#1-Relapse-WholeTumor	SLC8A3	14	70634566	Missense_Mutation	C	T	p.G192R	80	23	0.288	0.639	2	1	1	62	solute carrier family 8 (sodium/calcium exchanger), member 3	ENST00000381269.2
Case#1-Relapse-WholeTumor	LTBP2	14	74988722	Missense_Mutation	C	T	p.D894N	96	23	0.240	0.532	2	1	1	54	latent transforming growth factor beta binding protein 2	ENST00000261978.4
Case#1-Relapse-WholeTumor	YLPM1	14	75230659	Missense_Mutation	C	T	p.S156F	159	37	0.233	0.517	2	1	1	114	YLP motif containing 1	ENST00000552421.1
Case#1-Relapse-WholeTumor	TTLL5	14	76173416	Missense_Mutation	C	T	p.P214L	108	25	0.231	0.514	2	1	1	78	tubulin tyrosine ligase-like family, member 5	ENST00000298832.9
Case#1-Relapse-WholeTumor	ESRRB	14	76905755	Missense_Mutation	C	T	p.P20L	84	20	0.238	0.529	2	1	1	57	estrogen-related receptor beta	ENST00000509242.1
Case#1-Relapse-WholeTumor	KCNK10	14	88729793	Missense_Mutation	G	A	p.S47F	146	33	0.226	0.502	2	1	1	118	potassium channel, subfamily K, member 10	ENST00000340700.5
Case#1-Relapse-WholeTumor	FAM181A	14	94395357	Nonsense_Mutation	G	A	p.W304*	68	22	0.324	0.719	2	1	1	57	family with sequence similarity 181, member A	ENST00000267594.5
Case#1-Relapse-WholeTumor	SERPINA9	14	94936174	Missense_Mutation	C	T	p.A2T	43	17	0.395	0.879	2	1	1	32	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 9	ENST00000380365.3
Case#1-Relapse-WholeTumor	TCL1B	14	96152965	Splice_Site	G	A	p.R54K	159	19	0.119	0.266	2	1	1	104	T-cell leukemia/lymphoma 1B	ENST00000340722.7
Case#1-Relapse-WholeTumor	BDKRB2	14	96706787	Missense_Mutation	C	T	p.T41I	88	21	0.239	0.530	2	1	1	56	bradykinin receptor B2	ENST00000306005.3
Case#1-Relapse-WholeTumor	ATG2B	14	96813608	Missense_Mutation	G	A	p.S78F	101	13	0.129	0.286	2	1	1	96	autophagy related 2B	ENST00000359933.4
Case#1-Relapse-WholeTumor	AHNAK2	14	105416564	Missense_Mutation	G	A	p.P1742S	118	30	0.254	0.565	2	1	1	88	AHNAK nucleoprotein 2	ENST00000333244.5
Case#1-Relapse-WholeTumor	NPAP1	15	24922531	Missense_Mutation	C	T	p.S506F	139	62	0.446	0.991	2	2	0	117	nuclear pore associated protein 1	ENST00000329468.2
Case#1-Relapse-WholeTumor	RASGRP1	15	38786858	Missense_Mutation	G	A	p.L662F	72	43	0.597	1.327	2	2	0	61	RAS guanyl releasing protein 1 (calcium and DAG-regulated)	ENST00000310803.5
Case#1-Relapse-WholeTumor	SPG11	15	44955808	Missense_Mutation	G	A	p.A13V	15	6	0.400	0.889	2	2	0	10	spastic paraplegia 11 (autosomal recessive)	ENST00000261866.7
Case#1-Relapse-WholeTumor	C15orf43	15	45270782	Missense_Mutation	G	A	p.E207K	115	40	0.348	0.773	2	2	0	83	chromosome 15 open reading frame 43	ENST00000340827.3
Case#1-Relapse-WholeTumor	FAM227B	15	49833946	Missense_Mutation	C	G	p.E269Q	179	69	0.385	0.857	2	2	0	132	family with sequence similarity 227, member B	ENST00000299338.6
Case#1-Relapse-WholeTumor	TRPM7	15	50903300	Missense_Mutation	G	A	p.S757F	64	21	0.328	0.729	2	2	0	71	transient receptor potential cation channel, subfamily M, member 7	ENST00000313478.7
Case#1-Relapse-WholeTumor	WDR72	15	54025285	Missense_Mutation	G	A	p.T21I	89	25	0.281	0.624	2	2	0	44	WD repeat domain 72	ENST00000396328.1
Case#1-Relapse-WholeTumor	UNC13C	15	54586184	Missense_Mutation	G	A	p.E1304K	113	44	0.389	0.865	2	2	0	96	unc-13 homolog C (C. elegans)	ENST00000260323.11
Case#1-Relapse-WholeTumor	VPS13C	15	62212778	Missense_Mutation	C	T	p.M2377I	82	34	0.415	0.921	2	2	0	59	vacuolar protein sorting 13 homolog C (S. cerevisiae)	ENST00000261517.5
Case#1-Relapse-WholeTumor	DENND4A	15	65983748	Missense_Mutation	C	T	p.E1018K	109	47	0.431	0.958	2	2	0	79	DENN/MADD domain containing 4A	ENST00000431932.2
Case#1-Relapse-WholeTumor	MAP2K1	15	66729162	Missense_Mutation	C	T	p.P124S	165	71	0.430	0.956	2	2	0	144	mitogen-activated protein kinase kinase 1	ENST00000307102.5
Case#1-Relapse-WholeTumor	UBE2Q2	15	76152306	Missense_Mutation	C	T	p.P124S	511	244	0.477	1.061	2	2	0	392	ubiquitin-conjugating enzyme E2Q family member 2	ENST00000267938.4
Case#1-Relapse-WholeTumor	KIAA1024	15	79749651	Missense_Mutation	C	T	p.P388S	103	44	0.427	0.949	2	2	0	99	KIAA1024	ENST00000305428.3
Case#1-Relapse-WholeTumor	RP13-996F3.4	15	83015603	Missense_Mutation	T	C	p.T71A	711	321	0.451	1.003	2	2	0	580		ENST00000557886.1
Case#1-Relapse-WholeTumor	SLCO3A1	15	92459517	Missense_Mutation	G	A	p.E159K	98	48	0.490	1.088	2	2	0	55	solute carrier organic anion transporter family, member 3A1	ENST00000318445.6
Case#1-Relapse-WholeTumor	SLCO3A1	15	92669468	Missense_Mutation	T	C	p.V451A	67	19	0.284	0.630	2	2	0	67	solute carrier organic anion transporter family, member 3A1	ENST00000318445.6
Case#1-Relapse-WholeTumor	RAB11FIP3	16	476583	Missense_Mutation	C	T	p.L193F	33	11	0.333	1.148	1	1	0	25	RAB11 family interacting protein 3 (class II)	ENST00000262305.4
Case#1-Relapse-WholeTumor	TSC2	16	2111962	Nonsense_Mutation	C	T	p.Q404*	154	83	0.539	0.978	3	3	0	124	tuberous sclerosis 2	ENST00000219476.3
Case#1-Relapse-WholeTumor	PKD1	16	2147482	Missense_Mutation	C	T	p.E3415K	219	114	0.521	0.945	3	3	0	135	polycystic kidney disease 1 (autosomal dominant)	ENST00000262304.4
Case#1-Relapse-WholeTumor	TIGD7	16	3349540	Missense_Mutation	C	T	p.D359N	43	26	0.605	1.097	3	3	0	38	tigger transposable element derived 7	ENST00000396862.1
Case#1-Relapse-WholeTumor	CLUAP1	16	3554779	Missense_Mutation	C	T	p.R28C	139	82	0.590	1.071	3	3	0	109	clusterin associated protein 1	ENST00000576634.1
Case#1-Relapse-WholeTumor	ZNF500	16	4802975	Missense_Mutation	C	T	p.R282Q	101	63	0.624	1.132	3	3	0	75	zinc finger protein 500	ENST00000219478.6
Case#1-Relapse-WholeTumor	RBFOX1	16	7759066	Missense_Mutation	G	A	p.R335Q	165	84	0.509	0.924	3	3	0	105	RNA binding protein, fox-1 homolog (C. elegans) 1	ENST00000550418.1
Case#1-Relapse-WholeTumor	ACSM2A	16	20476954	Missense_Mutation	C	T	p.S98L	201	101	0.502	0.912	3	3	0	109	acyl-CoA synthetase medium-chain family member 2A	ENST00000573854.1
Case#1-Relapse-WholeTumor	USP31	16	23116773	Missense_Mutation	G	A	p.P360S	149	60	0.403	0.731	3	2	1	99	ubiquitin specific peptidase 31	ENST00000219689.7
Case#1-Relapse-WholeTumor	SCNN1G	16	23200795	Missense_Mutation	G	A	p.E141K	81	33	0.407	0.739	3	2	1	45	sodium channel, non-voltage-gated 1, gamma subunit	ENST00000300061.2
Case#1-Relapse-WholeTumor	RBBP6	16	24578724	Missense_Mutation	C	T	p.S617L	147	53	0.361	0.654	3	2	1	91	retinoblastoma binding protein 6	ENST00000319715.4
Case#1-Relapse-WholeTumor	NSMCE1	16	27237115	Missense_Mutation	T	C	p.K218R	133	17	0.128	0.232	3	2	1	110	non-SMC element 1 homolog (S. cerevisiae)	ENST00000361439.4
Case#1-Relapse-WholeTumor	KCTD13	16	29918330	Missense_Mutation	CC	TT	p.G285R	54	18	0.333	0.605	3	2	1	53	potassium channel tetramerization domain containing 13	ENST00000568000.1
Case#1-Relapse-WholeTumor	GPR56	16	57685420	Nonsense_Mutation	C	T	p.Q125*	61	21	0.344	0.625	3	2	1	28	G protein-coupled receptor 56	ENST00000388812.4
Case#1-Relapse-WholeTumor	CDH8	16	61687930	Missense_Mutation	C	T	p.R661Q	158	30	0.190	0.345	3	2	1	132	cadherin 8, type 2	ENST00000577390.1
Case#1-Relapse-WholeTumor	CDH8	16	61761117	Splice_Site	TC	AT	p.N473Y	91	31	0.341	0.618	3	2	1	61	cadherin 8, type 2	ENST00000577390.1
Case#1-Relapse-WholeTumor	ELMO3	16	67237233	Missense_Mutation	C	T	p.P631L	57	6	0.105	0.191	3	2	1	41	engulfment and cell motility 3	ENST00000360833.1
Case#1-Relapse-WholeTumor	KCTD19	16	67333336	Missense_Mutation	G	A	p.R306C	92	32	0.348	0.631	3	2	1	56	potassium channel tetramerization domain containing 19	ENST00000304372.5
Case#1-Relapse-WholeTumor	ESRP2	16	68265438	Missense_Mutation	C	T	p.E497K	129	22	0.171	0.310	3	2	1	64	epithelial splicing regulatory protein 2	ENST00000565858.1
Case#1-Relapse-WholeTumor	HYDIN	16	70995904	Missense_Mutation	C	T	p.E1976K	146	60	0.411	0.746	3	2	1	97	HYDIN, axonemal central pair apparatus protein	ENST00000393567.2
Case#1-Relapse-WholeTumor	ZNF23	16	71483009	Missense_Mutation	G	A	p.P307S	209	69	0.330	0.599	3	2	1	126	zinc finger protein 23	ENST00000393539.2
Case#1-Relapse-WholeTumor	ZFHX3	16	72827630	Missense_Mutation	C	G	p.G2984A	230	78	0.339	0.615	3	2	1	121	zinc finger homeobox 3	ENST00000268489.5
Case#1-Relapse-WholeTumor	FA2H	16	74750304	Missense_Mutation	G	A	p.S327F	110	29	0.264	0.478	3	2	1	71	fatty acid 2-hydroxylase	ENST00000219368.3
Case#1-Relapse-WholeTumor	CHST5	16	75563388	Missense_Mutation	C	T	p.A299T	73	15	0.205	0.373	3	2	1	32	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5	ENST00000336257.3
Case#1-Relapse-WholeTumor	CNTNAP4	16	76495889	Missense_Mutation	C	T	p.S460F	121	34	0.281	0.510	3	2	1	93	contactin associated protein-like 4	ENST00000476707.1
Case#1-Relapse-WholeTumor	VAT1L	16	77859352	Missense_Mutation	GG	AA	p.G192S	169	51	0.302	0.548	3	2	1	111	vesicle amine transport 1-like	ENST00000302536.2
Case#1-Relapse-WholeTumor	HSD17B2	16	82101883	Missense_Mutation	G	A	p.R125Q	220	44	0.200	0.363	3	2	1	136	hydroxysteroid (17-beta) dehydrogenase 2	ENST00000199936.4
Case#1-Relapse-WholeTumor	HSD17B2	16	82124611	Missense_Mutation	G	A	p.V257I	170	47	0.276	0.502	3	2	1	114	hydroxysteroid (17-beta) dehydrogenase 2	ENST00000199936.4

Case#1-Relapse-WholeTumor	CDH13	16	83711897	Missense_Mutation	G	A	p.G457S	191	42	0.220	0.399	3	2	1	121	cadherin 13	ENST00000566620.1
Case#1-Relapse-WholeTumor	TLDC1	16	84520527	Missense_Mutation	G	A	p.S223L	45	8	0.178	0.323	3	2	1	31	TBC/LysM-associated domain containing 1	ENST00000343629.6
Case#1-Relapse-WholeTumor	FOXC2	16	86601462	Missense_Mutation	C	T	p.S174F	103	41	0.398	0.722	3	2	1	64	forkhead box C2 (MFH-1, mesenchyme forkhead 1)	ENST00000320354.4
Case#1-Relapse-WholeTumor	ZCCHC14	16	87451194	Missense_Mutation	G	A	p.P282S	152	31	0.204	0.370	3	2	1	111	zinc finger, CCHC domain containing 14	ENST00000268616.4
Case#1-Relapse-WholeTumor	SLC7A5	16	87868107	Missense_Mutation	C	T	p.G461S	122	45	0.369	0.669	3	2	1	76	solute carrier family 7 (amino acid transporter light chain, L system), member 5	ENST00000261622.4
Case#1-Relapse-WholeTumor	CDT1	16	88871204	Missense_Mutation	G	C	p.R129P	137	57	0.416	0.755	3	2	1	81	chromatin licensing and DNA replication factor 1	ENST00000301019.4
Case#1-Relapse-WholeTumor	RNMTL1	17	685854	Missense_Mutation	CC	TT	p.S79F	42	14	0.333	0.741	2	1	1	32	RNA methyltransferase like 1	ENST00000304478.4
Case#1-Relapse-WholeTumor	SLC43A2	17	1494766	Splice_Site	C	T		68	15	0.221	0.490	2	1	1	50	solute carrier family 43 (amino acid system L transporter), member 2	ENST00000301335.5
Case#1-Relapse-WholeTumor	RTN4RL1	17	1840911	Missense_Mutation	G	A	p.L69F	219	54	0.247	0.548	2	1	1	204	reticulon 4 receptor-like 1	ENST00000331238.6
Case#1-Relapse-WholeTumor	SPNS2	17	4436361	Missense_Mutation	G	A	p.R342H	75	18	0.240	0.533	2	1	1	62	spinster homolog 2 (Drosophila)	ENST00000329078.3
Case#1-Relapse-WholeTumor	TM4SF5	17	4685876	Nonsense_Mutation	C	T	p.R113*	117	32	0.274	0.608	2	1	1	80	transmembrane 4 L six family member 5	ENST00000270560.3
Case#1-Relapse-WholeTumor	NLRP1	17	5462175	Missense_Mutation	G	A	p.P614L	93	25	0.269	0.597	2	1	1	70	NLR family, pyrin domain containing 1	ENST00000572272.1
Case#1-Relapse-WholeTumor	C17orf74	17	7329695	Missense_Mutation	C	T	p.R129C	206	49	0.238	0.529	2	1	1	125	chromosome 17 open reading frame 74	ENST00000333870.3
Case#1-Relapse-WholeTumor	ZBTB4	17	7365468	Missense_Mutation	G	A	p.P945S	189	50	0.265	0.588	2	1	1	146	zinc finger and BTB domain containing 4	ENST00000311403.4
Case#1-Relapse-WholeTumor	DNAH2	17	7710806	Missense_Mutation	C	T	p.R3211W	154	33	0.214	0.476	2	1	1	133	dynein, axonemal, heavy chain 2	ENST00000572933.1
Case#1-Relapse-WholeTumor	CHD3	17	7803300	Nonsense_Mutation	G	A	p.W877*	213	47	0.221	0.490	2	1	1	151	chromodomain helicase DNA binding protein 3	ENST00000330494.7
Case#1-Relapse-WholeTumor	MYH13	17	10267715	Missense_Mutation	C	T	p.E45K	174	28	0.161	0.358	2	1	1	164	myosin, heavy chain 13, skeletal muscle	ENST00000418404.3
Case#1-Relapse-WholeTumor	MYH8	17	10309451	Missense_Mutation	C	T	p.R780K	70	19	0.271	0.603	2	1	1	73	myosin, heavy chain 8, skeletal muscle, perinatal	ENST00000403437.2
Case#1-Relapse-WholeTumor	MYH8	17	10318445	Missense_Mutation	C	T	p.D265N	96	18	0.188	0.417	2	1	1	84	myosin, heavy chain 8, skeletal muscle, perinatal	ENST00000403437.2
Case#1-Relapse-WholeTumor	MYH4	17	10356117	Missense_Mutation	C	T	p.E1082K	118	24	0.203	0.452	2	1	1	79	myosin, heavy chain 4, skeletal muscle	ENST00000255381.2
Case#1-Relapse-WholeTumor	MYH2	17	10428903	Missense_Mutation	C	T	p.E1468K	109	26	0.239	0.530	2	1	1	73	myosin, heavy chain 2, skeletal muscle, adult	ENST00000245503.5
Case#1-Relapse-WholeTumor	MYH2	17	10446421	Missense_Mutation	C	T	p.E267K	114	29	0.254	0.565	2	1	1	90	myosin, heavy chain 2, skeletal muscle, adult	ENST00000245503.5
Case#1-Relapse-WholeTumor	MYH3	17	10533685	Missense_Mutation	C	T	p.D1793N	221	37	0.167	0.372	2	1	1	155	myosin, heavy chain 3, skeletal muscle, embryonic	ENST00000583535.1
Case#1-Relapse-WholeTumor	DNAH9	17	11556263	Missense_Mutation	G	A	p.E847K	90	24	0.267	0.593	2	1	1	78	dynein, axonemal, heavy chain 9	ENST00000262442.4
Case#1-Relapse-WholeTumor	DNAH9	17	11772460	Missense_Mutation	G	A	p.E3315K	98	19	0.194	0.431	2	1	1	86	dynein, axonemal, heavy chain 9	ENST00000262442.4
Case#1-Relapse-WholeTumor	FLCN	17	17118576	Missense_Mutation	A	G	p.V452A	65	17	0.262	0.581	2	1	1	45	folliculin	ENST00000285071.4
Case#1-Relapse-WholeTumor	TOM1L2	17	17797066	Missense_Mutation	C	T	p.R92Q	90	18	0.200	0.444	2	1	1	61	target of myb1-like 2 (chicken)	ENST00000379504.3
Case#1-Relapse-WholeTumor	ZNF286B	17	18565291	Missense_Mutation	G	A	p.L510F	328	38	0.116	0.257	2	1	1	255	zinc finger protein 286B	ENST00000545289.1
Case#1-Relapse-WholeTumor	EPN2	17	19189020	Missense_Mutation	C	T	p.P228L	45	7	0.156	0.346	2	1	1	42	epsin 2	ENST00000314728.5
Case#1-Relapse-WholeTumor	RNF112	17	19317435	Missense_Mutation	G	A	p.D285N	54	16	0.296	0.658	2	1	1	37	ring finger protein 112	ENST00000461366.1
Case#1-Relapse-WholeTumor	KIAA0100	17	26969968	Missense_Mutation	A	G	p.V145A	108	32	0.296	0.658	2	1	1	95	KIAA0100	ENST00000528896.2
Case#1-Relapse-WholeTumor	MYO18A	17	27493027	Missense_Mutation	G	A	p.P311L	29	10	0.345	0.766	2	1	1	26	myosin XVIIIA	ENST00000527372.1
Case#1-Relapse-WholeTumor	EFCAB5	17	28295941	Missense_Mutation	C	T	p.S108L	65	15	0.231	0.513	2	1	1	69	EF-hand calcium binding domain 5	ENST00000394835.3
Case#1-Relapse-WholeTumor	NF1	17	29548940	Missense_Mutation	G	A	p.E572K	126	20	0.159	0.353	2	1	1	85	neurofibromin 1	ENST00000358273.4
Case#1-Relapse-WholeTumor	COPRS	17	30180029	Missense_Mutation	G	A	p.P63S	121	24	0.198	0.441	2	1	1	87	coordinator of PRMT5, differentiation stimulator	ENST00000302362.6
Case#1-Relapse-WholeTumor	ZNF207	17	30693762	Missense_Mutation	C	T	p.P287S	89	24	0.270	0.599	2	1	1	67	zinc finger protein 207	ENST00000321233.6
Case#1-Relapse-WholeTumor	CDK5R1	17	30815557	Missense_Mutation	C	T	p.R307W	75	16	0.213	0.474	2	1	1	70	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	ENST00000313401.3
Case#1-Relapse-WholeTumor	CCL13	17	32685133	Missense_Mutation	C	T	p.H94Y	91	21	0.231	0.513	2	1	1	63	chemokine (C-C motif) ligand 13	ENST00000225844.2
Case#1-Relapse-WholeTumor	CCL18	17	34398362	Nonsense_Mutation	G	A	p.W77*	269	69	0.257	0.570	2	1	1	196	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	ENST00000004921.3
Case#1-Relapse-WholeTumor	MYO19	17	34858954	Missense_Mutation	G	A	p.P688L	169	40	0.237	0.526	2	1	1	108	myosin XIX	ENST00000431794.3
Case#1-Relapse-WholeTumor	PCGF2	17	36891693	Missense_Mutation	G	A	p.S273F	129	37	0.287	0.637	2	1	1	98	polycomb group ring finger 2	ENST00000580830.1
Case#1-Relapse-WholeTumor	PSMD3	17	38146126	Missense_Mutation	C	T	p.S274F	87	29	0.333	0.741	2	1	1	62	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	ENST00000264639.4
Case#1-Relapse-WholeTumor	KRT28	17	38956009	Missense_Mutation	G	A	p.S46F	59	8	0.136	0.301	2	1	1	43	keratin 28	ENST00000306658.7
Case#1-Relapse-WholeTumor	TMEM99	17	38990863	Missense_Mutation	C	T	p.S32F	94	20	0.213	0.473	2	1	1	81	transmembrane protein 99	ENST00000301665.3
Case#1-Relapse-WholeTumor	KRTAP9-8	17	39394394	Missense_Mutation	C	T	p.P31S	252	57	0.226	0.503	2	1	1	194	keratin associated protein 9-8	ENST00000254072.6
Case#1-Relapse-WholeTumor	KRTAP29-1	17	39458565	Missense_Mutation	G	A	p.P180L	49	14	0.286	0.635	2	1	1	51	keratin associated protein 29-1	ENST00000391353.1
Case#1-Relapse-WholeTumor	SPATA32	17	43332551	Missense_Mutation	G	A	p.T333I	248	52	0.210	0.466	2	1	1	203	spermatogenesis associated 32	ENST00000331780.4
Case#1-Relapse-WholeTumor	FAM117A	17	47793603	Nonsense_Mutation	G	A	p.R329*	113	37	0.327	0.594	3	2	1	76	family with sequence similarity 117, member A	ENST00000240364.2
Case#1-Relapse-WholeTumor	COL1A1	17	48275324	Missense_Mutation	C	T	p.E210K	121	24	0.198	0.360	3	2	1	72	collagen, type I, alpha 1	ENST00000225964.5
Case#1-Relapse-WholeTumor	PPM1E	17	57057800	Missense_Mutation	C	T	p.S559F	72	17	0.236	0.428	3	2	1	31	protein phosphatase, Mg2+/Mn2+ dependent, 1E	ENST00000308249.2
Case#1-Relapse-WholeTumor	CLTC	17	57746275	Missense_Mutation	C	T	p.P756S	184	63	0.342	0.621	3	2	1	129	clathrin, heavy chain (Hc)	ENST00000269122.3
Case#1-Relapse-WholeTumor	HELZ	17	65124841	Missense_Mutation	G	A	p.P1105S	115	32	0.278	0.505	3	2	1	72	helicase with zinc finger	ENST00000358691.5
Case#1-Relapse-WholeTumor	ABCA8	17	66865889	Missense_Mutation	C	T	p.V1515M	98	20	0.204	0.370	3	2	1	72	ATP-binding cassette, sub-family A (ABC1), member 8	ENST00000269080.2
Case#1-Relapse-WholeTumor	ABCA8	17	66933227	Missense_Mutation	C	T	p.E111K	122	16	0.131	0.238	3	2	1	39	ATP-binding cassette, sub-family A (ABC1), member 8	ENST00000269080.2
Case#1-Relapse-WholeTumor	SDK2	17	71375689	Splice_Site	C	T		126	21	0.167	0.302	3	2	1	81	sidekick cell adhesion molecule 2	ENST00000392650.3
Case#1-Relapse-WholeTumor	KIF19	17	72346896	Missense_Mutation	G	A	p.R480Q	181	59	0.326	0.592	3	2	1	131	kinesin family member 19	ENST00000389916.4
Case#1-Relapse-WholeTumor	GPRC5C	17	72436025	Missense_Mutation	C	T	p.P82L	64	17	0.266	0.482	3	2	1	45	G protein-coupled receptor, class C, group 5, member C	ENST00000481232.1
Case#1-Relapse-WholeTumor	NAT9	17	72771807	Missense_Mutation	C	T	p.G11R	137	40	0.292	0.530	3	2	1	81	N-acetyltransferase 9 (GCN5-related, putative)	ENST00000357814.3
Case#1-Relapse-WholeTumor	OTOP3	17	72931939	Missense_Mutation	G	A	p.G15R	80	24	0.300	0.544	3	2	1	53	otopetrin 3	ENST00000328801.4
Case#1-Relapse-WholeTumor	HID1	17	72958413	Missense_Mutation	G	A	p.S176F	113	17	0.150	0.273	3	2	1	53	HID1 domain containing	ENST00000425042.2
Case#1-Relapse-WholeTumor	ITGB4	17	73732763	Missense_Mutation	G	A	p.E660K	61	9	0.148	0.268	3	2	1	41	integrin, beta 4	ENST00000200181.3
Case#1-Relapse-WholeTumor	SEC14L1	17	75187009	Missense_Mutation	T	G	p.V63G	216	45	0.208	0.378	3	2	1	128	SEC14-like 1 (S. cerevisiae)	ENST00000413679.2
Case#1-Relapse-WholeTumor	DNAH17	17	76449428	Missense_Mutation	C	T	p.G3504E	120	18	0.150	0.272	3	2	1	61	dynein, axonemal, heavy chain 17	ENST00000585328.1
Case#1-Relapse-WholeTumor	DNAH17	17	76472670	Missense_Mutation	G	A	p.T2708I	236	46	0.195	0.354	3	2	1	182	dynein, axonemal, heavy chain 17	ENST00000585328.1
Case#1-Relapse-WholeTumor	GAA	17	78090886	Missense_Mutation	G	A	p.G770D	115	36	0.313	0.568	3	2	1	78	glucosidase, alpha; acid	ENST00000302262.3
Case#1-Relapse-WholeTumor	B3GNTL1	17	80904805	Missense_Mutation	C	T	p.G354S	78	14	0.179	0.326	3	2	1	50	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1	ENST00000320865.3
Case#1-Relapse-WholeTumor	DSC3	18	28588081	Missense_Mutation	C	T	p.E522K	150	35	0.233	0.519	2	1	1	106	desmocollin 3	ENST00000360428.4
Case#1-Relapse-WholeTumor	DSC3	18	28604431	Missense_Mutation	C	T	p.G220E	80	23	0.288	0.639	2	1	1	68	desmocollin 3	ENST00000360428.4
Case#1-Relapse-WholeTumor	CCDC178	18	30992024	Missense_Mutation	G	A	p.S10F	107	18	0.168	0.374	2	1	1	106	coiled-coil domain containing 178	ENST00000383096.3
Case#1-Relapse-WholeTumor	ASXL3	18	31323386	Missense_Mutation	C	T	p.P1192S	91	16	0.176	0.391	2	1	1	61	additional sex combs like transcriptional regulator 3	ENST00000269197.5
Case#1-Relapse-WholeTumor	ASXL3	18	31324221	Missense_Mutation	C	T	p.P1470L	111	22	0.198	0.440	2	1	1	71	additional sex combs like transcriptional regulator 3	ENST00000269197.5
Case#1-Relapse-WholeTumor	DTNA	18	32407618	Missense_Mutation	GG	AA	p.G358K	112	25	0.223	0.496	2	1	1	74	dystrobrevin, alpha	ENST00000399113.3
Case#1-Relapse-WholeTumor	LOXHD1	18	44184156	Missense_Mutation	C	T	p.D266N	66	17	0.258	0.572	2	1	1	38	lipoxygenase homology domains 1	ENST00000441551.2
Case#1-Relapse-WholeTumor	MYO5B	18	47432805	Missense_Mutation	C	T	p.G800R	41	14	0.341	0.759	2	1	1	26	myosin VB	ENST00000285039.7
Case#1-Relapse-WholeTumor	MAPK4	18	48248343	Missense_Mutation	G	A	p.E243K	67	13	0.194	0.431	2	1	1	65	mitogen-activated protein kinase 4	ENST00000400384.2
Case#1-Relapse-WholeTumor	DCC	18	50994327	Missense_Mutation	G	A	p.R1228Q	91	18	0.198	0.440	2	1	1	104	DCC netrin 1 receptor	ENST00000442544.2
Case#1-Relapse-WholeTumor	TCF4	18	52899872	Missense_Mutation	A	G	p.V506A	87	13	0.149	0.332	2	1	1	58	transcription factor 4	ENST00000356073.4
Case#1-Relapse-WholeTumor	ONECUT2	18	55143714	Missense_Mutation	C	T	p.S425F	39	12	0.308	0.684	2	1	1	25	one cut homeobox 2	ENST00000491143.2
Case#1-Relapse-WholeTumor	CDH20	18	59158012	Missense_Mutation	G	A	p.D76N	116	25	0.216	0.479	2	1	1	110	cadherin 20, type 2	ENST00000262717.4
Case#1-Relapse-WholeTumor	ZCCHC2	18	60241464	Missense_Mutation	C	T	p.S717F	121	15	0.124	0.275	2	1	1	119	zinc finger, CCHC domain containing 2	ENST00000269499.5
Case#1-Relapse-WholeTumor	SERPINB4	18	61309074	Missense_Mutation	C	T	p.E91K	232	53	0.228	0.508	2	1	1	209	serpin peptidase inhibitor, clade B (ovalbumin), member 4	ENST00000341074.5

Case#1-Relapse-WholeTumor	SERPINB7	18	61463608	Missense_Mutation	G	A	p.E149K	116	22	0.190	0.421	2	1	1	93	serpin peptidase inhibitor, clade B (ovalbumin), member 7	ENST00000398019.2
Case#1-Relapse-WholeTumor	PLK5	19	1527970	Missense_Mutation	C	T	p.A13V	120	31	0.258	0.574	2	1	1	102	polo-like kinase 5	ENST00000334770.4
Case#1-Relapse-WholeTumor	ZNF77	19	2933951	Missense_Mutation	G	A	p.P392S	159	41	0.258	0.573	2	1	1	108	zinc finger protein 77	ENST00000314531.4
Case#1-Relapse-WholeTumor	ZFR2	19	3810815	Missense_Mutation	A	C	p.V789G	202	33	0.163	0.363	2	1	1	156	zinc finger RNA binding protein 2	ENST00000262961.4
Case#1-Relapse-WholeTumor	LONP1	19	5719866	Missense_Mutation	C	T	p.G93E	27	6	0.222	0.494	2	1	1	25	lon peptidase 1, mitochondrial	ENST00000360614.3
Case#1-Relapse-WholeTumor	CTB-133G6.1	19	7437821	Missense_Mutation	G	A	p.G47R	71	16	0.225	0.501	2	1	1	76		ENST00000576789.1
Case#1-Relapse-WholeTumor	PNPLA6	19	7625627	Missense_Mutation	C	T	p.L1227F	78	19	0.244	0.541	2	1	1	59	patatin-like phospholipase domain containing 6	ENST00000221249.6
Case#1-Relapse-WholeTumor	STXBP2	19	7707219	Splice_Site	G	A	p.R265K	107	23	0.215	0.478	2	1	1	56	syntaxin binding protein 2	ENST00000221283.5
Case#1-Relapse-WholeTumor	ADAMTS10	19	8651078	Missense_Mutation	G	A	p.P863L	73	18	0.247	0.548	2	1	1	79	ADAM metallopeptidase with thrombospondin type 1 motif, 10	ENST00000597188.1
Case#1-Relapse-WholeTumor	ACTL9	19	8808786	Missense_Mutation	G	A	p.S89L	86	21	0.244	0.543	2	1	1	72	actin-like 9	ENST00000324436.3
Case#1-Relapse-WholeTumor	MUC16	19	9012820	Missense_Mutation	G	A	p.P12875L	432	78	0.181	0.401	2	1	1	364	mucin 16, cell surface associated	ENST00000397910.4
Case#1-Relapse-WholeTumor	MUC16	19	9014655	Missense_Mutation	GG	AA	p.R12774C	170	26	0.153	0.340	2	1	1	147	mucin 16, cell surface associated	ENST00000397910.4
Case#1-Relapse-WholeTumor	MUC16	19	9047086	Missense_Mutation	G	C	p.D11515E	187	32	0.171	0.380	2	1	1	157	mucin 16, cell surface associated	ENST00000397910.4
Case#1-Relapse-WholeTumor	MUC16	19	9048674	Missense_Mutation	C	T	p.G10986E	350	83	0.237	0.527	2	1	1	235	mucin 16, cell surface associated	ENST00000397910.4
Case#1-Relapse-WholeTumor	MUC16	19	9049967	Missense_Mutation	C	T	p.R10555K	199	54	0.271	0.603	2	1	1	125	mucin 16, cell surface associated	ENST00000397910.4
Case#1-Relapse-WholeTumor	MUC16	19	9068125	Missense_Mutation	C	T	p.E6441K	134	30	0.224	0.498	2	1	1	81	mucin 16, cell surface associated	ENST00000397910.4
Case#1-Relapse-WholeTumor	MUC16	19	9075553	Missense_Mutation	G	A	p.H3965Y	231	46	0.199	0.443	2	1	1	173	mucin 16, cell surface associated	ENST00000397910.4
Case#1-Relapse-WholeTumor	MUC16	19	9075565	Missense_Mutation	C	T	p.E3961K	223	39	0.175	0.389	2	1	1	168	mucin 16, cell surface associated	ENST00000397910.4
Case#1-Relapse-WholeTumor	MUC16	19	9082946	Missense_Mutation	C	T	p.G2957S	129	40	0.310	0.689	2	1	1	83	mucin 16, cell surface associated	ENST00000397910.4
Case#1-Relapse-WholeTumor	MUC16	19	9089678	Missense_Mutation	C	T	p.D713N	113	21	0.186	0.413	2	1	1	121	mucin 16, cell surface associated	ENST00000397910.4
Case#1-Relapse-WholeTumor	OR7D2	19	9297032	Missense_Mutation	C	T	p.T192I	94	17	0.181	0.402	2	1	1	75	olfactory receptor, family 7, subfamily D, member 2	ENST00000344248.2
Case#1-Relapse-WholeTumor	COL5A3	19	10089885	Missense_Mutation	C	T	p.E933K	63	10	0.159	0.353	2	1	1	55	collagen, type V, alpha 3	ENST00000264828.3
Case#1-Relapse-WholeTumor	PDE4A	19	10570404	Missense_Mutation	C	T	p.T445I	63	22	0.349	0.776	2	1	1	44	phosphodiesterase 4A, cAMP-specific	ENST00000352831.6
Case#1-Relapse-WholeTumor	ZNF763	19	12089022	Nonsense_Mutation	C	T	p.Q95*	247	40	0.162	0.360	2	1	1	181	zinc finger protein 763	ENST00000358987.3
Case#1-Relapse-WholeTumor	ZNF490	19	12692380	Missense_Mutation	G	A	p.S170F	192	46	0.240	0.532	2	1	1	139	zinc finger protein 490	ENST00000311437.6
Case#1-Relapse-WholeTumor	DNAJB1	19	14626756	Missense_Mutation	A	G	p.I340T	98	17	0.173	0.385	2	1	1	83	DnaJ (Hsp40) homolog, subfamily B, member 1	ENST00000254322.2
Case#1-Relapse-WholeTumor	OR7C1	19	14910162	Missense_Mutation	C	T	p.A263T	98	12	0.122	0.272	2	1	1	69	olfactory receptor, family 7, subfamily C, member 1	ENST00000248073.2
Case#1-Relapse-WholeTumor	CYP4F3	19	15769586	Missense_Mutation	C	T	p.P455L	140	32	0.229	0.508	2	1	1	78	cytochrome P450, family 4, subfamily F, polypeptide 3	ENST00000221307.8
Case#1-Relapse-WholeTumor	OR10H1	19	15918210	Missense_Mutation	A	G	p.L213P	265	24	0.091	0.201	2	1	1	220	olfactory receptor, family 10, subfamily H, member 1	ENST00000334920.2
Case#1-Relapse-WholeTumor	CYP4F11	19	16038276	Missense_Mutation	C	T	p.D121N	119	23	0.193	0.430	2	1	1	93	cytochrome P450, family 4, subfamily F, polypeptide 11	ENST00000402119.4
Case#1-Relapse-WholeTumor	CPAMD8	19	17068694	Missense_Mutation	C	T	p.E796K	70	16	0.229	0.508	2	1	1	70	C3 and PZP-like, alpha-2-macroglobulin domain containing 8	ENST00000443236.1
Case#1-Relapse-WholeTumor	CPAMD8	19	17091331	Missense_Mutation	G	A	p.R568C	103	27	0.262	0.583	2	1	1	87	C3 and PZP-like, alpha-2-macroglobulin domain containing 8	ENST00000443236.1
Case#1-Relapse-WholeTumor	UNC13A	19	17763477	Nonsense_Mutation	C	A	p.E468*	76	18	0.237	0.526	2	1	1	66	unc-13 homolog A (C. elegans)	ENST00000519716.2
Case#1-Relapse-WholeTumor	SLC5A5	19	17986906	Missense_Mutation	A	G	p.N230S	57	9	0.158	0.351	2	1	1	59	solute carrier family 5 (sodium/iodide cotransporter), member 5	ENST00000222248.3
Case#1-Relapse-WholeTumor	COMP	19	18899520	Missense_Mutation	C	T	p.G215S	15	5	0.333	0.741	2	1	1	16	cartilage oligomeric matrix protein	ENST00000222271.2
Case#1-Relapse-WholeTumor	UPF1	19	18961604	Missense_Mutation	C	T	p.P246L	108	31	0.287	0.638	2	1	1	82	UPF1 regulator of nonsense transcripts homolog (yeast)	ENST00000599848.1
Case#1-Relapse-WholeTumor	ZNF93	19	20045187	Missense_Mutation	C	T	p.H475Y	61	10	0.164	0.364	2	1	1	38	zinc finger protein 93	ENST00000343769.5
Case#1-Relapse-WholeTumor	ZNF90	19	20216075	Missense_Mutation	G	A	p.G59E	263	43	0.163	0.363	2	1	1	180	zinc finger protein 90	ENST00000418063.2
Case#1-Relapse-WholeTumor	ZNF714	19	21281116	Splice_Site	G	A	p.L14L	204	33	0.162	0.359	2	2	0	141	zinc finger protein 714	ENST00000596143.1
Case#1-Relapse-WholeTumor	ZNF208	19	22156497	Missense_Mutation	G	A	p.H447Y	73	13	0.178	0.396	2	1	1	89	zinc finger protein 208	ENST00000397126.4
Case#1-Relapse-WholeTumor	ZNF729	19	22496823	Missense_Mutation	C	T	p.H202Y	102	20	0.196	0.436	2	1	1	68	zinc finger protein 729	ENST00000601693.1
Case#1-Relapse-WholeTumor	ZNF728	19	23158524	Missense_Mutation	C	T	p.E539K	55	20	0.364	0.808	2	1	1	37	zinc finger protein 728	ENST00000594710.1
Case#1-Relapse-WholeTumor	POP4	19	30106202	Missense_Mutation	C	T	p.S193F	143	30	0.210	0.466	2	2	0	134	processing of precursor 4, ribonuclease P/MRP subunit (S. cerevisiae)	ENST00000585603.1
Case#1-Relapse-WholeTumor	URI1	19	30499976	Missense_Mutation	C	T	p.R251C	108	13	0.120	0.267	2	2	0	68	URI1, prefoldin-like chaperone	ENST00000542441.2
Case#1-Relapse-WholeTumor	KMT2B	19	36211511	Missense_Mutation	C	T	p.S421L	86	18	0.209	0.465	2	1	1	63	lysine (K)-specific methyltransferase 2B	ENST00000222270.7
Case#1-Relapse-WholeTumor	KMT2B	19	36211765	Missense_Mutation	C	T	p.P506S	50	8	0.160	0.356	2	1	1	32	lysine (K)-specific methyltransferase 2B	ENST00000222270.7
Case#1-Relapse-WholeTumor	WDR62	19	36592574	Missense_Mutation	G	C	p.E994Q	52	9	0.173	0.385	2	1	1	44	WD repeat domain 62	ENST00000270301.7
Case#1-Relapse-WholeTumor	ZNF382	19	37117458	Missense_Mutation	C	T	p.S220F	47	13	0.277	0.615	2	1	1	33	zinc finger protein 382	ENST00000292928.2
Case#1-Relapse-WholeTumor	ZNF527	19	37879964	Missense_Mutation	C	T	p.A338V	113	20	0.177	0.393	2	1	1	93	zinc finger protein 527	ENST00000436120.2
Case#1-Relapse-WholeTumor	WDR87	19	38379452	Missense_Mutation	C	T	p.R1581Q	255	36	0.141	0.314	2	1	1	212	WD repeat domain 87	ENST00000303868.5
Case#1-Relapse-WholeTumor	WDR87	19	38380329	Missense_Mutation	C	T	p.E1289K	68	12	0.176	0.392	2	1	1	67	WD repeat domain 87	ENST00000303868.5
Case#1-Relapse-WholeTumor	WDR87	19	38382235	Missense_Mutation	GG	AA	p.P1078L	165	29	0.176	0.391	2	1	1	104	WD repeat domain 87	ENST00000303868.5
Case#1-Relapse-WholeTumor	WDR87	19	38385303	Missense_Mutation	G	A	p.S308F	77	10	0.130	0.289	2	1	1	46	WD repeat domain 87	ENST00000303868.5
Case#1-Relapse-WholeTumor	RYR1	19	39051805	Missense_Mutation	C	T	p.S4112L	86	16	0.186	0.413	2	1	1	60	ryanodine receptor 1 (skeletal)	ENST00000359596.3
Case#1-Relapse-WholeTumor	RINL	19	39364598	Nonsense_Mutation	G	A	p.Q81*	48	7	0.146	0.324	2	1	1	46	Ras and Rab interactor-like	ENST00000591812.1
Case#1-Relapse-WholeTumor	FCGBP	19	40408433	Missense_Mutation	C	T	p.G1469E	173	26	0.150	0.334	2	1	1	141	Fc fragment of IgG binding protein	ENST00000221347.6
Case#1-Relapse-WholeTumor	CYP2A7	19	41387569	Missense_Mutation	C	T	p.A90T	120	36	0.300	0.667	2	1	1	80	cytochrome P450, family 2, subfamily A, polypeptide 7	ENST00000301146.4
Case#1-Relapse-WholeTumor	PSG6	19	43414930	Missense_Mutation	G	A	p.P170S	355	67	0.189	0.419	2	1	1	271	pregnancy specific beta-1-glycoprotein 6	ENST00000292125.2
Case#1-Relapse-WholeTumor	PSG9	19	43762572	Missense_Mutation	G	A	p.T342I	341	71	0.208	0.717	1	1	0	243	pregnancy specific beta-1-glycoprotein 9	ENST00000270077.3
Case#1-Relapse-WholeTumor	ZNF112	19	44832836	Missense_Mutation	G	A	p.P498S	82	14	0.171	0.379	2	1	1	72	zinc finger protein 112	ENST00000337401.4
Case#1-Relapse-WholeTumor	ZNF112	19	44833021	Missense_Mutation	A	G	p.V436A	46	10	0.217	0.483	2	1	1	40	zinc finger protein 112	ENST00000337401.4
Case#1-Relapse-WholeTumor	KLC3	19	45849897	Nonsense_Mutation	G	A	p.W118*	34	9	0.265	0.588	2	1	1	29	kinesin light chain 3	ENST00000391946.2
Case#1-Relapse-WholeTumor	FOSB	19	45974142	Missense_Mutation	A	T	p.T128S	66	15	0.227	0.505	2	1	1	58	FBJ murine osteosarcoma viral oncogene homolog B	ENST00000353609.3
Case#1-Relapse-WholeTumor	AC074212.3	19	46257749	Missense_Mutation	G	A	p.R190Q	67	18	0.269	0.597	2	1	1	51		ENST00000457052.2
Case#1-Relapse-WholeTumor	AC074212.3	19	46257839	Missense_Mutation	G	A	p.G220E	113	23	0.204	0.452	2	1	1	90		ENST00000457052.2
Case#1-Relapse-WholeTumor	SLC8A2	19	47941229	Splice_Site	C	T	p.G629G	59	13	0.220	0.490	2	1	1	59	solute carrier family 8 (sodium/calcium exchanger), member 2	ENST00000236877.6
Case#1-Relapse-WholeTumor	SLC17A7	19	49940011	Missense_Mutation	G	A	p.A37V	49	9	0.184	0.408	2	1	1	31	solute carrier family 17 (vesicular glutamate transporter), member 7	ENST00000221485.3
Case#1-Relapse-WholeTumor	MYH14	19	50775127	Missense_Mutation	C	T	p.R1024C	73	12	0.164	0.365	2	1	1	61	myosin, heavy chain 14, non-muscle	ENST00000596571.1
Case#1-Relapse-WholeTumor	MYBPC2	19	50939918	Missense_Mutation	CC	TA	p.R131S	71	9	0.127	0.282	2	1	1	87	myosin binding protein C, fast type	ENST00000357701.5
Case#1-Relapse-WholeTumor	KLK2	19	51380002	Missense_Mutation	G	A	p.E161K	71	13	0.183	0.407	2	1	1	63	kallikrein-related peptidase 2	ENST00000325321.3
Case#1-Relapse-WholeTumor	CTD-2616J11.4	19	51892732	Missense_Mutation	C	T	p.E23K	52	6	0.115	0.256	2	1	1	49		ENST00000574814.1
Case#1-Relapse-WholeTumor	SIGLEC8	19	51958757	Missense_Mutation	A	C	p.D322E	74	16	0.216	0.480	2	1	1	51	sialic acid binding Ig-like lectin 8	ENST00000321424.3
Case#1-Relapse-WholeTumor	SIGLEC6	19	52023425	Missense_Mutation	GG	TA	p.H425N	163	37	0.227	0.504	2	1	1	103	sialic acid binding Ig-like lectin 6	ENST00000425629.3
Case#1-Relapse-WholeTumor	ZNF528	19	52919060	Missense_Mutation	C	T	p.H319Y	116	16	0.138	0.307	2	1	1	86	zinc finger protein 528	ENST00000360465.3
Case#1-Relapse-WholeTumor	ZNF534	19	52941990	Missense_Mutation	C	T	p.T439I	137	25	0.182	0.406	2	1	1	111	zinc finger protein 534	ENST00000332323.6
Case#1-Relapse-WholeTumor	NLRP12	19	54327170	Missense_Mutation	C	T	p.E87K	87	18	0.207	0.460	2	1	1	107	NLR family, pyrin domain containing 12	ENST00000324134.6
Case#1-Relapse-WholeTumor	TARM1	19	54578294	Missense_Mutation	C	T	p.R48Q	67	9	0.134	0.299	2	1	1	41	T cell-interacting, activating receptor on myeloid cells 1	ENST00000432826.1
Case#1-Relapse-WholeTumor	LILRB2	19	54781428	Missense_Mutation	G	A	p.P446S	49	13	0.265	0.590	2	1	1	37	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2	ENST00000391749.4
Case#1-Relapse-WholeTumor	LILRB2	19	54783274	Missense_Mutation	C	T	p.R195K	209	53	0.254	0.564	2	1	1	162	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2	ENST00000391749.4
Case#1-Relapse-WholeTumor	NLRP7	19	55450454	Missense_Mutation	G	A	p.S578F	104	26	0.250	0.556	2	1	1	100	NLR family, pyrin domain containing 7	ENST00000590030.1
Case#1-Relapse-WholeTumor	PTPRH	19	55716732	Missense_Mutation	C	T	p.G194E	249	42	0.169	0.375	2	1	1	194	protein tyrosine phosphatase, receptor type, H	ENST00000376350.3

Case#1-Relapse-WholeTumor	EPN1	19	56200664	Splice_Site	C	T	p.P202L	101	26	0.257	0.572	2	1	1	75	epsin 1	ENST00000270460.6
Case#1-Relapse-WholeTumor	NLRP8	19	56490812	Missense_Mutation	C	T	p.L977F	117	20	0.171	0.380	2	1	1	71	NLR family, pyrin domain containing 8	ENST00000291971.3
Case#1-Relapse-WholeTumor	NLRP8	19	56499244	Missense_Mutation	G	A	p.G1038R	114	34	0.298	0.663	2	1	1	93	NLR family, pyrin domain containing 8	ENST00000291971.3
Case#1-Relapse-WholeTumor	USP29	19	57640501	Missense_Mutation	C	T	p.S153L	49	11	0.224	0.499	2	1	1	65	ubiquitin specific peptidase 29	ENST00000254181.4
Case#1-Relapse-WholeTumor	USP29	19	57640723	Missense_Mutation	C	T	p.S227L	50	12	0.240	0.533	2	1	1	40	ubiquitin specific peptidase 29	ENST00000254181.4
Case#1-Relapse-WholeTumor	USP29	19	57641208	Missense_Mutation	G	A	p.E389K	65	9	0.138	0.308	2	1	1	42	ubiquitin specific peptidase 29	ENST00000254181.4
Case#1-Relapse-WholeTumor	USP29	19	57642499	Missense_Mutation	C	T	p.P819L	105	26	0.248	0.550	2	1	1	74	ubiquitin specific peptidase 29	ENST00000254181.4
Case#1-Relapse-WholeTumor	ZNF418	19	58438869	Missense_Mutation	C	T	p.R227K	213	50	0.235	0.522	2	1	1	172	zinc finger protein 418	ENST00000396147.1
Case#1-Relapse-WholeTumor	ALLC	2	3743414	Frame_Shift_Del	TG	-	p.W207fs	150	27	0.180	0.400	2	1	1	127	allantoicase	ENST00000252505.3
Case#1-Relapse-WholeTumor	KIDINS220	2	8870915	Missense_Mutation	C	T	p.E1751K	185	55	0.297	0.661	2	1	1	121	kinase D-interacting substrate, 220kDa	ENST00000256707.3
Case#1-Relapse-WholeTumor	KCNS3	2	18112971	Nonsense_Mutation	G	A	p.W232*	86	18	0.209	0.465	2	1	1	64	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	ENST00000403915.1
Case#1-Relapse-WholeTumor	MFSD2B	2	24236215	Missense_Mutation	C	T	p.P53S	100	25	0.250	0.556	2	1	1	86	major facilitator superfamily domain containing 2B	ENST00000406420.3
Case#1-Relapse-WholeTumor	C2orf71	2	29294142	Missense_Mutation	G	A	p.P996S	86	14	0.163	0.362	2	1	1	58	chromosome 2 open reading frame 71	ENST00000331664.5
Case#1-Relapse-WholeTumor	VIT	2	37000987	Missense_Mutation	C	T	p.P245S	92	21	0.228	0.507	2	1	1	75	vitrin	ENST00000389975.3
Case#1-Relapse-WholeTumor	SLC8A1	2	40397451	Missense_Mutation	G	A	p.P670S	99	24	0.242	0.539	2	1	1	70	solute carrier family 8 (sodium/calcium exchanger), member 1	ENST00000403092.1
Case#1-Relapse-WholeTumor	PKDCC	2	42281304	Missense_Mutation	T	G	p.D297E	92	21	0.228	0.507	2	1	1	80	protein kinase domain containing, cytoplasmic	ENST00000294964.5
Case#1-Relapse-WholeTumor	SOCS5	2	46985901	Nonsense_Mutation	A	T	p.R78*	77	21	0.273	0.606	2	1	1	61	suppressor of cytokine signaling 5	ENST00000306503.5
Case#1-Relapse-WholeTumor	FSHR	2	49210079	Missense_Mutation	A	C	p.F214V	83	17	0.205	0.455	2	1	1	71	follicle stimulating hormone receptor	ENST00000406846.2
Case#1-Relapse-WholeTumor	PUS10	2	61235910	Missense_Mutation	C	G	p.D123H	63	16	0.254	0.564	2	1	1	48	pseudouridylate synthase 10	ENST00000316752.6
Case#1-Relapse-WholeTumor	C2orf74	2	61391520	Missense_Mutation	T	C	p.V148A	102	7	0.069	0.153	2	1	1	75	chromosome 2 open reading frame 74	ENST00000432605.1
Case#1-Relapse-WholeTumor	TIA1	2	70457971	Missense_Mutation	G	A	p.P47S	132	30	0.227	0.505	2	1	1	100	TIA1 cytotoxic granule-associated RNA binding protein	ENST00000433529.2
Case#1-Relapse-WholeTumor	MOGS	2	74689363	Missense_Mutation	G	A	p.P518L	155	37	0.239	0.530	2	1	1	130	mannosyl-oligosaccharide glucosidase	ENST00000233616.4
Case#1-Relapse-WholeTumor	M1AP	2	74842208	Missense_Mutation	CC	TT	p.G103E	60	10	0.167	0.370	2	1	1	56	meiosis 1 associated protein	ENST00000290536.5
Case#1-Relapse-WholeTumor	LRRTM4	2	77745733	Missense_Mutation	G	A	p.S421L	107	29	0.271	0.602	2	1	1	96	leucine rich repeat transmembrane neuronal 4	ENST00000409093.1
Case#1-Relapse-WholeTumor	CTNNA2	2	80874951	Missense_Mutation	C	T	p.S939L	46	10	0.217	0.483	2	1	1	50	catenin (cadherin-associated protein), alpha 2	ENST00000402739.4
Case#1-Relapse-WholeTumor	DNAH6	2	84880610	Missense_Mutation	T	G	p.V1749G	170	12	0.071	0.157	2	1	1	90	dynein, axonemal, heavy chain 6	ENST00000237449.6
Case#1-Relapse-WholeTumor	DNAH6	2	84896614	Missense_Mutation	G	A	p.G2096R	153	46	0.301	0.668	2	1	1	107	dynein, axonemal, heavy chain 6	ENST00000237449.6
Case#1-Relapse-WholeTumor	KCMF1	2	85255039	Missense_Mutation	G	A	p.G15E	114	22	0.193	0.429	2	1	1	89	potassium channel modulatory factor 1	ENST00000409785.4
Case#1-Relapse-WholeTumor	REEP1	2	86459757	Missense_Mutation	T	C	p.S196G	146	34	0.233	0.518	2	1	1	102	receptor accessory protein 1	ENST00000165698.5
Case#1-Relapse-WholeTumor	KRCC1	2	88327571	Missense_Mutation	G	A	p.S171L	90	22	0.244	0.543	2	1	1	43	lysine-rich coiled-coil 1	ENST00000347055.3
Case#1-Relapse-WholeTumor	PROM2	2	95951436	Missense_Mutation	T	A	p.L642Q	49	9	0.184	0.408	2	1	1	70	prominin 2	ENST00000317620.9
Case#1-Relapse-WholeTumor	CNGA3	2	99013039	Missense_Mutation	C	T	p.A469V	60	13	0.217	0.481	2	1	1	59	cyclic nucleotide gated channel alpha 3	ENST00000272602.2
Case#1-Relapse-WholeTumor	EIF5B	2	99980828	Missense_Mutation	C	T	p.S411F	51	12	0.235	0.523	2	1	1	36	eukaryotic translation initiation factor 5B	ENST00000289371.6
Case#1-Relapse-WholeTumor	AFF3	2	100203616	Splice_Site	C	T	p.S864N	214	47	0.220	0.488	2	1	1	168	AF4/FMR2 family, member 3	ENST00000409236.2
Case#1-Relapse-WholeTumor	ZC3H6	2	113080319	Missense_Mutation	C	T	p.P394S	105	26	0.248	0.550	2	1	1	77	zinc finger CCCH-type containing 6	ENST00000409871.1
Case#1-Relapse-WholeTumor	POLR1B	2	113308515	Missense_Mutation	C	T	p.T233I	229	48	0.210	0.466	2	1	1	132	polymerase (RNA) I polypeptide B, 128kDa	ENST00000263331.5
Case#1-Relapse-WholeTumor	IL1A	2	113539352	Nonsense_Mutation	G	A	p.Q50*	110	29	0.264	0.586	2	1	1	87	interleukin 1, alpha	ENST00000263339.3
Case#1-Relapse-WholeTumor	IL36B	2	113783785	Missense_Mutation	C	T	p.G96R	139	27	0.194	0.432	2	1	1	115	interleukin 36, beta	ENST00000259213.4
Case#1-Relapse-WholeTumor	TFCP2L1	2	121991768	Missense_Mutation	T	A	p.N366I	82	19	0.232	0.515	2	1	1	98	transcription factor CP2-like 1	ENST00000263707.5
Case#1-Relapse-WholeTumor	POTEF	2	130878027	Missense_Mutation	C	T	p.R21K	456	106	0.232	0.517	2	1	1	342	POTE ankyrin domain family, member F	ENST00000409914.2
Case#1-Relapse-WholeTumor	THSD7B	2	137814764	Missense_Mutation	C	T	p.S305L	77	21	0.273	0.606	2	1	1	88	thrombospondin, type I, domain containing 7B	ENST00000409968.1
Case#1-Relapse-WholeTumor	THSD7B	2	137990472	Missense_Mutation	G	A	p.G640E	146	36	0.247	0.548	2	1	1	139	thrombospondin, type I, domain containing 7B	ENST00000409968.1
Case#1-Relapse-WholeTumor	LRP1B	2	141202236	Missense_Mutation	C	G	p.C3357S	87	16	0.184	0.409	2	1	1	54	low density lipoprotein receptor-related protein 1B	ENST00000389484.3
Case#1-Relapse-WholeTumor	LRP1B	2	141473542	Splice_Site	C	A	p.G2008V	128	32	0.250	0.556	2	1	1	100	low density lipoprotein receptor-related protein 1B	ENST00000389484.3
Case#1-Relapse-WholeTumor	KYNU	2	143798132	Missense_Mutation	CC	TT	p.P393L	113	18	0.159	0.289	3	2	1	95	kynureninase	ENST00000264170.4
Case#1-Relapse-WholeTumor	NEB	2	152418675	Nonsense_Mutation	C	T	p.W4614*	198	46	0.232	0.422	3	2	1	126	nebulin	ENST00000172853.10
Case#1-Relapse-WholeTumor	NEB	2	152510597	Missense_Mutation	C	T	p.G2275E	129	29	0.225	0.408	3	2	1	70	nebulin	ENST00000172853.10
Case#1-Relapse-WholeTumor	GALNT5	2	158157341	Nonsense_Mutation	A	T	p.K757*	222	65	0.293	0.531	3	2	1	150	polypeptide N-acetylgalactosaminyltransferase 5	ENST00000259056.4
Case#1-Relapse-WholeTumor	PKP4	2	159533266	Missense_Mutation	C	T	p.S1048F	201	37	0.184	0.334	3	2	1	138	plakophilin 4	ENST00000389759.3
Case#1-Relapse-WholeTumor	ITGB6	2	160994079	Missense_Mutation	G	A	p.P509L	104	17	0.163	0.297	3	2	1	68	integrin, beta 6	ENST00000283249.2
Case#1-Relapse-WholeTumor	DPP4	2	162862292	Missense_Mutation	C	T	p.G672D	140	28	0.200	0.363	3	2	1	96	dipeptidyl-peptidase 4	ENST00000360534.3
Case#1-Relapse-WholeTumor	XIRP2	2	168114647	Missense_Mutation	G	A	p.E564K	36	5	0.139	0.252	3	2	1	33	xin actin-binding repeat containing 2	ENST00000409728.1
Case#1-Relapse-WholeTumor	LRP2	2	170129549	Missense_Mutation	CC	TT	p.G668E	123	50	0.407	0.738	3	2	1	84	low density lipoprotein receptor-related protein 2	ENST00000263816.3
Case#1-Relapse-WholeTumor	MYO3B	2	171055731	Missense_Mutation	G	A	p.G6R	79	18	0.228	0.414	3	2	1	66	myosin IIIB	ENST00000408978.4
Case#1-Relapse-WholeTumor	MYO3B	2	171070986	Missense_Mutation	C	T	p.A140V	120	16	0.133	0.242	3	2	1	76	myosin IIIB	ENST00000408978.4
Case#1-Relapse-WholeTumor	MYO3B	2	171323038	Missense_Mutation	C	T	p.S944F	90	40	0.444	0.807	3	2	1	58	myosin IIIB	ENST00000408978.4
Case#1-Relapse-WholeTumor	HOXD3	2	177034063	Frame_Shift_Del	C	-	p.A74fs	93	13	0.140	0.254	3	2	1	60	homeobox D3	ENST00000468418.3
Case#1-Relapse-WholeTumor	TTN	2	179418008	Nonsense_Mutation	C	T	p.W28232*	204	79	0.387	0.703	3	2	1	140	titin	ENST00000591111.1
Case#1-Relapse-WholeTumor	TTN	2	179418782	Missense_Mutation	C	T	p.E28045K	68	20	0.294	0.534	3	2	1	58	titin	ENST00000591111.1
Case#1-Relapse-WholeTumor	TTN	2	179425447	Missense_Mutation	G	A	p.S26830F	173	67	0.387	0.703	3	2	1	99	titin	ENST00000591111.1
Case#1-Relapse-WholeTumor	TTN	2	179439437	Missense_Mutation	C	T	p.G22167R	101	37	0.366	0.665	3	2	1	65	titin	ENST00000591111.1
Case#1-Relapse-WholeTumor	TTN	2	179444336	Missense_Mutation	C	T	p.G20889R	51	15	0.294	0.534	3	2	1	35	titin	ENST00000591111.1
Case#1-Relapse-WholeTumor	TTN	2	179452426	Missense_Mutation	G	A	p.P19563S	138	48	0.348	0.631	3	2	1	74	titin	ENST00000591111.1
Case#1-Relapse-WholeTumor	TTN	2	179457945	Missense_Mutation	C	T	p.D18023N	133	38	0.286	0.519	3	2	1	76	titin	ENST00000591111.1
Case#1-Relapse-WholeTumor	TTN	2	179497466	Missense_Mutation	C	T	p.D12782N	50	19	0.380	0.690	3	2	1	39	titin	ENST00000591111.1
Case#1-Relapse-WholeTumor	TTN	2	179536794	Missense_Mutation	C	T	p.E11337K	108	37	0.343	0.622	3	2	1	50	titin	ENST00000591111.1
Case#1-Relapse-WholeTumor	TTN	2	179595352	Missense_Mutation	G	A	p.H5653Y	59	6	0.102	0.185	3	2	1	45	titin	ENST00000591111.1
Case#1-Relapse-WholeTumor	TTN	2	179606079	Missense_Mutation	C	T	p.V3644M	108	25	0.231	0.420	3	2	1	60	titin	ENST00000591111.1
Case#1-Relapse-WholeTumor	CWC22	2	180837922	Missense_Mutation	C	T	p.V268M	97	7	0.072	0.131	3	2	1	67	CWC22 spliceosome-associated protein	ENST00000410053.3
Case#1-Relapse-WholeTumor	CWC22	2	180851449	Missense_Mutation	C	G	p.R60P	113	26	0.230	0.418	3	2	1	59	CWC22 spliceosome-associated protein	ENST00000410053.3
Case#1-Relapse-WholeTumor	COL3A1	2	189859537	Missense_Mutation	C	T	p.P479S	92	15	0.163	0.296	3	2	1	67	collagen, type III, alpha 1	ENST00000304636.3
Case#1-Relapse-WholeTumor	COL3A1	2	189862099	Missense_Mutation	G	A	p.G618E	141	43	0.305	0.553	3	2	1	105	collagen, type III, alpha 1	ENST00000304636.3
Case#1-Relapse-WholeTumor	COL5A2	2	189929752	Missense_Mutation	G	A	p.S532F	213	75	0.352	0.639	3	2	1	124	collagen, type V, alpha 2	ENST00000374866.3
Case#1-Relapse-WholeTumor	STAT4	2	191923476	Missense_Mutation	C	T	p.E352K	149	62	0.416	0.755	3	2	1	72	signal transducer and activator of transcription 4	ENST00000392320.2
Case#1-Relapse-WholeTumor	DNAH7	2	196681377	Missense_Mutation	C	T	p.E3246K	57	19	0.333	0.605	3	2	1	46	dynein, axonemal, heavy chain 7	ENST00000312428.6
Case#1-Relapse-WholeTumor	DNAH7	2	196681451	Missense_Mutation	G	A	p.A3221V	113	22	0.195	0.353	3	2	1	68	dynein, axonemal, heavy chain 7	ENST00000312428.6
Case#1-Relapse-WholeTumor	DNAH7	2	196681481	Missense_Mutation	G	A	p.S3211F	140	46	0.329	0.596	3	2	1	66	dynein, axonemal, heavy chain 7	ENST00000312428.6
Case#1-Relapse-WholeTumor	DNAH7	2	196788411	Missense_Mutation	G	A	p.H1245Y	61	10	0.164	0.298	3	2	1	38	dynein, axonemal, heavy chain 7	ENST00000312428.6
Case#1-Relapse-WholeTumor	DNAH7	2	196799425	Missense_Mutation	C	T	p.E1121K	172	43	0.250	0.454	3	2	1	103	dynein, axonemal, heavy chain 7	ENST00000312428.6
Case#1-Relapse-WholeTumor	HECW2	2	197184134	Missense_Mutation	C	T	p.A494T	38	9	0.237	0.430	3	2	1	25	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	ENST00000260983.3
Case#1-Relapse-WholeTumor	PLCL1	2	198948758	Missense_Mutation	G	A	p.E173K	106	15	0.142	0.257	3	2	1	68	phospholipase C-like 1	ENST00000428675.1
Case#1-Relapse-WholeTumor	AOX1	2	201470309	Missense_Mutation	G	A	p.D289N	181	63	0.348	0.632	3	2	1	119	aldehyde oxidase 1	ENST00000374700.2
Case#1-Relapse-WholeTumor	ADAM23	2	207474705	Missense_Mutation	G	A	p.G811S	71	25	0.352	0.639	3	2	1	46	ADAM metallopeptidase domain 23	ENST00000264377.3
Case#1-Relapse-WholeTumor	DYTN	2	207527804	Missense_Mutation	C	T	p.G486R	103	38	0.369	0.670	3	2	1	52	dystrotelin	ENST00000452335.2

Case#1-Relapse-WholeTumor	CRYGD	2	208989066	Missense_Mutation	C	T	p.E8K	291	97	0.333	0.605	3	2	1	209	crystallin, gamma D	ENST00000264376.4
Case#1-Relapse-WholeTumor	PTH2R	2	209324660	Missense_Mutation	CA	AG	p.Q319R	119	37	0.311	0.564	3	2	1	71	parathyroid hormone 2 receptor	ENST00000272847.2
Case#1-Relapse-WholeTumor	ERBB4	2	212570116	Splice_Site	C	T	p.G375G	261	33	0.126	0.229	3	2	1	159	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 4	ENST00000342788.4
Case#1-Relapse-WholeTumor	ACSL3	2	223795362	Missense_Mutation	C	T	p.P522S	161	54	0.335	0.609	3	2	1	111	acyl-CoA synthetase long-chain family member 3	ENST00000357430.3
Case#1-Relapse-WholeTumor	DOCK10	2	225761034	Missense_Mutation	C	T	p.G132R	104	32	0.308	0.558	3	2	1	63	dedicator of cytokinesis 10	ENST00000258390.7
Case#1-Relapse-WholeTumor	NYAP2	2	226446872	Missense_Mutation	G	A	p.E247K	103	32	0.311	0.564	3	2	1	67	neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adaptor 2	ENST00000272907.6
Case#1-Relapse-WholeTumor	COL4A4	2	227896939	Missense_Mutation	C	T	p.E1211K	60	11	0.183	0.333	3	2	1	43	collagen, type IV, alpha 4	ENST00000396625.3
Case#1-Relapse-WholeTumor	COL4A3	2	228104892	Missense_Mutation	C	T	p.P60S	90	24	0.267	0.484	3	2	1	58	collagen, type IV, alpha 3 (Goodpasture antigen)	ENST00000396578.3
Case#1-Relapse-WholeTumor	COL4A3	2	228154778	Missense_Mutation	G	A	p.G1015E	100	38	0.380	0.690	3	2	1	72	collagen, type IV, alpha 3 (Goodpasture antigen)	ENST00000396578.3
Case#1-Relapse-WholeTumor	PID1	2	229890516	Missense_Mutation	C	T	p.M195I	142	43	0.303	0.550	3	2	1	88	phosphotyrosine interaction domain containing 1	ENST00000354069.6
Case#1-Relapse-WholeTumor	SP140L	2	231223823	Missense_Mutation	C	T	p.H139Y	135	43	0.319	0.578	3	2	1	60	SP140 nuclear body protein-like	ENST00000415673.2
Case#1-Relapse-WholeTumor	SP100	2	231375877	Missense_Mutation	C	T	p.P697L	203	35	0.172	0.313	3	2	1	130	SP100 nuclear antigen	ENST00000264052.5
Case#1-Relapse-WholeTumor	GPR55	2	231775346	Missense_Mutation	G	A	p.T111I	121	47	0.388	0.705	3	2	1	76	G protein-coupled receptor 55	ENST00000392040.1
Case#1-Relapse-WholeTumor	INPP5D	2	234077959	Missense_Mutation	G	A	p.G510R	133	21	0.158	0.287	3	2	1	66	inositol polyphosphate-5-phosphatase, 145kDa	ENST00000359570.5
Case#1-Relapse-WholeTumor	MROH2A	2	234720599	Missense_Mutation	A	C	p.H882P	81	34	0.420	0.762	3	2	1	70	maestro heat-like repeat family member 2A	ENST00000389758.3
Case#1-Relapse-WholeTumor	ACKR3	2	237489127	Missense_Mutation	G	A	p.D7N	118	21	0.178	0.323	3	2	1	83	atypical chemokine receptor 3	ENST00000272928.3
Case#1-Relapse-WholeTumor	COL6A3	2	238283600	Missense_Mutation	G	A	p.P1045L	88	34	0.386	0.701	3	2	1	52	collagen, type VI, alpha 3	ENST00000295550.4
Case#1-Relapse-WholeTumor	ESPNL	2	239033910	Splice_Site	G	A		174	30	0.172	0.313	3	2	1	103	espin-like	ENST00000343063.3
Case#1-Relapse-WholeTumor	PER2	2	239155102	Missense_Mutation	G	A	p.P1228S	122	15	0.123	0.223	3	2	1	74	period circadian clock 2	ENST00000254657.3
Case#1-Relapse-WholeTumor	AQP12A	2	241631640	Missense_Mutation	G	A	p.M91I	203	42	0.207	0.375	3	2	1	106	aquaporin 12A	ENST00000337801.4
Case#1-Relapse-WholeTumor	SNED1	2	242003009	Missense_Mutation	G	A	p.D793N	104	16	0.154	0.279	3	2	1	70	sushi, nidogen and EGF-like domains 1	ENST00000310397.8
Case#1-Relapse-WholeTumor	PASK	2	242046876	Missense_Mutation	G	A	p.P1236S	137	25	0.182	0.331	3	2	1	94	PAS domain containing serine/threonine kinase	ENST00000405260.1
Case#1-Relapse-WholeTumor	NSFL1C	20	1424492	Missense_Mutation	G	A	p.L339F	72	14	0.194	0.432	2	1	1	64	NSFL1 (p97) cofactor (p47)	ENST00000216879.4
Case#1-Relapse-WholeTumor	CHGB	20	5903289	Missense_Mutation	G	A	p.E167K	44	11	0.250	0.556	2	1	1	27	chromogranin B (secretogranin 1)	ENST00000378961.4
Case#1-Relapse-WholeTumor	PAK7	20	9538323	Missense_Mutation	G	A	p.L559F	113	20	0.177	0.393	2	1	1	107	p21 protein (Cdc42/Rac)-activated kinase 7	ENST00000378429.3
Case#1-Relapse-WholeTumor	SNAP25	20	10256146	Missense_Mutation	G	A	p.E3K	103	20	0.194	0.431	2	1	1	85	synaptosomal-associated protein, 25kDa	ENST00000254976.2
Case#1-Relapse-WholeTumor	PET117	20	18122915	Missense_Mutation	C	T	p.L54F	138	26	0.188	0.419	2	1	1	106	PET117 homolog (S. cerevisiae)	ENST00000432901.3
Case#1-Relapse-WholeTumor	RIN2	20	19937290	Missense_Mutation	G	A	p.E113K	85	18	0.212	0.471	2	1	1	80	Ras and Rab interactor 2	ENST00000255006.6
Case#1-Relapse-WholeTumor	CRNKL1	20	20033087	Missense_Mutation	G	A	p.S128F	101	19	0.188	0.418	2	1	1	107	crooked neck pre-mRNA splicing factor 1	ENST00000377340.2
Case#1-Relapse-WholeTumor	C20orf26	20	20269392	Missense_Mutation	C	T	p.S979F	85	19	0.224	0.497	2	1	1	71		ENST00000245957.5
Case#1-Relapse-WholeTumor	GZF1	20	23346051	Missense_Mutation	C	T	p.T344I	133	34	0.256	0.568	2	1	1	100	GDNF-inducible zinc finger protein 1	ENST00000338121.5
Case#1-Relapse-WholeTumor	SYNDIG1	20	24523736	Start_Codon_SNP	G	A	p.M1I	115	15	0.130	0.290	2	1	1	89	synapse differentiation inducing 1	ENST00000376862.3
Case#1-Relapse-WholeTumor	CCM2L	20	30610584	Nonsense_Mutation	G	A	p.W352*	78	13	0.167	0.370	2	1	1	57	cerebral cavernous malformation 2-like	ENST00000300415.8
Case#1-Relapse-WholeTumor	BPIFB3	20	31656778	Splice_Site	C	T	p.S383F	51	8	0.157	0.349	2	1	1	63	BPI fold containing family B, member 3	ENST00000375494.3
Case#1-Relapse-WholeTumor	BPIFB4	20	31678582	Missense_Mutation	G	A	p.E374K	93	34	0.366	0.812	2	1	1	45	BPI fold containing family B, member 4	ENST00000375483.3
Case#1-Relapse-WholeTumor	KIAA1755	20	36869848	Missense_Mutation	G	A	p.P229S	103	34	0.330	0.734	2	1	1	74	KIAA1755	ENST00000279024.4
Case#1-Relapse-WholeTumor	FAM83D	20	37576624	Missense_Mutation	G	A	p.V283M	202	34	0.168	0.374	2	1	1	153	family with sequence similarity 83, member D	ENST00000217429.4
Case#1-Relapse-WholeTumor	PTPRT	20	40730906	Missense_Mutation	G	A	p.P1191L	55	10	0.182	0.404	2	1	1	68	protein tyrosine phosphatase, receptor type, T	ENST00000373187.1
Case#1-Relapse-WholeTumor	JPH2	20	42789002	Missense_Mutation	C	T	p.G142E	165	47	0.285	0.633	2	1	1	145	junctophilin 2	ENST00000372980.3
Case#1-Relapse-WholeTumor	SLPI	20	43883138	Missense_Mutation	C	T	p.G16E	107	24	0.224	0.498	2	1	1	66	secretory leukocyte peptidase inhibitor	ENST00000338380.2
Case#1-Relapse-WholeTumor	SPINT3	20	44144191	Missense_Mutation	G	C	p.R20G	44	12	0.273	0.606	2	1	1	37	serine peptidase inhibitor, Kunitz type, 3	ENST00000217428.6
Case#1-Relapse-WholeTumor	PCIF1	20	44574481	Missense_Mutation	G	A	p.G434R	128	23	0.180	0.399	2	1	1	84	PDX1 C-terminal inhibiting factor 1	ENST00000372409.3
Case#1-Relapse-WholeTumor	SLC12A5	20	44680479	Missense_Mutation	G	A	p.E806K	60	15	0.250	0.556	2	1	1	35	solute carrier family 12 (potassium/chloride transporter), member 5	ENST00000454036.2
Case#1-Relapse-WholeTumor	OCSTAMP	20	45174900	Missense_Mutation	G	A	p.S38F	68	18	0.265	0.588	2	1	1	33	osteoclast stimulatory transmembrane protein	ENST00000279028.2
Case#1-Relapse-WholeTumor	KCNB1	20	47990997	Missense_Mutation	G	A	p.S367F	84	21	0.250	0.556	2	1	1	34	potassium voltage-gated channel, Shab-related subfamily, member 1	ENST00000371741.4
Case#1-Relapse-WholeTumor	SLC9A8	20	48497530	Missense_Mutation	C	T	p.H410Y	129	32	0.248	0.551	2	1	1	91	solute carrier family 9, subfamily A (NHE8, cation proton antiporter 8), member 8	ENST00000361573.2
Case#1-Relapse-WholeTumor	KCNG1	20	49626157	Missense_Mutation	G	A	p.T240I	41	8	0.195	0.434	2	1	1	51	potassium voltage-gated channel, subfamily G, member 1	ENST00000371571.4
Case#1-Relapse-WholeTumor	TSHZ2	20	51870790	Missense_Mutation	G	A	p.D265N	159	36	0.226	0.503	2	1	1	102	teashirt zinc finger homeobox 2	ENST00000371497.5
Case#1-Relapse-WholeTumor	SYCP2	20	58439413	Missense_Mutation	C	T	p.E1516K	92	22	0.239	0.531	2	1	1	46	synaptonemal complex protein 2	ENST00000357552.3
Case#1-Relapse-WholeTumor	SLC17A9	20	61588121	Missense_Mutation	G	A	p.E22K	72	25	0.347	0.772	2	1	1	63	solute carrier family 17 (vesicular nucleotide transporter), member 9	ENST00000370351.4
Case#1-Relapse-WholeTumor	COL20A1	20	61945242	Splice_Site	C	T	p.S786F	93	16	0.172	0.382	2	1	1	111	collagen, type XX, alpha 1	ENST00000358894.6
Case#1-Relapse-WholeTumor	ZBTB46	20	62421662	Missense_Mutation	G	A	p.S150F	51	12	0.235	0.523	2	1	1	43	zinc finger and BTB domain containing 46	ENST00000245663.4
Case#1-Relapse-WholeTumor	APP	21	27326927	Missense_Mutation	G	A	p.A555V	104	27	0.260	0.577	2	1	1	47	amyloid beta (A4) precursor protein	ENST00000346798.3
Case#1-Relapse-WholeTumor	CYYR1	21	27840924	Missense_Mutation	C	T	p.E121K	116	14	0.121	0.268	2	1	1	88	cysteine/tyrosine-rich 1	ENST00000299340.4
Case#1-Relapse-WholeTumor	CYYR1	21	27840930	Missense_Mutation	C	T	p.D119N	115	25	0.217	0.483	2	1	1	89	cysteine/tyrosine-rich 1	ENST00000299340.4
Case#1-Relapse-WholeTumor	GRIK1	21	30949360	Missense_Mutation	G	A	p.S685L	165	44	0.267	0.593	2	1	1	82	glutamate receptor, ionotropic, kainate 1	ENST00000399907.1
Case#1-Relapse-WholeTumor	KRTAP24-1	21	31655093	Missense_Mutation	C	T	p.G53E	116	24	0.207	0.460	2	1	1	82	keratin associated protein 24-1	ENST00000340345.4
Case#1-Relapse-WholeTumor	C21orf54	21	34542053	Missense_Mutation	G	A	p.R39C	69	12	0.174	0.386	2	1	1	67	chromosome 21 open reading frame 54	ENST00000451980.2
Case#1-Relapse-WholeTumor	SLC5A3	21	35468687	Missense_Mutation	T	A	p.L397H	105	12	0.114	0.254	2	1	1	91	solute carrier family 5 (sodium/myo-inositol cotransporter), member 3	ENST00000381151.3
Case#1-Relapse-WholeTumor	KCNJ6	21	39087413	Missense_Mutation	G	A	p.S16F	50	14	0.280	0.622	2	1	1	44	potassium inwardly-rectifying channel, subfamily J, member 6	ENST00000609713.1
Case#1-Relapse-WholeTumor	ERG	21	39775479	Missense_Mutation	G	A	p.P188S	268	61	0.228	0.506	2	1	1	160	v-ets avian erythroblastosis virus E26 oncogene homolog	ENST00000417133.2
Case#1-Relapse-WholeTumor	B3GALT5	21	41033280	Missense_Mutation	C	T	p.T265I	120	40	0.333	0.741	2	1	1	76	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	ENST00000380620.4
Case#1-Relapse-WholeTumor	DSCAM	21	41496159	Missense_Mutation	C	T	p.R1220Q	166	32	0.193	0.428	2	1	1	144	Down syndrome cell adhesion molecule	ENST00000400454.1
Case#1-Relapse-WholeTumor	UBASH3A	21	43852263	Missense_Mutation	G	A	p.D408N	124	29	0.234	0.520	2	1	1	100	ubiquitin associated and SH3 domain containing A	ENST00000319294.6
Case#1-Relapse-WholeTumor	ITGB2	21	46320380	Missense_Mutation	C	T	p.G251D	256	60	0.234	0.521	2	1	1	218	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	ENST00000397850.2
Case#1-Relapse-WholeTumor	ADARB1	21	46624496	Missense_Mutation	C	T	p.S571F	130	23	0.177	0.393	2	1	1	118	adenosine deaminase, RNA-specific, B1	ENST00000360697.3
Case#1-Relapse-WholeTumor	PRMT2	21	48064312	Missense_Mutation	C	T	p.P80L	192	45	0.234	0.521	2	1	1	129	protein arginine methyltransferase 2	ENST00000397637.1
Case#1-Relapse-WholeTumor	PRMT2	21	48078714	Missense_Mutation	G	A	p.G238R	171	44	0.257	0.572	2	1	1	128	protein arginine methyltransferase 2	ENST00000397637.1
Case#1-Relapse-WholeTumor	PRMT2	21	48078777	Missense_Mutation	C	T	p.R259C	129	26	0.202	0.448	2	1	1	120	protein arginine methyltransferase 2	ENST00000397637.1
Case#1-Relapse-WholeTumor	HIRA	22	19348765	Missense_Mutation	GG	AA	p.L694F	110	27	0.245	0.545	2	1	1	85	histone cell cycle regulator	ENST00000263208.5
Case#1-Relapse-WholeTumor	MED15	22	20920814	Frame_Shift_Del	CAG	-	p.Q262fs	61	6	0.098	0.219	2	1	1	42	mediator complex subunit 15	ENST00000263205.7
Case#1-Relapse-WholeTumor	PI4KA	22	21065055	Missense_Mutation	CC	TT	p.G1947E	491	57	0.116	0.258	2	1	1	395	phosphatidylinositol 4-kinase, catalytic, alpha	ENST00000572273.1
Case#1-Relapse-WholeTumor	SUSD2	22	24579160	Missense_Mutation	C	T	p.S71F	618	98	0.159	0.352	2	1	1	476	sushi domain containing 2	ENST00000358321.3
Case#1-Relapse-WholeTumor	HORMAD2	22	30489987	Missense_Mutation	T	C	p.S16P	60	14	0.233	0.519	2	1	1	57	HORMA domain containing 2	ENST00000336726.6
Case#1-Relapse-WholeTumor	GATSL3	22	30682360	Missense_Mutation	G	A	p.P212L	88	35	0.398	0.884	2	1	1	53	GATS protein-like 3	ENST00000407689.3
Case#1-Relapse-WholeTumor	GAL3ST1	22	30951568	Missense_Mutation	C	T	p.R215Q	143	39	0.273	0.606	2	1	1	114	galactose-3-O-sulfotransferase 1	ENST00000402321.1
Case#1-Relapse-WholeTumor	PLA2G3	22	31534317	Missense_Mutation	G	A	p.P243S	99	18	0.182	0.404	2	1	1	66	phospholipase A2, group III	ENST00000215885.3

Case#1-Relapse-WholeTumor	CSF2RB	22	37326785	Missense_Mutation	C	T	p.P309S	32	10	0.313	0.694	2	1	1	34	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	ENST00000403662.3
Case#1-Relapse-WholeTumor	TST	22	37407121	Missense_Mutation	G	A	p.R281C	50	18	0.360	0.800	2	1	1	50	thiosulfate sulfurtransferase (rhodanese)	ENST00000403892.3
Case#1-Relapse-WholeTumor	POLR2F	22	38355466	Nonsense_Mutation	CC	AT	p.R69*	87	15	0.172	0.278	4	3	1	44	polymerase (RNA) II (DNA directed) polypeptide F	ENST00000442738.2
Case#1-Relapse-WholeTumor	CACNA1I	22	40045670	Missense_Mutation	G	A	p.G578S	59	30	0.508	0.819	4	3	1	47	calcium channel, voltage-dependent, T type, alpha 1I subunit	ENST00000402142.3
Case#1-Relapse-WholeTumor	C22orf46	22	42089609	Missense_Mutation	G	T	p.S120I	140	62	0.443	0.713	4	3	1	62	chromosome 22 open reading frame 46	ENST00000402966.1
Case#1-Relapse-WholeTumor	PHF21B	22	45309910	Missense_Mutation	G	A	p.P208L	59	19	0.322	0.519	4	3	1	20	PHD finger protein 21B	ENST00000313237.5
Case#1-Relapse-WholeTumor	MOV10L1	22	50596514	Missense_Mutation	C	T	p.P1032L	156	74	0.474	0.764	4	3	1	90	Mov10 RISC complex RNA helicase like 1	ENST00000262794.5
Case#1-Relapse-WholeTumor	NCAPH2	22	50960422	Missense_Mutation	CC	TT	p.H373Y	59	26	0.441	0.710	4	3	1	42	non-SMC condensin II complex, subunit H2	ENST00000420993.2
Case#1-Relapse-WholeTumor	CNTN4	3	3076318	Missense_Mutation	C	T	p.P596S	75	15	0.200	0.444	2	1	1	46	contactin 4	ENST00000397461.1
Case#1-Relapse-WholeTumor	GRM7	3	7456838	Missense_Mutation	C	T	p.R388C	108	17	0.157	0.350	2	1	1	93	glutamate receptor, metabotropic 7	ENST00000357716.4
Case#1-Relapse-WholeTumor	LHFPL4	3	9547825	Missense_Mutation	C	T	p.D157N	94	18	0.191	0.426	2	1	1	85	lipoma HMGIC fusion partner-like 4	ENST00000287585.6
Case#1-Relapse-WholeTumor	FGD5	3	14905742	Missense_Mutation	C	T	p.S878L	130	31	0.238	0.530	2	1	1	95	FYVE, RhoGEF and PH domain containing 5	ENST00000285046.5
Case#1-Relapse-WholeTumor	ZNF860	3	32031551	Missense_Mutation	C	T	p.S327L	172	28	0.163	0.362	2	1	1	157	zinc finger protein 860	ENST00000360311.4
Case#1-Relapse-WholeTumor	DYNC1LI1	3	32571819	Splice_Site	G	A	p.S381F	86	17	0.198	0.439	2	1	1	47	dynein, cytoplasmic 1, light intermediate chain 1	ENST00000273130.4
Case#1-Relapse-WholeTumor	TRANK1	3	36898824	Missense_Mutation	CC	TT	p.A753T	53	12	0.226	0.503	2	1	1	35	tetratricopeptide repeat and ankyrin repeat containing 1	ENST00000429976.2
Case#1-Relapse-WholeTumor	ITGA9	3	37544694	Missense_Mutation	G	A	p.G213E	70	14	0.200	0.444	2	1	1	57	integrin, alpha 9	ENST00000264741.5
Case#1-Relapse-WholeTumor	SCN5A	3	38592348	Missense_Mutation	C	T	p.D1839N	195	47	0.241	0.536	2	1	1	154	sodium channel, voltage-gated, type V, alpha subunit	ENST00000333535.4
Case#1-Relapse-WholeTumor	SCN5A	3	38622491	Missense_Mutation	C	A	p.E1053D	124	36	0.290	0.645	2	1	1	104	sodium channel, voltage-gated, type V, alpha subunit	ENST00000333535.4
Case#1-Relapse-WholeTumor	SCN5A	3	38622715	Missense_Mutation	C	T	p.D979N	44	8	0.182	0.404	2	1	1	31	sodium channel, voltage-gated, type V, alpha subunit	ENST00000333535.4
Case#1-Relapse-WholeTumor	SCN5A	3	38639391	Nonsense_Mutation	C	T	p.W697*	125	32	0.256	0.569	2	1	1	84	sodium channel, voltage-gated, type V, alpha subunit	ENST00000333535.4
Case#1-Relapse-WholeTumor	SCN10A	3	38791570	Missense_Mutation	G	A	p.L621F	132	35	0.265	0.589	2	1	1	95	sodium channel, voltage-gated, type X, alpha subunit	ENST00000449082.2
Case#1-Relapse-WholeTumor	SCN11A	3	38889195	Missense_Mutation	G	A	p.P1456S	29	5	0.172	0.383	2	1	1	45	sodium channel, voltage-gated, type XI, alpha subunit	ENST00000302328.3
Case#1-Relapse-WholeTumor	CSRNP1	3	39185792	Missense_Mutation	G	C	p.R206G	139	27	0.194	0.432	2	1	1	122	cysteine-serine-rich nuclear protein 1	ENST00000273153.5
Case#1-Relapse-WholeTumor	ZNF502	3	44763357	Missense_Mutation	C	T	p.P350S	92	24	0.261	0.580	2	1	1	71	zinc finger protein 502	ENST00000296091.4
Case#1-Relapse-WholeTumor	LIMD1	3	45637570	Missense_Mutation	C	T	p.S400F	91	20	0.220	0.488	2	1	1	65	LIM domains containing 1	ENST00000273317.4
Case#1-Relapse-WholeTumor	ELP6	3	47537648	Missense_Mutation	G	A	p.H238Y	126	28	0.222	0.494	2	1	1	84	elongator acetyltransferase complex subunit 6	ENST00000296149.4
Case#1-Relapse-WholeTumor	COL7A1	3	48629387	Missense_Mutation	G	A	p.S434F	68	19	0.279	0.621	2	1	1	69	collagen, type VII, alpha 1	ENST00000328333.8
Case#1-Relapse-WholeTumor	MAPKAPK3	3	50683142	Splice_Site	C	T	p.A210A	63	17	0.270	0.600	2	1	1	76	mitogen-activated protein kinase-activated protein kinase 3	ENST00000446044.1
Case#1-Relapse-WholeTumor	STAB1	3	52555427	Missense_Mutation	G	A	p.D1987N	98	25	0.255	0.567	2	1	1	99	stabilin 1	ENST00000321725.6
Case#1-Relapse-WholeTumor	CACNA2D3	3	55038797	Missense_Mutation	C	T	p.L900F	149	28	0.188	0.418	2	1	1	142	calcium channel, voltage-dependent, alpha 2/delta subunit 3	ENST00000474759.1
Case#1-Relapse-WholeTumor	ERC2	3	56041244	Missense_Mutation	C	T	p.E676K	74	13	0.176	0.390	2	1	1	55	ELKS/RAB6-interacting/CAST family member 2	ENST00000288221.6
Case#1-Relapse-WholeTumor	FAM3D	3	58625883	Missense_Mutation	C	T	p.G115E	108	26	0.241	0.535	2	1	1	72	family with sequence similarity 3, member D	ENST00000358781.2
Case#1-Relapse-WholeTumor	MAGI1	3	65464291	Missense_Mutation	G	A	p.P245S	237	46	0.194	0.431	2	1	1	181	membrane associated guanylate kinase, WW and PDZ domain containing 1	ENST00000497477.2
Case#1-Relapse-WholeTumor	SLC25A26	3	66287010	Missense_Mutation	C	T	p.P26S	161	42	0.261	0.580	2	1	1	101	solute carrier family 25 (S-adenosylmethionine carrier), member 26	ENST00000354883.6
Case#1-Relapse-WholeTumor	EOGT	3	69058856	Missense_Mutation	G	A	p.P48S	132	40	0.303	0.673	2	1	1	112	EGF domain-specific O-linked N-acetylglucosamine (GlcNAc) transferase	ENST00000383701.3
Case#1-Relapse-WholeTumor	ROBO2	3	77651579	Nonsense_Mutation	C	T	p.Q1025*	87	16	0.184	0.409	2	2	0	77	roundabout, axon guidance receptor, homolog 2 (Drosophila)	ENST00000461745.1
Case#1-Relapse-WholeTumor	ROBO2	3	77666845	Missense_Mutation	G	A	p.E1159K	132	30	0.227	0.505	2	2	0	82	roundabout, axon guidance receptor, homolog 2 (Drosophila)	ENST00000461745.1
Case#1-Relapse-WholeTumor	OR5K4	3	98073152	Missense_Mutation	G	A	p.G152E	169	41	0.243	0.539	2	1	1	100	olfactory receptor, family 5, subfamily K, member 4	ENST00000354924.2
Case#1-Relapse-WholeTumor	ZPLD1	3	102171955	Missense_Mutation	C	T	p.T100I	106	27	0.255	0.566	2	1	1	57	zona pellucida-like domain containing 1	ENST00000491959.1
Case#1-Relapse-WholeTumor	MORC1	3	108773587	Missense_Mutation	C	T	p.D440N	105	18	0.171	0.381	2	1	1	92	MORC family CW-type zinc finger 1	ENST00000483760.1
Case#1-Relapse-WholeTumor	MORC1	3	108813815	Missense_Mutation	G	A	p.S175F	73	8	0.110	0.244	2	1	1	80	MORC family CW-type zinc finger 1	ENST00000483760.1
Case#1-Relapse-WholeTumor	PHLDB2	3	111639198	Missense_Mutation	G	A	p.E645K	156	39	0.250	0.556	2	1	1	122	pleckstrin homology-like domain, family B, member 2	ENST00000431670.2
Case#1-Relapse-WholeTumor	PHLDB2	3	111651167	Missense_Mutation	C	T	p.L685F	88	17	0.193	0.429	2	1	1	61	pleckstrin homology-like domain, family B, member 2	ENST00000431670.2
Case#1-Relapse-WholeTumor	WDR52	3	113046507	Nonsense_Mutation	G	A	p.Q1426*	72	9	0.125	0.278	2	1	1	72		ENST00000393845.2
Case#1-Relapse-WholeTumor	WDR52	3	113063425	Missense_Mutation	G	A	p.P1067L	96	18	0.188	0.417	2	1	1	65		ENST00000393845.2
Case#1-Relapse-WholeTumor	PLA1A	3	119348287	Missense_Mutation	C	T	p.S448F	120	31	0.258	0.574	2	1	1	83	phospholipase A1 member A	ENST00000273371.4
Case#1-Relapse-WholeTumor	STXBP5L	3	121097634	Missense_Mutation	G	A	p.D774N	91	16	0.176	0.391	2	1	1	91	syntaxin binding protein 5-like	ENST00000273666.6
Case#1-Relapse-WholeTumor	PARP14	3	122437233	Missense_Mutation	C	T	p.P1412L	91	29	0.319	0.708	2	1	1	75	poly (ADP-ribose) polymerase family, member 14	ENST00000474629.2
Case#1-Relapse-WholeTumor	KALRN	3	124181467	Missense_Mutation	G	A	p.D1338N	116	29	0.250	0.556	2	1	1	97	kalirin, RhoGEF kinase	ENST00000240874.3
Case#1-Relapse-WholeTumor	GATA2	3	128205091	Missense_Mutation	G	A	p.T117I	21	6	0.286	0.635	2	1	1	22	GATA binding protein 2	ENST00000341105.2
Case#1-Relapse-WholeTumor	IFT122	3	129195534	Missense_Mutation	C	T	p.S346F	72	11	0.153	0.340	2	1	1	56	intraflagellar transport 122	ENST00000348417.2
Case#1-Relapse-WholeTumor	COL6A5	3	130095636	Missense_Mutation	T	G	p.D208E	93	13	0.140	0.311	2	1	1	56	collagen, type VI, alpha 5	ENST00000432398.2
Case#1-Relapse-WholeTumor	COL6A5	3	130107908	Missense_Mutation	C	T	p.H783Y	46	11	0.239	0.531	2	1	1	33	collagen, type VI, alpha 5	ENST00000432398.2
Case#1-Relapse-WholeTumor	PIK3R4	3	130424612	Missense_Mutation	G	A	p.P909S	117	22	0.188	0.418	2	1	1	109	phosphoinositide-3-kinase, regulatory subunit 4	ENST00000356763.3
Case#1-Relapse-WholeTumor	ESYT3	3	138195671	Missense_Mutation	C	G	p.T879S	55	15	0.273	0.606	2	1	1	41	extended synaptotagmin-like protein 3	ENST00000389567.4
Case#1-Relapse-WholeTumor	CLSTN2	3	140123566	Missense_Mutation	G	A	p.E199K	128	27	0.211	0.469	2	1	1	103	calsyntenin 2	ENST00000458420.3
Case#1-Relapse-WholeTumor	SLC25A36	3	140682046	Missense_Mutation	A	T	p.H121L	119	23	0.193	0.430	2	1	1	78	solute carrier family 25 (pyrimidine nucleotide carrier), member 36	ENST00000324194.6
Case#1-Relapse-WholeTumor	SIAH2	3	150480395	Missense_Mutation	G	A	p.P81L	50	13	0.260	0.578	2	1	1	28	siah E3 ubiquitin protein ligase 2	ENST00000312960.3
Case#1-Relapse-WholeTumor	SERPINI2	3	167182997	Missense_Mutation	G	A	p.P288L	80	28	0.350	0.778	2	1	1	55	serpin peptidase inhibitor, clade I (pancpin), member 2	ENST00000476257.1
Case#1-Relapse-WholeTumor	MECOM	3	168833574	Missense_Mutation	G	A	p.P508S	54	12	0.222	0.494	2	1	1	39	MDS1 and EVI1 complex locus	ENST00000464456.1
Case#1-Relapse-WholeTumor	TNIK	3	170828529	Missense_Mutation	C	T	p.G753E	78	14	0.179	0.399	2	1	1	69	TRAF2 and NCK interacting kinase	ENST00000436636.2
Case#1-Relapse-WholeTumor	CCDC39	3	180359793	Missense_Mutation	C	T	p.R621Q	190	41	0.216	0.480	2	1	1	162	coiled-coil domain containing 39	ENST00000442201.2
Case#1-Relapse-WholeTumor	CCDC39	3	180381704	Missense_Mutation	G	A	p.S54F	100	25	0.250	0.556	2	1	1	69	coiled-coil domain containing 39	ENST00000442201.2
Case#1-Relapse-WholeTumor	EIF4G1	3	184040441	Missense_Mutation	C	T	p.T573I	98	20	0.204	0.454	2	1	1	77	eukaryotic translation initiation factor 4 gamma, 1	ENST00000346169.2
Case#1-Relapse-WholeTumor	TMEM44	3	194325093	Missense_Mutation	GG	AA	p.P414S	90	20	0.222	0.494	2	1	1	64	transmembrane protein 44	ENST00000392432.2
Case#1-Relapse-WholeTumor	TMEM175	4	947137	Missense_Mutation	CC	TT	p.P208F	42	9	0.214	0.476	2	1	1	28	transmembrane protein 175	ENST00000264771.4
Case#1-Relapse-WholeTumor	SPON2	4	1164876	Missense_Mutation	C	T	p.D183N	14	7	0.500	1.111	2	1	1	13	spondin 2, extracellular matrix protein	ENST00000290902.5
Case#1-Relapse-WholeTumor	ADD1	4	2886385	Missense_Mutation	C	T	p.H168Y	179	34	0.190	0.422	2	1	1	143	adducin 1 (alpha)	ENST00000398129.1
Case#1-Relapse-WholeTumor	WFS1	4	6304145	Missense_Mutation	G	A	p.V875M	65	11	0.169	0.376	2	1	1	74	Wolfram syndrome 1 (wolframin)	ENST00000226760.1
Case#1-Relapse-WholeTumor	DEFB131	4	9452137	Missense_Mutation	G	A	p.R37K	57	16	0.281	0.624	2	2	0	68	defensin, beta 131	ENST00000334879.1
Case#1-Relapse-WholeTumor	ZNF518B	4	10447258	Missense_Mutation	C	T	p.R232K	137	21	0.153	0.341	2	1	1	91	zinc finger protein 518B	ENST00000326756.3
Case#1-Relapse-WholeTumor	CLNK	4	10669536	Splice_Site	C	T		55	13	0.236	0.525	2	1	1	26	cytokine-dependent hematopoietic cell linker	ENST00000226951.6
Case#1-Relapse-WholeTumor	CPEB2	4	15060828	Missense_Mutation	G	C	p.W421C	121	24	0.198	0.441	2	1	1	81	cytoplasmic polyadenylation element binding protein 2	ENST00000507071.1
Case#1-Relapse-WholeTumor	CD38	4	15826543	Missense_Mutation	T	C	p.F135L	132	30	0.227	0.505	2	1	1	96	CD38 molecule	ENST00000226279.3
Case#1-Relapse-WholeTumor	SLIT2	4	20535283	Missense_Mutation	C	T	p.R593C	163	29	0.178	0.395	2	1	1	118	slit homolog 2 (Drosophila)	ENST00000504154.1
Case#1-Relapse-WholeTumor	PPARGC1A	4	23816051	Missense_Mutation	G	A	p.S352F	73	15	0.205	0.457	2	1	1	54	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha	ENST00000264867.2
Case#1-Relapse-WholeTumor	SHISA3	4	42400323	Missense_Mutation	G	A	p.E84K	14	4	0.286	0.635	2	1	1	16	shisa family member 3	ENST00000319234.4
Case#1-Relapse-WholeTumor	KCTD8	4	44177183	Missense_Mutation	C	T	p.G349E	84	14	0.167	0.370	2	1	1	73	potassium channel tetramerization domain containing 8	ENST00000360029.3
Case#1-Relapse-WholeTumor	ATP10D	4	47525150	Missense_Mutation	G	A	p.G203R	188	45	0.239	0.532	2	1	1	142	ATPase, class V, type 10D	ENST00000273859.3

Case#1-Relapse-WholeTumor	CORIN	4	47765514	Missense_Mutation	C	T	p.E167K	162	37	0.228	0.508	2	1	1	125	corin, serine peptidase	ENST00000273857.4
Case#1-Relapse-WholeTumor	CWH43	4	48990626	Missense_Mutation	C	T	p.P59L	110	21	0.191	0.424	2	1	1	128	cell wall biogenesis 43 C-terminal homolog (S. cerevisiae)	ENST00000226432.4
Case#1-Relapse-WholeTumor	LPHN3	4	62813977	Missense_Mutation	G	A	p.A862T	142	30	0.211	0.469	2	1	1	102	latrophilin 3	ENST00000514591.1
Case#1-Relapse-WholeTumor	UGT2B11	4	70078385	Missense_Mutation	C	T	p.R259Q	342	71	0.208	0.461	2	1	1	284	UDP glucuronosyltransferase 2 family, polypeptide B11	ENST00000446444.1
Case#1-Relapse-WholeTumor	UGT2B28	4	70146763	Missense_Mutation	G	A	p.R182K	449	75	0.167	0.371	2	1	1	352	UDP glucuronosyltransferase 2 family, polypeptide B28	ENST00000335568.5
Case#1-Relapse-WholeTumor	UGT2B4	4	70359494	Missense_Mutation	C	T	p.D263N	297	62	0.209	0.464	2	1	1	268	UDP glucuronosyltransferase 2 family, polypeptide B4	ENST00000305107.6
Case#1-Relapse-WholeTumor	SMR3A	4	71232637	Missense_Mutation	C	T	p.P111S	215	49	0.228	0.506	2	1	1	172	submaxillary gland androgen regulated protein 3A	ENST00000226460.4
Case#1-Relapse-WholeTumor	ENAM	4	71501579	Missense_Mutation	C	T	p.P168S	51	6	0.118	0.261	2	1	1	43	enamelin	ENST00000396073.3
Case#1-Relapse-WholeTumor	AFP	4	74313262	Missense_Mutation	A	T	p.E309D	60	10	0.167	0.370	2	1	1	48	alpha-fetoprotein	ENST00000395792.2
Case#1-Relapse-WholeTumor	CXCL11	4	76955959	Missense_Mutation	C	A	p.R91I	44	10	0.227	0.505	2	1	1	51	chemokine (C-X-C motif) ligand 11	ENST00000503860.1
Case#1-Relapse-WholeTumor	FAM47E	4	77192919	Missense_Mutation	C	G	p.Q290E	81	20	0.247	0.549	2	1	1	52	family with sequence similarity 47, member E	ENST00000424749.2
Case#1-Relapse-WholeTumor	CNOT6L	4	78641776	Missense_Mutation	A	C	p.Y493D	139	36	0.259	0.576	2	1	1	86	CCR4-NOT transcription complex, subunit 6-like	ENST00000504123.1
Case#1-Relapse-WholeTumor	PRDM8	4	81121453	Splice_Site	G	A	p.R73R	160	32	0.200	0.444	2	1	1	127	PR domain containing 8	ENST00000504452.1
Case#1-Relapse-WholeTumor	PRDM8	4	81122675	Splice_Site	G	A	p.G151R	143	37	0.259	0.575	2	1	1	122	PR domain containing 8	ENST00000504452.1
Case#1-Relapse-WholeTumor	FGF5	4	81196152	Nonsense_Mutation	A	T	p.K149*	65	20	0.308	0.684	2	1	1	63	fibroblast growth factor 5	ENST00000312465.7
Case#1-Relapse-WholeTumor	BMP3	4	81967521	Missense_Mutation	G	A	p.E316K	65	11	0.169	0.376	2	1	1	67	bone morphogenetic protein 3	ENST00000282701.2
Case#1-Relapse-WholeTumor	AGPAT9	4	84502856	Missense_Mutation	C	T	p.S117F	156	35	0.224	0.499	2	1	1	153	1-acylglycerol-3-phosphate O-acyltransferase 9	ENST00000395226.2
Case#1-Relapse-WholeTumor	MAPK10	4	86985528	Missense_Mutation	T	C	p.D334G	96	26	0.271	0.602	2	1	1	88	mitogen-activated protein kinase 10	ENST00000359221.3
Case#1-Relapse-WholeTumor	PTPN13	4	87703357	Missense_Mutation	C	T	p.S1989F	47	12	0.255	0.567	2	1	1	48	protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	ENST00000411767.2
Case#1-Relapse-WholeTumor	SPARCL1	4	88400704	Missense_Mutation	G	A	p.P615L	109	26	0.239	0.530	2	1	1	80	SPARC-like 1 (hevin)	ENST00000282470.6
Case#1-Relapse-WholeTumor	DSPP	4	88533290	Missense_Mutation	G	A	p.E29K	113	20	0.177	0.393	2	1	1	71	dentin sialophosphoprotein	ENST00000282478.7
Case#1-Relapse-WholeTumor	STPG2	4	98893466	Missense_Mutation	C	T	p.E300K	64	12	0.188	0.417	2	1	1	41	sperm-tail PG-rich repeat containing 2	ENST00000295268.3
Case#1-Relapse-WholeTumor	ADH1A	4	100201412	Missense_Mutation	C	T	p.E285K	261	59	0.226	0.502	2	1	1	225	alcohol dehydrogenase 1A (class I), alpha polypeptide	ENST00000209668.2
Case#1-Relapse-WholeTumor	SLC9B2	4	103952935	Missense_Mutation	A	G	p.W393R	107	16	0.150	0.332	2	1	1	61	solute carrier family 9, subfamily B (NHA2, cation proton antiporter 2), member 2	ENST00000394785.3
Case#1-Relapse-WholeTumor	TACR3	4	104511147	Nonsense_Mutation	G	A	p.R364*	146	36	0.247	0.548	2	1	1	116	tachykinin receptor 3	ENST00000304883.2
Case#1-Relapse-WholeTumor	INTS12	4	106616723	Missense_Mutation	G	A	p.L87F	90	19	0.211	0.469	2	1	1	100	integrator complex subunit 12	ENST00000451321.2
Case#1-Relapse-WholeTumor	NPNT	4	106859527	Missense_Mutation	A	G	p.Q152R	71	20	0.282	0.626	2	1	1	43	nephronectin	ENST00000379987.2
Case#1-Relapse-WholeTumor	LEF1	4	109010280	Splice_Site	CC	TT	p.G183N	154	30	0.195	0.433	2	1	1	139	lymphoid enhancer-binding factor 1	ENST00000265165.1
Case#1-Relapse-WholeTumor	CASP6	4	110610646	Missense_Mutation	G	A	p.S241F	104	17	0.163	0.363	2	1	1	74	caspase 6, apoptosis-related cysteine peptidase	ENST00000265164.2
Case#1-Relapse-WholeTumor	PITX2	4	111539426	Missense_Mutation	G	A	p.P270L	147	36	0.245	0.544	2	1	1	149	paired-like homeodomain 2	ENST00000354925.2
Case#1-Relapse-WholeTumor	NDST4	4	115760590	Missense_Mutation	G	A	p.P744S	105	18	0.171	0.381	2	1	1	77	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4	ENST00000264363.2
Case#1-Relapse-WholeTumor	KIAA1109	4	123171565	Missense_Mutation	G	A	p.G1920D	59	10	0.169	0.377	2	1	1	46	KIAA1109	ENST00000264501.4
Case#1-Relapse-WholeTumor	KIAA1109	4	123246422	Missense_Mutation	C	T	p.R3648C	160	32	0.200	0.444	2	1	1	100	KIAA1109	ENST00000264501.4
Case#1-Relapse-WholeTumor	FAT4	4	126329769	Missense_Mutation	C	T	p.L1914F	71	12	0.169	0.376	2	1	1	68	FAT atypical cadherin 4	ENST00000394329.3
Case#1-Relapse-WholeTumor	FAT4	4	126411736	Missense_Mutation	G	A	p.E4587K	85	21	0.247	0.549	2	1	1	56	FAT atypical cadherin 4	ENST00000394329.3
Case#1-Relapse-WholeTumor	SLC25A31	4	128694685	Missense_Mutation	G	A	p.D302N	133	15	0.113	0.251	2	1	1	109	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 31	ENST00000281154.4
Case#1-Relapse-WholeTumor	PCDH18	4	138452420	Missense_Mutation	C	T	p.E275K	102	28	0.275	0.610	2	1	1	65	protocadherin 18	ENST00000344876.4
Case#1-Relapse-WholeTumor	FREM3	4	144621186	Missense_Mutation	G	A	p.H215Y	39	11	0.282	0.627	2	1	1	20	FRAS1 related extracellular matrix 3	ENST00000329798.5
Case#1-Relapse-WholeTumor	ZNF827	4	146697095	Missense_Mutation	A	C	p.C847G	92	18	0.196	0.435	2	1	1	76	zinc finger protein 827	ENST00000508784.1
Case#1-Relapse-WholeTumor	LRBA	4	151773393	Nonsense_Mutation	G	A	p.Q1157*	65	23	0.354	0.786	2	2	0	69	LPS-responsive vesicle trafficking, beach and anchor containing	ENST00000357115.3
Case#1-Relapse-WholeTumor	KIAA0922	4	154395012	Missense_Mutation	G	A	p.G71S	140	60	0.429	0.952	2	2	0	92	KIAA0922	ENST00000409663.3
Case#1-Relapse-WholeTumor	TLR2	4	154625114	Missense_Mutation	C	T	p.P352L	59	28	0.475	1.055	2	2	0	53	toll-like receptor 2	ENST00000260010.6
Case#1-Relapse-WholeTumor	DCHS2	4	155407624	Missense_Mutation	C	T	p.E694K	114	54	0.474	1.053	2	2	0	119	dachsous cadherin-related 2	ENST00000456341.2
Case#1-Relapse-WholeTumor	GLRB	4	158057765	Missense_Mutation	G	A	p.E148K	90	35	0.389	0.864	2	2	0	94	glycine receptor, beta	ENST00000264428.4
Case#1-Relapse-WholeTumor	FSTL5	4	162697192	Missense_Mutation	C	T	p.M148I	41	11	0.268	0.596	2	2	0	34	follistatin-like 5	ENST00000306100.5
Case#1-Relapse-WholeTumor	ANXA10	4	169049310	Missense_Mutation	G	A	p.G32R	75	24	0.320	0.711	2	2	0	76	annexin A10	ENST00000359299.3
Case#1-Relapse-WholeTumor	AGA	4	178358657	Missense_Mutation	G	A	p.P175L	111	46	0.414	0.921	2	2	0	116	aspartylglucosaminidase	ENST00000264595.2
Case#1-Relapse-WholeTumor	RP11-389E17.1	4	178896990	Missense_Mutation	G	A	p.D65N	147	68	0.463	1.593	1	1	0	160		ENST00000507870.1
Case#1-Relapse-WholeTumor	TENM3	4	183713919	Missense_Mutation	G	A	p.G2032S	56	21	0.375	1.292	1	1	0	52	teneurin transmembrane protein 3	ENST00000511685.1
Case#1-Relapse-WholeTumor	WWC2	4	184169952	Missense_Mutation	C	T	p.S273F	71	22	0.310	1.067	1	1	0	72	WW and C2 domain containing 2	ENST00000403733.3
Case#1-Relapse-WholeTumor	IRF2	4	185340707	Nonsense_Mutation	G	A	p.Q35*	53	9	0.170	0.585	1	1	0	44	interferon regulatory factor 2	ENST00000393593.3
Case#1-Relapse-WholeTumor	FAT1	4	187540106	Missense_Mutation	C	T	p.R2545K	54	19	0.352	1.212	1	1	0	62	FAT atypical cadherin 1	ENST00000441802.2
Case#1-Relapse-WholeTumor	PLEKHG4B	5	143609	Missense_Mutation	G	A	p.S245N	58	11	0.190	0.421	2	1	1	60	pleckstrin homology domain containing, family G (with RhoGef domain) member 4B	ENST00000283426.6
Case#1-Relapse-WholeTumor	CLPTM1L	5	1318560	Missense_Mutation	G	A	p.P514L	43	15	0.349	0.775	2	1	1	31	CLPTM1-like	ENST00000320895.5
Case#1-Relapse-WholeTumor	ADAMTS16	5	5187860	Missense_Mutation	G	A	p.G329E	155	33	0.213	0.473	2	1	1	118	ADAM metallopeptidase with thrombospondin type 1 motif, 16	ENST00000274181.7
Case#1-Relapse-WholeTumor	DNAH5	5	13735969	Missense_Mutation	G	A	p.S3843L	72	23	0.319	0.710	2	1	1	66	dynein, axonemal, heavy chain 5	ENST00000265104.4
Case#1-Relapse-WholeTumor	DNAH5	5	13850770	Missense_Mutation	G	A	p.S1702F	74	13	0.176	0.390	2	1	1	49	dynein, axonemal, heavy chain 5	ENST00000265104.4
Case#1-Relapse-WholeTumor	TRIO	5	14481656	Missense_Mutation	G	A	p.V2132M	120	32	0.267	0.593	2	1	1	98	trio Rho guanine nucleotide exchange factor	ENST00000344204.4
Case#1-Relapse-WholeTumor	CDH12	5	21783541	Missense_Mutation	G	A	p.T440I	123	27	0.220	0.488	2	1	1	97	cadherin 12, type 2 (N-cadherin 2)	ENST00000382254.1
Case#1-Relapse-WholeTumor	CDH10	5	24537668	Missense_Mutation	C	T	p.R116Q	103	24	0.233	0.518	2	1	1	87	cadherin 10, type 2 (T2-cadherin)	ENST00000264463.4
Case#1-Relapse-WholeTumor	CDH9	5	26881582	Missense_Mutation	C	T	p.R678K	103	17	0.165	0.367	2	1	1	80	cadherin 9, type 2 (T1-cadherin)	ENST00000231021.4
Case#1-Relapse-WholeTumor	ADAMTS12	5	33637846	Missense_Mutation	T	G	p.K575T	147	16	0.109	0.242	2	1	1	101	ADAM metallopeptidase with thrombospondin type 1 motif, 12	ENST00000504830.1
Case#1-Relapse-WholeTumor	UGT3A1	5	35965544	Missense_Mutation	G	A	p.P263S	181	36	0.199	0.442	2	1	1	151	UDP glycosyltransferase 3 family, polypeptide A1	ENST00000274278.3
Case#1-Relapse-WholeTumor	EGFLAM	5	38350705	Missense_Mutation	A	G	p.T132A	76	18	0.237	0.526	2	1	1	92	EGF-like, fibronectin type III and laminin G domains	ENST00000354891.3
Case#1-Relapse-WholeTumor	C7	5	40981538	Missense_Mutation	G	A	p.E799K	115	29	0.252	0.560	2	1	1	109	complement component 7	ENST00000313164.9
Case#1-Relapse-WholeTumor	C6	5	41155131	Nonsense_Mutation	G	A	p.Q682*	93	21	0.226	0.502	2	1	1	92	complement component 6	ENST00000263413.3
Case#1-Relapse-WholeTumor	C6	5	41159322	Missense_Mutation	G	A	p.S573F	37	11	0.297	0.661	2	1	1	39	complement component 6	ENST00000263413.3
Case#1-Relapse-WholeTumor	C6	5	41161821	Missense_Mutation	C	T	p.E478K	84	16	0.190	0.423	2	1	1	78	complement component 6	ENST00000263413.3
Case#1-Relapse-WholeTumor	GHR	5	42711363	Missense_Mutation	G	A	p.E225K	166	40	0.241	0.535	2	1	1	132	growth hormone receptor	ENST00000230882.4
Case#1-Relapse-WholeTumor	PARP8	5	50091115	Missense_Mutation	A	G	p.K431R	82	9	0.110	0.244	2	1	1	59	poly (ADP-ribose) polymerase family, member 8	ENST00000281631.5
Case#1-Relapse-WholeTumor	MOCS2	5	52397999	Missense_Mutation	C	T	p.E52K	106	23	0.217	0.482	2	1	1	100	molybdenum cofactor synthesis 2	ENST00000396954.3
Case#1-Relapse-WholeTumor	IPO11	5	61846195	Splice_Site	T	C	p.V751A	182	38	0.209	0.464	2	1	1	158	importin 11	ENST00000325324.6
Case#1-Relapse-WholeTumor	MARVELD2	5	68715684	Missense_Mutation	C	T	p.P158S	81	21	0.259	0.576	2	1	1	56	MARVEL domain containing 2	ENST00000325631.5
Case#1-Relapse-WholeTumor	MAP1B	5	71496188	Missense_Mutation	A	G	p.T2336A	38	10	0.263	0.585	2	1	1	25	microtubule-associated protein 1B	ENST00000296755.7
Case#1-Relapse-WholeTumor	ARHGEF28	5	73179596	Missense_Mutation	G	A	p.R981Q	100	25	0.250	0.556	2	1	1	97	Rho guanine nucleotide exchange factor (GEF) 28	ENST00000426542.2
Case#1-Relapse-WholeTumor	ANKRD31	5	74364391	Missense_Mutation	C	T	p.D1859N	143	43	0.301	0.668	2	1	1	99	ankyrin repeat domain 31	ENST00000274361.3
Case#1-Relapse-WholeTumor	GPR98	5	89933641	Missense_Mutation	G	A	p.D706N	184	33	0.179	0.399	2	1	1	156	G protein-coupled receptor 98	ENST00000405460.2
Case#1-Relapse-WholeTumor	GPR98	5	89970009	Missense_Mutation	G	A	p.E1690K	78	16	0.205	0.456	2	1	1	91	G protein-coupled receptor 98	ENST00000405460.2
Case#1-Relapse-WholeTumor	GPR98	5	89999523	Nonsense_Mutation	C	T	p.R2733*	112	21	0.188	0.417	2	1	1	100	G protein-coupled receptor 98	ENST00000405460.2
Case#1-Relapse-WholeTumor	GPR98	5	90059134	Missense_Mutation	G	A	p.E4045K	72	16	0.222	0.494	2	1	1	61	G protein-coupled receptor 98	ENST00000405460.2
Case#1-Relapse-WholeTumor	GPR98	5	90074406	Nonsense_Mutation	C	T	p.R4277*	48	11	0.229	0.509	2	1	1	45	G protein-coupled receptor 98	ENST00000405460.2

Case#1-Relapse-WholeTumor	GPR98	5	90136557	Missense_Mutation	C	T	p.P5592S	129	28	0.217	0.482	2	1	1	93	G protein-coupled receptor 98	ENST00000405460.2
Case#1-Relapse-WholeTumor	SLCO4C1	5	101592859	Missense_Mutation	C	T	p.E477K	121	29	0.240	0.533	2	1	1	81	solute carrier organic anion transporter family, member 4C1	ENST00000310954.6
Case#1-Relapse-WholeTumor	SLCO4C1	5	101606492	Missense_Mutation	C	T	p.R213K	51	11	0.216	0.479	2	1	1	44	solute carrier organic anion transporter family, member 4C1	ENST00000310954.6
Case#1-Relapse-WholeTumor	CAMK4	5	110820100	Missense_Mutation	G	A	p.G453E	53	11	0.208	0.461	2	1	1	19	calcium/calmodulin-dependent protein kinase IV	ENST00000282356.4
Case#1-Relapse-WholeTumor	EPB41L4A	5	111531361	Missense_Mutation	C	T	p.R474K	190	42	0.221	0.491	2	1	1	134	erythrocyte membrane protein band 4.1 like 4A	ENST00000261486.5
Case#1-Relapse-WholeTumor	SNCAIP	5	121786421	Missense_Mutation	G	A	p.E627K	68	14	0.206	0.458	2	1	1	76	synuclein, alpha interacting protein	ENST00000261368.8
Case#1-Relapse-WholeTumor	PRDM6	5	122506570	Missense_Mutation	C	T	p.P422S	124	34	0.274	0.609	2	1	1	106	PR domain containing 6	ENST00000407847.4
Case#1-Relapse-WholeTumor	SLC27A6	5	128302027	Missense_Mutation	G	T	p.R66I	112	26	0.232	0.516	2	1	1	60	solute carrier family 27 (fatty acid transporter), member 6	ENST00000262462.4
Case#1-Relapse-WholeTumor	ADAMTS19	5	129015556	Missense_Mutation	G	A	p.R863Q	103	16	0.155	0.345	2	1	1	65	ADAM metallopeptidase with thrombospondin type 1 motif, 19	ENST00000274487.4
Case#1-Relapse-WholeTumor	IL5	5	131879077	Missense_Mutation	C	T	p.E32K	151	29	0.192	0.427	2	1	1	93	interleukin 5	ENST00000231454.1
Case#1-Relapse-WholeTumor	PCDHA1	5	140166257	Missense_Mutation	G	A	p.D128N	151	40	0.265	0.589	2	1	1	102	protocadherin alpha 1	ENST00000504120.2
Case#1-Relapse-WholeTumor	PCDHA1	5	140167444	Missense_Mutation	GG	AA	p.D524N	293	61	0.208	0.463	2	1	1	221	protocadherin alpha 1	ENST00000504120.2
Case#1-Relapse-WholeTumor	PCDHA1	5	140167763	Missense_Mutation	G	A	p.E630K	332	74	0.223	0.495	2	1	1	291	protocadherin alpha 1	ENST00000504120.2
Case#1-Relapse-WholeTumor	PCDHA1	5	140168264	Missense_Mutation	G	A	p.G797S	64	17	0.266	0.590	2	1	1	59	protocadherin alpha 1	ENST00000504120.2
Case#1-Relapse-WholeTumor	PCDHA5	5	140203062	Nonsense_Mutation	C	T	p.R568*	256	54	0.211	0.469	2	1	1	199	protocadherin alpha 5	ENST00000529859.1
Case#1-Relapse-WholeTumor	PCDHA10	5	140237497	Missense_Mutation	C	T	p.R622C	194	87	0.448	0.997	2	1	1	142	protocadherin alpha 10	ENST00000307360.5
Case#1-Relapse-WholeTumor	PCDHA11	5	140250546	Missense_Mutation	C	T	p.P620S	290	67	0.231	0.513	2	1	1	195	protocadherin alpha 11	ENST00000398640.2
Case#1-Relapse-WholeTumor	PCDHA12	5	140255958	Missense_Mutation	G	A	p.E301K	93	20	0.215	0.478	2	1	1	92	protocadherin alpha 12	ENST00000398631.2
Case#1-Relapse-WholeTumor	PCDHA13	5	140264090	Missense_Mutation	G	A	p.G746E	135	29	0.215	0.477	2	1	1	80	protocadherin alpha 13	ENST00000289272.2
Case#1-Relapse-WholeTumor	PCDHB3	5	140481009	Missense_Mutation	C	T	p.S259F	60	14	0.233	0.519	2	1	1	47	protocadherin beta 3	ENST00000231130.2
Case#1-Relapse-WholeTumor	PCDHB3	5	140482613	Missense_Mutation	G	C	p.E794Q	134	31	0.231	0.514	2	1	1	94	protocadherin beta 3	ENST00000231130.2
Case#1-Relapse-WholeTumor	PCDHB5	5	140515701	Missense_Mutation	C	T	p.R229C	62	10	0.161	0.358	2	1	1	49	protocadherin beta 5	ENST00000231134.5
Case#1-Relapse-WholeTumor	PCDHB5	5	140516743	Missense_Mutation	C	T	p.P576L	154	29	0.188	0.418	2	1	1	103	protocadherin beta 5	ENST00000231134.5
Case#1-Relapse-WholeTumor	PCDHB17	5	140536565	Missense_Mutation	G	A	p.G330E	86	9	0.105	0.233	2	1	1	56	protocadherin beta 17 pseudogene	ENST00000539533.1
Case#1-Relapse-WholeTumor	PCDHB7	5	140554580	Missense_Mutation	C	T	p.R722C	387	32	0.083	0.184	2	1	1	329	protocadherin beta 7	ENST00000231137.3
Case#1-Relapse-WholeTumor	PCDHB10	5	140572324	Missense_Mutation	G	A	p.V67I	207	40	0.193	0.429	2	1	1	160	protocadherin beta 10	ENST00000239446.4
Case#1-Relapse-WholeTumor	PCDHB11	5	140580731	Missense_Mutation	G	A	p.E462K	260	47	0.181	0.402	2	1	1	244	protocadherin beta 11	ENST00000354757.3
Case#1-Relapse-WholeTumor	PCDHB11	5	140580900	Missense_Mutation	C	T	p.S518L	225	56	0.249	0.553	2	1	1	152	protocadherin beta 11	ENST00000354757.3
Case#1-Relapse-WholeTumor	PCDHB14	5	140604665	Missense_Mutation	C	T	p.R530C	188	39	0.207	0.461	2	1	1	179	protocadherin beta 14	ENST00000239449.4
Case#1-Relapse-WholeTumor	PCDHGB6	5	140788121	Missense_Mutation	C	T	p.H118Y	131	27	0.206	0.458	2	1	1	94	protocadherin gamma subfamily B, 6	ENST00000520790.1
Case#1-Relapse-WholeTumor	DIAPH1	5	140953145	Missense_Mutation	G	A	p.P758S	125	22	0.176	0.391	2	1	1	103	diaphanous-related formin 1	ENST00000398557.4
Case#1-Relapse-WholeTumor	FBXO38	5	147778581	Missense_Mutation	A	T	p.I50F	196	50	0.255	0.567	2	1	1	131	F-box protein 38	ENST00000340253.5
Case#1-Relapse-WholeTumor	FAT2	5	150911477	Missense_Mutation	G	A	p.S3161F	115	32	0.278	0.618	2	1	1	79	FAT atypical cadherin 2	ENST00000261800.5
Case#1-Relapse-WholeTumor	FAT2	5	150930357	Missense_Mutation	G	A	p.P1458S	121	23	0.190	0.422	2	1	1	76	FAT atypical cadherin 2	ENST00000261800.5
Case#1-Relapse-WholeTumor	GRIA1	5	153065789	Missense_Mutation	G	A	p.R345Q	88	15	0.170	0.379	2	1	1	97	glutamate receptor, ionotropic, AMPA 1	ENST00000285900.5
Case#1-Relapse-WholeTumor	DOCK2	5	169267845	Missense_Mutation	C	T	p.H930Y	203	52	0.256	0.569	2	1	1	133	dedicator of cytokinesis 2	ENST00000256935.8
Case#1-Relapse-WholeTumor	KCNIP1	5	170145803	Missense_Mutation	C	T	p.R46W	72	19	0.264	0.586	2	1	1	52	Kv channel interacting protein 1	ENST00000411494.1
Case#1-Relapse-WholeTumor	DRD1	5	174869582	Missense_Mutation	C	T	p.G174E	178	35	0.197	0.437	2	1	1	134	dopamine receptor D1	ENST00000393752.2
Case#1-Relapse-WholeTumor	GRM6	5	178416070	Missense_Mutation	G	A	p.A407V	139	29	0.209	0.464	2	1	1	108	glutamate receptor, metabotropic 6	ENST00000517717.1
Case#1-Relapse-WholeTumor	CNOT6	5	179992975	Nonsense_Mutation	C	T	p.Q239*	79	12	0.152	0.338	2	1	1	63	CCR4-NOT transcription complex, subunit 6	ENST00000393356.1
Case#1-Relapse-WholeTumor	TRIM52	5	180687373	Missense_Mutation	A	T	p.Y148N	209	53	0.254	0.564	2	1	1	159	tripartite motif containing 52	ENST00000327767.4
Case#1-Relapse-WholeTumor	PSMG4	6	3267914	Missense_Mutation	G	A	p.E114K	201	38	0.189	0.343	3	2	1	132	proteasome (prosome, macropain) assembly chaperone 4	ENST00000438998.2
Case#1-Relapse-WholeTumor	F13A1	6	6167714	Missense_Mutation	T	C	p.T629A	167	58	0.347	0.630	3	2	1	137	coagulation factor XIII, A1 polypeptide	ENST00000264870.3
Case#1-Relapse-WholeTumor	GFOD1	6	13365771	Missense_Mutation	G	A	p.P126L	121	43	0.355	0.645	3	2	1	61	glucose-fructose oxidoreductase domain containing 1	ENST00000379287.3
Case#1-Relapse-WholeTumor	HIST1H3B	6	26032069	Missense_Mutation	C	T	p.E74K	125	57	0.456	1.013	2	2	0	152	histone cluster 1, H3b	ENST00000244661.2
Case#1-Relapse-WholeTumor	HIST1H1E	6	26156625	Nonsense_Mutation	G	T	p.E3*	43	17	0.395	0.879	2	2	0	30	histone cluster 1, H1e	ENST00000304218.3
Case#1-Relapse-WholeTumor	ZKSCAN3	6	28333706	Missense_Mutation	A	G	p.T421A	97	7	0.072	0.160	2	2	0	79	zinc finger with KRAB and SCAN domains 3	ENST00000377255.3
Case#1-Relapse-WholeTumor	TULP1	6	35476999	Missense_Mutation	C	T	p.G270E	118	46	0.390	0.866	2	2	0	84	tubby like protein 1	ENST00000229771.6
Case#1-Relapse-WholeTumor	LRFN2	6	40400849	Missense_Mutation	C	T	p.E2K	54	29	0.537	1.193	2	2	0	44	leucine rich repeat and fibronectin type III domain containing 2	ENST00000338305.6
Case#1-Relapse-WholeTumor	KLHDC3	6	42986651	Missense_Mutation	C	T	p.R291C	100	54	0.540	1.200	2	2	0	68	kelch domain containing 3	ENST00000326974.4
Case#1-Relapse-WholeTumor	CD2AP	6	47522423	Missense_Mutation	G	T	p.L154F	90	44	0.489	1.086	2	2	0	106	CD2-associated protein	ENST00000359314.5
Case#1-Relapse-WholeTumor	PKHD1	6	51497504	Nonsense_Mutation	G	A	p.R3842*	82	40	0.488	1.084	2	2	0	80	polycystic kidney and hepatic disease 1 (autosomal recessive)	ENST00000371117.3
Case#1-Relapse-WholeTumor	IL17F	6	52101862	Missense_Mutation	G	A	p.S120F	110	41	0.373	0.828	2	2	0	88	interleukin 17F	ENST00000336123.4
Case#1-Relapse-WholeTumor	TINAG	6	54216156	Missense_Mutation	G	A	p.E363K	97	40	0.412	0.916	2	2	0	68	tubulointerstitial nephritis antigen	ENST00000259782.4
Case#1-Relapse-WholeTumor	HCRTR2	6	55039521	Missense_Mutation	G	A	p.E46K	143	68	0.476	1.057	2	2	0	153	hypocretin (orexin) receptor 2	ENST00000370862.3
Case#1-Relapse-WholeTumor	HMGCLL1	6	55304353	Missense_Mutation	C	T	p.G297E	127	50	0.394	0.875	2	2	0	111	3-hydroxymethyl-3-methylglutaryl-CoA lyase-like 1	ENST00000398661.2
Case#1-Relapse-WholeTumor	FKBP1C	6	63921759	Missense_Mutation	T	G	p.F100V	180	25	0.139	0.309	2	2	0	154	FK506 binding protein 1C	ENST00000370659.1
Case#1-Relapse-WholeTumor	LGSN	6	63990777	Missense_Mutation	G	A	p.P227S	28	9	0.321	0.714	2	2	0	30	lengsin, lens protein with glutamine synthetase domain	ENST00000370657.4
Case#1-Relapse-WholeTumor	BAI3	6	70071021	Missense_Mutation	G	A	p.D1286N	46	23	0.500	1.111	2	2	0	61	brain-specific angiogenesis inhibitor 3	ENST00000370598.1
Case#1-Relapse-WholeTumor	KHDC1L	6	73933892	Nonsense_Mutation	G	A	p.R98*	65	34	0.523	1.162	2	2	0	56	KH homology domain containing 1-like	ENST00000370388.3
Case#1-Relapse-WholeTumor	KHDC3L	6	74072881	Missense_Mutation	G	A	p.R78Q	89	35	0.393	0.874	2	2	0	90	KH domain containing 3-like, subcortical maternal complex member	ENST00000370367.3
Case#1-Relapse-WholeTumor	IMPG1	6	76660542	Missense_Mutation	C	T	p.E521K	104	49	0.471	1.047	2	2	0	100	interphotoreceptor matrix proteoglycan 1	ENST00000369950.3
Case#1-Relapse-WholeTumor	ME1	6	83949355	Splice_Site	C	T	p.G272E	54	19	0.352	0.782	2	2	0	50	malic enzyme 1, NADP(+)-dependent, cytosolic	ENST00000369705.3
Case#1-Relapse-WholeTumor	SNAP91	6	84333033	Missense_Mutation	G	A	p.P265L	93	39	0.419	0.932	2	2	0	75	synaptosomal-associated protein, 91kDa	ENST00000439399.2
Case#1-Relapse-WholeTumor	ORC3	6	88331115	Missense_Mutation	T	C	p.L344P	125	25	0.200	0.444	2	2	0	104	origin recognition complex, subunit 3	ENST00000392844.3
Case#1-Relapse-WholeTumor	GPRC6A	6	117128317	Missense_Mutation	G	A	p.S184L	67	27	0.403	0.896	2	2	0	75	G protein-coupled receptor, class C, group 6, member A	ENST00000310357.3
Case#1-Relapse-WholeTumor	RFX6	6	117198493	Missense_Mutation	C	G	p.Q19E	59	16	0.271	0.603	2	2	0	42	regulatory factor X, 6	ENST00000332958.2
Case#1-Relapse-WholeTumor	CLVS2	6	123377038	Missense_Mutation	C	T	p.P255S	97	6	0.062	0.137	2	2	0	61	clavesin 2	ENST00000275162.5
Case#1-Relapse-WholeTumor	PTPRK	6	128303984	Missense_Mutation	C	T	p.E1176K	136	61	0.449	0.997	2	2	0	130	protein tyrosine phosphatase, receptor type, K	ENST00000368215.3
Case#1-Relapse-WholeTumor	PDE7B	6	136508200	Missense_Mutation	G	A	p.E358K	36	11	0.306	0.679	2	2	0	44	phosphodiesterase 7B	ENST00000308191.6
Case#1-Relapse-WholeTumor	ADGB	6	147085186	Missense_Mutation	GA	TT	p.E1234L	95	32	0.337	0.749	2	2	0	79	androglobin	ENST00000397944.3
Case#1-Relapse-WholeTumor	SYNE1	6	152804270	Missense_Mutation	C	T	p.V434I	173	71	0.410	0.912	2	2	0	145	spectrin repeat containing, nuclear envelope 1	ENST00000367255.5
Case#1-Relapse-WholeTumor	FNDC1	6	159653652	Missense_Mutation	C	T	p.S703L	56	25	0.446	0.992	2	2	0	48	fibronectin type III domain containing 1	ENST00000297267.9
Case#1-Relapse-WholeTumor	RPS6KA2	6	166827406	Missense_Mutation	T	G	p.K651T	77	5	0.065	0.144	2	2	0	60	ribosomal protein S6 kinase, 90kDa, polypeptide 2	ENST00000265678.4
Case#1-Relapse-WholeTumor	DACT2	6	168709607	Missense_Mutation	C	T	p.S277N	145	77	0.531	1.180	2	2	0	98	dishevelled-binding antagonist of beta-catenin 2	ENST00000366795.3
Case#1-Relapse-WholeTumor	CARD11	7	2979559	Missense_Mutation	C	T	p.D230N	161	40	0.248	0.370	5	3	2	94	caspase recruitment domain family, member 11	ENST00000396946.4
Case#1-Relapse-WholeTumor	SDK1	7	4259755	Missense_Mutation	G	A	p.V1852M	144	35	0.243	0.362	5	3	2	60	sidekick cell adhesion molecule 1	ENST00000404826.2
Case#1-Relapse-WholeTumor	CYTH3	7	6210478	Missense_Mutation	GG	AA	p.P232S	120	51	0.425	0.633	5	3	2	60	cytohesin 3	ENST00000350796.3
Case#1-Relapse-WholeTumor	COL28A1	7	7421173	Splice_Site	A	G		186	71	0.382	0.568	5	3	2	68	collagen, type XXVIII, alpha 1	ENST00000399429.3
Case#1-Relapse-WholeTumor	AHR	7	17382668	Missense_Mutation	A	T	p.T843S	203	72	0.355	0.528	5	3	2	93	aryl hydrocarbon receptor	ENST00000242057.4
Case#1-Relapse-WholeTumor	MACC1	7	20197852	Missense_Mutation	C	T	p.R711K	84	34	0.405	0.603	5	3	2	39	metastasis associated in colon cancer 1	ENST00000400331.5
Case#1-Relapse-WholeTumor	ABCB5	7	20682869	Missense_Mutation	C	T	p.S126F	485	116	0.239	0.356	5	3	2	235	ATP-binding cassette, sub-family B (MDR/TAP), member 5	ENST00000404938.2
Case#1-Relapse-WholeTumor	RAPGEF5	7	22348019	Missense_Mutation	C	T	p.G207S	116	55	0.474	0.706	5	3	2	47	Rap guanine nucleotide exchange factor (GEF) 5	ENST00000405243.1
Case#1-Relapse-WholeTumor	STK31	7	23871758	Missense_Mutation	G	A	p.D945N	105	28	0.267	0.397	5	3	2	54	serine/threonine kinase 31	ENST00000355870.3

Case#1-Relapse-WholeTumor	MPP6	7	24690197	Missense_Mutation	G	A	p.D173N	289	90	0.311	0.464	5	3	2	139	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	ENST00000222644.5
Case#1-Relapse-WholeTumor	NPSR1	7	34698136	Missense_Mutation	G	A	p.G38R	221	37	0.167	0.249	5	3	2	120	neuropeptide S receptor 1	ENST00000360581.1
Case#1-Relapse-WholeTumor	HECW1	7	43485112	Missense_Mutation	G	A	p.E781K	160	58	0.363	0.540	5	3	2	73	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1	ENST00000395891.2
Case#1-Relapse-WholeTumor	NPC1L1	7	44553240	Missense_Mutation	C	T	p.V1296I	105	23	0.219	0.326	5	3	2	49	NPC1-like 1	ENST00000289547.4
Case#1-Relapse-WholeTumor	NACAD	7	45125328	Missense_Mutation	G	A	p.P151S	38	12	0.316	0.470	5	3	2	18	NAC alpha domain containing	ENST00000490531.2
Case#1-Relapse-WholeTumor	ABCA13	7	48259088	Missense_Mutation	G	A	p.R142Q	178	47	0.264	0.393	5	3	2	90	ATP-binding cassette, sub-family A (ABC1), member 13	ENST00000435803.1
Case#1-Relapse-WholeTumor	FIGNL1	7	50513407	Nonsense_Mutation	G	A	p.Q527*	118	36	0.305	0.454	5	3	2	82	fidgetin-like 1	ENST00000419119.1
Case#1-Relapse-WholeTumor	AUTS2	7	70255135	Missense_Mutation	CC	TT	p.S978F	25	8	0.320	0.516	4	2	2	14	autism susceptibility candidate 2	ENST00000342771.4
Case#1-Relapse-WholeTumor	VPS37D	7	73083819	Missense_Mutation	C	T	p.A70V	128	29	0.227	0.365	4	2	2	87	vacuolar protein sorting 37 homolog D (S. cerevisiae)	ENST00000324941.4
Case#1-Relapse-WholeTumor	PCLO	7	82582784	Missense_Mutation	AG	GA	p.S2495F	198	41	0.207	0.334	4	2	2	119	piccolo presynaptic cytomatrix protein	ENST00000333891.9
Case#1-Relapse-WholeTumor	PCLO	7	82583857	Missense_Mutation	T	C	p.T2138A	74	23	0.311	0.501	4	2	2	27	piccolo presynaptic cytomatrix protein	ENST00000333891.9
Case#1-Relapse-WholeTumor	SEMA3E	7	83035288	Missense_Mutation	C	T	p.G301R	150	48	0.320	0.516	4	2	2	90	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	ENST00000307792.3
Case#1-Relapse-WholeTumor	ZNF804B	7	88965621	Missense_Mutation	C	T	p.H1109Y	76	19	0.250	0.403	4	2	2	45	zinc finger protein 804B	ENST00000333190.4
Case#1-Relapse-WholeTumor	SAMD9	7	92731345	Missense_Mutation	C	T	p.E1356K	78	27	0.346	0.558	4	2	2	48	sterile alpha motif domain containing 9	ENST00000379958.2
Case#1-Relapse-WholeTumor	SAMD9	7	92734411	Missense_Mutation	C	T	p.E334K	96	28	0.292	0.470	4	2	2	56	sterile alpha motif domain containing 9	ENST00000379958.2
Case#1-Relapse-WholeTumor	CCDC132	7	92887505	Missense_Mutation	GC	AG	p.A153S	172	54	0.314	0.506	4	2	2	80	coiled-coil domain containing 132	ENST00000305866.5
Case#1-Relapse-WholeTumor	CALCR	7	93055859	Nonsense_Mutation	G	A	p.Q412*	169	47	0.278	0.448	4	2	2	82	calcitonin receptor	ENST00000394441.1
Case#1-Relapse-WholeTumor	PPP1R9A	7	94539496	Missense_Mutation	G	A	p.R24Q	124	47	0.379	0.611	4	2	2	86	protein phosphatase 1, regulatory subunit 9A	ENST00000433881.1
Case#1-Relapse-WholeTumor	PON1	7	94947634	Splice_Site	C	T		146	39	0.267	0.430	4	2	2	78	paraoxonase 1	ENST00000222381.3
Case#1-Relapse-WholeTumor	SPDYE3	7	99910811	Missense_Mutation	G	A	p.R271K	1205	126	0.105	0.168	4	2	2	582	speedy/RINGO cell cycle regulator family member E3	ENST00000332397.6
Case#1-Relapse-WholeTumor	MYL10	7	101256829	Missense_Mutation	G	A	p.P203S	145	41	0.283	0.456	4	2	2	61	myosin, light chain 10, regulatory	ENST00000223167.4
Case#1-Relapse-WholeTumor	RELN	7	103185660	Missense_Mutation	C	T	p.G2145E	149	33	0.221	0.357	4	2	2	59	reelin	ENST00000428762.1
Case#1-Relapse-WholeTumor	KMT2E	7	104746993	Missense_Mutation	G	A	p.R874Q	104	25	0.240	0.387	4	2	2	62	lysine (K)-specific methyltransferase 2E	ENST00000311117.3
Case#1-Relapse-WholeTumor	ATXN7L1	7	105255069	Missense_Mutation	G	A	p.S571L	350	113	0.323	0.520	4	2	2	162	ataxin 7-like 1	ENST00000419735.3
Case#1-Relapse-WholeTumor	PNPLA8	7	108119753	Missense_Mutation	A	G	p.V650A	161	15	0.093	0.169	3	2	1	117	patatin-like phospholipase domain containing 8	ENST00000422087.1
Case#1-Relapse-WholeTumor	RNF133	7	122338165	Missense_Mutation	G	A	p.R270C	129	16	0.124	0.225	3	2	1	99	ring finger protein 133	ENST00000340112.2
Case#1-Relapse-WholeTumor	GRM8	7	126173610	Missense_Mutation	T	A	p.N609I	69	18	0.261	0.473	3	2	1	45	glutamate receptor, metabotropic 8	ENST00000339582.2
Case#1-Relapse-WholeTumor	FSCN3	7	127236471	Missense_Mutation	C	T	p.R311C	134	18	0.134	0.244	3	2	1	86	fascin actin-bundling protein 3, testicular	ENST00000265825.5
Case#1-Relapse-WholeTumor	PRRT4	7	127999744	Missense_Mutation	A	G	p.L101S	89	12	0.135	0.245	3	2	1	62	proline-rich transmembrane protein 4	ENST00000446477.2
Case#1-Relapse-WholeTumor	MKLN1	7	131130539	Missense_Mutation	C	T	p.R468C	90	25	0.278	0.504	3	2	1	62	muskelin 1, intracellular mediator containing kelch motifs	ENST00000352689.6
Case#1-Relapse-WholeTumor	CHRM2	7	136700756	Missense_Mutation	G	A	p.E382K	120	13	0.108	0.197	3	2	1	99	cholinergic receptor, muscarinic 2	ENST00000445907.2
Case#1-Relapse-WholeTumor	BRAF	7	140453136	Missense_Mutation	AC	TT	p.V600K	125	47	0.376	0.682	3	2	1	78	B-Raf proto-oncogene, serine/threonine kinase	ENST00000288602.6
Case#1-Relapse-WholeTumor	MGAM	7	141731583	Missense_Mutation	G	A	p.G525E	115	45	0.391	0.710	3	2	1	69	maltase-glucoamylase (alpha-glucosidase)	ENST00000549489.2
Case#1-Relapse-WholeTumor	MGAM	7	141755895	Splice_Site	G	A	p.M1193I	129	20	0.155	0.281	3	2	1	106	maltase-glucoamylase (alpha-glucosidase)	ENST00000549489.2
Case#1-Relapse-WholeTumor	MGAM	7	141765190	Missense_Mutation	C	T	p.P1514S	300	72	0.240	0.436	3	2	1	231	maltase-glucoamylase (alpha-glucosidase)	ENST00000549489.2
Case#1-Relapse-WholeTumor	RP11-1220K2.2	7	141837268	Missense_Mutation	C	T	p.R295C	100	38	0.380	0.690	3	2	1	74		ENST00000477922.3
Case#1-Relapse-WholeTumor	RP11-1220K2.2	7	141896372	Missense_Mutation	G	A	p.M1496I	143	55	0.385	0.698	3	2	1	96		ENST00000477922.3
Case#1-Relapse-WholeTumor	PRSS58	7	141954881	Missense_Mutation	C	T	p.D144N	122	41	0.336	NA	NA	NA	NA	76	protease, serine, 58	ENST00000552471.1
Case#1-Relapse-WholeTumor	EPHB6	7	142563271	Missense_Mutation	C	T	p.P330S	102	12	0.118	0.214	3	2	1	61	EPH receptor B6	ENST00000392957.2
Case#1-Relapse-WholeTumor	TRPV6	7	142571199	Splice_Site	A	G		158	10	0.063	0.115	3	2	1	81	transient receptor potential cation channel, subfamily V, member 6	ENST00000359396.3
Case#1-Relapse-WholeTumor	TRPV6	7	142571416	Missense_Mutation	C	T	p.D525N	176	59	0.335	0.608	3	2	1	126	transient receptor potential cation channel, subfamily V, member 6	ENST00000359396.3
Case#1-Relapse-WholeTumor	C7orf34	7	142636842	Missense_Mutation	C	T	p.P67S	118	19	0.161	0.292	3	2	1	52	chromosome 7 open reading frame 34	ENST00000409607.3
Case#1-Relapse-WholeTumor	ZYX	7	143080204	Missense_Mutation	C	T	p.P271L	124	28	0.226	0.410	3	2	1	88	zyxin	ENST00000322764.5
Case#1-Relapse-WholeTumor	AGAP3	7	150817198	Missense_Mutation	G	A	p.R137Q	98	31	0.316	0.574	3	2	1	63	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3	ENST00000463381.1
Case#1-Relapse-WholeTumor	KMT2C	7	152012392	Nonsense_Mutation	C	A	p.E141*	141	47	0.333	0.605	3	2	1	76	lysine (K)-specific methyltransferase 2C	ENST00000262189.6
Case#1-Relapse-WholeTumor	PTPRN2	7	157691406	Missense_Mutation	C	T	p.E583K	108	34	0.315	0.571	3	2	1	99	protein tyrosine phosphatase, receptor type, N polypeptide 2	ENST00000389418.4
Case#1-Relapse-WholeTumor	ERICH1	8	565233	Missense_Mutation	C	T	p.G343E	157	34	0.217	0.481	2	1	1	137	glutamate-rich 1	ENST00000522706.1
Case#1-Relapse-WholeTumor	CSMD1	8	3443759	Missense_Mutation	G	A	p.S375L	53	5	0.094	0.210	2	1	1	53	CUB and Sushi multiple domains 1	ENST00000520002.1
Case#1-Relapse-WholeTumor	CSMD1	8	3611472	Missense_Mutation	C	T	p.G304E	149	38	0.255	0.567	2	1	1	46	CUB and Sushi multiple domains 1	ENST00000520002.1
Case#1-Relapse-WholeTumor	CSMD1	8	4495009	Missense_Mutation	G	A	p.P53S	86	10	0.116	0.258	2	1	1	85	CUB and Sushi multiple domains 1	ENST00000520002.1
Case#1-Relapse-WholeTumor	RP1L1	8	10468628	Missense_Mutation	G	A	p.P994S	20	5	0.250	0.556	2	1	1	21	retinitis pigmentosa 1-like 1	ENST00000382483.3
Case#1-Relapse-WholeTumor	RP1L1	8	10470500	Missense_Mutation	C	T	p.E370K	53	15	0.283	0.629	2	1	1	30	retinitis pigmentosa 1-like 1	ENST00000382483.3
Case#1-Relapse-WholeTumor	PINX1	8	10692188	Nonsense_Mutation	C	T	p.W39*	110	29	0.264	0.586	2	1	1	86	PIN2/TERF1 interacting, telomerase inhibitor 1	ENST00000314787.3
Case#1-Relapse-WholeTumor	XKR6	8	10756097	Missense_Mutation	A	G	p.F431L	151	29	0.192	0.427	2	1	1	150	XK, Kell blood group complex subunit-related family, member 6	ENST00000416569.2
Case#1-Relapse-WholeTumor	HR	8	21984943	Missense_Mutation	G	A	p.L338F	97	28	0.289	0.641	2	1	1	58	hair growth associated	ENST00000381418.4
Case#1-Relapse-WholeTumor	PIWIL2	8	22147376	Missense_Mutation	G	A	p.D335N	186	39	0.210	0.466	2	1	1	139	piwi-like RNA-mediated gene silencing 2	ENST00000454009.2
Case#1-Relapse-WholeTumor	CCAR2	8	22475911	Missense_Mutation	C	T	p.A708V	144	39	0.271	0.602	2	1	1	108	cell cycle and apoptosis regulator 2	ENST00000308511.4
Case#1-Relapse-WholeTumor	LOXL2	8	23185913	Missense_Mutation	C	T	p.G378S	71	13	0.183	0.407	2	1	1	50	lysyl oxidase-like 2	ENST00000389131.3
Case#1-Relapse-WholeTumor	ADAM7	8	24323251	Missense_Mutation	G	A	p.D118N	82	21	0.256	0.569	2	1	1	71	ADAM metallopeptidase domain 7	ENST00000175238.6
Case#1-Relapse-WholeTumor	DOCK5	8	25159955	Missense_Mutation	C	T	p.P321S	109	23	0.211	0.469	2	1	1	82	dedicator of cytokinesis 5	ENST00000276440.7
Case#1-Relapse-WholeTumor	EBF2	8	25720235	Missense_Mutation	C	T	p.R363K	133	26	0.195	0.434	2	1	1	110	early B-cell factor 2	ENST00000520164.1
Case#1-Relapse-WholeTumor	MBOAT4	8	29989645	Missense_Mutation	C	T	p.M374I	64	12	0.188	0.417	2	1	1	39	membrane bound O-acyltransferase domain containing 4	ENST00000320542.3
Case#1-Relapse-WholeTumor	C8orf86	8	38369913	Missense_Mutation	C	T	p.E222K	75	11	0.147	0.326	2	1	1	78	chromosome 8 open reading frame 86	ENST00000358138.1
Case#1-Relapse-WholeTumor	ADAM18	8	39495126	Missense_Mutation	C	T	p.S244F	190	39	0.205	0.456	2	1	1	127	ADAM metallopeptidase domain 18	ENST00000265707.5
Case#1-Relapse-WholeTumor	IDO2	8	39845422	Missense_Mutation	G	A	p.G161E	158	26	0.165	0.366	2	1	1	120	indoleamine 2,3-dioxygenase 2	ENST00000389060.4
Case#1-Relapse-WholeTumor	IDO2	8	39847249	Nonsense_Mutation	C	T	p.Q187*	97	22	0.227	0.504	2	1	1	71	indoleamine 2,3-dioxygenase 2	ENST00000389060.4
Case#1-Relapse-WholeTumor	C8orf4	8	40011065	Missense_Mutation	G	A	p.R5Q	96	14	0.146	0.324	2	1	1	86	chromosome 8 open reading frame 4	ENST00000315792.3
Case#1-Relapse-WholeTumor	KAT6A	8	41791491	Missense_Mutation	G	A	p.P1416L	41	8	0.195	0.434	2	1	1	34	K(lysine) acetyltransferase 6A	ENST00000396930.3
Case#1-Relapse-WholeTumor	PLAG1	8	57079775	Missense_Mutation	G	A	p.S177F	139	25	0.180	0.326	3	2	1	100	pleiomorphic adenoma gene 1	ENST00000316981.3
Case#1-Relapse-WholeTumor	CHD7	8	61655631	Frame_Shift_Del	C	-	p.T547fs	96	19	0.198	0.359	3	2	1	60	chromodomain helicase DNA binding protein 7	ENST00000423902.2
Case#1-Relapse-WholeTumor	PREX2	8	68956771	Missense_Mutation	C	T	p.R297C	193	27	0.140	0.254	3	2	1	119	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2	ENST00000288368.4
Case#1-Relapse-WholeTumor	PREX2	8	69011995	Missense_Mutation	C	T	p.P878S	54	5	0.093	0.168	3	2	1	41	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2	ENST00000288368.4
Case#1-Relapse-WholeTumor	PRDM14	8	70978523	Missense_Mutation	G	A	p.P377L	72	25	0.347	0.630	3	2	1	36	PR domain containing 14	ENST00000276594.2
Case#1-Relapse-WholeTumor	SBSPON	8	73993418	Missense_Mutation	G	A	p.P82L	99	28	0.283	0.513	3	2	1	77	somatomedin B and thrombospondin, type 1 domain containing	ENST00000297354.6
Case#1-Relapse-WholeTumor	ZFHX4	8	77619801	Missense_Mutation	G	A	p.E871K	79	26	0.329	0.597	3	2	1	66	zinc finger homeobox 4	ENST00000521891.2
Case#1-Relapse-WholeTumor	ZFHX4	8	77766277	Missense_Mutation	A	G	p.K2374E	77	13	0.169	0.306	3	2	1	41	zinc finger homeobox 4	ENST00000521891.2
Case#1-Relapse-WholeTumor	ZFHX4	8	77768230	Missense_Mutation	C	T	p.H3025Y	90	36	0.400	0.726	3	2	1	75	zinc finger homeobox 4	ENST00000521891.2
Case#1-Relapse-WholeTumor	PMP2	8	82359603	Missense_Mutation	C	T	p.G7S	114	12	0.105	0.191	3	2	1	58	peripheral myelin protein 2	ENST00000256103.2
Case#1-Relapse-WholeTumor	CNGB3	8	87683207	Missense_Mutation	C	T	p.G153E	171	35	0.205	0.371	3	2	1	95	cyclic nucleotide gated channel beta 3	ENST00000320005.5

Case#1-Relapse-WholeTumor	DECR1	8	91049114	Missense_Mutation	C	T	p.S204L	132	36	0.273	0.495	3	2	1	77	2,4-dienoyl CoA reductase 1, mitochondrial	ENST00000220764.2
Case#1-Relapse-WholeTumor	RUNX1T1	8	93026848	Missense_Mutation	C	T	p.E143K	239	35	0.146	0.266	3	2	1	33	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	ENST00000523629.1
Case#1-Relapse-WholeTumor	VPS13B	8	100286557	Missense_Mutation	C	T	p.P883S	137	19	0.139	0.252	3	2	1	111	vacuolar protein sorting 13 homolog B (yeast)	ENST00000358544.2
Case#1-Relapse-WholeTumor	C8orf56	8	104145509	Missense_Mutation	G	A	p.P22S	95	16	0.168	0.306	3	2	1	61		ENST00000436771.1
Case#1-Relapse-WholeTumor	RIMS2	8	105263362	Missense_Mutation	G	A	p.E1286K	150	27	0.180	0.327	3	2	1	83	regulating synaptic membrane exocytosis 2	ENST00000436393.2
Case#1-Relapse-WholeTumor	PKHD1L1	8	110477181	Missense_Mutation	C	T	p.A2707V	158	17	0.108	0.195	3	2	1	128	polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1	ENST00000378402.5
Case#1-Relapse-WholeTumor	PKHD1L1	8	110477423	Missense_Mutation	T	G	p.F2788V	148	17	0.115	0.208	3	2	1	94	polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1	ENST00000378402.5
Case#1-Relapse-WholeTumor	KCNV1	8	110980535	Missense_Mutation	C	T	p.D429N	142	23	0.162	0.294	3	2	1	82	potassium channel, subfamily V, member 1	ENST00000524391.1
Case#1-Relapse-WholeTumor	CSMD3	8	113421156	Missense_Mutation	G	A	p.S1834F	106	49	0.462	0.839	3	2	1	59	CUB and Sushi multiple domains 3	ENST00000297405.5
Case#1-Relapse-WholeTumor	CSMD3	8	113599347	Missense_Mutation	C	T	p.G1278E	235	81	0.345	0.626	3	2	1	172	CUB and Sushi multiple domains 3	ENST00000297405.5
Case#1-Relapse-WholeTumor	SNTB1	8	121706062	Missense_Mutation	G	A	p.P220S	200	39	0.195	0.354	3	2	1	126	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	ENST00000395601.3
Case#1-Relapse-WholeTumor	FER1L6	8	125131868	Missense_Mutation	C	T	p.S1804L	229	49	0.214	0.388	3	2	1	130	fer-1-like family member 6	ENST00000522917.1
Case#1-Relapse-WholeTumor	NDUFB9	8	125555473	Missense_Mutation	C	T	p.P83S	172	66	0.384	0.696	3	2	1	94	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa	ENST00000276689.3
Case#1-Relapse-WholeTumor	GSDMC	8	130760796	Missense_Mutation	G	A	p.S493F	52	27	0.519	0.942	3	2	1	34	gasdermin C	ENST00000276708.4
Case#1-Relapse-WholeTumor	ADCY8	8	131949386	Missense_Mutation	G	A	p.P472S	163	43	0.264	0.479	3	2	1	93	adenylate cyclase 8 (brain)	ENST00000286355.5
Case#1-Relapse-WholeTumor	GPR20	8	142367729	Missense_Mutation	C	T	p.D99N	239	44	0.184	0.334	3	2	1	142	G protein-coupled receptor 20	ENST00000377741.3
Case#1-Relapse-WholeTumor	KCNV2	9	2717824	Missense_Mutation	A	G	p.S29G	85	6	0.071	0.157	2	1	1	76	potassium channel, subfamily V, member 2	ENST00000382082.3
Case#1-Relapse-WholeTumor	RFX3	9	3266260	Missense_Mutation	C	T	p.G468D	71	12	0.169	0.376	2	1	1	69	regulatory factor X, 3 (influences HLA class II expression)	ENST00000382004.3
Case#1-Relapse-WholeTumor	FREM1	9	14792882	Splice_Site	C	T	p.K1280K	31	11	0.355	0.789	2	1	1	33	FRAS1 related extracellular matrix 1	ENST00000380880.3
Case#1-Relapse-WholeTumor	FREM1	9	14805118	Missense_Mutation	G	A	p.H1103Y	126	34	0.270	0.600	2	1	1	102	FRAS1 related extracellular matrix 1	ENST00000380880.3
Case#1-Relapse-WholeTumor	IFNA10	9	21206889	Nonsense_Mutation	G	A	p.Q70*	414	80	0.193	0.429	2	1	1	331	interferon, alpha 10	ENST00000357374.2
Case#1-Relapse-WholeTumor	AQP3	9	33442091	Missense_Mutation	C	T	p.E277K	46	13	0.283	0.628	2	1	1	32	aquaporin 3 (Gill blood group)	ENST00000297991.4
Case#1-Relapse-WholeTumor	PRSS3	9	33796734	Missense_Mutation	C	T	p.S102F	262	64	0.244	0.543	2	1	1	181	protease, serine, 3	ENST00000361005.5
Case#1-Relapse-WholeTumor	UBAP1	9	34251519	Missense_Mutation	G	A	p.G500R	47	8	0.170	0.378	2	1	1	38	ubiquitin associated protein 1	ENST00000297661.4
Case#1-Relapse-WholeTumor	DNAJB5	9	34996535	Missense_Mutation	C	T	p.P162L	49	11	0.224	0.499	2	1	1	59	DnaJ (Hsp40) homolog, subfamily B, member 5	ENST00000541010.1
Case#1-Relapse-WholeTumor	RUSC2	9	35555066	Missense_Mutation	C	T	p.T675I	77	17	0.221	0.491	2	1	1	44	RUN and SH3 domain containing 2	ENST00000455600.1
Case#1-Relapse-WholeTumor	TPM2	9	35689195	Missense_Mutation	G	A	p.S63F	82	18	0.220	0.488	2	1	1	89	tropomyosin 2 (beta)	ENST00000360958.2
Case#1-Relapse-WholeTumor	NPR2	9	35808639	Missense_Mutation	G	C	p.R949P	93	6	0.065	0.143	2	1	1	80	natriuretic peptide receptor 2	ENST00000342694.2
Case#1-Relapse-WholeTumor	PCSK5	9	78601062	Missense_Mutation	A	C	p.Q104H	116	6	0.052	0.115	2	1	1	79	proprotein convertase subtilisin/kexin type 5	ENST00000545128.1
Case#1-Relapse-WholeTumor	PRUNE2	9	79324306	Missense_Mutation	G	A	p.P962S	96	16	0.167	0.370	2	1	1	93	prune homolog 2 (Drosophila)	ENST00000376718.3
Case#1-Relapse-WholeTumor	PRUNE2	9	79324742	Nonsense_Mutation	C	T	p.W816*	118	40	0.339	0.753	2	1	1	77	prune homolog 2 (Drosophila)	ENST00000376718.3
Case#1-Relapse-WholeTumor	VPS13A	9	79968418	Missense_Mutation	C	T	p.P2505S	107	25	0.234	0.519	2	1	1	60	vacuolar protein sorting 13 homolog A (S. cerevisiae)	ENST00000360280.3
Case#1-Relapse-WholeTumor	SPATA31D1	9	84605355	Nonsense_Mutation	C	T	p.Q86*	113	21	0.186	0.413	2	1	1	121	SPATA31 subfamily D, member 1	ENST00000344803.2
Case#1-Relapse-WholeTumor	SPATA31D1	9	84606542	Missense_Mutation	C	T	p.S386F	148	34	0.230	0.511	2	1	1	112	SPATA31 subfamily D, member 1	ENST00000344803.2
Case#1-Relapse-WholeTumor	SPATA31D1	9	84607427	Missense_Mutation	C	T	p.S681F	211	49	0.232	0.516	2	1	1	170	SPATA31 subfamily D, member 1	ENST00000344803.2
Case#1-Relapse-WholeTumor	SPATA31D1	9	84607702	Nonsense_Mutation	C	T	p.Q773*	189	30	0.159	0.353	2	1	1	165	SPATA31 subfamily D, member 1	ENST00000344803.2
Case#1-Relapse-WholeTumor	SPATA31D1	9	84609831	Nonsense_Mutation	CC	AT	p.Q1483*	47	7	0.149	0.331	2	1	1	50	SPATA31 subfamily D, member 1	ENST00000344803.2
Case#1-Relapse-WholeTumor	SYK	9	93641149	Missense_Mutation	A	C	p.N499H	138	15	0.109	0.242	2	2	0	131	spleen tyrosine kinase	ENST00000375754.4
Case#1-Relapse-WholeTumor	ROR2	9	94519791	Missense_Mutation	C	T	p.G76S	109	30	0.275	0.612	2	2	0	99	receptor tyrosine kinase-like orphan receptor 2	ENST00000375708.3
Case#1-Relapse-WholeTumor	NOL8	9	95078125	Missense_Mutation	G	A	p.S261F	122	48	0.393	0.874	2	2	0	69	nucleolar protein 8	ENST00000535387.1
Case#1-Relapse-WholeTumor	OR13C5	9	107361140	Missense_Mutation	C	T	p.M185I	171	37	0.216	0.481	2	2	0	125	olfactory receptor, family 13, subfamily C, member 5	ENST00000374779.2
Case#1-Relapse-WholeTumor	ZNF462	9	109701335	Missense_Mutation	C	T	p.S2125F	85	15	0.176	0.392	2	2	0	75	zinc finger protein 462	ENST00000277225.5
Case#1-Relapse-WholeTumor	EPB41L4B	9	111970274	Missense_Mutation	G	A	p.P603L	94	20	0.213	0.473	2	2	0	91	erythrocyte membrane protein band 4.1 like 4B	ENST00000374566.3
Case#1-Relapse-WholeTumor	C9orf84	9	114476724	Splice_Site	C	A		131	23	0.176	0.390	2	2	0	119	chromosome 9 open reading frame 84	ENST00000318737.4
Case#1-Relapse-WholeTumor	WDR31	9	116079120	Missense_Mutation	G	A	p.S338F	112	27	0.241	0.536	2	2	0	101	WD repeat domain 31	ENST00000374193.4
Case#1-Relapse-WholeTumor	AMBP	9	116840393	Missense_Mutation	C	T	p.E33K	136	24	0.176	0.392	2	2	0	121	alpha-1-microglobulin/bikunin precursor	ENST00000265132.3
Case#1-Relapse-WholeTumor	COL27A1	9	117063995	Missense_Mutation	C	T	p.P1615S	80	28	0.350	0.778	2	2	0	78	collagen, type XXVII, alpha 1	ENST00000356083.3
Case#1-Relapse-WholeTumor	AKNA	9	117099465	Missense_Mutation	C	T	p.E1397K	71	17	0.239	0.532	2	2	0	53	AT-hook transcription factor	ENST00000307564.4
Case#1-Relapse-WholeTumor	TNFSF8	9	117668179	Splice_Site	C	T	p.G80E	106	13	0.123	0.273	2	2	0	74	tumor necrosis factor (ligand) superfamily, member 8	ENST00000223795.2
Case#1-Relapse-WholeTumor	PAPPA	9	118997855	Missense_Mutation	G	A	p.D891N	104	21	0.202	0.449	2	2	0	101	pregnancy-associated plasma protein A, pappalysin 1	ENST00000328252.3
Case#1-Relapse-WholeTumor	ASTN2	9	119770412	Missense_Mutation	C	T	p.R517K	112	29	0.259	0.575	2	2	0	106	astrotactin 2	ENST00000313400.4
Case#1-Relapse-WholeTumor	CRB2	9	126135412	Splice_Site	G	T		98	20	0.204	0.454	2	2	0	84	crumbs family member 2	ENST00000373631.3
Case#1-Relapse-WholeTumor	FAM102A	9	130710478	Missense_Mutation	G	A	p.S163F	115	22	0.191	0.425	2	2	0	105	family with sequence similarity 102, member A	ENST00000373095.1
Case#1-Relapse-WholeTumor	FAM73B	9	131804656	Missense_Mutation	C	T	p.A57V	85	14	0.165	0.366	2	2	0	55	family with sequence similarity 73, member B	ENST00000358369.4
Case#1-Relapse-WholeTumor	GPR107	9	132869775	Splice_Site	G	A	p.W421*	46	12	0.261	0.580	2	2	0	42	G protein-coupled receptor 107	ENST00000372406.1
Case#1-Relapse-WholeTumor	MED22	9	136208432	Missense_Mutation	G	A	p.P176S	44	27	0.614	1.364	2	2	0	23	mediator complex subunit 22	ENST00000491289.1
Case#1-Relapse-WholeTumor	SARDH	9	136536738	Missense_Mutation	G	A	p.R749W	129	30	0.233	0.517	2	2	0	88	sarcosine dehydrogenase	ENST00000371872.4
Case#1-Relapse-WholeTumor	COL5A1	9	137693800	Splice_Site	G	A	p.G985S	118	47	0.398	0.885	2	2	0	90	collagen, type V, alpha 1	ENST00000371817.3
Case#1-Relapse-WholeTumor	C9orf62	9	138236023	Missense_Mutation	G	A	p.G77R	55	16	0.291	0.646	2	2	0	67	chromosome 9 open reading frame 62	ENST00000320778.2
Case#1-Relapse-WholeTumor	PMPCA	9	139311617	Missense_Mutation	C	T	p.A283V	101	20	0.198	0.440	2	2	0	71	peptidase (mitochondrial processing) alpha	ENST00000371717.3
Case#1-Relapse-WholeTumor	LCN15	9	139658209	Missense_Mutation	G	A	p.A88V	67	37	0.552	1.227	2	2	0	52	lipocalin 15	ENST00000316144.5
Case#1-Relapse-WholeTumor	ABCA2	9	139916431	Missense_Mutation	G	A	p.P196L	129	27	0.209	0.465	2	2	0	91	ATP-binding cassette, sub-family A (ABC1), member 2	ENST00000371605.3
Case#1-Relapse-WholeTumor	KAL1	X	8553349	Missense_Mutation	C	T	p.R272Q	75	33	0.440	NA	NA	NA	NA	56	Kallmann syndrome 1 sequence	ENST00000262648.3
Case#1-Relapse-WholeTumor	MBTPS2	X	21863393	Missense_Mutation	C	T	p.P110L	57	32	0.561	NA	NA	NA	NA	41	membrane-bound transcription factor peptidase, site 2	ENST00000379484.5
Case#1-Relapse-WholeTumor	MAGEB6	X	26212568	Missense_Mutation	T	C	p.L202S	72	35	0.486	NA	NA	NA	NA	63	melanoma antigen family B, 6	ENST00000379034.1
Case#1-Relapse-WholeTumor	DCAF8L2	X	27765397	Missense_Mutation	G	A	p.E129K	56	27	0.482	NA	NA	NA	NA	39	DDB1 and CUL4 associated factor 8-like 2	ENST00000451261.2
Case#1-Relapse-WholeTumor	DCAF8L1	X	27999214	Missense_Mutation	C	T	p.E80K	152	51	0.336	NA	NA	NA	NA	95	DDB1 and CUL4 associated factor 8-like 1	ENST00000441525.1
Case#1-Relapse-WholeTumor	MAGEB2	X	30237541	Missense_Mutation	G	A	p.E282K	65	29	0.446	NA	NA	NA	NA	77	melanoma antigen family B, 2	ENST00000378988.4
Case#1-Relapse-WholeTumor	FAM47A	X	34149036	Missense_Mutation	C	T	p.E454K	95	35	0.368	NA	NA	NA	NA	61	family with sequence similarity 47, member A	ENST00000346193.3
Case#1-Relapse-WholeTumor	CXorf22	X	35984681	Splice_Site	G	A		23	11	0.478	NA	NA	NA	NA	27	chromosome X open reading frame 22	ENST00000297866.5
Case#1-Relapse-WholeTumor	CXorf30	X	36337365	Missense_Mutation	G	A	p.D242N	33	18	0.545	NA	NA	NA	NA	25	chromosome X open reading frame 30	ENST00000378657.4
Case#1-Relapse-WholeTumor	USP9X	X	41048592	Frame_Shift_Ins	-	ACGA	p.-1282fs	96	48	0.500	NA	NA	NA	NA	65	ubiquitin specific peptidase 9, X-linked	ENST00000324545.8
Case#1-Relapse-WholeTumor	USP9X	X	41075197	Missense_Mutation	C	T	p.L1793F	147	55	0.374	NA	NA	NA	NA	93	ubiquitin specific peptidase 9, X-linked	ENST00000324545.8
Case#1-Relapse-WholeTumor	DDX3X	X	41205773	Missense_Mutation	C	G	p.L505V	103	46	0.447	NA	NA	NA	NA	79	DEAD (Asp-Glu-Ala-Asp) box helicase 3, X-linked	ENST00000399959.2
Case#1-Relapse-WholeTumor	CACNA1F	X	49067877	Missense_Mutation	G	A	p.P1400S	48	20	0.417	NA	NA	NA	NA	35	calcium channel, voltage-dependent, L type, alpha 1F subunit	ENST00000376265.2
Case#1-Relapse-WholeTumor	CCNB3	X	50051581	Missense_Mutation	G	A	p.D138N	87	45	0.517	NA	NA	NA	NA	51	cyclin B3	ENST00000376042.1
Case#1-Relapse-WholeTumor	KIAA2022	X	73960373	Missense_Mutation	G	A	p.P1340L	34	20	0.588	NA	NA	NA	NA	22	KIAA2022	ENST00000055682.6
Case#1-Relapse-WholeTumor	KIAA2022	X	73961246	Missense_Mutation	G	A	p.S1049F	70	27	0.386	NA	NA	NA	NA	61	KIAA2022	ENST00000055682.6
Case#1-Relapse-WholeTumor	CYSLTR1	X	77529237	Missense_Mutation	C	T	p.E3K	16	7	0.438	NA	NA	NA	NA	21	cysteinyl leukotriene receptor 1	ENST00000373304.3
Case#1-Relapse-WholeTumor	PCDH19	X	99551514	Missense_Mutation	GG	AA	p.H1070Y	33	13	0.394	NA	NA	NA	NA	22	protocadherin 19	ENST00000373034.4

Case#1-Relapse-WholeTumor	TAF7L	X	100531091	Missense_Mutation	A	G	p.I394T	36	12	0.333	NA	NA	NA	NA	25	TAF7-like RNA polymerase II, TATA box binding protein (TBP)-associated factor, 50kDa	ENST00000372907.3
Case#1-Relapse-WholeTumor	ESX1	X	103499146	Missense_Mutation	CC	AT	p.G65D	24	11	0.458	NA	NA	NA	NA	22	ESX homeobox 1	ENST00000372588.4
Case#1-Relapse-WholeTumor	NRK	X	105132299	Missense_Mutation	G	A	p.D89N	33	20	0.606	NA	NA	NA	NA	31	Nik related kinase	ENST00000243300.9
Case#1-Relapse-WholeTumor	CAPN6	X	110497543	Missense_Mutation	G	A	p.S85F	86	28	0.326	NA	NA	NA	NA	60	calpain 6	ENST00000324068.1
Case#1-Relapse-WholeTumor	LRCH2	X	114358531	Missense_Mutation	G	A	p.P609L	54	28	0.519	NA	NA	NA	NA	53	leucine-rich repeats and calponin homology (CH) domain containing 2	ENST00000317135.8
Case#1-Relapse-WholeTumor	TENM1	X	123838976	Missense_Mutation	G	A	p.S301F	94	37	0.394	NA	NA	NA	NA	78	teneurin transmembrane protein 1	ENST00000371130.3
Case#1-Relapse-WholeTumor	ARHGAP36	X	130220631	Missense_Mutation	C	T	p.S493F	69	22	0.319	NA	NA	NA	NA	55	Rho GTPase activating protein 36	ENST00000276211.5
Case#1-Relapse-WholeTumor	GPR112	X	135431303	Missense_Mutation	C	T	p.S1813F	53	18	0.340	NA	NA	NA	NA	52	G protein-coupled receptor 112	ENST00000394143.1
Case#1-Relapse-WholeTumor	F9	X	138643980	Missense_Mutation	G	A	p.R379Q	45	24	0.533	NA	NA	NA	NA	30	coagulation factor IX	ENST00000218099.2
Case#1-Relapse-WholeTumor	BGN	X	152772308	Missense_Mutation	G	A	p.E233K	48	15	0.313	NA	NA	NA	NA	32	biglycan	ENST00000331595.4
Case#1-Relapse-WholeTumor	PDZD4	X	153071546	Frame_Shift_Del	CA	-	p.*177fs	95	34	0.358	NA	NA	NA	NA	72	PDZ domain containing 4	ENST00000164640.4
Case#1-Relapse-WholeTumor	SLC9B1P1	Y	13501691	Missense_Mutation	G	A	p.S173L	95	37	0.389	NA	NA	NA	NA	67	solute carrier family 9, subfamily B (NHA1, cation proton antiporter 1), member 1 pseudogene 1	ENST00000331172.6
Case#1-Baseline-WholeTumor	PRDM16	1	3321331	Missense_Mutation	G	A	p.E305K	86	28	0.326	0.412	2	1	1	62	PR domain containing 16	ENST00000270722.5
Case#1-Baseline-WholeTumor	EXOSC10	1	11158126	Missense_Mutation	G	A	p.P67S	69	30	0.435	0.550	2	1	1	59	exosome component 10	ENST00000376936.4
Case#1-Baseline-WholeTumor	PLOD1	1	12017971	Missense_Mutation	G	A	p.E272K	121	52	0.430	0.544	2	1	1	114	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	ENST00000196061.4
Case#1-Baseline-WholeTumor	PRAMEF4	1	12941719	Missense_Mutation	C	T	p.M277I	559	105	0.188	0.238	2	1	1	694	PRAME family member 4	ENST00000235349.5
Case#1-Baseline-WholeTumor	PRAMEF22	1	13036403	Missense_Mutation	G	A	p.E159K	312	66	0.212	0.268	2	1	1	441	PRAME family member 22	ENST00000376187.1
Case#1-Baseline-WholeTumor	RSC1A1	1	15987133	Missense_Mutation	C	T	p.S257F	35	14	0.400	0.506	2	1	1	35	regulatory solute carrier protein, family 1, member 1	ENST00000345034.1
Case#1-Baseline-WholeTumor	FAM131C	1	16385124	Missense_Mutation	GG	AA	p.S217F	142	20	0.141	0.178	2	1	1	132	family with sequence similarity 131, member C	ENST00000375662.4
Case#1-Baseline-WholeTumor	FBXO42	1	16577779	Missense_Mutation	G	A	p.P514S	62	21	0.339	0.429	2	1	1	69	F-box protein 42	ENST00000375592.3
Case#1-Baseline-WholeTumor	NBPF1	1	16892277	Missense_Mutation	G	A	p.A972V	133	11	0.083	0.105	2	1	1	74	neuroblastoma breakpoint family, member 1	ENST00000430580.2
Case#1-Baseline-WholeTumor	NBPF1	1	16895613	Missense_Mutation	G	A	p.H857Y	1129	109	0.097	0.122	2	1	1	1742	neuroblastoma breakpoint family, member 1	ENST00000430580.2
Case#1-Baseline-WholeTumor	UBR4	1	19411143	Nonsense_Mutation	G	A	p.Q4955*	91	28	0.308	0.389	2	1	1	94	ubiquitin protein ligase E3 component n-recognin 4	ENST00000375254.3
Case#1-Baseline-WholeTumor	HSPG2	1	22170753	Missense_Mutation	G	A	p.S2835F	104	30	0.288	0.365	2	1	1	72	heparan sulfate proteoglycan 2	ENST00000374695.3
Case#1-Baseline-WholeTumor	LACTBL1	1	23285254	Missense_Mutation	C	T	p.M159I	48	16	0.333	0.422	2	1	1	55	lactamase, beta-like 1	ENST00000426928.2
Case#1-Baseline-WholeTumor	IL22RA1	1	24447965	Missense_Mutation	G	A	p.A352V	97	40	0.412	0.522	2	1	1	96	interleukin 22 receptor, alpha 1	ENST00000270800.1
Case#1-Baseline-WholeTumor	YTHDF2	1	29070382	Missense_Mutation	C	G	p.L534V	127	44	0.346	0.439	2	1	1	112	YTH domain family, member 2	ENST00000373812.3
Case#1-Baseline-WholeTumor	CSMD2	1	34037163	Nonsense_Mutation	C	T	p.W2642*	81	27	0.333	0.422	2	1	1	88	CUB and Sushi multiple domains 2	ENST00000373381.4
Case#1-Baseline-WholeTumor	CSMD2	1	34128655	Missense_Mutation	C	T	p.D237N	43	20	0.465	0.589	2	1	1	37	CUB and Sushi multiple domains 2	ENST00000373380.1
Case#1-Baseline-WholeTumor	CSMD2	1	34401378	Missense_Mutation	G	A	p.P232L	28	8	0.286	0.362	2	1	1	27	CUB and Sushi multiple domains 2	ENST00000373381.4
Case#1-Baseline-WholeTumor	ZMYM4	1	35885142	Missense_Mutation	C	T	p.P1504L	79	38	0.481	0.609	2	1	1	125	zinc finger, MYM-type 4	ENST00000314607.6
Case#1-Baseline-WholeTumor	MACF1	1	39823309	Missense_Mutation	C	T	p.S3901F	75	31	0.413	0.523	2	1	1	67	microtubule-actin crosslinking factor 1	ENST00000372915.3
Case#1-Baseline-WholeTumor	NFYC	1	41236181	Frame_Shift_Ins	-	C	p.HP353fs	71	27	0.380	0.481	2	1	1	77	nuclear transcription factor Y, gamma	ENST00000308733.5
Case#1-Baseline-WholeTumor	C1orf50	1	43240949	Missense_Mutation	C	T	p.P162S	66	24	0.364	0.460	2	1	1	74	chromosome 1 open reading frame 50	ENST00000372525.5
Case#1-Baseline-WholeTumor	KLF17	1	44595265	Missense_Mutation	C	T	p.P108S	61	20	0.328	0.415	2	1	1	48	Kruppel-like factor 17	ENST00000372299.3
Case#1-Baseline-WholeTumor	PTCH2	1	45297861	Missense_Mutation	GG	AA	p.L140F	78	30	0.385	0.487	2	1	1	90	patched 2	ENST00000372192.3
Case#1-Baseline-WholeTumor	SLC5A9	1	48694988	Missense_Mutation	C	T	p.L121F	66	28	0.424	0.537	2	1	1	67	solute carrier family 5 (sodium/sugar cotransporter), member 9	ENST00000438567.2
Case#1-Baseline-WholeTumor	ECHDC2	1	53370732	Missense_Mutation	G	A	p.T163I	93	43	0.462	0.585	2	1	1	77	enoyl CoA hydratase domain containing 2	ENST00000371522.4
Case#1-Baseline-WholeTumor	PODN	1	53543414	Missense_Mutation	G	A	p.E314K	65	27	0.415	0.526	2	1	1	66	podocan	ENST00000312553.5
Case#1-Baseline-WholeTumor	FAM151A	1	55088975	Missense_Mutation	G	A	p.L32F	150	42	0.280	0.354	2	1	1	153	family with sequence similarity 151, member A	ENST00000302250.2
Case#1-Baseline-WholeTumor	TTC22	1	55266809	Missense_Mutation	C	T	p.D10N	48	20	0.417	0.527	2	1	1	40	tetratricopeptide repeat domain 22	ENST00000371276.4
Case#1-Baseline-WholeTumor	C1orf168	1	57219580	Missense_Mutation	C	T	p.E387K	94	26	0.277	0.350	2	1	1	124	chromosome 1 open reading frame 168	ENST00000343433.6
Case#1-Baseline-WholeTumor	C1orf168	1	57257903	Missense_Mutation	G	A	p.P195S	49	9	0.184	0.232	2	1	1	69	chromosome 1 open reading frame 168	ENST00000343433.6
Case#1-Baseline-WholeTumor	C1orf168	1	57257998	Missense_Mutation	C	T	p.G163E	60	19	0.317	0.401	2	1	1	73	chromosome 1 open reading frame 168	ENST00000343433.6
Case#1-Baseline-WholeTumor	C8B	1	57417854	Splice_Site	C	T		81	37	0.457	0.578	2	1	1	99	complement component 8, beta polypeptide	ENST00000371237.4
Case#1-Baseline-WholeTumor	FGGY	1	60139762	Missense_Mutation	C	T	p.A490V	101	48	0.475	0.602	2	1	1	117	FGGY carbohydrate kinase domain containing	ENST00000303721.7
Case#1-Baseline-WholeTumor	L1TD1	1	62676451	Nonsense_Mutation	C	T	p.Q669*	36	14	0.389	0.492	2	1	1	39	LINE-1 type transposase domain containing 1	ENST00000498273.1
Case#1-Baseline-WholeTumor	PGM1	1	64125279	Missense_Mutation	C	T	p.S541F	46	17	0.370	0.468	2	1	1	59	phosphoglucomutase 1	ENST00000371084.3
Case#1-Baseline-WholeTumor	CACHD1	1	65131810	Missense_Mutation	G	A	p.G783S	72	30	0.417	0.527	2	1	1	76	cache domain containing 1	ENST00000371073.2
Case#1-Baseline-WholeTumor	TCTEX1D1	1	67242961	Missense_Mutation	A	C	p.M122L	67	30	0.448	0.567	2	1	1	84	Tctex1 domain containing 1	ENST00000282670.2
Case#1-Baseline-WholeTumor	DEPDC1	1	68944934	Missense_Mutation	C	T	p.G669R	70	27	0.386	0.488	2	1	1	66	DEP domain containing 1	ENST00000456315.2
Case#1-Baseline-WholeTumor	LRRC7	1	70504734	Missense_Mutation	G	A	p.G1038E	69	31	0.449	0.569	2	1	1	47	leucine rich repeat containing 7	ENST00000035383.5
Case#1-Baseline-WholeTumor	SLC44A5	1	75708615	Missense_Mutation	C	T	p.E143K	61	16	0.262	0.332	2	1	1	73	solute carrier family 44, member 5	ENST00000370855.5
Case#1-Baseline-WholeTumor	AK5	1	77752704	Missense_Mutation	G	A	p.E47K	88	37	0.420	0.532	2	1	1	103	adenylate kinase 5	ENST00000354567.2
Case#1-Baseline-WholeTumor	GIPC2	1	78560732	Missense_Mutation	C	T	p.H175Y	93	36	0.387	0.490	2	1	1	104	GIPC PDZ domain containing family, member 2	ENST00000370759.3
Case#1-Baseline-WholeTumor	CLCA2	1	86913369	Missense_Mutation	G	A	p.G631E	80	32	0.400	0.506	2	1	1	101	chloride channel accessory 2	ENST00000370565.4
Case#1-Baseline-WholeTumor	LRRC8B	1	90048448	Missense_Mutation	CC	TT	p.S80F	44	13	0.295	0.374	2	1	1	49	leucine rich repeat containing 8 family, member B	ENST00000330947.2
Case#1-Baseline-WholeTumor	F3	1	95005853	Missense_Mutation	C	T	p.E58K	103	44	0.427	0.541	2	1	1	141	coagulation factor III (thromboplastin, tissue factor)	ENST00000334047.7
Case#1-Baseline-WholeTumor	DPYD	1	98293682	Missense_Mutation	C	T	p.R74Q	38	12	0.316	0.400	2	1	1	66	dihydropyrimidine dehydrogenase	ENST00000370192.3
Case#1-Baseline-WholeTumor	OLFM3	1	102270241	Nonsense_Mutation	A	C	p.Y330*	53	26	0.491	0.621	2	1	1	84	olfactomedin 3	ENST00000338858.5
Case#1-Baseline-WholeTumor	COL11A1	1	103364320	Missense_Mutation	C	T	p.G1384S	113	36	0.319	0.403	2	1	1	119	collagen, type XI, alpha 1	ENST00000370096.3
Case#1-Baseline-WholeTumor	COL11A1	1	103463909	Missense_Mutation	C	T	p.G718E	77	24	0.312	0.395	2	1	1	124	collagen, type XI, alpha 1	ENST00000370096.3
Case#1-Baseline-WholeTumor	CELSR2	1	109813876	Missense_Mutation	C	T	p.S2545F	65	26	0.400	0.506	2	1	1	63	cadherin, EGF LAG seven-pass G-type receptor 2	ENST00000271332.3
Case#1-Baseline-WholeTumor	MYBPHL	1	109839414	Nonsense_Mutation	G	A	p.Q241*	125	58	0.464	0.587	2	1	1	121	myosin binding protein H-like	ENST00000357155.1
Case#1-Baseline-WholeTumor	AHCYL1	1	110527681	Frame_Shift_Ins	-	TGCC	p.-4fs	97	31	0.320	0.405	2	1	1	35	adenosylhomocysteinase-like 1	ENST00000369799.5
Case#1-Baseline-WholeTumor	LRIG2	1	113666581	Missense_Mutation	C	T	p.S1019L	74	26	0.351	0.445	2	1	1	84	leucine-rich repeats and immunoglobulin-like domains 2	ENST00000361127.5
Case#1-Baseline-WholeTumor	DENND2C	1	115164674	Missense_Mutation	G	A	p.P357S	126	50	0.397	0.502	2	1	1	165	DENN/MADD domain containing 2C	ENST00000393274.1
Case#1-Baseline-WholeTumor	SYCP1	1	115487554	Missense_Mutation	G	A	p.R702Q	93	38	0.409	0.517	2	1	1	96	synaptonemal complex protein 1	ENST00000369522.3
Case#1-Baseline-WholeTumor	NGF	1	115829131	Missense_Mutation	C	T	p.E96K	68	20	0.294	0.372	2	1	1	61	nerve growth factor (beta polypeptide)	ENST00000369512.2
Case#1-Baseline-WholeTumor	IGSF3	1	117142910	Missense_Mutation	G	A	p.S561F	68	23	0.338	0.428	2	1	1	54	immunoglobulin superfamily, member 3	ENST00000369486.3
Case#1-Baseline-WholeTumor	WDR3	1	118481139	Missense_Mutation	T	A	p.D179E	76	29	0.382	0.483	2	1	1	98	WD repeat domain 3	ENST00000349139.5
Case#1-Baseline-WholeTumor	SPAG17	1	118624140	Missense_Mutation	C	T	p.E630K	60	16	0.267	0.338	2	1	1	67	sperm associated antigen 17	ENST00000336338.5
Case#1-Baseline-WholeTumor	HSD3B2	1	119964548	Missense_Mutation	G	A	p.E142K	89	28	0.315	0.398	2	1	1	104	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2	ENST00000543831.1
Case#1-Baseline-WholeTumor	HSD3B2	1	119965208	Missense_Mutation	C	T	p.R362W	79	30	0.380	0.481	2	1	1	112	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2	ENST00000543831.1
Case#1-Baseline-WholeTumor	ANKRD35	1	145561858	Missense_Mutation	CC	TT	p.P516L	82	21	0.256	0.301	3	2	1	66	ankyrin repeat domain 35	ENST00000355594.4
Case#1-Baseline-WholeTumor	FCGR1A	1	149759943	Missense_Mutation	C	T	p.S110F	270	155	0.574	0.676	3	2	1	242	Fc fragment of IgG, high affinity Ia, receptor (CD64)	ENST00000369168.4
Case#1-Baseline-WholeTumor	TCHH	1	152080664	Nonsense_Mutation	G	A	p.Q1677*	118	34	0.288	0.339	3	2	1	82	trichohyalin	ENST00000368804.1
Case#1-Baseline-WholeTumor	TCHH	1	152082830	Missense_Mutation	C	T	p.E955K	89	22	0.247	0.291	3	2	1	72	trichohyalin	ENST00000368804.1
Case#1-Baseline-WholeTumor	HRNR	1	152190971	Missense_Mutation	C	T	p.G1045D	305	78	0.256	0.301	3	2	1	246	hornerin	ENST00000368801.2
Case#1-Baseline-WholeTumor	FLG	1	152280808	Missense_Mutation	C	T	p.G2185E	332	76	0.229	0.269	3	2	1	335	filaggrin	ENST00000368799.1

Case#1-Baseline-WholeTumor	FLG	1	152283826	Missense_Mutation	G	A	p.S1179F	324	90	0.278	0.327	3	2	1	338	filaggrin	ENST00000368799.1
Case#1-Baseline-WholeTumor	FLG	1	152284345	Missense_Mutation	C	T	p.G1006E	230	76	0.330	0.389	3	2	1	225	filaggrin	ENST00000368799.1
Case#1-Baseline-WholeTumor	FLG2	1	152325229	Missense_Mutation	C	T	p.G1678E	275	84	0.305	0.360	3	2	1	315	filaggrin family member 2	ENST00000388718.5
Case#1-Baseline-WholeTumor	CRNN	1	152382120	Missense_Mutation	C	T	p.G480S	121	8	0.066	0.078	3	2	1	84	cornulin	ENST00000271835.3
Case#1-Baseline-WholeTumor	CRNN	1	152383101	Nonsense_Mutation	G	A	p.Q153*	61	30	0.492	0.579	3	2	1	53	cornulin	ENST00000271835.3
Case#1-Baseline-WholeTumor	S100A3	1	153520165	Missense_Mutation	G	A	p.S100F	188	54	0.287	0.338	3	2	1	128	S100 calcium binding protein A3	ENST00000368713.3
Case#1-Baseline-WholeTumor	SNAPIN	1	153633746	Missense_Mutation	G	A	p.G127E	98	19	0.194	0.228	3	2	1	79	SNAP-associated protein	ENST00000368685.5
Case#1-Baseline-WholeTumor	NUP210L	1	154062058	Nonsense_Mutation	G	A	p.R734*	78	17	0.218	0.257	3	2	1	50	nucleoporin 210kDa-like	ENST00000368559.3
Case#1-Baseline-WholeTumor	UBAP2L	1	154228226	Missense_Mutation	C	T	p.L718F	109	32	0.294	0.346	3	2	1	73	ubiquitin associated protein 2-like	ENST00000361546.2
Case#1-Baseline-WholeTumor	BCAN	1	156622520	Missense_Mutation	C	T	p.S593F	37	12	0.324	0.382	3	2	1	34	brevican	ENST00000329117.5
Case#1-Baseline-WholeTumor	PRCC	1	156756716	Missense_Mutation	C	T	p.S278F	57	5	0.088	0.103	3	2	1	72	papillary renal cell carcinoma (translocation-associated)	ENST00000271526.4
Case#1-Baseline-WholeTumor	FCRL2	1	157737021	Splice_Site	C	A	p.G388*	35	6	0.171	0.202	3	2	1	36	Fc receptor-like 2	ENST00000361516.3
Case#1-Baseline-WholeTumor	OR10T2	1	158368898	Missense_Mutation	C	T	p.G120E	52	18	0.346	0.407	3	2	1	39	olfactory receptor, family 10, subfamily T, member 2	ENST00000334438.1
Case#1-Baseline-WholeTumor	OR10X1	1	158548760	Missense_Mutation	C	T	p.M310I	116	32	0.276	0.325	3	2	1	104	olfactory receptor, family 10, subfamily X, member 1 (gene/pseudogene)	ENST00000368150.1
Case#1-Baseline-WholeTumor	SPTA1	1	158585076	Nonsense_Mutation	G	A	p.Q2240*	113	28	0.248	0.292	3	2	1	86	spectrin, alpha, erythrocytic 1	ENST00000368147.4
Case#1-Baseline-WholeTumor	OR6K3	1	158687250	Missense_Mutation	C	T	p.R235K	86	15	0.174	0.205	3	2	1	63	olfactory receptor, family 6, subfamily K, member 3	ENST00000368146.1
Case#1-Baseline-WholeTumor	OR6N1	1	158736124	Missense_Mutation	C	T	p.A117T	75	43	0.573	0.675	3	2	1	72	olfactory receptor, family 6, subfamily N, member 1	ENST00000335094.2
Case#1-Baseline-WholeTumor	OR10J1	1	159410110	Missense_Mutation	T	G	p.F188V	102	32	0.314	0.369	3	2	1	98	olfactory receptor, family 10, subfamily J, member 1	ENST00000423932.3
Case#1-Baseline-WholeTumor	CRP	1	159683805	Missense_Mutation	G	A	p.S62F	34	20	0.588	0.692	3	2	1	51	C-reactive protein, pentraxin-related	ENST00000255030.5
Case#1-Baseline-WholeTumor	SLAMF8	1	159799815	Missense_Mutation	C	T	p.S67F	53	32	0.604	0.711	3	2	1	30	SLAM family member 8	ENST00000289707.5
Case#1-Baseline-WholeTumor	LY9	1	160783554	Missense_Mutation	G	A	p.E195K	91	19	0.209	0.246	3	2	1	110	lymphocyte antigen 9	ENST00000263285.6
Case#1-Baseline-WholeTumor	ITLN1	1	160851081	Nonsense_Mutation	G	A	p.Q143*	126	28	0.222	0.262	3	2	1	110	intelectin 1 (galactofuranose binding)	ENST00000326245.3
Case#1-Baseline-WholeTumor	FCGR3A	1	161518217	Missense_Mutation	G	A	p.H105Y	345	36	0.104	0.123	3	2	1	244	Fc fragment of IgG, low affinity IIIa, receptor (CD16a)	ENST00000436743.1
Case#1-Baseline-WholeTumor	UHMK1	1	162487933	Missense_Mutation	C	T	p.P356S	189	42	0.222	0.262	3	2	1	133	U2AF homology motif (UHM) kinase 1	ENST00000489294.1
Case#1-Baseline-WholeTumor	RGS5	1	163122504	Missense_Mutation	C	T	p.G74R	96	52	0.542	0.638	3	2	1	63	regulator of G-protein signaling 5	ENST00000313961.5
Case#1-Baseline-WholeTumor	MAEL	1	166960705	Missense_Mutation	GG	AA	p.G106N	111	32	0.288	0.339	3	2	1	104	maelstrom spermatogenic transposon silencer	ENST00000367872.4
Case#1-Baseline-WholeTumor	CD247	1	167402275	Missense_Mutation	C	T	p.D139N	54	31	0.574	0.676	3	2	1	48	CD247 molecule	ENST00000362089.5
Case#1-Baseline-WholeTumor	ADCY10	1	167871277	Missense_Mutation	C	T	p.G90E	109	32	0.294	0.346	3	2	1	80	adenylate cyclase 10 (soluble)	ENST00000367851.4
Case#1-Baseline-WholeTumor	NME7	1	169292461	Missense_Mutation	C	T	p.E58K	78	30	0.385	0.453	3	2	1	55	NME/NM23 family member 7	ENST00000367811.3
Case#1-Baseline-WholeTumor	CCDC181	1	169391259	Missense_Mutation	A	T	p.L137H	33	6	0.182	0.214	3	2	1	29	coiled-coil domain containing 181	ENST00000367806.3
Case#1-Baseline-WholeTumor	FMO4	1	171292331	Splice_Site	G	A	p.K107K	84	10	0.119	0.140	3	2	1	97	flavin containing monooxygenase 4	ENST00000367749.3
Case#1-Baseline-WholeTumor	SLC9C2	1	173545816	Missense_Mutation	C	T	p.E296K	63	23	0.365	0.430	3	2	1	32	solute carrier family 9, member C2 (putative)	ENST00000367714.3
Case#1-Baseline-WholeTumor	SLC9C2	1	173567152	Missense_Mutation	G	A	p.P83L	95	29	0.305	0.359	3	2	1	43	solute carrier family 9, member C2 (putative)	ENST00000367714.3
Case#1-Baseline-WholeTumor	TNN	1	175046583	Missense_Mutation	C	T	p.P10L	35	10	0.286	0.336	3	2	1	25	tenascin N	ENST00000239462.4
Case#1-Baseline-WholeTumor	TNR	1	175293631	Missense_Mutation	C	T	p.G1273E	127	22	0.173	0.204	3	2	1	93	tenascin R	ENST00000367674.2
Case#1-Baseline-WholeTumor	TNR	1	175324709	Missense_Mutation	G	A	p.S1060F	84	25	0.298	0.350	3	2	1	85	tenascin R	ENST00000367674.2
Case#1-Baseline-WholeTumor	TNR	1	175325572	Missense_Mutation	C	T	p.G1001R	138	41	0.297	0.350	3	2	1	124	tenascin R	ENST00000367674.2
Case#1-Baseline-WholeTumor	TNR	1	175331865	Missense_Mutation	C	T	p.E930K	209	133	0.636	0.749	3	2	1	226	tenascin R	ENST00000367674.2
Case#1-Baseline-WholeTumor	PAPPA2	1	176525628	Missense_Mutation	G	A	p.R57Q	65	15	0.231	0.272	3	2	1	106	pappalysin 2	ENST00000367662.3
Case#1-Baseline-WholeTumor	PAPPA2	1	176709218	Missense_Mutation	C	T	p.S1346L	65	15	0.231	0.272	3	2	1	85	pappalysin 2	ENST00000367662.3
Case#1-Baseline-WholeTumor	ASTN1	1	176926845	Missense_Mutation	G	A	p.S627L	79	21	0.266	0.313	3	2	1	106	astrotactin 1	ENST00000367654.3
Case#1-Baseline-WholeTumor	ASTN1	1	177133719	Missense_Mutation	C	T	p.E32K	48	12	0.250	0.294	3	2	1	31	astrotactin 1	ENST00000367654.3
Case#1-Baseline-WholeTumor	RASAL2	1	178423643	Missense_Mutation	G	A	p.G543R	123	30	0.244	0.287	3	2	1	74	RAS protein activator like 2	ENST00000462775.1
Case#1-Baseline-WholeTumor	QSOX1	1	180158768	Missense_Mutation	C	T	p.P367S	82	28	0.341	0.402	3	2	1	79	quiescin Q6 sulfhydryl oxidase 1	ENST00000367602.3
Case#1-Baseline-WholeTumor	CACNA1E	1	181695231	Nonsense_Mutation	C	T	p.Q725*	69	30	0.435	0.512	3	2	1	79	calcium channel, voltage-dependent, R type, alpha 1E subunit	ENST00000367573.2
Case#1-Baseline-WholeTumor	RGSL1	1	182443171	Missense_Mutation	G	A	p.E309K	53	15	0.283	0.333	3	2	1	50	regulator of G-protein signaling like 1	ENST00000294854.8
Case#1-Baseline-WholeTumor	NMNAT2	1	183261971	Missense_Mutation	G	C	p.R66G	68	13	0.191	0.225	3	2	1	63	nicotinamide nucleotide adenylyltransferase 2	ENST00000287713.6
Case#1-Baseline-WholeTumor	SMG7	1	183498642	Nonsense_Mutation	C	T	p.R273*	114	23	0.202	0.238	3	2	1	87	SMG7 nonsense mediated mRNA decay factor	ENST00000347615.2
Case#1-Baseline-WholeTumor	FAM129A	1	184764464	Missense_Mutation	C	T	p.E812K	52	14	0.269	0.317	3	2	1	50	family with sequence similarity 129, member A	ENST00000367511.3
Case#1-Baseline-WholeTumor	HMCN1	1	186059892	Missense_Mutation	C	T	p.P3244S	80	17	0.213	0.250	3	2	1	70	hemicentin 1	ENST00000271588.4
Case#1-Baseline-WholeTumor	HMCN1	1	186084051	Missense_Mutation	C	T	p.R3793C	116	34	0.293	0.345	3	2	1	98	hemicentin 1	ENST00000271588.4
Case#1-Baseline-WholeTumor	PRG4	1	186276622	Missense_Mutation	G	A	p.E591K	102	25	0.245	0.289	3	2	1	76	proteoglycan 4	ENST00000445192.2
Case#1-Baseline-WholeTumor	PDC	1	186413125	Missense_Mutation	C	T	p.E243K	103	24	0.233	0.274	3	2	1	97	phosducin	ENST00000391997.2
Case#1-Baseline-WholeTumor	UCHL5	1	192993057	Nonsense_Mutation	G	A	p.R217*	77	26	0.338	0.398	3	2	1	52	ubiquitin carboxyl-terminal hydrolase L5	ENST00000367455.4
Case#1-Baseline-WholeTumor	PTPRC	1	198718604	Missense_Mutation	G	A	p.D998N	65	32	0.492	0.580	3	2	1	51	protein tyrosine phosphatase, receptor type, C	ENST00000367376.2
Case#1-Baseline-WholeTumor	CACNA1S	1	201039480	Missense_Mutation	GG	AA	p.P760L	65	42	0.646	0.761	3	2	1	27	calcium channel, voltage-dependent, L type, alpha 1S subunit	ENST00000362061.3
Case#1-Baseline-WholeTumor	PKP1	1	201294101	Missense_Mutation	C	T	p.L644F	99	30	0.303	0.357	3	2	1	78	plakophilin 1	ENST00000352845.3
Case#1-Baseline-WholeTumor	LGR6	1	202287440	Missense_Mutation	C	T	p.S670F	118	37	0.314	0.369	3	2	1	59	leucine-rich repeat containing G protein-coupled receptor 6	ENST00000367278.3
Case#1-Baseline-WholeTumor	FMOD	1	203317046	Missense_Mutation	G	A	p.T118I	137	41	0.299	0.352	3	2	1	97	fibromodulin	ENST00000354955.4
Case#1-Baseline-WholeTumor	NFASC	1	204949527	Missense_Mutation	G	A	p.G736R	121	27	0.223	0.263	3	2	1	83	neurofascin	ENST00000401399.1
Case#1-Baseline-WholeTumor	CR1	1	207751155	Missense_Mutation	C	T	p.P1515S	282	166	0.589	0.693	3	2	1	276	complement component (3b/4b) receptor 1 (Knops blood group)	ENST00000367049.4
Case#1-Baseline-WholeTumor	C1orf74	1	209956207	Missense_Mutation	G	A	p.S258F	76	32	0.421	0.496	3	2	1	61	chromosome 1 open reading frame 74	ENST00000294811.1
Case#1-Baseline-WholeTumor	KCNH1	1	211263988	Missense_Mutation	C	T	p.E119K	111	36	0.324	0.382	3	2	1	95	potassium voltage-gated channel, subfamily H (eag-related), member 1	ENST00000271751.4
Case#1-Baseline-WholeTumor	USH2A	1	216498829	Missense_Mutation	G	A	p.P321S	108	65	0.602	0.709	3	2	1	89	Usher syndrome 2A (autosomal recessive, mild)	ENST00000307340.3
Case#1-Baseline-WholeTumor	C1orf65	1	223568085	Missense_Mutation	A	G	p.N423S	39	8	0.205	0.241	3	2	1	21		ENST00000366875.3
Case#1-Baseline-WholeTumor	DNAH14	1	225380471	Missense_Mutation	G	A	p.G1488E	63	12	0.190	0.224	3	2	1	53	dynein, axonemal, heavy chain 14	ENST00000445597.2
Case#1-Baseline-WholeTumor	IBA57	1	228362852	Missense_Mutation	C	T	p.P237S	223	132	0.592	0.697	3	2	1	150	IBA57, iron-sulfur cluster assembly homolog (S. cerevisiae)	ENST00000366711.3
Case#1-Baseline-WholeTumor	OBSCN	1	228444456	Missense_Mutation	G	A	p.E1472K	354	94	0.266	0.313	3	2	1	190	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	ENST00000422127.1
Case#1-Baseline-WholeTumor	OBSCN	1	228467086	Missense_Mutation	C	T	p.T2446I	253	68	0.269	0.316	3	2	1	124	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	ENST00000422127.1
Case#1-Baseline-WholeTumor	OBSCN	1	228480416	Missense_Mutation	C	T	p.A3599V	228	68	0.298	0.351	3	2	1	164	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	ENST00000422127.1
Case#1-Baseline-WholeTumor	OBSCN	1	228563861	Missense_Mutation	GG	AA	p.G7647K	147	47	0.320	NA	NA	NA	NA	91	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	ENST00000422127.1
Case#1-Baseline-WholeTumor	PCNXL2	1	233388499	Missense_Mutation	C	T	p.E624K	64	11	0.172	0.202	3	2	1	57	pecanex-like 2 (Drosophila)	ENST00000258229.9
Case#1-Baseline-WholeTumor	TARBP1	1	234565167	Missense_Mutation	G	A	p.P956S	71	16	0.225	0.265	3	2	1	69	TAR (HIV-1) RNA binding protein 1	ENST00000040877.1
Case#1-Baseline-WholeTumor	B3GALNT2	1	235658121	Missense_Mutation	G	A	p.P44S	113	31	0.274	0.323	3	2	1	80	beta-1,3-N-acetylgalactosaminyltransferase 2	ENST00000366600.3
Case#1-Baseline-WholeTumor	LYST	1	235926080	Missense_Mutation	GG	AA	p.L2065F	97	32	0.330	0.388	3	2	1	60	lysosomal trafficking regulator	ENST00000389794.3
Case#1-Baseline-WholeTumor	RYR2	1	237675076	Missense_Mutation	C	T	p.S936L	68	29	0.426	0.502	3	2	1	57	ryanodine receptor 2 (cardiac)	ENST00000366574.2
Case#1-Baseline-WholeTumor	RYR2	1	237948261	Missense_Mutation	G	A	p.E4417K	71	38	0.535	0.630	3	2	1	44	ryanodine receptor 2 (cardiac)	ENST00000366574.2
Case#1-Baseline-WholeTumor	RYR2	1	237965216	Splice_Site	C	T	p.N4717N	131	30	0.229	0.270	3	2	1	112	ryanodine receptor 2 (cardiac)	ENST00000366574.2
Case#1-Baseline-WholeTumor	CHRM3	1	240071811	Missense_Mutation	G	A	p.E354K	21	13	0.619	0.729	3	2	1	21	cholinergic receptor, muscarinic 3	ENST00000255380.4
Case#1-Baseline-WholeTumor	RGS7	1	241262011	Missense_Mutation	G	A	p.R44C	122	35	0.287	0.338	3	2	1	107	regulator of G-protein signaling 7	ENST00000407727.1
Case#1-Baseline-WholeTumor	AKT3	1	243736329	Missense_Mutation	C	T	p.E240K	99	32	0.323	0.381	3	2	1	85	v-akt murine thymoma viral oncogene homolog 3	ENST00000366539.1
Case#1-Baseline-WholeTumor	NLRP3	1	247586553	Missense_Mutation	CG	TA	p.S102L	225	61	0.271	0.319	3	2	1	180	NLR family, pyrin domain containing 3	ENST00000336119.3
Case#1-Baseline-WholeTumor	OR2G3	1	247769009	Missense_Mutation	G	A	p.G41E	134	36	0.269	0.316	3	2	1	105	olfactory receptor, family 2, subfamily G, member 3	ENST00000320002.2

Case#1-Baseline-WholeTumor	OR6F1	1	247875661	Missense_Mutation	C	T	p.G133R	66	20	0.303	0.357	3	2	1	55	olfactory receptor, family 6, subfamily F, member 1	ENST00000302084.2
Case#1-Baseline-WholeTumor	OR2L3	1	248224777	Missense_Mutation	G	A	p.R265Q	243	75	0.309	0.363	3	2	1	251	olfactory receptor, family 2, subfamily L, member 3	ENST00000359959.3
Case#1-Baseline-WholeTumor	OR2M3	1	248366400	Missense_Mutation	G	A	p.D11N	199	57	0.286	0.337	3	2	1	200	olfactory receptor, family 2, subfamily M, member 3	ENST00000456743.1
Case#1-Baseline-WholeTumor	OR2M3	1	248366416	Missense_Mutation	G	A	p.G16E	204	59	0.289	0.340	3	2	1	199	olfactory receptor, family 2, subfamily M, member 3	ENST00000456743.1
Case#1-Baseline-WholeTumor	OR2T7	1	248604980	Missense_Mutation	C	T	p.P158L	191	38	0.199	0.234	3	2	1	183	olfactory receptor, family 2, subfamily T, member 7	ENST00000460972.3
Case#1-Baseline-WholeTumor	OR2T27	1	248813686	Missense_Mutation	G	A	p.P167L	88	40	0.455	0.535	3	2	1	82	olfactory receptor, family 2, subfamily T, member 27	ENST00000344889.3
Case#1-Baseline-WholeTumor	ADARB2	10	1779337	Missense_Mutation	G	A	p.S3L	71	51	0.718	1.100	1	1	0	77	adenosine deaminase, RNA-specific, B2 (non-functional)	ENST00000381312.1
Case#1-Baseline-WholeTumor	CAMK1D	10	12856222	Missense_Mutation	G	A	p.E224K	43	26	0.605	0.926	1	1	0	123	calcium/calmodulin-dependent protein kinase ID	ENST00000378847.3
Case#1-Baseline-WholeTumor	VIM	10	17271596	Missense_Mutation	GG	AA	p.G59N	16	6	0.375	0.475	2	1	1	14	vimentin	ENST00000224237.5
Case#1-Baseline-WholeTumor	C10orf112	10	19498265	Missense_Mutation	G	A	p.D179N	35	15	0.429	0.542	2	1	1	41		ENST00000454679.2
Case#1-Baseline-WholeTumor	C10orf112	10	19636906	Missense_Mutation	A	T	p.I666F	43	23	0.535	0.677	2	1	1	50		ENST00000454679.2
Case#1-Baseline-WholeTumor	PLXDC2	10	20335803	Missense_Mutation	T	A	p.D110E	73	24	0.329	0.416	2	1	1	104	plexin domain containing 2	ENST00000377252.4
Case#1-Baseline-WholeTumor	THNSL1	10	25313606	Missense_Mutation	C	T	p.S485F	48	21	0.438	0.554	2	1	1	72	threonine synthase-like 1 (S. cerevisiae)	ENST00000524413.1
Case#1-Baseline-WholeTumor	SVIL	10	29840084	Missense_Mutation	G	A	p.S90L	56	19	0.339	0.429	2	1	1	89	supervillin	ENST00000355867.4
Case#1-Baseline-WholeTumor	GPRIN2	10	46999649	Missense_Mutation	G	A	p.A257T	43	7	0.163	0.206	2	1	1	47	G protein regulated inducer of neurite outgrowth 2	ENST00000374317.1
Case#1-Baseline-WholeTumor	ZNF488	10	48370630	Missense_Mutation	G	A	p.R33K	177	72	0.407	0.515	2	1	1	154	zinc finger protein 488	ENST00000395702.2
Case#1-Baseline-WholeTumor	FRMPD2	10	49446153	Missense_Mutation	C	G	p.A268P	57	9	0.158	0.200	2	1	1	58	FERM and PDZ domain containing 2	ENST00000374201.3
Case#1-Baseline-WholeTumor	WDFY4	10	50028286	Missense_Mutation	G	A	p.G1838E	24	7	0.292	0.369	2	1	1	38	WDFY family member 4	ENST00000325239.5
Case#1-Baseline-WholeTumor	C10orf128	10	50374999	Missense_Mutation	G	T	p.F51L	34	14	0.412	0.521	2	1	1	56	chromosome 10 open reading frame 128	ENST00000474718.1
Case#1-Baseline-WholeTumor	OGDHL	10	50943359	Missense_Mutation	C	T	p.G983E	97	40	0.412	0.522	2	1	1	110	oxoglutarate dehydrogenase-like	ENST00000374103.4
Case#1-Baseline-WholeTumor	SGMS1	10	52103527	Missense_Mutation	T	C	p.I116M	65	20	0.308	0.389	2	1	1	78	sphingomyelin synthase 1	ENST00000361781.2
Case#1-Baseline-WholeTumor	A1CF	10	52595855	Missense_Mutation	C	T	p.A195T	102	48	0.471	0.596	2	1	1	89	APOBEC1 complementation factor	ENST00000373993.1
Case#1-Baseline-WholeTumor	MBL2	10	54531257	Missense_Mutation	G	A	p.P47S	51	22	0.431	0.546	2	1	1	67	mannose-binding lectin (protein C) 2, soluble	ENST00000373968.3
Case#1-Baseline-WholeTumor	PCDH15	10	55569228	Missense_Mutation	C	T	p.E1528K	94	36	0.383	0.485	2	1	1	119	protocadherin-related 15	ENST00000395445.1
Case#1-Baseline-WholeTumor	PCDH15	10	55582166	Missense_Mutation	A	T	p.F1774I	14	3	0.214	0.271	2	1	1	19	protocadherin-related 15	ENST00000320301.6
Case#1-Baseline-WholeTumor	PCDH15	10	55582867	Missense_Mutation	G	A	p.S1540L	87	39	0.448	0.567	2	1	1	112	protocadherin-related 15	ENST00000320301.6
Case#1-Baseline-WholeTumor	PCDH15	10	55945022	Missense_Mutation	C	T	p.D438N	60	21	0.350	0.443	2	1	1	92	protocadherin-related 15	ENST00000320301.6
Case#1-Baseline-WholeTumor	FAM13C	10	61112097	Missense_Mutation	T	G	p.N86T	100	45	0.450	0.570	2	1	1	97	family with sequence similarity 13, member C	ENST00000373868.2
Case#1-Baseline-WholeTumor	ANK3	10	61824037	Missense_Mutation	C	T	p.R4110K	38	8	0.211	0.266	2	1	1	35	ankyrin 3, node of Ranvier (ankyrin G)	ENST00000280772.2
Case#1-Baseline-WholeTumor	ARID5B	10	63850676	Missense_Mutation	C	T	p.P485L	34	12	0.353	0.447	2	1	1	24	AT rich interactive domain 5B (MRF1-like)	ENST00000279873.7
Case#1-Baseline-WholeTumor	JMJD1C	10	64960426	Missense_Mutation	G	A	p.R1696C	101	44	0.436	0.551	2	1	1	127	jumonji domain containing 1C	ENST00000399262.2
Case#1-Baseline-WholeTumor	RUFY2	10	70139242	Missense_Mutation	T	C	p.I382V	35	6	0.171	0.217	2	1	1	23	RUN and FYVE domain containing 2	ENST00000602465.1
Case#1-Baseline-WholeTumor	CCAR1	10	70508974	Missense_Mutation	G	A	p.G303E	135	48	0.356	0.450	2	1	1	119	cell division cycle and apoptosis regulator 1	ENST00000265872.6
Case#1-Baseline-WholeTumor	PALD1	10	72300880	Missense_Mutation	C	T	p.A644V	80	30	0.375	0.475	2	1	1	50	phosphatase domain containing, paladin 1	ENST00000263563.6
Case#1-Baseline-WholeTumor	PRF1	10	72358636	Missense_Mutation	C	T	p.E281K	107	44	0.411	0.521	2	1	1	78	perforin 1 (pore forming protein)	ENST00000441259.1
Case#1-Baseline-WholeTumor	CDH23	10	73500633	Missense_Mutation	G	A	p.V1520M	85	33	0.388	0.491	2	1	1	86	cadherin-related 23	ENST00000224721.6
Case#1-Baseline-WholeTumor	P4HA1	10	74806804	Missense_Mutation	G	A	p.P319L	107	46	0.430	0.544	2	1	1	100	prolyl 4-hydroxylase, alpha polypeptide I	ENST00000307116.2
Case#1-Baseline-WholeTumor	TTC18	10	75034301	Missense_Mutation	G	A	p.H979Y	67	28	0.418	0.529	2	1	1	87		ENST00000310715.3
Case#1-Baseline-WholeTumor	PTEN	10	89720808	Missense_Mutation	T	C	p.L320S	69	55	0.797	1.009	2	2	0	49	phosphatase and tensin homolog	ENST00000371953.3
Case#1-Baseline-WholeTumor	BTAF1	10	93719750	Missense_Mutation	C	T	p.R368C	88	71	0.807	1.021	2	2	0	94	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa	ENST00000265990.6
Case#1-Baseline-WholeTumor	PLCE1	10	95791077	Missense_Mutation	G	A	p.E92K	37	31	0.838	1.061	2	2	0	56	phospholipase C, epsilon 1	ENST00000371380.3
Case#1-Baseline-WholeTumor	TCTN3	10	97440329	Missense_Mutation	G	A	p.S497F	67	57	0.851	1.077	2	2	0	95	tectonic family member 3	ENST00000371217.5
Case#1-Baseline-WholeTumor	SEC31B	10	102269137	Missense_Mutation	G	A	p.P112L	37	30	0.811	1.026	2	2	0	38	SEC31 homolog B (S. cerevisiae)	ENST00000370345.3
Case#1-Baseline-WholeTumor	SORCS3	10	106918686	Missense_Mutation	G	A	p.E556K	38	28	0.737	0.933	2	2	0	76	sortilin-related VPS10 domain containing receptor 3	ENST00000369701.3
Case#1-Baseline-WholeTumor	PNLIPRP3	10	118203946	Missense_Mutation	G	A	p.G126D	52	39	0.750	0.949	2	2	0	72	pancreatic lipase-related protein 3	ENST00000369230.3
Case#1-Baseline-WholeTumor	TACC2	10	123847216	Missense_Mutation	C	T	p.S1734F	63	51	0.810	1.025	2	2	0	94	transforming, acidic coiled-coil containing protein 2	ENST00000369005.1
Case#1-Baseline-WholeTumor	CTBP2	10	126691950	Missense_Mutation	A	G	p.V57A	143	18	0.126	NA	NA	NA	NA	94	C-terminal binding protein 2	ENST00000337195.5
Case#1-Baseline-WholeTumor	NPS	10	129350899	Missense_Mutation	C	T	p.S89L	28	26	0.929	1.175	2	2	0	58	neuropeptide S	ENST00000398023.1
Case#1-Baseline-WholeTumor	MKI67	10	129914052	Missense_Mutation	G	A	p.S207F	36	27	0.750	0.949	2	2	0	51	marker of proliferation Ki-67	ENST00000368654.3
Case#1-Baseline-WholeTumor	AL450307.1	10	133608090	Missense_Mutation	G	A	p.P96S	55	46	0.836	1.059	2	2	0	43		ENST00000341866.3
Case#1-Baseline-WholeTumor	TTC40	10	134699335	Missense_Mutation	C	T	p.A1145T	50	39	0.780	0.987	2	2	0	39		ENST00000368586.5
Case#1-Baseline-WholeTumor	MUC6	11	1016547	Missense_Mutation	G	A	p.S2085F	150	49	0.327	0.414	2	1	1	179	mucin 6, oligomeric mucus/gel-forming	ENST00000421673.2
Case#1-Baseline-WholeTumor	MUC5B	11	1270408	Missense_Mutation	G	A	p.A4100T	272	61	0.224	0.284	2	1	1	211	mucin 5B, oligomeric mucus/gel-forming	ENST00000529681.1
Case#1-Baseline-WholeTumor	OR52R1	11	4825594	Missense_Mutation	C	T	p.G6E	88	29	0.330	0.417	2	1	1	89	olfactory receptor, family 52, subfamily R, member 1	ENST00000356069.2
Case#1-Baseline-WholeTumor	OR51S1	11	4870024	Missense_Mutation	G	A	p.H139Y	61	13	0.213	0.270	2	1	1	88	olfactory receptor, family 51, subfamily S, member 1	ENST00000322101.2
Case#1-Baseline-WholeTumor	OR51G1	11	4945500	Missense_Mutation	C	T	p.G24S	88	34	0.386	0.489	2	1	1	117	olfactory receptor, family 51, subfamily G, member 1	ENST00000321961.2
Case#1-Baseline-WholeTumor	MMP26	11	5013192	Splice_Site	A	C		15	9	0.600	0.759	2	1	1	20	matrix metallopeptidase 26	ENST00000380390.1
Case#1-Baseline-WholeTumor	OR52J3	11	5068546	Missense_Mutation	G	A	p.R264Q	59	25	0.424	0.536	2	1	1	100	olfactory receptor, family 52, subfamily J, member 3	ENST00000380370.1
Case#1-Baseline-WholeTumor	OR52E2	11	5079909	Missense_Mutation	C	T	p.E317K	63	29	0.460	0.583	2	1	1	86	olfactory receptor, family 52, subfamily E, member 2	ENST00000321522.2
Case#1-Baseline-WholeTumor	OR51B2	11	5345263	Missense_Mutation	C	T	p.E89K	22	6	0.273	0.345	2	1	1	40	olfactory receptor, family 51, subfamily B, member 2	ENST00000328813.2
Case#1-Baseline-WholeTumor	OR51I2	11	5475346	Missense_Mutation	G	A	p.D210N	139	44	0.317	0.401	2	1	1	190	olfactory receptor, family 51, subfamily I, member 2	ENST00000341449.2
Case#1-Baseline-WholeTumor	UBQLN3	11	5529629	Missense_Mutation	G	A	p.S387F	72	31	0.431	0.545	2	1	1	77	ubiquilin 3	ENST00000311659.4
Case#1-Baseline-WholeTumor	TRIM22	11	5730807	Nonsense_Mutation	C	T	p.R476*	70	27	0.386	0.488	2	1	1	76	tripartite motif containing 22	ENST00000379965.3
Case#1-Baseline-WholeTumor	OR56B4	11	6129543	Missense_Mutation	G	A	p.E179K	37	11	0.297	0.376	2	1	1	50	olfactory receptor, family 56, subfamily B, member 4	ENST00000316529.3
Case#1-Baseline-WholeTumor	NLRP10	11	7981652	Missense_Mutation	C	T	p.E503K	51	14	0.275	0.347	2	1	1	57	NLR family, pyrin domain containing 10	ENST00000328600.2
Case#1-Baseline-WholeTumor	KCNC1	11	17793758	Missense_Mutation	C	T	p.P373S	48	25	0.521	0.659	2	1	1	35	potassium voltage-gated channel, Shaw-related subfamily, member 1	ENST00000379472.3
Case#1-Baseline-WholeTumor	SPTY2D1	11	18633868	Nonsense_Mutation	G	A	p.R627*	81	24	0.296	0.375	2	1	1	69	SPT2, Suppressor of Ty, domain containing 1 (S. cerevisiae)	ENST00000336349.5
Case#1-Baseline-WholeTumor	NAV2	11	20099567	Missense_Mutation	C	T	p.T1755I	54	24	0.444	0.563	2	1	1	43	neuron navigator 2	ENST00000396087.3
Case#1-Baseline-WholeTumor	NELL1	11	21581750	Missense_Mutation	C	T	p.A601V	73	28	0.384	0.486	2	1	1	82	NEL-like 1 (chicken)	ENST00000357134.5
Case#1-Baseline-WholeTumor	CREB3L1	11	46334162	Splice_Site	G	A		118	40	0.339	0.429	2	1	1	96	cAMP responsive element binding protein 3-like 1	ENST00000529193.1
Case#1-Baseline-WholeTumor	PTPRJ	11	48157838	Nonsense_Mutation	AC	TT	p.Q622*	46	11	0.239	0.303	2	1	1	72	protein tyrosine phosphatase, receptor type, J	ENST00000418331.2
Case#1-Baseline-WholeTumor	OR4C5	11	48387693	Frame_Shift_Del	C	-	p.E109fs	42	11	0.262	0.332	2	1	1	55	olfactory receptor, family 4, subfamily C, member 5	ENST00000319813.3
Case#1-Baseline-WholeTumor	OR4A47	11	48510661	Missense_Mutation	G	A	p.G106D	64	18	0.281	0.356	2	1	1	81	olfactory receptor, family 4, subfamily A, member 47	ENST00000446524.1
Case#1-Baseline-WholeTumor	OR5D14	11	55563272	Missense_Mutation	C	T	p.P81S	80	27	0.338	0.427	2	1	1	181	olfactory receptor, family 5, subfamily D, member 14	ENST00000335605.1
Case#1-Baseline-WholeTumor	OR5M9	11	56230749	Missense_Mutation	C	T	p.M43I	53	16	0.302	0.382	2	1	1	54	olfactory receptor, family 5, subfamily M, member 9	ENST00000279791.1
Case#1-Baseline-WholeTumor	OR5M8	11	56258275	Missense_Mutation	G	A	p.T191I	171	68	0.398	0.503	2	1	1	241	olfactory receptor, family 5, subfamily M, member 8	ENST00000327216.2
Case#1-Baseline-WholeTumor	OR5AP2	11	56408980	Nonsense_Mutation	C	T	p.W312*	60	13	0.217	0.274	2	1	1	88	olfactory receptor, family 5, subfamily AP, member 2	ENST00000302981.1
Case#1-Baseline-WholeTumor	OR5AK2	11	56756827	Missense_Mutation	G	A	p.G147S	73	39	0.534	0.676	2	1	1	125	olfactory receptor, family 5, subfamily AK, member 2	ENST00000326855.2
Case#1-Baseline-WholeTumor	OR4D6	11	59224841	Missense_Mutation	G	A	p.M136I	73	25	0.342	0.434	2	1	1	102	olfactory receptor, family 4, subfamily D, member 6	ENST00000300127.2
Case#1-Baseline-WholeTumor	TUT1	11	62348929	Missense_Mutation	G	C	p.S173C	101	41	0.406	0.514	2	1	1	82	terminal uridylyl transferase 1, U6 snRNA-specific	ENST00000476907.1
Case#1-Baseline-WholeTumor	SLC22A9	11	63141402	Missense_Mutation	G	A	p.G233E	73	23	0.315	0.399	2	1	1	87	solute carrier family 22 (organic anion transporter), member 9	ENST00000279178.3
Case#1-Baseline-WholeTumor	PLCB3	11	64028965	Nonsense_Mutation	C	T	p.R609*	96	39	0.406	0.514	2	1	1	89	phospholipase C, beta 3 (phosphatidylinositol-specific)	ENST00000540288.1
Case#1-Baseline-WholeTumor	RPS6KA4	11	64129178	Missense_Mutation	C	T	p.T239I	108	29	0.269	0.340	2	1	1	64	ribosomal protein S6 kinase, 90kDa, polypeptide 4	ENST00000334205.4

Case#1-Baseline-WholeTumor	ATG2A	11	64664948	Missense_Mutation	GG	AA	p.L1696F	116	46	0.397	0.502	2	1	1	113	autophagy related 2A	ENST00000377264.3
Case#1-Baseline-WholeTumor	CTSW	11	65649988	Missense_Mutation	T	C	p.S177P	100	30	0.300	0.380	2	1	1	69	cathepsin W	ENST00000307886.3
Case#1-Baseline-WholeTumor	CD248	11	66082544	Missense_Mutation	C	T	p.S652N	51	18	0.353	0.447	2	1	1	48	CD248 molecule, endosialin	ENST00000311330.3
Case#1-Baseline-WholeTumor	SPTBN2	11	66455082	Missense_Mutation	C	T	p.G2180R	53	18	0.340	0.430	2	1	1	33	spectrin, beta, non-erythrocytic 2	ENST00000533211.1
Case#1-Baseline-WholeTumor	TBX10	11	67402378	Missense_Mutation	G	A	p.P96S	90	42	0.467	0.591	2	1	1	72	T-box 10	ENST00000335385.3
Case#1-Baseline-WholeTumor	FGF3	11	69625429	Missense_Mutation	G	A	p.H122Y	123	51	0.415	0.525	2	1	1	116	fibroblast growth factor 3	ENST00000334134.2
Case#1-Baseline-WholeTumor	INPPL1	11	71944487	Missense_Mutation	CC	TT	p.R682W	42	22	0.524	0.663	2	1	1	53	inositol polyphosphate phosphatase-like 1	ENST00000298229.2
Case#1-Baseline-WholeTumor	GDPD4	11	76944167	Missense_Mutation	G	A	p.P431L	100	37	0.370	0.468	2	1	1	146	glycerophosphodiester phosphodiesterase domain containing 4	ENST00000376217.2
Case#1-Baseline-WholeTumor	NARS2	11	78277192	Missense_Mutation	G	A	p.H167Y	52	20	0.385	0.487	2	1	1	65	asparaginyl-tRNA synthetase 2, mitochondrial (putative)	ENST00000281038.5
Case#1-Baseline-WholeTumor	EED	11	85988157	Missense_Mutation	T	C	p.F368L	110	41	0.373	0.472	2	1	1	114	embryonic ectoderm development	ENST00000263360.6
Case#1-Baseline-WholeTumor	TRIM77	11	89450921	Missense_Mutation	G	A	p.D412N	137	47	0.343	0.434	2	1	1	154	tripartite motif containing 77	ENST00000398290.3
Case#1-Baseline-WholeTumor	FAT3	11	92085636	Missense_Mutation	G	A	p.E120K	45	20	0.444	0.563	2	1	1	95	FAT atypical cadherin 3	ENST00000298047.6
Case#1-Baseline-WholeTumor	CCDC67	11	93127766	Missense_Mutation	G	A	p.E395K	53	16	0.302	0.382	2	1	1	56	coiled-coil domain containing 67	ENST00000298050.3
Case#1-Baseline-WholeTumor	HEPHL1	11	93839165	Missense_Mutation	G	A	p.G972R	83	34	0.410	0.519	2	1	1	89	hephaestin-like 1	ENST00000315765.9
Case#1-Baseline-WholeTumor	CNTN5	11	99872774	Missense_Mutation	G	A	p.G296R	107	35	0.327	0.414	2	1	1	118	contactin 5	ENST00000524871.1
Case#1-Baseline-WholeTumor	CNTN5	11	99872807	Missense_Mutation	C	T	p.P307S	102	44	0.431	0.546	2	1	1	135	contactin 5	ENST00000524871.1
Case#1-Baseline-WholeTumor	CNTN5	11	100061937	Missense_Mutation	G	A	p.E554K	105	41	0.390	0.494	2	1	1	166	contactin 5	ENST00000524871.1
Case#1-Baseline-WholeTumor	CNTN5	11	100168399	Missense_Mutation	GA	AT	p.R786N	120	41	0.342	0.432	2	1	1	186	contactin 5	ENST00000524871.1
Case#1-Baseline-WholeTumor	MMP8	11	102589181	Missense_Mutation	G	A	p.P250S	102	32	0.314	0.397	2	1	1	124	matrix metallopeptidase 8 (neutrophil collagenase)	ENST00000236826.3
Case#1-Baseline-WholeTumor	DYNC2H1	11	103092818	Missense_Mutation	C	T	p.S3056L	117	41	0.350	0.444	2	1	1	86	dynein, cytoplasmic 2, heavy chain 1	ENST00000375735.2
Case#1-Baseline-WholeTumor	CWF19L2	11	107309831	Missense_Mutation	A	G	p.S217P	104	15	0.144	0.183	2	1	1	95	CWF19-like 2, cell cycle control (S. pombe)	ENST00000282251.5
Case#1-Baseline-WholeTumor	NCAM1	11	113076767	Nonsense_Mutation	C	T	p.R47*	69	23	0.333	0.422	2	1	1	67	neural cell adhesion molecule 1	ENST00000533760.1
Case#1-Baseline-WholeTumor	ZW10	11	113629345	Missense_Mutation	G	A	p.P222S	100	24	0.240	0.304	2	1	1	122	zw10 kinetochore protein	ENST00000200135.3
Case#1-Baseline-WholeTumor	NXPE2	11	114577134	Missense_Mutation	C	T	p.H388Y	57	29	0.509	0.644	2	1	1	61	neurexophilin and PC-esterase domain family, member 2	ENST00000389586.4
Case#1-Baseline-WholeTumor	PAFAH1B2	11	117038213	Missense_Mutation	C	T	p.S163L	78	23	0.295	0.373	2	1	1	65	platelet-activating factor acetylhydrolase 1b, catalytic subunit 2 (30kDa)	ENST00000527958.1
Case#1-Baseline-WholeTumor	CEP164	11	117234205	Missense_Mutation	G	A	p.G250S	143	9	0.063	0.080	2	1	1	126	centrosomal protein 164kDa	ENST00000278935.3
Case#1-Baseline-WholeTumor	KMT2A	11	118362000	Missense_Mutation	C	T	p.H1596Y	98	35	0.357	0.452	2	1	1	102	lysine (K)-specific methyltransferase 2A	ENST00000389506.5
Case#1-Baseline-WholeTumor	PDZD3	11	119057283	Missense_Mutation	G	A	p.G138R	35	15	0.429	0.542	2	1	1	51	PDZ domain containing 3	ENST00000531114.1
Case#1-Baseline-WholeTumor	CBL	11	119169212	Missense_Mutation	C	T	p.S799F	87	33	0.379	0.480	2	1	1	131	Cbl proto-oncogene, E3 ubiquitin protein ligase	ENST00000264033.4
Case#1-Baseline-WholeTumor	SORL1	11	121367627	Missense_Mutation	G	A	p.E270K	74	27	0.365	0.462	2	1	1	96	sortilin-related receptor, L(DLR class) A repeats containing	ENST00000260197.7
Case#1-Baseline-WholeTumor	OR8D4	11	123777185	Missense_Mutation	G	A	p.G16E	43	13	0.302	0.383	2	1	1	68	olfactory receptor, family 8, subfamily D, member 4	ENST00000321355.2
Case#1-Baseline-WholeTumor	OR8D4	11	123778058	Missense_Mutation	G	A	p.R307K	45	15	0.333	0.422	2	1	1	48	olfactory receptor, family 8, subfamily D, member 4	ENST00000321355.2
Case#1-Baseline-WholeTumor	OR10S1	11	123848326	Missense_Mutation	A	G	p.F25L	67	24	0.358	0.453	2	1	1	114	olfactory receptor, family 10, subfamily S, member 1	ENST00000531945.1
Case#1-Baseline-WholeTumor	SRPR	11	126136477	Missense_Mutation	GG	AA	p.P245F	103	51	0.495	0.627	2	1	1	91	signal recognition particle receptor (docking protein)	ENST00000332118.6
Case#1-Baseline-WholeTumor	SRPR	11	126138630	Missense_Mutation	A	G	p.S24P	109	47	0.431	0.546	2	1	1	93	signal recognition particle receptor (docking protein)	ENST00000332118.6
Case#1-Baseline-WholeTumor	ARHGAP32	11	128840469	Missense_Mutation	G	A	p.R1533C	97	38	0.392	0.496	2	1	1	175	Rho GTPase activating protein 32	ENST00000310343.9
Case#1-Baseline-WholeTumor	ADAMTS8	11	130286943	Missense_Mutation	C	T	p.D330N	80	27	0.338	0.427	2	1	1	85	ADAM metallopeptidase with thrombospondin type 1 motif, 8	ENST00000257359.6
Case#1-Baseline-WholeTumor	NCAPD3	11	134080186	Missense_Mutation	GG	AA	p.P182L	73	29	0.397	0.503	2	1	1	114	non-SMC condensin II complex, subunit D3	ENST00000534548.2
Case#1-Baseline-WholeTumor	DCP1B	12	2061631	Missense_Mutation	G	A	p.S492F	96	35	0.365	0.461	2	1	1	114	decapping mRNA 1B	ENST00000280665.6
Case#1-Baseline-WholeTumor	AC005841.1	12	2966135	Missense_Mutation	C	T	p.E27K	105	38	0.362	0.458	2	1	1	111		ENST00000382678.3
Case#1-Baseline-WholeTumor	GALNT8	12	4870294	Nonsense_Mutation	G	A	p.W448*	21	6	0.286	0.362	2	1	1	58	polypeptide N-acetylgalactosaminyltransferase 8	ENST00000252318.2
Case#1-Baseline-WholeTumor	KCNA5	12	5154520	Missense_Mutation	C	T	p.R403C	43	20	0.465	0.589	2	1	1	56	potassium voltage-gated channel, shaker-related subfamily, member 5	ENST00000252321.3
Case#1-Baseline-WholeTumor	CD163	12	7637740	Missense_Mutation	C	T	p.E911K	44	16	0.364	0.460	2	1	1	54	CD163 molecule	ENST00000359156.4
Case#1-Baseline-WholeTumor	PRB3	12	11420444	Missense_Mutation	C	G	p.E247Q	65	4	0.062	0.078	2	1	1	74	proline-rich protein BstNI subfamily 3	ENST00000279573.7
Case#1-Baseline-WholeTumor	PRB2	12	11546665	Missense_Mutation	C	T	p.G116E	258	68	0.264	0.334	2	1	1	359	proline-rich protein BstNI subfamily 2	ENST00000389362.4
Case#1-Baseline-WholeTumor	GRIN2B	12	13906630	Missense_Mutation	C	T	p.D211N	42	14	0.333	0.422	2	1	1	62	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	ENST00000609686.1
Case#1-Baseline-WholeTumor	PIK3C2G	12	18658227	Splice_Site	C	T	p.A1011V	77	29	0.377	0.477	2	1	1	93	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 gamma	ENST00000266497.5
Case#1-Baseline-WholeTumor	SLCO1B1	12	21329769	Missense_Mutation	C	T	p.S140F	55	27	0.491	0.621	2	1	1	69	solute carrier organic anion transporter family, member 1B1	ENST00000256958.2
Case#1-Baseline-WholeTumor	SOX5	12	23687236	Missense_Mutation	C	T	p.D737N	172	61	0.355	0.449	2	1	1	154	SRY (sex determining region Y)-box 5	ENST00000451604.2
Case#1-Baseline-WholeTumor	BCAT1	12	24970979	Missense_Mutation	C	T	p.G375E	123	44	0.358	0.453	2	1	1	107	branched chain amino-acid transaminase 1, cytosolic	ENST00000261192.7
Case#1-Baseline-WholeTumor	CAPRIN2	12	30882208	Missense_Mutation	C	T	p.E386K	24	9	0.375	0.475	2	1	1	20	caprin family member 2	ENST00000395805.2
Case#1-Baseline-WholeTumor	C12orf40	12	40114658	Missense_Mutation	G	A	p.E522K	57	19	0.333	0.422	2	1	1	63	chromosome 12 open reading frame 40	ENST00000324616.5
Case#1-Baseline-WholeTumor	MUC19	12	40821867	Missense_Mutation	G	A	p.V206I	143	10	0.070	0.089	2	1	1	163	mucin 19, oligomeric	ENST00000454784.4
Case#1-Baseline-WholeTumor	MUC19	12	40832004	Missense_Mutation	G	A	p.E515K	43	21	0.488	0.618	2	1	1	68	mucin 19, oligomeric	ENST00000454784.4
Case#1-Baseline-WholeTumor	ARID2	12	46287234	Missense_Mutation	C	T	p.P1727S	53	21	0.396	0.502	2	1	1	63	AT rich interactive domain 2 (ARID, RFX-like)	ENST00000334344.6
Case#1-Baseline-WholeTumor	PCED1B	12	47629420	Missense_Mutation	G	A	p.E192K	183	74	0.404	0.512	2	1	1	135	PC-esterase domain containing 1B	ENST00000546455.1
Case#1-Baseline-WholeTumor	SENP1	12	48439118	Missense_Mutation	C	T	p.R641Q	123	39	0.317	0.401	2	1	1	127	SUMO1/sentrin specific peptidase 1	ENST00000004980.5
Case#1-Baseline-WholeTumor	RND1	12	49254905	Missense_Mutation	C	T	p.E110K	17	4	0.235	0.298	2	1	1	30	Rho family GTPase 1	ENST00000309739.5
Case#1-Baseline-WholeTumor	TFCP2	12	51510103	Missense_Mutation	T	C	p.D151G	65	26	0.400	0.506	2	1	1	57	transcription factor CP2	ENST00000257915.5
Case#1-Baseline-WholeTumor	SCN8A	12	52184276	Missense_Mutation	C	T	p.P1505L	61	28	0.459	0.581	2	1	1	79	sodium channel, voltage gated, type VIII, alpha subunit	ENST00000354534.6
Case#1-Baseline-WholeTumor	KRT71	12	52943113	Missense_Mutation	CC	AT	p.R227H	34	8	0.235	0.298	2	1	1	64	keratin 71	ENST00000267119.5
Case#1-Baseline-WholeTumor	SOAT2	12	53512909	Splice_Site	C	T	p.A304V	46	19	0.413	0.523	2	1	1	47	sterol O-acyltransferase 2	ENST00000301466.3
Case#1-Baseline-WholeTumor	ITGB7	12	53590388	Missense_Mutation	G	A	p.A264V	100	47	0.470	0.595	2	1	1	60	integrin, beta 7	ENST00000267082.5
Case#1-Baseline-WholeTumor	GPR84	12	54757016	Missense_Mutation	C	T	p.R207Q	65	24	0.369	0.467	2	1	1	96	G protein-coupled receptor 84	ENST00000551809.1
Case#1-Baseline-WholeTumor	OR6C74	12	55641512	Nonsense_Mutation	G	A	p.W147*	66	28	0.424	0.537	2	1	1	82	olfactory receptor, family 6, subfamily C, member 74	ENST00000343870.4
Case#1-Baseline-WholeTumor	OR6C75	12	55759151	Missense_Mutation	G	A	p.G86E	42	15	0.357	0.452	2	1	1	60	olfactory receptor, family 6, subfamily C, member 75	ENST00000343399.3
Case#1-Baseline-WholeTumor	OR6C65	12	55795213	Missense_Mutation	G	A	p.E301K	44	14	0.318	0.403	2	1	1	59	olfactory receptor, family 6, subfamily C, member 65	ENST00000379665.2
Case#1-Baseline-WholeTumor	PMEL	12	56359790	Missense_Mutation	A	T	p.D2E	46	20	0.435	0.550	2	1	1	57	premelanosome protein	ENST00000548747.1
Case#1-Baseline-WholeTumor	SMARCC2	12	56565658	Missense_Mutation	C	T	p.D633N	72	23	0.319	0.404	2	1	1	63	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	ENST00000267064.4
Case#1-Baseline-WholeTumor	PAN2	12	56718253	Missense_Mutation	G	A	p.R585C	61	29	0.475	0.602	2	1	1	79	PAN2 poly(A) specific ribonuclease subunit	ENST00000425394.2
Case#1-Baseline-WholeTumor	HSD17B6	12	57167760	Missense_Mutation	G	A	p.G42R	64	24	0.375	0.475	2	1	1	83	hydroxysteroid (17-beta) dehydrogenase 6	ENST00000554643.1
Case#1-Baseline-WholeTumor	B4GALNT1	12	58025711	Missense_Mutation	C	T	p.E69K	80	36	0.450	0.570	2	1	1	48	beta-1,4-N-acetyl-galactosaminyl transferase 1	ENST00000341156.4
Case#1-Baseline-WholeTumor	AGAP2	12	58125350	Missense_Mutation	G	A	p.P677S	123	44	0.358	0.453	2	1	1	122	ArfGAP with GTPase domain, ankyrin repeat and PH domain 2	ENST00000547588.1
Case#1-Baseline-WholeTumor	OTOGL	12	80704481	Missense_Mutation	G	A	p.D1133N	57	24	0.421	0.533	2	1	1	66	otogelin-like	ENST00000547103.1
Case#1-Baseline-WholeTumor	PTPRQ	12	81062909	Missense_Mutation	G	A	p.E2102K	116	39	0.336	0.426	2	1	1	194	protein tyrosine phosphatase, receptor type, Q	ENST00000266688.5
Case#1-Baseline-WholeTumor	METTL25	12	82796892	Missense_Mutation	T	A	p.F421Y	84	40	0.476	0.603	2	1	1	87	methyltransferase like 25	ENST00000248306.3
Case#1-Baseline-WholeTumor	METTL25	12	82871108	Nonsense_Mutation	C	T	p.R566*	118	43	0.364	0.461	2	1	1	133	methyltransferase like 25	ENST00000248306.3
Case#1-Baseline-WholeTumor	TMCC3	12	94976130	Missense_Mutation	G	A	p.S88L	62	19	0.306	0.388	2	1	1	47	transmembrane and coiled-coil domain family 3	ENST00000261226.4
Case#1-Baseline-WholeTumor	APAF1	12	99060110	Missense_Mutation	C	A	p.T446K	62	7	0.113	0.143	2	1	1	61	apoptotic peptidase activating factor 1	ENST00000551964.1
Case#1-Baseline-WholeTumor	NUAK1	12	106461083	Missense_Mutation	C	T	p.D495N	33	10	0.303	0.384	2	1	1	55	NUAK family, SNF1-like kinase, 1	ENST00000261402.2
Case#1-Baseline-WholeTumor	NUAK1	12	106500267	Missense_Mutation	C	T	p.D93N	83	30	0.361	0.458	2	1	1	126	NUAK family, SNF1-like kinase, 1	ENST00000261402.2

Case#1-Baseline-WholeTumor	CMKLR1	12	108686645	Missense_Mutation	G	A	p.S32F	41	14	0.341	0.432	2	1	1	79	chemokine-like receptor 1	ENST00000312143.7
Case#1-Baseline-WholeTumor	ATXN2	12	111951289	Missense_Mutation	G	A	p.S637F	68	27	0.397	0.503	2	1	1	74	ataxin 2	ENST00000377617.3
Case#1-Baseline-WholeTumor	NOS1	12	117728218	Missense_Mutation	C	T	p.G289E	35	15	0.429	0.542	2	1	1	56	nitric oxide synthase 1 (neuronal)	ENST00000338101.4
Case#1-Baseline-WholeTumor	KSR2	12	117993071	Missense_Mutation	G	A	p.S474F	119	58	0.487	0.617	2	1	1	143	kinase suppressor of ras 2	ENST00000339824.5
Case#1-Baseline-WholeTumor	SRRM4	12	119592176	Missense_Mutation	G	A	p.R507Q	151	58	0.384	0.486	2	1	1	131	serine/arginine repetitive matrix 4	ENST00000267260.4
Case#1-Baseline-WholeTumor	TMEM132B	12	126138174	Missense_Mutation	G	A	p.D719N	97	30	0.309	0.391	2	1	1	108	transmembrane protein 132B	ENST00000299308.3
Case#1-Baseline-WholeTumor	TMEM132C	12	129178431	Missense_Mutation	G	A	p.D503N	49	18	0.367	0.465	2	1	1	91	transmembrane protein 132C	ENST00000435159.2
Case#1-Baseline-WholeTumor	TMEM132C	12	129180403	Missense_Mutation	G	A	p.E562K	58	29	0.500	0.633	2	1	1	84	transmembrane protein 132C	ENST00000435159.2
Case#1-Baseline-WholeTumor	ANKLE2	12	133313612	Missense_Mutation	G	A	p.S487F	43	15	0.349	0.442	2	1	1	36	ankyrin repeat and LEM domain containing 2	ENST00000357997.5
Case#1-Baseline-WholeTumor	TUBA3C	13	19751150	Missense_Mutation	G	A	p.P325S	269	120	0.446	0.565	2	1	1	195	tubulin, alpha 3c	ENST00000400113.3
Case#1-Baseline-WholeTumor	TUBA3C	13	19751338	Missense_Mutation	T	C	p.Y262C	229	75	0.328	0.415	2	1	1	234	tubulin, alpha 3c	ENST00000400113.3
Case#1-Baseline-WholeTumor	GJA3	13	20716277	Missense_Mutation	C	T	p.G384E	24	12	0.500	0.633	2	1	1	18	gap junction protein, alpha 3, 46kDa	ENST00000241125.3
Case#1-Baseline-WholeTumor	USP12	13	27669805	Missense_Mutation	G	A	p.P169L	142	58	0.408	0.481	3	2	1	108	ubiquitin specific peptidase 12	ENST00000282344.6
Case#1-Baseline-WholeTumor	MTUS2	13	29599268	Missense_Mutation	G	A	p.D155N	104	48	0.462	0.543	3	2	1	81	microtubule associated tumor suppressor candidate 2	ENST00000431530.3
Case#1-Baseline-WholeTumor	TEX26	13	31513914	Splice_Site	C	T	p.R49C	79	33	0.418	0.492	3	2	1	90	testis expressed 26	ENST00000380473.3
Case#1-Baseline-WholeTumor	FRY	13	32776086	Missense_Mutation	C	T	p.P1252L	76	22	0.289	0.341	3	2	1	87	furry homolog (Drosophila)	ENST00000380250.3
Case#1-Baseline-WholeTumor	BRCA2	13	32930694	Missense_Mutation	C	T	p.S2522F	59	24	0.407	0.479	3	2	1	50	breast cancer 2, early onset	ENST00000380152.3
Case#1-Baseline-WholeTumor	KL	13	33629411	Missense_Mutation	C	T	p.P520S	45	17	0.378	0.445	3	2	1	82	klotho	ENST00000380099.3
Case#1-Baseline-WholeTumor	NBEA	13	36141110	Missense_Mutation	G	A	p.E2331K	54	23	0.426	0.501	3	2	1	59	neurobeachin	ENST00000400445.3
Case#1-Baseline-WholeTumor	POSTN	13	38156628	Missense_Mutation	G	A	p.R423C	97	50	0.515	0.607	3	2	1	97	periostin, osteoblast specific factor	ENST00000379747.4
Case#1-Baseline-WholeTumor	FREM2	13	39261986	Missense_Mutation	G	A	p.V169I	124	54	0.435	0.513	3	2	1	94	FRAS1 related extracellular matrix protein 2	ENST00000280481.7
Case#1-Baseline-WholeTumor	PROSER1	13	39585573	Missense_Mutation	G	A	p.P922S	68	30	0.441	0.519	3	2	1	76	proline and serine rich 1	ENST00000352251.3
Case#1-Baseline-WholeTumor	COG3	13	46090309	Missense_Mutation	A	G	p.K614R	59	19	0.322	0.379	3	2	1	66	component of oligomeric golgi complex 3	ENST00000349995.5
Case#1-Baseline-WholeTumor	LRCH1	13	47315930	Missense_Mutation	C	T	p.L712F	106	38	0.358	0.422	3	2	1	145	leucine-rich repeats and calponin homology (CH) domain containing 1	ENST00000389798.3
Case#1-Baseline-WholeTumor	PCDH17	13	58208790	Missense_Mutation	A	C	p.M704L	64	13	0.203	0.239	3	2	1	54	protocadherin 17	ENST00000377918.3
Case#1-Baseline-WholeTumor	DACH1	13	72049903	Missense_Mutation	C	T	p.R704Q	82	33	0.402	0.474	3	2	1	110	dachshund family transcription factor 1	ENST00000359684.2
Case#1-Baseline-WholeTumor	LMO7	13	76287325	Missense_Mutation	C	G	p.T78R	243	99	0.407	0.480	3	2	1	262	LIM domain 7	ENST00000341547.4
Case#1-Baseline-WholeTumor	MYCBP2	13	77642818	Missense_Mutation	G	A	p.S3980F	124	50	0.403	0.475	3	2	1	125	MYC binding protein 2, E3 ubiquitin protein ligase	ENST00000544440.2
Case#1-Baseline-WholeTumor	DNAJC3	13	96412327	Nonsense_Mutation	C	T	p.R194*	85	32	0.376	0.443	3	2	1	88	DnaJ (Hsp40) homolog, subfamily C, member 3	ENST00000602402.1
Case#1-Baseline-WholeTumor	CCDC168	13	103386677	Missense_Mutation	G	A	p.S828F	82	41	0.500	0.589	3	2	1	115	coiled-coil domain containing 168	ENST00000322527.2
Case#1-Baseline-WholeTumor	CCDC168	13	103387112	Missense_Mutation	G	A	p.S683F	64	27	0.422	0.497	3	2	1	51	coiled-coil domain containing 168	ENST00000322527.2
Case#1-Baseline-WholeTumor	CCDC168	13	103387773	Missense_Mutation	C	T	p.E463K	108	50	0.463	0.545	3	2	1	131	coiled-coil domain containing 168	ENST00000322527.2
Case#1-Baseline-WholeTumor	BIVM	13	103474115	Missense_Mutation	G	A	p.E242K	86	36	0.419	0.493	3	2	1	94	basic, immunoglobulin-like variable motif containing	ENST00000257336.1
Case#1-Baseline-WholeTumor	SLC10A2	13	103718383	Missense_Mutation	G	A	p.L73F	49	17	0.347	0.408	3	2	1	61	solute carrier family 10 (sodium/bile acid cotransporter), member 2	ENST00000245312.3
Case#1-Baseline-WholeTumor	DAOA	13	106124931	Missense_Mutation	G	A	p.G60R	173	66	0.382	0.449	3	2	1	156	D-amino acid oxidase activator	ENST00000375936.3
Case#1-Baseline-WholeTumor	MCF2L	13	113744025	Missense_Mutation	C	T	p.P1009L	67	24	0.358	0.422	3	2	1	50	MCF.2 cell line derived transforming sequence-like	ENST00000375608.3
Case#1-Baseline-WholeTumor	OR4K15	14	20444378	Missense_Mutation	C	T	p.S234F	129	42	0.326	0.412	2	1	1	217	olfactory receptor, family 4, subfamily K, member 15	ENST00000305051.5
Case#1-Baseline-WholeTumor	OR4L1	14	20529068	Missense_Mutation	C	A	p.L289M	15	4	0.267	0.338	2	1	1	39	olfactory receptor, family 4, subfamily L, member 1	ENST00000315683.1
Case#1-Baseline-WholeTumor	OR4K17	14	20585661	Missense_Mutation	G	A	p.M32I	81	41	0.506	0.641	2	1	1	106	olfactory receptor, family 4, subfamily K, member 17	ENST00000315543.4
Case#1-Baseline-WholeTumor	OR4K17	14	20586032	Missense_Mutation	C	T	p.A156V	37	14	0.378	0.479	2	1	1	78	olfactory receptor, family 4, subfamily K, member 17	ENST00000315543.4
Case#1-Baseline-WholeTumor	OR11H6	14	20692146	Missense_Mutation	C	T	p.S93F	27	9	0.333	0.422	2	1	1	38	olfactory receptor, family 11, subfamily H, member 6	ENST00000315519.2
Case#1-Baseline-WholeTumor	TOX4	14	21955823	Missense_Mutation	G	A	p.G97R	23	13	0.565	0.715	2	1	1	48	TOX high mobility group box family member 4	ENST00000405508.1
Case#1-Baseline-WholeTumor	ACIN1	14	23562690	Nonsense_Mutation	G	A	p.Q126*	147	48	0.327	0.413	2	1	1	142	apoptotic chromatin condensation inducer 1	ENST00000262710.1
Case#1-Baseline-WholeTumor	MYH6	14	23858841	Missense_Mutation	C	T	p.D1274N	107	34	0.318	0.402	2	1	1	96	myosin, heavy chain 6, cardiac muscle, alpha	ENST00000356287.3
Case#1-Baseline-WholeTumor	MYH6	14	23862245	Missense_Mutation	C	T	p.E1043K	44	16	0.364	0.460	2	1	1	81	myosin, heavy chain 6, cardiac muscle, alpha	ENST00000356287.3
Case#1-Baseline-WholeTumor	MYH7	14	23902319	Missense_Mutation	C	T	p.D107N	103	31	0.301	0.381	2	1	1	122	myosin, heavy chain 7, cardiac muscle, beta	ENST00000355349.3
Case#1-Baseline-WholeTumor	NGDN	14	23946546	Missense_Mutation	G	T	p.G284V	187	67	0.358	0.454	2	1	1	262	neuroguidin, EIF4E binding protein	ENST00000408901.3
Case#1-Baseline-WholeTumor	IRF9	14	24633109	Missense_Mutation	G	A	p.G173E	20	6	0.300	0.380	2	1	1	17	interferon regulatory factor 9	ENST00000396864.3
Case#1-Baseline-WholeTumor	HECTD1	14	31598018	Missense_Mutation	G	A	p.S1520F	42	16	0.381	0.482	2	1	1	41	HECT domain containing E3 ubiquitin protein ligase 1	ENST00000399332.1
Case#1-Baseline-WholeTumor	NPAS3	14	33684576	Missense_Mutation	G	A	p.G110E	84	35	0.417	0.527	2	1	1	98	neuronal PAS domain protein 3	ENST00000356141.4
Case#1-Baseline-WholeTumor	TTC6	14	38218445	Missense_Mutation	G	C	p.D889H	27	9	0.333	0.422	2	1	1	28	tetratricopeptide repeat domain 6	ENST00000553443.1
Case#1-Baseline-WholeTumor	TTC6	14	38311413	Missense_Mutation	C	T	p.R494C	54	33	0.611	0.774	2	1	1	75	tetratricopeptide repeat domain 6	ENST00000476979.1
Case#1-Baseline-WholeTumor	MIA2	14	39717294	Missense_Mutation	C	T	p.P506S	21	7	0.333	0.422	2	1	1	32	melanoma inhibitory activity 2	ENST00000280082.3
Case#1-Baseline-WholeTumor	SOS2	14	50585402	Missense_Mutation	G	A	p.P1220L	140	62	0.443	0.561	2	1	1	130	son of sevenless homolog 2 (Drosophila)	ENST00000216373.5
Case#1-Baseline-WholeTumor	PYGL	14	51379841	Missense_Mutation	C	T	p.G509E	50	14	0.280	0.354	2	1	1	34	phosphorylase, glycogen, liver	ENST00000216392.7
Case#1-Baseline-WholeTumor	PTGDR	14	52734740	Missense_Mutation	G	A	p.V70I	51	27	0.529	0.670	2	1	1	47	prostaglandin D2 receptor (DP)	ENST00000306051.2
Case#1-Baseline-WholeTumor	ERO1L	14	53119962	Missense_Mutation	C	T	p.E294K	97	39	0.402	0.509	2	1	1	82	ERO1-like (S. cerevisiae)	ENST00000395686.3
Case#1-Baseline-WholeTumor	C14orf37	14	58605950	Missense_Mutation	C	T	p.E43K	145	61	0.421	0.533	2	1	1	173	chromosome 14 open reading frame 37	ENST00000267485.7
Case#1-Baseline-WholeTumor	DACT1	14	59113232	Missense_Mutation	G	A	p.G631R	103	40	0.388	0.492	2	1	1	81	dishevelled-binding antagonist of beta-catenin 1	ENST00000335867.4
Case#1-Baseline-WholeTumor	CCDC175	14	60005543	Nonsense_Mutation	C	T	p.W457*	42	21	0.500	0.633	2	1	1	32	coiled-coil domain containing 175	ENST00000537690.2
Case#1-Baseline-WholeTumor	C14orf39	14	60935167	Missense_Mutation	C	T	p.E255K	48	19	0.396	0.501	2	1	1	39	chromosome 14 open reading frame 39	ENST00000321731.3
Case#1-Baseline-WholeTumor	KCNH5	14	63174459	Missense_Mutation	C	T	p.E912K	63	20	0.317	0.402	2	1	1	68	potassium voltage-gated channel, subfamily H (eag-related), member 5	ENST00000322893.7
Case#1-Baseline-WholeTumor	SMOC1	14	70480115	Missense_Mutation	G	A	p.G318E	69	28	0.406	0.514	2	1	1	66	SPARC related modular calcium binding 1	ENST00000381280.4
Case#1-Baseline-WholeTumor	SLC8A3	14	70527657	Splice_Site	C	T		53	15	0.283	0.358	2	1	1	41	solute carrier family 8 (sodium/calcium exchanger), member 3	ENST00000381269.2
Case#1-Baseline-WholeTumor	SLC8A3	14	70634566	Missense_Mutation	C	T	p.G192R	47	21	0.447	0.566	2	1	1	62	solute carrier family 8 (sodium/calcium exchanger), member 3	ENST00000381269.2
Case#1-Baseline-WholeTumor	LTBP2	14	74988722	Missense_Mutation	C	T	p.D894N	66	23	0.348	0.441	2	1	1	54	latent transforming growth factor beta binding protein 2	ENST00000261978.4
Case#1-Baseline-WholeTumor	YLPM1	14	75230659	Missense_Mutation	C	T	p.S156F	138	49	0.355	0.449	2	1	1	114	YLP motif containing 1	ENST00000552421.1
Case#1-Baseline-WholeTumor	TTLL5	14	76173416	Missense_Mutation	C	T	p.P214L	65	30	0.462	0.584	2	1	1	78	tubulin tyrosine ligase-like family, member 5	ENST00000298832.9
Case#1-Baseline-WholeTumor	ESRRB	14	76905755	Missense_Mutation	C	T	p.P20L	79	34	0.430	0.545	2	1	1	57	estrogen-related receptor beta	ENST00000509242.1
Case#1-Baseline-WholeTumor	KCNK10	14	88729793	Missense_Mutation	G	A	p.S47F	150	54	0.360	0.456	2	1	1	118	potassium channel, subfamily K, member 10	ENST00000340700.5
Case#1-Baseline-WholeTumor	FAM181A	14	94395357	Nonsense_Mutation	G	A	p.W304*	49	12	0.245	0.310	2	1	1	57	family with sequence similarity 181, member A	ENST00000267594.5
Case#1-Baseline-WholeTumor	SERPINA9	14	94936174	Missense_Mutation	C	T	p.A2T	17	8	0.471	0.596	2	1	1	32	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 9	ENST00000380365.3
Case#1-Baseline-WholeTumor	TCL1B	14	96152965	Splice_Site	G	A	p.R54K	117	46	0.393	0.498	2	1	1	104	T-cell leukemia/lymphoma 1B	ENST00000340722.7
Case#1-Baseline-WholeTumor	BDKRB2	14	96706787	Missense_Mutation	C	T	p.T41I	36	8	0.222	0.281	2	1	1	56	bradykinin receptor B2	ENST00000306005.3
Case#1-Baseline-WholeTumor	ATG2B	14	96813608	Missense_Mutation	G	A	p.S78F	73	23	0.315	0.399	2	1	1	96	autophagy related 2B	ENST00000359933.4
Case#1-Baseline-WholeTumor	AHNAK2	14	105416564	Missense_Mutation	G	A	p.P1742S	88	36	0.409	0.518	2	1	1	88	AHNAK nucleoprotein 2	ENST00000333244.5
Case#1-Baseline-WholeTumor	OR4N4	15	22382897	Missense_Mutation	A	G	p.Y142C	27	5	0.185	0.234	2	1	1	145	olfactory receptor, family 4, subfamily N, member 4	ENST00000328795.4
Case#1-Baseline-WholeTumor	RP11-467N20.5	15	23407013	Missense_Mutation	C	T	p.R608K	221	14	0.063	0.080	2	1	1	169		ENST00000558241.1
Case#1-Baseline-WholeTumor	NPAP1	15	24922531	Missense_Mutation	C	T	p.S506F	90	71	0.789	0.999	2	1	1	117	nuclear pore associated protein 1	ENST00000329468.2
Case#1-Baseline-WholeTumor	RASGRP1	15	38786858	Missense_Mutation	G	A	p.L662F	42	33	0.786	0.995	2	2	0	61	RAS guanyl releasing protein 1 (calcium and DAG-regulated)	ENST00000310803.5
Case#1-Baseline-WholeTumor	SPG11	15	44955808	Missense_Mutation	G	A	p.A13V	12	10	0.833	1.055	2	2	0	10	spastic paraplegia 11 (autosomal recessive)	ENST00000261866.7

Case#1-Baseline-WholeTumor	C15orf43	15	45270782	Missense_Mutation	G	A	p.E207K	50	41	0.820	1.038	2	2	0	83	chromosome 15 open reading frame 43	ENST00000340827.3
Case#1-Baseline-WholeTumor	FAM227B	15	49833946	Missense_Mutation	C	G	p.E269Q	155	133	0.858	1.086	2	2	0	132	family with sequence similarity 227, member B	ENST00000299338.6
Case#1-Baseline-WholeTumor	TRPM7	15	50903300	Missense_Mutation	G	A	p.S757F	48	40	0.833	1.055	2	2	0	71	transient receptor potential cation channel, subfamily M, member 7	ENST00000313478.7
Case#1-Baseline-WholeTumor	WDR72	15	54025285	Missense_Mutation	G	A	p.T21I	38	32	0.842	1.066	2	2	0	44	WD repeat domain 72	ENST00000396328.1
Case#1-Baseline-WholeTumor	UNC13C	15	54586184	Missense_Mutation	G	A	p.E1304K	69	52	0.754	0.954	2	2	0	96	unc-13 homolog C (C. elegans)	ENST00000260323.11
Case#1-Baseline-WholeTumor	VPS13C	15	62212778	Missense_Mutation	C	T	p.M2377I	47	36	0.766	0.970	2	2	0	59	vacuolar protein sorting 13 homolog C (S. cerevisiae)	ENST00000261517.5
Case#1-Baseline-WholeTumor	DENND4A	15	65983748	Missense_Mutation	C	T	p.E1018K	69	51	0.739	0.936	2	2	0	79	DENN/MADD domain containing 4A	ENST00000431932.2
Case#1-Baseline-WholeTumor	MAP2K1	15	66729162	Missense_Mutation	C	T	p.P124S	95	68	0.716	0.906	2	2	0	144	mitogen-activated protein kinase kinase 1	ENST00000307102.5
Case#1-Baseline-WholeTumor	UBE2Q2	15	76152306	Missense_Mutation	C	T	p.P124S	291	230	0.790	1.000	2	2	0	392	ubiquitin-conjugating enzyme E2Q family member 2	ENST00000267938.4
Case#1-Baseline-WholeTumor	KIAA1024	15	79749651	Missense_Mutation	C	T	p.P388S	63	46	0.730	0.924	2	2	0	99	KIAA1024	ENST00000305428.3
Case#1-Baseline-WholeTumor	RP13-996F3.4	15	83015603	Missense_Mutation	T	C	p.T71A	373	295	0.791	1.001	2	1	1	580		ENST00000557886.1
Case#1-Baseline-WholeTumor	SLCO3A1	15	92459517	Missense_Mutation	G	A	p.E159K	123	93	0.756	0.957	2	2	0	55	solute carrier organic anion transporter family, member 3A1	ENST00000318445.6
Case#1-Baseline-WholeTumor	SLCO3A1	15	92669468	Missense_Mutation	T	C	p.V451A	40	27	0.675	0.854	2	2	0	67	solute carrier organic anion transporter family, member 3A1	ENST00000318445.6
Case#1-Baseline-WholeTumor	RAB11FIP3	16	476583	Missense_Mutation	C	T	p.L193F	37	15	0.405	0.513	2	1	1	25	RAB11 family interacting protein 3 (class II)	ENST00000262305.4
Case#1-Baseline-WholeTumor	UBE2I	16	1364309	Missense_Mutation	C	T	p.P28S	173	66	0.382	0.483	2	1	1	122	ubiquitin-conjugating enzyme E2I	ENST00000355803.4
Case#1-Baseline-WholeTumor	TSC2	16	2111962	Nonsense_Mutation	C	T	p.Q404*	149	69	0.463	0.586	2	1	1	124	tuberous sclerosis 2	ENST00000219476.3
Case#1-Baseline-WholeTumor	PKD1	16	2147482	Missense_Mutation	C	T	p.E3415K	186	92	0.495	0.626	2	1	1	135	polycystic kidney disease 1 (autosomal dominant)	ENST00000262304.4
Case#1-Baseline-WholeTumor	E4F1	16	2283990	Splice_Site	C	T	p.T458T	104	42	0.404	0.511	2	1	1	99	E4F transcription factor 1	ENST00000301727.4
Case#1-Baseline-WholeTumor	ABCA3	16	2328371	Missense_Mutation	C	T	p.D1546N	81	30	0.370	0.469	2	1	1	72	ATP-binding cassette, sub-family A (ABC1), member 3	ENST00000301732.5
Case#1-Baseline-WholeTumor	TIGD7	16	3349540	Missense_Mutation	C	T	p.D359N	34	15	0.441	0.558	2	1	1	38	tigger transposable element derived 7	ENST00000396862.1
Case#1-Baseline-WholeTumor	CLUAP1	16	3554779	Missense_Mutation	C	T	p.R28C	114	47	0.412	0.522	2	1	1	109	clusterin associated protein 1	ENST00000576634.1
Case#1-Baseline-WholeTumor	C16orf96	16	4625472	Missense_Mutation	G	A	p.G331R	79	26	0.329	0.417	2	1	1	93	chromosome 16 open reading frame 96	ENST00000444310.4
Case#1-Baseline-WholeTumor	ZNF500	16	4802975	Missense_Mutation	C	T	p.R282Q	97	44	0.454	0.574	2	1	1	75	zinc finger protein 500	ENST00000219478.6
Case#1-Baseline-WholeTumor	RBFOX1	16	7759066	Missense_Mutation	G	A	p.R335Q	102	37	0.363	0.459	2	1	1	105	RNA binding protein, fox-1 homolog (C. elegans) 1	ENST00000550418.1
Case#1-Baseline-WholeTumor	ACSM2A	16	20476954	Missense_Mutation	C	T	p.S98L	137	35	0.255	0.323	2	1	1	109	acyl-CoA synthetase medium-chain family member 2A	ENST00000573854.1
Case#1-Baseline-WholeTumor	ACSM2B	16	20570685	Missense_Mutation	C	T	p.E88K	35	11	0.314	0.398	2	1	1	55	acyl-CoA synthetase medium-chain family member 2B	ENST00000329697.6
Case#1-Baseline-WholeTumor	ACSM1	16	20693784	Splice_Site	C	T	p.G135G	171	42	0.246	0.311	2	1	1	195	acyl-CoA synthetase medium-chain family member 1	ENST00000307493.4
Case#1-Baseline-WholeTumor	USP31	16	23116773	Missense_Mutation	G	A	p.P360S	108	47	0.435	0.551	2	1	1	99	ubiquitin specific peptidase 31	ENST00000219689.7
Case#1-Baseline-WholeTumor	SCNN1G	16	23200795	Missense_Mutation	G	A	p.E141K	38	23	0.605	0.766	2	1	1	45	sodium channel, non-voltage-gated 1, gamma subunit	ENST00000300061.2
Case#1-Baseline-WholeTumor	RBBP6	16	24578724	Missense_Mutation	C	T	p.S617L	74	29	0.392	0.496	2	1	1	91	retinoblastoma binding protein 6	ENST00000319715.4
Case#1-Baseline-WholeTumor	KCTD13	16	29918330	Missense_Mutation	CC	TT	p.G285R	64	27	0.422	0.534	2	1	1	53	potassium channel tetramerization domain containing 13	ENST00000568000.1
Case#1-Baseline-WholeTumor	GPR56	16	57685420	Nonsense_Mutation	C	T	p.Q125*	40	16	0.400	0.506	2	1	1	28	G protein-coupled receptor 56	ENST00000388812.4
Case#1-Baseline-WholeTumor	CDH8	16	61687930	Missense_Mutation	C	T	p.R661Q	65	35	0.538	0.682	2	1	1	132	cadherin 8, type 2	ENST00000577390.1
Case#1-Baseline-WholeTumor	CDH8	16	61761117	Splice_Site	TC	AT	p.N473Y	41	10	0.244	0.309	2	1	1	61	cadherin 8, type 2	ENST00000577390.1
Case#1-Baseline-WholeTumor	ELMO3	16	67237233	Missense_Mutation	C	T	p.P631L	26	10	0.385	0.487	2	1	1	41	engulfment and cell motility 3	ENST00000360833.1
Case#1-Baseline-WholeTumor	KCTD19	16	67333336	Missense_Mutation	G	A	p.R306C	58	16	0.276	0.349	2	1	1	56	potassium channel tetramerization domain containing 19	ENST00000304372.5
Case#1-Baseline-WholeTumor	ESRP2	16	68265438	Missense_Mutation	C	T	p.E497K	65	36	0.554	0.701	2	1	1	64	epithelial splicing regulatory protein 2	ENST00000565858.1
Case#1-Baseline-WholeTumor	WWP2	16	69969798	Missense_Mutation	C	T	p.P629S	53	20	0.377	0.478	2	1	1	76	WW domain containing E3 ubiquitin protein ligase 2	ENST00000359154.2
Case#1-Baseline-WholeTumor	HYDIN	16	70995904	Missense_Mutation	C	T	p.E1976K	52	17	0.327	0.414	2	1	1	97	HYDIN, axonemal central pair apparatus protein	ENST00000393567.2
Case#1-Baseline-WholeTumor	ZNF23	16	71483009	Missense_Mutation	G	A	p.P307S	98	31	0.316	0.400	2	1	1	126	zinc finger protein 23	ENST00000393539.2
Case#1-Baseline-WholeTumor	ZFHX3	16	72827630	Missense_Mutation	C	G	p.G2984A	82	20	0.244	0.309	2	1	1	121	zinc finger homeobox 3	ENST00000268489.5
Case#1-Baseline-WholeTumor	FA2H	16	74750304	Missense_Mutation	G	A	p.S327F	65	29	0.446	0.565	2	1	1	71	fatty acid 2-hydroxylase	ENST00000219368.3
Case#1-Baseline-WholeTumor	CHST5	16	75563388	Missense_Mutation	C	T	p.A299T	65	32	0.492	0.623	2	1	1	32	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5	ENST00000336257.3
Case#1-Baseline-WholeTumor	CNTNAP4	16	76495889	Missense_Mutation	C	T	p.S460F	50	8	0.160	0.203	2	1	1	93	contactin associated protein-like 4	ENST00000476707.1
Case#1-Baseline-WholeTumor	VAT1L	16	77859352	Missense_Mutation	GG	AA	p.G192S	84	25	0.298	0.377	2	1	1	111	vesicle amine transport 1-like	ENST00000302536.2
Case#1-Baseline-WholeTumor	HSD17B2	16	82101883	Missense_Mutation	G	A	p.R125Q	104	35	0.337	0.426	2	1	1	136	hydroxysteroid (17-beta) dehydrogenase 2	ENST00000199936.4
Case#1-Baseline-WholeTumor	HSD17B2	16	82124611	Missense_Mutation	G	A	p.V257I	85	23	0.271	0.343	2	1	1	114	hydroxysteroid (17-beta) dehydrogenase 2	ENST00000199936.4
Case#1-Baseline-WholeTumor	CDH13	16	83711897	Missense_Mutation	G	A	p.G457S	85	39	0.459	0.581	2	1	1	121	cadherin 13	ENST00000566620.1
Case#1-Baseline-WholeTumor	TLDC1	16	84520527	Missense_Mutation	G	A	p.S223L	27	10	0.370	0.469	2	1	1	31	TBC/LysM-associated domain containing 1	ENST00000343629.6
Case#1-Baseline-WholeTumor	FOXC2	16	86601462	Missense_Mutation	C	T	p.S174F	51	11	0.216	0.273	2	1	1	64	forkhead box C2 (MFH-1, mesenchyme forkhead 1)	ENST00000320354.4
Case#1-Baseline-WholeTumor	ZCCHC14	16	87451194	Missense_Mutation	G	A	p.P282S	117	54	0.462	0.584	2	1	1	111	zinc finger, CCHC domain containing 14	ENST00000268616.4
Case#1-Baseline-WholeTumor	SLC7A5	16	87868107	Missense_Mutation	C	T	p.G461S	71	16	0.225	0.285	2	1	1	76	solute carrier family 7 (amino acid transporter light chain, L system), member 5	ENST00000261622.4
Case#1-Baseline-WholeTumor	CDT1	16	88871204	Missense_Mutation	G	C	p.R129P	89	23	0.258	0.327	2	1	1	81	chromatin licensing and DNA replication factor 1	ENST00000301019.4
Case#1-Baseline-WholeTumor	RNMTL1	17	685854	Missense_Mutation	CC	TT	p.S79F	34	15	0.441	0.558	2	1	1	32	RNA methyltransferase like 1	ENST00000304478.4
Case#1-Baseline-WholeTumor	SLC43A2	17	1494766	Splice_Site	C	T		75	34	0.453	0.574	2	1	1	50	solute carrier family 43 (amino acid system L transporter), member 2	ENST00000301335.5
Case#1-Baseline-WholeTumor	RTN4RL1	17	1840911	Missense_Mutation	G	A	p.L69F	220	100	0.455	0.575	2	1	1	204	reticulon 4 receptor-like 1	ENST00000331238.6
Case#1-Baseline-WholeTumor	SPNS2	17	4436361	Missense_Mutation	G	A	p.R342H	75	27	0.360	0.456	2	1	1	62	spinster homolog 2 (Drosophila)	ENST00000329078.3
Case#1-Baseline-WholeTumor	TM4SF5	17	4685876	Nonsense_Mutation	C	T	p.R113*	107	47	0.439	0.556	2	1	1	80	transmembrane 4 L six family member 5	ENST00000270560.3
Case#1-Baseline-WholeTumor	NLRP1	17	5462175	Missense_Mutation	G	A	p.P614L	47	12	0.255	0.323	2	1	1	70	NLR family, pyrin domain containing 1	ENST00000572272.1
Case#1-Baseline-WholeTumor	C17orf74	17	7329695	Missense_Mutation	C	T	p.R129C	206	82	0.398	0.504	2	1	1	125	chromosome 17 open reading frame 74	ENST00000333870.3
Case#1-Baseline-WholeTumor	ZBTB4	17	7365468	Missense_Mutation	G	A	p.P945S	162	76	0.469	0.594	2	1	1	146	zinc finger and BTB domain containing 4	ENST00000311403.4
Case#1-Baseline-WholeTumor	DNAH2	17	7710806	Missense_Mutation	C	T	p.R3211W	145	52	0.359	0.454	2	1	1	133	dynein, axonemal, heavy chain 2	ENST00000572933.1
Case#1-Baseline-WholeTumor	CHD3	17	7803300	Nonsense_Mutation	G	A	p.W877*	141	56	0.397	0.503	2	1	1	151	chromodomain helicase DNA binding protein 3	ENST00000330494.7
Case#1-Baseline-WholeTumor	MYH13	17	10267715	Missense_Mutation	C	T	p.E45K	125	36	0.288	0.365	2	1	1	164	myosin, heavy chain 13, skeletal muscle	ENST00000418404.3
Case#1-Baseline-WholeTumor	MYH8	17	10309451	Missense_Mutation	C	T	p.R780K	60	27	0.450	0.570	2	1	1	73	myosin, heavy chain 8, skeletal muscle, perinatal	ENST00000403437.2
Case#1-Baseline-WholeTumor	MYH8	17	10318445	Missense_Mutation	C	T	p.D265N	55	23	0.418	0.529	2	1	1	84	myosin, heavy chain 8, skeletal muscle, perinatal	ENST00000403437.2
Case#1-Baseline-WholeTumor	MYH4	17	10356117	Missense_Mutation	C	T	p.E1082K	45	30	0.667	0.844	2	1	1	79	myosin, heavy chain 4, skeletal muscle	ENST00000255381.2
Case#1-Baseline-WholeTumor	MYH2	17	10428903	Missense_Mutation	C	T	p.E1468K	64	21	0.328	0.415	2	1	1	73	myosin, heavy chain 2, skeletal muscle, adult	ENST00000245503.5
Case#1-Baseline-WholeTumor	MYH2	17	10446421	Missense_Mutation	C	T	p.E267K	72	26	0.361	0.457	2	1	1	90	myosin, heavy chain 2, skeletal muscle, adult	ENST00000245503.5
Case#1-Baseline-WholeTumor	MYH3	17	10533685	Missense_Mutation	C	T	p.D1793N	107	50	0.467	0.592	2	1	1	155	myosin, heavy chain 3, skeletal muscle, embryonic	ENST00000583535.1
Case#1-Baseline-WholeTumor	DNAH9	17	11556263	Missense_Mutation	G	A	p.E847K	57	18	0.316	0.400	2	1	1	78	dynein, axonemal, heavy chain 9	ENST00000262442.4
Case#1-Baseline-WholeTumor	DNAH9	17	11772460	Missense_Mutation	G	A	p.E3315K	67	23	0.343	0.435	2	1	1	86	dynein, axonemal, heavy chain 9	ENST00000262442.4
Case#1-Baseline-WholeTumor	FLCN	17	17118576	Missense_Mutation	A	G	p.V452A	66	27	0.409	0.518	2	1	1	45	folliculin	ENST00000285071.4
Case#1-Baseline-WholeTumor	TOM1L2	17	17797066	Missense_Mutation	C	T	p.R92Q	52	21	0.404	0.511	2	1	1	61	target of myb1-like 2 (chicken)	ENST00000379504.3
Case#1-Baseline-WholeTumor	ZNF286B	17	18565291	Missense_Mutation	G	A	p.L510F	254	60	0.236	0.299	2	1	1	255	zinc finger protein 286B	ENST00000545289.1
Case#1-Baseline-WholeTumor	EPN2	17	19189020	Missense_Mutation	C	T	p.P228L	65	29	0.446	0.565	2	1	1	42	epsin 2	ENST00000314728.5
Case#1-Baseline-WholeTumor	RNF112	17	19317435	Missense_Mutation	G	A	p.D285N	36	11	0.306	0.387	2	1	1	37	ring finger protein 112	ENST00000461366.1
Case#1-Baseline-WholeTumor	KIAA0100	17	26969968	Missense_Mutation	A	G	p.V145A	73	35	0.479	0.607	2	1	1	95	KIAA0100	ENST00000528896.2
Case#1-Baseline-WholeTumor	MYO18A	17	27493027	Missense_Mutation	G	A	p.P311L	40	16	0.400	0.506	2	1	1	26	myosin XVIIIA	ENST00000527372.1
Case#1-Baseline-WholeTumor	EFCAB5	17	28295941	Missense_Mutation	C	T	p.S108L	56	14	0.250	0.316	2	1	1	69	EF-hand calcium binding domain 5	ENST00000394835.3
Case#1-Baseline-WholeTumor	NF1	17	29548940	Missense_Mutation	G	A	p.E572K	83	26	0.313	0.397	2	1	1	85	neurofibromin 1	ENST00000358273.4
Case#1-Baseline-WholeTumor	COPRS	17	30180029	Missense_Mutation	G	A	p.P63S	81	36	0.444	0.563	2	1	1	87	coordinator of PRMT5, differentiation stimulator	ENST00000302362.6

Case#1-Baseline-WholeTumor	ZNF207	17	30693762	Missense_Mutation	C	T	p.P287S	55	25	0.455	0.575	2	1	1	67	zinc finger protein 207	ENST00000321233.6
Case#1-Baseline-WholeTumor	CDK5R1	17	30815557	Missense_Mutation	C	T	p.R307W	61	24	0.393	0.498	2	1	1	70	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	ENST00000313401.3
Case#1-Baseline-WholeTumor	CCL13	17	32685133	Missense_Mutation	C	T	p.H94Y	52	23	0.442	0.560	2	1	1	63	chemokine (C-C motif) ligand 13	ENST00000225844.2
Case#1-Baseline-WholeTumor	CCL18	17	34398362	Nonsense_Mutation	G	A	p.W77*	159	72	0.453	0.573	2	1	1	196	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	ENST00000004921.3
Case#1-Baseline-WholeTumor	MYO19	17	34858954	Missense_Mutation	G	A	p.P688L	126	50	0.397	0.502	2	1	1	108	myosin XIX	ENST00000431794.3
Case#1-Baseline-WholeTumor	SYNRG	17	35880726	Missense_Mutation	G	A	p.S1231F	52	17	0.327	0.414	2	1	1	56	synergin, gamma	ENST00000339208.6
Case#1-Baseline-WholeTumor	TBC1D3F	17	36288299	Nonsense_Mutation	C	T	p.Q129*	702	61	0.087	0.110	2	1	1	844	TBC1 domain family, member 3F	ENST00000327454.6
Case#1-Baseline-WholeTumor	PCGF2	17	36891693	Missense_Mutation	G	A	p.S273F	144	74	0.514	0.650	2	1	1	98	polycomb group ring finger 2	ENST00000580830.1
Case#1-Baseline-WholeTumor	PSMD3	17	38146126	Missense_Mutation	C	T	p.S274F	50	26	0.520	0.658	2	1	1	62	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	ENST00000264639.4
Case#1-Baseline-WholeTumor	KRT28	17	38956009	Missense_Mutation	G	A	p.S46F	33	9	0.273	0.345	2	1	1	43	keratin 28	ENST00000306658.7
Case#1-Baseline-WholeTumor	TMEM99	17	38990863	Missense_Mutation	C	T	p.S32F	55	17	0.309	0.391	2	1	1	81	transmembrane protein 99	ENST00000301665.3
Case#1-Baseline-WholeTumor	KRTAP9-8	17	39394394	Missense_Mutation	C	T	p.P31S	207	47	0.227	0.287	2	1	1	194	keratin associated protein 9-8	ENST00000254072.6
Case#1-Baseline-WholeTumor	KRTAP29-1	17	39458565	Missense_Mutation	G	A	p.P180L	43	24	0.558	0.707	2	1	1	51	keratin associated protein 29-1	ENST00000391353.1
Case#1-Baseline-WholeTumor	SPATA32	17	43332551	Missense_Mutation	G	A	p.T333I	173	70	0.405	0.512	2	1	1	203	spermatogenesis associated 32	ENST00000331780.4
Case#1-Baseline-WholeTumor	FAM117A	17	47793603	Nonsense_Mutation	G	A	p.R329*	68	37	0.544	0.641	3	2	1	76	family with sequence similarity 117, member A	ENST00000240364.2
Case#1-Baseline-WholeTumor	COL1A1	17	48275324	Missense_Mutation	C	T	p.E210K	113	26	0.230	0.271	3	2	1	72	collagen, type I, alpha 1	ENST00000225964.5
Case#1-Baseline-WholeTumor	PPM1E	17	57057800	Missense_Mutation	C	T	p.S559F	31	5	0.161	0.190	3	2	1	31	protein phosphatase, Mg2+/Mn2+ dependent, 1E	ENST00000308249.2
Case#1-Baseline-WholeTumor	CLTC	17	57746275	Missense_Mutation	C	T	p.P756S	164	87	0.530	0.624	3	2	1	129	clathrin, heavy chain (Hc)	ENST00000269122.3
Case#1-Baseline-WholeTumor	HELZ	17	65124841	Missense_Mutation	G	A	p.P1105S	109	67	0.615	0.724	3	2	1	72	helicase with zinc finger	ENST00000358691.5
Case#1-Baseline-WholeTumor	ABCA8	17	66865889	Missense_Mutation	C	T	p.V1515M	79	25	0.316	0.373	3	2	1	72	ATP-binding cassette, sub-family A (ABC1), member 8	ENST00000269080.2
Case#1-Baseline-WholeTumor	ABCA8	17	66933227	Missense_Mutation	C	T	p.E111K	82	18	0.220	0.258	3	2	1	39	ATP-binding cassette, sub-family A (ABC1), member 8	ENST00000269080.2
Case#1-Baseline-WholeTumor	SDK2	17	71375689	Splice_Site	C	T		144	30	0.208	0.245	3	2	1	81	sidekick cell adhesion molecule 2	ENST00000392650.3
Case#1-Baseline-WholeTumor	KIF19	17	72346896	Missense_Mutation	G	A	p.R480Q	167	98	0.587	0.691	3	2	1	131	kinesin family member 19	ENST00000389916.4
Case#1-Baseline-WholeTumor	GPRC5C	17	72436025	Missense_Mutation	C	T	p.P82L	43	7	0.163	0.192	3	2	1	45	G protein-coupled receptor, class C, group 5, member C	ENST00000481232.1
Case#1-Baseline-WholeTumor	NAT9	17	72771807	Missense_Mutation	C	T	p.G11R	119	66	0.555	0.653	3	2	1	81	N-acetyltransferase 9 (GCN5-related, putative)	ENST00000357814.3
Case#1-Baseline-WholeTumor	OTOP3	17	72931939	Missense_Mutation	G	A	p.G15R	140	82	0.586	0.690	3	2	1	53	otopetrin 3	ENST00000328801.4
Case#1-Baseline-WholeTumor	HID1	17	72958413	Missense_Mutation	G	A	p.S176F	116	32	0.276	0.325	3	2	1	53	HID1 domain containing	ENST00000425042.2
Case#1-Baseline-WholeTumor	ITGB4	17	73732763	Missense_Mutation	G	A	p.E660K	64	8	0.125	0.147	3	2	1	41	integrin, beta 4	ENST00000200181.3
Case#1-Baseline-WholeTumor	SEC14L1	17	75187009	Missense_Mutation	T	G	p.V63G	162	30	0.185	0.218	3	2	1	128	SEC14-like 1 (S. cerevisiae)	ENST00000413679.2
Case#1-Baseline-WholeTumor	DNAH17	17	76449428	Missense_Mutation	C	T	p.G3504E	114	22	0.193	0.227	3	2	1	61	dynein, axonemal, heavy chain 17	ENST00000585328.1
Case#1-Baseline-WholeTumor	DNAH17	17	76472670	Missense_Mutation	G	A	p.T2708I	220	53	0.241	0.284	3	2	1	182	dynein, axonemal, heavy chain 17	ENST00000585328.1
Case#1-Baseline-WholeTumor	GAA	17	78090886	Missense_Mutation	G	A	p.G770D	116	73	0.629	0.741	3	2	1	78	glucosidase, alpha; acid	ENST00000302262.3
Case#1-Baseline-WholeTumor	B3GNTL1	17	80904805	Missense_Mutation	C	T	p.G354S	84	26	0.310	0.364	3	2	1	50	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1	ENST00000320865.3
Case#1-Baseline-WholeTumor	DSC3	18	28588081	Missense_Mutation	C	T	p.E522K	93	33	0.355	0.449	2	1	1	106	desmocollin 3	ENST00000360428.4
Case#1-Baseline-WholeTumor	DSC3	18	28604431	Missense_Mutation	C	T	p.G220E	57	30	0.526	0.666	2	1	1	68	desmocollin 3	ENST00000360428.4
Case#1-Baseline-WholeTumor	CCDC178	18	30992024	Missense_Mutation	G	A	p.S10F	69	23	0.333	0.422	2	1	1	106	coiled-coil domain containing 178	ENST00000383096.3
Case#1-Baseline-WholeTumor	ASXL3	18	31323386	Missense_Mutation	C	T	p.P1192S	54	24	0.444	0.563	2	1	1	61	additional sex combs like transcriptional regulator 3	ENST00000269197.5
Case#1-Baseline-WholeTumor	ASXL3	18	31324221	Missense_Mutation	C	T	p.P1470L	45	15	0.333	0.422	2	1	1	71	additional sex combs like transcriptional regulator 3	ENST00000269197.5
Case#1-Baseline-WholeTumor	DTNA	18	32407618	Missense_Mutation	GG	AA	p.G358K	57	18	0.316	0.400	2	1	1	74	dystrobrevin, alpha	ENST00000399113.3
Case#1-Baseline-WholeTumor	LOXHD1	18	44184156	Missense_Mutation	C	T	p.D266N	27	10	0.370	0.469	2	1	1	38	lipoxygenase homology domains 1	ENST00000441551.2
Case#1-Baseline-WholeTumor	MYO5B	18	47432805	Missense_Mutation	C	T	p.G800R	26	16	0.615	0.779	2	1	1	26	myosin VB	ENST00000285039.7
Case#1-Baseline-WholeTumor	MAPK4	18	48248343	Missense_Mutation	G	A	p.E243K	37	13	0.351	0.445	2	1	1	65	mitogen-activated protein kinase 4	ENST00000400384.2
Case#1-Baseline-WholeTumor	DCC	18	50994327	Missense_Mutation	G	A	p.R1228Q	64	23	0.359	0.455	2	1	1	104	DCC netrin 1 receptor	ENST00000442544.2
Case#1-Baseline-WholeTumor	TCF4	18	52899872	Missense_Mutation	A	G	p.V506A	48	13	0.271	0.343	2	1	1	58	transcription factor 4	ENST00000356073.4
Case#1-Baseline-WholeTumor	ONECUT2	18	55143714	Missense_Mutation	C	T	p.S425F	22	12	0.545	0.690	2	1	1	25	one cut homeobox 2	ENST00000491143.2
Case#1-Baseline-WholeTumor	CDH20	18	59158012	Missense_Mutation	G	A	p.D76N	72	23	0.319	0.404	2	1	1	110	cadherin 20, type 2	ENST00000262717.4
Case#1-Baseline-WholeTumor	ZCCHC2	18	60241464	Missense_Mutation	C	T	p.S717F	81	26	0.321	0.406	2	1	1	119	zinc finger, CCHC domain containing 2	ENST00000269499.5
Case#1-Baseline-WholeTumor	SERPINB4	18	61309074	Missense_Mutation	C	T	p.E91K	118	47	0.398	0.504	2	1	1	209	serpin peptidase inhibitor, clade B (ovalbumin), member 4	ENST00000341074.5
Case#1-Baseline-WholeTumor	SERPINB7	18	61463608	Missense_Mutation	G	A	p.E149K	78	31	0.397	0.503	2	1	1	93	serpin peptidase inhibitor, clade B (ovalbumin), member 7	ENST00000398019.2
Case#1-Baseline-WholeTumor	PLK5	19	1527970	Missense_Mutation	C	T	p.A13V	111	41	0.369	0.468	2	1	1	102	polo-like kinase 5	ENST00000334770.4
Case#1-Baseline-WholeTumor	ZNF77	19	2933951	Missense_Mutation	G	A	p.P392S	90	39	0.433	0.549	2	1	1	108	zinc finger protein 77	ENST00000314531.4
Case#1-Baseline-WholeTumor	ZFR2	19	3810815	Missense_Mutation	A	C	p.V789G	202	71	0.351	0.445	2	1	1	156	zinc finger RNA binding protein 2	ENST00000262961.4
Case#1-Baseline-WholeTumor	LONP1	19	5719866	Missense_Mutation	C	T	p.G93E	22	10	0.455	0.575	2	1	1	25	lon peptidase 1, mitochondrial	ENST00000360614.3
Case#1-Baseline-WholeTumor	CTB-133G6.1	19	7437821	Missense_Mutation	G	A	p.G47R	63	26	0.413	0.522	2	1	1	76		ENST00000576789.1
Case#1-Baseline-WholeTumor	PNPLA6	19	7625627	Missense_Mutation	C	T	p.L1227F	68	30	0.441	0.558	2	1	1	59	patatin-like phospholipase domain containing 6	ENST00000221249.6
Case#1-Baseline-WholeTumor	STXBP2	19	7707219	Splice_Site	G	A	p.R265K	76	39	0.513	0.650	2	1	1	56	syntaxin binding protein 2	ENST00000221283.5
Case#1-Baseline-WholeTumor	ADAMTS10	19	8651078	Missense_Mutation	G	A	p.P863L	76	22	0.289	0.366	2	1	1	79	ADAM metallopeptidase with thrombospondin type 1 motif, 10	ENST00000597188.1
Case#1-Baseline-WholeTumor	ACTL9	19	8808786	Missense_Mutation	G	A	p.S89L	81	38	0.469	0.594	2	1	1	72	actin-like 9	ENST00000324436.3
Case#1-Baseline-WholeTumor	MUC16	19	9012820	Missense_Mutation	G	A	p.P12875L	273	79	0.289	0.366	2	1	1	364	mucin 16, cell surface associated	ENST00000397910.4
Case#1-Baseline-WholeTumor	MUC16	19	9014655	Missense_Mutation	GG	AA	p.R12774C	112	26	0.232	0.294	2	1	1	147	mucin 16, cell surface associated	ENST00000397910.4
Case#1-Baseline-WholeTumor	MUC16	19	9017469	Missense_Mutation	GG	AA	p.R12619C	202	22	0.109	0.138	2	1	1	256	mucin 16, cell surface associated	ENST00000397910.4
Case#1-Baseline-WholeTumor	MUC16	19	9047086	Missense_Mutation	G	C	p.D11515E	103	44	0.427	0.541	2	1	1	157	mucin 16, cell surface associated	ENST00000397910.4
Case#1-Baseline-WholeTumor	MUC16	19	9048674	Missense_Mutation	C	T	p.G10986E	163	64	0.393	0.497	2	1	1	235	mucin 16, cell surface associated	ENST00000397910.4
Case#1-Baseline-WholeTumor	MUC16	19	9049967	Missense_Mutation	C	T	p.R10555K	105	33	0.314	0.398	2	1	1	125	mucin 16, cell surface associated	ENST00000397910.4
Case#1-Baseline-WholeTumor	MUC16	19	9068125	Missense_Mutation	C	T	p.E6441K	48	15	0.313	0.396	2	1	1	81	mucin 16, cell surface associated	ENST00000397910.4
Case#1-Baseline-WholeTumor	MUC16	19	9075553	Missense_Mutation	G	A	p.H3965Y	110	39	0.355	0.449	2	1	1	173	mucin 16, cell surface associated	ENST00000397910.4
Case#1-Baseline-WholeTumor	MUC16	19	9075565	Missense_Mutation	C	T	p.E3961K	109	43	0.394	0.499	2	1	1	168	mucin 16, cell surface associated	ENST00000397910.4
Case#1-Baseline-WholeTumor	MUC16	19	9082946	Missense_Mutation	C	T	p.G2957S	79	32	0.405	0.513	2	1	1	83	mucin 16, cell surface associated	ENST00000397910.4
Case#1-Baseline-WholeTumor	MUC16	19	9089678	Missense_Mutation	C	T	p.D713N	94	45	0.479	0.606	2	1	1	121	mucin 16, cell surface associated	ENST00000397910.4
Case#1-Baseline-WholeTumor	OR7D2	19	9297032	Missense_Mutation	C	T	p.T192I	63	17	0.270	0.342	2	1	1	75	olfactory receptor, family 7, subfamily D, member 2	ENST00000344248.2
Case#1-Baseline-WholeTumor	COL5A3	19	10089885	Missense_Mutation	C	T	p.E933K	34	14	0.412	0.521	2	1	1	55	collagen, type V, alpha 3	ENST00000264828.3
Case#1-Baseline-WholeTumor	DNMT1	19	10305571	Missense_Mutation	G	A	p.P2L	36	15	0.417	0.527	2	1	1	9	DNA (cytosine-5-)-methyltransferase 1	ENST00000340748.4
Case#1-Baseline-WholeTumor	PDE4A	19	10570404	Missense_Mutation	C	T	p.T445I	44	14	0.318	0.403	2	1	1	44	phosphodiesterase 4A, cAMP-specific	ENST00000352831.6
Case#1-Baseline-WholeTumor	ZNF763	19	12089022	Nonsense_Mutation	C	T	p.Q95*	113	34	0.301	0.381	2	1	1	181	zinc finger protein 763	ENST00000358987.3
Case#1-Baseline-WholeTumor	ZNF490	19	12692380	Missense_Mutation	G	A	p.S170F	116	56	0.483	0.611	2	1	1	139	zinc finger protein 490	ENST00000311437.6
Case#1-Baseline-WholeTumor	DNAJB1	19	14626756	Missense_Mutation	A	G	p.I340T	70	26	0.371	0.470	2	1	1	83	DnaJ (Hsp40) homolog, subfamily B, member 1	ENST00000254322.2
Case#1-Baseline-WholeTumor	OR7C1	19	14910162	Missense_Mutation	C	T	p.A263T	79	26	0.329	0.417	2	1	1	69	olfactory receptor, family 7, subfamily C, member 1	ENST00000248073.2
Case#1-Baseline-WholeTumor	CYP4F3	19	15769586	Missense_Mutation	C	T	p.P455L	99	41	0.414	0.524	2	1	1	78	cytochrome P450, family 4, subfamily F, polypeptide 3	ENST00000221307.8
Case#1-Baseline-WholeTumor	CYP4F11	19	16038276	Missense_Mutation	C	T	p.D121N	51	18	0.353	0.447	2	1	1	93	cytochrome P450, family 4, subfamily F, polypeptide 11	ENST00000402119.4
Case#1-Baseline-WholeTumor	CPAMD8	19	17068694	Missense_Mutation	C	T	p.E796K	64	20	0.313	0.396	2	1	1	70	C3 and PZP-like, alpha-2-macroglobulin domain containing 8	ENST00000443236.1
Case#1-Baseline-WholeTumor	CPAMD8	19	17091331	Missense_Mutation	G	A	p.R568C	74	21	0.284	0.359	2	1	1	87	C3 and PZP-like, alpha-2-macroglobulin domain containing 8	ENST00000443236.1
Case#1-Baseline-WholeTumor	UNC13A	19	17763477	Nonsense_Mutation	C	A	p.E468*	54	17	0.315	0.398	2	1	1	66	unc-13 homolog A (C. elegans)	ENST00000519716.2
Case#1-Baseline-WholeTumor	SLC5A5	19	17986906	Missense_Mutation	A	G	p.N230S	41	17	0.415	0.525	2	1	1	59	solute carrier family 5 (sodium/iodide cotransporter), member 5	ENST00000222248.3

Case#1-Baseline-WholeTumor	COMP	19	18899520	Missense_Mutation	C	T	p.G215S	25	9	0.360	0.456	2	1	1	16	cartilage oligomeric matrix protein	ENST00000222271.2
Case#1-Baseline-WholeTumor	UPF1	19	18961604	Missense_Mutation	C	T	p.P246L	152	59	0.388	0.491	2	1	1	82	UPF1 regulator of nonsense transcripts homolog (yeast)	ENST00000599848.1
Case#1-Baseline-WholeTumor	ZNF93	19	20045187	Missense_Mutation	C	T	p.H475Y	32	8	0.250	0.316	2	1	1	38	zinc finger protein 93	ENST00000343769.5
Case#1-Baseline-WholeTumor	AC007204.1	19	20048638	Missense_Mutation	C	T	p.G1E	120	44	0.367	0.464	2	1	1	122		ENST00000595282.1
Case#1-Baseline-WholeTumor	ZNF90	19	20216075	Missense_Mutation	G	A	p.G59E	172	71	0.413	0.523	2	1	1	180	zinc finger protein 90	ENST00000418063.2
Case#1-Baseline-WholeTumor	ZNF714	19	21281116	Splice_Site	G	A	p.L14L	120	42	0.350	0.443	2	1	1	141	zinc finger protein 714	ENST00000596143.1
Case#1-Baseline-WholeTumor	ZNF208	19	22156497	Missense_Mutation	G	A	p.H447Y	66	24	0.364	0.460	2	1	1	89	zinc finger protein 208	ENST00000397126.4
Case#1-Baseline-WholeTumor	ZNF729	19	22496823	Missense_Mutation	C	T	p.H202Y	59	19	0.322	0.408	2	1	1	68	zinc finger protein 729	ENST00000601693.1
Case#1-Baseline-WholeTumor	ZNF728	19	23158524	Missense_Mutation	C	T	p.E539K	36	12	0.333	0.422	2	1	1	37	zinc finger protein 728	ENST00000594710.1
Case#1-Baseline-WholeTumor	POP4	19	30106202	Missense_Mutation	C	T	p.S193F	103	34	0.330	0.418	2	1	1	134	processing of precursor 4, ribonuclease P/MRP subunit (S. cerevisiae)	ENST00000585603.1
Case#1-Baseline-WholeTumor	URI1	19	30499976	Missense_Mutation	C	T	p.R251C	59	19	0.322	0.408	2	1	1	68	URI1, prefoldin-like chaperone	ENST00000542441.2
Case#1-Baseline-WholeTumor	KMT2B	19	36211511	Missense_Mutation	C	T	p.S421L	54	26	0.481	0.609	2	1	1	63	lysine (K)-specific methyltransferase 2B	ENST00000222270.7
Case#1-Baseline-WholeTumor	KMT2B	19	36211765	Missense_Mutation	C	T	p.P506S	53	20	0.377	0.478	2	1	1	32	lysine (K)-specific methyltransferase 2B	ENST00000222270.7
Case#1-Baseline-WholeTumor	WDR62	19	36592574	Missense_Mutation	G	C	p.E994Q	56	25	0.446	0.565	2	1	1	44	WD repeat domain 62	ENST00000270301.7
Case#1-Baseline-WholeTumor	ZNF382	19	37117458	Missense_Mutation	C	T	p.S220F	34	15	0.441	0.558	2	1	1	33	zinc finger protein 382	ENST00000292928.2
Case#1-Baseline-WholeTumor	ZNF527	19	37879964	Missense_Mutation	C	T	p.A338V	83	26	0.313	0.397	2	1	1	93	zinc finger protein 527	ENST00000436120.2
Case#1-Baseline-WholeTumor	WDR87	19	38376099	Missense_Mutation	C	T	p.D2699N	41	16	0.390	0.494	2	1	1	34	WD repeat domain 87	ENST00000303868.5
Case#1-Baseline-WholeTumor	WDR87	19	38379452	Missense_Mutation	C	T	p.R1581Q	146	64	0.438	0.555	2	1	1	212	WD repeat domain 87	ENST00000303868.5
Case#1-Baseline-WholeTumor	WDR87	19	38380329	Missense_Mutation	C	T	p.E1289K	29	15	0.517	0.655	2	1	1	67	WD repeat domain 87	ENST00000303868.5
Case#1-Baseline-WholeTumor	WDR87	19	38382235	Missense_Mutation	GG	AA	p.P1078L	95	41	0.432	0.546	2	1	1	33	WD repeat domain 87	ENST00000303868.5
Case#1-Baseline-WholeTumor	WDR87	19	38385303	Missense_Mutation	G	A	p.S308F	32	9	0.281	0.356	2	1	1	46	WD repeat domain 87	ENST00000303868.5
Case#1-Baseline-WholeTumor	RYR1	19	39051805	Missense_Mutation	C	T	p.S4112L	92	33	0.359	0.454	2	1	1	60	ryanodine receptor 1 (skeletal)	ENST00000359596.3
Case#1-Baseline-WholeTumor	RINL	19	39364598	Nonsense_Mutation	G	A	p.Q81*	40	13	0.325	0.411	2	1	1	46	Ras and Rab interactor-like	ENST00000591812.1
Case#1-Baseline-WholeTumor	AC011500.1	19	39930255	Missense_Mutation	C	T	p.P15L	29	14	0.483	0.611	2	1	1	22		ENST00000396843.1
Case#1-Baseline-WholeTumor	FCGBP	19	40408433	Missense_Mutation	C	T	p.G1469E	127	35	0.276	0.349	2	1	1	141	Fc fragment of IgG binding protein	ENST00000221347.6
Case#1-Baseline-WholeTumor	CYP2A7	19	41387569	Missense_Mutation	C	T	p.A90T	119	30	0.252	0.319	2	1	1	80	cytochrome P450, family 2, subfamily A, polypeptide 7	ENST00000301146.4
Case#1-Baseline-WholeTumor	PSG6	19	43414930	Missense_Mutation	G	A	p.P170S	185	72	0.389	0.493	2	1	1	271	pregnancy specific beta-1-glycoprotein 6	ENST00000292125.2
Case#1-Baseline-WholeTumor	PSG9	19	43762572	Missense_Mutation	G	A	p.T342I	219	87	0.397	0.503	2	1	1	243	pregnancy specific beta-1-glycoprotein 9	ENST00000270077.3
Case#1-Baseline-WholeTumor	ZNF112	19	44832836	Missense_Mutation	G	A	p.P498S	50	19	0.380	0.481	2	1	1	72	zinc finger protein 112	ENST00000337401.4
Case#1-Baseline-WholeTumor	ZNF112	19	44833021	Missense_Mutation	A	G	p.V436A	35	15	0.429	0.542	2	1	1	40	zinc finger protein 112	ENST00000337401.4
Case#1-Baseline-WholeTumor	KLC3	19	45849897	Nonsense_Mutation	G	A	p.W118*	29	7	0.241	0.306	2	1	1	29	kinesin light chain 3	ENST00000391946.2
Case#1-Baseline-WholeTumor	FOSB	19	45974142	Missense_Mutation	A	T	p.T128S	77	25	0.325	0.411	2	1	1	58	FBJ murine osteosarcoma viral oncogene homolog B	ENST00000353609.3
Case#1-Baseline-WholeTumor	AC074212.3	19	46257749	Missense_Mutation	G	A	p.R190Q	57	30	0.526	0.666	2	1	1	51		ENST00000457052.2
Case#1-Baseline-WholeTumor	AC074212.3	19	46257839	Missense_Mutation	G	A	p.G220E	81	26	0.321	0.406	2	1	1	90		ENST00000457052.2
Case#1-Baseline-WholeTumor	SLC8A2	19	47941229	Splice_Site	C	T	p.G629G	50	16	0.320	0.405	2	1	1	59	solute carrier family 8 (sodium/calcium exchanger), member 2	ENST00000236877.6
Case#1-Baseline-WholeTumor	SLC17A7	19	49940011	Missense_Mutation	G	A	p.A37V	66	29	0.439	0.556	2	1	1	31	solute carrier family 17 (vesicular glutamate transporter), member 7	ENST00000221485.3
Case#1-Baseline-WholeTumor	MYH14	19	50775127	Missense_Mutation	C	T	p.R1024C	54	22	0.407	0.516	2	1	1	61	myosin, heavy chain 14, non-muscle	ENST00000596571.1
Case#1-Baseline-WholeTumor	POLD1	19	50906324	Missense_Mutation	C	T	p.P329S	37	15	0.405	0.513	2	1	1	28	polymerase (DNA directed), delta 1, catalytic subunit	ENST00000440232.2
Case#1-Baseline-WholeTumor	MYBPC2	19	50939918	Missense_Mutation	CC	TA	p.R131S	70	19	0.271	0.344	2	1	1	87	myosin binding protein C, fast type	ENST00000357701.5
Case#1-Baseline-WholeTumor	SHANK1	19	51172351	Missense_Mutation	G	A	p.P956S	17	4	0.235	0.298	2	1	1	24	SH3 and multiple ankyrin repeat domains 1	ENST00000293441.1
Case#1-Baseline-WholeTumor	KLK2	19	51380002	Missense_Mutation	G	A	p.E161K	33	14	0.424	0.537	2	1	1	63	kallikrein-related peptidase 2	ENST00000325321.3
Case#1-Baseline-WholeTumor	CTD-2616J11.4	19	51892732	Missense_Mutation	C	T	p.E23K	46	16	0.348	0.440	2	1	1	49		ENST00000574814.1
Case#1-Baseline-WholeTumor	SIGLEC8	19	51958757	Missense_Mutation	A	C	p.D322E	59	11	0.186	0.236	2	1	1	51	sialic acid binding Ig-like lectin 8	ENST00000321424.3
Case#1-Baseline-WholeTumor	SIGLEC6	19	52023425	Missense_Mutation	GG	TA	p.H425N	104	45	0.433	0.548	2	1	1	103	sialic acid binding Ig-like lectin 6	ENST00000425629.3
Case#1-Baseline-WholeTumor	ZNF528	19	52919060	Missense_Mutation	C	T	p.H319Y	63	26	0.413	0.522	2	1	1	86	zinc finger protein 528	ENST00000360465.3
Case#1-Baseline-WholeTumor	ZNF534	19	52941990	Missense_Mutation	C	T	p.T439I	65	25	0.385	0.487	2	1	1	111	zinc finger protein 534	ENST00000332323.6
Case#1-Baseline-WholeTumor	NLRP12	19	54327170	Missense_Mutation	C	T	p.E87K	87	32	0.368	0.466	2	1	1	107	NLR family, pyrin domain containing 12	ENST00000324134.6
Case#1-Baseline-WholeTumor	TARM1	19	54578294	Missense_Mutation	C	T	p.R48Q	74	27	0.365	0.462	2	1	1	41	T cell-interacting, activating receptor on myeloid cells 1	ENST00000432826.1
Case#1-Baseline-WholeTumor	LILRB2	19	54781428	Missense_Mutation	G	A	p.P446S	36	8	0.222	0.281	2	1	1	35	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2	ENST00000391749.4
Case#1-Baseline-WholeTumor	LILRB2	19	54783274	Missense_Mutation	C	T	p.R195K	98	34	0.347	0.439	2	1	1	162	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2	ENST00000391749.4
Case#1-Baseline-WholeTumor	NLRP7	19	55450454	Missense_Mutation	G	A	p.S578F	59	25	0.424	0.536	2	1	1	100	NLR family, pyrin domain containing 7	ENST00000590030.1
Case#1-Baseline-WholeTumor	PTPRH	19	55716732	Missense_Mutation	C	T	p.G194E	178	81	0.455	0.576	2	1	1	194	protein tyrosine phosphatase, receptor type, H	ENST00000376350.3
Case#1-Baseline-WholeTumor	EPN1	19	56200664	Splice_Site	C	T	p.P202L	106	32	0.302	0.382	2	1	1	75	epsin 1	ENST00000270460.6
Case#1-Baseline-WholeTumor	NLRP8	19	56490812	Missense_Mutation	C	T	p.L977F	72	31	0.431	0.545	2	1	1	71	NLR family, pyrin domain containing 8	ENST00000291971.3
Case#1-Baseline-WholeTumor	NLRP8	19	56499244	Missense_Mutation	G	A	p.G1038R	90	39	0.433	0.549	2	1	1	93	NLR family, pyrin domain containing 8	ENST00000291971.3
Case#1-Baseline-WholeTumor	USP29	19	57640501	Missense_Mutation	C	T	p.S153L	38	9	0.237	0.300	2	1	1	65	ubiquitin specific peptidase 29	ENST00000254181.4
Case#1-Baseline-WholeTumor	USP29	19	57641208	Missense_Mutation	G	A	p.E389K	32	13	0.406	0.514	2	1	1	42	ubiquitin specific peptidase 29	ENST00000254181.4
Case#1-Baseline-WholeTumor	USP29	19	57642499	Missense_Mutation	C	T	p.P819L	45	16	0.356	0.450	2	1	1	74	ubiquitin specific peptidase 29	ENST00000254181.4
Case#1-Baseline-WholeTumor	ZNF418	19	58438869	Missense_Mutation	C	T	p.R227K	116	36	0.310	0.393	2	1	1	172	zinc finger protein 418	ENST00000396147.1
Case#1-Baseline-WholeTumor	ALLC	2	3743414	Frame_Shift_Del	TG	-	p.W207fs	72	29	0.403	0.510	2	1	1	127	allantoicase	ENST00000252505.3
Case#1-Baseline-WholeTumor	KIDINS220	2	8870915	Missense_Mutation	C	T	p.E1751K	100	39	0.390	0.494	2	1	1	121	kinase D-interacting substrate, 220kDa	ENST00000256707.3
Case#1-Baseline-WholeTumor	KCNS3	2	18112971	Nonsense_Mutation	G	A	p.W232*	45	18	0.400	0.506	2	1	1	64	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	ENST00000403915.1
Case#1-Baseline-WholeTumor	MFSD2B	2	24236215	Missense_Mutation	C	T	p.P53S	80	28	0.350	0.443	2	1	1	86	major facilitator superfamily domain containing 2B	ENST00000406420.3
Case#1-Baseline-WholeTumor	C2orf71	2	29294142	Missense_Mutation	G	A	p.P996S	61	27	0.443	0.560	2	1	1	58	chromosome 2 open reading frame 71	ENST00000331664.5
Case#1-Baseline-WholeTumor	VIT	2	37000987	Missense_Mutation	C	T	p.P245S	79	22	0.278	0.353	2	1	1	75	vitrin	ENST00000389975.3
Case#1-Baseline-WholeTumor	SLC8A1	2	40397451	Missense_Mutation	G	A	p.P670S	52	12	0.231	0.292	2	1	1	70	solute carrier family 8 (sodium/calcium exchanger), member 1	ENST00000403092.1
Case#1-Baseline-WholeTumor	PKDCC	2	42281304	Missense_Mutation	T	G	p.D297E	128	51	0.398	0.504	2	1	1	80	protein kinase domain containing, cytoplasmic	ENST00000294964.5
Case#1-Baseline-WholeTumor	SOCS5	2	46985901	Nonsense_Mutation	A	T	p.R78*	41	17	0.415	0.525	2	1	1	61	suppressor of cytokine signaling 5	ENST00000306503.5
Case#1-Baseline-WholeTumor	FSHR	2	49210079	Missense_Mutation	A	C	p.F214V	65	30	0.462	0.584	2	1	1	71	follicle stimulating hormone receptor	ENST00000406846.2
Case#1-Baseline-WholeTumor	TIA1	2	70457971	Missense_Mutation	G	A	p.P47S	96	38	0.396	0.501	2	1	1	100	TIA1 cytotoxic granule-associated RNA binding protein	ENST00000433529.2
Case#1-Baseline-WholeTumor	C2orf78	2	74043397	Missense_Mutation	G	A	p.G683S	19	8	0.421	0.533	2	1	1	32	chromosome 2 open reading frame 78	ENST00000409561.1
Case#1-Baseline-WholeTumor	MOGS	2	74689363	Missense_Mutation	G	A	p.P518L	112	36	0.321	0.407	2	1	1	130	mannosyl-oligosaccharide glucosidase	ENST00000233616.4
Case#1-Baseline-WholeTumor	M1AP	2	74842208	Missense_Mutation	CC	TT	p.G103E	48	23	0.479	0.607	2	1	1	56	meiosis 1 associated protein	ENST00000290536.5
Case#1-Baseline-WholeTumor	LRRTM4	2	77745733	Missense_Mutation	G	A	p.S421L	78	37	0.474	0.600	2	1	1	96	leucine rich repeat transmembrane neuronal 4	ENST00000409093.1
Case#1-Baseline-WholeTumor	CTNNA2	2	80874951	Missense_Mutation	C	T	p.S939L	32	15	0.469	0.593	2	1	1	50	catenin (cadherin-associated protein), alpha 2	ENST00000402739.4
Case#1-Baseline-WholeTumor	DNAH6	2	84896614	Missense_Mutation	G	A	p.G2096R	70	31	0.443	0.561	2	1	1	107	dynein, axonemal, heavy chain 6	ENST00000237449.6
Case#1-Baseline-WholeTumor	KCMF1	2	85255039	Missense_Mutation	G	A	p.G15E	72	29	0.403	0.510	2	1	1	89	potassium channel modulatory factor 1	ENST00000409785.4
Case#1-Baseline-WholeTumor	REEP1	2	86459757	Missense_Mutation	T	C	p.S196G	153	47	0.307	0.389	2	1	1	102	receptor accessory protein 1	ENST00000165698.5
Case#1-Baseline-WholeTumor	KRCC1	2	88327571	Missense_Mutation	G	A	p.S171L	45	18	0.400	0.506	2	1	1	43	lysine-rich coiled-coil 1	ENST00000347055.3
Case#1-Baseline-WholeTumor	PROM2	2	95951436	Missense_Mutation	T	A	p.L642Q	68	28	0.412	0.521	2	1	1	70	prominin 2	ENST00000317620.9

Case#1-Baseline-WholeTumor	CNGA3	2	99013039	Missense_Mutation	C	T	p.A469V	46	24	0.522	0.660	2	1	1	59	cyclic nucleotide gated channel alpha 3	ENST00000272602.2
Case#1-Baseline-WholeTumor	EIF5B	2	99980828	Missense_Mutation	C	T	p.S411F	31	10	0.323	0.408	2	1	1	36	eukaryotic translation initiation factor 5B	ENST00000289371.6
Case#1-Baseline-WholeTumor	AFF3	2	100203616	Splice_Site	C	T	p.S864N	142	52	0.366	0.464	2	1	1	168	AF4/FMR2 family, member 3	ENST00000409236.2
Case#1-Baseline-WholeTumor	ZC3H6	2	113080319	Missense_Mutation	C	T	p.P394S	63	28	0.444	0.563	2	1	1	77	zinc finger CCCH-type containing 6	ENST00000409871.1
Case#1-Baseline-WholeTumor	POLR1B	2	113308515	Missense_Mutation	C	T	p.T233I	153	47	0.307	0.389	2	1	1	132	polymerase (RNA) I polypeptide B, 128kDa	ENST00000263331.5
Case#1-Baseline-WholeTumor	IL1A	2	113539352	Nonsense_Mutation	G	A	p.Q50*	74	32	0.432	0.547	2	1	1	87	interleukin 1, alpha	ENST00000263339.3
Case#1-Baseline-WholeTumor	IL36B	2	113783785	Missense_Mutation	C	T	p.G96R	98	37	0.378	0.478	2	1	1	115	interleukin 36, beta	ENST00000259213.4
Case#1-Baseline-WholeTumor	IWS1	2	128263292	Nonsense_Mutation	C	A	p.G63*	31	4	0.129	0.163	2	1	1	32	IWS1 homolog (S. cerevisiae)	ENST00000295321.4
Case#1-Baseline-WholeTumor	POTEF	2	130878027	Missense_Mutation	C	T	p.R21K	294	84	0.286	0.362	2	1	1	342	POTE ankyrin domain family, member F	ENST00000409914.2
Case#1-Baseline-WholeTumor	THSD7B	2	137814764	Missense_Mutation	C	T	p.S305L	43	19	0.442	0.559	2	1	1	88	thrombospondin, type I, domain containing 7B	ENST00000409968.1
Case#1-Baseline-WholeTumor	THSD7B	2	137990472	Missense_Mutation	G	A	p.G640E	72	21	0.292	0.369	2	1	1	139	thrombospondin, type I, domain containing 7B	ENST00000409968.1
Case#1-Baseline-WholeTumor	LRP1B	2	141202236	Missense_Mutation	C	G	p.C3357S	39	22	0.564	0.714	2	1	1	54	low density lipoprotein receptor-related protein 1B	ENST00000389484.3
Case#1-Baseline-WholeTumor	LRP1B	2	141473542	Splice_Site	C	A	p.G2008V	92	27	0.293	0.371	2	1	1	100	low density lipoprotein receptor-related protein 1B	ENST00000389484.3
Case#1-Baseline-WholeTumor	KYNU	2	143798132	Missense_Mutation	CC	TT	p.P393L	64	26	0.406	0.514	2	1	1	95	kynureninase	ENST00000264170.4
Case#1-Baseline-WholeTumor	NEB	2	152418675	Nonsense_Mutation	C	T	p.W4614*	86	34	0.395	0.500	2	1	1	126	nebulin	ENST00000172853.10
Case#1-Baseline-WholeTumor	NEB	2	152510597	Missense_Mutation	C	T	p.G2275E	52	16	0.308	0.389	2	1	1	70	nebulin	ENST00000172853.10
Case#1-Baseline-WholeTumor	GALNT5	2	158157341	Nonsense_Mutation	A	T	p.K757*	128	58	0.453	0.574	2	1	1	150	polypeptide N-acetylgalactosaminyltransferase 5	ENST00000259056.4
Case#1-Baseline-WholeTumor	PKP4	2	159533266	Missense_Mutation	C	T	p.S1048F	87	39	0.448	0.567	2	1	1	138	plakophilin 4	ENST00000389759.3
Case#1-Baseline-WholeTumor	ITGB6	2	160994079	Missense_Mutation	G	A	p.P509L	55	19	0.345	0.437	2	1	1	68	integrin, beta 6	ENST00000283249.2
Case#1-Baseline-WholeTumor	DPP4	2	162862292	Missense_Mutation	C	T	p.G672D	68	18	0.265	0.335	2	1	1	96	dipeptidyl-peptidase 4	ENST00000360534.3
Case#1-Baseline-WholeTumor	XIRP2	2	168114647	Missense_Mutation	G	A	p.E564K	22	7	0.318	0.403	2	1	1	33	xin actin-binding repeat containing 2	ENST00000409728.1
Case#1-Baseline-WholeTumor	LRP2	2	170129549	Missense_Mutation	CC	TT	p.G668E	48	16	0.333	0.422	2	1	1	84	low density lipoprotein receptor-related protein 2	ENST00000263816.3
Case#1-Baseline-WholeTumor	MYO3B	2	171055731	Missense_Mutation	G	A	p.G6R	36	15	0.417	0.527	2	1	1	66	myosin IIIB	ENST00000408978.4
Case#1-Baseline-WholeTumor	MYO3B	2	171070986	Missense_Mutation	C	T	p.A140V	48	20	0.417	0.527	2	1	1	76	myosin IIIB	ENST00000408978.4
Case#1-Baseline-WholeTumor	MYO3B	2	171323038	Missense_Mutation	C	T	p.S944F	46	17	0.370	0.468	2	1	1	58	myosin IIIB	ENST00000408978.4
Case#1-Baseline-WholeTumor	HOXD3	2	177034063	Frame_Shift_Del	C	-	p.A74fs	46	10	0.217	0.275	2	1	1	60	homeobox D3	ENST00000468418.3
Case#1-Baseline-WholeTumor	TTN	2	179418008	Nonsense_Mutation	C	T	p.W28232*	97	25	0.258	0.326	2	1	1	140	titin	ENST00000591111.1
Case#1-Baseline-WholeTumor	TTN	2	179418782	Missense_Mutation	C	T	p.E28045K	50	16	0.320	0.405	2	1	1	58	titin	ENST00000591111.1
Case#1-Baseline-WholeTumor	TTN	2	179425447	Missense_Mutation	G	A	p.S26830F	80	31	0.388	0.491	2	1	1	99	titin	ENST00000591111.1
Case#1-Baseline-WholeTumor	TTN	2	179439437	Missense_Mutation	C	T	p.G22167R	58	19	0.328	0.415	2	1	1	65	titin	ENST00000591111.1
Case#1-Baseline-WholeTumor	TTN	2	179444336	Missense_Mutation	C	T	p.G20889R	37	14	0.378	0.479	2	1	1	35	titin	ENST00000591111.1
Case#1-Baseline-WholeTumor	TTN	2	179452426	Missense_Mutation	G	A	p.P19563S	67	26	0.388	0.491	2	1	1	74	titin	ENST00000591111.1
Case#1-Baseline-WholeTumor	TTN	2	179457945	Missense_Mutation	C	T	p.D18023N	54	21	0.389	0.492	2	1	1	76	titin	ENST00000591111.1
Case#1-Baseline-WholeTumor	TTN	2	179497466	Missense_Mutation	C	T	p.D12782N	16	4	0.250	0.316	2	1	1	39	titin	ENST00000591111.1
Case#1-Baseline-WholeTumor	TTN	2	179536794	Missense_Mutation	C	T	p.E11337K	62	21	0.339	0.429	2	1	1	50	titin	ENST00000591111.1
Case#1-Baseline-WholeTumor	TTN	2	179595352	Missense_Mutation	G	A	p.H5653Y	38	13	0.342	0.433	2	1	1	45	titin	ENST00000591111.1
Case#1-Baseline-WholeTumor	TTN	2	179606079	Missense_Mutation	C	T	p.V3644M	57	24	0.421	0.533	2	1	1	60	titin	ENST00000591111.1
Case#1-Baseline-WholeTumor	CWC22	2	180851449	Missense_Mutation	C	G	p.R60P	50	23	0.460	0.582	2	1	1	59	CWC22 spliceosome-associated protein	ENST00000410053.3
Case#1-Baseline-WholeTumor	COL3A1	2	189859537	Missense_Mutation	C	T	p.P479S	61	20	0.328	0.415	2	1	1	67	collagen, type III, alpha 1	ENST00000304636.3
Case#1-Baseline-WholeTumor	COL3A1	2	189862099	Missense_Mutation	G	A	p.G618E	66	28	0.424	0.537	2	1	1	105	collagen, type III, alpha 1	ENST00000304636.3
Case#1-Baseline-WholeTumor	COL5A2	2	189929752	Missense_Mutation	G	A	p.S532F	137	54	0.394	0.499	2	1	1	124	collagen, type V, alpha 2	ENST00000374866.3
Case#1-Baseline-WholeTumor	STAT4	2	191923476	Missense_Mutation	C	T	p.E352K	73	28	0.384	0.486	2	1	1	72	signal transducer and activator of transcription 4	ENST00000392320.2
Case#1-Baseline-WholeTumor	DNAH7	2	196681377	Missense_Mutation	C	T	p.E3246K	39	16	0.410	0.519	2	1	1	46	dynein, axonemal, heavy chain 7	ENST00000312428.6
Case#1-Baseline-WholeTumor	DNAH7	2	196681451	Missense_Mutation	G	A	p.A3221V	67	28	0.418	0.529	2	1	1	68	dynein, axonemal, heavy chain 7	ENST00000312428.6
Case#1-Baseline-WholeTumor	DNAH7	2	196681481	Missense_Mutation	G	A	p.S3211F	84	30	0.357	0.452	2	1	1	66	dynein, axonemal, heavy chain 7	ENST00000312428.6
Case#1-Baseline-WholeTumor	DNAH7	2	196788411	Missense_Mutation	G	A	p.H1245Y	37	15	0.405	0.513	2	1	1	38	dynein, axonemal, heavy chain 7	ENST00000312428.6
Case#1-Baseline-WholeTumor	DNAH7	2	196799425	Missense_Mutation	C	T	p.E1121K	94	32	0.340	0.431	2	1	1	103	dynein, axonemal, heavy chain 7	ENST00000312428.6
Case#1-Baseline-WholeTumor	HECW2	2	197184134	Missense_Mutation	C	T	p.A494T	20	8	0.400	0.506	2	1	1	25	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	ENST00000260983.3
Case#1-Baseline-WholeTumor	PLCL1	2	198948758	Missense_Mutation	G	A	p.E173K	54	17	0.315	0.398	2	1	1	68	phospholipase C-like 1	ENST00000428675.1
Case#1-Baseline-WholeTumor	AOX1	2	201470309	Missense_Mutation	G	A	p.D289N	91	26	0.286	0.362	2	1	1	119	aldehyde oxidase 1	ENST00000374700.2
Case#1-Baseline-WholeTumor	ADAM23	2	207474705	Missense_Mutation	G	A	p.G811S	31	14	0.452	0.572	2	1	1	46	ADAM metallopeptidase domain 23	ENST00000264377.3
Case#1-Baseline-WholeTumor	DYTN	2	207527804	Missense_Mutation	C	T	p.G486R	53	18	0.340	0.430	2	1	1	52	dystrotelin	ENST00000452335.2
Case#1-Baseline-WholeTumor	CRYGD	2	208989066	Missense_Mutation	C	T	p.E8K	282	104	0.369	0.467	2	1	1	209	crystallin, gamma D	ENST00000264376.4
Case#1-Baseline-WholeTumor	PTH2R	2	209324660	Missense_Mutation	CA	AG	p.Q319R	37	17	0.459	0.582	2	1	1	71	parathyroid hormone 2 receptor	ENST00000272847.2
Case#1-Baseline-WholeTumor	ERBB4	2	212570116	Splice_Site	C	T	p.G375G	139	52	0.374	0.474	2	1	1	159	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 4	ENST00000342788.4
Case#1-Baseline-WholeTumor	ACSL3	2	223795362	Missense_Mutation	C	T	p.P522S	121	41	0.339	0.429	2	1	1	111	acyl-CoA synthetase long-chain family member 3	ENST00000357430.3
Case#1-Baseline-WholeTumor	DOCK10	2	225761034	Missense_Mutation	C	T	p.G132R	41	15	0.366	0.463	2	1	1	63	dedicator of cytokinesis 10	ENST00000258390.7
Case#1-Baseline-WholeTumor	NYAP2	2	226446872	Missense_Mutation	G	A	p.E247K	64	23	0.359	0.455	2	1	1	67	neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adaptor 2	ENST00000272907.6
Case#1-Baseline-WholeTumor	COL4A4	2	227896939	Missense_Mutation	C	T	p.E1211K	36	16	0.444	0.563	2	1	1	43	collagen, type IV, alpha 4	ENST00000396625.3
Case#1-Baseline-WholeTumor	COL4A3	2	228104892	Missense_Mutation	C	T	p.P60S	42	21	0.500	0.633	2	1	1	58	collagen, type IV, alpha 3 (Goodpasture antigen)	ENST00000396578.3
Case#1-Baseline-WholeTumor	COL4A3	2	228154778	Missense_Mutation	G	A	p.G1015E	56	20	0.357	0.452	2	1	1	72	collagen, type IV, alpha 3 (Goodpasture antigen)	ENST00000396578.3
Case#1-Baseline-WholeTumor	PID1	2	229890516	Missense_Mutation	C	T	p.M195I	72	30	0.417	0.527	2	1	1	88	phosphotyrosine interaction domain containing 1	ENST00000354069.6
Case#1-Baseline-WholeTumor	SP140L	2	231223823	Missense_Mutation	C	T	p.H139Y	83	36	0.434	0.549	2	1	1	60	SP140 nuclear body protein-like	ENST00000415673.2
Case#1-Baseline-WholeTumor	SP100	2	231375877	Missense_Mutation	C	T	p.P697L	112	41	0.366	0.463	2	1	1	130	SP100 nuclear antigen	ENST00000264052.5
Case#1-Baseline-WholeTumor	GPR55	2	231775346	Missense_Mutation	G	A	p.T111I	56	16	0.286	0.362	2	1	1	76	G protein-coupled receptor 55	ENST00000392040.1
Case#1-Baseline-WholeTumor	INPP5D	2	234077959	Missense_Mutation	G	A	p.G510R	67	28	0.418	0.529	2	1	1	66	inositol polyphosphate-5-phosphatase, 145kDa	ENST00000359570.5
Case#1-Baseline-WholeTumor	MROH2A	2	234720599	Missense_Mutation	A	C	p.H882P	56	20	0.357	0.452	2	1	1	70	maestro heat-like repeat family member 2A	ENST00000389758.3
Case#1-Baseline-WholeTumor	ACKR3	2	237489127	Missense_Mutation	G	A	p.D7N	80	37	0.463	0.585	2	1	1	83	atypical chemokine receptor 3	ENST00000272928.3
Case#1-Baseline-WholeTumor	COL6A3	2	238283600	Missense_Mutation	G	A	p.P1045L	64	25	0.391	0.494	2	1	1	52	collagen, type VI, alpha 3	ENST00000295550.4
Case#1-Baseline-WholeTumor	ESPNL	2	239033910	Splice_Site	G	A		154	66	0.429	0.542	2	1	1	103	espin-like	ENST00000343063.3
Case#1-Baseline-WholeTumor	PER2	2	239155102	Missense_Mutation	G	A	p.P1228S	82	26	0.317	0.401	2	1	1	74	period circadian clock 2	ENST00000254657.3
Case#1-Baseline-WholeTumor	AQP12A	2	241631640	Missense_Mutation	G	A	p.M91I	146	67	0.459	0.581	2	1	1	106	aquaporin 12A	ENST00000337801.4
Case#1-Baseline-WholeTumor	SNED1	2	242003009	Missense_Mutation	G	A	p.D793N	83	35	0.422	0.534	2	1	1	70	sushi, nidogen and EGF-like domains 1	ENST00000310397.8
Case#1-Baseline-WholeTumor	PASK	2	242046876	Missense_Mutation	G	A	p.P1236S	76	29	0.382	0.483	2	1	1	94	PAS domain containing serine/threonine kinase	ENST00000405260.1
Case#1-Baseline-WholeTumor	NSFL1C	20	1424492	Missense_Mutation	G	A	p.L339F	78	32	0.410	0.519	2	1	1	64	NSFL1 (p97) cofactor (p47)	ENST00000216879.4
Case#1-Baseline-WholeTumor	CHGB	20	5903289	Missense_Mutation	G	A	p.E167K	28	9	0.321	0.407	2	1	1	27	chromogranin B (secretogranin 1)	ENST00000378961.4
Case#1-Baseline-WholeTumor	PAK7	20	9538323	Missense_Mutation	G	A	p.L559F	71	22	0.310	0.392	2	1	1	107	p21 protein (Cdc42/Rac)-activated kinase 7	ENST00000378429.3
Case#1-Baseline-WholeTumor	SNAP25	20	10256146	Missense_Mutation	G	A	p.E3K	80	24	0.300	0.380	2	1	1	85	synaptosomal-associated protein, 25kDa	ENST00000254976.2
Case#1-Baseline-WholeTumor	PET117	20	18122915	Missense_Mutation	C	T	p.L54F	105	44	0.419	0.530	2	1	1	106	PET117 homolog (S. cerevisiae)	ENST00000432901.3
Case#1-Baseline-WholeTumor	RIN2	20	19937290	Missense_Mutation	G	A	p.E113K	56	21	0.375	0.475	2	1	1	80	Ras and Rab interactor 2	ENST00000255006.6
Case#1-Baseline-WholeTumor	CRNKL1	20	20033087	Missense_Mutation	G	A	p.S128F	117	48	0.410	0.519	2	1	1	107	crooked neck pre-mRNA splicing factor 1	ENST00000377340.2
Case#1-Baseline-WholeTumor	C20orf26	20	20269392	Missense_Mutation	C	T	p.S979F	73	27	0.370	0.468	2	1	1	71		ENST00000245957.5
Case#1-Baseline-WholeTumor	GZF1	20	23346051	Missense_Mutation	C	T	p.T344I	138	44	0.319	0.404	2	1	1	100	GDNF-inducible zinc finger protein 1	ENST00000338121.5
Case#1-Baseline-WholeTumor	SYNDIG1	20	24523736	Start_Codon_SNP	G	A	p.M1I	82	43	0.524	0.664	2	1	1	89	synapse differentiation inducing 1	ENST00000376862.3

Case#1-Baseline-WholeTumor	CCM2L	20	30610584	Nonsense_Mutation	G	A	p.W352*	59	17	0.288	0.365	2	1	1	57	cerebral cavernous malformation 2-like	ENST00000300415.8
Case#1-Baseline-WholeTumor	BPIFB3	20	31656778	Splice_Site	C	T	p.S383F	34	11	0.324	0.410	2	1	1	63	BPI fold containing family B, member 3	ENST00000375494.3
Case#1-Baseline-WholeTumor	BPIFB4	20	31678582	Missense_Mutation	G	A	p.E374K	49	19	0.388	0.491	2	1	1	45	BPI fold containing family B, member 4	ENST00000375483.3
Case#1-Baseline-WholeTumor	SOGA1	20	35431407	Missense_Mutation	G	A	p.S826F	43	13	0.302	0.383	2	1	1	22	suppressor of glucose, autophagy associated 1	ENST00000357779.3
Case#1-Baseline-WholeTumor	KIAA1755	20	36869848	Missense_Mutation	G	A	p.P229S	53	17	0.321	0.406	2	1	1	74	KIAA1755	ENST00000279024.4
Case#1-Baseline-WholeTumor	PTPRT	20	40730906	Missense_Mutation	G	A	p.P1191L	48	20	0.417	0.527	2	1	1	68	protein tyrosine phosphatase, receptor type, T	ENST00000373187.1
Case#1-Baseline-WholeTumor	JPH2	20	42789002	Missense_Mutation	C	T	p.G142E	208	83	0.399	0.505	2	1	1	145	junctophilin 2	ENST00000372980.3
Case#1-Baseline-WholeTumor	C20orf62	20	43090908	Missense_Mutation	C	T	p.D44N	30	12	0.400	0.506	2	1	1	31	chromosome 20 open reading frame 62	ENST00000372910.3
Case#1-Baseline-WholeTumor	SLPI	20	43883138	Missense_Mutation	C	T	p.G16E	54	19	0.352	0.445	2	1	1	66	secretory leukocyte peptidase inhibitor	ENST00000338380.2
Case#1-Baseline-WholeTumor	SPINT3	20	44144191	Missense_Mutation	G	C	p.R20G	28	9	0.321	0.407	2	1	1	37	serine peptidase inhibitor, Kunitz type, 3	ENST00000217428.6
Case#1-Baseline-WholeTumor	PCIF1	20	44574481	Missense_Mutation	G	A	p.G434R	89	31	0.348	0.441	2	1	1	84	PDX1 C-terminal inhibiting factor 1	ENST00000372409.3
Case#1-Baseline-WholeTumor	SLC12A5	20	44680479	Missense_Mutation	G	A	p.E806K	31	9	0.290	0.367	2	1	1	35	solute carrier family 12 (potassium/chloride transporter), member 5	ENST00000454036.2
Case#1-Baseline-WholeTumor	OCSTAMP	20	45174900	Missense_Mutation	G	A	p.S38F	66	23	0.348	0.441	2	1	1	33	osteoclast stimulatory transmembrane protein	ENST00000279028.2
Case#1-Baseline-WholeTumor	KCNB1	20	47990997	Missense_Mutation	G	A	p.S367F	33	14	0.424	0.537	2	1	1	34	potassium voltage-gated channel, Shab-related subfamily, member 1	ENST00000371741.4
Case#1-Baseline-WholeTumor	SLC9A8	20	48497530	Missense_Mutation	C	T	p.H410Y	74	26	0.351	0.445	2	1	1	91	solute carrier family 9, subfamily A (NHE8, cation proton antiporter 8), member 8	ENST00000361573.2
Case#1-Baseline-WholeTumor	KCNG1	20	49626157	Missense_Mutation	G	A	p.T240I	76	34	0.447	0.566	2	1	1	51	potassium voltage-gated channel, subfamily G, member 1	ENST00000371571.4
Case#1-Baseline-WholeTumor	TSHZ2	20	51870790	Missense_Mutation	G	A	p.D265N	85	37	0.435	0.551	2	1	1	102	teashirt zinc finger homeobox 2	ENST00000371497.5
Case#1-Baseline-WholeTumor	SYCP2	20	58439413	Missense_Mutation	C	T	p.E1516K	60	21	0.350	0.443	2	1	1	46	synaptonemal complex protein 2	ENST00000357552.3
Case#1-Baseline-WholeTumor	SLC17A9	20	61588121	Missense_Mutation	G	A	p.E22K	76	27	0.355	0.450	2	1	1	63	solute carrier family 17 (vesicular nucleotide transporter), member 9	ENST00000370351.4
Case#1-Baseline-WholeTumor	COL20A1	20	61945242	Splice_Site	C	T	p.S786F	98	31	0.316	0.400	2	1	1	111	collagen, type XX, alpha 1	ENST00000358894.6
Case#1-Baseline-WholeTumor	ZBTB46	20	62421662	Missense_Mutation	G	A	p.S150F	50	19	0.380	0.481	2	1	1	43	zinc finger and BTB domain containing 46	ENST00000245663.4
Case#1-Baseline-WholeTumor	APP	21	27326927	Missense_Mutation	G	A	p.A555V	53	17	0.321	0.406	2	1	1	47	amyloid beta (A4) precursor protein	ENST00000346798.3
Case#1-Baseline-WholeTumor	CYYR1	21	27840924	Missense_Mutation	C	T	p.E121K	61	22	0.361	0.457	2	1	1	88	cysteine/tyrosine-rich 1	ENST00000299340.4
Case#1-Baseline-WholeTumor	CYYR1	21	27840930	Missense_Mutation	C	T	p.D119N	67	27	0.403	0.510	2	1	1	89	cysteine/tyrosine-rich 1	ENST00000299340.4
Case#1-Baseline-WholeTumor	GRIK1	21	30949360	Missense_Mutation	G	A	p.S685L	80	32	0.400	0.506	2	1	1	82	glutamate receptor, ionotropic, kainate 1	ENST00000399907.1
Case#1-Baseline-WholeTumor	KRTAP24-1	21	31655093	Missense_Mutation	C	T	p.G53E	51	15	0.294	0.372	2	1	1	82	keratin associated protein 24-1	ENST00000340345.4
Case#1-Baseline-WholeTumor	C21orf54	21	34542053	Missense_Mutation	G	A	p.R39C	62	24	0.387	0.490	2	1	1	67	chromosome 21 open reading frame 54	ENST00000451980.2
Case#1-Baseline-WholeTumor	KCNJ6	21	39087413	Missense_Mutation	G	A	p.S16F	27	13	0.481	0.609	2	1	1	44	potassium inwardly-rectifying channel, subfamily J, member 6	ENST00000609713.1
Case#1-Baseline-WholeTumor	ERG	21	39775479	Missense_Mutation	G	A	p.P188S	155	60	0.387	0.490	2	1	1	160	v-ets avian erythroblastosis virus E26 oncogene homolog	ENST00000417133.2
Case#1-Baseline-WholeTumor	B3GALT5	21	41033280	Missense_Mutation	C	T	p.T265I	53	18	0.340	0.430	2	1	1	76	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	ENST00000380620.4
Case#1-Baseline-WholeTumor	DSCAM	21	41496159	Missense_Mutation	C	T	p.R1220Q	109	44	0.404	0.511	2	1	1	144	Down syndrome cell adhesion molecule	ENST00000400454.1
Case#1-Baseline-WholeTumor	UBASH3A	21	43852263	Missense_Mutation	G	A	p.D408N	77	24	0.312	0.395	2	1	1	100	ubiquitin associated and SH3 domain containing A	ENST00000319294.6
Case#1-Baseline-WholeTumor	ITGB2	21	46320380	Missense_Mutation	C	T	p.G251D	271	91	0.336	0.425	2	1	1	218	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	ENST00000397850.2
Case#1-Baseline-WholeTumor	ADARB1	21	46624496	Missense_Mutation	C	T	p.S571F	81	24	0.296	0.375	2	1	1	118	adenosine deaminase, RNA-specific, B1	ENST00000360697.3
Case#1-Baseline-WholeTumor	PRMT2	21	48064312	Missense_Mutation	C	T	p.P80L	149	55	0.369	0.467	2	1	1	129	protein arginine methyltransferase 2	ENST00000397637.1
Case#1-Baseline-WholeTumor	PRMT2	21	48078714	Missense_Mutation	G	A	p.G238R	112	52	0.464	0.588	2	1	1	128	protein arginine methyltransferase 2	ENST00000397637.1
Case#1-Baseline-WholeTumor	PRMT2	21	48078777	Missense_Mutation	C	T	p.R259C	74	28	0.378	0.479	2	1	1	120	protein arginine methyltransferase 2	ENST00000397637.1
Case#1-Baseline-WholeTumor	HIRA	22	19348765	Missense_Mutation	GG	AA	p.L694F	58	14	0.241	0.306	2	1	1	85	histone cell cycle regulator	ENST00000263208.5
Case#1-Baseline-WholeTumor	PI4KA	22	21065055	Missense_Mutation	CC	TT	p.G1947E	348	78	0.224	0.284	2	1	1	395	phosphatidylinositol 4-kinase, catalytic, alpha	ENST00000572273.1
Case#1-Baseline-WholeTumor	SUSD2	22	24579160	Missense_Mutation	C	T	p.S71F	441	139	0.315	0.399	2	1	1	476	sushi domain containing 2	ENST00000358321.3
Case#1-Baseline-WholeTumor	HORMAD2	22	30489987	Missense_Mutation	T	C	p.S16P	44	14	0.318	0.403	2	1	1	57	HORMA domain containing 2	ENST00000336726.6
Case#1-Baseline-WholeTumor	GATSL3	22	30682360	Missense_Mutation	G	A	p.P212L	51	20	0.392	0.496	2	1	1	53	GATS protein-like 3	ENST00000407689.3
Case#1-Baseline-WholeTumor	GAL3ST1	22	30951568	Missense_Mutation	C	T	p.R215Q	148	48	0.324	0.411	2	1	1	114	galactose-3-O-sulfotransferase 1	ENST00000402321.1
Case#1-Baseline-WholeTumor	PLA2G3	22	31534317	Missense_Mutation	G	A	p.P243S	55	19	0.345	0.437	2	1	1	66	phospholipase A2, group III	ENST00000215885.3
Case#1-Baseline-WholeTumor	CSF2RB	22	37326785	Missense_Mutation	C	T	p.P309S	37	11	0.297	0.376	2	1	1	34	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	ENST00000403662.3
Case#1-Baseline-WholeTumor	TST	22	37407121	Missense_Mutation	G	A	p.R281C	47	14	0.298	0.377	2	1	1	50	thiosulfate sulfurtransferase (rhodanese)	ENST00000403892.3
Case#1-Baseline-WholeTumor	POLR2F	22	38355466	Nonsense_Mutation	CC	AT	p.R69*	52	14	0.269	0.341	2	1	1	44	polymerase (RNA) II (DNA directed) polypeptide F	ENST00000442738.2
Case#1-Baseline-WholeTumor	CACNA1I	22	40045670	Missense_Mutation	G	A	p.G578S	43	22	0.512	0.648	2	1	1	47	calcium channel, voltage-dependent, T type, alpha 1I subunit	ENST00000402142.3
Case#1-Baseline-WholeTumor	PHF21B	22	45309910	Missense_Mutation	G	A	p.P208L	34	21	0.618	0.782	2	1	1	20	PHD finger protein 21B	ENST00000313237.5
Case#1-Baseline-WholeTumor	MOV10L1	22	50596514	Missense_Mutation	C	T	p.P1032L	103	57	0.553	0.701	2	1	1	90	Mov10 RISC complex RNA helicase like 1	ENST00000262794.5
Case#1-Baseline-WholeTumor	NCAPH2	22	50960422	Missense_Mutation	CC	TT	p.H373Y	37	13	0.351	0.445	2	1	1	42	non-SMC condensin II complex, subunit H2	ENST00000420993.2
Case#1-Baseline-WholeTumor	CNTN4	3	3076318	Missense_Mutation	C	T	p.P596S	60	28	0.467	0.549	3	2	1	46	contactin 4	ENST00000397461.1
Case#1-Baseline-WholeTumor	GRM7	3	7456838	Missense_Mutation	C	T	p.R388C	98	38	0.388	0.456	3	2	1	93	glutamate receptor, metabotropic 7	ENST00000357716.4
Case#1-Baseline-WholeTumor	LHFPL4	3	9547825	Missense_Mutation	C	T	p.D157N	114	40	0.351	0.413	3	2	1	85	lipoma HMGIC fusion partner-like 4	ENST00000287585.6
Case#1-Baseline-WholeTumor	FGD5	3	14905742	Missense_Mutation	C	T	p.S878L	109	43	0.394	0.464	3	2	1	95	FYVE, RhoGEF and PH domain containing 5	ENST00000285046.5
Case#1-Baseline-WholeTumor	ZNF860	3	32031551	Missense_Mutation	C	T	p.S327L	151	41	0.272	0.320	3	2	1	157	zinc finger protein 860	ENST00000360311.4
Case#1-Baseline-WholeTumor	DYNC1LI1	3	32571819	Splice_Site	G	A	p.S381F	74	29	0.392	0.461	3	2	1	47	dynein, cytoplasmic 1, light intermediate chain 1	ENST00000273130.4
Case#1-Baseline-WholeTumor	TRANK1	3	36898824	Missense_Mutation	CC	TT	p.A753T	40	24	0.600	0.706	3	2	1	35	tetratricopeptide repeat and ankyrin repeat containing 1	ENST00000429976.2
Case#1-Baseline-WholeTumor	ITGA9	3	37544694	Missense_Mutation	G	A	p.G213E	65	37	0.569	0.670	3	2	1	57	integrin, alpha 9	ENST00000264741.5
Case#1-Baseline-WholeTumor	SCN5A	3	38592348	Missense_Mutation	C	T	p.D1839N	196	97	0.495	0.583	3	2	1	154	sodium channel, voltage-gated, type V, alpha subunit	ENST00000333535.4
Case#1-Baseline-WholeTumor	SCN5A	3	38622491	Missense_Mutation	C	A	p.E1053D	159	73	0.459	0.540	3	2	1	104	sodium channel, voltage-gated, type V, alpha subunit	ENST00000333535.4
Case#1-Baseline-WholeTumor	SCN5A	3	38622715	Missense_Mutation	C	T	p.D979N	62	24	0.387	0.456	3	2	1	31	sodium channel, voltage-gated, type V, alpha subunit	ENST00000333535.4
Case#1-Baseline-WholeTumor	SCN5A	3	38639391	Nonsense_Mutation	C	T	p.W697*	96	31	0.323	0.380	3	2	1	84	sodium channel, voltage-gated, type V, alpha subunit	ENST00000333535.4
Case#1-Baseline-WholeTumor	SCN10A	3	38791570	Missense_Mutation	G	A	p.L621F	67	37	0.552	0.650	3	2	1	95	sodium channel, voltage-gated, type X, alpha subunit	ENST00000449082.2
Case#1-Baseline-WholeTumor	SCN11A	3	38889189	Missense_Mutation	GG	AA	p.P1458S	36	19	0.528	0.621	3	2	1	49	sodium channel, voltage-gated, type XI, alpha subunit	ENST00000302328.3
Case#1-Baseline-WholeTumor	SCN11A	3	38889195	Missense_Mutation	G	A	p.P1456S	36	11	0.306	0.360	3	2	1	45	sodium channel, voltage-gated, type XI, alpha subunit	ENST00000302328.3
Case#1-Baseline-WholeTumor	CSRNP1	3	39185792	Missense_Mutation	G	C	p.R206G	184	70	0.380	0.448	3	2	1	122	cysteine-serine-rich nuclear protein 1	ENST00000273153.5
Case#1-Baseline-WholeTumor	ZNF502	3	44763357	Missense_Mutation	C	T	p.P350S	80	42	0.525	0.618	3	2	1	71	zinc finger protein 502	ENST00000296091.4
Case#1-Baseline-WholeTumor	LIMD1	3	45637570	Missense_Mutation	C	T	p.S400F	85	40	0.471	0.554	3	2	1	65	LIM domains containing 1	ENST00000273317.4
Case#1-Baseline-WholeTumor	ELP6	3	47537648	Missense_Mutation	G	A	p.H238Y	92	34	0.370	0.435	3	2	1	84	elongator acetyltransferase complex subunit 6	ENST00000296149.4
Case#1-Baseline-WholeTumor	COL7A1	3	48629387	Missense_Mutation	G	A	p.S434F	101	52	0.515	0.606	3	2	1	69	collagen, type VII, alpha 1	ENST00000328333.8
Case#1-Baseline-WholeTumor	MAPKAPK3	3	50683142	Splice_Site	C	T	p.A210A	72	28	0.389	0.458	3	2	1	76	mitogen-activated protein kinase-activated protein kinase 3	ENST00000446044.1
Case#1-Baseline-WholeTumor	STAB1	3	52555427	Missense_Mutation	G	A	p.D1987N	111	34	0.306	0.361	3	2	1	99	stabilin 1	ENST00000321725.6
Case#1-Baseline-WholeTumor	CACNA2D3	3	55038797	Missense_Mutation	C	T	p.L900F	131	30	0.229	0.270	3	2	1	142	calcium channel, voltage-dependent, alpha 2/delta subunit 3	ENST00000474759.1
Case#1-Baseline-WholeTumor	ERC2	3	56041244	Missense_Mutation	C	T	p.E676K	61	29	0.475	0.560	3	2	1	55	ELKS/RAB6-interacting/CAST family member 2	ENST00000288221.6
Case#1-Baseline-WholeTumor	FAM3D	3	58625883	Missense_Mutation	C	T	p.G115E	91	43	0.473	0.556	3	2	1	72	family with sequence similarity 3, member D	ENST00000358781.2
Case#1-Baseline-WholeTumor	MAGI1	3	65464291	Missense_Mutation	G	A	p.P245S	153	75	0.490	0.577	3	2	1	181	membrane associated guanylate kinase, WW and PDZ domain containing 1	ENST00000497477.2

Case#1-Baseline-WholeTumor	SLC25A26	3	66287010	Missense_Mutation	C	T	p.P26S	135	46	0.341	0.401	3	2	1	101	solute carrier family 25 (S-adenosylmethionine carrier), member 26	ENST00000354883.6
Case#1-Baseline-WholeTumor	EOGT	3	69058856	Missense_Mutation	G	A	p.P48S	107	33	0.308	0.363	3	2	1	112	EGF domain-specific O-linked N-acetylglucosamine (GlcNAc) transferase	ENST00000383701.3
Case#1-Baseline-WholeTumor	ROBO2	3	77651579	Nonsense_Mutation	C	T	p.Q1025*	71	24	0.338	0.398	3	2	1	77	roundabout, axon guidance receptor, homolog 2 (Drosophila)	ENST00000461745.1
Case#1-Baseline-WholeTumor	ROBO2	3	77666845	Missense_Mutation	G	A	p.E1159K	88	30	0.341	0.401	3	2	1	82	roundabout, axon guidance receptor, homolog 2 (Drosophila)	ENST00000461745.1
Case#1-Baseline-WholeTumor	OR5K4	3	98073152	Missense_Mutation	G	A	p.G152E	109	35	0.321	0.406	2	1	1	100	olfactory receptor, family 5, subfamily K, member 4	ENST00000354924.2
Case#1-Baseline-WholeTumor	ZPLD1	3	102171955	Missense_Mutation	C	T	p.T100I	79	35	0.443	0.561	2	1	1	57	zona pellucida-like domain containing 1	ENST00000491959.1
Case#1-Baseline-WholeTumor	MORC1	3	108773587	Missense_Mutation	C	T	p.D440N	82	36	0.439	0.556	2	1	1	92	MORC family CW-type zinc finger 1	ENST00000483760.1
Case#1-Baseline-WholeTumor	MORC1	3	108813815	Missense_Mutation	G	A	p.S175F	54	19	0.352	0.445	2	1	1	80	MORC family CW-type zinc finger 1	ENST00000483760.1
Case#1-Baseline-WholeTumor	PHLDB2	3	111639198	Missense_Mutation	G	A	p.E645K	118	47	0.398	0.504	2	1	1	122	pleckstrin homology-like domain, family B, member 2	ENST00000431670.2
Case#1-Baseline-WholeTumor	PHLDB2	3	111651167	Missense_Mutation	C	T	p.L685F	67	32	0.478	0.605	2	1	1	61	pleckstrin homology-like domain, family B, member 2	ENST00000431670.2
Case#1-Baseline-WholeTumor	WDR52	3	113046507	Nonsense_Mutation	G	A	p.Q1426*	59	18	0.305	0.386	2	1	1	72		ENST00000393845.2
Case#1-Baseline-WholeTumor	WDR52	3	113063425	Missense_Mutation	G	A	p.P1067L	96	42	0.438	0.554	2	1	1	65		ENST00000393845.2
Case#1-Baseline-WholeTumor	PLA1A	3	119348287	Missense_Mutation	C	T	p.S448F	90	43	0.478	0.605	2	1	1	83	phospholipase A1 member A	ENST00000273371.4
Case#1-Baseline-WholeTumor	STXBP5L	3	121097634	Missense_Mutation	G	A	p.D774N	78	28	0.359	0.454	2	1	1	91	syntaxin binding protein 5-like	ENST00000273666.6
Case#1-Baseline-WholeTumor	PARP14	3	122437233	Missense_Mutation	C	T	p.P1412L	68	23	0.338	0.428	2	1	1	75	poly (ADP-ribose) polymerase family, member 14	ENST00000474629.2
Case#1-Baseline-WholeTumor	KALRN	3	124181467	Missense_Mutation	G	A	p.D1338N	90	34	0.378	0.478	2	1	1	97	kalirin, RhoGEF kinase	ENST00000240874.3
Case#1-Baseline-WholeTumor	GATA2	3	128205091	Missense_Mutation	G	A	p.T117I	19	7	0.368	0.466	2	1	1	22	GATA binding protein 2	ENST00000341105.2
Case#1-Baseline-WholeTumor	IFT122	3	129195534	Missense_Mutation	C	T	p.S346F	54	15	0.278	0.352	2	1	1	56	intraflagellar transport 122	ENST00000348417.2
Case#1-Baseline-WholeTumor	COL6A5	3	130095636	Missense_Mutation	T	G	p.D208E	61	25	0.410	0.519	2	1	1	56	collagen, type VI, alpha 5	ENST00000432398.2
Case#1-Baseline-WholeTumor	COL6A5	3	130107908	Missense_Mutation	C	T	p.H783Y	24	10	0.417	0.527	2	1	1	33	collagen, type VI, alpha 5	ENST00000432398.2
Case#1-Baseline-WholeTumor	PIK3R4	3	130424612	Missense_Mutation	G	A	p.P909S	82	31	0.378	0.479	2	1	1	109	phosphoinositide-3-kinase, regulatory subunit 4	ENST00000356763.3
Case#1-Baseline-WholeTumor	ESYT3	3	138195671	Missense_Mutation	C	G	p.T879S	37	17	0.459	0.582	2	1	1	41	extended synaptotagmin-like protein 3	ENST00000389567.4
Case#1-Baseline-WholeTumor	CLSTN2	3	140123566	Missense_Mutation	G	A	p.E199K	85	31	0.365	0.462	2	1	1	103	calsyntenin 2	ENST00000458420.3
Case#1-Baseline-WholeTumor	SLC25A36	3	140682046	Missense_Mutation	A	T	p.H121L	94	41	0.436	0.552	2	1	1	78	solute carrier family 25 (pyrimidine nucleotide carrier), member 36	ENST00000324194.6
Case#1-Baseline-WholeTumor	SIAH2	3	150480395	Missense_Mutation	G	A	p.P81L	49	15	0.306	0.387	2	1	1	28	siah E3 ubiquitin protein ligase 2	ENST00000312960.3
Case#1-Baseline-WholeTumor	SERPINI2	3	167182997	Missense_Mutation	G	A	p.P288L	56	22	0.393	0.497	2	1	1	55	serpin peptidase inhibitor, clade I (pancpin), member 2	ENST00000476257.1
Case#1-Baseline-WholeTumor	MECOM	3	168833574	Missense_Mutation	G	A	p.P508S	45	20	0.444	0.563	2	1	1	39	MDS1 and EVI1 complex locus	ENST00000464456.1
Case#1-Baseline-WholeTumor	TNIK	3	170828529	Missense_Mutation	C	T	p.G753E	71	24	0.338	0.428	2	1	1	69	TRAF2 and NCK interacting kinase	ENST00000436636.2
Case#1-Baseline-WholeTumor	CCDC39	3	180359793	Missense_Mutation	C	T	p.R621Q	126	46	0.365	0.462	2	1	1	162	coiled-coil domain containing 39	ENST00000442201.2
Case#1-Baseline-WholeTumor	CCDC39	3	180381704	Missense_Mutation	G	A	p.S54F	71	28	0.394	0.499	2	1	1	69	coiled-coil domain containing 39	ENST00000442201.2
Case#1-Baseline-WholeTumor	EIF4G1	3	184040441	Missense_Mutation	C	T	p.T573I	62	22	0.355	0.449	2	1	1	77	eukaryotic translation initiation factor 4 gamma, 1	ENST00000346169.2
Case#1-Baseline-WholeTumor	TMEM44	3	194325093	Missense_Mutation	GG	AA	p.P414S	101	39	0.386	0.489	2	1	1	64	transmembrane protein 44	ENST00000392432.2
Case#1-Baseline-WholeTumor	TMEM175	4	947137	Missense_Mutation	CC	TT	p.P208F	35	13	0.371	0.470	2	1	1	28	transmembrane protein 175	ENST00000264771.4
Case#1-Baseline-WholeTumor	SPON2	4	1164876	Missense_Mutation	C	T	p.D183N	17	6	0.353	0.447	2	1	1	13	spondin 2, extracellular matrix protein	ENST00000290902.5
Case#1-Baseline-WholeTumor	ADD1	4	2886385	Missense_Mutation	C	T	p.H168Y	108	37	0.343	0.434	2	1	1	143	adducin 1 (alpha)	ENST00000398129.1
Case#1-Baseline-WholeTumor	WFS1	4	6304145	Missense_Mutation	G	A	p.V875M	99	40	0.404	0.511	2	1	1	74	Wolfram syndrome 1 (wolframin)	ENST00000226760.1
Case#1-Baseline-WholeTumor	DEFB131	4	9452137	Missense_Mutation	G	A	p.R37K	50	21	0.420	0.532	2	1	1	68	defensin, beta 131	ENST00000334879.1
Case#1-Baseline-WholeTumor	ZNF518B	4	10447258	Missense_Mutation	C	T	p.R232K	88	27	0.307	0.388	2	1	1	91	zinc finger protein 518B	ENST00000326756.3
Case#1-Baseline-WholeTumor	CLNK	4	10669536	Splice_Site	C	T		35	16	0.457	0.579	2	1	1	26	cytokine-dependent hematopoietic cell linker	ENST00000226951.6
Case#1-Baseline-WholeTumor	CPEB2	4	15060828	Missense_Mutation	G	C	p.W421C	92	38	0.413	0.523	2	1	1	81	cytoplasmic polyadenylation element binding protein 2	ENST00000507071.1
Case#1-Baseline-WholeTumor	CD38	4	15826543	Missense_Mutation	T	C	p.F135L	90	39	0.433	0.549	2	1	1	96	CD38 molecule	ENST00000226279.3
Case#1-Baseline-WholeTumor	SLIT2	4	20535283	Missense_Mutation	C	T	p.R593C	113	54	0.478	0.605	2	1	1	118	slit homolog 2 (Drosophila)	ENST00000504154.1
Case#1-Baseline-WholeTumor	SHISA3	4	42400323	Missense_Mutation	G	A	p.E84K	19	10	0.526	0.666	2	1	1	16	shisa family member 3	ENST00000319234.4
Case#1-Baseline-WholeTumor	KCTD8	4	44177183	Missense_Mutation	C	T	p.G349E	44	20	0.455	0.575	2	1	1	73	potassium channel tetramerization domain containing 8	ENST00000360029.3
Case#1-Baseline-WholeTumor	ATP10D	4	47525150	Missense_Mutation	G	A	p.G203R	104	36	0.346	0.438	2	1	1	142	ATPase, class V, type 10D	ENST00000273859.3
Case#1-Baseline-WholeTumor	CORIN	4	47765514	Missense_Mutation	C	T	p.E167K	106	45	0.425	0.537	2	1	1	125	corin, serine peptidase	ENST00000273857.4
Case#1-Baseline-WholeTumor	CWH43	4	48990626	Missense_Mutation	C	T	p.P59L	102	42	0.412	0.521	2	1	1	128	cell wall biogenesis 43 C-terminal homolog (S. cerevisiae)	ENST00000226432.4
Case#1-Baseline-WholeTumor	LPHN3	4	62813977	Missense_Mutation	G	A	p.A862T	93	26	0.280	0.354	2	1	1	102	latrophilin 3	ENST00000514591.1
Case#1-Baseline-WholeTumor	UGT2B11	4	70078385	Missense_Mutation	C	T	p.R259Q	207	85	0.411	0.520	2	1	1	284	UDP glucuronosyltransferase 2 family, polypeptide B11	ENST00000446444.1
Case#1-Baseline-WholeTumor	UGT2B28	4	70146763	Missense_Mutation	G	A	p.R182K	187	68	0.364	0.460	2	1	1	352	UDP glucuronosyltransferase 2 family, polypeptide B28	ENST00000335568.5
Case#1-Baseline-WholeTumor	UGT2B4	4	70359494	Missense_Mutation	C	T	p.D263N	160	66	0.413	0.522	2	1	1	268	UDP glucuronosyltransferase 2 family, polypeptide B4	ENST00000305107.6
Case#1-Baseline-WholeTumor	SMR3A	4	71232637	Missense_Mutation	C	T	p.P111S	137	53	0.387	0.490	2	1	1	172	submaxillary gland androgen regulated protein 3A	ENST00000226460.4
Case#1-Baseline-WholeTumor	ENAM	4	71501579	Missense_Mutation	C	T	p.P168S	47	16	0.340	0.431	2	1	1	43	enamelin	ENST00000396073.3
Case#1-Baseline-WholeTumor	AFP	4	74313262	Missense_Mutation	A	T	p.E309D	30	11	0.367	0.464	2	1	1	48	alpha-fetoprotein	ENST00000395792.2
Case#1-Baseline-WholeTumor	CXCL11	4	76955959	Missense_Mutation	C	A	p.R91I	30	13	0.433	0.549	2	1	1	51	chemokine (C-X-C motif) ligand 11	ENST00000503860.1
Case#1-Baseline-WholeTumor	FAM47E	4	77192919	Missense_Mutation	C	G	p.Q290E	46	18	0.391	0.495	2	1	1	52	family with sequence similarity 47, member E	ENST00000424749.2
Case#1-Baseline-WholeTumor	CNOT6L	4	78641776	Missense_Mutation	A	C	p.Y493D	67	33	0.493	0.623	2	1	1	86	CCR4-NOT transcription complex, subunit 6-like	ENST00000504123.1
Case#1-Baseline-WholeTumor	BMP2K	4	79792083	Frame_Shift_Del	CAG	-	p.Q486fs	90	7	0.078	0.098	2	1	1	83	BMP2 inducible kinase	ENST00000335016.5
Case#1-Baseline-WholeTumor	PRDM8	4	81121453	Splice_Site	G	A	p.R73R	98	38	0.388	0.491	2	1	1	127	PR domain containing 8	ENST00000504452.1
Case#1-Baseline-WholeTumor	PRDM8	4	81122675	Splice_Site	G	A	p.G151R	117	49	0.419	0.530	2	1	1	122	PR domain containing 8	ENST00000504452.1
Case#1-Baseline-WholeTumor	FGF5	4	81196152	Nonsense_Mutation	A	T	p.K149*	68	32	0.471	0.596	2	1	1	63	fibroblast growth factor 5	ENST00000312465.7
Case#1-Baseline-WholeTumor	BMP3	4	81967521	Missense_Mutation	G	A	p.E316K	57	25	0.439	0.555	2	1	1	67	bone morphogenetic protein 3	ENST00000282701.2
Case#1-Baseline-WholeTumor	AGPAT9	4	84502856	Missense_Mutation	C	T	p.S117F	101	43	0.426	0.539	2	1	1	153	1-acylglycerol-3-phosphate O-acyltransferase 9	ENST00000395226.2
Case#1-Baseline-WholeTumor	MAPK10	4	86985528	Missense_Mutation	T	C	p.D334G	60	13	0.217	0.274	2	1	1	88	mitogen-activated protein kinase 10	ENST00000359221.3
Case#1-Baseline-WholeTumor	PTPN13	4	87703357	Missense_Mutation	C	T	p.S1989F	38	19	0.500	0.633	2	1	1	48	protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	ENST00000411767.2
Case#1-Baseline-WholeTumor	SPARCL1	4	88400704	Missense_Mutation	G	A	p.P615L	79	31	0.392	0.497	2	1	1	80	SPARC-like 1 (hevin)	ENST00000282470.6
Case#1-Baseline-WholeTumor	DSPP	4	88533290	Missense_Mutation	G	A	p.E29K	60	14	0.233	0.295	2	1	1	71	dentin sialophosphoprotein	ENST00000282478.7
Case#1-Baseline-WholeTumor	STPG2	4	98893466	Missense_Mutation	C	T	p.E300K	51	24	0.471	0.596	2	1	1	41	sperm-tail PG-rich repeat containing 2	ENST00000295268.3
Case#1-Baseline-WholeTumor	ADH1A	4	100201412	Missense_Mutation	C	T	p.E285K	165	71	0.430	0.545	2	1	1	225	alcohol dehydrogenase 1A (class I), alpha polypeptide	ENST00000209668.2
Case#1-Baseline-WholeTumor	SLC9B1	4	103822321	Missense_Mutation	C	T	p.D501N	595	31	0.052	0.066	2	1	1	800	solute carrier family 9, subfamily B (NHA1, cation proton antiporter 1), member 1	ENST00000296422.7
Case#1-Baseline-WholeTumor	SLC9B2	4	103952935	Missense_Mutation	A	G	p.W393R	67	26	0.388	0.491	2	1	1	61	solute carrier family 9, subfamily B (NHA2, cation proton antiporter 2), member 2	ENST00000394785.3
Case#1-Baseline-WholeTumor	TACR3	4	104511147	Nonsense_Mutation	G	A	p.R364*	84	34	0.405	0.512	2	1	1	116	tachykinin receptor 3	ENST00000304883.2
Case#1-Baseline-WholeTumor	INTS12	4	106616723	Missense_Mutation	G	A	p.L87F	94	25	0.266	0.337	2	1	1	100	integrator complex subunit 12	ENST00000451321.2
Case#1-Baseline-WholeTumor	NPNT	4	106859527	Missense_Mutation	A	G	p.Q152R	33	19	0.576	0.729	2	1	1	43	nephronectin	ENST00000379987.2
Case#1-Baseline-WholeTumor	LEF1	4	109010280	Splice_Site	CC	TT	p.G183N	148	50	0.338	0.428	2	1	1	139	lymphoid enhancer-binding factor 1	ENST00000265165.1
Case#1-Baseline-WholeTumor	CASP6	4	110610646	Missense_Mutation	G	A	p.S241F	97	23	0.237	0.300	2	1	1	74	caspase 6, apoptosis-related cysteine peptidase	ENST00000265164.2
Case#1-Baseline-WholeTumor	PITX2	4	111539426	Missense_Mutation	G	A	p.P270L	152	59	0.388	0.491	2	1	1	149	paired-like homeodomain 2	ENST00000354925.2
Case#1-Baseline-WholeTumor	NDST4	4	115760590	Missense_Mutation	G	A	p.P744S	80	39	0.488	0.617	2	1	1	77	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4	ENST00000264363.2
Case#1-Baseline-WholeTumor	KIAA1109	4	123171565	Missense_Mutation	G	A	p.G1920D	49	18	0.367	0.465	2	1	1	46	KIAA1109	ENST00000264501.4

Case#1-Baseline-WholeTumor	KIAA1109	4	123246422	Missense_Mutation	C	T	p.R3648C	80	22	0.275	0.348	2	1	1	100	KIAA1109	ENST00000264501.4
Case#1-Baseline-WholeTumor	FAT4	4	126329769	Missense_Mutation	C	T	p.L1914F	61	17	0.279	0.353	2	1	1	68	FAT atypical cadherin 4	ENST00000394329.3
Case#1-Baseline-WholeTumor	FAT4	4	126411736	Missense_Mutation	G	A	p.E4587K	45	18	0.400	0.506	2	1	1	56	FAT atypical cadherin 4	ENST00000394329.3
Case#1-Baseline-WholeTumor	SLC25A31	4	128694685	Missense_Mutation	G	A	p.D302N	98	24	0.245	0.310	2	1	1	109	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 31	ENST00000281154.4
Case#1-Baseline-WholeTumor	PCDH18	4	138452420	Missense_Mutation	C	T	p.E275K	51	15	0.294	0.372	2	1	1	65	protocadherin 18	ENST00000344876.4
Case#1-Baseline-WholeTumor	FREM3	4	144621186	Missense_Mutation	G	A	p.H215Y	27	12	0.444	0.563	2	1	1	20	FRAS1 related extracellular matrix 3	ENST00000329798.5
Case#1-Baseline-WholeTumor	ZNF827	4	146697095	Missense_Mutation	A	C	p.C847G	85	37	0.435	0.551	2	1	1	76	zinc finger protein 827	ENST00000508784.1
Case#1-Baseline-WholeTumor	LRBA	4	151773393	Nonsense_Mutation	G	A	p.Q1157*	41	27	0.659	0.834	2	2	0	69	LPS-responsive vesicle trafficking, beach and anchor containing	ENST00000357115.3
Case#1-Baseline-WholeTumor	KIAA0922	4	154395012	Missense_Mutation	G	A	p.G71S	77	53	0.688	0.871	2	2	0	92	KIAA0922	ENST00000409663.3
Case#1-Baseline-WholeTumor	TLR2	4	154625114	Missense_Mutation	C	T	p.P352L	35	25	0.714	0.904	2	2	0	53	toll-like receptor 2	ENST00000260010.6
Case#1-Baseline-WholeTumor	DCHS2	4	155407624	Missense_Mutation	C	T	p.E694K	78	63	0.808	1.022	2	2	0	119	dachsous cadherin-related 2	ENST00000456341.2
Case#1-Baseline-WholeTumor	GLRB	4	158057765	Missense_Mutation	G	A	p.E148K	59	52	0.881	1.116	2	2	0	94	glycine receptor, beta	ENST00000264428.4
Case#1-Baseline-WholeTumor	FSTL5	4	162697192	Missense_Mutation	C	T	p.M148I	23	22	0.957	1.211	2	2	0	34	follistatin-like 5	ENST00000306100.5
Case#1-Baseline-WholeTumor	ANXA10	4	169049310	Missense_Mutation	G	A	p.G32R	60	53	0.883	1.118	2	2	0	76	annexin A10	ENST00000359299.3
Case#1-Baseline-WholeTumor	AGA	4	178358657	Missense_Mutation	G	A	p.P175L	87	71	0.816	1.033	2	2	0	116	aspartylglucosaminidase	ENST00000264595.2
Case#1-Baseline-WholeTumor	RP11-389E17.1	4	178896990	Missense_Mutation	G	A	p.D65N	80	67	0.838	1.060	2	2	0	160		ENST00000507870.1
Case#1-Baseline-WholeTumor	TENM3	4	183713919	Missense_Mutation	G	A	p.G2032S	26	16	0.615	0.943	1	1	0	52	teneurin transmembrane protein 3	ENST00000511685.1
Case#1-Baseline-WholeTumor	WWC2	4	184169952	Missense_Mutation	C	T	p.S273F	34	22	0.647	0.991	1	1	0	72	WW and C2 domain containing 2	ENST00000403733.3
Case#1-Baseline-WholeTumor	IRF2	4	185340707	Nonsense_Mutation	G	A	p.Q35*	23	14	0.609	0.932	1	1	0	44	interferon regulatory factor 2	ENST00000393593.3
Case#1-Baseline-WholeTumor	FAT1	4	187540106	Missense_Mutation	C	T	p.R2545K	25	15	0.600	0.919	1	1	0	62	FAT atypical cadherin 1	ENST00000441802.2
Case#1-Baseline-WholeTumor	PLEKHG4B	5	143609	Missense_Mutation	G	A	p.S245N	50	11	0.220	0.278	2	1	1	60	pleckstrin homology domain containing, family G (with RhoGef domain) member 4B	ENST00000283426.6
Case#1-Baseline-WholeTumor	CLPTM1L	5	1318560	Missense_Mutation	G	A	p.P514L	45	14	0.311	0.394	2	1	1	31	CLPTM1-like	ENST00000320895.5
Case#1-Baseline-WholeTumor	ADAMTS16	5	5187860	Missense_Mutation	G	A	p.G329E	96	33	0.344	0.435	2	1	1	118	ADAM metallopeptidase with thrombospondin type 1 motif, 16	ENST00000274181.7
Case#1-Baseline-WholeTumor	DNAH5	5	13735969	Missense_Mutation	G	A	p.S3843L	64	26	0.406	0.514	2	1	1	66	dynein, axonemal, heavy chain 5	ENST00000265104.4
Case#1-Baseline-WholeTumor	DNAH5	5	13850770	Missense_Mutation	G	A	p.S1702F	39	13	0.333	0.422	2	1	1	49	dynein, axonemal, heavy chain 5	ENST00000265104.4
Case#1-Baseline-WholeTumor	TRIO	5	14481656	Missense_Mutation	G	A	p.V2132M	117	51	0.436	0.552	2	1	1	98	trio Rho guanine nucleotide exchange factor	ENST00000344204.4
Case#1-Baseline-WholeTumor	CDH12	5	21783541	Missense_Mutation	G	A	p.T440I	75	30	0.400	0.506	2	1	1	97	cadherin 12, type 2 (N-cadherin 2)	ENST00000382254.1
Case#1-Baseline-WholeTumor	CDH10	5	24537668	Missense_Mutation	C	T	p.R116Q	57	20	0.351	0.444	2	1	1	87	cadherin 10, type 2 (T2-cadherin)	ENST00000264463.4
Case#1-Baseline-WholeTumor	CDH9	5	26881582	Missense_Mutation	C	T	p.R678K	63	16	0.254	0.321	2	1	1	80	cadherin 9, type 2 (T1-cadherin)	ENST00000231021.4
Case#1-Baseline-WholeTumor	UGT3A1	5	35965544	Missense_Mutation	G	A	p.P263S	95	31	0.326	0.413	2	1	1	151	UDP glycosyltransferase 3 family, polypeptide A1	ENST00000274278.3
Case#1-Baseline-WholeTumor	EGFLAM	5	38350705	Missense_Mutation	A	G	p.T132A	76	14	0.184	0.233	2	1	1	92	EGF-like, fibronectin type III and laminin G domains	ENST00000354891.3
Case#1-Baseline-WholeTumor	C7	5	40981538	Missense_Mutation	G	A	p.E799K	83	31	0.373	0.473	2	1	1	109	complement component 7	ENST00000313164.9
Case#1-Baseline-WholeTumor	C6	5	41155131	Nonsense_Mutation	G	A	p.Q682*	86	31	0.360	0.456	2	1	1	92	complement component 6	ENST00000263413.3
Case#1-Baseline-WholeTumor	C6	5	41159322	Missense_Mutation	G	A	p.S573F	22	10	0.455	0.575	2	1	1	31	complement component 6	ENST00000263413.3
Case#1-Baseline-WholeTumor	C6	5	41161821	Missense_Mutation	C	T	p.E478K	49	26	0.531	0.672	2	1	1	78	complement component 6	ENST00000263413.3
Case#1-Baseline-WholeTumor	GHR	5	42711363	Missense_Mutation	G	A	p.E225K	87	20	0.230	0.291	2	1	1	132	growth hormone receptor	ENST00000230882.4
Case#1-Baseline-WholeTumor	MOCS2	5	52397999	Missense_Mutation	C	T	p.E52K	69	17	0.246	0.312	2	1	1	100	molybdenum cofactor synthesis 2	ENST00000396954.3
Case#1-Baseline-WholeTumor	IPO11	5	61846195	Splice_Site	T	C	p.V751A	116	57	0.491	0.622	2	1	1	158	importin 11	ENST00000325324.6
Case#1-Baseline-WholeTumor	MARVELD2	5	68715684	Missense_Mutation	C	T	p.P158S	35	13	0.371	0.470	2	1	1	56	MARVEL domain containing 2	ENST00000325631.5
Case#1-Baseline-WholeTumor	MAP1B	5	71496188	Missense_Mutation	A	G	p.T2336A	25	12	0.480	0.608	2	1	1	25	microtubule-associated protein 1B	ENST00000296755.7
Case#1-Baseline-WholeTumor	ARHGEF28	5	73179596	Missense_Mutation	G	A	p.R981Q	88	39	0.443	0.561	2	1	1	97	Rho guanine nucleotide exchange factor (GEF) 28	ENST00000426542.2
Case#1-Baseline-WholeTumor	ANKRD31	5	74364391	Missense_Mutation	C	T	p.D1859N	95	29	0.305	0.386	2	1	1	99	ankyrin repeat domain 31	ENST00000274361.3
Case#1-Baseline-WholeTumor	GPR98	5	89933641	Missense_Mutation	G	A	p.D706N	120	37	0.308	0.390	2	1	1	156	G protein-coupled receptor 98	ENST00000405460.2
Case#1-Baseline-WholeTumor	GPR98	5	89970009	Missense_Mutation	G	A	p.E1690K	70	22	0.314	0.398	2	1	1	91	G protein-coupled receptor 98	ENST00000405460.2
Case#1-Baseline-WholeTumor	GPR98	5	89999523	Nonsense_Mutation	C	T	p.R2733*	59	27	0.458	0.579	2	1	1	100	G protein-coupled receptor 98	ENST00000405460.2
Case#1-Baseline-WholeTumor	GPR98	5	90059134	Missense_Mutation	G	A	p.E4045K	55	19	0.345	0.437	2	1	1	61	G protein-coupled receptor 98	ENST00000405460.2
Case#1-Baseline-WholeTumor	GPR98	5	90074406	Nonsense_Mutation	C	T	p.R4277*	49	19	0.388	0.491	2	1	1	45	G protein-coupled receptor 98	ENST00000405460.2
Case#1-Baseline-WholeTumor	GPR98	5	90136557	Missense_Mutation	C	T	p.P5592S	78	27	0.346	0.438	2	1	1	93	G protein-coupled receptor 98	ENST00000405460.2
Case#1-Baseline-WholeTumor	SLCO4C1	5	101592859	Missense_Mutation	C	T	p.E477K	79	36	0.456	0.577	2	1	1	81	solute carrier organic anion transporter family, member 4C1	ENST00000310954.6
Case#1-Baseline-WholeTumor	SLCO4C1	5	101606492	Missense_Mutation	C	T	p.R213K	29	11	0.379	0.480	2	1	1	44	solute carrier organic anion transporter family, member 4C1	ENST00000310954.6
Case#1-Baseline-WholeTumor	CAMK4	5	110820100	Missense_Mutation	G	A	p.G453E	34	11	0.324	0.410	2	1	1	19	calcium/calmodulin-dependent protein kinase IV	ENST00000282356.4
Case#1-Baseline-WholeTumor	EPB41L4A	5	111531361	Missense_Mutation	C	T	p.R474K	92	31	0.337	0.427	2	1	1	134	erythrocyte membrane protein band 4.1 like 4A	ENST00000261486.5
Case#1-Baseline-WholeTumor	SNCAIP	5	121786421	Missense_Mutation	G	A	p.E627K	41	17	0.415	0.525	2	1	1	76	synuclein, alpha interacting protein	ENST00000261368.8
Case#1-Baseline-WholeTumor	PRDM6	5	122506570	Missense_Mutation	C	T	p.P422S	79	30	0.380	0.481	2	1	1	106	PR domain containing 6	ENST00000407847.4
Case#1-Baseline-WholeTumor	SLC27A6	5	128302027	Missense_Mutation	G	T	p.R66I	69	24	0.348	0.440	2	1	1	60	solute carrier family 27 (fatty acid transporter), member 6	ENST00000262462.4
Case#1-Baseline-WholeTumor	ADAMTS19	5	129015556	Missense_Mutation	G	A	p.R863Q	66	30	0.455	0.575	2	1	1	65	ADAM metallopeptidase with thrombospondin type 1 motif, 19	ENST00000274487.4
Case#1-Baseline-WholeTumor	IL5	5	131879077	Missense_Mutation	C	T	p.E32K	67	23	0.343	0.435	2	1	1	93	interleukin 5	ENST00000231454.1
Case#1-Baseline-WholeTumor	PCDHA1	5	140166257	Missense_Mutation	G	A	p.D128N	99	39	0.394	0.499	2	1	1	102	protocadherin alpha 1	ENST00000504120.2
Case#1-Baseline-WholeTumor	PCDHA1	5	140167444	Missense_Mutation	GG	AA	p.D524N	331	116	0.350	0.444	2	1	1	221	protocadherin alpha 1	ENST00000504120.2
Case#1-Baseline-WholeTumor	PCDHA1	5	140167763	Missense_Mutation	G	A	p.E630K	377	148	0.393	0.497	2	1	1	291	protocadherin alpha 1	ENST00000504120.2
Case#1-Baseline-WholeTumor	PCDHA1	5	140168264	Missense_Mutation	G	A	p.G797S	34	16	0.471	0.596	2	1	1	59	protocadherin alpha 1	ENST00000504120.2
Case#1-Baseline-WholeTumor	PCDHA5	5	140203062	Nonsense_Mutation	C	T	p.R568*	282	123	0.436	0.552	2	1	1	199	protocadherin alpha 5	ENST00000529859.1
Case#1-Baseline-WholeTumor	PCDHA10	5	140237497	Missense_Mutation	C	T	p.R622C	169	133	0.787	0.996	2	1	1	142	protocadherin alpha 10	ENST00000307360.5
Case#1-Baseline-WholeTumor	PCDHA11	5	140250546	Missense_Mutation	C	T	p.P620S	317	135	0.426	0.539	2	1	1	195	protocadherin alpha 11	ENST00000398640.2
Case#1-Baseline-WholeTumor	PCDHA12	5	140255958	Missense_Mutation	G	A	p.E301K	56	22	0.393	0.497	2	1	1	92	protocadherin alpha 12	ENST00000398631.2
Case#1-Baseline-WholeTumor	PCDHA13	5	140264090	Missense_Mutation	G	A	p.G746E	163	63	0.387	0.489	2	1	1	80	protocadherin alpha 13	ENST00000289272.2
Case#1-Baseline-WholeTumor	PCDHB3	5	140481009	Missense_Mutation	C	T	p.S259F	42	23	0.548	0.693	2	1	1	47	protocadherin beta 3	ENST00000231130.2
Case#1-Baseline-WholeTumor	PCDHB3	5	140482613	Missense_Mutation	G	C	p.E794Q	102	38	0.373	0.472	2	1	1	94	protocadherin beta 3	ENST00000231130.2
Case#1-Baseline-WholeTumor	PCDHB5	5	140515701	Missense_Mutation	C	T	p.R229C	47	19	0.404	0.512	2	1	1	49	protocadherin beta 5	ENST00000231134.5
Case#1-Baseline-WholeTumor	PCDHB5	5	140516743	Missense_Mutation	C	T	p.P576L	201	77	0.383	0.485	2	1	1	103	protocadherin beta 5	ENST00000231134.5
Case#1-Baseline-WholeTumor	PCDHB17	5	140536565	Missense_Mutation	G	A	p.G330E	43	18	0.419	0.530	2	1	1	56	protocadherin beta 17 pseudogene	ENST00000539533.1
Case#1-Baseline-WholeTumor	PCDHB7	5	140554580	Missense_Mutation	C	T	p.R722C	346	58	0.168	0.212	2	1	1	329	protocadherin beta 7	ENST00000231137.3
Case#1-Baseline-WholeTumor	PCDHB7	5	140554769	Missense_Mutation	C	T	p.R785C	343	51	0.149	0.188	2	1	1	406	protocadherin beta 7	ENST00000231137.3
Case#1-Baseline-WholeTumor	PCDHB10	5	140572324	Missense_Mutation	G	A	p.V67I	142	30	0.211	0.267	2	1	1	160	protocadherin beta 10	ENST00000239446.4
Case#1-Baseline-WholeTumor	PCDHB11	5	140580731	Missense_Mutation	G	A	p.E462K	207	89	0.430	0.544	2	1	1	244	protocadherin beta 11	ENST00000354757.3
Case#1-Baseline-WholeTumor	PCDHB11	5	140580900	Missense_Mutation	C	T	p.S518L	198	88	0.444	0.563	2	1	1	152	protocadherin beta 11	ENST00000354757.3
Case#1-Baseline-WholeTumor	PCDHB14	5	140604665	Missense_Mutation	C	T	p.R530C	213	92	0.432	0.547	2	1	1	179	protocadherin beta 14	ENST00000239449.4
Case#1-Baseline-WholeTumor	PCDHGB6	5	140788121	Missense_Mutation	C	T	p.H118Y	82	33	0.402	0.509	2	1	1	94	protocadherin gamma subfamily B, 6	ENST00000520790.1
Case#1-Baseline-WholeTumor	DIAPH1	5	140953145	Missense_Mutation	G	A	p.P758S	133	53	0.398	0.504	2	1	1	103	diaphanous-related formin 1	ENST00000398557.4
Case#1-Baseline-WholeTumor	FBXO38	5	147778581	Missense_Mutation	A	T	p.I50F	126	45	0.357	0.452	2	1	1	131	F-box protein 38	ENST00000340253.5
Case#1-Baseline-WholeTumor	FAT2	5	150911477	Missense_Mutation	G	A	p.S3161F	133	73	0.549	0.695	2	1	1	79	FAT atypical cadherin 2	ENST00000261800.5
Case#1-Baseline-WholeTumor	FAT2	5	150930357	Missense_Mutation	G	A	p.P1458S	78	31	0.397	0.503	2	1	1	76	FAT atypical cadherin 2	ENST00000261800.5
Case#1-Baseline-WholeTumor	GRIA1	5	153065789	Missense_Mutation	G	A	p.R345Q	63	30	0.476	0.603	2	1	1	97	glutamate receptor, ionotropic, AMPA 1	ENST00000285900.5

Case#1-Baseline-WholeTumor	DOCK2	5	169267845	Missense_Mutation	C	T	p.H930Y	125	46	0.368	0.466	2	1	1	133	dedicator of cytokinesis 2	ENST00000256935.8
Case#1-Baseline-WholeTumor	KCNIP1	5	170145803	Missense_Mutation	C	T	p.R46W	42	17	0.405	0.512	2	1	1	52	Kv channel interacting protein 1	ENST00000411494.1
Case#1-Baseline-WholeTumor	DRD1	5	174869582	Missense_Mutation	C	T	p.G174E	100	31	0.310	0.365	3	2	1	134	dopamine receptor D1	ENST00000393752.2
Case#1-Baseline-WholeTumor	GRM6	5	178416070	Missense_Mutation	G	A	p.A407V	128	37	0.289	0.340	3	2	1	108	glutamate receptor, metabotropic 6	ENST00000517717.1
Case#1-Baseline-WholeTumor	CNOT6	5	179992975	Nonsense_Mutation	C	T	p.Q239*	77	40	0.519	0.612	3	2	1	63	CCR4-NOT transcription complex, subunit 6	ENST00000393356.1
Case#1-Baseline-WholeTumor	TRIM52	5	180687373	Missense_Mutation	A	T	p.Y148N	140	41	0.293	NA	NA	NA	NA	159	tripartite motif containing 52	ENST00000327767.4
Case#1-Baseline-WholeTumor	PSMG4	6	3267914	Missense_Mutation	G	A	p.E114K	119	63	0.529	0.623	3	2	1	132	proteasome (prosome, macropain) assembly chaperone 4	ENST00000438998.2
Case#1-Baseline-WholeTumor	F13A1	6	6167714	Missense_Mutation	T	C	p.T629A	99	22	0.222	0.262	3	2	1	137	coagulation factor XIII, A1 polypeptide	ENST00000264870.3
Case#1-Baseline-WholeTumor	HIST1H3B	6	26032069	Missense_Mutation	C	T	p.E74K	95	55	0.579	0.887	1	1	0	152	histone cluster 1, H3b	ENST00000244661.2
Case#1-Baseline-WholeTumor	TULP1	6	35476999	Missense_Mutation	C	T	p.G270E	36	17	0.472	0.723	1	1	0	84	tubby like protein 1	ENST00000229771.6
Case#1-Baseline-WholeTumor	LRFN2	6	40400849	Missense_Mutation	C	T	p.E2K	35	21	0.600	0.919	1	1	0	44	leucine rich repeat and fibronectin type III domain containing 2	ENST00000338305.6
Case#1-Baseline-WholeTumor	KLHDC3	6	42986651	Missense_Mutation	C	T	p.R291C	46	40	0.870	1.332	1	1	0	68	kelch domain containing 3	ENST00000326974.4
Case#1-Baseline-WholeTumor	CD2AP	6	47522423	Missense_Mutation	G	T	p.L154F	53	42	0.792	1.214	1	1	0	106	CD2-associated protein	ENST00000359314.5
Case#1-Baseline-WholeTumor	PKHD1	6	51497504	Nonsense_Mutation	G	A	p.R3842*	53	36	0.679	1.040	1	1	0	80	polycystic kidney and hepatic disease 1 (autosomal recessive)	ENST00000371117.3
Case#1-Baseline-WholeTumor	IL17F	6	52101862	Missense_Mutation	G	A	p.S120F	46	29	0.630	0.966	1	1	0	88	interleukin 17F	ENST00000336123.4
Case#1-Baseline-WholeTumor	TINAG	6	54216156	Missense_Mutation	G	A	p.E363K	51	31	0.608	0.931	1	1	0	68	tubulointerstitial nephritis antigen	ENST00000259782.4
Case#1-Baseline-WholeTumor	HCRTR2	6	55039521	Missense_Mutation	G	A	p.E46K	66	42	0.636	0.975	1	1	0	153	hypocretin (orexin) receptor 2	ENST00000370862.3
Case#1-Baseline-WholeTumor	HMGCLL1	6	55304353	Missense_Mutation	C	T	p.G297E	32	23	0.719	1.101	1	1	0	111	3-hydroxymethyl-3-methylglutaryl-CoA lyase-like 1	ENST00000398661.2
Case#1-Baseline-WholeTumor	BAI3	6	70071021	Missense_Mutation	G	A	p.D1286N	17	11	0.647	0.991	1	1	0	61	brain-specific angiogenesis inhibitor 3	ENST00000370598.1
Case#1-Baseline-WholeTumor	KHDC1L	6	73933892	Nonsense_Mutation	G	A	p.R98*	23	15	0.652	0.999	1	1	0	56	KH homology domain containing 1-like	ENST00000370388.3
Case#1-Baseline-WholeTumor	KHDC3L	6	74072881	Missense_Mutation	G	A	p.R78Q	34	21	0.618	0.946	1	1	0	90	KH domain containing 3-like, subcortical maternal complex member	ENST00000370367.3
Case#1-Baseline-WholeTumor	IMPG1	6	76660542	Missense_Mutation	C	T	p.E521K	35	22	0.629	0.963	1	1	0	100	interphotoreceptor matrix proteoglycan 1	ENST00000369950.3
Case#1-Baseline-WholeTumor	ME1	6	83949355	Splice_Site	C	T	p.G272E	25	18	0.720	1.103	1	1	0	50	malic enzyme 1, NADP(+)-dependent, cytosolic	ENST00000369705.3
Case#1-Baseline-WholeTumor	SNAP91	6	84333033	Missense_Mutation	G	A	p.P265L	35	23	0.657	1.007	1	1	0	75	synaptosomal-associated protein, 91kDa	ENST00000439399.2
Case#1-Baseline-WholeTumor	KIAA1009	6	84884944	Missense_Mutation	G	T	p.Q596K	26	5	0.192	0.295	1	1	0	51		ENST00000403245.3
Case#1-Baseline-WholeTumor	GPRC6A	6	117128317	Missense_Mutation	G	A	p.S184L	24	13	0.542	0.830	1	1	0	75	G protein-coupled receptor, class C, group 6, member A	ENST00000310357.3
Case#1-Baseline-WholeTumor	RFX6	6	117198493	Missense_Mutation	C	G	p.Q19E	37	31	0.838	1.283	1	1	0	42	regulatory factor X, 6	ENST00000332958.2
Case#1-Baseline-WholeTumor	PTPRK	6	128303984	Missense_Mutation	C	T	p.E1176K	65	49	0.754	1.155	1	1	0	130	protein tyrosine phosphatase, receptor type, K	ENST00000368215.3
Case#1-Baseline-WholeTumor	PDE7B	6	136508200	Missense_Mutation	G	A	p.E358K	28	17	0.607	0.930	1	1	0	44	phosphodiesterase 7B	ENST00000308191.6
Case#1-Baseline-WholeTumor	ADGB	6	147085186	Missense_Mutation	GA	TT	p.E1234L	36	28	0.778	1.191	1	1	0	79	androglobin	ENST00000397944.3
Case#1-Baseline-WholeTumor	SYNE1	6	152804270	Missense_Mutation	C	T	p.V434I	68	44	0.647	0.991	1	1	0	145	spectrin repeat containing, nuclear envelope 1	ENST00000367255.5
Case#1-Baseline-WholeTumor	FNDC1	6	159653652	Missense_Mutation	C	T	p.S703L	44	23	0.523	0.801	1	1	0	48	fibronectin type III domain containing 1	ENST00000297267.9
Case#1-Baseline-WholeTumor	DACT2	6	168709607	Missense_Mutation	C	T	p.S277N	84	57	0.679	1.039	1	1	0	98	dishevelled-binding antagonist of beta-catenin 2	ENST00000366795.3
Case#1-Baseline-WholeTumor	CARD11	7	2979559	Missense_Mutation	C	T	p.D230N	97	27	0.278	0.328	3	2	1	94	caspase recruitment domain family, member 11	ENST00000396946.4
Case#1-Baseline-WholeTumor	SDK1	7	4259755	Missense_Mutation	G	A	p.V1852M	118	42	0.356	0.419	3	2	1	60	sidekick cell adhesion molecule 1	ENST00000404826.2
Case#1-Baseline-WholeTumor	CYTH3	7	6210478	Missense_Mutation	GG	AA	p.P232S	97	49	0.505	0.595	3	2	1	60	cytohesin 3	ENST00000350796.3
Case#1-Baseline-WholeTumor	COL28A1	7	7421173	Splice_Site	A	G		103	60	0.583	0.686	3	2	1	68	collagen, type XXVIII, alpha 1	ENST00000399429.3
Case#1-Baseline-WholeTumor	AHR	7	17382668	Missense_Mutation	A	T	p.T843S	137	80	0.584	0.687	3	2	1	93	aryl hydrocarbon receptor	ENST00000242057.4
Case#1-Baseline-WholeTumor	MACC1	7	20197852	Missense_Mutation	C	T	p.R711K	35	24	0.686	0.807	3	2	1	39	metastasis associated in colon cancer 1	ENST00000400331.5
Case#1-Baseline-WholeTumor	ABCB5	7	20682869	Missense_Mutation	C	T	p.S126F	221	59	0.267	0.314	3	2	1	235	ATP-binding cassette, sub-family B (MDR/TAP), member 5	ENST00000404938.2
Case#1-Baseline-WholeTumor	RAPGEF5	7	22348019	Missense_Mutation	C	T	p.G207S	73	43	0.589	0.693	3	2	1	47	Rap guanine nucleotide exchange factor (GEF) 5	ENST00000405243.1
Case#1-Baseline-WholeTumor	STK31	7	23871758	Missense_Mutation	G	A	p.D945N	46	31	0.674	0.793	3	2	1	54	serine/threonine kinase 31	ENST00000355870.3
Case#1-Baseline-WholeTumor	MPP6	7	24690197	Missense_Mutation	G	A	p.D173N	153	80	0.523	0.616	3	2	1	139	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	ENST00000222644.5
Case#1-Baseline-WholeTumor	NPSR1	7	34698136	Missense_Mutation	G	A	p.G38R	93	26	0.280	0.329	3	2	1	120	neuropeptide S receptor 1	ENST00000360581.1
Case#1-Baseline-WholeTumor	HECW1	7	43485112	Missense_Mutation	G	A	p.E781K	158	89	0.563	0.663	3	2	1	73	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1	ENST00000395891.2
Case#1-Baseline-WholeTumor	ABCA13	7	48259088	Missense_Mutation	G	A	p.R142Q	132	40	0.303	0.357	3	2	1	90	ATP-binding cassette, sub-family A (ABC1), member 13	ENST00000435803.1
Case#1-Baseline-WholeTumor	FIGNL1	7	50513407	Nonsense_Mutation	G	A	p.Q527*	64	11	0.172	0.202	3	2	1	82	fidgetin-like 1	ENST00000419119.1
Case#1-Baseline-WholeTumor	AUTS2	7	70255135	Missense_Mutation	CC	TT	p.S978F	13	8	0.615	0.724	3	2	1	14	autism susceptibility candidate 2	ENST00000342771.4
Case#1-Baseline-WholeTumor	VPS37D	7	73083819	Missense_Mutation	C	T	p.A70V	162	41	0.253	0.298	3	2	1	87	vacuolar protein sorting 37 homolog D (S. cerevisiae)	ENST00000324941.4
Case#1-Baseline-WholeTumor	PCLO	7	82582784	Missense_Mutation	AG	GA	p.S2495F	105	59	0.562	0.661	3	2	1	119	piccolo presynaptic cytomatrix protein	ENST00000333891.9
Case#1-Baseline-WholeTumor	PCLO	7	82583857	Missense_Mutation	T	C	p.T2138A	33	20	0.606	0.713	3	2	1	27	piccolo presynaptic cytomatrix protein	ENST00000333891.9
Case#1-Baseline-WholeTumor	SEMA3E	7	83035288	Missense_Mutation	C	T	p.G301R	93	51	0.548	0.646	3	2	1	90	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	ENST00000307792.3
Case#1-Baseline-WholeTumor	ZNF804B	7	88965621	Missense_Mutation	C	T	p.H1109Y	57	31	0.544	0.640	3	2	1	45	zinc finger protein 804B	ENST00000333190.4
Case#1-Baseline-WholeTumor	SAMD9	7	92731345	Missense_Mutation	C	T	p.E1356K	64	41	0.641	0.754	3	2	1	48	sterile alpha motif domain containing 9	ENST00000379958.2
Case#1-Baseline-WholeTumor	SAMD9	7	92734411	Missense_Mutation	C	T	p.E334K	60	35	0.583	0.687	3	2	1	56	sterile alpha motif domain containing 9	ENST00000379958.2
Case#1-Baseline-WholeTumor	CCDC132	7	92887505	Missense_Mutation	GC	AG	p.A153S	117	74	0.632	0.745	3	2	1	80	coiled-coil domain containing 132	ENST00000305866.5
Case#1-Baseline-WholeTumor	CALCR	7	93055859	Nonsense_Mutation	G	A	p.Q412*	141	35	0.248	0.292	3	2	1	82	calcitonin receptor	ENST00000394441.1
Case#1-Baseline-WholeTumor	PPP1R9A	7	94539496	Missense_Mutation	G	A	p.R24Q	95	13	0.137	0.161	3	2	1	86	protein phosphatase 1, regulatory subunit 9A	ENST00000433881.1
Case#1-Baseline-WholeTumor	PON1	7	94947634	Splice_Site	C	T		112	56	0.500	0.589	3	2	1	78	paraoxonase 1	ENST00000222381.3
Case#1-Baseline-WholeTumor	MYL10	7	101256829	Missense_Mutation	G	A	p.P203S	73	19	0.260	0.306	3	2	1	61	myosin, light chain 10, regulatory	ENST00000223167.4
Case#1-Baseline-WholeTumor	RELN	7	103185660	Missense_Mutation	C	T	p.G2145E	92	18	0.196	0.230	3	2	1	59	reelin	ENST00000428762.1
Case#1-Baseline-WholeTumor	KMT2E	7	104746993	Missense_Mutation	G	A	p.R874Q	104	17	0.163	0.192	3	2	1	62	lysine (K)-specific methyltransferase 2E	ENST00000311117.3
Case#1-Baseline-WholeTumor	ATXN7L1	7	105255069	Missense_Mutation	G	A	p.S571L	232	53	0.228	0.269	3	2	1	162	ataxin 7-like 1	ENST00000419735.3
Case#1-Baseline-WholeTumor	RNF133	7	122338165	Missense_Mutation	G	A	p.R270C	78	13	0.167	0.196	3	2	1	99	ring finger protein 133	ENST00000340112.2
Case#1-Baseline-WholeTumor	GRM8	7	126173610	Missense_Mutation	T	A	p.N609I	46	22	0.478	0.563	3	2	1	45	glutamate receptor, metabotropic 8	ENST00000339582.2
Case#1-Baseline-WholeTumor	FSCN3	7	127236471	Missense_Mutation	C	T	p.R311C	114	22	0.193	0.227	3	2	1	86	fascin actin-bundling protein 3, testicular	ENST00000265825.5
Case#1-Baseline-WholeTumor	PRRT4	7	127999744	Missense_Mutation	A	G	p.L101S	79	23	0.291	0.343	3	2	1	62	proline-rich transmembrane protein 4	ENST00000446477.2
Case#1-Baseline-WholeTumor	MKLN1	7	131130539	Missense_Mutation	C	T	p.R468C	75	47	0.627	0.738	3	2	1	62	muskelin 1, intracellular mediator containing kelch motifs	ENST00000352689.6
Case#1-Baseline-WholeTumor	CHRM2	7	136700756	Missense_Mutation	G	A	p.E382K	83	12	0.145	0.170	3	2	1	99	cholinergic receptor, muscarinic 2	ENST00000445907.2
Case#1-Baseline-WholeTumor	BRAF	7	140453136	Missense_Mutation	AC	TT	p.V600K	117	67	0.573	0.674	3	2	1	78	B-Raf proto-oncogene, serine/threonine kinase	ENST00000288602.6
Case#1-Baseline-WholeTumor	MGAM	7	141731583	Missense_Mutation	G	A	p.G525E	61	39	0.639	0.753	3	2	1	69	maltase-glucoamylase (alpha-glucosidase)	ENST00000549489.2
Case#1-Baseline-WholeTumor	MGAM	7	141755895	Splice_Site	G	A	p.M1193I	116	34	0.293	0.345	3	2	1	106	maltase-glucoamylase (alpha-glucosidase)	ENST00000549489.2
Case#1-Baseline-WholeTumor	MGAM	7	141765190	Missense_Mutation	C	T	p.P1514S	250	112	0.448	0.527	3	2	1	231	maltase-glucoamylase (alpha-glucosidase)	ENST00000549489.2
Case#1-Baseline-WholeTumor	RP11-1220K2.2	7	141837268	Missense_Mutation	C	T	p.R295C	80	52	0.650	0.765	3	2	1	74		ENST00000477922.3
Case#1-Baseline-WholeTumor	RP11-1220K2.2	7	141896372	Missense_Mutation	G	A	p.M1496I	110	55	0.500	0.589	3	2	1	96		ENST00000477922.3
Case#1-Baseline-WholeTumor	PRSS58	7	141954881	Missense_Mutation	C	T	p.D144N	95	61	0.642	0.756	3	2	1	76	protease, serine, 58	ENST00000552471.1
Case#1-Baseline-WholeTumor	EPHB6	7	142563271	Missense_Mutation	C	T	p.P330S	72	16	0.222	0.262	3	2	1	61	EPH receptor B6	ENST00000392957.2
Case#1-Baseline-WholeTumor	TRPV6	7	142571416	Missense_Mutation	C	T	p.D525N	105	61	0.581	0.684	3	2	1	126	transient receptor potential cation channel, subfamily V, member 6	ENST00000359396.3
Case#1-Baseline-WholeTumor	C7orf34	7	142636842	Missense_Mutation	C	T	p.P67S	86	22	0.256	0.301	3	2	1	52	chromosome 7 open reading frame 34	ENST00000409607.3
Case#1-Baseline-WholeTumor	ZYX	7	143080204	Missense_Mutation	C	T	p.P271L	121	23	0.190	0.224	3	2	1	88	zyxin	ENST00000322764.5
Case#1-Baseline-WholeTumor	AGAP3	7	150817198	Missense_Mutation	G	A	p.R137Q	99	58	0.586	0.690	3	2	1	63	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3	ENST00000463381.1

Case#1-Baseline-WholeTumor	KMT2C	7	152012392	Nonsense_Mutation	C	A	p.E141*	114	74	0.649	0.764	3	2	1	76	lysine (K)-specific methyltransferase 2C	ENST00000262189.6
Case#1-Baseline-WholeTumor	PTPRN2	7	157691406	Missense_Mutation	C	T	p.E583K	112	57	0.509	0.599	3	2	1	99	protein tyrosine phosphatase, receptor type, N polypeptide 2	ENST00000389418.4
Case#1-Baseline-WholeTumor	ERICH1	8	565233	Missense_Mutation	C	T	p.G343E	80	29	0.363	0.459	2	1	1	137	glutamate-rich 1	ENST00000522706.1
Case#1-Baseline-WholeTumor	CSMD1	8	3443759	Missense_Mutation	G	A	p.S375L	50	23	0.460	0.582	2	1	1	53	CUB and Sushi multiple domains 1	ENST00000520002.1
Case#1-Baseline-WholeTumor	CSMD1	8	3611472	Missense_Mutation	C	T	p.G304E	93	35	0.376	0.476	2	1	1	115	CUB and Sushi multiple domains 1	ENST00000520002.1
Case#1-Baseline-WholeTumor	CSMD1	8	4495009	Missense_Mutation	G	A	p.P53S	89	42	0.472	0.597	2	1	1	85	CUB and Sushi multiple domains 1	ENST00000520002.1
Case#1-Baseline-WholeTumor	RP1L1	8	10468628	Missense_Mutation	G	A	p.P994S	20	4	0.200	0.253	2	1	1	21	retinitis pigmentosa 1-like 1	ENST00000382483.3
Case#1-Baseline-WholeTumor	RP1L1	8	10470500	Missense_Mutation	C	T	p.E370K	37	11	0.297	0.376	2	1	1	30	retinitis pigmentosa 1-like 1	ENST00000382483.3
Case#1-Baseline-WholeTumor	PINX1	8	10692188	Nonsense_Mutation	C	T	p.W39*	71	27	0.380	0.481	2	1	1	86	PIN2/TERF1 interacting, telomerase inhibitor 1	ENST00000314787.3
Case#1-Baseline-WholeTumor	XKR6	8	10756097	Missense_Mutation	A	G	p.F431L	92	39	0.424	0.537	2	1	1	150	XK, Kell blood group complex subunit-related family, member 6	ENST00000416569.2
Case#1-Baseline-WholeTumor	HR	8	21984943	Missense_Mutation	G	A	p.L338F	85	29	0.341	0.432	2	1	1	58	hair growth associated	ENST00000381418.4
Case#1-Baseline-WholeTumor	PIWIL2	8	22147376	Missense_Mutation	G	A	p.D335N	118	41	0.347	0.440	2	1	1	139	piwi-like RNA-mediated gene silencing 2	ENST00000454009.2
Case#1-Baseline-WholeTumor	CCAR2	8	22475911	Missense_Mutation	C	T	p.A708V	95	31	0.326	0.413	2	1	1	108	cell cycle and apoptosis regulator 2	ENST00000308511.4
Case#1-Baseline-WholeTumor	RHOBTB2	8	22864490	Missense_Mutation	GG	AA	p.V245M	23	8	0.348	0.440	2	1	1	32	Rho-related BTB domain containing 2	ENST00000251822.6
Case#1-Baseline-WholeTumor	LOXL2	8	23185913	Missense_Mutation	C	T	p.G378S	48	20	0.417	0.527	2	1	1	50	lysyl oxidase-like 2	ENST00000389131.3
Case#1-Baseline-WholeTumor	ADAM7	8	24323251	Missense_Mutation	G	A	p.D118N	48	19	0.396	0.501	2	1	1	71	ADAM metallopeptidase domain 7	ENST00000175238.6
Case#1-Baseline-WholeTumor	DOCK5	8	25159955	Missense_Mutation	C	T	p.P321S	90	38	0.422	0.534	2	1	1	82	dedicator of cytokinesis 5	ENST00000276440.7
Case#1-Baseline-WholeTumor	EBF2	8	25720235	Missense_Mutation	C	T	p.R363K	87	37	0.425	0.538	2	1	1	110	early B-cell factor 2	ENST00000520164.1
Case#1-Baseline-WholeTumor	MBOAT4	8	29989645	Missense_Mutation	C	T	p.M374I	31	12	0.387	0.490	2	1	1	39	membrane bound O-acyltransferase domain containing 4	ENST00000320542.3
Case#1-Baseline-WholeTumor	C8orf86	8	38369913	Missense_Mutation	C	T	p.E222K	62	24	0.387	0.490	2	1	1	78	chromosome 8 open reading frame 86	ENST00000358138.1
Case#1-Baseline-WholeTumor	ADAM18	8	39495126	Missense_Mutation	C	T	p.S244F	104	44	0.423	0.536	2	1	1	127	ADAM metallopeptidase domain 18	ENST00000265707.5
Case#1-Baseline-WholeTumor	IDO2	8	39845422	Missense_Mutation	G	A	p.G161E	93	38	0.409	0.517	2	1	1	120	indoleamine 2,3-dioxygenase 2	ENST00000389060.4
Case#1-Baseline-WholeTumor	IDO2	8	39847249	Nonsense_Mutation	C	T	p.Q187*	75	27	0.360	0.456	2	1	1	71	indoleamine 2,3-dioxygenase 2	ENST00000389060.4
Case#1-Baseline-WholeTumor	C8orf4	8	40011065	Missense_Mutation	G	A	p.R5Q	59	19	0.322	0.408	2	1	1	86	chromosome 8 open reading frame 4	ENST00000315792.3
Case#1-Baseline-WholeTumor	KAT6A	8	41791491	Missense_Mutation	G	A	p.P1416L	33	14	0.424	0.537	2	1	1	34	K(lysine) acetyltransferase 6A	ENST00000396930.3
Case#1-Baseline-WholeTumor	PLAG1	8	57079775	Missense_Mutation	G	A	p.S177F	94	26	0.277	0.326	3	2	1	100	pleiomorphic adenoma gene 1	ENST00000316981.3
Case#1-Baseline-WholeTumor	CHD7	8	61655631	Frame_Shift_Del	C	-	p.T547fs	58	19	0.328	0.386	3	2	1	60	chromodomain helicase DNA binding protein 7	ENST00000423902.2
Case#1-Baseline-WholeTumor	PREX2	8	68956771	Missense_Mutation	C	T	p.R297C	135	30	0.222	0.262	3	2	1	119	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2	ENST00000288368.4
Case#1-Baseline-WholeTumor	PREX2	8	69011995	Missense_Mutation	C	T	p.P878S	33	11	0.333	0.392	3	2	1	41	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2	ENST00000288368.4
Case#1-Baseline-WholeTumor	PREX2	8	69104673	Missense_Mutation	C	T	p.S1506F	63	17	0.270	0.318	3	2	1	66	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2	ENST00000288368.4
Case#1-Baseline-WholeTumor	PRDM14	8	70978523	Missense_Mutation	G	A	p.P377L	53	23	0.434	0.511	3	2	1	36	PR domain containing 14	ENST00000276594.2
Case#1-Baseline-WholeTumor	SBSPON	8	73993418	Missense_Mutation	G	A	p.P82L	56	31	0.554	0.652	3	2	1	77	somatomedin B and thrombospondin, type 1 domain containing	ENST00000297354.6
Case#1-Baseline-WholeTumor	ZFHX4	8	77619801	Missense_Mutation	G	A	p.E871K	49	17	0.347	0.408	3	2	1	66	zinc finger homeobox 4	ENST00000521891.2
Case#1-Baseline-WholeTumor	ZFHX4	8	77766277	Missense_Mutation	A	G	p.K2374E	45	11	0.244	0.288	3	2	1	41	zinc finger homeobox 4	ENST00000521891.2
Case#1-Baseline-WholeTumor	ZFHX4	8	77768230	Missense_Mutation	C	T	p.H3025Y	65	35	0.538	0.634	3	2	1	75	zinc finger homeobox 4	ENST00000521891.2
Case#1-Baseline-WholeTumor	PMP2	8	82359603	Missense_Mutation	C	T	p.G7S	95	27	0.284	0.335	3	2	1	58	peripheral myelin protein 2	ENST00000256103.2
Case#1-Baseline-WholeTumor	CNGB3	8	87683207	Missense_Mutation	C	T	p.G153E	114	27	0.237	0.279	3	2	1	95	cyclic nucleotide gated channel beta 3	ENST00000320005.5
Case#1-Baseline-WholeTumor	DECR1	8	91049114	Missense_Mutation	C	T	p.S204L	81	45	0.556	0.654	3	2	1	77	2,4-dienoyl CoA reductase 1, mitochondrial	ENST00000220764.2
Case#1-Baseline-WholeTumor	RUNX1T1	8	93026848	Missense_Mutation	C	T	p.E143K	146	38	0.260	0.306	3	2	1	33	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	ENST00000523629.1
Case#1-Baseline-WholeTumor	VPS13B	8	100286557	Missense_Mutation	C	T	p.P883S	111	35	0.315	0.371	3	2	1	111	vacuolar protein sorting 13 homolog B (yeast)	ENST00000358544.2
Case#1-Baseline-WholeTumor	C8orf56	8	104145509	Missense_Mutation	G	A	p.P22S	89	22	0.247	0.291	3	2	1	61		ENST00000436771.1
Case#1-Baseline-WholeTumor	RIMS2	8	105263362	Missense_Mutation	G	A	p.E1286K	100	32	0.320	0.377	3	2	1	83	regulating synaptic membrane exocytosis 2	ENST00000436393.2
Case#1-Baseline-WholeTumor	PKHD1L1	8	110477181	Missense_Mutation	C	T	p.A2707V	124	40	0.323	0.380	3	2	1	128	polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1	ENST00000378402.5
Case#1-Baseline-WholeTumor	KCNV1	8	110980535	Missense_Mutation	C	T	p.D429N	101	33	0.327	0.385	3	2	1	82	potassium channel, subfamily V, member 1	ENST00000524391.1
Case#1-Baseline-WholeTumor	CSMD3	8	113421156	Missense_Mutation	G	A	p.S1834F	76	48	0.632	0.744	3	2	1	59	CUB and Sushi multiple domains 3	ENST00000297405.5
Case#1-Baseline-WholeTumor	CSMD3	8	113599347	Missense_Mutation	C	T	p.G1278E	176	102	0.580	0.682	3	2	1	172	CUB and Sushi multiple domains 3	ENST00000297405.5
Case#1-Baseline-WholeTumor	SNTB1	8	121706062	Missense_Mutation	G	A	p.P220S	150	51	0.340	0.400	3	2	1	126	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	ENST00000395601.3
Case#1-Baseline-WholeTumor	FER1L6	8	125131868	Missense_Mutation	C	T	p.S1804L	133	37	0.278	0.327	3	2	1	130	fer-1-like family member 6	ENST00000522917.1
Case#1-Baseline-WholeTumor	NDUFB9	8	125555473	Missense_Mutation	C	T	p.P83S	139	70	0.504	0.593	3	2	1	94	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa	ENST00000276689.3
Case#1-Baseline-WholeTumor	GSDMC	8	130760796	Missense_Mutation	G	A	p.S493F	45	25	0.556	0.654	3	2	1	34	gasdermin C	ENST00000276708.4
Case#1-Baseline-WholeTumor	ADCY8	8	131949386	Missense_Mutation	G	A	p.P472S	123	46	0.374	0.440	3	2	1	93	adenylate cyclase 8 (brain)	ENST00000286355.5
Case#1-Baseline-WholeTumor	GPR20	8	142367729	Missense_Mutation	C	T	p.D99N	242	56	0.231	0.272	3	2	1	142	G protein-coupled receptor 20	ENST00000377741.3
Case#1-Baseline-WholeTumor	RFX3	9	3266260	Missense_Mutation	C	T	p.G468D	41	16	0.390	0.494	2	1	1	69	regulatory factor X, 3 (influences HLA class II expression)	ENST00000382004.3
Case#1-Baseline-WholeTumor	FREM1	9	14792882	Splice_Site	C	T	p.K1280K	31	9	0.290	0.367	2	1	1	33	FRAS1 related extracellular matrix 1	ENST00000380880.3
Case#1-Baseline-WholeTumor	FREM1	9	14805118	Missense_Mutation	G	A	p.H1103Y	66	30	0.455	0.575	2	1	1	102	FRAS1 related extracellular matrix 1	ENST00000380880.3
Case#1-Baseline-WholeTumor	IFNA10	9	21206889	Nonsense_Mutation	G	A	p.Q70*	205	73	0.356	0.451	2	1	1	331	interferon, alpha 10	ENST00000357374.2
Case#1-Baseline-WholeTumor	AQP3	9	33442091	Missense_Mutation	C	T	p.E277K	37	9	0.243	0.308	2	1	1	32	aquaporin 3 (Gill blood group)	ENST00000297991.4
Case#1-Baseline-WholeTumor	PRSS3	9	33796734	Missense_Mutation	C	T	p.S102F	172	58	0.337	0.427	2	1	1	168	protease, serine, 3	ENST00000361005.5
Case#1-Baseline-WholeTumor	UBAP1	9	34251519	Missense_Mutation	G	A	p.G500R	27	9	0.333	0.422	2	1	1	38	ubiquitin associated protein 1	ENST00000297661.4
Case#1-Baseline-WholeTumor	DNAJB5	9	34996535	Missense_Mutation	C	T	p.P162L	51	16	0.314	0.397	2	1	1	59	DnaJ (Hsp40) homolog, subfamily B, member 5	ENST00000541010.1
Case#1-Baseline-WholeTumor	RUSC2	9	35555066	Missense_Mutation	C	T	p.T675I	66	28	0.424	0.537	2	1	1	44	RUN and SH3 domain containing 2	ENST00000455600.1
Case#1-Baseline-WholeTumor	TPM2	9	35689195	Missense_Mutation	G	A	p.S63F	75	31	0.413	0.523	2	1	1	89	tropomyosin 2 (beta)	ENST00000360958.2
Case#1-Baseline-WholeTumor	CR769776.1	9	69380339	Missense_Mutation	G	A	p.S31L	556	30	0.054	0.068	2	1	1	472		ENST00000414341.2
Case#1-Baseline-WholeTumor	PRUNE2	9	79244209	Splice_Site	A	-		24	7	0.292	0.369	2	1	1	23	prune homolog 2 (Drosophila)	ENST00000376718.3
Case#1-Baseline-WholeTumor	PRUNE2	9	79324306	Missense_Mutation	G	A	p.P962S	47	17	0.362	0.458	2	1	1	93	prune homolog 2 (Drosophila)	ENST00000376718.3
Case#1-Baseline-WholeTumor	PRUNE2	9	79324742	Nonsense_Mutation	C	T	p.W816*	64	29	0.453	0.574	2	1	1	77	prune homolog 2 (Drosophila)	ENST00000376718.3
Case#1-Baseline-WholeTumor	VPS13A	9	79968418	Missense_Mutation	C	T	p.P2505S	75	28	0.373	0.473	2	1	1	60	vacuolar protein sorting 13 homolog A (S. cerevisiae)	ENST00000360280.3
Case#1-Baseline-WholeTumor	SPATA31D1	9	84605355	Nonsense_Mutation	C	T	p.Q86*	89	44	0.494	0.626	2	1	1	121	SPATA31 subfamily D, member 1	ENST00000344803.2
Case#1-Baseline-WholeTumor	SPATA31D1	9	84606542	Missense_Mutation	C	T	p.S386F	62	20	0.323	0.408	2	1	1	112	SPATA31 subfamily D, member 1	ENST00000344803.2
Case#1-Baseline-WholeTumor	SPATA31D1	9	84607427	Missense_Mutation	C	T	p.S681F	119	50	0.420	0.532	2	1	1	170	SPATA31 subfamily D, member 1	ENST00000344803.2
Case#1-Baseline-WholeTumor	SPATA31D1	9	84607702	Nonsense_Mutation	C	T	p.Q773*	119	43	0.361	0.457	2	1	1	165	SPATA31 subfamily D, member 1	ENST00000344803.2
Case#1-Baseline-WholeTumor	SPATA31D1	9	84609831	Nonsense_Mutation	CC	AT	p.Q1483*	30	10	0.333	0.422	2	1	1	50	SPATA31 subfamily D, member 1	ENST00000344803.2
Case#1-Baseline-WholeTumor	ROR2	9	94519791	Missense_Mutation	C	T	p.G76S	85	41	0.482	0.611	2	2	0	99	receptor tyrosine kinase-like orphan receptor 2	ENST00000375708.3
Case#1-Baseline-WholeTumor	NOL8	9	95078125	Missense_Mutation	G	A	p.S261F	55	47	0.855	1.082	2	2	0	69	nucleolar protein 8	ENST00000535387.1
Case#1-Baseline-WholeTumor	OR13C5	9	107361140	Missense_Mutation	C	T	p.M185I	97	40	0.412	0.522	2	2	0	125	olfactory receptor, family 13, subfamily C, member 5	ENST00000374779.2
Case#1-Baseline-WholeTumor	ZNF462	9	109701335	Missense_Mutation	C	T	p.S2125F	59	18	0.305	0.386	2	2	0	75	zinc finger protein 462	ENST00000277225.5
Case#1-Baseline-WholeTumor	EPB41L4B	9	111970274	Missense_Mutation	G	A	p.P603L	73	26	0.356	0.451	2	2	0	91	erythrocyte membrane protein band 4.1 like 4B	ENST00000374566.3
Case#1-Baseline-WholeTumor	C9orf84	9	114476724	Splice_Site	C	A		93	28	0.301	0.381	2	2	0	119	chromosome 9 open reading frame 84	ENST00000318737.4
Case#1-Baseline-WholeTumor	WDR31	9	116079120	Missense_Mutation	G	A	p.S338F	77	31	0.403	0.510	2	2	0	101	WD repeat domain 31	ENST00000374193.4

Case#1-Baseline-WholeTumor	AMBP	9	116840393	Missense_Mutation	C	T	p.E33K	148	60	0.405	0.513	2	2	0	121	alpha-1-microglobulin/bikunin precursor	ENST00000265132.3
Case#1-Baseline-WholeTumor	COL27A1	9	117063995	Missense_Mutation	C	T	p.P1615S	59	30	0.508	0.644	2	2	0	78	collagen, type XXVII, alpha 1	ENST00000356083.3
Case#1-Baseline-WholeTumor	AKNA	9	117099465	Missense_Mutation	C	T	p.E1397K	94	34	0.362	0.458	2	2	0	53	AT-hook transcription factor	ENST00000307564.4
Case#1-Baseline-WholeTumor	TNFSF8	9	117668179	Splice_Site	C	T	p.G80E	73	25	0.342	0.434	2	2	0	74	tumor necrosis factor (ligand) superfamily, member 8	ENST00000223795.2
Case#1-Baseline-WholeTumor	PAPPA	9	118997855	Missense_Mutation	G	A	p.D891N	74	24	0.324	0.411	2	2	0	101	pregnancy-associated plasma protein A, pappalysin 1	ENST00000328252.3
Case#1-Baseline-WholeTumor	ASTN2	9	119770412	Missense_Mutation	C	T	p.R517K	78	32	0.410	0.519	2	2	0	106	astrotactin 2	ENST00000313400.4
Case#1-Baseline-WholeTumor	CRB2	9	126135412	Splice_Site	G	T		102	38	0.373	0.472	2	2	0	84	crumbs family member 2	ENST00000373631.3
Case#1-Baseline-WholeTumor	FAM102A	9	130710478	Missense_Mutation	G	A	p.S163F	128	49	0.383	0.485	2	2	0	105	family with sequence similarity 102, member A	ENST00000373095.1
Case#1-Baseline-WholeTumor	FAM73B	9	131804656	Missense_Mutation	C	T	p.A57V	67	31	0.463	0.586	2	2	0	55	family with sequence similarity 73, member B	ENST00000358369.4
Case#1-Baseline-WholeTumor	GPR107	9	132869775	Splice_Site	G	A	p.W421*	41	11	0.268	0.340	2	2	0	42	G protein-coupled receptor 107	ENST00000372406.1
Case#1-Baseline-WholeTumor	MED22	9	136208432	Missense_Mutation	G	A	p.P176S	39	33	0.846	1.071	2	2	0	23	mediator complex subunit 22	ENST00000491289.1
Case#1-Baseline-WholeTumor	SARDH	9	136536738	Missense_Mutation	G	A	p.R749W	123	36	0.293	0.370	2	2	0	88	sarcosine dehydrogenase	ENST00000371872.4
Case#1-Baseline-WholeTumor	COL5A1	9	137693800	Splice_Site	G	A	p.G985S	85	50	0.588	0.745	2	2	0	90	collagen, type V, alpha 1	ENST00000371817.3
Case#1-Baseline-WholeTumor	C9orf62	9	138236023	Missense_Mutation	G	A	p.G77R	60	20	0.333	0.422	2	2	0	67	chromosome 9 open reading frame 62	ENST00000320778.2
Case#1-Baseline-WholeTumor	PMPCA	9	139311617	Missense_Mutation	C	T	p.A283V	105	43	0.410	0.518	2	2	0	71	peptidase (mitochondrial processing) alpha	ENST00000371717.3
Case#1-Baseline-WholeTumor	LCN15	9	139658209	Missense_Mutation	G	A	p.A88V	49	40	0.816	1.033	2	2	0	52	lipocalin 15	ENST00000316144.5
Case#1-Baseline-WholeTumor	KIAA1984	9	139694569	Missense_Mutation	A	C	p.D129A	10	10	1.000	1.266	2	2	0	10		ENST00000338005.6
Case#1-Baseline-WholeTumor	ABCA2	9	139915386	Missense_Mutation	G	A	p.A341V	27	10	0.370	0.469	2	2	0	11	ATP-binding cassette, sub-family A (ABC1), member 2	ENST00000371605.3
Case#1-Baseline-WholeTumor	ABCA2	9	139916431	Missense_Mutation	G	A	p.P196L	106	39	0.368	0.466	2	2	0	91	ATP-binding cassette, sub-family A (ABC1), member 2	ENST00000371605.3
Case#1-Baseline-WholeTumor	KAL1	X	8553349	Missense_Mutation	C	T	p.R272Q	46	35	0.761	0.963	2	1	1	56	Kallmann syndrome 1 sequence	ENST00000262648.3
Case#1-Baseline-WholeTumor	FAM9A	X	8763346	Frame_Shift_Del	CTG	-	p.Q202fs	32	6	0.188	0.237	2	1	1	32	family with sequence similarity 9, member A	ENST00000543214.1
Case#1-Baseline-WholeTumor	WWC3	X	10093137	Missense_Mutation	G	A	p.E634K	94	24	0.255	0.323	2	1	1	45	WWC family member 3	ENST00000380861.4
Case#1-Baseline-WholeTumor	MBTPS2	X	21863393	Missense_Mutation	C	T	p.P110L	36	32	0.889	1.125	2	1	1	41	membrane-bound transcription factor peptidase, site 2	ENST00000379484.5
Case#1-Baseline-WholeTumor	MAGEB6	X	26212568	Missense_Mutation	T	C	p.L202S	47	35	0.745	0.943	2	1	1	63	melanoma antigen family B, 6	ENST00000379034.1
Case#1-Baseline-WholeTumor	DCAF8L2	X	27765397	Missense_Mutation	G	A	p.E129K	21	12	0.571	0.723	2	1	1	39	DDB1 and CUL4 associated factor 8-like 2	ENST00000451261.2
Case#1-Baseline-WholeTumor	DCAF8L1	X	27999214	Missense_Mutation	C	T	p.E80K	64	37	0.578	0.732	2	1	1	95	DDB1 and CUL4 associated factor 8-like 1	ENST00000441525.1
Case#1-Baseline-WholeTumor	MAGEB2	X	30237541	Missense_Mutation	G	A	p.E282K	53	46	0.868	1.099	2	1	1	77	melanoma antigen family B, 2	ENST00000378988.4
Case#1-Baseline-WholeTumor	FAM47A	X	34149036	Missense_Mutation	C	T	p.E454K	60	45	0.750	0.949	2	1	1	61	family with sequence similarity 47, member A	ENST00000346193.3
Case#1-Baseline-WholeTumor	CXorf22	X	35984681	Splice_Site	G	A		19	11	0.579	0.733	2	1	1	27	chromosome X open reading frame 22	ENST00000297866.5
Case#1-Baseline-WholeTumor	CXorf30	X	36337365	Missense_Mutation	G	A	p.D242N	27	25	0.926	1.172	2	1	1	25	chromosome X open reading frame 30	ENST00000378657.4
Case#1-Baseline-WholeTumor	USP9X	X	41048592	Frame_Shift_Ins	-	ACGA	p.-1282fs	64	46	0.719	0.910	2	1	1	65	ubiquitin specific peptidase 9, X-linked	ENST00000324545.8
Case#1-Baseline-WholeTumor	USP9X	X	41075197	Missense_Mutation	C	T	p.L1793F	78	61	0.782	0.990	2	1	1	93	ubiquitin specific peptidase 9, X-linked	ENST00000324545.8
Case#1-Baseline-WholeTumor	DDX3X	X	41205773	Missense_Mutation	C	G	p.L505V	58	46	0.793	1.004	2	1	1	79	DEAD (Asp-Glu-Ala-Asp) box helicase 3, X-linked	ENST00000399959.2
Case#1-Baseline-WholeTumor	CACNA1F	X	49067877	Missense_Mutation	G	A	p.P1400S	18	17	0.944	1.195	2	1	1	35	calcium channel, voltage-dependent, L type, alpha 1F subunit	ENST00000376265.2
Case#1-Baseline-WholeTumor	CCNB3	X	50051581	Missense_Mutation	G	A	p.D138N	50	42	0.840	1.063	2	1	1	51	cyclin B3	ENST00000376042.1
Case#1-Baseline-WholeTumor	KIAA2022	X	73960373	Missense_Mutation	G	A	p.P1340L	16	14	0.875	1.108	2	1	1	22	KIAA2022	ENST00000055682.6
Case#1-Baseline-WholeTumor	KIAA2022	X	73961246	Missense_Mutation	G	A	p.S1049F	34	18	0.529	0.670	2	1	1	61	KIAA2022	ENST00000055682.6
Case#1-Baseline-WholeTumor	CYSLTR1	X	77529237	Missense_Mutation	C	T	p.E3K	17	10	0.588	0.745	2	1	1	21	cysteinyl leukotriene receptor 1	ENST00000373304.3
Case#1-Baseline-WholeTumor	PCDH19	X	99551514	Missense_Mutation	GG	AA	p.H1070Y	26	17	0.654	0.828	2	1	1	22	protocadherin 19	ENST00000373034.4
Case#1-Baseline-WholeTumor	NRK	X	105132299	Missense_Mutation	G	A	p.D89N	29	25	0.862	1.091	2	1	1	31	Nik related kinase	ENST00000243300.9
Case#1-Baseline-WholeTumor	CAPN6	X	110497543	Missense_Mutation	G	A	p.S85F	47	37	0.787	0.996	2	1	1	60	calpain 6	ENST00000324068.1
Case#1-Baseline-WholeTumor	LRCH2	X	114358531	Missense_Mutation	G	A	p.P609L	26	21	0.808	1.022	2	1	1	53	leucine-rich repeats and calponin homology (CH) domain containing 2	ENST00000317135.8
Case#1-Baseline-WholeTumor	TENM1	X	123838976	Missense_Mutation	G	A	p.S301F	34	29	0.853	1.080	2	1	1	78	teneurin transmembrane protein 1	ENST00000371130.3
Case#1-Baseline-WholeTumor	ARHGAP36	X	130220631	Missense_Mutation	C	T	p.S493F	47	38	0.809	1.023	2	1	1	55	Rho GTPase activating protein 36	ENST00000276211.5
Case#1-Baseline-WholeTumor	GPR112	X	135431303	Missense_Mutation	C	T	p.S1813F	35	20	0.571	0.723	2	1	1	52	G protein-coupled receptor 112	ENST00000394143.1
Case#1-Baseline-WholeTumor	F9	X	138643980	Missense_Mutation	G	A	p.R379Q	23	16	0.696	0.881	2	1	1	30	coagulation factor IX	ENST00000218099.2
Case#1-Baseline-WholeTumor	BGN	X	152772308	Missense_Mutation	G	A	p.E233K	24	22	0.917	1.160	2	1	1	32	biglycan	ENST00000331595.4
Case#1-Baseline-WholeTumor	PDZD4	X	153071546	Frame_Shift_Del	CA	-	p.*177fs	52	40	0.769	0.974	2	1	1	72	PDZ domain containing 4	ENST00000164640.4
Case#1-Baseline-WholeTumor	SLC9B1P1	Y	13501691	Missense_Mutation	G	A	p.S173L	44	38	0.864	1.093	2	1	1	67	solute carrier family 9, subfamily B (NHA1, cation proton antiporter 1), member 1 pseudogene 1	ENST00000331172.6
Case#4-Baseline-WholeTumor	NADK	1	1686040	Missense_Mutation	G	T	p.N262K	57	7	0.123	0.133	3	2	1	84	NAD kinase	ENST00000341426.5
Case#4-Baseline-WholeTumor	TTC34	1	2704099	Missense_Mutation	C	T	p.A88T	43	5	0.116	0.131	2	2	0	49	tetratricopeptide repeat domain 34	ENST00000401095.3
Case#4-Baseline-WholeTumor	MTOR	1	11190667	Missense_Mutation	GG	AA	p.T1844I	117	68	0.581	0.629	3	2	1	136	mechanistic target of rapamycin (serine/threonine kinase)	ENST00000361445.4
Case#4-Baseline-WholeTumor	PRAMEF15	1	13645819	Missense_Mutation	G	A	p.V117I	345	93	0.270	0.292	3	2	1	482	PRAME family member 15	ENST00000330087.5
Case#4-Baseline-WholeTumor	LRRC38	1	13839611	Missense_Mutation	T	C	p.N160D	73	40	0.548	0.593	3	2	1	88	leucine rich repeat containing 38	ENST00000376085.3
Case#4-Baseline-WholeTumor	PADI2	1	17413045	Missense_Mutation	G	A	p.H269Y	64	37	0.578	0.626	3	2	1	88	peptidyl arginine deiminase, type II	ENST00000375486.4
Case#4-Baseline-WholeTumor	KLHDC7A	1	18808983	Missense_Mutation	A	T	p.E503V	47	12	0.255	0.276	3	2	1	47	kelch domain containing 7A	ENST00000400664.1
Case#4-Baseline-WholeTumor	TMCO2	1	40717118	Missense_Mutation	A	G	p.K134R	30	7	0.233	0.253	3	2	1	41	transmembrane and coiled-coil domains 2	ENST00000372766.3
Case#4-Baseline-WholeTumor	CCDC30	1	43032087	Nonsense_Mutation	C	T	p.R266*	47	11	0.234	0.253	3	2	1	58	coiled-coil domain containing 30	ENST00000340612.4
Case#4-Baseline-WholeTumor	LDLRAD1	1	54480008	Missense_Mutation	G	A	p.R35C	30	12	0.400	0.433	3	2	1	28	low density lipoprotein receptor class A domain containing 1	ENST00000371360.1
Case#4-Baseline-WholeTumor	LEPR	1	66101926	Missense_Mutation	G	A	p.G909D	103	39	0.379	0.410	3	2	1	144	leptin receptor	ENST00000349533.6
Case#4-Baseline-WholeTumor	C1orf173	1	75038204	Missense_Mutation	C	T	p.E1064K	139	86	0.619	0.670	3	2	1	153		ENST00000326665.5
Case#4-Baseline-WholeTumor	C1orf173	1	75055582	Missense_Mutation	C	T	p.E637K	100	66	0.660	0.714	3	2	1	118		ENST00000326665.5
Case#4-Baseline-WholeTumor	LPHN2	1	82434986	Missense_Mutation	G	A	p.R879Q	125	36	0.288	0.312	3	2	1	136	latrophilin 2	ENST00000370728.1
Case#4-Baseline-WholeTumor	RPF1	1	84956083	Missense_Mutation	A	G	p.K182E	97	56	0.577	0.625	3	2	1	110	ribosome production factor 1 homolog (S. cerevisiae)	ENST00000370654.5
Case#4-Baseline-WholeTumor	PRPF38B	1	109242103	Missense_Mutation	C	T	p.R368C	71	21	0.296	0.320	3	2	1	69	pre-mRNA processing factor 38B	ENST00000370025.4
Case#4-Baseline-WholeTumor	DENND2D	1	111734940	Splice_Site	C	T		45	15	0.333	0.361	3	2	1	39	DENN/MADD domain containing 2D	ENST00000357640.4
Case#4-Baseline-WholeTumor	SYCP1	1	115417165	Missense_Mutation	G	A	p.D213N	79	45	0.570	0.617	3	2	1	106	synaptonemal complex protein 1	ENST00000369522.3
Case#4-Baseline-WholeTumor	VPS72	1	151149374	Missense_Mutation	C	T	p.G292R	61	29	0.475	0.505	4	2	2	50	vacuolar protein sorting 72 homolog (S. cerevisiae)	ENST00000354473.4
Case#4-Baseline-WholeTumor	ZNF687	1	151261061	Missense_Mutation	C	T	p.R725C	172	82	0.477	0.506	4	2	2	169	zinc finger protein 687	ENST00000368879.2
Case#4-Baseline-WholeTumor	KPRP	1	152733503	Missense_Mutation	C	T	p.P480L	61	15	0.246	0.261	4	2	2	50	keratinocyte proline-rich protein	ENST00000606109.1
Case#4-Baseline-WholeTumor	ADAM15	1	155029553	Missense_Mutation	C	T	p.T375I	109	57	0.523	0.555	4	2	2	101	ADAM metallopeptidase domain 15	ENST00000356955.2
Case#4-Baseline-WholeTumor	CRP	1	159683802	Missense_Mutation	G	A	p.S63L	80	37	0.463	0.491	4	2	2	63	C-reactive protein, pentraxin-related	ENST00000255030.5
Case#4-Baseline-WholeTumor	MAEL	1	166973432	Missense_Mutation	A	G	p.K180R	150	33	0.220	0.234	4	2	2	134	maelstrom spermatogenic transposon silencer	ENST00000367872.4
Case#4-Baseline-WholeTumor	F5	1	169511368	Missense_Mutation	G	A	p.P987L	112	46	0.411	0.436	4	2	2	111	coagulation factor V (proaccelerin, labile factor)	ENST00000367797.3
Case#4-Baseline-WholeTumor	FMO3	1	171086425	Missense_Mutation	G	A	p.G481E	106	54	0.509	0.541	4	2	2	91	flavin containing monooxygenase 3	ENST00000367755.4
Case#4-Baseline-WholeTumor	PRRC2C	1	171544097	Missense_Mutation	C	T	p.S2260F	69	28	0.406	0.431	4	2	2	67	proline-rich coiled-coil 2C	ENST00000338920.4
Case#4-Baseline-WholeTumor	BRINP3	1	190068089	Missense_Mutation	G	A	p.P454S	139	60	0.432	0.458	4	2	2	100	bone morphogenetic protein/retinoic acid inducible neural-specific 3	ENST00000367462.3
Case#4-Baseline-WholeTumor	PPFIA4	1	203008264	Missense_Mutation	C	T	p.S43F	123	58	0.472	0.501	4	2	2	100	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4	ENST00000447715.2
Case#4-Baseline-WholeTumor	MYBPH	1	203144538	Missense_Mutation	G	A	p.S86F	92	16	0.174	0.185	4	2	2	73	myosin binding protein H	ENST00000255416.4
Case#4-Baseline-WholeTumor	CNTN2	1	205034965	Missense_Mutation	G	A	p.G582R	79	21	0.266	0.282	4	2	2	66	contactin 2 (axonal)	ENST00000331830.4
Case#4-Baseline-WholeTumor	USH2A	1	215901656	Missense_Mutation	C	T	p.E3928K	99	49	0.495	0.526	4	2	2	72	Usher syndrome 2A (autosomal recessive, mild)	ENST00000307340.3

Case#4-Baseline-WholeTumor	USH2A	1	216017763	Missense_Mutation	G	A	p.S3044L	77	34	0.442	0.469	4	2	2	76	Usher syndrome 2A (autosomal recessive, mild)	ENST00000307340.3
Case#4-Baseline-WholeTumor	PCNXL2	1	233137282	Splice_Site	CC	TT	p.D1700N	54	10	0.185	0.197	4	2	2	49	pecanex-like 2 (Drosophila)	ENST00000258229.9
Case#4-Baseline-WholeTumor	PCNXL2	1	233160921	Nonsense_Mutation	G	A	p.R1526*	180	74	0.411	0.437	4	2	2	142	pecanex-like 2 (Drosophila)	ENST00000258229.9
Case#4-Baseline-WholeTumor	TBCE	1	235611744	Missense_Mutation	G	A	p.E494K	167	77	0.461	0.490	4	2	2	166	tubulin folding cofactor E	ENST00000366601.3
Case#4-Baseline-WholeTumor	LYST	1	235972935	Missense_Mutation	G	A	p.R395C	77	35	0.455	0.483	4	2	2	75	lysosomal trafficking regulator	ENST00000389794.3
Case#4-Baseline-WholeTumor	LGALS8	1	236700836	Missense_Mutation	C	T	p.P29S	181	83	0.459	0.487	4	2	2	173	lectin, galactoside-binding, soluble, 8	ENST00000366584.4
Case#4-Baseline-WholeTumor	OR1C1	1	247921002	Missense_Mutation	C	T	p.R236K	110	56	0.509	0.541	4	2	2	85	olfactory receptor, family 1, subfamily C, member 1	ENST00000408896.2
Case#4-Baseline-WholeTumor	OR2L3	1	248224011	Missense_Mutation	G	A	p.D10N	385	172	0.447	0.474	4	2	2	391	olfactory receptor, family 2, subfamily L, member 3	ENST00000359959.3
Case#4-Baseline-WholeTumor	UPF2	10	12041915	Missense_Mutation	A	G	p.L583P	115	38	0.330	0.358	3	2	1	115	UPF2 regulator of nonsense transcripts homolog (yeast)	ENST00000356352.2
Case#4-Baseline-WholeTumor	CACNB2	10	18827189	Nonsense_Mutation	G	A	p.W461*	118	35	0.297	0.321	3	2	1	105	calcium channel, voltage-dependent, beta 2 subunit	ENST00000324631.7
Case#4-Baseline-WholeTumor	PLXDC2	10	20506484	Missense_Mutation	C	T	p.P418S	48	26	0.542	0.586	3	2	1	71	plexin domain containing 2	ENST00000377252.4
Case#4-Baseline-WholeTumor	NEBL	10	21120508	Missense_Mutation	T	A	p.D485V	48	14	0.292	0.316	3	2	1	74	nebulette	ENST00000377122.4
Case#4-Baseline-WholeTumor	NEBL	10	21158766	Missense_Mutation	G	A	p.S162F	86	25	0.291	0.315	3	2	1	98	nebulette	ENST00000377122.4
Case#4-Baseline-WholeTumor	PTCHD3	10	27703109	Missense_Mutation	G	A	p.A24V	80	51	0.638	0.690	3	2	1	70	patched domain containing 3	ENST00000438700.3
Case#4-Baseline-WholeTumor	SVIL	10	29769741	Splice_Site	T	G	p.E1701A	65	4	0.062	0.067	3	2	1	68	supervillin	ENST00000355867.4
Case#4-Baseline-WholeTumor	WDFY4	10	50098714	Missense_Mutation	G	A	p.E2420K	118	78	0.661	0.715	3	2	1	122	WDFY family member 4	ENST00000325239.5
Case#4-Baseline-WholeTumor	C10orf71	10	50534837	Missense_Mutation	C	T	p.P1416L	57	11	0.193	0.209	3	2	1	35	chromosome 10 open reading frame 71	ENST00000374144.3
Case#4-Baseline-WholeTumor	ADAMTS14	10	72513650	Missense_Mutation	G	A	p.G942R	68	38	0.559	0.605	3	2	1	47	ADAM metallopeptidase with thrombospondin type 1 motif, 14	ENST00000373207.1
Case#4-Baseline-WholeTumor	ZMIZ1	10	81050867	Missense_Mutation	A	G	p.Q231R	36	23	0.639	0.692	3	2	1	52	zinc finger, MIZ-type containing 1	ENST00000334512.5
Case#4-Baseline-WholeTumor	NUTM2B	10	81463478	Missense_Mutation	G	A	p.G38E	555	127	0.229	0.248	3	2	1	692	NUT family member 2B	ENST00000429828.1
Case#4-Baseline-WholeTumor	PLCE1	10	95790940	Missense_Mutation	G	A	p.R46Q	44	17	0.386	0.418	3	2	1	54	phospholipase C, epsilon 1	ENST00000371380.3
Case#4-Baseline-WholeTumor	FGF8	10	103534967	Missense_Mutation	G	A	p.P26S	12	4	0.333	0.361	3	2	1	16	fibroblast growth factor 8 (androgen-induced)	ENST00000344255.3
Case#4-Baseline-WholeTumor	FAM160B1	10	116606884	Missense_Mutation	C	T	p.S535L	76	24	0.316	0.342	3	2	1	96	family with sequence similarity 160, member B1	ENST00000369248.4
Case#4-Baseline-WholeTumor	DMBT1	10	124352006	Missense_Mutation	G	A	p.D799N	390	125	0.321	0.347	3	2	1	441	deleted in malignant brain tumors 1	ENST00000338354.3
Case#4-Baseline-WholeTumor	NAP1L4	11	2981039	Missense_Mutation	G	A	p.P236L	150	38	0.253	0.274	3	2	1	172	nucleosome assembly protein 1-like 4	ENST00000380542.4
Case#4-Baseline-WholeTumor	OR52A1	11	5173208	Missense_Mutation	G	A	p.P131L	65	23	0.354	0.383	3	2	1	75	olfactory receptor, family 52, subfamily A, member 1	ENST00000380367.1
Case#4-Baseline-WholeTumor	OTOG	11	17667291	Splice_Site	G	A	p.V2860M	55	24	0.436	0.472	3	2	1	55	otogelin	ENST00000399391.2
Case#4-Baseline-WholeTumor	LDHAL6A	11	18487261	Missense_Mutation	G	A	p.D108N	134	88	0.657	0.711	3	2	1	184	lactate dehydrogenase A-like 6A	ENST00000280706.2
Case#4-Baseline-WholeTumor	QSER1	11	32956744	Missense_Mutation	C	T	p.R1185C	93	25	0.269	0.291	3	2	1	102	glutamine and serine rich 1	ENST00000399302.2
Case#4-Baseline-WholeTumor	OR8K3	11	56086143	Missense_Mutation	G	A	p.D121N	116	70	0.603	0.653	3	2	1	141	olfactory receptor, family 8, subfamily K, member 3	ENST00000312711.1
Case#4-Baseline-WholeTumor	SLC22A9	11	63177274	Splice_Site	G	A	p.E534E	41	12	0.293	0.317	3	2	1	59	solute carrier family 22 (organic anion transporter), member 9	ENST00000279178.3
Case#4-Baseline-WholeTumor	CHKA	11	67821505	Frame_Shift_Del	G	-	p.Q442fs	67	20	0.299	0.323	3	2	1	66	choline kinase alpha	ENST00000265689.4
Case#4-Baseline-WholeTumor	CHKA	11	67821509	Missense_Mutation	GT	AA	p.Y440F	60	20	0.333	0.361	3	2	1	68	choline kinase alpha	ENST00000265689.4
Case#4-Baseline-WholeTumor	SHANK2	11	70333333	Missense_Mutation	C	T	p.S643N	96	52	0.542	0.586	3	2	1	83	SH3 and multiple ankyrin repeat domains 2	ENST00000423696.2
Case#4-Baseline-WholeTumor	NUMA1	11	71732302	Missense_Mutation	G	T	p.D136E	125	39	0.312	0.338	3	2	1	131	nuclear mitotic apparatus protein 1	ENST00000393695.3
Case#4-Baseline-WholeTumor	TENM4	11	78467872	Missense_Mutation	C	T	p.G912R	104	24	0.231	0.250	3	2	1	90	teneurin transmembrane protein 4	ENST00000278550.7
Case#4-Baseline-WholeTumor	SYTL2	11	85432002	Splice_Site	C	T	p.G487D	49	13	0.265	0.287	3	2	1	61	synaptotagmin-like 2	ENST00000528231.1
Case#4-Baseline-WholeTumor	MFRP	11	119215694	Missense_Mutation	G	A	p.P221L	26	15	0.577	0.648	2	1	1	42	membrane frizzled-related protein	ENST00000530681.1
Case#4-Baseline-WholeTumor	OR8B4	11	124294532	Missense_Mutation	G	A	p.P79L	68	33	0.485	0.545	2	1	1	104	olfactory receptor, family 8, subfamily B, member 4	ENST00000356130.3
Case#4-Baseline-WholeTumor	CACNA1C	12	2224470	Missense_Mutation	C	T	p.P44S	24	14	0.583	0.631	3	2	1	42	calcium channel, voltage-dependent, L type, alpha 1C subunit	ENST00000347598.4
Case#4-Baseline-WholeTumor	FGF23	12	4479934	Missense_Mutation	C	T	p.E111K	55	36	0.655	0.708	3	2	1	54	fibroblast growth factor 23	ENST00000237837.1
Case#4-Baseline-WholeTumor	COPS7A	12	6838423	Missense_Mutation	A	T	p.Y113F	75	51	0.680	0.736	3	2	1	123	COP9 signalosome subunit 7A	ENST00000543155.1
Case#4-Baseline-WholeTumor	PZP	12	9312946	Missense_Mutation	C	T	p.E1005K	111	40	0.360	0.390	3	2	1	144	pregnancy-zone protein	ENST00000261336.2
Case#4-Baseline-WholeTumor	KCNJ8	12	21919327	Missense_Mutation	C	T	p.R202Q	123	69	0.561	0.607	3	2	1	180	potassium inwardly-rectifying channel, subfamily J, member 8	ENST00000240662.2
Case#4-Baseline-WholeTumor	OR8S1	12	48921750	Missense_Mutation	C	T	p.A315V	79	21	0.266	0.288	3	2	1	84	olfactory receptor, family 8, subfamily S, member 1	ENST00000310194.1
Case#4-Baseline-WholeTumor	KRT2	12	53038873	Missense_Mutation	C	T	p.G617E	110	75	0.682	0.738	3	2	1	115	keratin 2	ENST00000309680.3
Case#4-Baseline-WholeTumor	TENC1	12	53448151	Missense_Mutation	G	A	p.D150N	30	9	0.300	0.325	3	2	1	47	tensin like C1 domain containing phosphatase (tensin 2)	ENST00000314250.6
Case#4-Baseline-WholeTumor	AMHR2	12	53818171	Missense_Mutation	C	T	p.P50L	59	40	0.678	0.734	3	2	1	75	anti-Mullerian hormone receptor, type II	ENST00000257863.4
Case#4-Baseline-WholeTumor	OR6C6	12	55688227	Missense_Mutation	C	T	p.E264K	151	47	0.311	0.337	3	2	1	184	olfactory receptor, family 6, subfamily C, member 6	ENST00000358433.2
Case#4-Baseline-WholeTumor	GLI1	12	57865324	Missense_Mutation	C	T	p.S934F	48	36	0.750	0.812	3	2	1	40	GLI family zinc finger 1	ENST00000228682.2
Case#4-Baseline-WholeTumor	TPH2	12	72338095	Missense_Mutation	C	T	p.H93Y	89	17	0.191	0.207	3	2	1	93	tryptophan hydroxylase 2	ENST00000333850.3
Case#4-Baseline-WholeTumor	RASSF9	12	86198686	Missense_Mutation	G	C	p.H368D	118	38	0.322	0.349	3	2	1	129	Ras association (RalGDS/AF-6) domain family (N-terminal) member 9	ENST00000361228.3
Case#4-Baseline-WholeTumor	C12orf50	12	88379663	Missense_Mutation	GG	AA	p.H364Y	188	47	0.250	0.271	3	2	1	230	chromosome 12 open reading frame 50	ENST00000298699.2
Case#4-Baseline-WholeTumor	NR2C1	12	95456418	Missense_Mutation	C	T	p.G51S	97	5	0.052	0.056	3	2	1	152	nuclear receptor subfamily 2, group C, member 1	ENST00000333003.5
Case#4-Baseline-WholeTumor	TCHP	12	110352340	Nonsense_Mutation	C	T	p.R410*	70	39	0.557	0.603	3	2	1	93	trichoplein, keratin filament binding	ENST00000312777.5
Case#4-Baseline-WholeTumor	SDS	12	113835043	Missense_Mutation	C	T	p.E194K	53	19	0.358	0.388	3	2	1	59	serine dehydratase	ENST00000257549.4
Case#4-Baseline-WholeTumor	CCDC60	12	119943001	Missense_Mutation	C	T	p.P259L	62	35	0.565	0.611	3	2	1	63	coiled-coil domain containing 60	ENST00000327554.2
Case#4-Baseline-WholeTumor	TMEM132C	12	129190442	Missense_Mutation	G	A	p.E977K	70	23	0.329	0.356	3	2	1	62	transmembrane protein 132C	ENST00000435159.2
Case#4-Baseline-WholeTumor	FLT1	13	28964230	Missense_Mutation	C	T	p.G558R	149	84	0.564	0.592	5	3	2	111	fms-related tyrosine kinase 1	ENST00000282397.4
Case#4-Baseline-WholeTumor	DAOA	13	106142269	Missense_Mutation	C	T	p.H101Y	199	25	0.126	0.132	5	3	2	107	D-amino acid oxidase activator	ENST00000375936.3
Case#4-Baseline-WholeTumor	F7	13	113773045	Missense_Mutation	G	A	p.R375Q	170	65	0.382	0.401	5	3	2	131	coagulation factor VII (serum prothrombin conversion accelerator)	ENST00000375581.3
Case#4-Baseline-WholeTumor	TFDP1	13	114288253	Missense_Mutation	G	C	p.V175L	194	66	0.340	0.357	5	3	2	135	transcription factor Dp-1	ENST00000375370.5
Case#4-Baseline-WholeTumor	OR4M1	14	20249212	Missense_Mutation	C	T	p.S244F	533	45	0.084	0.091	3	2	1	646	olfactory receptor, family 4, subfamily M, member 1	ENST00000315957.4
Case#4-Baseline-WholeTumor	OR4K15	14	20444431	Missense_Mutation	C	T	p.R252C	249	148	0.594	0.643	3	2	1	281	olfactory receptor, family 4, subfamily K, member 15	ENST00000305051.5
Case#4-Baseline-WholeTumor	KLHL33	14	20897784	Missense_Mutation	G	A	p.S309F	45	33	0.733	0.794	3	2	1	42	kelch-like family member 33	ENST00000344581.4
Case#4-Baseline-WholeTumor	CHD8	14	21876604	Missense_Mutation	G	A	p.A866V	43	12	0.279	0.302	3	2	1	65	chromodomain helicase DNA binding protein 8	ENST00000557364.1
Case#4-Baseline-WholeTumor	ADCK1	14	78392234	Missense_Mutation	G	C	p.C379S	98	29	0.296	0.320	3	2	1	120	aarF domain containing kinase 1	ENST00000238561.5
Case#4-Baseline-WholeTumor	CATSPERB	14	92139225	Missense_Mutation	G	A	p.L372F	97	28	0.289	0.312	3	2	1	98	catsper channel auxiliary subunit beta	ENST00000256343.3
Case#4-Baseline-WholeTumor	AHNAK2	14	105404695	Missense_Mutation	C	T	p.R5698Q	114	33	0.289	0.313	3	2	1	141	AHNAK nucleoprotein 2	ENST00000333244.5
Case#4-Baseline-WholeTumor	OR4M2	15	22369306	Missense_Mutation	C	T	p.S244F	754	143	0.190	0.201	4	2	2	725	olfactory receptor, family 4, subfamily M, member 2	ENST00000332663.2
Case#4-Baseline-WholeTumor	GOLGA8I	15	23260815	Missense_Mutation	C	T	p.S199F	371	80	0.216	0.229	4	2	2	315	golgin A8 family, member I	ENST00000450802.3
Case#4-Baseline-WholeTumor	NUTM1	15	34640641	Missense_Mutation	C	T	p.P163L	62	25	0.403	0.428	4	2	2	71	NUT midline carcinoma, family member 1	ENST00000333756.4
Case#4-Baseline-WholeTumor	EIF2AK4	15	40324409	Nonsense_Mutation	C	T	p.Q1567*	151	65	0.430	0.457	4	2	2	143	eukaryotic translation initiation factor 2 alpha kinase 4	ENST00000263791.5
Case#4-Baseline-WholeTumor	POLR2M	15	57999140	Missense_Mutation	C	T	p.L34F	84	36	0.429	0.455	4	2	2	72	polymerase (RNA) II (DNA directed) polypeptide M	ENST00000299638.3
Case#4-Baseline-WholeTumor	GRAMD2	15	72460887	Missense_Mutation	G	T	p.N71K	104	51	0.490	0.521	4	2	2	102	GRAM domain containing 2	ENST00000309731.7
Case#4-Baseline-WholeTumor	ADAMTSL3	15	84683394	Missense_Mutation	CC	TT	p.L1359F	211	93	0.441	0.468	4	2	2	186	ADAMTS-like 3	ENST00000286744.5
Case#4-Baseline-WholeTumor	TICRR	15	90152048	Nonsense_Mutation	C	T	p.R913*	78	41	0.526	0.558	4	2	2	90	TOPBP1-interacting checkpoint and replication regulator	ENST00000268138.7
Case#4-Baseline-WholeTumor	MCTP2	15	94901781	Missense_Mutation	G	A	p.G414D	234	103	0.440	0.467	4	2	2	211	multiple C2 domains, transmembrane 2	ENST00000357742.4
Case#4-Baseline-WholeTumor	USP7	16	8993559	Missense_Mutation	C	A	p.D789Y	133	63	0.474	0.503	4	2	2	105	ubiquitin specific peptidase 7 (herpes virus-associated)	ENST00000344836.4
Case#4-Baseline-WholeTumor	SMG1	16	18879649	Missense_Mutation	G	A	p.R1020C	591	214	0.362	0.384	4	3	1	521	SMG1 phosphatidylinositol 3-kinase-related kinase	ENST00000446231.2
Case#4-Baseline-WholeTumor	ITGAL	16	30486653	Missense_Mutation	G	A	p.G64E	55	30	0.545	0.579	4	2	2	43	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)	ENST00000356798.6
Case#4-Baseline-WholeTumor	SLC6A2	16	55733504	Missense_Mutation	G	A	p.G510R	243	115	0.473	0.502	4	2	2	232	solute carrier family 6 (neurotransmitter transporter), member 2	ENST00000379906.2

Case#4-Baseline-WholeTumor	CDH8	16	61687811	Missense_Mutation	T	G	p.K701Q	157	79	0.503	0.534	4	2	2	160	cadherin 8, type 2	ENST00000577390.1
Case#4-Baseline-WholeTumor	TSNAXIP1	16	67859956	Missense_Mutation	GG	AA	p.R320Q	94	43	0.457	0.486	4	2	2	65	translin-associated factor X interacting protein 1	ENST00000388833.3
Case#4-Baseline-WholeTumor	COG4	16	70515672	Missense_Mutation	T	C	p.N701D	129	58	0.450	0.477	4	2	2	92	component of oligomeric golgi complex 4	ENST00000323786.5
Case#4-Baseline-WholeTumor	HYDIN	16	70942713	Missense_Mutation	C	T	p.E2686K	77	31	0.403	0.427	4	2	2	81	HYDIN, axonemal central pair apparatus protein	ENST00000393567.2
Case#4-Baseline-WholeTumor	ZFHX3	16	72829347	Missense_Mutation	C	T	p.E2412K	205	91	0.444	0.471	4	2	2	236	zinc finger homeobox 3	ENST00000268489.5
Case#4-Baseline-WholeTumor	LDHD	16	75148750	Missense_Mutation	CC	TT	p.R148Q	123	52	0.423	0.449	4	2	2	81	lactate dehydrogenase D	ENST00000450168.2
Case#4-Baseline-WholeTumor	CNTNAP4	16	76483672	Missense_Mutation	C	T	p.H333Y	113	60	0.531	0.564	4	2	2	96	contactin associated protein-like 4	ENST00000476707.1
Case#4-Baseline-WholeTumor	CDH13	16	83711861	Missense_Mutation	G	A	p.E445K	115	49	0.426	0.452	4	2	2	108	cadherin 13	ENST00000566620.1
Case#4-Baseline-WholeTumor	OSGIN1	16	83994638	Missense_Mutation	C	T	p.P233L	53	19	0.358	0.381	4	2	2	51	oxidative stress induced growth inhibitor 1	ENST00000343939.2
Case#4-Baseline-WholeTumor	ATP2C2	16	84482262	Missense_Mutation	G	A	p.E543K	104	48	0.462	0.490	4	2	2	91	ATPase, Ca++ transporting, type 2C, member 2	ENST00000262429.4
Case#4-Baseline-WholeTumor	JPH3	16	87678017	Missense_Mutation	C	T	p.P179L	62	32	0.516	0.548	4	2	2	28	junctophilin 3	ENST00000284262.2
Case#4-Baseline-WholeTumor	RPL13	16	89628073	Missense_Mutation	G	A	p.A112T	80	7	0.088	0.093	4	2	2	72	ribosomal protein L13	ENST00000393099.3
Case#4-Baseline-WholeTumor	RTN4RL1	17	1841037	Missense_Mutation	G	A	p.R27W	73	5	0.068	0.074	3	2	1	61	reticulon 4 receptor-like 1	ENST00000331238.6
Case#4-Baseline-WholeTumor	RAP1GAP2	17	2898660	Missense_Mutation	G	A	p.G315E	149	48	0.322	0.349	3	2	1	196	RAP1 GTPase activating protein 2	ENST00000254695.8
Case#4-Baseline-WholeTumor	KIF1C	17	4904574	Missense_Mutation	A	G	p.M81V	54	33	0.611	0.661	3	2	1	64	kinesin family member 1C	ENST00000320785.5
Case#4-Baseline-WholeTumor	NLRP1	17	5487064	Missense_Mutation	G	A	p.H72Y	68	28	0.412	0.446	3	2	1	76	NLR family, pyrin domain containing 1	ENST00000572272.1
Case#4-Baseline-WholeTumor	PER1	17	8047180	Missense_Mutation	G	A	p.P826S	21	6	0.286	0.309	3	2	1	25	period circadian clock 1	ENST00000317276.4
Case#4-Baseline-WholeTumor	SHISA6	17	11461607	Missense_Mutation	G	A	p.E497K	23	8	0.348	0.376	3	2	1	29	shisa family member 6	ENST00000409168.3
Case#4-Baseline-WholeTumor	MYOCD	17	12649264	Missense_Mutation	C	T	p.P334S	90	52	0.578	0.625	3	2	1	124	myocardin	ENST00000343344.4
Case#4-Baseline-WholeTumor	MYO15A	17	18025233	Missense_Mutation	C	T	p.P1040L	90	53	0.589	0.637	3	2	1	94	myosin XVA	ENST00000205890.5
Case#4-Baseline-WholeTumor	CDRT15L2	17	20483109	Missense_Mutation	G	A	p.G18E	118	35	0.297	0.321	3	2	1	137	CMT1A duplicated region transcript 15-like 2	ENST00000399044.1
Case#4-Baseline-WholeTumor	TNFAIP1	17	26667468	Nonsense_Mutation	CC	TT	p.Q114*	62	35	0.565	0.611	3	2	1	109	tumor necrosis factor, alpha-induced protein 1 (endothelial)	ENST00000226225.2
Case#4-Baseline-WholeTumor	TAOK1	17	27822642	Missense_Mutation	A	T	p.D299V	99	40	0.404	0.437	3	2	1	133	TAO kinase 1	ENST00000261716.3
Case#4-Baseline-WholeTumor	GOSR1	17	28849280	Missense_Mutation	C	T	p.P213S	99	31	0.313	0.339	3	2	1	123	golgi SNAP receptor complex member 1	ENST00000225724.5
Case#4-Baseline-WholeTumor	ATAD5	17	29185321	Missense_Mutation	C	G	p.S979C	104	34	0.327	0.354	3	2	1	149	ATPase family, AAA domain containing 5	ENST00000321990.4
Case#4-Baseline-WholeTumor	KRTAP9-1	17	39346139	Splice_Site	A	G	p.M1V	149	9	0.060	0.065	3	2	1	188	keratin associated protein 9-1	ENST00000398470.1
Case#4-Baseline-WholeTumor	COL1A1	17	48264079	Missense_Mutation	G	A	p.R1246W	116	50	0.431	0.467	3	2	1	142	collagen, type I, alpha 1	ENST00000225964.5
Case#4-Baseline-WholeTumor	KIF2B	17	51900425	Missense_Mutation	C	T	p.P11S	84	30	0.357	0.387	3	2	1	95	kinesin family member 2B	ENST00000268919.4
Case#4-Baseline-WholeTumor	LPO	17	56329738	Missense_Mutation	C	T	p.P326S	56	36	0.643	0.696	3	2	1	68	lactoperoxidase	ENST00000262290.4
Case#4-Baseline-WholeTumor	ACE	17	61556450	Missense_Mutation	C	T	p.S167F	64	42	0.656	0.710	3	2	1	57	angiotensin I converting enzyme	ENST00000290866.4
Case#4-Baseline-WholeTumor	ACE	17	61584653	Missense_Mutation	G	A	p.G693E	78	16	0.205	0.222	3	2	1	90	angiotensin I converting enzyme	ENST00000577647.1
Case#4-Baseline-WholeTumor	FTSJ3	17	61902413	Missense_Mutation	G	A	p.P236S	61	36	0.590	0.639	3	2	1	110	FtsJ homolog 3 (E. coli)	ENST00000427159.2
Case#4-Baseline-WholeTumor	CD300E	17	72613262	Missense_Mutation	G	A	p.S128F	62	32	0.516	0.559	3	2	1	96	CD300e molecule	ENST00000328630.3
Case#4-Baseline-WholeTumor	ENTHD2	17	79207827	Missense_Mutation	GG	AA	p.P110F	45	25	0.556	0.601	3	2	1	75	ENTH domain containing 2	ENST00000300714.3
Case#4-Baseline-WholeTumor	EMILIN2	18	2891737	Missense_Mutation	G	A	p.E538K	67	14	0.209	0.226	3	2	1	68	elastin microfibril interfacer 2	ENST00000254528.3
Case#4-Baseline-WholeTumor	PIEZO2	18	10800407	Missense_Mutation	C	T	p.E436K	85	49	0.576	0.624	3	2	1	110	piezo-type mechanosensitive ion channel component 2	ENST00000503781.3
Case#4-Baseline-WholeTumor	NOL4	18	31709882	Missense_Mutation	C	T	p.G123R	42	24	0.571	0.619	3	2	1	36	nucleolar protein 4	ENST00000261592.5
Case#4-Baseline-WholeTumor	SETBP1	18	42531243	Missense_Mutation	G	A	p.M646I	25	13	0.520	0.563	3	2	1	25	SET binding protein 1	ENST00000282030.5
Case#4-Baseline-WholeTumor	PIAS2	18	44470629	Missense_Mutation	G	T	p.P138Q	104	25	0.240	0.260	3	2	1	108	protein inhibitor of activated STAT, 2	ENST00000585916.1
Case#4-Baseline-WholeTumor	DYM	18	46784814	Missense_Mutation	G	A	p.S434F	54	13	0.241	0.261	3	2	1	80	dymeclin	ENST00000269445.6
Case#4-Baseline-WholeTumor	MRO	18	48333099	Missense_Mutation	GT	AA	p.T74F	117	35	0.299	0.324	3	2	1	102	maestro	ENST00000428869.2
Case#4-Baseline-WholeTumor	CDH20	18	59167645	Missense_Mutation	G	A	p.D191N	122	67	0.549	0.594	3	2	1	142	cadherin 20, type 2	ENST00000262717.4
Case#4-Baseline-WholeTumor	STXBP2	19	7707710	Splice_Site	G	A		73	26	0.356	0.378	4	2	2	59	syntaxin binding protein 2	ENST00000221283.5
Case#4-Baseline-WholeTumor	COL5A3	19	10103734	Missense_Mutation	C	T	p.G587R	71	34	0.479	0.508	4	2	2	64	collagen, type V, alpha 3	ENST00000264828.3
Case#4-Baseline-WholeTumor	CD97	19	14507986	Nonsense_Mutation	G	A	p.W192*	218	94	0.431	0.458	4	2	2	207	CD97 molecule	ENST00000242786.5
Case#4-Baseline-WholeTumor	CALR3	19	16601198	Missense_Mutation	G	A	p.S126L	109	52	0.477	0.507	4	2	2	50	calreticulin 3	ENST00000269881.3
Case#4-Baseline-WholeTumor	SSBP4	19	18541675	Missense_Mutation	G	T	p.V102F	129	60	0.465	0.494	4	2	2	129	single stranded DNA binding protein 4	ENST00000270061.7
Case#4-Baseline-WholeTumor	SLC7A10	19	33700222	Missense_Mutation	C	T	p.R478K	69	33	0.478	0.508	4	2	2	56	solute carrier family 7 (neutral amino acid transporter light chain, asc system), member 10	ENST00000253188.4
Case#4-Baseline-WholeTumor	LGI4	19	35622939	Missense_Mutation	C	T	p.E108K	77	32	0.416	0.441	4	2	2	69	leucine-rich repeat LGI family, member 4	ENST00000310123.3
Case#4-Baseline-WholeTumor	CTD-2162K18.4	19	37266288	Splice_Site	G	T	p.G45V	108	29	0.269	0.285	4	2	2	112		ENST00000590750.1
Case#4-Baseline-WholeTumor	WDR87	19	38379375	Nonsense_Mutation	T	A	p.R1607*	201	55	0.274	0.296	3	2	1	211	WD repeat domain 87	ENST00000303868.5
Case#4-Baseline-WholeTumor	FCGBP	19	40419960	Missense_Mutation	C	T	p.D1012N	61	21	0.344	0.373	3	2	1	53	Fc fragment of IgG binding protein	ENST00000221347.6
Case#4-Baseline-WholeTumor	ZNF284	19	44586178	Missense_Mutation	C	T	p.S52F	114	49	0.430	0.465	3	2	1	157	zinc finger protein 284	ENST00000421176.3
Case#4-Baseline-WholeTumor	SLC8A2	19	47935658	Missense_Mutation	G	A	p.P719S	52	29	0.558	0.604	3	2	1	39	solute carrier family 8 (sodium/calcium exchanger), member 2	ENST00000236877.6
Case#4-Baseline-WholeTumor	PPP1R15A	19	49377424	Missense_Mutation	G	A	p.G312S	68	7	0.103	0.111	3	2	1	41	protein phosphatase 1, regulatory subunit 15A	ENST00000200453.5
Case#4-Baseline-WholeTumor	PPP1R15A	19	49377436	Missense_Mutation	G	C	p.A316P	77	8	0.104	0.112	3	2	1	41	protein phosphatase 1, regulatory subunit 15A	ENST00000200453.5
Case#4-Baseline-WholeTumor	NR1H2	19	50885729	Missense_Mutation	C	T	p.P418L	16	3	0.188	0.203	3	2	1	31	nuclear receptor subfamily 1, group H, member 2	ENST00000253727.5
Case#4-Baseline-WholeTumor	VN1R4	19	53770381	Missense_Mutation	G	T	p.R180S	372	77	0.207	0.224	3	2	1	352	vomeronasal 1 receptor 4	ENST00000311170.4
Case#4-Baseline-WholeTumor	LILRA4	19	54848929	Missense_Mutation	G	A	p.P232S	96	54	0.563	0.609	3	2	1	103	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 4	ENST00000291759.4
Case#4-Baseline-WholeTumor	PEG3	19	57327232	Missense_Mutation	C	T	p.E860K	85	34	0.400	0.433	3	2	1	96	paternally expressed 3	ENST00000326441.9
Case#4-Baseline-WholeTumor	SLC27A5	19	59010979	Missense_Mutation	T	G	p.E516A	77	31	0.403	0.436	3	2	1	92	solute carrier family 27 (fatty acid transporter), member 5	ENST00000263093.2
Case#4-Baseline-WholeTumor	KCNF1	2	11053119	Missense_Mutation	C	G	p.F189L	106	63	0.594	0.643	3	2	1	129	potassium voltage-gated channel, subfamily F, member 1	ENST00000295082.1
Case#4-Baseline-WholeTumor	C2orf44	2	24261224	Nonsense_Mutation	G	A	p.R381*	95	31	0.326	0.353	3	2	1	113	chromosome 2 open reading frame 44	ENST00000295148.4
Case#4-Baseline-WholeTumor	C2orf16	2	27800620	Missense_Mutation	G	A	p.G394E	63	16	0.254	0.275	3	2	1	92	chromosome 2 open reading frame 16	ENST00000408964.2
Case#4-Baseline-WholeTumor	XDH	2	31588406	Missense_Mutation	C	A	p.G821C	34	9	0.265	0.287	3	2	1	63	xanthine dehydrogenase	ENST00000379416.3
Case#4-Baseline-WholeTumor	LTBP1	2	33585726	Missense_Mutation	G	A	p.D1355N	53	43	0.811	0.878	3	2	1	81	latent transforming growth factor beta binding protein 1	ENST00000404816.2
Case#4-Baseline-WholeTumor	LTBP1	2	33589369	Missense_Mutation	C	T	p.P1496S	142	40	0.282	0.305	3	2	1	168	latent transforming growth factor beta binding protein 1	ENST00000404816.2
Case#4-Baseline-WholeTumor	GKN1	2	69201798	Missense_Mutation	C	T	p.R11C	116	39	0.336	0.364	3	2	1	161	gastrokine 1	ENST00000377938.2
Case#4-Baseline-WholeTumor	RETSAT	2	85571180	Missense_Mutation	G	A	p.S492F	156	51	0.327	0.354	3	2	1	173	retinol saturase (all-trans-retinol 13,14-reductase)	ENST00000295802.4
Case#4-Baseline-WholeTumor	RGPD2	2	88125212	Missense_Mutation	C	G	p.A13P	89	5	0.056	0.061	3	2	1	94	RANBP2-like and GRIP domain containing 2	ENST00000398146.3
Case#4-Baseline-WholeTumor	SNRNP200	2	96952860	Missense_Mutation	G	A	p.H1175Y	84	50	0.595	0.644	3	2	1	135	small nuclear ribonucleoprotein 200kDa (U5)	ENST00000323853.5
Case#4-Baseline-WholeTumor	SLC9A2	2	103299820	Missense_Mutation	G	A	p.V369I	126	79	0.627	0.679	3	2	1	116	solute carrier family 9, subfamily A (NHE2, cation proton antiporter 2), member 2	ENST00000233969.2
Case#4-Baseline-WholeTumor	FHL2	2	105990066	Missense_Mutation	G	A	p.S94F	127	30	0.236	0.256	3	2	1	131	four and a half LIM domains 2	ENST00000409807.1
Case#4-Baseline-WholeTumor	RGPD3	2	107041320	Missense_Mutation	C	T	p.D1035N	629	122	0.194	0.210	3	2	1	724	RANBP2-like and GRIP domain containing 3	ENST00000409886.3
Case#4-Baseline-WholeTumor	SLC5A7	2	108622595	Missense_Mutation	G	A	p.A278T	91	29	0.319	0.345	3	2	1	107	solute carrier family 5 (sodium/choline cotransporter), member 7	ENST00000264047.2
Case#4-Baseline-WholeTumor	RGPD8	2	113190990	Nonsense_Mutation	G	T	p.S14*	56	6	0.107	0.116	3	2	1	76	RANBP2-like and GRIP domain containing 8	ENST00000302558.3
Case#4-Baseline-WholeTumor	NT5DC4	2	113480696	Missense_Mutation	C	T	p.S163F	79	46	0.582	0.630	3	2	1	84	5'-nucleotidase domain containing 4	ENST00000327581.4
Case#4-Baseline-WholeTumor	MCM6	2	136609000	Missense_Mutation	G	A	p.A630V	72	24	0.333	0.361	3	2	1	105	minichromosome maintenance complex component 6	ENST00000264156.2
Case#4-Baseline-WholeTumor	LRP1B	2	141986902	Missense_Mutation	C	T	p.E234K	82	42	0.512	0.554	3	2	1	116	low density lipoprotein receptor-related protein 1B	ENST00000389484.3
Case#4-Baseline-WholeTumor	KCNJ3	2	155711406	Missense_Mutation	G	A	p.E363K	136	54	0.397	0.430	3	2	1	118	potassium inwardly-rectifying channel, subfamily J, member 3	ENST00000295101.2
Case#4-Baseline-WholeTumor	FASTKD1	2	170419831	Missense_Mutation	G	A	p.S159F	61	14	0.230	0.248	3	2	1	69	FAST kinase domains 1	ENST00000453153.2
Case#4-Baseline-WholeTumor	TTN	2	179413763	Missense_Mutation	C	T	p.D29223N	184	55	0.299	0.324	3	2	1	195	titin	ENST00000591111.1

Case#4-Baseline-WholeTumor	ZNF804A	2	185801210	Missense_Mutation	C	T	p.L363F	67	24	0.358	0.388	3	2	1	76	zinc finger protein 804A	ENST00000302277.6
Case#4-Baseline-WholeTumor	COL3A1	2	189849494	Missense_Mutation	G	A	p.G30R	88	55	0.625	0.676	3	2	1	104	collagen, type III, alpha 1	ENST00000304636.3
Case#4-Baseline-WholeTumor	COL5A2	2	189916185	Missense_Mutation	G	A	p.P931L	68	42	0.618	0.669	3	2	1	91	collagen, type V, alpha 2	ENST00000374866.3
Case#4-Baseline-WholeTumor	SLC39A10	2	196548592	Missense_Mutation	A	G	p.N393S	68	44	0.647	0.700	3	2	1	98	solute carrier family 39 (zinc transporter), member 10	ENST00000409086.3
Case#4-Baseline-WholeTumor	HECW2	2	197297876	Nonsense_Mutation	C	T	p.W91*	94	48	0.511	0.553	3	2	1	120	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	ENST00000260983.3
Case#4-Baseline-WholeTumor	SPATS2L	2	201342647	Missense_Mutation	C	T	p.R524W	109	64	0.587	0.636	3	2	1	111	spermatogenesis associated, serine-rich 2-like	ENST00000358677.5
Case#4-Baseline-WholeTumor	PTH2R	2	209309571	Missense_Mutation	C	T	p.S271L	136	8	0.059	0.064	3	2	1	145	parathyroid hormone 2 receptor	ENST00000272847.2
Case#4-Baseline-WholeTumor	ABCA12	2	215910594	Missense_Mutation	C	T	p.S280N	63	18	0.286	0.309	3	2	1	83	ATP-binding cassette, sub-family A (ABC1), member 12	ENST00000272895.7
Case#4-Baseline-WholeTumor	TNS1	2	218669225	Missense_Mutation	T	C	p.N1722S	68	7	0.103	0.111	3	2	1	80	tensin 1	ENST00000171887.4
Case#4-Baseline-WholeTumor	PLCD4	2	219486254	Missense_Mutation	G	C	p.E158Q	236	78	0.331	0.358	3	2	1	259	phospholipase C, delta 4	ENST00000450993.2
Case#4-Baseline-WholeTumor	COL4A3	2	228137815	Missense_Mutation	G	A	p.G637R	39	21	0.538	0.583	3	2	1	29	collagen, type IV, alpha 3 (Goodpasture antigen)	ENST00000396578.3
Case#4-Baseline-WholeTumor	SPHKAP	2	228882374	Missense_Mutation	G	A	p.R1066W	40	12	0.300	0.325	3	2	1	56	SPHK1 interactor, AKAP domain containing	ENST00000392056.3
Case#4-Baseline-WholeTumor	ALPP	2	233244930	Missense_Mutation	G	C	p.R231P	183	17	0.093	0.101	3	2	1	149	alkaline phosphatase, placental	ENST00000392027.2
Case#4-Baseline-WholeTumor	LRRFIP1	2	238668783	Missense_Mutation	A	G	p.Q275R	136	8	0.059	0.064	3	2	1	153	leucine rich repeat (in FLII) interacting protein 1	ENST00000392000.4
Case#4-Baseline-WholeTumor	SIRPG	20	1629760	Missense_Mutation	C	T	p.R123Q	407	179	0.440	0.476	3	2	1	406	signal-regulatory protein gamma	ENST00000303415.3
Case#4-Baseline-WholeTumor	PTPRA	20	2985771	Nonsense_Mutation	C	T	p.R261*	233	93	0.399	0.424	4	2	2	235	protein tyrosine phosphatase, receptor type, A	ENST00000216877.6
Case#4-Baseline-WholeTumor	PTPRT	20	41408885	Missense_Mutation	C	T	p.E181K	166	61	0.367	0.390	4	2	2	147	protein tyrosine phosphatase, receptor type, T	ENST00000373187.1
Case#4-Baseline-WholeTumor	WFDC12	20	43752816	Missense_Mutation	C	T	p.G57E	85	36	0.424	0.450	4	2	2	89	WAP four-disulfide core domain 12	ENST00000372785.3
Case#4-Baseline-WholeTumor	SLC12A5	20	44663604	Missense_Mutation	G	A	p.E47K	223	84	0.377	0.400	4	2	2	229	solute carrier family 12 (potassium/chloride transporter), member 5	ENST00000454036.2
Case#4-Baseline-WholeTumor	SULF2	20	46307419	Splice_Site	C	T		83	39	0.470	0.499	4	2	2	72	sulfatase 2	ENST00000359930.4
Case#4-Baseline-WholeTumor	CSE1L	20	47688977	Missense_Mutation	T	G	p.V308G	153	57	0.373	0.396	4	2	2	133	CSE1 chromosome segregation 1-like (yeast)	ENST00000262982.2
Case#4-Baseline-WholeTumor	TSHZ2	20	51872411	Missense_Mutation	C	T	p.A805V	95	50	0.526	0.559	4	2	2	70	teashirt zinc finger homeobox 2	ENST00000371497.5
Case#4-Baseline-WholeTumor	EDN3	20	57876722	Missense_Mutation	G	A	p.D104N	123	53	0.431	0.458	4	2	2	120	endothelin 3	ENST00000337938.2
Case#4-Baseline-WholeTumor	CDH26	20	58562571	Nonsense_Mutation	C	T	p.R301*	105	46	0.438	0.465	4	2	2	89	cadherin 26	ENST00000244047.5
Case#4-Baseline-WholeTumor	ZNF512B	20	62595699	Missense_Mutation	G	A	p.S436F	88	39	0.443	0.471	4	2	2	73	zinc finger protein 512B	ENST00000450537.1
Case#4-Baseline-WholeTumor	DOPEY2	21	37603196	Missense_Mutation	C	T	p.S705F	86	5	0.058	0.062	4	2	2	102	dopey family member 2	ENST00000399151.3
Case#4-Baseline-WholeTumor	TXNRD2	22	19907099	Missense_Mutation	C	A	p.A66S	103	8	0.078	0.082	4	2	2	73	thioredoxin reductase 2	ENST00000400521.1
Case#4-Baseline-WholeTumor	IL2RB	22	37524258	Missense_Mutation	G	A	p.P512S	70	31	0.443	0.470	4	2	2	54	interleukin 2 receptor, beta	ENST00000216223.5
Case#4-Baseline-WholeTumor	ITPR1	3	4725411	Missense_Mutation	G	A	p.V1128M	92	31	0.337	0.365	3	2	1	101	inositol 1,4,5-trisphosphate receptor, type 1	ENST00000443694.2
Case#4-Baseline-WholeTumor	GRM7	3	7456752	Missense_Mutation	G	A	p.R359K	107	41	0.383	0.415	3	2	1	132	glutamate receptor, metabotropic 7	ENST00000357716.4
Case#4-Baseline-WholeTumor	FANCD2OS	3	10146268	Missense_Mutation	A	G	p.L64P	186	12	0.065	0.070	3	2	1	191	FANCD2 opposite strand	ENST00000450660.2
Case#4-Baseline-WholeTumor	IRAK2	3	10251282	Missense_Mutation	C	T	p.P145L	41	8	0.195	0.211	3	2	1	43	interleukin-1 receptor-associated kinase 2	ENST00000256458.4
Case#4-Baseline-WholeTumor	RFTN1	3	16399542	Missense_Mutation	C	T	p.G348D	52	40	0.769	0.833	3	2	1	64	raftlin, lipid raft linker 1	ENST00000334133.4
Case#4-Baseline-WholeTumor	SCN5A	3	38674744	Missense_Mutation	C	T	p.E19K	64	37	0.578	0.626	3	2	1	80	sodium channel, voltage-gated, type V, alpha subunit	ENST00000333535.4
Case#4-Baseline-WholeTumor	SCN10A	3	38751016	Missense_Mutation	G	A	p.L1412F	119	77	0.647	0.700	3	2	1	155	sodium channel, voltage-gated, type X, alpha subunit	ENST00000449082.2
Case#4-Baseline-WholeTumor	SCN11A	3	38888372	Missense_Mutation	C	T	p.R1730K	236	129	0.547	0.592	3	2	1	304	sodium channel, voltage-gated, type XI, alpha subunit	ENST00000302328.3
Case#4-Baseline-WholeTumor	MYRIP	3	40291738	Missense_Mutation	C	T	p.S763L	96	35	0.365	0.395	3	2	1	118	myosin VIIA and Rab interacting protein	ENST00000302541.6
Case#4-Baseline-WholeTumor	FAM198A	3	43074665	Missense_Mutation	T	C	p.S304P	54	18	0.333	0.361	3	2	1	62	family with sequence similarity 198, member A	ENST00000430121.2
Case#4-Baseline-WholeTumor	FLNB	3	58118606	Missense_Mutation	G	A	p.E1488K	118	38	0.322	0.349	3	2	1	147	filamin B, beta	ENST00000295956.4
Case#4-Baseline-WholeTumor	FLNB	3	58133951	Missense_Mutation	C	T	p.S1916F	97	26	0.268	0.290	3	2	1	91	filamin B, beta	ENST00000295956.4
Case#4-Baseline-WholeTumor	UBA3	3	69120709	Missense_Mutation	A	C	p.N108K	84	22	0.262	0.283	3	2	1	73	ubiquitin-like modifier activating enzyme 3	ENST00000361055.4
Case#4-Baseline-WholeTumor	ROBO2	3	77571939	Missense_Mutation	G	A	p.D274N	64	19	0.297	0.321	3	2	1	87	roundabout, axon guidance receptor, homolog 2 (Drosophila)	ENST00000461745.1
Case#4-Baseline-WholeTumor	CD96	3	111319630	Missense_Mutation	C	G	p.S335C	71	24	0.338	0.366	3	2	1	73	CD96 molecule	ENST00000283285.5
Case#4-Baseline-WholeTumor	ZDHHC23	3	113673125	Missense_Mutation	A	G	p.K247R	69	4	0.058	0.063	3	2	1	88	zinc finger, DHHC-type containing 23	ENST00000330212.3
Case#4-Baseline-WholeTumor	DRD3	3	113858514	Missense_Mutation	G	A	p.P186S	59	34	0.576	0.624	3	2	1	54	dopamine receptor D3	ENST00000460779.1
Case#4-Baseline-WholeTumor	COL6A6	3	130289826	Missense_Mutation	G	A	p.D856N	91	59	0.648	0.702	3	2	1	100	collagen, type VI, alpha 6	ENST00000358511.6
Case#4-Baseline-WholeTumor	PRR23B	3	138739020	Missense_Mutation	C	T	p.E162K	76	50	0.658	0.712	3	2	1	74	proline rich 23B	ENST00000329447.5
Case#4-Baseline-WholeTumor	CLSTN2	3	140140069	Missense_Mutation	C	T	p.T247I	204	126	0.618	0.669	3	2	1	253	calsyntenin 2	ENST00000458420.3
Case#4-Baseline-WholeTumor	PLS1	3	142408605	Missense_Mutation	C	T	p.P376L	70	23	0.329	0.356	3	2	1	90	plastin 1	ENST00000337777.3
Case#4-Baseline-WholeTumor	MECOM	3	168834174	Missense_Mutation	G	A	p.P308S	141	41	0.291	0.315	3	2	1	165	MDS1 and EVI1 complex locus	ENST00000464456.1
Case#4-Baseline-WholeTumor	LRRIQ4	3	169540280	Missense_Mutation	G	A	p.E191K	95	32	0.337	0.365	3	2	1	121	leucine-rich repeats and IQ motif containing 4	ENST00000340806.6
Case#4-Baseline-WholeTumor	LIPH	3	185237097	Splice_Site	C	T	p.G240E	50	30	0.600	0.649	3	2	1	55	lipase, member H	ENST00000296252.4
Case#4-Baseline-WholeTumor	TP63	3	189585721	Missense_Mutation	G	A	p.E328K	90	27	0.300	0.325	3	2	1	105	tumor protein p63	ENST00000264731.3
Case#4-Baseline-WholeTumor	DLG1	3	196786775	Missense_Mutation	G	A	p.S834F	70	21	0.300	0.325	3	2	1	87	discs, large homolog 1 (Drosophila)	ENST00000419354.1
Case#4-Baseline-WholeTumor	ERVMER34-1	4	53610260	Nonsense_Mutation	CC	TT	p.W476*	171	97	0.567	0.602	4	2	2	49	endogenous retrovirus group MER34, member 1	ENST00000443173.1
Case#4-Baseline-WholeTumor	SULT1E1	4	70723251	Missense_Mutation	C	T	p.D38N	131	54	0.412	0.438	4	2	2	135	sulfotransferase family 1E, estrogen-preferring, member 1	ENST00000226444.3
Case#4-Baseline-WholeTumor	SDAD1	4	76877139	Nonsense_Mutation	G	A	p.R669*	191	81	0.424	0.450	4	2	2	175	SDA1 domain containing 1	ENST00000356260.5
Case#4-Baseline-WholeTumor	ADH7	4	100341946	Missense_Mutation	T	G	p.K202T	99	46	0.465	0.493	4	2	2	76	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	ENST00000209665.4
Case#4-Baseline-WholeTumor	DNAJB14	4	100827712	Nonsense_Mutation	G	A	p.R232*	128	56	0.438	0.465	4	2	2	139	DnaJ (Hsp40) homolog, subfamily B, member 14	ENST00000442697.2
Case#4-Baseline-WholeTumor	TET2	4	106197130	Missense_Mutation	T	G	p.D1821E	56	34	0.607	0.645	4	2	2	60	tet methylcytosine dioxygenase 2	ENST00000540549.1
Case#4-Baseline-WholeTumor	NDST4	4	115750954	Missense_Mutation	CC	TT	p.830_831MD>IN	78	31	0.397	0.422	4	2	2	90	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4	ENST00000264363.2
Case#4-Baseline-WholeTumor	NR3C2	4	149041348	Missense_Mutation	C	T	p.E868K	70	38	0.543	0.576	4	2	2	65	nuclear receptor subfamily 3, group C, member 2	ENST00000358102.3
Case#4-Baseline-WholeTumor	AADAT	4	170983060	Missense_Mutation	G	A	p.P407S	75	42	0.560	0.595	4	2	2	68	aminoadipate aminotransferase	ENST00000337664.4
Case#4-Baseline-WholeTumor	TENM3	4	183696244	Missense_Mutation	G	A	p.E1748K	105	50	0.476	0.506	4	2	2	78	teneurin transmembrane protein 3	ENST00000511685.1
Case#4-Baseline-WholeTumor	TENM3	4	183710475	Missense_Mutation	G	A	p.G1845E	154	68	0.442	0.469	4	2	2	136	teneurin transmembrane protein 3	ENST00000511685.1
Case#4-Baseline-WholeTumor	KIAA0947	5	5464375	Missense_Mutation	C	T	p.P1643L	70	26	0.371	0.402	3	2	1	71		ENST00000296564.7
Case#4-Baseline-WholeTumor	PRDM9	5	23526641	Missense_Mutation	G	A	p.G482R	145	85	0.586	0.635	3	2	1	179	PR domain containing 9	ENST00000296682.3
Case#4-Baseline-WholeTumor	NIPBL	5	37014813	Missense_Mutation	C	T	p.S1530F	32	7	0.219	0.237	3	2	1	51	Nipped-B homolog (Drosophila)	ENST00000282516.8
Case#4-Baseline-WholeTumor	DDX4	5	55077770	Missense_Mutation	G	A	p.D196N	101	31	0.307	0.332	3	2	1	139	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4	ENST00000505374.1
Case#4-Baseline-WholeTumor	ANKRA2	5	72858439	Missense_Mutation	C	T	p.V90M	87	59	0.678	0.734	3	2	1	114	ankyrin repeat, family A (RFXANK-like), 2	ENST00000296785.3
Case#4-Baseline-WholeTumor	IQGAP2	5	75866423	Nonsense_Mutation	C	T	p.R108*	199	122	0.613	0.664	3	2	1	236	IQ motif containing GTPase activating protein 2	ENST00000274364.6
Case#4-Baseline-WholeTumor	PCSK1	5	95729001	Missense_Mutation	C	T	p.D656N	116	40	0.345	0.373	3	2	1	136	proprotein convertase subtilisin/kexin type 1	ENST00000311106.3
Case#4-Baseline-WholeTumor	PCDHA10	5	140237666	Missense_Mutation	C	T	p.S678L	158	48	0.304	0.329	3	2	1	174	protocadherin alpha 10	ENST00000307360.5
Case#4-Baseline-WholeTumor	PCDHB5	5	140515210	Missense_Mutation	G	A	p.R65Q	48	30	0.625	0.676	3	2	1	53	protocadherin beta 5	ENST00000231134.5
Case#4-Baseline-WholeTumor	PCDHB6	5	140530818	Missense_Mutation	G	A	p.G327E	96	47	0.490	0.530	3	2	1	133	protocadherin beta 6	ENST00000231136.1
Case#4-Baseline-WholeTumor	PCDHGA10	5	140795122	Missense_Mutation	C	T	p.P794S	186	65	0.349	0.378	3	2	1	203	protocadherin gamma subfamily A, 10	ENST00000398610.2
Case#4-Baseline-WholeTumor	GABRP	5	170222377	Missense_Mutation	G	A	p.G136R	86	20	0.233	0.252	3	2	1	78	gamma-aminobutyric acid (GABA) A receptor, pi	ENST00000518525.1
Case#4-Baseline-WholeTumor	F13A1	6	6224978	Missense_Mutation	C	A	p.S305I	247	83	0.336	0.348	7	5	2	139	coagulation factor XIII, A1 polypeptide	ENST00000264870.3
Case#4-Baseline-WholeTumor	HIVEP1	6	12121325	Missense_Mutation	CC	TT	p.P433F	157	19	0.121	0.125	7	5	2	106	human immunodeficiency virus type I enhancer binding protein 1	ENST00000379388.2
Case#4-Baseline-WholeTumor	ANKS1A	6	34951202	Splice_Site	GG	AA	p.G338K	145	43	0.297	0.307	7	5	2	79	ankyrin repeat and sterile alpha motif domain containing 1A	ENST00000360359.3
Case#4-Baseline-WholeTumor	FAM83B	6	54735423	Missense_Mutation	C	T	p.P127S	115	30	0.261	0.270	7	5	2	52	family with sequence similarity 83, member B	ENST00000306858.7
Case#4-Baseline-WholeTumor	FAM83B	6	54806267	Missense_Mutation	C	G	p.S833C	134	23	0.172	0.178	7	5	2	90	family with sequence similarity 83, member B	ENST00000306858.7
Case#4-Baseline-WholeTumor	GFRAL	6	55196568	Nonsense_Mutation	T	G	p.Y26*	256	32	0.125	0.129	7	5	2	127	GDNF family receptor alpha like	ENST00000340465.2
Case#4-Baseline-WholeTumor	GFRAL	6	55198740	Missense_Mutation	C	T	p.S105L	190	121	0.637	0.659	7	5	2	107	GDNF family receptor alpha like	ENST00000340465.2

Case#4-Baseline-WholeTumor	DST	6	56422239	Missense_Mutation	G	T	p.Q4629K	338	195	0.577	0.597	7	5	2	198	dystonin	ENST00000361203.3
Case#4-Baseline-WholeTumor	PRIM2	6	57512471	Splice_Site	G	A		305	45	0.148	0.155	5	3	2	324	primase, DNA, polypeptide 2 (58kDa)	ENST00000389488.2
Case#4-Baseline-WholeTumor	THEMIS	6	128135008	Missense_Mutation	C	T	p.D260N	56	51	0.911	1.023	2	2	0	85	thymocyte selection associated	ENST00000368248.2
Case#4-Baseline-WholeTumor	PTPRK	6	128326312	Missense_Mutation	C	T	p.R803Q	77	73	0.948	1.065	2	2	0	120	protein tyrosine phosphatase, receptor type, K	ENST00000368215.3
Case#4-Baseline-WholeTumor	GPR146	7	1097183	Missense_Mutation	G	A	p.G11E	107	11	0.103	0.116	2	1	1	180	G protein-coupled receptor 146	ENST00000397095.1
Case#4-Baseline-WholeTumor	HDAC9	7	18788735	Missense_Mutation	G	A	p.E670K	57	26	0.456	0.513	2	1	1	106	histone deacetylase 9	ENST00000432645.2
Case#4-Baseline-WholeTumor	HDAC9	7	18993787	Missense_Mutation	G	A	p.D983N	38	17	0.447	0.503	2	1	1	69	histone deacetylase 9	ENST00000432645.2
Case#4-Baseline-WholeTumor	ABCB5	7	20795083	Missense_Mutation	G	A	p.G1204R	38	16	0.421	0.473	2	1	1	55	ATP-binding cassette, sub-family B (MDR/TAP), member 5	ENST00000404938.2
Case#4-Baseline-WholeTumor	CPVL	7	29160604	Missense_Mutation	C	T	p.R25H	59	5	0.085	0.095	2	1	1	107	carboxypeptidase, vitellogenic-like	ENST00000409850.1
Case#4-Baseline-WholeTumor	SPDYE1	7	44047066	Missense_Mutation	T	C	p.C278R	280	25	0.089	0.100	2	1	1	434	speedy/RINGO cell cycle regulator family member E1	ENST00000258704.3
Case#4-Baseline-WholeTumor	C7orf72	7	50180972	Missense_Mutation	C	T	p.T358I	45	6	0.133	0.150	2	1	1	47	chromosome 7 open reading frame 72	ENST00000297001.6
Case#4-Baseline-WholeTumor	STYXL1	7	75633078	Missense_Mutation	A	G	p.I232T	37	18	0.486	0.547	2	1	1	64	serine/threonine/tyrosine interacting-like 1	ENST00000248600.1
Case#4-Baseline-WholeTumor	PCLO	7	82581909	Missense_Mutation	G	A	p.P2787L	142	52	0.366	0.411	2	1	1	220	piccolo presynaptic cytomatrix protein	ENST00000333891.9
Case#4-Baseline-WholeTumor	TECPR1	7	97866139	Missense_Mutation	G	A	p.A377V	38	11	0.289	0.325	2	1	1	79	tectonin beta-propeller repeat containing 1	ENST00000447648.2
Case#4-Baseline-WholeTumor	BRAF	7	140453135	Missense_Mutation	CA	TT	p.V600E	48	16	0.333	0.375	2	1	1	84	B-Raf proto-oncogene, serine/threonine kinase	ENST00000288602.6
Case#4-Baseline-WholeTumor	CLEC5A	7	141635733	Missense_Mutation	C	T	p.E76K	85	33	0.388	0.436	2	1	1	130	C-type lectin domain family 5, member A	ENST00000546910.1
Case#4-Baseline-WholeTumor	MGAM	7	141750519	Missense_Mutation	C	T	p.S887L	59	23	0.390	0.438	2	1	1	132	maltase-glucoamylase (alpha-glucosidase)	ENST00000549489.2
Case#4-Baseline-WholeTumor	RP11-1220K2.2	7	141889282	Nonsense_Mutation	G	A	p.W1441*	92	38	0.413	0.464	2	1	1	167		ENST00000477922.3
Case#4-Baseline-WholeTumor	OR6B1	7	143701367	Missense_Mutation	C	T	p.S93F	148	70	0.473	0.531	2	1	1	246	olfactory receptor, family 6, subfamily B, member 1	ENST00000408922.2
Case#4-Baseline-WholeTumor	MYOM2	8	2077195	Missense_Mutation	G	A	p.E1259K	77	22	0.286	0.309	3	2	1	90	myomesin 2	ENST00000262113.4
Case#4-Baseline-WholeTumor	CSMD1	8	3263699	Nonsense_Mutation	C	A	p.G707*	51	19	0.373	0.403	3	2	1	66	CUB and Sushi multiple domains 1	ENST00000520002.1
Case#4-Baseline-WholeTumor	ZNF705G	8	7215569	Missense_Mutation	G	A	p.H278Y	627	187	0.298	0.323	3	2	1	727	zinc finger protein 705G	ENST00000400156.4
Case#4-Baseline-WholeTumor	FZD3	8	28385409	Missense_Mutation	C	T	p.P378S	143	97	0.678	0.734	3	2	1	217	frizzled class receptor 3	ENST00000240093.3
Case#4-Baseline-WholeTumor	DUSP4	8	29195991	Missense_Mutation	G	A	p.L203F	76	48	0.632	0.684	3	2	1	103	dual specificity phosphatase 4	ENST00000240100.2
Case#4-Baseline-WholeTumor	C8orf86	8	38370002	Missense_Mutation	G	A	p.P192L	99	30	0.303	0.328	3	2	1	129	chromosome 8 open reading frame 86	ENST00000358138.1
Case#4-Baseline-WholeTumor	TACC1	8	38684765	Missense_Mutation	C	T	p.S511F	155	107	0.690	0.747	3	2	1	136	transforming, acidic coiled-coil containing protein 1	ENST00000317827.4
Case#4-Baseline-WholeTumor	ZMAT4	8	40532391	Missense_Mutation	G	A	p.P137S	76	45	0.592	0.641	3	2	1	87	zinc finger, matrin-type 4	ENST00000297737.6
Case#4-Baseline-WholeTumor	ANK1	8	41573301	Missense_Mutation	C	T	p.E491K	97	63	0.649	0.703	3	2	1	122	ankyrin 1, erythrocytic	ENST00000347528.4
Case#4-Baseline-WholeTumor	HOOK3	8	42841811	Missense_Mutation	C	T	p.R469C	86	28	0.326	0.352	3	2	1	117	hook microtubule-tethering protein 3	ENST00000307602.4
Case#4-Baseline-WholeTumor	SNTG1	8	51415354	Missense_Mutation	A	T	p.N127I	33	18	0.545	0.590	3	2	1	31	syntrophin, gamma 1	ENST00000522124.1
Case#4-Baseline-WholeTumor	PXDNL	8	52320757	Nonsense_Mutation	G	A	p.Q1143*	77	43	0.558	0.604	3	2	1	93	peroxidasin homolog (Drosophila)-like	ENST00000356297.4
Case#4-Baseline-WholeTumor	NKAIN3	8	63492222	Missense_Mutation	G	A	p.R60Q	105	65	0.619	0.670	3	2	1	135	Na+/K+ transporting ATPase interacting 3	ENST00000523211.1
Case#4-Baseline-WholeTumor	MCMDC2	8	67789615	Missense_Mutation	C	T	p.P106L	84	39	0.464	0.503	3	2	1	116	minichromosome maintenance domain containing 2	ENST00000422365.2
Case#4-Baseline-WholeTumor	FABP4	8	82392716	Missense_Mutation	G	A	p.S64F	81	21	0.259	0.281	3	2	1	66	fatty acid binding protein 4, adipocyte	ENST00000256104.4
Case#4-Baseline-WholeTumor	LRRCC1	8	86049698	Splice_Site	G	A		72	18	0.250	0.271	3	2	1	69	leucine rich repeat and coiled-coil centrosomal protein 1	ENST00000360375.3
Case#4-Baseline-WholeTumor	SLC7A13	8	87226860	Missense_Mutation	G	A	p.P399S	80	23	0.288	0.311	3	2	1	71	solute carrier family 7 (anionic amino acid transporter), member 13	ENST00000297524.3
Case#4-Baseline-WholeTumor	CNGB3	8	87645012	Missense_Mutation	C	T	p.G430R	77	53	0.688	0.745	3	2	1	114	cyclic nucleotide gated channel beta 3	ENST00000320005.5
Case#4-Baseline-WholeTumor	SYBU	8	110587514	Missense_Mutation	G	A	p.A538V	71	16	0.225	0.244	3	2	1	62	syntabulin (syntaxin-interacting)	ENST00000422135.1
Case#4-Baseline-WholeTumor	FAM84B	8	127569041	Missense_Mutation	C	G	p.W198C	58	16	0.276	0.299	3	2	1	73	family with sequence similarity 84, member B	ENST00000304916.3
Case#4-Baseline-WholeTumor	POU5F1B	8	128428150	Missense_Mutation	CC	TT	p.P14S	87	57	0.655	0.709	3	2	1	76	POU class 5 homeobox 1B	ENST00000465342.2
Case#4-Baseline-WholeTumor	ASAP1	8	131130447	Nonsense_Mutation	G	A	p.Q614*	58	35	0.603	0.653	3	2	1	72	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	ENST00000518721.1
Case#4-Baseline-WholeTumor	EEF1D	8	144663474	Missense_Mutation	C	T	p.G72S	40	8	0.200	0.216	3	2	1	51	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	ENST00000529272.1
Case#4-Baseline-WholeTumor	EPPK1	8	144940260	Missense_Mutation	C	T	p.D2388N	206	11	0.053	0.058	3	2	1	132	epiplakin 1	ENST00000525985.1
Case#4-Baseline-WholeTumor	SCRT1	8	145559810	Nonsense_Mutation	T	A	p.K8*	36	28	0.778	0.842	3	2	1	42	scratch family zinc finger 1	ENST00000332135.4
Case#4-Baseline-WholeTumor	SLC39A4	8	145639726	Missense_Mutation	T	C	p.T357A	111	9	0.081	0.088	3	2	1	118	solute carrier family 39 (zinc transporter), member 4	ENST00000301305.3
Case#4-Baseline-WholeTumor	TONSL	8	145666213	Missense_Mutation	C	T	p.R351Q	100	31	0.310	0.336	3	2	1	106	tonsoku-like, DNA repair protein	ENST00000409379.3
Case#4-Baseline-WholeTumor	C8orf33	8	146278132	Missense_Mutation	G	A	p.R56K	86	32	0.372	0.403	3	2	1	96	chromosome 8 open reading frame 33	ENST00000331434.6
Case#4-Baseline-WholeTumor	IFNA7	9	21201768	Missense_Mutation	G	A	p.P133S	234	200	0.855	0.960	2	2	0	363	interferon, alpha 7	ENST00000239347.3
Case#4-Baseline-WholeTumor	GALT	9	34646742	Missense_Mutation	C	T	p.A14V	85	38	0.447	0.502	2	2	0	156	galactose-1-phosphate uridylyltransferase	ENST00000378842.3
Case#4-Baseline-WholeTumor	ANKRD18A	9	38571130	Missense_Mutation	C	A	p.A183S	75	5	0.067	0.075	2	2	0	139	ankyrin repeat domain 18A	ENST00000566717.2
Case#4-Baseline-WholeTumor	SPATA31A7	9	65506215	Missense_Mutation	C	T	p.E449K	161	89	0.553	0.621	2	1	1	276	SPATA31 subfamily A, member 7	ENST00000355045.2
Case#4-Baseline-WholeTumor	C9orf84	9	114454544	Missense_Mutation	T	C	p.E1174G	86	6	0.070	0.078	2	2	0	126	chromosome 9 open reading frame 84	ENST00000318737.4
Case#4-Baseline-WholeTumor	TNFSF15	9	117568247	Missense_Mutation	C	T	p.E16K	23	20	0.870	0.977	2	2	0	38	tumor necrosis factor (ligand) superfamily, member 15	ENST00000374045.4
Case#4-Baseline-WholeTumor	GOLGA1	9	127661645	Missense_Mutation	G	A	p.T425M	29	4	0.138	0.155	2	2	0	72	golgin A1	ENST00000373555.4
Case#4-Baseline-WholeTumor	PNPLA7	9	140358581	Missense_Mutation	C	T	p.D1050N	41	6	0.146	0.164	2	2	0	48	patatin-like phospholipase domain containing 7	ENST00000277531.4
Case#4-Baseline-WholeTumor	CLCN4	X	10181775	Missense_Mutation	G	A	p.G544E	89	87	0.978	1.038	4	3	1	76	chloride channel, voltage-sensitive 4	ENST00000380833.4
Case#4-Baseline-WholeTumor	TLR8	X	12938028	Missense_Mutation	G	A	p.R290Q	71	65	0.915	0.972	4	3	1	53	toll-like receptor 8	ENST00000218032.6
Case#4-Baseline-WholeTumor	MAOB	X	43698248	Nonsense_Mutation	G	A	p.Q49*	22	21	0.955	1.014	4	3	1	38	monoamine oxidase B	ENST00000378069.4
Case#4-Baseline-WholeTumor	POF1B	X	84562231	Missense_Mutation	T	G	p.T368P	40	37	0.925	0.982	4	3	1	47	premature ovarian failure, 1B	ENST00000262753.4
Case#4-Baseline-WholeTumor	PCDH19	X	99661471	Missense_Mutation	C	T	p.E709K	16	15	0.938	0.995	4	3	1	30	protocadherin 19	ENST00000373034.4
Case#4-Baseline-WholeTumor	ESX1	X	103495543	Missense_Mutation	C	T	p.R196Q	52	48	0.923	0.980	4	3	1	42	ESX homeobox 1	ENST00000372588.4
Case#4-Baseline-WholeTumor	COL4A5	X	107819152	Missense_Mutation	C	T	p.P187S	39	37	0.949	1.007	4	3	1	34	collagen, type IV, alpha 5	ENST00000361603.2
Case#4-Baseline-WholeTumor	RBMXL3	X	114424215	Missense_Mutation	G	A	p.G71S	54	47	0.870	0.924	4	3	1	54	RNA binding motif protein, X-linked-like 3	ENST00000424776.3
Case#4-Baseline-WholeTumor	SLC6A14	X	115590023	Missense_Mutation	G	A	p.E611K	40	39	0.975	1.035	4	3	1	34	solute carrier family 6 (amino acid transporter), member 14	ENST00000371900.4
Case#4-Baseline-WholeTumor	THOC2	X	122759828	Missense_Mutation	G	A	p.R998C	61	57	0.934	0.992	4	3	1	60	THO complex 2	ENST00000245838.8
Case#4-Baseline-WholeTumor	IGSF1	X	130411997	Missense_Mutation	C	T	p.G718E	76	73	0.961	1.020	4	3	1	61	immunoglobulin superfamily, member 1	ENST00000361420.3
Case#4-Baseline-WholeTumor	F8	X	154156921	Missense_Mutation	C	T	p.R1715Q	55	17	0.309	0.328	4	3	1	59	coagulation factor VIII, procoagulant component	ENST00000360256.4
Case#4-Relapse-WholeTumor	NADK	1	1696717	Missense_Mutation	C	A	p.K43N	137	29	0.212	0.261	3	2	1	95	NAD kinase	ENST00000341426.5
Case#4-Relapse-WholeTumor	MORN1	1	2252916	Missense_Mutation	C	T	p.G467D	24	4	0.167	0.206	3	2	1	29	MORN repeat containing 1	ENST00000378531.3
Case#4-Relapse-WholeTumor	TTC34	1	2704099	Missense_Mutation	C	T	p.A88T	54	14	0.259	0.441	1	1	0	49	tetratricopeptide repeat domain 34	ENST00000401095.3
Case#4-Relapse-WholeTumor	MTOR	1	11190667	Missense_Mutation	GG	AA	p.T1844I	111	47	0.423	0.523	3	2	1	136	mechanistic target of rapamycin (serine/threonine kinase)	ENST00000361445.4
Case#4-Relapse-WholeTumor	LRRC38	1	13839611	Missense_Mutation	T	C	p.N160D	123	65	0.528	0.652	3	2	1	88	leucine rich repeat containing 38	ENST00000376085.3
Case#4-Relapse-WholeTumor	PADI2	1	17413045	Missense_Mutation	G	A	p.H269Y	85	45	0.529	0.653	3	2	1	88	peptidyl arginine deiminase, type II	ENST00000375486.4
Case#4-Relapse-WholeTumor	KLHDC7A	1	18808983	Missense_Mutation	A	T	p.E503V	43	12	0.279	0.344	3	2	1	44	kelch domain containing 7A	ENST00000400664.1
Case#4-Relapse-WholeTumor	ALDH4A1	1	19200985	Missense_Mutation	C	A	p.Q517H	243	48	0.198	0.244	3	2	1	174	aldehyde dehydrogenase 4 family, member A1	ENST00000375341.3
Case#4-Relapse-WholeTumor	VWA5B1	1	20656824	Missense_Mutation	A	G	p.N469S	98	5	0.051	0.063	3	2	1	103	von Willebrand factor A domain containing 5B1	ENST00000375079.2
Case#4-Relapse-WholeTumor	TMCO2	1	40717118	Missense_Mutation	A	G	p.K134R	52	12	0.231	0.285	3	2	1	41	transmembrane and coiled-coil domains 2	ENST00000372766.3
Case#4-Relapse-WholeTumor	CCDC30	1	43032087	Nonsense_Mutation	C	T	p.R266*	86	19	0.221	0.273	3	2	1	58	coiled-coil domain containing 30	ENST00000340612.4
Case#4-Relapse-WholeTumor	TOE1	1	45806991	Missense_Mutation	G	A	p.G71E	133	35	0.263	0.325	3	2	1	149	target of EGR1, member 1 (nuclear)	ENST00000372090.5
Case#4-Relapse-WholeTumor	LDLRAD1	1	54480008	Missense_Mutation	G	A	p.R35C	64	17	0.266	0.328	3	2	1	28	low density lipoprotein receptor class A domain containing 1	ENST00000371360.1
Case#4-Relapse-WholeTumor	CDCP2	1	54606804	Missense_Mutation	C	T	p.G244R	183	21	0.115	0.142	3	2	1	129	CUB domain containing protein 2	ENST00000371330.1
Case#4-Relapse-WholeTumor	LEPR	1	66101926	Missense_Mutation	G	A	p.G909D	220	54	0.245	0.303	3	2	1	144	leptin receptor	ENST00000349533.6
Case#4-Relapse-WholeTumor	C1orf173	1	75038204	Missense_Mutation	C	T	p.E1064K	225	104	0.462	0.570	3	2	1	153		ENST00000326665.5

Case#4-Relapse-WholeTumor	C1orf173	1	75055582	Missense_Mutation	C	T	p.E637K	130	59	0.454	0.560	3	2	1	118		ENST00000326665.5
Case#4-Relapse-WholeTumor	LPHN2	1	82434986	Missense_Mutation	G	A	p.R879Q	283	59	0.208	0.257	3	2	1	136	latrophilin 2	ENST00000370728.1
Case#4-Relapse-WholeTumor	RPF1	1	84956083	Missense_Mutation	A	G	p.K182E	198	107	0.540	0.667	3	2	1	110	ribosome production factor 1 homolog (S. cerevisiae)	ENST00000370654.5
Case#4-Relapse-WholeTumor	PRPF38B	1	109242103	Missense_Mutation	C	T	p.R368C	74	22	0.297	0.367	3	2	1	69	pre-mRNA processing factor 38B	ENST00000370025.4
Case#4-Relapse-WholeTumor	DENND2D	1	111734940	Splice_Site	C	T		59	17	0.288	0.356	3	2	1	39	DENN/MADD domain containing 2D	ENST00000357640.4
Case#4-Relapse-WholeTumor	SYCP1	1	115417165	Missense_Mutation	G	A	p.D213N	165	73	0.442	0.546	3	2	1	106	synaptonemal complex protein 1	ENST00000369522.3
Case#4-Relapse-WholeTumor	TBX15	1	119427467	Missense_Mutation	A	C	p.M566R	118	7	0.059	0.073	3	2	1	104	T-box 15	ENST00000369429.3
Case#4-Relapse-WholeTumor	VPS72	1	151149374	Missense_Mutation	C	T	p.G292R	57	28	0.491	0.578	4	2	2	50	vacuolar protein sorting 72 homolog (S. cerevisiae)	ENST00000354473.4
Case#4-Relapse-WholeTumor	ZNF687	1	151260293	Missense_Mutation	A	G	p.N509S	114	25	0.219	0.258	4	2	2	96	zinc finger protein 687	ENST00000368879.2
Case#4-Relapse-WholeTumor	ZNF687	1	151261061	Missense_Mutation	C	T	p.R725C	232	82	0.353	0.416	4	2	2	169	zinc finger protein 687	ENST00000368879.2
Case#4-Relapse-WholeTumor	KPRP	1	152733503	Missense_Mutation	C	T	p.P480L	77	17	0.221	0.260	4	2	2	50	keratinocyte proline-rich protein	ENST00000606109.1
Case#4-Relapse-WholeTumor	ADAM15	1	155029553	Missense_Mutation	C	T	p.T375I	98	31	0.316	0.372	4	2	2	101	ADAM metallopeptidase domain 15	ENST00000356955.2
Case#4-Relapse-WholeTumor	HDGF	1	156713558	Missense_Mutation	G	A	p.P201L	86	6	0.070	0.082	4	2	2	77	hepatoma-derived growth factor	ENST00000357325.5
Case#4-Relapse-WholeTumor	SH2D2A	1	156784085	Splice_Site	C	A	p.E104*	121	24	0.198	0.233	4	2	2	71	SH2 domain containing 2A	ENST00000368199.3
Case#4-Relapse-WholeTumor	CRP	1	159683802	Missense_Mutation	G	A	p.S63L	101	38	0.376	0.442	4	2	2	63	C-reactive protein, pentraxin-related	ENST00000255030.5
Case#4-Relapse-WholeTumor	FCRLA	1	161683136	Missense_Mutation	G	A	p.R366Q	124	9	0.073	0.085	4	2	2	62	Fc receptor-like A	ENST00000236938.6
Case#4-Relapse-WholeTumor	MAEL	1	166973432	Missense_Mutation	A	G	p.K180R	187	36	0.193	0.226	4	2	2	134	maelstrom spermatogenic transposon silencer	ENST00000367872.4
Case#4-Relapse-WholeTumor	F5	1	169511368	Missense_Mutation	G	A	p.P987L	207	90	0.435	0.511	4	2	2	111	coagulation factor V (proaccelerin, labile factor)	ENST00000367797.3
Case#4-Relapse-WholeTumor	FMO3	1	171086425	Missense_Mutation	G	A	p.G481E	107	37	0.346	0.407	4	2	2	91	flavin containing monooxygenase 3	ENST00000367755.4
Case#4-Relapse-WholeTumor	PRRC2C	1	171544097	Missense_Mutation	C	T	p.S2260F	142	52	0.366	0.431	4	2	2	67	proline-rich coiled-coil 2C	ENST00000338920.4
Case#4-Relapse-WholeTumor	BRINP3	1	190068089	Missense_Mutation	G	A	p.P454S	116	45	0.388	0.456	4	2	2	100	bone morphogenetic protein/retinoic acid inducible neural-specific 3	ENST00000367462.3
Case#4-Relapse-WholeTumor	PPFIA4	1	203008264	Missense_Mutation	C	T	p.S43F	128	47	0.367	0.432	4	2	2	100	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4	ENST00000447715.2
Case#4-Relapse-WholeTumor	MYBPH	1	203144538	Missense_Mutation	G	A	p.S86F	65	11	0.169	0.199	4	2	2	73	myosin binding protein H	ENST00000255416.4
Case#4-Relapse-WholeTumor	CNTN2	1	205034965	Missense_Mutation	G	A	p.G582R	120	19	0.158	0.186	4	2	2	66	contactin 2 (axonal)	ENST00000331830.4
Case#4-Relapse-WholeTumor	PLXNA2	1	208390113	Missense_Mutation	C	A	p.W385C	72	15	0.208	0.245	4	2	2	45	plexin A2	ENST00000367033.3
Case#4-Relapse-WholeTumor	USH2A	1	215901656	Missense_Mutation	C	T	p.E3928K	144	57	0.396	0.465	4	2	2	72	Usher syndrome 2A (autosomal recessive, mild)	ENST00000307340.3
Case#4-Relapse-WholeTumor	USH2A	1	216017763	Missense_Mutation	G	A	p.S3044L	139	59	0.424	0.499	4	2	2	76	Usher syndrome 2A (autosomal recessive, mild)	ENST00000307340.3
Case#4-Relapse-WholeTumor	DNAH14	1	225268433	Missense_Mutation	T	A	p.I974N	166	31	0.187	0.220	4	2	2	95	dynein, axonemal, heavy chain 14	ENST00000445597.2
Case#4-Relapse-WholeTumor	AGT	1	230845977	Missense_Mutation	G	A	p.T207M	58	5	0.086	0.101	4	2	2	47	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	ENST00000366667.4
Case#4-Relapse-WholeTumor	PCNXL2	1	233137282	Splice_Site	CC	TT	p.D1700N	76	15	0.197	0.232	4	2	2	49	pecanex-like 2 (Drosophila)	ENST00000258229.9
Case#4-Relapse-WholeTumor	PCNXL2	1	233160921	Nonsense_Mutation	G	A	p.R1526*	117	51	0.436	0.512	4	2	2	142	pecanex-like 2 (Drosophila)	ENST00000258229.9
Case#4-Relapse-WholeTumor	TBCE	1	235611744	Missense_Mutation	G	A	p.E494K	321	117	0.364	0.429	4	2	2	166	tubulin folding cofactor E	ENST00000366601.3
Case#4-Relapse-WholeTumor	LYST	1	235972935	Missense_Mutation	G	A	p.R395C	113	50	0.442	0.520	4	2	2	75	lysosomal trafficking regulator	ENST00000389794.3
Case#4-Relapse-WholeTumor	GREM2	1	240656550	Missense_Mutation	G	C	p.Q76E	197	10	0.051	0.060	4	2	2	187	gremlin 2, DAN family BMP antagonist	ENST00000318160.4
Case#4-Relapse-WholeTumor	OR1C1	1	247921002	Missense_Mutation	C	T	p.R236K	100	40	0.400	0.470	4	2	2	85	olfactory receptor, family 1, subfamily C, member 1	ENST00000408896.2
Case#4-Relapse-WholeTumor	OR2L2	1	248202474	Missense_Mutation	A	G	p.Q302R	385	66	0.171	0.202	4	2	2	222	olfactory receptor, family 2, subfamily L, member 2	ENST00000366479.2
Case#4-Relapse-WholeTumor	OR2L3	1	248224011	Missense_Mutation	G	A	p.D10N	511	202	0.395	0.465	4	2	2	391	olfactory receptor, family 2, subfamily L, member 3	ENST00000359959.3
Case#4-Relapse-WholeTumor	PITRM1	10	3191823	Missense_Mutation	C	T	p.V621I	99	7	0.071	0.087	3	2	1	83	pitrilysin metallopeptidase 1	ENST00000224949.4
Case#4-Relapse-WholeTumor	UPF2	10	12041915	Missense_Mutation	A	G	p.L583P	196	41	0.209	0.258	3	2	1	115	UPF2 regulator of nonsense transcripts homolog (yeast)	ENST00000356352.2
Case#4-Relapse-WholeTumor	CACNB2	10	18827189	Nonsense_Mutation	G	A	p.W461*	193	46	0.238	0.294	3	2	1	105	calcium channel, voltage-dependent, beta 2 subunit	ENST00000324631.7
Case#4-Relapse-WholeTumor	PLXDC2	10	20506484	Missense_Mutation	C	T	p.P418S	65	38	0.585	0.722	3	2	1	71	plexin domain containing 2	ENST00000377252.4
Case#4-Relapse-WholeTumor	NEBL	10	21158766	Missense_Mutation	G	A	p.S162F	135	28	0.207	0.256	3	2	1	98	nebulette	ENST00000377122.4
Case#4-Relapse-WholeTumor	PTCHD3	10	27703109	Missense_Mutation	G	A	p.A24V	123	65	0.528	0.652	3	2	1	70	patched domain containing 3	ENST00000438700.3
Case#4-Relapse-WholeTumor	MTPAP	10	30602756	Missense_Mutation	G	C	p.Q511E	164	44	0.268	0.331	3	2	1	128	mitochondrial poly(A) polymerase	ENST00000263063.4
Case#4-Relapse-WholeTumor	WDFY4	10	50098714	Missense_Mutation	G	A	p.E2420K	137	70	0.511	0.601	4	2	2	122	WDFY family member 4	ENST00000325239.5
Case#4-Relapse-WholeTumor	C10orf71	10	50534837	Missense_Mutation	C	T	p.P1416L	89	28	0.315	0.370	4	2	2	35	chromosome 10 open reading frame 71	ENST00000374144.3
Case#4-Relapse-WholeTumor	ADAMTS14	10	72513650	Missense_Mutation	G	A	p.G942R	50	23	0.460	0.568	3	2	1	47	ADAM metallopeptidase with thrombospondin type 1 motif, 14	ENST00000373207.1
Case#4-Relapse-WholeTumor	SEC24C	10	75519952	Missense_Mutation	G	T	p.G220C	36	10	0.278	0.343	3	2	1	50	SEC24 family member C	ENST00000339365.2
Case#4-Relapse-WholeTumor	ZMIZ1	10	81050867	Missense_Mutation	A	G	p.Q231R	45	20	0.444	0.549	3	2	1	52	zinc finger, MIZ-type containing 1	ENST00000334512.5
Case#4-Relapse-WholeTumor	NUTM2B	10	81463478	Missense_Mutation	G	A	p.G38E	1040	186	0.179	0.221	3	2	1	692	NUT family member 2B	ENST00000429828.1
Case#4-Relapse-WholeTumor	PLCE1	10	95790940	Missense_Mutation	G	A	p.R46Q	61	17	0.279	0.344	3	2	1	54	phospholipase C, epsilon 1	ENST00000371380.3
Case#4-Relapse-WholeTumor	FGF8	10	103534967	Missense_Mutation	G	A	p.P26S	17	9	0.529	0.653	3	2	1	16	fibroblast growth factor 8 (androgen-induced)	ENST00000344255.3
Case#4-Relapse-WholeTumor	FAM160B1	10	116606884	Missense_Mutation	C	T	p.S535L	221	52	0.235	0.290	3	2	1	96	family with sequence similarity 160, member B1	ENST00000369248.4
Case#4-Relapse-WholeTumor	DMBT1	10	124352006	Missense_Mutation	G	A	p.D799N	439	83	0.189	0.233	3	2	1	441	deleted in malignant brain tumors 1	ENST00000338354.3
Case#4-Relapse-WholeTumor	TTC40	10	134647622	Missense_Mutation	T	A	p.Q2291L	57	19	0.333	0.411	3	2	1	48		ENST00000368586.5
Case#4-Relapse-WholeTumor	NAP1L4	11	2981039	Missense_Mutation	G	A	p.P236L	248	59	0.238	0.294	3	2	1	172	nucleosome assembly protein 1-like 4	ENST00000380542.4
Case#4-Relapse-WholeTumor	OR52A1	11	5173208	Missense_Mutation	G	A	p.P131L	66	15	0.227	0.281	3	2	1	75	olfactory receptor, family 52, subfamily A, member 1	ENST00000380367.1
Case#4-Relapse-WholeTumor	OTOG	11	17667291	Splice_Site	G	A	p.V2860M	75	17	0.227	0.280	3	2	1	55	otogelin	ENST00000399391.2
Case#4-Relapse-WholeTumor	LDHAL6A	11	18487261	Missense_Mutation	G	A	p.D108N	230	129	0.561	0.692	3	2	1	184	lactate dehydrogenase A-like 6A	ENST00000280706.2
Case#4-Relapse-WholeTumor	QSER1	11	32956744	Missense_Mutation	C	T	p.R1185C	195	44	0.226	0.278	3	2	1	102	glutamine and serine rich 1	ENST00000399302.2
Case#4-Relapse-WholeTumor	OR8K3	11	56086143	Missense_Mutation	G	A	p.D121N	113	64	0.566	0.699	3	2	1	141	olfactory receptor, family 8, subfamily K, member 3	ENST00000312711.1
Case#4-Relapse-WholeTumor	METTL12	11	62434173	Missense_Mutation	G	A	p.G125S	77	5	0.065	0.080	3	2	1	84	methyltransferase like 12	ENST00000532971.1
Case#4-Relapse-WholeTumor	SLC22A9	11	63177274	Splice_Site	G	A	p.E534E	128	27	0.211	0.260	3	2	1	59	solute carrier family 22 (organic anion transporter), member 9	ENST00000279178.3
Case#4-Relapse-WholeTumor	CHKA	11	67821505	Frame_Shift_Del	G	-	p.Q442fs	84	15	0.179	0.220	3	2	1	66	choline kinase alpha	ENST00000265689.4
Case#4-Relapse-WholeTumor	CHKA	11	67821509	Missense_Mutation	GT	AA	p.Y440F	77	15	0.195	0.240	3	2	1	68	choline kinase alpha	ENST00000265689.4
Case#4-Relapse-WholeTumor	SHANK2	11	70333333	Missense_Mutation	C	T	p.S643N	132	67	0.508	0.626	3	2	1	83	SH3 and multiple ankyrin repeat domains 2	ENST00000423696.2
Case#4-Relapse-WholeTumor	MYO7A	11	76853783	Missense_Mutation	T	C	p.L16S	115	9	0.078	0.097	3	2	1	138	myosin VIIA	ENST00000409709.3
Case#4-Relapse-WholeTumor	TENM4	11	78467872	Missense_Mutation	C	T	p.G912R	84	17	0.202	0.250	3	2	1	90	teneurin transmembrane protein 4	ENST00000278550.7
Case#4-Relapse-WholeTumor	MFRP	11	119215694	Missense_Mutation	G	A	p.P221L	32	20	0.625	0.771	3	2	1	42	membrane frizzled-related protein	ENST00000530681.1
Case#4-Relapse-WholeTumor	OR8B4	11	124294532	Missense_Mutation	G	A	p.P79L	157	96	0.611	0.755	3	2	1	104	olfactory receptor, family 8, subfamily B, member 4	ENST00000356130.3
Case#4-Relapse-WholeTumor	CACNA1C	12	2224470	Missense_Mutation	C	T	p.P44S	38	19	0.500	0.617	3	2	1	42	calcium channel, voltage-dependent, L type, alpha 1C subunit	ENST00000347598.4
Case#4-Relapse-WholeTumor	FGF23	12	4479934	Missense_Mutation	C	T	p.E111K	123	61	0.496	0.612	3	2	1	54	fibroblast growth factor 23	ENST00000237837.1
Case#4-Relapse-WholeTumor	ANO2	12	6030405	Missense_Mutation	A	G	p.V108A	133	8	0.060	0.074	3	2	1	89	anoctamin 2, calcium activated chloride channel	ENST00000356134.5
Case#4-Relapse-WholeTumor	COPS7A	12	6838423	Missense_Mutation	A	T	p.Y113F	127	59	0.465	0.573	3	2	1	123	COP9 signalosome subunit 7A	ENST00000543155.1
Case#4-Relapse-WholeTumor	GPR162	12	6936122	Missense_Mutation	C	T	p.T507I	90	21	0.233	0.288	3	2	1	42	G protein-coupled receptor 162	ENST00000311268.3
Case#4-Relapse-WholeTumor	PZP	12	9312946	Missense_Mutation	C	T	p.E1005K	133	31	0.233	0.288	3	2	1	144	pregnancy-zone protein	ENST00000261336.2
Case#4-Relapse-WholeTumor	PRB4	12	11461549	Missense_Mutation	G	C	p.P123R	113	32	0.283	0.350	3	2	1	155	proline-rich protein BstNI subfamily 4	ENST00000535904.1
Case#4-Relapse-WholeTumor	PRB4	12	11461706	Missense_Mutation	G	T	p.P71T	203	46	0.227	0.280	3	2	1	164	proline-rich protein BstNI subfamily 4	ENST00000535904.1
Case#4-Relapse-WholeTumor	KCNJ8	12	21919327	Missense_Mutation	C	T	p.R202Q	173	86	0.497	0.614	3	2	1	180	potassium inwardly-rectifying channel, subfamily J, member 8	ENST00000240662.2
Case#4-Relapse-WholeTumor	OR8S1	12	48921750	Missense_Mutation	C	T	p.A315V	176	41	0.233	0.288	3	2	1	84	olfactory receptor, family 8, subfamily S, member 1	ENST00000310194.1
Case#4-Relapse-WholeTumor	KRT2	12	53038873	Missense_Mutation	C	T	p.G617E	88	50	0.568	0.701	3	2	1	115	keratin 2	ENST00000309680.3
Case#4-Relapse-WholeTumor	KRT78	12	53242440	Missense_Mutation	A	G	p.L92P	159	13	0.082	0.101	3	2	1	117	keratin 78	ENST00000304620.4
Case#4-Relapse-WholeTumor	TENC1	12	53448151	Missense_Mutation	G	A	p.D150N	74	19	0.257	0.317	3	2	1	47	tensin like C1 domain containing phosphatase (tensin 2)	ENST00000314250.6

Case#4-Relapse-WholeTumor	AMHR2	12	53818171	Missense_Mutation	C	T	p.P50L	63	29	0.460	0.568	3	2	1	75	anti-Mullerian hormone receptor, type II	ENST00000257863.4
Case#4-Relapse-WholeTumor	OR6C6	12	55688227	Missense_Mutation	C	T	p.E264K	240	60	0.250	0.309	3	2	1	184	olfactory receptor, family 6, subfamily C, member 6	ENST00000358433.2
Case#4-Relapse-WholeTumor	GLI1	12	57865324	Missense_Mutation	C	T	p.S934F	74	42	0.568	0.701	3	2	1	40	GLI family zinc finger 1	ENST00000228682.2
Case#4-Relapse-WholeTumor	ARHGAP9	12	57869131	Missense_Mutation	G	A	p.R518W	36	10	0.278	0.343	3	2	1	14	Rho GTPase activating protein 9	ENST00000356411.2
Case#4-Relapse-WholeTumor	TPH2	12	72338095	Missense_Mutation	C	T	p.H93Y	150	33	0.220	0.272	3	2	1	93	tryptophan hydroxylase 2	ENST00000333850.3
Case#4-Relapse-WholeTumor	ATXN7L3B	12	74932048	Missense_Mutation	G	C	p.E52D	164	45	0.274	0.339	3	2	1	157	ataxin 7-like 3B	ENST00000519948.2
Case#4-Relapse-WholeTumor	RASSF9	12	86198686	Missense_Mutation	G	C	p.H368D	89	24	0.270	0.333	3	2	1	129	Ras association (RalGDS/AF-6) domain family (N-terminal) member 9	ENST00000361228.3
Case#4-Relapse-WholeTumor	C12orf50	12	88379663	Missense_Mutation	GG	AA	p.H364Y	281	65	0.231	0.285	3	2	1	230	chromosome 12 open reading frame 50	ENST00000298699.2
Case#4-Relapse-WholeTumor	C12orf50	12	88390205	Missense_Mutation	T	C	p.T143A	118	25	0.212	0.261	3	2	1	80	chromosome 12 open reading frame 50	ENST00000298699.2
Case#4-Relapse-WholeTumor	TCHP	12	110352340	Nonsense_Mutation	C	T	p.R410*	91	35	0.385	0.520	2	1	1	93	trichoplein, keratin filament binding	ENST00000312777.5
Case#4-Relapse-WholeTumor	SDS	12	113835043	Missense_Mutation	C	T	p.E194K	40	16	0.400	0.541	2	1	1	59	serine dehydratase	ENST00000257549.4
Case#4-Relapse-WholeTumor	RBM19	12	114374887	Missense_Mutation	T	C	p.T665A	126	9	0.071	0.097	2	1	1	116	RNA binding motif protein 19	ENST00000545145.2
Case#4-Relapse-WholeTumor	CCDC60	12	119943001	Missense_Mutation	C	T	p.P259L	72	19	0.264	0.357	2	1	1	63	coiled-coil domain containing 60	ENST00000327554.2
Case#4-Relapse-WholeTumor	TMEM132C	12	129190442	Missense_Mutation	G	A	p.E977K	43	23	0.535	0.723	2	1	1	62	transmembrane protein 132C	ENST00000435159.2
Case#4-Relapse-WholeTumor	FLT1	13	28964230	Missense_Mutation	C	T	p.G558R	158	86	0.544	0.621	5	3	2	111	fms-related tyrosine kinase 1	ENST00000282397.4
Case#4-Relapse-WholeTumor	PCDH9	13	66879162	Splice_Site	T	G		86	21	0.244	0.279	5	3	2	70	protocadherin 9	ENST00000377865.2
Case#4-Relapse-WholeTumor	UGGT2	13	96589308	Missense_Mutation	C	A	p.G616V	276	55	0.199	0.227	5	3	2	125	UDP-glucose glycoprotein glucosyltransferase 2	ENST00000376747.3
Case#4-Relapse-WholeTumor	DAOA	13	106142269	Missense_Mutation	C	T	p.H101Y	259	42	0.162	0.185	5	3	2	107	D-amino acid oxidase activator	ENST00000375936.3
Case#4-Relapse-WholeTumor	COL4A1	13	110838794	Missense_Mutation	C	A	p.G612V	72	15	0.208	0.238	5	3	2	33	collagen, type IV, alpha 1	ENST00000375820.4
Case#4-Relapse-WholeTumor	F7	13	113773045	Missense_Mutation	G	A	p.R375Q	205	66	0.322	0.367	5	3	2	131	coagulation factor VII (serum prothrombin conversion accelerator)	ENST00000375581.3
Case#4-Relapse-WholeTumor	TFDP1	13	114288253	Missense_Mutation	G	C	p.V175L	324	101	0.312	0.356	5	3	2	135	transcription factor Dp-1	ENST00000375370.5
Case#4-Relapse-WholeTumor	OR4M1	14	20249212	Missense_Mutation	C	T	p.S244F	653	52	0.080	0.094	4	3	1	646	olfactory receptor, family 4, subfamily M, member 1	ENST00000315957.4
Case#4-Relapse-WholeTumor	OR4K15	14	20444431	Missense_Mutation	C	T	p.R252C	267	113	0.423	0.522	3	2	1	281	olfactory receptor, family 4, subfamily K, member 15	ENST00000305051.5
Case#4-Relapse-WholeTumor	KLHL33	14	20897784	Missense_Mutation	G	A	p.S309F	55	25	0.455	0.561	3	2	1	42	kelch-like family member 33	ENST00000344581.4
Case#4-Relapse-WholeTumor	CHD8	14	21876604	Missense_Mutation	G	A	p.A866V	98	30	0.306	0.378	3	2	1	65	chromodomain helicase DNA binding protein 8	ENST00000557364.1
Case#4-Relapse-WholeTumor	C14orf39	14	60932752	Missense_Mutation	G	A	p.A306V	117	7	0.060	0.074	3	2	1	65	chromosome 14 open reading frame 39	ENST00000321731.3
Case#4-Relapse-WholeTumor	CATSPERB	14	92139225	Missense_Mutation	G	A	p.L372F	195	54	0.277	0.342	3	2	1	98	catsper channel auxiliary subunit beta	ENST00000256343.3
Case#4-Relapse-WholeTumor	ZFYVE21	14	104199095	Missense_Mutation	A	C	p.H222P	83	15	0.181	0.223	3	2	1	82	zinc finger, FYVE domain containing 21	ENST00000311141.2
Case#4-Relapse-WholeTumor	AHNAK2	14	105404695	Missense_Mutation	C	T	p.R5698Q	185	39	0.211	0.260	3	2	1	141	AHNAK nucleoprotein 2	ENST00000333244.5
Case#4-Relapse-WholeTumor	OR4M2	15	22369306	Missense_Mutation	C	T	p.S244F	977	154	0.158	0.180	5	3	2	725	olfactory receptor, family 4, subfamily M, member 2	ENST00000332663.2
Case#4-Relapse-WholeTumor	GOLGA8I	15	23260815	Missense_Mutation	C	T	p.S199F	623	114	0.183	0.209	5	3	2	315	golgin A8 family, member I	ENST00000450802.3
Case#4-Relapse-WholeTumor	NUTM1	15	34640641	Missense_Mutation	C	T	p.P163L	56	12	0.214	0.264	3	2	1	71	NUT midline carcinoma, family member 1	ENST00000333756.4
Case#4-Relapse-WholeTumor	EIF2AK4	15	40324409	Nonsense_Mutation	C	T	p.Q1567*	197	57	0.289	0.357	3	2	1	143	eukaryotic translation initiation factor 2 alpha kinase 4	ENST00000263791.5
Case#4-Relapse-WholeTumor	POLR2M	15	57999140	Missense_Mutation	C	T	p.L34F	122	40	0.328	0.385	4	2	2	72	polymerase (RNA) II (DNA directed) polypeptide M	ENST00000299638.3
Case#4-Relapse-WholeTumor	GRAMD2	15	72460887	Missense_Mutation	G	T	p.N71K	117	41	0.350	0.412	4	2	2	102	GRAM domain containing 2	ENST00000309731.7
Case#4-Relapse-WholeTumor	CCDC33	15	74622678	Missense_Mutation	G	A	p.S480N	118	9	0.076	0.090	4	2	2	82	coiled-coil domain containing 33	ENST00000398814.3
Case#4-Relapse-WholeTumor	ADAMTSL3	15	84683394	Missense_Mutation	CC	TT	p.L1359F	225	77	0.342	0.390	5	3	2	186	ADAMTS-like 3	ENST00000286744.5
Case#4-Relapse-WholeTumor	TICRR	15	90152048	Nonsense_Mutation	C	T	p.R913*	215	83	0.386	0.454	4	2	2	90	TOPBP1-interacting checkpoint and replication regulator	ENST00000268138.7
Case#4-Relapse-WholeTumor	MCTP2	15	94901781	Missense_Mutation	G	A	p.G414D	378	119	0.315	0.370	4	2	2	211	multiple C2 domains, transmembrane 2	ENST00000357742.4
Case#4-Relapse-WholeTumor	WDR24	16	736857	Missense_Mutation	C	T	p.G537S	83	20	0.241	0.283	4	2	2	63	WD repeat domain 24	ENST00000248142.6
Case#4-Relapse-WholeTumor	USP7	16	8993559	Missense_Mutation	C	A	p.D789Y	227	101	0.445	0.523	4	2	2	105	ubiquitin specific peptidase 7 (herpes virus-associated)	ENST00000344836.4
Case#4-Relapse-WholeTumor	SMG1	16	18879649	Missense_Mutation	G	A	p.R1020C	1505	348	0.231	0.264	5	4	1	521	SMG1 phosphatidylinositol 3-kinase-related kinase	ENST00000446231.2
Case#4-Relapse-WholeTumor	ITGAL	16	30486653	Missense_Mutation	G	A	p.G64E	62	37	0.597	0.681	5	3	2	43	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)	ENST00000356798.6
Case#4-Relapse-WholeTumor	SLC6A2	16	55733504	Missense_Mutation	G	A	p.G510R	216	81	0.375	0.441	4	2	2	232	solute carrier family 6 (neurotransmitter transporter), member 2	ENST00000379906.2
Case#4-Relapse-WholeTumor	CDH8	16	61687811	Missense_Mutation	T	G	p.K701Q	175	74	0.423	0.497	4	2	2	160	cadherin 8, type 2	ENST00000577390.1
Case#4-Relapse-WholeTumor	TSNAXIP1	16	67859956	Missense_Mutation	GG	AA	p.R320Q	60	23	0.383	0.451	4	2	2	65	translin-associated factor X interacting protein 1	ENST00000388833.3
Case#4-Relapse-WholeTumor	COG4	16	70515672	Missense_Mutation	T	C	p.N701D	166	65	0.392	0.460	4	2	2	92	component of oligomeric golgi complex 4	ENST00000323786.5
Case#4-Relapse-WholeTumor	HYDIN	16	70942713	Missense_Mutation	C	T	p.E2686K	137	48	0.350	0.412	4	2	2	81	HYDIN, axonemal central pair apparatus protein	ENST00000393567.2
Case#4-Relapse-WholeTumor	ZFHX3	16	72829347	Missense_Mutation	C	T	p.E2412K	211	99	0.469	0.552	4	2	2	236	zinc finger homeobox 3	ENST00000268489.5
Case#4-Relapse-WholeTumor	LDHD	16	75148750	Missense_Mutation	CC	TT	p.R148Q	170	65	0.382	0.450	4	2	2	81	lactate dehydrogenase D	ENST00000450168.2
Case#4-Relapse-WholeTumor	CNTNAP4	16	76483672	Missense_Mutation	C	T	p.H333Y	107	44	0.411	0.483	4	2	2	96	contactin associated protein-like 4	ENST00000476707.1
Case#4-Relapse-WholeTumor	CDH13	16	83711861	Missense_Mutation	G	A	p.E445K	208	83	0.399	0.469	4	2	2	108	cadherin 13	ENST00000566620.1
Case#4-Relapse-WholeTumor	OSGIN1	16	83994638	Missense_Mutation	C	T	p.P233L	122	38	0.311	0.366	4	2	2	51	oxidative stress induced growth inhibitor 1	ENST00000343939.2
Case#4-Relapse-WholeTumor	ATP2C2	16	84482262	Missense_Mutation	G	A	p.E543K	133	49	0.368	0.433	4	2	2	91	ATPase, Ca++ transporting, type 2C, member 2	ENST00000262429.4
Case#4-Relapse-WholeTumor	JPH3	16	87678017	Missense_Mutation	C	T	p.P179L	128	59	0.461	0.542	4	2	2	28	junctophilin 3	ENST00000284262.2
Case#4-Relapse-WholeTumor	RAP1GAP2	17	2898660	Missense_Mutation	G	A	p.G315E	163	78	0.479	0.591	3	2	1	196	RAP1 GTPase activating protein 2	ENST00000254695.8
Case#4-Relapse-WholeTumor	PELP1	17	4578435	Missense_Mutation	C	G	p.V405L	90	23	0.256	0.315	3	2	1	44	proline, glutamate and leucine rich protein 1	ENST00000574876.1
Case#4-Relapse-WholeTumor	KIF1C	17	4904574	Missense_Mutation	A	G	p.M81V	66	21	0.318	0.393	3	2	1	64	kinesin family member 1C	ENST00000320785.5
Case#4-Relapse-WholeTumor	NLRP1	17	5487064	Missense_Mutation	G	A	p.H72Y	80	41	0.513	0.633	3	2	1	76	NLR family, pyrin domain containing 1	ENST00000572272.1
Case#4-Relapse-WholeTumor	NEURL4	17	7229766	Missense_Mutation	G	T	p.N398K	139	33	0.237	0.293	3	2	1	154	neuralized E3 ubiquitin protein ligase 4	ENST00000399464.2
Case#4-Relapse-WholeTumor	PER1	17	8047180	Missense_Mutation	G	A	p.P826S	18	10	0.556	0.686	3	2	1	25	period circadian clock 1	ENST00000317276.4
Case#4-Relapse-WholeTumor	MYOCD	17	12649264	Missense_Mutation	C	T	p.P334S	158	39	0.247	0.305	3	2	1	124	myocardin	ENST00000343344.4
Case#4-Relapse-WholeTumor	MYO15A	17	18025233	Missense_Mutation	C	T	p.P1040L	63	19	0.302	0.372	3	2	1	94	myosin XVA	ENST00000205890.5
Case#4-Relapse-WholeTumor	CDRT15L2	17	20483109	Missense_Mutation	G	A	p.G18E	139	66	0.475	0.586	3	2	1	137	CMT1A duplicated region transcript 15-like 2	ENST00000399044.1
Case#4-Relapse-WholeTumor	TNFAIP1	17	26667468	Nonsense_Mutation	CC	TT	p.Q114*	86	16	0.186	0.230	3	2	1	109	tumor necrosis factor, alpha-induced protein 1 (endothelial)	ENST00000226225.2
Case#4-Relapse-WholeTumor	TAOK1	17	27822642	Missense_Mutation	A	T	p.D299V	186	47	0.253	0.312	3	2	1	133	TAO kinase 1	ENST00000261716.3
Case#4-Relapse-WholeTumor	GOSR1	17	28849280	Missense_Mutation	C	T	p.P213S	146	70	0.479	0.592	3	2	1	123	golgi SNAP receptor complex member 1	ENST00000225724.5
Case#4-Relapse-WholeTumor	TBC1D29	17	28890301	Missense_Mutation	G	A	p.S104N	60	6	0.100	0.123	3	2	1	47	TBC1 domain family, member 29	ENST00000580161.1
Case#4-Relapse-WholeTumor	ATAD5	17	29185321	Missense_Mutation	C	G	p.S979C	135	63	0.467	0.576	3	2	1	149	ATPase family, AAA domain containing 5	ENST00000321990.4
Case#4-Relapse-WholeTumor	SLFN12	17	33749919	Missense_Mutation	A	C	p.S43R	132	7	0.053	0.065	3	2	1	176	schlafen family member 12	ENST00000394562.1
Case#4-Relapse-WholeTumor	SLFN12L	17	33806164	Nonsense_Mutation	C	T	p.W355*	162	35	0.216	0.267	3	2	1	112	schlafen family member 12-like	ENST00000260908.7
Case#4-Relapse-WholeTumor	C17orf98	17	36997503	Missense_Mutation	T	C	p.Q47R	117	6	0.051	0.063	3	2	1	73	chromosome 17 open reading frame 98	ENST00000398575.4
Case#4-Relapse-WholeTumor	KRT36	17	39643646	Missense_Mutation	G	A	p.T315M	91	10	0.110	0.136	3	2	1	95	keratin 36	ENST00000328119.6
Case#4-Relapse-WholeTumor	COL1A1	17	48264079	Missense_Mutation	G	A	p.R1246W	112	27	0.241	0.298	3	2	1	142	collagen, type I, alpha 1	ENST00000225964.5
Case#4-Relapse-WholeTumor	KIF2B	17	51900425	Missense_Mutation	C	T	p.P11S	163	70	0.429	0.530	3	2	1	95	kinesin family member 2B	ENST00000268919.4
Case#4-Relapse-WholeTumor	LPO	17	56329738	Missense_Mutation	C	T	p.P326S	86	21	0.244	0.301	3	2	1	68	lactoperoxidase	ENST00000262290.4
Case#4-Relapse-WholeTumor	ACE	17	61556450	Missense_Mutation	C	T	p.S167F	80	21	0.263	0.324	3	2	1	57	angiotensin I converting enzyme	ENST00000290866.4
Case#4-Relapse-WholeTumor	ACE	17	61584653	Missense_Mutation	G	A	p.G693E	85	49	0.576	0.711	3	2	1	90	angiotensin I converting enzyme	ENST00000577647.1
Case#4-Relapse-WholeTumor	FTSJ3	17	61902413	Missense_Mutation	G	A	p.P236S	108	27	0.250	0.309	3	2	1	110	FtsJ homolog 3 (E. coli)	ENST00000427159.2
Case#4-Relapse-WholeTumor	TTYH2	17	72240177	Missense_Mutation	T	G	p.S265A	112	10	0.089	0.110	3	2	1	64	tweety family member 2	ENST00000269346.4
Case#4-Relapse-WholeTumor	CD300E	17	72613262	Missense_Mutation	G	A	p.S128F	102	24	0.235	0.290	3	2	1	96	CD300e molecule	ENST00000328630.3
Case#4-Relapse-WholeTumor	ENTHD2	17	79207827	Missense_Mutation	GG	AA	p.P110F	87	23	0.264	0.326	3	2	1	75	ENTH domain containing 2	ENST00000300714.3

Case#4-Relapse-WholeTumor	PIEZO2	18	10800407	Missense_Mutation	C	T	p.E436K	96	70	0.729	0.985	2	2	0	110	piezo-type mechanosensitive ion channel component 2	ENST00000503781.3
Case#4-Relapse-WholeTumor	NOL4	18	31709882	Missense_Mutation	C	T	p.G123R	75	48	0.640	0.865	2	2	0	36	nucleolar protein 4	ENST00000261592.5
Case#4-Relapse-WholeTumor	SETBP1	18	42531243	Missense_Mutation	G	A	p.M646I	22	19	0.864	1.167	2	2	0	25	SET binding protein 1	ENST00000282030.5
Case#4-Relapse-WholeTumor	PIAS2	18	44470629	Missense_Mutation	G	T	p.P138Q	75	26	0.347	0.468	2	2	0	108	protein inhibitor of activated STAT, 2	ENST00000585916.1
Case#4-Relapse-WholeTumor	DYM	18	46784814	Missense_Mutation	G	A	p.S434F	95	38	0.400	0.541	2	2	0	80	dymeclin	ENST00000269445.6
Case#4-Relapse-WholeTumor	CDH20	18	59167645	Missense_Mutation	G	A	p.D191N	116	79	0.681	0.920	2	2	0	142	cadherin 20, type 2	ENST00000262717.4
Case#4-Relapse-WholeTumor	NDUFS7	19	1388538	Missense_Mutation	C	T	p.P23L	115	7	0.061	0.072	4	2	2	60	NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)	ENST00000233627.9
Case#4-Relapse-WholeTumor	MKNK2	19	2039727	Missense_Mutation	C	T	p.R428Q	56	4	0.071	0.084	4	2	2	72	MAP kinase interacting serine/threonine kinase 2	ENST00000591601.1
Case#4-Relapse-WholeTumor	STXBP2	19	7707710	Splice_Site	G	A		93	43	0.462	0.544	4	2	2	59	syntaxin binding protein 2	ENST00000221283.5
Case#4-Relapse-WholeTumor	MUC16	19	8962010	Missense_Mutation	A	T	p.I14456N	140	33	0.236	0.277	4	2	2	61	mucin 16, cell surface associated	ENST00000397910.4
Case#4-Relapse-WholeTumor	COL5A3	19	10103734	Missense_Mutation	C	T	p.G587R	134	65	0.485	0.570	4	2	2	64	collagen, type V, alpha 3	ENST00000264828.3
Case#4-Relapse-WholeTumor	ZNF844	19	12184876	Missense_Mutation	A	C	p.N12H	631	125	0.198	0.233	4	2	2	373	zinc finger protein 844	ENST00000439326.3
Case#4-Relapse-WholeTumor	hsa-mir-1199	19	14185226	Missense_Mutation	T	C	p.V198A	144	10	0.069	0.082	4	2	2	46		ENST00000587086.1
Case#4-Relapse-WholeTumor	CD97	19	14507986	Nonsense_Mutation	G	A	p.W192*	248	97	0.391	0.460	4	2	2	207	CD97 molecule	ENST00000242786.5
Case#4-Relapse-WholeTumor	CALR3	19	16601198	Missense_Mutation	G	A	p.S126L	197	78	0.396	0.465	4	2	2	50	calreticulin 3	ENST00000269881.3
Case#4-Relapse-WholeTumor	NWD1	19	16855265	Missense_Mutation	A	G	p.I78V	213	15	0.070	0.083	4	2	2	92	NACHT and WD repeat domain containing 1	ENST00000552788.1
Case#4-Relapse-WholeTumor	SSBP4	19	18541675	Missense_Mutation	G	T	p.V102F	252	90	0.357	0.420	4	2	2	129	single stranded DNA binding protein 4	ENST00000270061.7
Case#4-Relapse-WholeTumor	SLC7A10	19	33700222	Missense_Mutation	C	T	p.R478K	98	48	0.490	0.576	4	2	2	56	solute carrier family 7 (neutral amino acid transporter light chain, asc system), member 10	ENST00000253188.4
Case#4-Relapse-WholeTumor	LGI4	19	35622939	Missense_Mutation	C	T	p.E108K	94	36	0.383	0.450	4	2	2	69	leucine-rich repeat LGI family, member 4	ENST00000310123.3
Case#4-Relapse-WholeTumor	CTD-2162K18.4	19	37266288	Splice_Site	G	T	p.G45V	279	60	0.215	0.253	4	2	2	112		ENST00000590750.1
Case#4-Relapse-WholeTumor	WDR87	19	38379375	Nonsense_Mutation	T	A	p.R1607*	327	66	0.202	0.237	4	2	2	211	WD repeat domain 87	ENST00000303868.5
Case#4-Relapse-WholeTumor	FCGBP	19	40419960	Missense_Mutation	C	T	p.D1012N	83	23	0.277	0.326	4	2	2	53	Fc fragment of IgG binding protein	ENST00000221347.6
Case#4-Relapse-WholeTumor	ZNF284	19	44586178	Missense_Mutation	C	T	p.S52F	201	85	0.423	0.497	4	2	2	157	zinc finger protein 284	ENST00000421176.3
Case#4-Relapse-WholeTumor	SLC8A2	19	47935658	Missense_Mutation	G	A	p.P719S	70	31	0.443	0.521	4	2	2	39	solute carrier family 8 (sodium/calcium exchanger), member 2	ENST00000236877.6
Case#4-Relapse-WholeTumor	CARD8	19	48737706	Nonsense_Mutation	A	T	p.C10*	173	10	0.058	0.068	4	2	2	113	caspase recruitment domain family, member 8	ENST00000359009.4
Case#4-Relapse-WholeTumor	FUT2	19	49206674	Nonsense_Mutation	G	A	p.W154*	134	11	0.082	0.097	4	2	2	99	fucosyltransferase 2 (secretor status included)	ENST00000425340.2
Case#4-Relapse-WholeTumor	NR1H2	19	50885729	Missense_Mutation	C	T	p.P418L	61	12	0.197	0.231	4	2	2	32	nuclear receptor subfamily 1, group H, member 2	ENST00000253727.5
Case#4-Relapse-WholeTumor	VN1R4	19	53770381	Missense_Mutation	G	T	p.R180S	578	82	0.142	0.167	4	2	2	352	vomeronasal 1 receptor 4	ENST00000311170.4
Case#4-Relapse-WholeTumor	LILRA4	19	54848929	Missense_Mutation	G	A	p.P232S	152	56	0.368	0.455	3	2	1	103	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 4	ENST00000291759.4
Case#4-Relapse-WholeTumor	PEG3	19	57327232	Missense_Mutation	C	T	p.E860K	113	35	0.310	0.364	4	2	2	96	paternally expressed 3	ENST00000326441.9
Case#4-Relapse-WholeTumor	SLC27A5	19	59010979	Missense_Mutation	T	G	p.E516A	193	79	0.409	0.481	4	2	2	92	solute carrier family 27 (fatty acid transporter), member 5	ENST00000263093.2
Case#4-Relapse-WholeTumor	KCNF1	2	11053119	Missense_Mutation	C	G	p.F189L	162	104	0.642	0.868	2	2	0	129	potassium voltage-gated channel, subfamily F, member 1	ENST00000295082.1
Case#4-Relapse-WholeTumor	XDH	2	31588406	Missense_Mutation	C	A	p.G821C	44	16	0.364	0.491	2	2	0	63	xanthine dehydrogenase	ENST00000379416.3
Case#4-Relapse-WholeTumor	LTBP1	2	33585726	Missense_Mutation	G	A	p.D1355N	84	66	0.786	1.062	2	2	0	81	latent transforming growth factor beta binding protein 1	ENST00000404816.2
Case#4-Relapse-WholeTumor	FSHR	2	49189921	Missense_Mutation	C	T	p.S680N	123	7	0.057	0.077	2	2	0	122	follicle stimulating hormone receptor	ENST00000406846.2
Case#4-Relapse-WholeTumor	GKN1	2	69201798	Missense_Mutation	C	T	p.R11C	131	34	0.260	0.320	3	2	1	161	gastrokine 1	ENST00000377938.2
Case#4-Relapse-WholeTumor	RETSAT	2	85571180	Missense_Mutation	G	A	p.S492F	275	54	0.196	0.242	3	2	1	173	retinol saturase (all-trans-retinol 13,14-reductase)	ENST00000295802.4
Case#4-Relapse-WholeTumor	GPAT2	2	96688929	Missense_Mutation	G	A	p.R692C	96	24	0.250	0.309	3	2	1	89	glycerol-3-phosphate acyltransferase 2, mitochondrial	ENST00000434632.1
Case#4-Relapse-WholeTumor	SNRNP200	2	96952860	Missense_Mutation	G	A	p.H1175Y	104	47	0.452	0.558	3	2	1	135	small nuclear ribonucleoprotein 200kDa (U5)	ENST00000323853.5
Case#4-Relapse-WholeTumor	INPP4A	2	99172244	Missense_Mutation	A	G	p.T604A	117	6	0.051	0.060	4	3	1	115	inositol polyphosphate-4-phosphatase, type I, 107kDa	ENST00000523221.1
Case#4-Relapse-WholeTumor	SLC9A2	2	103299820	Missense_Mutation	G	A	p.V369I	135	53	0.393	0.462	4	3	1	116	solute carrier family 9, subfamily A (NHE2, cation proton antiporter 2), member 2	ENST00000233969.2
Case#4-Relapse-WholeTumor	FHL2	2	105990066	Missense_Mutation	G	A	p.S94F	179	39	0.218	0.256	4	3	1	131	four and a half LIM domains 2	ENST00000409807.1
Case#4-Relapse-WholeTumor	RGPD3	2	107041320	Missense_Mutation	C	T	p.D1035N	1456	240	0.165	0.194	4	3	1	724	RANBP2-like and GRIP domain containing 3	ENST00000409886.3
Case#4-Relapse-WholeTumor	SLC5A7	2	108622595	Missense_Mutation	G	A	p.A278T	144	36	0.250	0.294	4	3	1	107	solute carrier family 5 (sodium/choline cotransporter), member 7	ENST00000264047.2
Case#4-Relapse-WholeTumor	POLR1B	2	113309473	Missense_Mutation	C	T	p.S295L	267	16	0.060	0.070	4	3	1	207	polymerase (RNA) I polypeptide B, 128kDa	ENST00000263331.5
Case#4-Relapse-WholeTumor	NT5DC4	2	113480696	Missense_Mutation	C	T	p.S163F	77	42	0.545	0.641	4	3	1	84	5'-nucleotidase domain containing 4	ENST00000327581.4
Case#4-Relapse-WholeTumor	MCM6	2	136609000	Missense_Mutation	G	A	p.A630V	147	46	0.313	0.368	4	2	2	105	minichromosome maintenance complex component 6	ENST00000264156.2
Case#4-Relapse-WholeTumor	LRP1B	2	141986902	Missense_Mutation	C	T	p.E234K	169	75	0.444	0.522	4	2	2	116	low density lipoprotein receptor-related protein 1B	ENST00000389484.3
Case#4-Relapse-WholeTumor	KCNJ3	2	155711406	Missense_Mutation	G	A	p.E363K	237	105	0.443	0.521	4	2	2	41	potassium inwardly-rectifying channel, subfamily J, member 3	ENST00000295101.2
Case#4-Relapse-WholeTumor	KLHL41	2	170366728	Missense_Mutation	G	C	p.C147S	172	31	0.180	0.212	4	2	2	77	kelch-like family member 41	ENST00000284669.1
Case#4-Relapse-WholeTumor	FASTKD1	2	170419831	Missense_Mutation	G	A	p.S159F	110	43	0.391	0.460	4	2	2	69	FAST kinase domains 1	ENST00000453153.2
Case#4-Relapse-WholeTumor	SCRN3	2	175268898	Missense_Mutation	G	A	p.M203I	154	46	0.299	0.351	4	2	2	90	secernin 3	ENST00000272732.6
Case#4-Relapse-WholeTumor	TTN	2	179413763	Missense_Mutation	C	T	p.D29223N	161	71	0.441	0.518	4	2	2	195	titin	ENST00000591111.1
Case#4-Relapse-WholeTumor	ZNF804A	2	185801210	Missense_Mutation	C	T	p.L363F	93	28	0.301	0.354	4	2	2	76	zinc finger protein 804A	ENST00000302277.6
Case#4-Relapse-WholeTumor	COL3A1	2	189849494	Missense_Mutation	G	A	p.G30R	171	64	0.374	0.440	4	2	2	104	collagen, type III, alpha 1	ENST00000304636.3
Case#4-Relapse-WholeTumor	COL5A2	2	189916185	Missense_Mutation	G	A	p.P931L	127	52	0.409	0.481	4	2	2	91	collagen, type V, alpha 2	ENST00000374866.3
Case#4-Relapse-WholeTumor	SLC39A10	2	196548592	Missense_Mutation	A	G	p.N393S	177	61	0.345	0.405	4	2	2	98	solute carrier family 39 (zinc transporter), member 10	ENST00000409086.3
Case#4-Relapse-WholeTumor	HECW2	2	197297876	Nonsense_Mutation	C	T	p.W91*	209	86	0.411	0.484	4	2	2	120	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	ENST00000260983.3
Case#4-Relapse-WholeTumor	SPATS2L	2	201342647	Missense_Mutation	C	T	p.R524W	129	55	0.426	0.501	4	2	2	111	spermatogenesis associated, serine-rich 2-like	ENST00000358677.5
Case#4-Relapse-WholeTumor	ABCA12	2	215910594	Missense_Mutation	C	T	p.S280N	110	22	0.200	0.235	4	2	2	83	ATP-binding cassette, sub-family A (ABC1), member 12	ENST00000272895.7
Case#4-Relapse-WholeTumor	PLCD4	2	219486254	Missense_Mutation	G	C	p.E158Q	419	169	0.403	0.474	4	2	2	259	phospholipase C, delta 4	ENST00000450993.2
Case#4-Relapse-WholeTumor	CUL3	2	225400319	Missense_Mutation	G	T	p.L102I	161	22	0.137	0.161	4	2	2	90	cullin 3	ENST00000264414.4
Case#4-Relapse-WholeTumor	COL4A3	2	228137815	Missense_Mutation	G	A	p.G637R	54	25	0.463	0.544	4	2	2	29	collagen, type IV, alpha 3 (Goodpasture antigen)	ENST00000396578.3
Case#4-Relapse-WholeTumor	SPHKAP	2	228882374	Missense_Mutation	G	A	p.R1066W	103	42	0.408	0.479	4	2	2	56	SPHK1 interactor, AKAP domain containing	ENST00000392056.3
Case#4-Relapse-WholeTumor	SIRPG	20	1629760	Missense_Mutation	C	T	p.R123Q	526	202	0.384	0.451	4	3	1	406	signal-regulatory protein gamma	ENST00000303415.3
Case#4-Relapse-WholeTumor	PTPRA	20	2985771	Nonsense_Mutation	C	T	p.R261*	326	112	0.344	0.404	4	2	2	235	protein tyrosine phosphatase, receptor type, A	ENST00000216877.6
Case#4-Relapse-WholeTumor	PTPRT	20	41408885	Missense_Mutation	C	T	p.E181K	199	84	0.422	0.496	4	2	2	147	protein tyrosine phosphatase, receptor type, T	ENST00000373187.1
Case#4-Relapse-WholeTumor	WFDC12	20	43752816	Missense_Mutation	C	T	p.G57E	136	52	0.382	0.450	4	2	2	89	WAP four-disulfide core domain 12	ENST00000372785.3
Case#4-Relapse-WholeTumor	ZSWIM1	20	44512136	Missense_Mutation	C	T	p.A302V	92	25	0.272	0.319	4	2	2	83	zinc finger, SWIM-type containing 1	ENST00000372523.1
Case#4-Relapse-WholeTumor	SLC12A5	20	44663604	Missense_Mutation	G	A	p.E47K	241	81	0.336	0.395	4	2	2	229	solute carrier family 12 (potassium/chloride transporter), member 5	ENST00000454036.2
Case#4-Relapse-WholeTumor	SULF2	20	46307419	Splice_Site	C	T		111	43	0.387	0.455	4	2	2	72	sulfatase 2	ENST00000359930.4
Case#4-Relapse-WholeTumor	CSE1L	20	47688977	Missense_Mutation	T	G	p.V308G	262	108	0.412	0.485	4	2	2	133	CSE1 chromosome segregation 1-like (yeast)	ENST00000262982.2
Case#4-Relapse-WholeTumor	TSHZ2	20	51872411	Missense_Mutation	C	T	p.A805V	121	56	0.463	0.544	4	2	2	70	teashirt zinc finger homeobox 2	ENST00000371497.5
Case#4-Relapse-WholeTumor	EDN3	20	57876722	Missense_Mutation	G	A	p.D104N	187	73	0.390	0.459	4	2	2	120	endothelin 3	ENST00000337938.2
Case#4-Relapse-WholeTumor	CDH26	20	58562571	Nonsense_Mutation	C	T	p.R301*	201	84	0.418	0.491	4	2	2	89	cadherin 26	ENST00000244047.5
Case#4-Relapse-WholeTumor	ZNF512B	20	62595699	Missense_Mutation	G	A	p.S436F	144	56	0.389	0.457	4	2	2	73	zinc finger protein 512B	ENST00000450537.1
Case#4-Relapse-WholeTumor	ETS2	21	40188935	Missense_Mutation	A	T	p.N170I	194	34	0.175	0.206	4	2	2	99	v-ets avian erythroblastosis virus E26 oncogene homolog 2	ENST00000360214.3
Case#4-Relapse-WholeTumor	FAM230A	22	20710213	Missense_Mutation	A	T	p.T649S	428	39	0.091	0.096	13	9	4	58	family with sequence similarity 230, member A	ENST00000434783.3
Case#4-Relapse-WholeTumor	IL2RB	22	37524258	Missense_Mutation	G	A	p.P512S	118	44	0.373	0.438	4	2	2	54	interleukin 2 receptor, beta	ENST00000216223.5
Case#4-Relapse-WholeTumor	PLXNB2	22	50721492	Missense_Mutation	C	T	p.V935I	93	7	0.075	0.088	4	2	2	65	plexin B2	ENST00000449103.1

Case#4-Relapse-WholeTumor	SHANK3	22	51117034	Missense_Mutation	G	T	p.D121Y	167	33	0.198	0.232	4	2	2	78	SH3 and multiple ankyrin repeat domains 3	ENST00000414786.2
Case#4-Relapse-WholeTumor	ITPR1	3	4725411	Missense_Mutation	G	A	p.V1128M	134	37	0.276	0.341	3	2	1	101	inositol 1,4,5-trisphosphate receptor, type 1	ENST00000443694.2
Case#4-Relapse-WholeTumor	GRM7	3	7456752	Missense_Mutation	G	A	p.R359K	162	25	0.154	0.190	3	2	1	132	glutamate receptor, metabotropic 7	ENST00000357716.4
Case#4-Relapse-WholeTumor	IRAK2	3	10251282	Missense_Mutation	C	T	p.P145L	91	27	0.297	0.366	3	2	1	43	interleukin-1 receptor-associated kinase 2	ENST00000256458.4
Case#4-Relapse-WholeTumor	RFTN1	3	16399542	Missense_Mutation	C	T	p.G348D	95	45	0.474	0.585	3	2	1	64	raftlin, lipid raft linker 1	ENST00000334133.4
Case#4-Relapse-WholeTumor	SCN5A	3	38674744	Missense_Mutation	C	T	p.E19K	73	40	0.548	0.676	3	2	1	80	sodium channel, voltage-gated, type V, alpha subunit	ENST00000333535.4
Case#4-Relapse-WholeTumor	SCN10A	3	38751016	Missense_Mutation	G	A	p.L1412F	151	70	0.464	0.572	3	2	1	155	sodium channel, voltage-gated, type X, alpha subunit	ENST00000449082.2
Case#4-Relapse-WholeTumor	SCN11A	3	38888372	Missense_Mutation	C	T	p.R1730K	210	93	0.443	0.547	3	2	1	304	sodium channel, voltage-gated, type XI, alpha subunit	ENST00000302328.3
Case#4-Relapse-WholeTumor	MYRIP	3	40291738	Missense_Mutation	C	T	p.S763L	144	33	0.229	0.283	3	2	1	118	myosin VIIA and Rab interacting protein	ENST00000302541.6
Case#4-Relapse-WholeTumor	FAM198A	3	43074665	Missense_Mutation	T	C	p.S304P	86	12	0.140	0.172	3	2	1	62	family with sequence similarity 198, member A	ENST00000430121.2
Case#4-Relapse-WholeTumor	FAM198A	3	43074831	Missense_Mutation	G	A	p.R359Q	110	7	0.064	0.079	3	2	1	78	family with sequence similarity 198, member A	ENST00000430121.2
Case#4-Relapse-WholeTumor	RAD54L2	3	51668017	Missense_Mutation	T	A	p.F370I	93	7	0.075	0.093	3	2	1	76	RAD54-like 2 (S. cerevisiae)	ENST00000409535.2
Case#4-Relapse-WholeTumor	DNAH1	3	52430526	Missense_Mutation	G	A	p.G3801D	103	6	0.058	0.072	3	2	1	68	dynein, axonemal, heavy chain 1	ENST00000420323.2
Case#4-Relapse-WholeTumor	FLNB	3	58118606	Missense_Mutation	G	A	p.E1488K	156	41	0.263	0.324	3	2	1	147	filamin B, beta	ENST00000295956.4
Case#4-Relapse-WholeTumor	FLNB	3	58133951	Missense_Mutation	C	T	p.S1916F	127	38	0.299	0.369	3	2	1	91	filamin B, beta	ENST00000295956.4
Case#4-Relapse-WholeTumor	UBA3	3	69120709	Missense_Mutation	A	C	p.N108K	173	60	0.347	0.428	3	2	1	73	ubiquitin-like modifier activating enzyme 3	ENST00000361055.4
Case#4-Relapse-WholeTumor	ROBO2	3	77571939	Missense_Mutation	G	A	p.D274N	93	30	0.323	0.398	3	2	1	87	roundabout, axon guidance receptor, homolog 2 (Drosophila)	ENST00000461745.1
Case#4-Relapse-WholeTumor	CD96	3	111319630	Missense_Mutation	C	G	p.S335C	126	33	0.262	0.323	3	2	1	73	CD96 molecule	ENST00000283285.5
Case#4-Relapse-WholeTumor	DRD3	3	113858514	Missense_Mutation	G	A	p.P186S	66	35	0.530	0.655	3	2	1	54	dopamine receptor D3	ENST00000460779.1
Case#4-Relapse-WholeTumor	COL6A6	3	130289826	Missense_Mutation	G	A	p.D856N	153	82	0.536	0.661	3	2	1	100	collagen, type VI, alpha 6	ENST00000358511.6
Case#4-Relapse-WholeTumor	PRR23B	3	138739020	Missense_Mutation	C	T	p.E162K	115	54	0.470	0.580	3	2	1	74	proline rich 23B	ENST00000329447.5
Case#4-Relapse-WholeTumor	CLSTN2	3	140140069	Missense_Mutation	C	T	p.T247I	193	101	0.523	0.646	3	2	1	253	calsyntenin 2	ENST00000458420.3
Case#4-Relapse-WholeTumor	PLS1	3	142408605	Missense_Mutation	C	T	p.P376L	98	14	0.143	0.176	3	2	1	90	plastin 1	ENST00000337777.3
Case#4-Relapse-WholeTumor	MECOM	3	168834174	Missense_Mutation	G	A	p.P308S	214	62	0.290	0.358	3	2	1	165	MDS1 and EVI1 complex locus	ENST00000464456.1
Case#4-Relapse-WholeTumor	LRRIQ4	3	169540280	Missense_Mutation	G	A	p.E191K	149	46	0.309	0.381	3	2	1	121	leucine-rich repeats and IQ motif containing 4	ENST00000340806.6
Case#4-Relapse-WholeTumor	LIPH	3	185237097	Splice_Site	C	T	p.G240E	91	43	0.473	0.583	3	2	1	55	lipase, member H	ENST00000296252.4
Case#4-Relapse-WholeTumor	TP63	3	189585721	Missense_Mutation	G	A	p.E328K	196	51	0.260	0.321	3	2	1	105	tumor protein p63	ENST00000264731.3
Case#4-Relapse-WholeTumor	DLG1	3	196786775	Missense_Mutation	G	A	p.S834F	96	21	0.219	0.270	3	2	1	87	discs, large homolog 1 (Drosophila)	ENST00000419354.1
Case#4-Relapse-WholeTumor	DHX15	4	24531266	Missense_Mutation	G	A	p.T743I	223	38	0.170	0.200	4	2	2	176	DEAH (Asp-Glu-Ala-His) box helicase 15	ENST00000336812.4
Case#4-Relapse-WholeTumor	ERVMER34-1	4	53610260	Nonsense_Mutation	CC	TT	p.W476*	140	52	0.371	0.437	4	2	2	49	endogenous retrovirus group MER34, member 1	ENST00000443173.1
Case#4-Relapse-WholeTumor	SULT1E1	4	70723251	Missense_Mutation	C	T	p.D38N	213	84	0.394	0.464	4	2	2	135	sulfotransferase family 1E, estrogen-preferring, member 1	ENST00000226444.3
Case#4-Relapse-WholeTumor	SDAD1	4	76877139	Nonsense_Mutation	G	A	p.R669*	267	117	0.438	0.515	4	2	2	175	SDA1 domain containing 1	ENST00000356260.5
Case#4-Relapse-WholeTumor	GRID2	4	94138027	Missense_Mutation	T	C	p.C310R	259	55	0.212	0.250	4	2	2	146	glutamate receptor, ionotropic, delta 2	ENST00000282020.4
Case#4-Relapse-WholeTumor	ADH7	4	100341946	Missense_Mutation	T	G	p.K202T	128	62	0.484	0.569	4	2	2	76	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	ENST00000209665.4
Case#4-Relapse-WholeTumor	DNAJB14	4	100827712	Nonsense_Mutation	G	A	p.R232*	197	79	0.401	0.471	4	2	2	139	DnaJ (Hsp40) homolog, subfamily B, member 14	ENST00000442697.2
Case#4-Relapse-WholeTumor	BANK1	4	102839287	Missense_Mutation	G	A	p.A383T	106	7	0.066	0.078	4	2	2	62	B-cell scaffold protein with ankyrin repeats 1	ENST00000322953.4
Case#4-Relapse-WholeTumor	TET2	4	106197130	Missense_Mutation	T	G	p.D1821E	78	27	0.346	0.407	4	2	2	60	tet methylcytosine dioxygenase 2	ENST00000540549.1
Case#4-Relapse-WholeTumor	NDST4	4	115750954	Missense_Mutation	CC	TT	p.830_831MD>IN	92	39	0.424	0.498	4	2	2	90	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4	ENST00000264363.2
Case#4-Relapse-WholeTumor	INPP4B	4	143094937	Missense_Mutation	A	G	p.S403P	150	30	0.200	0.235	4	2	2	112	inositol polyphosphate-4-phosphatase, type II, 105kDa	ENST00000513000.1
Case#4-Relapse-WholeTumor	NR3C2	4	149041348	Missense_Mutation	C	T	p.E868K	99	42	0.424	0.499	4	2	2	65	nuclear receptor subfamily 3, group C, member 2	ENST00000358102.3
Case#4-Relapse-WholeTumor	RPS3A	4	152024138	Missense_Mutation	A	C	p.Q38P	206	11	0.053	0.063	4	2	2	124	ribosomal protein S3A	ENST00000509736.1
Case#4-Relapse-WholeTumor	AADAT	4	170983060	Missense_Mutation	G	A	p.P407S	106	36	0.340	0.399	4	2	2	68	aminoadipate aminotransferase	ENST00000337664.4
Case#4-Relapse-WholeTumor	TENM3	4	183696244	Missense_Mutation	G	A	p.E1748K	127	57	0.449	0.528	4	2	2	78	teneurin transmembrane protein 3	ENST00000511685.1
Case#4-Relapse-WholeTumor	TENM3	4	183710475	Missense_Mutation	G	A	p.G1845E	280	100	0.357	0.420	4	2	2	136	teneurin transmembrane protein 3	ENST00000511685.1
Case#4-Relapse-WholeTumor	KIAA0947	5	5464375	Missense_Mutation	C	T	p.P1643L	119	25	0.210	0.259	3	2	1	71		ENST00000296564.7
Case#4-Relapse-WholeTumor	PRDM9	5	23526641	Missense_Mutation	G	A	p.G482R	246	120	0.488	0.602	3	2	1	179	PR domain containing 9	ENST00000296682.3
Case#4-Relapse-WholeTumor	NIPBL	5	37014813	Missense_Mutation	C	T	p.S1530F	83	13	0.157	0.193	3	2	1	51	Nipped-B homolog (Drosophila)	ENST00000282516.8
Case#4-Relapse-WholeTumor	DDX4	5	55077770	Missense_Mutation	G	A	p.D196N	187	53	0.283	0.350	3	2	1	139	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4	ENST00000505374.1
Case#4-Relapse-WholeTumor	ANKRA2	5	72858439	Missense_Mutation	C	T	p.V90M	210	110	0.524	0.647	3	2	1	114	ankyrin repeat, family A (RFXANK-like), 2	ENST00000296785.3
Case#4-Relapse-WholeTumor	IQGAP2	5	75866423	Nonsense_Mutation	C	T	p.R108*	358	172	0.480	0.593	3	2	1	236	IQ motif containing GTPase activating protein 2	ENST00000274364.6
Case#4-Relapse-WholeTumor	AGGF1	5	76332468	Missense_Mutation	G	T	p.V202L	116	8	0.069	0.085	3	2	1	84	angiogenic factor with G patch and FHA domains 1	ENST00000312916.7
Case#4-Relapse-WholeTumor	PCSK1	5	95729001	Missense_Mutation	C	T	p.D656N	100	21	0.210	0.259	3	2	1	136	proprotein convertase subtilisin/kexin type 1	ENST00000311106.3
Case#4-Relapse-WholeTumor	PCDHA10	5	140237666	Missense_Mutation	C	T	p.S678L	140	37	0.264	0.326	3	2	1	174	protocadherin alpha 10	ENST00000307360.5
Case#4-Relapse-WholeTumor	PCDHB5	5	140515210	Missense_Mutation	G	A	p.R65Q	59	36	0.610	0.753	3	2	1	53	protocadherin beta 5	ENST00000231134.5
Case#4-Relapse-WholeTumor	PCDHB6	5	140530818	Missense_Mutation	G	A	p.G327E	193	93	0.482	0.595	3	2	1	133	protocadherin beta 6	ENST00000231136.1
Case#4-Relapse-WholeTumor	PCDHGB3	5	140750285	Missense_Mutation	G	T	p.M108I	170	49	0.288	0.356	3	2	1	124	protocadherin gamma subfamily B, 3	ENST00000576222.1
Case#4-Relapse-WholeTumor	PCDHGA10	5	140795122	Missense_Mutation	C	T	p.P794S	288	77	0.267	0.330	3	2	1	203	protocadherin gamma subfamily A, 10	ENST00000398610.2
Case#4-Relapse-WholeTumor	GABRP	5	170222377	Missense_Mutation	G	A	p.G136R	137	24	0.175	0.216	3	2	1	78	gamma-aminobutyric acid (GABA) A receptor, pi	ENST00000518525.1
Case#4-Relapse-WholeTumor	STK10	5	171532741	Splice_Site	C	A	p.W263C	75	16	0.213	0.263	3	2	1	65	serine/threonine kinase 10	ENST00000176763.5
Case#4-Relapse-WholeTumor	F13A1	6	6224978	Missense_Mutation	C	A	p.S305I	361	97	0.269	0.300	6	4	2	139	coagulation factor XIII, A1 polypeptide	ENST00000264870.3
Case#4-Relapse-WholeTumor	HIVEP1	6	12121325	Missense_Mutation	CC	TT	p.P433F	218	28	0.128	0.143	6	4	2	106	human immunodeficiency virus type I enhancer binding protein 1	ENST00000379388.2
Case#4-Relapse-WholeTumor	ANKS1A	6	34951202	Splice_Site	GG	AA	p.G338K	301	86	0.286	0.319	6	4	2	79	ankyrin repeat and sterile alpha motif domain containing 1A	ENST00000360359.3
Case#4-Relapse-WholeTumor	FAM83B	6	54735423	Missense_Mutation	C	T	p.P127S	108	17	0.157	0.176	6	4	2	52	family with sequence similarity 83, member B	ENST00000306858.7
Case#4-Relapse-WholeTumor	FAM83B	6	54806267	Missense_Mutation	C	G	p.S833C	194	33	0.170	0.190	6	4	2	90	family with sequence similarity 83, member B	ENST00000306858.7
Case#4-Relapse-WholeTumor	GFRAL	6	55198740	Missense_Mutation	C	T	p.S105L	395	206	0.522	0.583	6	4	2	107	GDNF family receptor alpha like	ENST00000340465.2
Case#4-Relapse-WholeTumor	DST	6	56422239	Missense_Mutation	G	T	p.Q4629K	494	267	0.540	0.604	6	4	2	198	dystonin	ENST00000361203.3
Case#4-Relapse-WholeTumor	PRIM2	6	57512471	Splice_Site	G	A		494	72	0.146	0.166	5	3	2	324	primase, DNA, polypeptide 2 (58kDa)	ENST00000389488.2
Case#4-Relapse-WholeTumor	KHDC3L	6	74073531	Missense_Mutation	C	G	p.A201G	77	10	0.130	0.176	2	2	0	91	KH domain containing 3-like, subcortical maternal complex member	ENST00000370367.3
Case#4-Relapse-WholeTumor	THEMIS	6	128135008	Missense_Mutation	C	T	p.D260N	87	61	0.701	0.947	2	2	0	85	thymocyte selection associated	ENST00000368248.2
Case#4-Relapse-WholeTumor	PTPRK	6	128326312	Missense_Mutation	C	T	p.R803Q	108	74	0.685	0.926	2	2	0	120	protein tyrosine phosphatase, receptor type, K	ENST00000368215.3
Case#4-Relapse-WholeTumor	BCLAF1	6	136593183	Missense_Mutation	G	C	p.H665D	228	20	0.088	0.103	4	2	2	86	BCL2-associated transcription factor 1	ENST00000531224.1
Case#4-Relapse-WholeTumor	NOX3	6	155761246	Missense_Mutation	G	T	p.T171K	60	5	0.083	0.113	2	2	0	53	NADPH oxidase 3	ENST00000159060.2
Case#4-Relapse-WholeTumor	SUN1	7	881668	Missense_Mutation	C	T	p.H118Y	85	7	0.082	0.111	2	1	1	82	Sad1 and UNC84 domain containing 1	ENST00000405266.1
Case#4-Relapse-WholeTumor	CCZ1B	7	6844574	Missense_Mutation	C	G	p.M367I	130	12	0.092	0.125	2	1	1	126	CCZ1 vacuolar protein trafficking and biogenesis associated homolog B (S. cerevisiae)	ENST00000316731.8
Case#4-Relapse-WholeTumor	VWDE	7	12396999	Missense_Mutation	A	T	p.S1139R	85	28	0.329	0.445	2	1	1	131	von Willebrand factor D and EGF domains	ENST00000275358.3
Case#4-Relapse-WholeTumor	HDAC9	7	18788735	Missense_Mutation	G	A	p.E670K	96	27	0.281	0.380	2	1	1	106	histone deacetylase 9	ENST00000432645.2
Case#4-Relapse-WholeTumor	HDAC9	7	18993787	Missense_Mutation	G	A	p.D983N	65	21	0.323	0.437	2	1	1	69	histone deacetylase 9	ENST00000432645.2
Case#4-Relapse-WholeTumor	ABCB5	7	20795083	Missense_Mutation	G	A	p.G1204R	75	29	0.387	0.523	2	1	1	55	ATP-binding cassette, sub-family B (MDR/TAP), member 5	ENST00000404938.2
Case#4-Relapse-WholeTumor	C7orf31	7	25181912	Missense_Mutation	T	C	p.H300R	108	7	0.065	0.088	2	1	1	59	chromosome 7 open reading frame 31	ENST00000409280.1
Case#4-Relapse-WholeTumor	STYXL1	7	75633078	Missense_Mutation	A	G	p.I232T	56	10	0.179	0.241	2	1	1	64	serine/threonine/tyrosine interacting-like 1	ENST00000248600.1
Case#4-Relapse-WholeTumor	PCLO	7	82581909	Missense_Mutation	G	A	p.P2787L	132	46	0.348	0.471	2	1	1	220	piccolo presynaptic cytomatrix protein	ENST00000333891.9
Case#4-Relapse-WholeTumor	TECPR1	7	97866139	Missense_Mutation	G	A	p.A377V	75	26	0.347	0.468	2	1	1	79	tectonin beta-propeller repeat containing 1	ENST00000447648.2
Case#4-Relapse-WholeTumor	SH2B2	7	101928495	Missense_Mutation	G	C	p.A16P	72	5	0.069	0.094	2	1	1	50	SH2B adaptor protein 2	ENST00000536178.1

Case#4-Relapse-WholeTumor	POT1	7	124503424	Missense_Mutation	C	T	p.G176R	102	45	0.441	0.596	2	1	1	95	protection of telomeres 1	ENST00000357628.3
Case#4-Relapse-WholeTumor	LRGUK	7	133932357	Missense_Mutation	T	C	p.M678T	116	8	0.069	0.093	2	1	1	66	leucine-rich repeats and guanylate kinase domain containing	ENST00000285928.2
Case#4-Relapse-WholeTumor	BRAF	7	140453135	Missense_Mutation	CA	TT	p.V600E	119	44	0.370	0.500	2	1	1	84	B-Raf proto-oncogene, serine/threonine kinase	ENST00000288602.6
Case#4-Relapse-WholeTumor	CLEC5A	7	141635733	Missense_Mutation	C	T	p.E76K	90	38	0.422	0.571	2	1	1	130	C-type lectin domain family 5, member A	ENST00000546910.1
Case#4-Relapse-WholeTumor	MGAM	7	141750519	Missense_Mutation	C	T	p.S887L	97	37	0.381	0.515	2	1	1	132	maltase-glucoamylase (alpha-glucosidase)	ENST00000549489.2
Case#4-Relapse-WholeTumor	RP11-1220K2.2	7	141889282	Nonsense_Mutation	G	A	p.W1441*	143	61	0.427	0.576	2	1	1	167		ENST00000477922.3
Case#4-Relapse-WholeTumor	CTAGE15	7	143270172	Missense_Mutation	A	G	p.E421G	105	9	0.086	0.116	2	1	1	117	CTAGE family, member 15	ENST00000420911.2
Case#4-Relapse-WholeTumor	OR6B1	7	143701367	Missense_Mutation	C	T	p.S93F	142	33	0.232	0.314	2	1	1	246	olfactory receptor, family 6, subfamily B, member 1	ENST00000408922.2
Case#4-Relapse-WholeTumor	LRRC61	7	150034378	Missense_Mutation	A	G	p.N143S	21	4	0.190	0.257	2	1	1	53	leucine rich repeat containing 61	ENST00000359623.4
Case#4-Relapse-WholeTumor	MYOM2	8	2077195	Missense_Mutation	G	A	p.E1259K	175	31	0.177	0.208	4	2	2	90	myomesin 2	ENST00000262113.4
Case#4-Relapse-WholeTumor	ZNF705G	8	7215569	Missense_Mutation	G	A	p.H278Y	1191	238	0.200	0.235	4	2	2	727	zinc finger protein 705G	ENST00000400156.4
Case#4-Relapse-WholeTumor	PCM1	8	17817553	Missense_Mutation	G	T	p.A691S	117	6	0.051	0.063	3	2	1	120	pericentriolar material 1	ENST00000519253.1
Case#4-Relapse-WholeTumor	FZD3	8	28385409	Missense_Mutation	C	T	p.P378S	292	146	0.500	0.617	3	2	1	217	frizzled class receptor 3	ENST00000240093.3
Case#4-Relapse-WholeTumor	DUSP4	8	29195991	Missense_Mutation	G	A	p.L203F	99	47	0.475	0.586	3	2	1	103	dual specificity phosphatase 4	ENST00000240100.2
Case#4-Relapse-WholeTumor	C8orf86	8	38370002	Missense_Mutation	G	A	p.P192L	159	41	0.258	0.318	3	2	1	129	chromosome 8 open reading frame 86	ENST00000358138.1
Case#4-Relapse-WholeTumor	TACC1	8	38684765	Missense_Mutation	C	T	p.S511F	201	96	0.478	0.589	3	2	1	136	transforming, acidic coiled-coil containing protein 1	ENST00000317827.4
Case#4-Relapse-WholeTumor	ZMAT4	8	40532391	Missense_Mutation	G	A	p.P137S	99	44	0.444	0.549	3	2	1	87	zinc finger, matrin-type 4	ENST00000297737.6
Case#4-Relapse-WholeTumor	ANK1	8	41573301	Missense_Mutation	C	T	p.E491K	94	55	0.585	0.722	3	2	1	122	ankyrin 1, erythrocytic	ENST00000347528.4
Case#4-Relapse-WholeTumor	HOOK3	8	42841811	Missense_Mutation	C	T	p.R469C	149	30	0.201	0.249	3	2	1	117	hook microtubule-tethering protein 3	ENST00000307602.4
Case#4-Relapse-WholeTumor	SNTG1	8	51415354	Missense_Mutation	A	T	p.N127I	79	47	0.595	0.734	3	2	1	31	syntrophin, gamma 1	ENST00000522124.1
Case#4-Relapse-WholeTumor	PXDNL	8	52320757	Nonsense_Mutation	G	A	p.Q1143*	110	49	0.445	0.550	3	2	1	93	peroxidasin homolog (Drosophila)-like	ENST00000356297.4
Case#4-Relapse-WholeTumor	NKAIN3	8	63492222	Missense_Mutation	G	A	p.R60Q	119	62	0.521	0.643	3	2	1	135	Na+/K+ transporting ATPase interacting 3	ENST00000523211.1
Case#4-Relapse-WholeTumor	MCMDC2	8	67789615	Missense_Mutation	C	T	p.P106L	139	62	0.446	0.551	3	2	1	116	minichromosome maintenance domain containing 2	ENST00000422365.2
Case#4-Relapse-WholeTumor	FABP4	8	82392716	Missense_Mutation	G	A	p.S64F	133	31	0.233	0.288	3	2	1	66	fatty acid binding protein 4, adipocyte	ENST00000256104.4
Case#4-Relapse-WholeTumor	LRRCC1	8	86049698	Splice_Site	G	A		94	20	0.213	0.263	3	2	1	69	leucine rich repeat and coiled-coil centrosomal protein 1	ENST00000360375.3
Case#4-Relapse-WholeTumor	SLC7A13	8	87226860	Missense_Mutation	G	A	p.P399S	124	30	0.242	0.299	3	2	1	71	solute carrier family 7 (anionic amino acid transporter), member 13	ENST00000297524.3
Case#4-Relapse-WholeTumor	CNGB3	8	87645012	Missense_Mutation	C	T	p.G430R	113	53	0.469	0.579	3	2	1	114	cyclic nucleotide gated channel beta 3	ENST00000320005.5
Case#4-Relapse-WholeTumor	SYBU	8	110587514	Missense_Mutation	G	A	p.A538V	114	24	0.211	0.260	3	2	1	62	syntabulin (syntaxin-interacting)	ENST00000422135.1
Case#4-Relapse-WholeTumor	FAM84B	8	127569041	Missense_Mutation	C	G	p.W198C	81	27	0.333	0.411	3	2	1	73	family with sequence similarity 84, member B	ENST00000304916.3
Case#4-Relapse-WholeTumor	POU5F1B	8	128428150	Missense_Mutation	CC	TT	p.P14S	117	69	0.590	0.728	3	2	1	76	POU class 5 homeobox 1B	ENST00000465342.2
Case#4-Relapse-WholeTumor	ASAP1	8	131130447	Nonsense_Mutation	G	A	p.Q614*	165	76	0.461	0.568	3	2	1	72	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	ENST00000518721.1
Case#4-Relapse-WholeTumor	EEF1D	8	144663474	Missense_Mutation	C	T	p.G72S	90	19	0.211	0.261	3	2	1	51	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	ENST00000529272.1
Case#4-Relapse-WholeTumor	SCRT1	8	145559810	Nonsense_Mutation	T	A	p.K8*	97	53	0.546	0.674	3	2	1	42	scratch family zinc finger 1	ENST00000332135.4
Case#4-Relapse-WholeTumor	TONSL	8	145666213	Missense_Mutation	C	T	p.R351Q	121	36	0.298	0.367	3	2	1	106	tonsoku-like, DNA repair protein	ENST00000409379.3
Case#4-Relapse-WholeTumor	C8orf33	8	146278132	Missense_Mutation	G	A	p.R56K	173	47	0.272	0.335	3	2	1	96	chromosome 8 open reading frame 33	ENST00000331434.6
Case#4-Relapse-WholeTumor	AK3	9	4740973	Missense_Mutation	C	T	p.G39R	54	37	0.685	0.926	2	2	0	28	adenylate kinase 3	ENST00000381809.3
Case#4-Relapse-WholeTumor	IFNA7	9	21201768	Missense_Mutation	G	A	p.P133S	299	213	0.712	0.963	2	2	0	96	interferon, alpha 7	ENST00000239347.3
Case#4-Relapse-WholeTumor	GALT	9	34646742	Missense_Mutation	C	T	p.A14V	116	30	0.259	0.349	2	2	0	156	galactose-1-phosphate uridylyltransferase	ENST00000378842.3
Case#4-Relapse-WholeTumor	SPATA31A7	9	65506215	Missense_Mutation	C	T	p.E449K	242	59	0.244	0.301	3	2	1	276	SPATA31 subfamily A, member 7	ENST00000355045.2
Case#4-Relapse-WholeTumor	ERCC6L2	9	98638288	Start_Codon_SNP	A	G	p.M1V	80	8	0.100	0.135	2	2	0	52	excision repair cross-complementation group 6-like 2	ENST00000288985.7
Case#4-Relapse-WholeTumor	CTNNAL1	9	111727670	Missense_Mutation	C	G	p.E527Q	117	7	0.060	0.081	2	2	0	102	catenin (cadherin-associated protein), alpha-like 1	ENST00000325551.4
Case#4-Relapse-WholeTumor	EPB41L4B	9	111945049	Missense_Mutation	T	G	p.N816T	154	11	0.071	0.097	2	2	0	154	erythrocyte membrane protein band 4.1 like 4B	ENST00000374566.3
Case#4-Relapse-WholeTumor	C9orf84	9	114454544	Missense_Mutation	T	C	p.E1174G	112	6	0.054	0.072	2	2	0	126	chromosome 9 open reading frame 84	ENST00000318737.4
Case#4-Relapse-WholeTumor	TNFSF15	9	117568247	Missense_Mutation	C	T	p.E16K	38	23	0.605	0.818	2	2	0	38	tumor necrosis factor (ligand) superfamily, member 15	ENST00000374045.4
Case#4-Relapse-WholeTumor	DNLZ	9	139256468	Missense_Mutation	C	G	p.S178T	35	6	0.171	0.232	2	2	0	49	DNL-type zinc finger	ENST00000371738.3
Case#4-Relapse-WholeTumor	EXD3	9	140243844	Missense_Mutation	C	T	p.C545Y	27	4	0.148	0.200	2	2	0	28	exonuclease 3'-5' domain containing 3	ENST00000340951.4
Case#4-Relapse-WholeTumor	CLCN4	X	10181775	Missense_Mutation	G	A	p.G544E	106	84	0.792	NA	NA	NA	NA	76	chloride channel, voltage-sensitive 4	ENST00000380833.4
Case#4-Relapse-WholeTumor	TLR8	X	12938028	Missense_Mutation	G	A	p.R290Q	73	57	0.781	NA	NA	NA	NA	53	toll-like receptor 8	ENST00000218032.6
Case#4-Relapse-WholeTumor	MAOB	X	43656509	Missense_Mutation	C	A	p.A161S	59	6	0.102	NA	NA	NA	NA	70	monoamine oxidase B	ENST00000378069.4
Case#4-Relapse-WholeTumor	MAOB	X	43698248	Nonsense_Mutation	G	A	p.Q49*	33	26	0.788	NA	NA	NA	NA	38	monoamine oxidase B	ENST00000378069.4
Case#4-Relapse-WholeTumor	STARD8	X	67937976	Missense_Mutation	G	A	p.R327Q	100	6	0.060	NA	NA	NA	NA	75	StAR-related lipid transfer (START) domain containing 8	ENST00000252336.6
Case#4-Relapse-WholeTumor	MAGEE1	X	75648447	Missense_Mutation	G	T	p.G42C	113	43	0.381	NA	NA	NA	NA	80	melanoma antigen family E, 1	ENST00000361470.2
Case#4-Relapse-WholeTumor	POF1B	X	84562231	Missense_Mutation	T	G	p.T368P	51	39	0.765	NA	NA	NA	NA	47	premature ovarian failure, 1B	ENST00000262753.4
Case#4-Relapse-WholeTumor	PCDH19	X	99661471	Missense_Mutation	C	T	p.E709K	22	17	0.773	NA	NA	NA	NA	30	protocadherin 19	ENST00000373034.4
Case#4-Relapse-WholeTumor	ESX1	X	103495543	Missense_Mutation	C	T	p.R196Q	39	33	0.846	NA	NA	NA	NA	42	ESX homeobox 1	ENST00000372588.4
Case#4-Relapse-WholeTumor	COL4A5	X	107819152	Missense_Mutation	C	T	p.P187S	59	54	0.915	NA	NA	NA	NA	34	collagen, type IV, alpha 5	ENST00000361603.2
Case#4-Relapse-WholeTumor	RBMXL3	X	114424215	Missense_Mutation	G	A	p.G71S	131	96	0.733	NA	NA	NA	NA	54	RNA binding motif protein, X-linked-like 3	ENST00000424776.3
Case#4-Relapse-WholeTumor	SLC6A14	X	115590023	Missense_Mutation	G	A	p.E611K	78	62	0.795	NA	NA	NA	NA	34	solute carrier family 6 (amino acid transporter), member 14	ENST00000371900.4
Case#4-Relapse-WholeTumor	THOC2	X	122759828	Missense_Mutation	G	A	p.R998C	144	131	0.910	NA	NA	NA	NA	60	THO complex 2	ENST00000245838.8
Case#4-Relapse-WholeTumor	IGSF1	X	130411997	Missense_Mutation	C	T	p.G718E	101	80	0.792	NA	NA	NA	NA	61	immunoglobulin superfamily, member 1	ENST00000361420.3
Case#4-Relapse-WholeTumor	ABCD1	X	153002661	Missense_Mutation	G	C	p.V482L	134	37	0.276	NA	NA	NA	NA	91	ATP-binding cassette, sub-family D (ALD), member 1	ENST00000218104.3
Case#4-Relapse-WholeTumor	F8	X	154156921	Missense_Mutation	C	T	p.R1715Q	87	43	0.494	NA	NA	NA	NA	59	coagulation factor VIII, procoagulant component	ENST00000360256.4
Case#2-Baseline-M420	UBR4	1	19446148	Missense_Mutation	G	A	p.S3453F	141	64	0.454	0.466	4	2	2	95	ubiquitin protein ligase E3 component n-recognin 4	ENST00000375254.3
Case#2-Baseline-M420	USP48	1	22074689	Nonsense_Mutation	G	A	p.R284*	133	56	0.421	0.432	4	2	2	112	ubiquitin specific peptidase 48	ENST00000308271.9
Case#2-Baseline-M420	CSMD2	1	34158630	Missense_Mutation	C	T	p.E191K	135	55	0.407	0.418	4	2	2	153	CUB and Sushi multiple domains 2	ENST00000373380.1
Case#2-Baseline-M420	GUCA2A	1	42629134	Missense_Mutation	G	A	p.P75S	99	46	0.465	0.477	4	2	2	114	guanylate cyclase activator 2A (guanylin)	ENST00000357001.2
Case#2-Baseline-M420	YBX1	1	43162403	Missense_Mutation	C	T	p.P149S	242	105	0.434	0.445	4	2	2	256	Y box binding protein 1	ENST00000321358.7
Case#2-Baseline-M420	EIF2B3	1	45316632	Missense_Mutation	C	T	p.M450I	144	52	0.361	0.371	4	2	2	127	eukaryotic translation initiation factor 2B, subunit 3 gamma, 58kDa	ENST00000360403.2
Case#2-Baseline-M420	TMEM69	1	46159342	Missense_Mutation	T	G	p.F170C	222	102	0.459	0.472	4	2	2	205	transmembrane protein 69	ENST00000372025.4
Case#2-Baseline-M420	NRD1	1	52287201	Missense_Mutation	C	T	p.V464M	106	63	0.594	0.610	4	2	2	107	nardilysin (N-arginine dibasic convertase)	ENST00000354831.7
Case#2-Baseline-M420	MROH7	1	55167778	Missense_Mutation	C	T	p.R1101C	108	47	0.435	0.447	4	2	2	115	maestro heat-like repeat family member 7	ENST00000421030.2
Case#2-Baseline-M420	NFIA	1	61554113	Missense_Mutation	A	G	p.N107S	157	74	0.471	0.484	4	2	2	152	nuclear factor I/A	ENST00000403491.3
Case#2-Baseline-M420	WDR78	1	67292573	Missense_Mutation	G	A	p.P757S	207	95	0.459	0.471	4	2	2	184	WD repeat domain 78	ENST00000371026.3
Case#2-Baseline-M420	OVGP1	1	111957517	Missense_Mutation	T	C	p.S536G	76	27	0.355	0.365	4	2	2	39	oviductal glycoprotein 1, 120kDa	ENST00000369732.3
Case#2-Baseline-M420	MAGI3	1	114201725	Nonsense_Mutation	GTC	TAA	p.V885*	71	22	0.310	0.318	4	2	2	76	membrane associated guanylate kinase, WW and PDZ domain containing 3	ENST00000307546.9
Case#2-Baseline-M420	CD101	1	117554348	Missense_Mutation	C	T	p.L201F	162	64	0.395	0.405	4	2	2	141	CD101 molecule	ENST00000256652.4
Case#2-Baseline-M420	SPRR3	1	152975659	Frame_Shift_Del	GAGCCAGGCT GTACCAAGGT CCCT	-	p.E55fs	302	53	0.175	0.180	4	2	2	295	small proline-rich protein 3	ENST00000295367.4
Case#2-Baseline-M420	FCRL5	1	157494225	Missense_Mutation	G	A	p.H695Y	151	56	0.371	0.381	4	2	2	138	Fc receptor-like 5	ENST00000361835.3
Case#2-Baseline-M420	OR10K1	1	158435851	Missense_Mutation	C	T	p.P167L	176	85	0.483	0.496	4	2	2	169	olfactory receptor, family 10, subfamily K, member 1	ENST00000289451.2

Case#2-Baseline-M420	SPTA1	1	158582643	Missense_Mutation	C	G	p.E2366D	104	46	0.442	0.454	4	2	2	112	spectrin, alpha, erythrocytic 1	ENST00000368147.4
Case#2-Baseline-M420	ADCY10	1	167830176	Missense_Mutation	C	T	p.R581Q	181	88	0.486	0.499	4	2	2	162	adenylate cyclase 10 (soluble)	ENST00000367851.4
Case#2-Baseline-M420	FMO1	1	171254450	Missense_Mutation	G	A	p.D456N	179	86	0.480	0.493	4	2	2	145	flavin containing monooxygenase 1	ENST00000354841.4
Case#2-Baseline-M420	FASLG	1	172634863	Missense_Mutation	G	A	p.E185K	129	59	0.457	0.469	4	2	2	124	Fas ligand (TNF superfamily, member 6)	ENST00000367721.2
Case#2-Baseline-M420	SLC9C2	1	173506151	Missense_Mutation	C	T	p.G529R	111	54	0.486	0.499	4	2	2	129	solute carrier family 9, member C2 (putative)	ENST00000367714.3
Case#2-Baseline-M420	CFH	1	196709900	Missense_Mutation	G	T	p.W978C	131	60	0.458	0.470	4	2	2	141	complement factor H	ENST00000367429.4
Case#2-Baseline-M420	KIF21B	1	200944701	Missense_Mutation	C	T	p.G1514R	83	34	0.410	0.420	4	2	2	85	kinesin family member 21B	ENST00000422435.2
Case#2-Baseline-M420	NUAK2	1	205272869	Missense_Mutation	GG	AA	p.P532L	88	41	0.466	0.478	4	2	2	59	NUAK family, SNF1-like kinase, 2	ENST00000367157.3
Case#2-Baseline-M420	KCNH1	1	211093144	Missense_Mutation	C	T	p.G434R	291	143	0.491	0.504	4	2	2	277	potassium voltage-gated channel, subfamily H (eag-related), member 1	ENST00000271751.4
Case#2-Baseline-M420	USH2A	1	215972377	Missense_Mutation	C	T	p.G3277E	176	91	0.517	0.531	4	2	2	204	Usher syndrome 2A (autosomal recessive, mild)	ENST00000307340.3
Case#2-Baseline-M420	USH2A	1	216061902	Missense_Mutation	C	T	p.E2697K	110	54	0.491	0.504	4	2	2	119	Usher syndrome 2A (autosomal recessive, mild)	ENST00000307340.3
Case#2-Baseline-M420	DISP1	1	223176405	Missense_Mutation	C	T	p.P556S	129	57	0.442	0.453	4	2	2	88	dispatched homolog 1 (Drosophila)	ENST00000284476.6
Case#2-Baseline-M420	SUSD4	1	223396814	Missense_Mutation	G	T	p.D407E	62	26	0.419	0.430	4	2	2	62	sushi domain containing 4	ENST00000343846.3
Case#2-Baseline-M420	OBSCN	1	228494211	Missense_Mutation	G	A	p.G3933E	89	46	0.517	0.530	4	2	2	83	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	ENST00000422127.1
Case#2-Baseline-M420	ABCB10	1	229683251	Missense_Mutation	T	A	p.M306L	211	107	0.507	0.520	4	2	2	198	ATP-binding cassette, sub-family B (MDR/TAP), member 10	ENST00000344517.4
Case#2-Baseline-M420	PCNXL2	1	233270779	Missense_Mutation	C	T	p.V1273M	210	99	0.471	0.484	4	2	2	169	pecanex-like 2 (Drosophila)	ENST00000258229.9
Case#2-Baseline-M420	OR1C1	1	247920918	Missense_Mutation	G	A	p.S264F	125	57	0.456	0.468	4	2	2	134	olfactory receptor, family 1, subfamily C, member 1	ENST00000408896.2
Case#2-Baseline-M420	ARHGAP22	10	49791162	Missense_Mutation	G	A	p.R24W	32	32	1.000	1.053	2	2	0	72	Rho GTPase activating protein 22	ENST00000249601.4
Case#2-Baseline-M420	DLG5	10	79580911	Missense_Mutation	G	A	p.R1111C	49	48	0.980	1.031	2	2	0	83	discs, large homolog 5 (Drosophila)	ENST00000372391.2
Case#2-Baseline-M420	MUC6	11	1030779	Splice_Site	GC	TT	p.A229N	35	33	0.943	0.992	2	2	0	51	mucin 6, oligomeric mucus/gel-forming	ENST00000421673.2
Case#2-Baseline-M420	OR51I1	11	5461851	Missense_Mutation	GG	AA	p.T298I	58	56	0.966	1.016	2	2	0	127	olfactory receptor, family 51, subfamily I, member 1	ENST00000380211.1
Case#2-Baseline-M420	OR5P2	11	7818171	Missense_Mutation	C	T	p.E107K	84	83	0.988	1.040	2	2	0	158	olfactory receptor, family 5, subfamily P, member 2	ENST00000329434.2
Case#2-Baseline-M420	OR4A16	11	55110683	Missense_Mutation	C	T	p.P3S	64	64	1.000	1.053	2	2	0	140	olfactory receptor, family 4, subfamily A, member 16	ENST00000314721.2
Case#2-Baseline-M420	CTNND1	11	57564280	Missense_Mutation	G	A	p.G258R	108	100	0.926	0.975	2	2	0	210	catenin (cadherin-associated protein), delta 1	ENST00000399050.4
Case#2-Baseline-M420	IGHMBP2	11	68675723	Missense_Mutation	G	A	p.D123N	46	44	0.957	1.007	2	2	0	128	immunoglobulin mu binding protein 2	ENST00000255078.3
Case#2-Baseline-M420	TRIM77	11	89444610	Nonsense_Mutation	G	A	p.W148*	56	50	0.893	0.940	2	2	0	116	tripartite motif containing 77	ENST00000398290.3
Case#2-Baseline-M420	MMP20	11	102487610	Missense_Mutation	G	A	p.P103S	78	76	0.974	1.026	2	2	0	151	matrix metallopeptidase 20	ENST00000260228.2
Case#2-Baseline-M420	GRAMD1B	11	123465478	Nonsense_Mutation	C	T	p.Q126*	75	74	0.987	1.039	2	2	0	98	GRAM domain containing 1B	ENST00000529750.1
Case#2-Baseline-M420	KCNJ5	11	128781214	Missense_Mutation	G	A	p.G16R	70	64	0.914	0.962	2	2	0	146	potassium inwardly-rectifying channel, subfamily J, member 5	ENST00000338350.4
Case#2-Baseline-M420	ADAMTS15	11	130339181	Missense_Mutation	G	A	p.D523N	34	30	0.882	0.929	2	2	0	74	ADAM metallopeptidase with thrombospondin type 1 motif, 15	ENST00000299164.2
Case#2-Baseline-M420	PRMT8	12	3649955	Missense_Mutation	G	A	p.E87K	140	73	0.521	0.535	4	2	2	142	protein arginine methyltransferase 8	ENST00000382622.3
Case#2-Baseline-M420	VWF	12	6103165	Missense_Mutation	A	T	p.L2154Q	140	65	0.464	0.477	4	2	2	109	von Willebrand factor	ENST00000261405.5
Case#2-Baseline-M420	CD163L1	12	7521564	Splice_Site	GA	-		94	15	0.160	0.164	4	2	2	84	CD163 molecule-like 1	ENST00000313599.3
Case#2-Baseline-M420	PIK3C2G	12	18716366	Missense_Mutation	C	T	p.S1238L	118	51	0.432	0.444	4	2	2	108	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 gamma	ENST00000266497.5
Case#2-Baseline-M420	SLCO1B3	12	21069126	Missense_Mutation	G	A	p.G685E	231	131	0.567	0.582	4	2	2	155	solute carrier organic anion transporter family, member 1B3	ENST00000381545.3
Case#2-Baseline-M420	KCNJ8	12	21918938	Missense_Mutation	C	T	p.E332K	173	84	0.486	0.498	4	2	2	162	potassium inwardly-rectifying channel, subfamily J, member 8	ENST00000240662.2
Case#2-Baseline-M420	SLC38A4	12	47178369	Missense_Mutation	C	T	p.G150E	66	62	0.939	0.989	2	2	0	97	solute carrier family 38, member 4	ENST00000447411.1
Case#2-Baseline-M420	DIP2B	12	51118670	Splice_Site	G	A		71	65	0.915	0.964	2	1	1	151	DIP2 disco-interacting protein 2 homolog B (Drosophila)	ENST00000301180.5
Case#2-Baseline-M420	MYO1A	12	57422920	Missense_Mutation	C	T	p.E1001K	45	42	0.933	0.982	2	2	0	81	myosin IA	ENST00000442789.2
Case#2-Baseline-M420	C12orf55	12	97180611	Missense_Mutation	G	A	p.E2872K	56	53	0.946	0.996	2	2	0	106		ENST00000524981.4
Case#2-Baseline-M420	GNPTAB	12	102153816	Missense_Mutation	G	T	p.P1081T	82	79	0.963	1.014	2	2	0	136	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	ENST00000299314.7
Case#2-Baseline-M420	TDG	12	104376924	Missense_Mutation	C	T	p.R209C	74	72	0.973	1.024	2	2	0	112	thymine-DNA glycosylase	ENST00000392872.3
Case#2-Baseline-M420	CUX2	12	111757876	Missense_Mutation	C	T	p.T688I	76	65	0.855	0.900	2	2	0	108	cut-like homeobox 2	ENST00000261726.6
Case#2-Baseline-M420	DNAH10	12	124267722	Missense_Mutation	G	A	p.E243K	92	85	0.924	0.973	2	2	0	162	dynein, axonemal, heavy chain 10	ENST00000409039.3
Case#2-Baseline-M420	BRCA2	13	32930738	Missense_Mutation	C	T	p.H2537Y	53	52	0.981	1.033	2	2	0	96	breast cancer 2, early onset	ENST00000380152.3
Case#2-Baseline-M420	NBEA	13	36124642	Missense_Mutation	G	A	p.G2205E	86	83	0.965	1.016	2	2	0	151	neurobeachin	ENST00000400445.3
Case#2-Baseline-M420	NFKBIA	14	35871725	Missense_Mutation	G	A	p.P261S	45	44	0.978	1.029	2	2	0	93	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	ENST00000216797.5
Case#2-Baseline-M420	TTC6	14	38151975	Missense_Mutation	G	A	p.E355K	61	57	0.934	0.984	2	2	0	126	tetratricopeptide repeat domain 6	ENST00000553443.1
Case#2-Baseline-M420	KCNH5	14	63453861	Missense_Mutation	G	C	p.R160G	98	93	0.949	0.999	2	2	0	142	potassium voltage-gated channel, subfamily H (eag-related), member 5	ENST00000322893.7
Case#2-Baseline-M420	ABCD4	14	74764632	Splice_Site	C	T		88	42	0.477	0.502	2	2	0	184	ATP-binding cassette, sub-family D (ALD), member 4	ENST00000356924.4
Case#2-Baseline-M420	OR4M2	15	22369306	Missense_Mutation	C	T	p.S244F	720	161	0.224	0.229	4	2	2	727	olfactory receptor, family 4, subfamily M, member 2	ENST00000332663.2
Case#2-Baseline-M420	FMN1	15	33261614	Missense_Mutation	T	C	p.E763G	160	62	0.388	0.398	4	2	2	117	formin 1	ENST00000559047.1
Case#2-Baseline-M420	SLC28A2	15	45545451	Missense_Mutation	C	T	p.S13F	161	77	0.478	0.491	4	2	2	145	solute carrier family 28 (concentrative nucleoside transporter), member 2	ENST00000347644.3
Case#2-Baseline-M420	CYP1A2	15	75042116	Missense_Mutation	G	A	p.E13K	150	69	0.460	0.472	4	2	2	149	cytochrome P450, family 1, subfamily A, polypeptide 2	ENST00000343932.4
Case#2-Baseline-M420	KIAA1199	15	81188289	Nonsense_Mutation	G	A	p.W433*	199	97	0.487	0.500	4	2	2	184		ENST00000394685.3
Case#2-Baseline-M420	PKD1	16	2160895	Missense_Mutation	G	A	p.R1425C	368	151	0.410	0.421	4	2	2	323	polycystic kidney disease 1 (autosomal dominant)	ENST00000262304.4
Case#2-Baseline-M420	DNAH3	16	20974716	Missense_Mutation	C	T	p.G3497E	190	84	0.442	0.454	4	2	2	181	dynein, axonemal, heavy chain 3	ENST00000261383.3
Case#2-Baseline-M420	DNAH3	16	21086851	Missense_Mutation	C	T	p.E1001K	120	50	0.417	0.428	4	2	2	92	dynein, axonemal, heavy chain 3	ENST00000261383.3
Case#2-Baseline-M420	TNRC6A	16	24815560	Nonsense_Mutation	C	T	p.R1253*	113	56	0.496	0.509	4	2	2	103	trinucleotide repeat containing 6A	ENST00000395799.3
Case#2-Baseline-M420	STX1B	16	31004546	Missense_Mutation	G	C	p.R231G	115	45	0.391	0.402	4	2	2	121	syntaxin 1B	ENST00000215095.5
Case#2-Baseline-M420	ITGAM	16	31309065	Splice_Site	G	A		84	44	0.524	0.538	4	2	2	94	integrin, alpha M (complement component 3 receptor 3 subunit)	ENST00000287497.8
Case#2-Baseline-M420	ITGAM	16	31309202	Missense_Mutation	A	T	p.E545V	97	57	0.588	0.603	4	2	2	98	integrin, alpha M (complement component 3 receptor 3 subunit)	ENST00000287497.8
Case#2-Baseline-M420	PAPD5	16	50263084	Missense_Mutation	C	T	p.R538C	107	43	0.402	0.412	4	2	2	117	PAP associated domain containing 5	ENST00000561678.1
Case#2-Baseline-M420	OGFOD1	16	56504605	Missense_Mutation	C	T	p.P396L	107	43	0.402	0.412	4	2	2	81	2-oxoglutarate and iron-dependent oxygenase domain containing 1	ENST00000566157.1
Case#2-Baseline-M420	SLC12A3	16	56947280	Missense_Mutation	G	A	p.G1010E	253	129	0.510	0.523	4	2	2	244	solute carrier family 12 (sodium/chloride transporter), member 3	ENST00000563236.1
Case#2-Baseline-M420	EXOC3L1	16	67221347	Missense_Mutation	C	T	p.G274E	90	45	0.500	0.513	4	2	2	61	exocyst complex component 3-like 1	ENST00000314586.6
Case#2-Baseline-M420	HYDIN	16	70977759	Missense_Mutation	G	A	p.L2209F	57	32	0.561	0.576	4	2	2	46	HYDIN, axonemal central pair apparatus protein	ENST00000393567.2
Case#2-Baseline-M420	HYDIN	16	71009082	Missense_Mutation	C	T	p.D1577N	857	204	0.238	0.244	4	2	2	872	HYDIN, axonemal central pair apparatus protein	ENST00000393567.2
Case#2-Baseline-M420	CHST4	16	71570816	Nonsense_Mutation	G	A	p.W79*	154	73	0.474	0.487	4	2	2	126	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4	ENST00000338482.5
Case#2-Baseline-M420	JPH3	16	87678364	Missense_Mutation	G	A	p.D295N	394	176	0.447	0.458	4	2	2	387	junctophilin 3	ENST00000284262.2
Case#2-Baseline-M420	DNAH2	17	7702025	Missense_Mutation	G	A	p.E2850K	111	31	0.279	0.289	3	2	1	125	dynein, axonemal, heavy chain 2	ENST00000572933.1
Case#2-Baseline-M420	MYH4	17	10358940	Missense_Mutation	A	T	p.F722Y	141	90	0.638	0.661	3	2	1	213	myosin, heavy chain 4, skeletal muscle	ENST00000255381.2
Case#2-Baseline-M420	DNAH9	17	11607590	Missense_Mutation	G	A	p.G1741D	127	49	0.386	0.399	3	2	1	141	dynein, axonemal, heavy chain 9	ENST00000262442.4
Case#2-Baseline-M420	KRTAP4-5	17	39305785	Missense_Mutation	A	T	p.C79S	384	82	0.214	0.221	3	2	1	362	keratin associated protein 4-5	ENST00000343246.4
Case#2-Baseline-M420	ZNF385C	17	40181094	Splice_Site	G	A	p.A226V	37	10	0.270	0.280	3	2	1	63	zinc finger protein 385C	ENST00000436535.3
Case#2-Baseline-M420	CDC27	17	45234357	Missense_Mutation	G	A	p.S255F	131	7	0.053	0.055	3	2	1	132	cell division cycle 27	ENST00000066544.3
Case#2-Baseline-M420	IGF2BP1	17	47126787	Missense_Mutation	C	T	p.A572V	101	27	0.267	0.277	3	2	1	101	insulin-like growth factor 2 mRNA binding protein 1	ENST00000290341.3
Case#2-Baseline-M420	SGCA	17	48245845	Missense_Mutation	G	A	p.E166K	141	91	0.645	0.668	3	2	1	167	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)	ENST00000262018.3

Case#2-Baseline-M420	CD300A	17	72477896	Missense_Mutation	A	T	p.N233I	143	80	0.559	0.579	3	2	1	200	CD300a molecule	ENST00000360141.3
Case#2-Baseline-M420	RBFOX3	17	77100159	Missense_Mutation	G	A	p.S137F	89	54	0.607	0.628	3	2	1	105	RNA binding protein, fox-1 homolog (C. elegans) 3	ENST00000453134.2
Case#2-Baseline-M420	EMILIN2	18	2891917	Missense_Mutation	G	A	p.E598K	89	25	0.281	0.291	3	2	1	112	elastin microfibril interfacer 2	ENST00000254528.3
Case#2-Baseline-M420	IMPACT	18	22023054	Missense_Mutation	C	T	p.P178S	100	61	0.610	0.631	3	2	1	82	impact RWD domain protein	ENST00000284202.4
Case#2-Baseline-M420	DSC1	18	28714538	Missense_Mutation	CC	TT	p.D625N	95	52	0.547	0.567	3	2	1	114	desmocollin 1	ENST00000257198.5
Case#2-Baseline-M420	ALPK2	18	56196344	Missense_Mutation	G	A	p.S1827F	114	71	0.623	0.645	3	2	1	108	alpha-kinase 2	ENST00000361673.3
Case#2-Baseline-M420	SERPINB8	18	61652436	Missense_Mutation	G	T	p.S226I	119	36	0.303	0.313	3	2	1	141	serpin peptidase inhibitor, clade B (ovalbumin), member 8	ENST00000397985.2
Case#2-Baseline-M420	CNDP1	18	72250811	Missense_Mutation	C	T	p.P442S	157	44	0.280	0.290	3	2	1	188	carnosine dipeptidase 1 (metallopeptidase M20 family)	ENST00000358821.3
Case#2-Baseline-M420	PTBP1	19	805050	Missense_Mutation	C	T	p.T252M	160	76	0.475	0.488	4	2	2	185	polypyrimidine tract binding protein 1	ENST00000349038.4
Case#2-Baseline-M420	GNG7	19	2515129	Missense_Mutation	G	A	p.S33F	150	72	0.480	0.493	4	2	2	147	guanine nucleotide binding protein (G protein), gamma 7	ENST00000382159.3
Case#2-Baseline-M420	MAP2K2	19	4110574	Missense_Mutation	G	C	p.P128R	131	51	0.389	0.400	4	2	2	162	mitogen-activated protein kinase kinase 2	ENST00000262948.5
Case#2-Baseline-M420	MUC16	19	9061537	Missense_Mutation	C	T	p.E8637K	180	88	0.489	0.502	4	2	2	158	mucin 16, cell surface associated	ENST00000397910.4
Case#2-Baseline-M420	MUC16	19	9082813	Missense_Mutation	G	A	p.S3001L	159	70	0.440	0.452	4	2	2	167	mucin 16, cell surface associated	ENST00000397910.4
Case#2-Baseline-M420	MUC16	19	9085250	Missense_Mutation	C	T	p.E2189K	171	93	0.544	0.558	4	2	2	154	mucin 16, cell surface associated	ENST00000397910.4
Case#2-Baseline-M420	OR7G3	19	9236942	Missense_Mutation	G	A	p.P229S	189	94	0.497	0.510	4	2	2	168	olfactory receptor, family 7, subfamily G, member 3	ENST00000305444.2
Case#2-Baseline-M420	ZNF560	19	9577307	Missense_Mutation	C	G	p.Q772H	295	138	0.468	0.480	4	2	2	264	zinc finger protein 560	ENST00000301480.4
Case#2-Baseline-M420	ZNF563	19	12429713	Missense_Mutation	G	A	p.H376Y	388	179	0.461	0.473	4	2	2	406	zinc finger protein 563	ENST00000293725.5
Case#2-Baseline-M420	EMR3	19	14769339	Missense_Mutation	C	G	p.E127Q	52	4	0.077	0.079	4	2	2	69	egf-like module containing, mucin-like, hormone receptor-like 3	ENST00000253673.5
Case#2-Baseline-M420	ABHD8	19	17412109	Missense_Mutation	C	T	p.G106E	18	8	0.444	0.456	4	2	2	20	abhydrolase domain containing 8	ENST00000247706.3
Case#2-Baseline-M420	ARHGAP35	19	47422066	Missense_Mutation	C	T	p.P45L	266	118	0.444	0.455	4	2	2	282	Rho GTPase activating protein 35	ENST00000404338.3
Case#2-Baseline-M420	SCAF1	19	50156247	Missense_Mutation	CC	TT	p.R868C	334	128	0.383	0.393	4	2	2	339	SR-related CTD-associated factor 1	ENST00000360565.3
Case#2-Baseline-M420	LILRB5	19	54759398	Missense_Mutation	C	T	p.A235T	237	116	0.489	0.502	4	2	2	197	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5	ENST00000316219.5
Case#2-Baseline-M420	LILRA1	19	55107746	Missense_Mutation	C	T	p.P351S	205	85	0.415	0.426	4	2	2	214	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1	ENST00000251372.3
Case#2-Baseline-M420	CAD	2	27464912	Missense_Mutation	C	T	p.S1943F	123	61	0.496	0.509	4	2	2	131	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	ENST00000403525.1
Case#2-Baseline-M420	HEATR5B	2	37234373	Missense_Mutation	G	A	p.H1533Y	152	69	0.454	0.466	4	2	2	135	HEAT repeat containing 5B	ENST00000233099.5
Case#2-Baseline-M420	USP34	2	61633078	Missense_Mutation	T	A	p.N106I	97	45	0.464	0.476	4	2	2	96	ubiquitin specific peptidase 34	ENST00000398571.2
Case#2-Baseline-M420	CNTNAP5	2	125175155	Missense_Mutation	G	A	p.G173R	149	73	0.490	0.503	4	2	2	148	contactin associated protein-like 5	ENST00000431078.1
Case#2-Baseline-M420	GPR39	2	133402871	Missense_Mutation	C	T	p.R352W	152	70	0.461	0.473	4	2	2	136	G protein-coupled receptor 39	ENST00000329321.3
Case#2-Baseline-M420	LRP1B	2	141607835	Missense_Mutation	G	A	p.P1592L	150	73	0.487	0.499	4	2	2	137	low density lipoprotein receptor-related protein 1B	ENST00000389484.3
Case#2-Baseline-M420	NEB	2	152427025	Missense_Mutation	C	T	p.E4001K	135	70	0.519	0.532	4	2	2	88	nebulin	ENST00000172853.10
Case#2-Baseline-M420	FMNL2	2	153497396	Missense_Mutation	G	A	p.G421E	154	67	0.435	0.447	4	2	2	133	formin-like 2	ENST00000475377.2
Case#2-Baseline-M420	DCAF17	2	172325510	Missense_Mutation	C	A	p.F317L	146	67	0.459	0.471	4	2	2	94	DDB1 and CUL4 associated factor 17	ENST00000375255.3
Case#2-Baseline-M420	PDE1A	2	183011865	Missense_Mutation	G	A	p.H527Y	78	44	0.564	0.579	4	2	2	69	phosphodiesterase 1A, calmodulin-dependent	ENST00000435564.1
Case#2-Baseline-M420	SLC40A1	2	190428486	Missense_Mutation	C	T	p.R409Q	163	71	0.436	0.447	4	2	2	155	solute carrier family 40 (iron-regulated transporter), member 1	ENST00000261024.2
Case#2-Baseline-M420	STAT4	2	191919251	Missense_Mutation	C	T	p.E406K	141	71	0.504	0.517	4	2	2	141	signal transducer and activator of transcription 4	ENST00000392320.2
Case#2-Baseline-M420	DNAH7	2	196799458	Missense_Mutation	C	T	p.E1110K	148	69	0.466	0.478	4	2	2	129	dynein, axonemal, heavy chain 7	ENST00000312428.6
Case#2-Baseline-M420	CRYGA	2	209025650	Missense_Mutation	C	T	p.E135K	201	91	0.453	0.465	4	2	2	173	crystallin, gamma A	ENST00000304502.4
Case#2-Baseline-M420	PTH2R	2	209302602	Missense_Mutation	G	A	p.G136E	110	55	0.500	0.513	4	2	2	111	parathyroid hormone 2 receptor	ENST00000272847.2
Case#2-Baseline-M420	ARPC2	2	219093493	Missense_Mutation	C	T	p.P48S	131	60	0.458	0.470	4	2	2	130	actin related protein 2/3 complex, subunit 2, 34kDa	ENST00000295685.10
Case#2-Baseline-M420	ACSL3	2	223782833	Missense_Mutation	A	G	p.N209S	120	57	0.475	0.488	4	2	2	95	acyl-CoA synthetase long-chain family member 3	ENST00000357430.3
Case#2-Baseline-M420	COL4A3	2	228109667	Splice_Site	G	A	p.G94R	204	98	0.480	0.493	4	2	2	166	collagen, type IV, alpha 3 (Goodpasture antigen)	ENST00000396578.3
Case#2-Baseline-M420	INPP5D	2	234112887	Missense_Mutation	C	T	p.P1019S	114	61	0.535	0.549	4	2	2	105	inositol polyphosphate-5-phosphatase, 145kDa	ENST00000359570.5
Case#2-Baseline-M420	COL6A3	2	238296599	Missense_Mutation	C	T	p.G313E	195	90	0.462	0.474	4	2	2	152	collagen, type VI, alpha 3	ENST00000295550.4
Case#2-Baseline-M420	RBM44	2	238733043	Nonsense_Mutation	G	A	p.W811*	205	84	0.410	0.421	4	2	2	41	RNA binding motif protein 44	ENST00000409864.1
Case#2-Baseline-M420	CHGB	20	5903578	Missense_Mutation	C	T	p.S263F	102	47	0.461	0.473	4	2	2	81	chromogranin B (secretogranin 1)	ENST00000378961.4
Case#2-Baseline-M420	HAO1	20	7886973	Missense_Mutation	C	T	p.M183I	79	31	0.392	0.403	4	2	2	66	hydroxyacid oxidase (glycolate oxidase) 1	ENST00000378789.3
Case#2-Baseline-M420	SLX4IP	20	10603749	Nonsense_Mutation	C	T	p.R317*	160	70	0.438	0.449	4	2	2	135	SLX4 interacting protein	ENST00000334534.5
Case#2-Baseline-M420	TTLL9	20	30513896	Splice_Site	T	A		166	84	0.506	0.519	4	2	2	129	tubulin tyrosine ligase-like family, member 9	ENST00000375938.4
Case#2-Baseline-M420	SAMHD1	20	35545391	Missense_Mutation	C	T	p.R305K	108	32	0.296	0.307	3	2	1	98	SAM domain and HD domain 1	ENST00000262878.4
Case#2-Baseline-M420	PABPC1L	20	43559255	Missense_Mutation	C	T	p.A376V	119	68	0.571	0.591	3	2	1	166	poly(A) binding protein, cytoplasmic 1-like	ENST00000217073.2
Case#2-Baseline-M420	PABPC1L	20	43566704	Missense_Mutation	G	A	p.E550K	113	33	0.292	0.302	3	2	1	152	poly(A) binding protein, cytoplasmic 1-like	ENST00000217073.2
Case#2-Baseline-M420	ZNF334	20	45133364	Nonsense_Mutation	G	A	p.Q13*	137	40	0.292	0.302	3	2	1	145	zinc finger protein 334	ENST00000347606.4
Case#2-Baseline-M420	FAM217B	20	58519207	Missense_Mutation	CC	TT	p.A70V	80	44	0.550	0.569	3	2	1	117	family with sequence similarity 217, member B	ENST00000358293.3
Case#2-Baseline-M420	USP25	21	17250160	Nonsense_Mutation	C	T	p.R949*	199	81	0.407	0.418	4	2	2	167	ubiquitin specific peptidase 25	ENST00000285679.6
Case#2-Baseline-M420	GRIK1	21	31062192	Missense_Mutation	G	A	p.R134C	135	66	0.489	0.502	4	2	2	117	glutamate receptor, ionotropic, kainate 1	ENST00000399907.1
Case#2-Baseline-M420	IFNAR2	21	34635507	Missense_Mutation	C	T	p.S417F	135	71	0.526	0.540	4	2	2	138	interferon (alpha, beta and omega) receptor 2	ENST00000342136.4
Case#2-Baseline-M420	ABCG1	21	43714725	Missense_Mutation	C	T	p.T588I	100	50	0.500	0.513	4	2	2	115	ATP-binding cassette, sub-family G (WHITE), member 1	ENST00000361802.2
Case#2-Baseline-M420	KRTAP10-11	21	46067102	Missense_Mutation	C	T	p.P243S	189	78	0.413	0.424	4	2	2	197	keratin associated protein 10-11	ENST00000334670.8
Case#2-Baseline-M420	COL18A1	21	46914475	Missense_Mutation	G	A	p.R1205Q	127	49	0.386	0.396	4	2	2	111	collagen, type XVIII, alpha 1	ENST00000359759.4
Case#2-Baseline-M420	PCNT	21	47836080	Missense_Mutation	C	T	p.S2083F	199	92	0.462	0.474	4	2	2	169	pericentrin	ENST00000359568.5
Case#2-Baseline-M420	RIMBP3	22	20456945	Missense_Mutation	G	A	p.P1453S	222	84	0.378	0.392	3	2	1	280	RIMS binding protein 3	ENST00000426804.1
Case#2-Baseline-M420	LZTR1	22	21343110	Missense_Mutation	C	T	p.T181M	110	43	0.391	0.405	3	2	1	111	leucine-zipper-like transcription regulator 1	ENST00000215739.8
Case#2-Baseline-M420	PIWIL3	22	25155951	Missense_Mutation	C	G	p.Q36H	82	19	0.232	0.244	2	2	0	110	piwi-like RNA-mediated gene silencing 3	ENST00000332271.5
Case#2-Baseline-M420	CABP7	22	30124619	Splice_Site	G	A	p.G85D	79	39	0.494	0.507	4	2	2	66	calcium binding protein 7	ENST00000216144.3
Case#2-Baseline-M420	EIF3D	22	36916707	Missense_Mutation	C	T	p.R165H	79	37	0.468	0.481	4	2	2	75	eukaryotic translation initiation factor 3, subunit D	ENST00000216190.8
Case#2-Baseline-M420	PARVB	22	44489874	Missense_Mutation	T	C	p.V60A	114	60	0.526	0.540	4	2	2	104	parvin, beta	ENST00000338758.7
Case#2-Baseline-M420	NUP210	3	13372082	Missense_Mutation	G	A	p.P1330S	240	115	0.479	0.492	4	2	2	199	nucleoporin 210kDa	ENST00000254508.5
Case#2-Baseline-M420	SLC4A7	3	27498171	Missense_Mutation	C	T	p.E2K	140	64	0.457	0.469	4	2	2	140	solute carrier family 4, sodium bicarbonate cotransporter, member 7	ENST00000295736.5
Case#2-Baseline-M420	SCN5A	3	38592057	Missense_Mutation	G	A	p.L1936F	119	53	0.445	0.457	4	2	2	93	sodium channel, voltage-gated, type V, alpha subunit	ENST00000333535.4
Case#2-Baseline-M420	CSRNP1	3	39185707	Missense_Mutation	C	T	p.R234Q	238	105	0.441	0.453	4	2	2	184	cysteine-serine-rich nuclear protein 1	ENST00000273153.5
Case#2-Baseline-M420	LRRC2	3	46593024	Missense_Mutation	G	A	p.R20C	155	69	0.445	0.457	4	2	2	169	leucine rich repeat containing 2	ENST00000395905.3
Case#2-Baseline-M420	UBA7	3	49847517	Missense_Mutation	AC	TT	p.V578K	96	36	0.375	0.385	4	2	2	115	ubiquitin-like modifier activating enzyme 7	ENST00000333486.3
Case#2-Baseline-M420	DOCK3	3	51127760	Missense_Mutation	G	A	p.E231K	125	52	0.416	0.427	4	2	2	158	dedicator of cytokinesis 3	ENST00000266037.9
Case#2-Baseline-M420	LRTM1	3	54961931	Splice_Site	C	G		144	65	0.451	0.463	4	2	2	153	leucine-rich repeats and transmembrane domains 1	ENST00000273286.5
Case#2-Baseline-M420	PTPRG	3	62216967	Missense_Mutation	G	A	p.R786K	39	18	0.462	0.474	4	2	2	48	protein tyrosine phosphatase, receptor type, G	ENST00000474889.1
Case#2-Baseline-M420	DHFRL1	3	93779809	Missense_Mutation	A	G	p.C183R	182	94	0.516	0.530	4	2	2	165	dihydrofolate reductase-like 1	ENST00000394221.2
Case#2-Baseline-M420	SLC9C1	3	111996674	Missense_Mutation	T	G	p.N118H	144	60	0.417	0.428	4	2	2	147	solute carrier family 9, subfamily C (Na+-transporting carboxylic acid decarboxylase), member 1	ENST00000305815.5
Case#2-Baseline-M420	KALRN	3	124201655	Splice_Site	G	A	p.E1396K	118	57	0.483	0.496	4	2	2	121	kalirin, RhoGEF kinase	ENST00000240874.3
Case#2-Baseline-M420	COL6A5	3	130141610	Missense_Mutation	G	A	p.G1695E	118	46	0.390	0.400	4	2	2	110	collagen, type VI, alpha 5	ENST00000432398.2
Case#2-Baseline-M420	ACKR4	3	132319698	Missense_Mutation	C	T	p.P153S	360	81	0.225	0.231	4	2	2	334	atypical chemokine receptor 4	ENST00000249887.2

Case#2-Baseline-M420	WDR49	3	167254723	Missense_Mutation	C	T	p.G278E	187	82	0.439	0.450	4	2	2	156	WD repeat domain 49	ENST00000308378.3
Case#2-Baseline-M420	RGS12	4	3432545	Missense_Mutation	C	T	p.A1326V	134	84	0.627	0.649	3	2	1	187	regulator of G-protein signaling 12	ENST00000344733.5
Case#2-Baseline-M420	SLIT2	4	20619226	Missense_Mutation	C	T	p.P1434L	129	81	0.628	0.650	3	2	1	157	slit homolog 2 (Drosophila)	ENST00000504154.1
Case#2-Baseline-M420	KLHL5	4	39116817	Missense_Mutation	C	T	p.S693F	84	36	0.429	0.444	3	2	1	90	kelch-like family member 5	ENST00000504108.1
Case#2-Baseline-M420	RBM47	4	40440602	Missense_Mutation	C	T	p.M103I	134	40	0.299	0.309	3	2	1	179	RNA binding motif protein 47	ENST00000381793.2
Case#2-Baseline-M420	ENAM	4	71509437	Missense_Mutation	C	T	p.S765F	117	37	0.316	0.327	3	2	1	124	enamelin	ENST00000396073.3
Case#2-Baseline-M420	FREM3	4	144620448	Missense_Mutation	C	T	p.D461N	120	66	0.550	0.569	3	2	1	168	FRAS1 related extracellular matrix 3	ENST00000329798.5
Case#2-Baseline-M420	ANXA10	4	169049272	Missense_Mutation	C	T	p.P19L	62	24	0.387	0.401	3	2	1	90	annexin A10	ENST00000359299.3
Case#2-Baseline-M420	SPATA4	4	177116616	Missense_Mutation	C	T	p.R33Q	160	45	0.281	0.291	3	2	1	214	spermatogenesis associated 4	ENST00000280191.2
Case#2-Baseline-M420	TENM3	4	183714432	Missense_Mutation	G	A	p.E2203K	107	61	0.570	0.590	3	2	1	138	teneurin transmembrane protein 3	ENST00000511685.1
Case#2-Baseline-M420	DNAH5	5	13885322	Missense_Mutation	C	T	p.G920E	70	27	0.386	0.396	4	2	2	64	dynein, axonemal, heavy chain 5	ENST00000265104.4
Case#2-Baseline-M420	C9	5	39341716	Missense_Mutation	GG	AA	p.P90L	163	71	0.436	0.447	4	2	2	170	complement component 9	ENST00000263408.4
Case#2-Baseline-M420	CMYA5	5	79026782	Missense_Mutation	C	T	p.P732S	123	60	0.488	0.501	4	2	2	108	cardiomyopathy associated 5	ENST00000446378.2
Case#2-Baseline-M420	KIF3A	5	132056301	Splice_Site	G	A	p.R206C	148	75	0.507	0.520	4	2	2	129	kinesin family member 3A	ENST00000378746.4
Case#2-Baseline-M420	PCDHA4	5	140188687	Missense_Mutation	G	A	p.E639K	407	175	0.430	0.441	4	2	2	438	protocadherin alpha 4	ENST00000530339.1
Case#2-Baseline-M420	PCDHB8	5	140558546	Missense_Mutation	G	A	p.E311K	182	76	0.418	0.429	4	2	2	162	protocadherin beta 8	ENST00000239444.2
Case#2-Baseline-M420	SPINK14	5	147549340	Missense_Mutation	G	T	p.L15F	144	60	0.417	0.428	4	2	2	103	serine peptidase inhibitor, Kazal type 14 (putative)	ENST00000356972.1
Case#2-Baseline-M420	SYNPO	5	150027783	Missense_Mutation	CC	TT	p.P227S	132	58	0.439	0.451	4	2	2	111	synaptopodin	ENST00000394243.1
Case#2-Baseline-M420	BTNL9	5	180474954	Missense_Mutation	C	T	p.P46L	155	70	0.452	0.463	4	2	2	125	butyrophilin-like 9	ENST00000327705.9
Case#2-Baseline-M420	PRSS16	6	27222499	Missense_Mutation	C	T	p.P393L	76	35	0.461	0.473	4	2	2	82	protease, serine, 16 (thymus)	ENST00000230582.3
Case#2-Baseline-M420	TREML2	6	41162493	Missense_Mutation	G	A	p.A152V	139	69	0.496	0.509	4	2	2	152	triggering receptor expressed on myeloid cells-like 2	ENST00000483722.1
Case#2-Baseline-M420	BMP5	6	55739516	Missense_Mutation	C	T	p.E50K	174	82	0.471	0.484	4	2	2	176	bone morphogenetic protein 5	ENST00000370830.3
Case#2-Baseline-M420	COL19A1	6	70866106	Missense_Mutation	G	A	p.D723N	154	76	0.494	0.506	4	2	2	150	collagen, type XIX, alpha 1	ENST00000322773.4
Case#2-Baseline-M420	NR2E1	6	108502798	Missense_Mutation	C	T	p.A313V	98	41	0.418	0.429	4	2	2	88	nuclear receptor subfamily 2, group E, member 1	ENST00000368986.4
Case#2-Baseline-M420	ASF1A	6	119222008	Missense_Mutation	G	A	p.G63S	148	68	0.459	0.472	4	2	2	174	anti-silencing function 1A histone chaperone	ENST00000229595.5
Case#2-Baseline-M420	THEMIS	6	128134071	Missense_Mutation	G	A	p.T572I	200	91	0.455	0.467	4	2	2	173	thymocyte selection associated	ENST00000368248.2
Case#2-Baseline-M420	MYB	6	135517046	Missense_Mutation	C	T	p.S370L	137	60	0.438	0.449	4	2	2	181	v-myb avian myeloblastosis viral oncogene homolog	ENST00000367814.4
Case#2-Baseline-M420	VTA1	6	142510629	Missense_Mutation	G	A	p.E160K	177	76	0.429	0.441	4	2	2	172	vesicle (multivesicular body) trafficking 1	ENST00000367630.4
Case#2-Baseline-M420	OPRM1	6	154412483	Missense_Mutation	G	A	p.R347Q	201	96	0.478	0.490	4	2	2	198	opioid receptor, mu 1	ENST00000330432.7
Case#2-Baseline-M420	LPA	6	161027508	Splice_Site	C	T		311	140	0.450	0.462	4	2	2	282	lipoprotein, Lp(a)	ENST00000316300.5
Case#2-Baseline-M420	VWDE	7	12373192	Missense_Mutation	T	A	p.I1553F	293	112	0.382	0.387	9	5	4	127	von Willebrand factor D and EGF domains	ENST00000275358.3
Case#2-Baseline-M420	SNX10	7	26400626	Missense_Mutation	GG	AA	p.R19K	269	123	0.457	0.463	9	5	4	109	sorting nexin 10	ENST00000338523.4
Case#2-Baseline-M420	ZNF716	7	57528786	Missense_Mutation	C	T	p.H207Y	573	193	0.337	NA	NA	NA	NA	256	zinc finger protein 716	ENST00000420713.1
Case#2-Baseline-M420	SAMD9	7	92734447	Nonsense_Mutation	G	A	p.Q322*	135	135	1.000	1.018	6	6	0	102	sterile alpha motif domain containing 9	ENST00000379958.2
Case#2-Baseline-M420	BRAF	7	140453145	Missense_Mutation	AG	GA	p.L597S	217	217	1.000	1.018	6	6	0	155	B-Raf proto-oncogene, serine/threonine kinase	ENST00000288602.6
Case#2-Baseline-M420	CSMD1	8	2830815	Missense_Mutation	T	G	p.N2917T	132	70	0.530	0.544	4	2	2	105	CUB and Sushi multiple domains 1	ENST00000520002.1
Case#2-Baseline-M420	CSMD1	8	2949047	Missense_Mutation	G	A	p.R2427C	110	44	0.400	0.411	4	2	2	117	CUB and Sushi multiple domains 1	ENST00000520002.1
Case#2-Baseline-M420	RP1L1	8	10470320	Nonsense_Mutation	G	A	p.Q430*	133	58	0.436	0.448	4	2	2	145	retinitis pigmentosa 1-like 1	ENST00000382483.3
Case#2-Baseline-M420	KIF13B	8	29037719	Missense_Mutation	G	A	p.R208C	182	83	0.456	0.468	4	2	2	202	kinesin family member 13B	ENST00000524189.1
Case#2-Baseline-M420	RP1	8	55538384	Missense_Mutation	G	A	p.E648K	136	77	0.566	0.586	3	2	1	156	retinitis pigmentosa 1 (autosomal dominant)	ENST00000220676.1
Case#2-Baseline-M420	RP1	8	55538858	Missense_Mutation	G	A	p.E806K	143	35	0.245	0.253	3	2	1	152	retinitis pigmentosa 1 (autosomal dominant)	ENST00000220676.1
Case#2-Baseline-M420	RP1	8	55540103	Missense_Mutation	C	T	p.P1221S	115	74	0.643	0.666	3	2	1	139	retinitis pigmentosa 1 (autosomal dominant)	ENST00000220676.1
Case#2-Baseline-M420	SLCO5A1	8	70617305	Missense_Mutation	C	T	p.S528N	153	50	0.327	0.338	3	2	1	207	solute carrier organic anion transporter family, member 5A1	ENST00000260126.4
Case#2-Baseline-M420	OTUD6B	8	92090825	Missense_Mutation	A	G	p.Y216C	109	30	0.275	0.285	3	2	1	128	OTU domain containing 6B	ENST00000285420.4
Case#2-Baseline-M420	STK3	8	99591892	Splice_Site	C	T	p.S316S	98	61	0.622	0.644	3	2	1	117	serine/threonine kinase 3	ENST00000419617.2
Case#2-Baseline-M420	UBR5	8	103297416	Missense_Mutation	C	T	p.A1879T	51	22	0.431	0.447	3	2	1	63	ubiquitin protein ligase E3 component n-recognin 5	ENST00000520539.1
Case#2-Baseline-M420	TAF1L	9	32632916	Missense_Mutation	G	A	p.R888C	275	121	0.440	0.452	4	2	2	188	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 210kDa-like	ENST00000242310.4
Case#2-Baseline-M420	TAF1L	9	32633779	Missense_Mutation	C	T	p.R600Q	199	96	0.482	0.495	4	2	2	178	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 210kDa-like	ENST00000242310.4
Case#2-Baseline-M420	PCSK5	9	78936451	Missense_Mutation	G	A	p.G1306E	118	40	0.339	0.351	3	2	1	109	proprotein convertase subtilisin/kexin type 5	ENST00000545128.1
Case#2-Baseline-M420	UBQLN1	9	86300989	Nonsense_Mutation	G	A	p.Q88*	81	22	0.272	0.281	3	2	1	117	ubiquilin 1	ENST00000376395.4
Case#2-Baseline-M420	WNK2	9	95997111	Missense_Mutation	C	T	p.P366L	159	98	0.616	0.638	3	2	1	156	WNK lysine deficient protein kinase 2	ENST00000297954.4
Case#2-Baseline-M420	FBP2	9	97349720	Missense_Mutation	C	T	p.G68R	142	79	0.556	0.576	3	2	1	203	fructose-1,6-bisphosphatase 2	ENST00000375337.3
Case#2-Baseline-M420	CYLC2	9	105767002	Missense_Mutation	G	A	p.G69E	73	26	0.356	0.369	3	2	1	102	cylicin, basic protein of sperm head cytoskeleton 2	ENST00000374798.3
Case#2-Baseline-M420	OR13D1	9	107457064	Missense_Mutation	G	A	p.R121K	150	88	0.587	0.607	3	2	1	151	olfactory receptor, family 13, subfamily D, member 1	ENST00000318763.5
Case#2-Baseline-M420	AMBP	9	116825001	Missense_Mutation	C	T	p.G214E	150	71	0.473	0.486	4	2	2	113	alpha-1-microglobulin/bikunin precursor	ENST00000265132.3
Case#2-Baseline-M420	COL27A1	9	116958238	Splice_Site	G	A		163	74	0.454	0.466	4	2	2	58	collagen, type XXVII, alpha 1	ENST00000356083.3
Case#2-Baseline-M420	OR1N1	9	125289493	Missense_Mutation	C	T	p.G27E	178	88	0.494	0.507	4	2	2	158	olfactory receptor, family 1, subfamily N, member 1	ENST00000304880.2
Case#2-Baseline-M420	RPL7A	9	136217582	Splice_Site	C	T	p.S209L	131	32	0.244	0.253	3	2	1	175	ribosomal protein L7a	ENST00000323345.6
Case#2-Baseline-M420	OLFM1	9	138011716	Missense_Mutation	C	T	p.P384S	101	56	0.554	0.574	3	2	1	120	olfactomedin 1	ENST00000371793.3
Case#2-Baseline-M420	KCNT1	9	138649216	Missense_Mutation	G	A	p.E231K	121	77	0.636	0.659	3	2	1	164	potassium channel, subfamily T, member 1	ENST00000263604.3
Case#2-Baseline-M420	FAM166A	9	140139847	Missense_Mutation	C	T	p.G145E	167	96	0.575	0.595	3	2	1	188	family with sequence similarity 166, member A	ENST00000344774.4
Case#2-Baseline-M420	DCAF8L1	X	27997672	Nonsense_Mutation	G	A	p.R594*	111	110	0.991	NA	NA	NA	NA	97	DDB1 and CUL4 associated factor 8-like 1	ENST00000441525.1
Case#2-Baseline-M420	MAGEE2	X	75003604	Missense_Mutation	C	T	p.R428Q	97	95	0.979	NA	NA	NA	NA	87	melanoma antigen family E, 2	ENST00000373359.2
Case#2-Baseline-M420	MUM1L1	X	105451316	Missense_Mutation	G	A	p.D631N	56	55	0.982	NA	NA	NA	NA	59	melanoma associated antigen (mutated) 1-like 1	ENST00000357175.2
Case#2-Baseline-M420	COL4A5	X	107909764	Missense_Mutation	G	A	p.E1165K	61	59	0.967	NA	NA	NA	NA	76	collagen, type IV, alpha 5	ENST00000361603.2
Case#2-Relapse-WholeTumor	UBR4	1	19446148	Missense_Mutation	G	A	p.S3453F	158	65	0.411	0.573	4	2	2	95	ubiquitin protein ligase E3 component n-recognin 4	ENST00000375254.3
Case#2-Relapse-WholeTumor	USP48	1	22074689	Nonsense_Mutation	G	A	p.R284*	160	62	0.388	0.540	4	2	2	112	ubiquitin specific peptidase 48	ENST00000308271.9
Case#2-Relapse-WholeTumor	CD164L2	1	27708822	Nonsense_Mutation	A	T	p.C108*	210	12	0.057	0.080	4	2	2	153	CD164 sialomucin-like 2	ENST00000374030.1
Case#2-Relapse-WholeTumor	CSMD2	1	34158630	Missense_Mutation	C	T	p.E191K	206	76	0.369	0.514	4	2	2	153	CUB and Sushi multiple domains 2	ENST00000373380.1
Case#2-Relapse-WholeTumor	GUCA2A	1	42629134	Missense_Mutation	G	A	p.P75S	177	68	0.384	0.535	4	2	2	114	guanylate cyclase activator 2A (guanylin)	ENST00000357001.2
Case#2-Relapse-WholeTumor	YBX1	1	43162403	Missense_Mutation	C	T	p.P149S	366	114	0.311	0.434	4	2	2	256	Y box binding protein 1	ENST00000321358.7
Case#2-Relapse-WholeTumor	EIF2B3	1	45316632	Missense_Mutation	C	T	p.M450I	167	56	0.335	0.467	4	2	2	127	eukaryotic translation initiation factor 2B, subunit 3 gamma, 58kDa	ENST00000360403.2
Case#2-Relapse-WholeTumor	ZSWIM5	1	45501872	Missense_Mutation	G	A	p.A665V	145	12	0.083	0.115	4	2	2	103	zinc finger, SWIM-type containing 5	ENST00000359600.5
Case#2-Relapse-WholeTumor	TMEM69	1	46159342	Missense_Mutation	T	G	p.F170C	301	107	0.355	0.495	4	2	2	205	transmembrane protein 69	ENST00000372025.4
Case#2-Relapse-WholeTumor	NRD1	1	52287201	Missense_Mutation	C	T	p.V464M	137	44	0.321	0.447	4	2	2	107	nardilysin (N-arginine dibasic convertase)	ENST00000354831.7
Case#2-Relapse-WholeTumor	MROH7	1	55167778	Missense_Mutation	C	T	p.R1101C	169	55	0.325	0.453	4	2	2	115	maestro heat-like repeat family member 7	ENST00000421030.2
Case#2-Relapse-WholeTumor	C8A	1	57333319	Missense_Mutation	T	G	p.C39G	200	27	0.135	0.188	4	2	2	147	complement component 8, alpha polypeptide	ENST00000361249.3
Case#2-Relapse-WholeTumor	NFIA	1	61554113	Missense_Mutation	A	G	p.N107S	204	65	0.319	0.444	4	2	2	152	nuclear factor I/A	ENST00000403491.3
Case#2-Relapse-WholeTumor	WDR78	1	67292573	Missense_Mutation	G	A	p.P757S	254	93	0.366	0.510	4	2	2	184	WD repeat domain 78	ENST00000371026.3
Case#2-Relapse-WholeTumor	OVGP1	1	111957517	Missense_Mutation	T	C	p.S536G	73	27	0.370	0.564	3	2	1	39	oviductal glycoprotein 1, 120kDa	ENST00000369732.3
Case#2-Relapse-WholeTumor	MAGI3	1	114201725	Nonsense_Mutation	GTC	TAA	p.V885*	84	31	0.369	0.562	3	2	1	76	membrane associated guanylate kinase, WW and PDZ domain containing 3	ENST00000307546.9

Case#2-Relapse-WholeTumor	CD101	1	117554348	Missense_Mutation	C	T	p.L201F	145	53	0.366	0.557	3	2	1	141	CD101 molecule	ENST00000256652.4
Case#2-Relapse-WholeTumor	SPRR3	1	152975659	Frame_Shift_Del	GAGCCAGGCT GTACCAAGGT CCCT	-	p.E55fs	347	61	0.176	0.268	3	2	1	295	small proline-rich protein 3	ENST00000295367.4
Case#2-Relapse-WholeTumor	FCRL5	1	157494225	Missense_Mutation	G	A	p.H695Y	187	41	0.219	0.334	3	2	1	138	Fc receptor-like 5	ENST00000361835.3
Case#2-Relapse-WholeTumor	OR10K1	1	158435851	Missense_Mutation	C	T	p.P167L	220	89	0.405	0.616	3	2	1	169	olfactory receptor, family 10, subfamily K, member 1	ENST00000289451.2
Case#2-Relapse-WholeTumor	SPTA1	1	158582643	Missense_Mutation	C	G	p.E2366D	125	53	0.424	0.646	3	2	1	112	spectrin, alpha, erythrocytic 1	ENST00000368147.4
Case#2-Relapse-WholeTumor	ADCY10	1	167830176	Missense_Mutation	C	T	p.R581Q	190	42	0.221	0.337	3	2	1	162	adenylate cyclase 10 (soluble)	ENST00000367851.4
Case#2-Relapse-WholeTumor	FMO1	1	171254450	Missense_Mutation	G	A	p.D456N	178	26	0.146	0.223	3	2	1	145	flavin containing monooxygenase 1	ENST00000354841.4
Case#2-Relapse-WholeTumor	FASLG	1	172634863	Missense_Mutation	G	A	p.E185K	143	26	0.182	0.277	3	2	1	124	Fas ligand (TNF superfamily, member 6)	ENST00000367721.2
Case#2-Relapse-WholeTumor	SLC9C2	1	173506151	Missense_Mutation	C	T	p.G529R	174	36	0.207	0.315	3	2	1	129	solute carrier family 9, member C2 (putative)	ENST00000367714.3
Case#2-Relapse-WholeTumor	CFH	1	196709900	Missense_Mutation	G	T	p.W978C	153	37	0.242	0.369	3	2	1	141	complement factor H	ENST00000367429.4
Case#2-Relapse-WholeTumor	KIF21B	1	200944701	Missense_Mutation	C	T	p.G1514R	110	24	0.218	0.332	3	2	1	85	kinesin family member 21B	ENST00000422435.2
Case#2-Relapse-WholeTumor	NUAK2	1	205272869	Missense_Mutation	GG	AA	p.P532L	113	53	0.469	0.715	3	2	1	59	NUAK family, SNF1-like kinase, 2	ENST00000367157.3
Case#2-Relapse-WholeTumor	FCAMR	1	207140983	Missense_Mutation	C	T	p.R18K	241	15	0.062	0.095	3	2	1	201	Fc receptor, IgA, IgM, high affinity	ENST00000324852.4
Case#2-Relapse-WholeTumor	KCNH1	1	211093144	Missense_Mutation	C	T	p.G434R	301	131	0.435	0.663	3	2	1	277	potassium voltage-gated channel, subfamily H (eag-related), member 1	ENST00000271751.4
Case#2-Relapse-WholeTumor	USH2A	1	215972377	Missense_Mutation	C	T	p.G3277E	216	51	0.236	0.360	3	2	1	204	Usher syndrome 2A (autosomal recessive, mild)	ENST00000307340.3
Case#2-Relapse-WholeTumor	USH2A	1	216061902	Missense_Mutation	C	T	p.E2697K	160	41	0.256	0.390	3	2	1	119	Usher syndrome 2A (autosomal recessive, mild)	ENST00000307340.3
Case#2-Relapse-WholeTumor	DISP1	1	223176405	Missense_Mutation	C	T	p.P556S	133	53	0.398	0.607	3	2	1	88	dispatched homolog 1 (Drosophila)	ENST00000284476.6
Case#2-Relapse-WholeTumor	SUSD4	1	223396814	Missense_Mutation	G	T	p.D407E	74	18	0.243	0.371	3	2	1	62	sushi domain containing 4	ENST00000343846.3
Case#2-Relapse-WholeTumor	SDE2	1	226180122	Missense_Mutation	C	T	p.R166H	135	23	0.170	0.260	3	2	1	91	SDE2 telomere maintenance homolog (S. pombe)	ENST00000272091.7
Case#2-Relapse-WholeTumor	OBSCN	1	228494211	Missense_Mutation	G	A	p.G3933E	107	26	0.243	0.370	3	2	1	83	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	ENST00000422127.1
Case#2-Relapse-WholeTumor	ABCB10	1	229683251	Missense_Mutation	T	A	p.M306L	251	104	0.414	0.631	3	2	1	198	ATP-binding cassette, sub-family B (MDR/TAP), member 10	ENST00000344517.4
Case#2-Relapse-WholeTumor	PCNXL2	1	233270779	Missense_Mutation	C	T	p.V1273M	223	48	0.215	0.328	3	2	1	169	pecanex-like 2 (Drosophila)	ENST00000258229.9
Case#2-Relapse-WholeTumor	OR1C1	1	247920918	Missense_Mutation	G	A	p.S264F	110	19	0.173	0.308	2	1	1	134	olfactory receptor, family 1, subfamily C, member 1	ENST00000408896.2
Case#2-Relapse-WholeTumor	DCLRE1C	10	14977485	Missense_Mutation	C	T	p.M147I	121	47	0.388	0.694	2	2	0	35	DNA cross-link repair 1C	ENST00000378278.2
Case#2-Relapse-WholeTumor	DCLRE1C	10	14977523	Missense_Mutation	C	T	p.G135R	113	46	0.407	0.727	2	2	0	35	DNA cross-link repair 1C	ENST00000378278.2
Case#2-Relapse-WholeTumor	ARHGAP22	10	49791162	Missense_Mutation	G	A	p.R24W	52	27	0.519	0.927	2	2	0	72	Rho GTPase activating protein 22	ENST00000249601.4
Case#2-Relapse-WholeTumor	DLG5	10	79580911	Missense_Mutation	G	A	p.R1111C	77	35	0.455	0.812	2	2	0	83	discs, large homolog 5 (Drosophila)	ENST00000372391.2
Case#2-Relapse-WholeTumor	LRIT1	10	85993828	Splice_Site	C	T		98	14	0.143	0.255	2	2	0	115	leucine-rich repeat, immunoglobulin-like and transmembrane domains 1	ENST00000372105.3
Case#2-Relapse-WholeTumor	MUC6	11	1030779	Splice_Site	GC	TT	p.A229N	34	16	0.471	0.840	2	2	0	51	mucin 6, oligomeric mucus/gel-forming	ENST00000421673.2
Case#2-Relapse-WholeTumor	OR51I1	11	5461851	Missense_Mutation	GG	AA	p.T298I	131	60	0.458	0.818	2	2	0	127	olfactory receptor, family 51, subfamily I, member 1	ENST00000380211.1
Case#2-Relapse-WholeTumor	OR5P2	11	7818171	Missense_Mutation	C	T	p.E107K	126	80	0.635	1.134	2	2	0	158	olfactory receptor, family 5, subfamily P, member 2	ENST00000329434.2
Case#2-Relapse-WholeTumor	OR4A16	11	55110683	Missense_Mutation	C	T	p.P3S	99	51	0.515	0.920	2	2	0	140	olfactory receptor, family 4, subfamily A, member 16	ENST00000314721.2
Case#2-Relapse-WholeTumor	CTNND1	11	57564280	Missense_Mutation	G	A	p.G258R	187	106	0.567	1.012	2	2	0	210	catenin (cadherin-associated protein), delta 1	ENST00000399050.4
Case#2-Relapse-WholeTumor	PCNXL3	11	65384461	Missense_Mutation	A	T	p.Q107L	60	26	0.433	0.774	2	2	0	53	pecanex-like 3 (Drosophila)	ENST00000355703.3
Case#2-Relapse-WholeTumor	IGHMBP2	11	68675723	Missense_Mutation	G	A	p.D123N	110	58	0.527	0.942	2	2	0	128	immunoglobulin mu binding protein 2	ENST00000255078.3
Case#2-Relapse-WholeTumor	TRIM77	11	89444610	Nonsense_Mutation	G	A	p.W148*	82	43	0.524	0.936	2	2	0	116	tripartite motif containing 77	ENST00000398290.3
Case#2-Relapse-WholeTumor	MMP20	11	102487610	Missense_Mutation	G	A	p.P103S	150	86	0.573	1.024	2	2	0	151	matrix metallopeptidase 20	ENST00000260228.2
Case#2-Relapse-WholeTumor	GRIA4	11	105789535	Missense_Mutation	A	G	p.K456R	165	44	0.267	0.476	2	2	0	150	glutamate receptor, ionotropic, AMPA 4	ENST00000530497.1
Case#2-Relapse-WholeTumor	GRAMD1B	11	123465478	Nonsense_Mutation	C	T	p.Q126*	108	65	0.602	1.075	2	2	0	98	GRAM domain containing 1B	ENST00000529750.1
Case#2-Relapse-WholeTumor	KCNJ5	11	128781214	Missense_Mutation	G	A	p.G16R	125	76	0.608	1.086	2	2	0	146	potassium inwardly-rectifying channel, subfamily J, member 5	ENST00000338350.4
Case#2-Relapse-WholeTumor	ADAMTS15	11	130339181	Missense_Mutation	G	A	p.D523N	72	37	0.514	0.918	2	2	0	74	ADAM metallopeptidase with thrombospondin type 1 motif, 15	ENST00000299164.2
Case#2-Relapse-WholeTumor	DCP1B	12	2058318	Frame_Shift_Del	G	-	p.P569fs	167	41	0.246	0.374	3	2	1	133	decapping mRNA 1B	ENST00000280665.6
Case#2-Relapse-WholeTumor	PRMT8	12	3649955	Missense_Mutation	G	A	p.E87K	159	26	0.164	0.249	3	2	1	142	protein arginine methyltransferase 8	ENST00000382622.3
Case#2-Relapse-WholeTumor	VWF	12	6103165	Missense_Mutation	A	T	p.L2154Q	123	49	0.398	0.607	3	2	1	109	von Willebrand factor	ENST00000261405.5
Case#2-Relapse-WholeTumor	CD163L1	12	7521564	Splice_Site	GA	-		126	24	0.190	0.290	3	2	1	84	CD163 molecule-like 1	ENST00000313599.3
Case#2-Relapse-WholeTumor	PRH2	12	11083425	Missense_Mutation	G	A	p.G89R	332	37	0.111	0.170	3	2	1	260	proline-rich protein HaeIII subfamily 2	ENST00000396400.3
Case#2-Relapse-WholeTumor	PIK3C2G	12	18716366	Missense_Mutation	C	T	p.S1238L	139	27	0.194	0.296	3	2	1	108	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 gamma	ENST00000266497.5
Case#2-Relapse-WholeTumor	PIK3C2G	12	18716381	Missense_Mutation	CA	AT	p.S1243Y	147	28	0.190	0.290	3	2	1	114	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 gamma	ENST00000266497.5
Case#2-Relapse-WholeTumor	SLCO1B3	12	21069126	Missense_Mutation	G	A	p.G685E	242	45	0.186	0.283	3	2	1	155	solute carrier organic anion transporter family, member 1B3	ENST00000381545.3
Case#2-Relapse-WholeTumor	KCNJ8	12	21918938	Missense_Mutation	C	T	p.E332K	174	80	0.460	0.701	3	2	1	162	potassium inwardly-rectifying channel, subfamily J, member 8	ENST00000240662.2
Case#2-Relapse-WholeTumor	SLC38A4	12	47178369	Missense_Mutation	C	T	p.G150E	116	70	0.603	1.078	2	2	0	97	solute carrier family 38, member 4	ENST00000447411.1
Case#2-Relapse-WholeTumor	DIP2B	12	51118670	Splice_Site	G	A		98	53	0.541	0.966	2	2	0	151	DIP2 disco-interacting protein 2 homolog B (Drosophila)	ENST00000301180.5
Case#2-Relapse-WholeTumor	KRT2	12	53042832	Missense_Mutation	G	T	p.L306M	151	47	0.311	0.556	2	2	0	147	keratin 2	ENST00000309680.3
Case#2-Relapse-WholeTumor	KRT76	12	53162841	Missense_Mutation	C	T	p.V525I	181	47	0.260	0.464	2	2	0	215	keratin 76	ENST00000332411.2
Case#2-Relapse-WholeTumor	MYO1A	12	57422920	Missense_Mutation	C	T	p.E1001K	66	31	0.470	0.839	2	2	0	81	myosin IA	ENST00000442789.2
Case#2-Relapse-WholeTumor	C12orf55	12	97180611	Missense_Mutation	G	A	p.E2872K	77	40	0.519	0.928	2	2	0	106		ENST00000524981.4
Case#2-Relapse-WholeTumor	GNPTAB	12	102153816	Missense_Mutation	G	T	p.P1081T	116	55	0.474	0.847	2	2	0	136	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	ENST00000299314.7
Case#2-Relapse-WholeTumor	TDG	12	104376924	Missense_Mutation	C	T	p.R209C	92	55	0.598	1.068	2	2	0	112	thymine-DNA glycosylase	ENST00000392872.3
Case#2-Relapse-WholeTumor	CUX2	12	111757876	Missense_Mutation	C	T	p.T688I	141	80	0.567	1.013	2	2	0	108	cut-like homeobox 2	ENST00000261726.6
Case#2-Relapse-WholeTumor	ATXN2	12	111924586	Missense_Mutation	G	T	p.F921L	68	16	0.235	0.420	2	2	0	69	ataxin 2	ENST00000377617.3
Case#2-Relapse-WholeTumor	DNAH10	12	124267722	Missense_Mutation	G	A	p.E243K	172	100	0.581	1.038	2	2	0	162	dynein, axonemal, heavy chain 10	ENST00000409039.3
Case#2-Relapse-WholeTumor	BRCA2	13	32930738	Missense_Mutation	C	T	p.H2537Y	102	58	0.569	1.015	2	2	0	96	breast cancer 2, early onset	ENST00000380152.3
Case#2-Relapse-WholeTumor	NBEA	13	36124642	Missense_Mutation	G	A	p.G2205E	146	80	0.548	0.978	2	2	0	151	neurobeachin	ENST00000400445.3
Case#2-Relapse-WholeTumor	NFKBIA	14	35871725	Missense_Mutation	G	A	p.P261S	88	54	0.614	1.096	2	2	0	93	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	ENST00000216797.5
Case#2-Relapse-WholeTumor	TTC6	14	38151975	Missense_Mutation	G	A	p.E355K	104	64	0.615	1.099	2	2	0	126	tetratricopeptide repeat domain 6	ENST00000553443.1
Case#2-Relapse-WholeTumor	KCNH5	14	63453861	Missense_Mutation	G	C	p.R160G	149	70	0.470	0.839	2	2	0	142	potassium voltage-gated channel, subfamily H (eag-related), member 5	ENST00000322893.7
Case#2-Relapse-WholeTumor	ABCD4	14	74764632	Splice_Site	C	T		172	43	0.250	0.446	2	2	0	184	ATP-binding cassette, sub-family D (ALD), member 4	ENST00000356924.4
Case#2-Relapse-WholeTumor	OR4M2	15	22369306	Missense_Mutation	C	T	p.S244F	838	159	0.190	0.289	3	2	1	727	olfactory receptor, family 4, subfamily M, member 2	ENST00000332663.2
Case#2-Relapse-WholeTumor	FMN1	15	33261614	Missense_Mutation	T	C	p.E763G	166	65	0.392	0.597	3	2	1	117	formin 1	ENST00000559047.1
Case#2-Relapse-WholeTumor	SLC28A2	15	45545451	Missense_Mutation	C	T	p.S13F	164	52	0.317	0.483	3	2	1	145	solute carrier family 28 (concentrative nucleoside transporter), member 2	ENST00000347644.3
Case#2-Relapse-WholeTumor	CYP1A2	15	75042116	Missense_Mutation	G	A	p.E13K	153	60	0.392	0.598	3	2	1	149	cytochrome P450, family 1, subfamily A, polypeptide 2	ENST00000343932.4
Case#2-Relapse-WholeTumor	KIAA1199	15	81188289	Nonsense_Mutation	G	A	p.W433*	225	89	0.396	0.603	3	2	1	184		ENST00000394685.3
Case#2-Relapse-WholeTumor	LRRK1	15	101606184	Missense_Mutation	C	G	p.P1848A	76	17	0.224	0.341	3	2	1	65	leucine-rich repeat kinase 1	ENST00000388948.3
Case#2-Relapse-WholeTumor	PKD1	16	2160895	Missense_Mutation	G	A	p.R1425C	386	89	0.231	0.351	3	2	1	323	polycystic kidney disease 1 (autosomal dominant)	ENST00000262304.4
Case#2-Relapse-WholeTumor	DNAH3	16	20974716	Missense_Mutation	C	T	p.G3497E	188	64	0.340	0.519	3	2	1	181	dynein, axonemal, heavy chain 3	ENST00000261383.3

Case#2-Relapse-WholeTumor	DNAH3	16	21086851	Missense_Mutation	C	T	p.E1001K	96	36	0.375	0.571	3	2	1	92	dynein, axonemal, heavy chain 3	ENST00000261383.3
Case#2-Relapse-WholeTumor	TMEM159	16	21185368	Missense_Mutation	C	G	p.C101W	127	26	0.205	0.312	3	2	1	124	transmembrane protein 159	ENST00000233047.4
Case#2-Relapse-WholeTumor	SCNN1G	16	23223460	Missense_Mutation	C	A	p.H428N	137	10	0.073	0.111	3	2	1	85	sodium channel, non-voltage-gated 1, gamma subunit	ENST00000300061.2
Case#2-Relapse-WholeTumor	TNRC6A	16	24815560	Nonsense_Mutation	C	T	p.R1253*	121	26	0.215	0.327	3	2	1	103	trinucleotide repeat containing 6A	ENST00000395799.3
Case#2-Relapse-WholeTumor	PRR14	16	30666042	Missense_Mutation	CG	TT	p.R251F	97	16	0.165	0.251	3	2	1	79	proline rich 14	ENST00000542965.2
Case#2-Relapse-WholeTumor	STX1B	16	31004546	Missense_Mutation	G	C	p.R231G	139	25	0.180	0.274	3	2	1	121	syntaxin 1B	ENST00000215095.5
Case#2-Relapse-WholeTumor	ITGAM	16	31309065	Splice_Site	G	A		88	30	0.341	0.519	3	2	1	94	integrin, alpha M (complement component 3 receptor 3 subunit)	ENST00000287497.8
Case#2-Relapse-WholeTumor	ITGAM	16	31309202	Missense_Mutation	A	T	p.E545V	102	27	0.265	0.403	3	2	1	98	integrin, alpha M (complement component 3 receptor 3 subunit)	ENST00000287497.8
Case#2-Relapse-WholeTumor	PAPD5	16	50263084	Missense_Mutation	C	T	p.R538C	133	28	0.211	0.321	3	2	1	117	PAP associated domain containing 5	ENST00000561678.1
Case#2-Relapse-WholeTumor	OGFOD1	16	56504605	Missense_Mutation	C	T	p.P396L	112	20	0.179	0.272	3	2	1	81	2-oxoglutarate and iron-dependent oxygenase domain containing 1	ENST00000566157.1
Case#2-Relapse-WholeTumor	SLC12A3	16	56947280	Missense_Mutation	G	A	p.G1010E	341	133	0.390	0.594	3	2	1	244	solute carrier family 12 (sodium/chloride transporter), member 3	ENST00000563236.1
Case#2-Relapse-WholeTumor	NLRC5	16	57110766	Missense_Mutation	G	A	p.C1596Y	89	26	0.292	0.445	3	2	1	84	NLR family, CARD domain containing 5	ENST00000262510.6
Case#2-Relapse-WholeTumor	EXOC3L1	16	67221347	Missense_Mutation	C	T	p.G274E	72	32	0.444	0.677	3	2	1	61	exocyst complex component 3-like 1	ENST00000314586.6
Case#2-Relapse-WholeTumor	HYDIN	16	70977759	Missense_Mutation	G	A	p.L2209F	64	38	0.594	0.905	3	2	1	46	HYDIN, axonemal central pair apparatus protein	ENST00000393567.2
Case#2-Relapse-WholeTumor	HYDIN	16	71007260	Missense_Mutation	T	G	p.M1789L	316	36	0.114	0.174	3	2	1	271	HYDIN, axonemal central pair apparatus protein	ENST00000393567.2
Case#2-Relapse-WholeTumor	HYDIN	16	71009082	Missense_Mutation	C	T	p.D1577N	951	207	0.218	0.332	3	2	1	872	HYDIN, axonemal central pair apparatus protein	ENST00000393567.2
Case#2-Relapse-WholeTumor	CHST4	16	71570816	Nonsense_Mutation	G	A	p.W79*	167	76	0.455	0.693	3	2	1	126	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4	ENST00000338482.5
Case#2-Relapse-WholeTumor	PHLPP2	16	71683269	Missense_Mutation	C	T	p.E1166K	206	23	0.112	0.170	3	2	1	132	PH domain and leucine rich repeat protein phosphatase 2	ENST00000568954.1
Case#2-Relapse-WholeTumor	JPH3	16	87678364	Missense_Mutation	G	A	p.D295N	456	86	0.189	0.287	3	2	1	387	junctophilin 3	ENST00000284262.2
Case#2-Relapse-WholeTumor	DNAH2	17	7702025	Missense_Mutation	G	A	p.E2850K	119	32	0.269	0.480	2	1	1	125	dynein, axonemal, heavy chain 2	ENST00000572933.1
Case#2-Relapse-WholeTumor	KCNAB3	17	7827771	Missense_Mutation	A	T	p.Y225N	155	42	0.271	0.484	2	1	1	163	potassium voltage-gated channel, shaker-related subfamily, beta member 3	ENST00000303790.2
Case#2-Relapse-WholeTumor	USP43	17	9583599	Nonsense_Mutation	G	T	p.E341*	115	24	0.209	0.373	2	1	1	111	ubiquitin specific peptidase 43	ENST00000285199.7
Case#2-Relapse-WholeTumor	MYH4	17	10358940	Missense_Mutation	A	T	p.F722Y	155	44	0.284	0.507	2	1	1	213	myosin, heavy chain 4, skeletal muscle	ENST00000255381.2
Case#2-Relapse-WholeTumor	DNAH9	17	11607590	Missense_Mutation	G	A	p.G1741D	134	37	0.276	0.493	2	1	1	141	dynein, axonemal, heavy chain 9	ENST00000262442.4
Case#2-Relapse-WholeTumor	CSF3	17	38172825	Missense_Mutation	C	A	p.P134T	172	46	0.267	0.478	2	1	1	182	colony stimulating factor 3 (granulocyte)	ENST00000225474.2
Case#2-Relapse-WholeTumor	ZNF385C	17	40181094	Splice_Site	G	A	p.A226V	69	19	0.275	0.492	2	1	1	63	zinc finger protein 385C	ENST00000436535.3
Case#2-Relapse-WholeTumor	IGF2BP1	17	47126787	Missense_Mutation	C	T	p.A572V	165	32	0.194	0.296	3	2	1	101	insulin-like growth factor 2 mRNA binding protein 1	ENST00000290341.3
Case#2-Relapse-WholeTumor	SGCA	17	48245845	Missense_Mutation	G	A	p.E166K	205	77	0.376	0.572	3	2	1	167	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)	ENST00000262018.3
Case#2-Relapse-WholeTumor	CD300A	17	72477896	Missense_Mutation	A	T	p.N233I	211	73	0.346	0.527	3	2	1	200	CD300a molecule	ENST00000360141.3
Case#2-Relapse-WholeTumor	RBFOX3	17	77100159	Missense_Mutation	G	A	p.S137F	163	74	0.454	0.692	3	2	1	105	RNA binding protein, fox-1 homolog (C. elegans) 3	ENST00000453134.2
Case#2-Relapse-WholeTumor	RNF213	17	78346865	Missense_Mutation	G	C	p.R4281P	194	18	0.093	0.141	3	2	1	139	ring finger protein 213	ENST00000582970.1
Case#2-Relapse-WholeTumor	EMILIN2	18	2891917	Missense_Mutation	G	A	p.E598K	168	29	0.173	0.263	3	2	1	112	elastin microfibril interfacer 2	ENST00000254528.3
Case#2-Relapse-WholeTumor	TMEM200C	18	5890552	Missense_Mutation	G	A	p.A504V	57	17	0.298	0.454	3	2	1	43	transmembrane protein 200C	ENST00000581347.2
Case#2-Relapse-WholeTumor	IMPACT	18	22023054	Missense_Mutation	C	T	p.P178S	116	42	0.362	0.552	3	2	1	82	impact RWD domain protein	ENST00000284202.4
Case#2-Relapse-WholeTumor	DSC1	18	28714538	Missense_Mutation	CC	TT	p.D625N	126	52	0.413	0.629	3	2	1	114	desmocollin 1	ENST00000257198.5
Case#2-Relapse-WholeTumor	ALPK2	18	56196344	Missense_Mutation	G	A	p.S1827F	131	68	0.519	0.791	3	2	1	108	alpha-kinase 2	ENST00000361673.3
Case#2-Relapse-WholeTumor	SERPINB8	18	61652436	Missense_Mutation	G	T	p.S226I	162	28	0.173	0.263	3	2	1	141	serpin peptidase inhibitor, clade B (ovalbumin), member 8	ENST00000397985.2
Case#2-Relapse-WholeTumor	CNDP1	18	72250811	Missense_Mutation	C	T	p.P442S	207	46	0.222	0.339	3	2	1	188	carnosine dipeptidase 1 (metallopeptidase M20 family)	ENST00000358821.3
Case#2-Relapse-WholeTumor	PTBP1	19	805050	Missense_Mutation	C	T	p.T252M	287	145	0.505	0.704	4	3	1	185	polypyrimidine tract binding protein 1	ENST00000349038.4
Case#2-Relapse-WholeTumor	GNG7	19	2515129	Missense_Mutation	G	A	p.S33F	200	35	0.175	0.267	3	2	1	147	guanine nucleotide binding protein (G protein), gamma 7	ENST00000382159.3
Case#2-Relapse-WholeTumor	MAP2K2	19	4110574	Missense_Mutation	G	C	p.P128R	160	57	0.356	0.543	3	2	1	162	mitogen-activated protein kinase kinase 2	ENST00000262948.5
Case#2-Relapse-WholeTumor	MUC16	19	9061537	Missense_Mutation	C	T	p.E8637K	205	74	0.361	0.550	3	2	1	158	mucin 16, cell surface associated	ENST00000397910.4
Case#2-Relapse-WholeTumor	MUC16	19	9064668	Missense_Mutation	G	C	p.S7593C	228	44	0.193	0.294	3	2	1	177	mucin 16, cell surface associated	ENST00000397910.4
Case#2-Relapse-WholeTumor	MUC16	19	9082813	Missense_Mutation	G	A	p.S3001L	186	46	0.247	0.377	3	2	1	167	mucin 16, cell surface associated	ENST00000397910.4
Case#2-Relapse-WholeTumor	MUC16	19	9085250	Missense_Mutation	C	T	p.E2189K	146	67	0.459	0.699	3	2	1	154	mucin 16, cell surface associated	ENST00000397910.4
Case#2-Relapse-WholeTumor	OR7G3	19	9236942	Missense_Mutation	G	A	p.P229S	167	34	0.204	0.310	3	2	1	168	olfactory receptor, family 7, subfamily G, member 3	ENST00000305444.2
Case#2-Relapse-WholeTumor	ZNF560	19	9577307	Missense_Mutation	C	G	p.Q772H	310	55	0.177	0.270	3	2	1	264	zinc finger protein 560	ENST00000301480.4
Case#2-Relapse-WholeTumor	ZNF563	19	12429713	Missense_Mutation	G	A	p.H376Y	422	86	0.204	0.311	3	2	1	406	zinc finger protein 563	ENST00000293725.5
Case#2-Relapse-WholeTumor	ABHD8	19	17412109	Missense_Mutation	C	T	p.G106E	18	7	0.389	0.593	3	2	1	20	abhydrolase domain containing 8	ENST00000247706.3
Case#2-Relapse-WholeTumor	ARHGAP35	19	47422066	Missense_Mutation	C	T	p.P45L	325	146	0.449	0.685	3	2	1	282	Rho GTPase activating protein 35	ENST00000404338.3
Case#2-Relapse-WholeTumor	LHB	19	49519534	Missense_Mutation	G	A	p.P73S	463	82	0.177	0.270	3	2	1	386	luteinizing hormone beta polypeptide	ENST00000221421.2
Case#2-Relapse-WholeTumor	SCAF1	19	50156247	Missense_Mutation	CC	TT	p.R868C	380	145	0.382	0.581	3	2	1	339	SR-related CTD-associated factor 1	ENST00000360565.3
Case#2-Relapse-WholeTumor	LILRB5	19	54759398	Missense_Mutation	C	T	p.A235T	312	126	0.404	0.615	3	2	1	197	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5	ENST00000316219.5
Case#2-Relapse-WholeTumor	LILRA1	19	55107746	Missense_Mutation	C	T	p.P351S	267	124	0.464	0.708	3	2	1	214	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1	ENST00000251372.3
Case#2-Relapse-WholeTumor	ZNF324B	19	58966688	Missense_Mutation	CG	TT	p.P126L	246	49	0.199	0.304	3	2	1	227	zinc finger protein 324B	ENST00000336614.4
Case#2-Relapse-WholeTumor	CAD	2	27464912	Missense_Mutation	C	T	p.S1943F	150	65	0.433	0.660	3	2	1	131	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	ENST00000403525.1
Case#2-Relapse-WholeTumor	C2orf16	2	27803529	Missense_Mutation	G	A	p.A1364T	142	34	0.239	0.365	3	2	1	131	chromosome 2 open reading frame 16	ENST00000408964.2
Case#2-Relapse-WholeTumor	HEATR5B	2	37234373	Missense_Mutation	G	A	p.H1533Y	180	75	0.417	0.635	3	2	1	135	HEAT repeat containing 5B	ENST00000233099.5
Case#2-Relapse-WholeTumor	HNRNPLL	2	38809081	Missense_Mutation	T	C	p.Y259C	204	44	0.216	0.329	3	2	1	192	heterogeneous nuclear ribonucleoprotein L-like	ENST00000449105.3
Case#2-Relapse-WholeTumor	USP34	2	61633078	Missense_Mutation	T	A	p.N106I	106	49	0.462	0.704	3	2	1	96	ubiquitin specific peptidase 34	ENST00000398571.2
Case#2-Relapse-WholeTumor	DUSP11	2	73993587	Missense_Mutation	C	T	p.R298Q	234	49	0.209	0.319	3	2	1	199	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	ENST00000272444.3
Case#2-Relapse-WholeTumor	FAM178B	2	97613588	Missense_Mutation	C	T	p.D497N	124	61	0.492	0.750	3	2	1	105	family with sequence similarity 178, member B	ENST00000417561.3
Case#2-Relapse-WholeTumor	CNTNAP5	2	125175155	Missense_Mutation	G	A	p.G173R	142	57	0.401	0.612	3	2	1	148	contactin associated protein-like 5	ENST00000431078.1
Case#2-Relapse-WholeTumor	MYO7B	2	128366350	Missense_Mutation	C	T	p.S904F	358	57	0.159	0.243	3	2	1	311	myosin VIIB	ENST00000409816.2
Case#2-Relapse-WholeTumor	GPR39	2	133402871	Missense_Mutation	C	T	p.R352W	190	83	0.437	0.666	3	2	1	136	G protein-coupled receptor 39	ENST00000329231.3
Case#2-Relapse-WholeTumor	LRP1B	2	141607835	Missense_Mutation	G	A	p.P1592L	181	38	0.210	0.320	3	2	1	137	low density lipoprotein receptor-related protein 1B	ENST00000389484.3
Case#2-Relapse-WholeTumor	NEB	2	152427025	Missense_Mutation	C	T	p.E4001K	134	26	0.194	0.296	3	2	1	88	nebulin	ENST00000172853.10
Case#2-Relapse-WholeTumor	FMNL2	2	153497396	Missense_Mutation	G	A	p.G421E	188	32	0.170	0.259	3	2	1	133	formin-like 2	ENST00000475377.2
Case#2-Relapse-WholeTumor	DCAF17	2	172325510	Missense_Mutation	C	A	p.F317L	157	75	0.478	0.728	3	2	1	94	DDB1 and CUL4 associated factor 17	ENST00000375255.3
Case#2-Relapse-WholeTumor	PDE1A	2	183011865	Missense_Mutation	G	A	p.H527Y	98	22	0.224	0.342	3	2	1	69	phosphodiesterase 1A, calmodulin-dependent	ENST00000435564.1
Case#2-Relapse-WholeTumor	SLC40A1	2	190428486	Missense_Mutation	C	T	p.R409Q	195	41	0.210	0.320	3	2	1	155	solute carrier family 40 (iron-regulated transporter), member 1	ENST00000261024.2
Case#2-Relapse-WholeTumor	STAT4	2	191919251	Missense_Mutation	C	T	p.E406K	171	69	0.404	0.615	3	2	1	141	signal transducer and activator of transcription 4	ENST00000392320.2
Case#2-Relapse-WholeTumor	DNAH7	2	196762426	Missense_Mutation	G	C	p.P1538A	239	45	0.188	0.287	3	2	1	191	dynein, axonemal, heavy chain 7	ENST00000312428.6
Case#2-Relapse-WholeTumor	DNAH7	2	196799458	Missense_Mutation	C	T	p.E1110K	155	28	0.181	0.275	3	2	1	129	dynein, axonemal, heavy chain 7	ENST00000312428.6
Case#2-Relapse-WholeTumor	CRYGA	2	209025650	Missense_Mutation	C	T	p.E135K	229	99	0.432	0.659	3	2	1	173	crystallin, gamma A	ENST00000304502.4
Case#2-Relapse-WholeTumor	PTH2R	2	209302602	Missense_Mutation	G	A	p.G136E	142	27	0.190	0.290	3	2	1	111	parathyroid hormone 2 receptor	ENST00000272847.2
Case#2-Relapse-WholeTumor	ARPC2	2	219093493	Missense_Mutation	C	T	p.P48S	142	63	0.444	0.676	3	2	1	130	actin related protein 2/3 complex, subunit 2, 34kDa	ENST00000295685.10
Case#2-Relapse-WholeTumor	PNKD	2	219206288	Missense_Mutation	C	T	p.R186W	261	16	0.061	0.093	3	2	1	208	paroxysmal nonkinesigenic dyskinesia	ENST00000273077.4
Case#2-Relapse-WholeTumor	ACSL3	2	223782833	Missense_Mutation	A	G	p.N209S	127	20	0.157	0.240	3	2	1	95	acyl-CoA synthetase long-chain family member 3	ENST00000357430.3
Case#2-Relapse-WholeTumor	COL4A3	2	228109667	Splice_Site	G	A	p.G94R	218	47	0.216	0.329	3	2	1	166	collagen, type IV, alpha 3 (Goodpasture antigen)	ENST00000396578.3

Case#2-Relapse-WholeTumor	CHRNG	2	233408368	Missense_Mutation	C	T	p.R332W	167	38	0.228	0.347	3	2	1	122	cholinergic receptor, nicotinic, gamma (muscle)	ENST00000389494.3
Case#2-Relapse-WholeTumor	INPP5D	2	234112887	Missense_Mutation	C	T	p.P1019S	142	54	0.380	0.579	3	2	1	105	inositol polyphosphate-5-phosphatase, 145kDa	ENST00000359570.5
Case#2-Relapse-WholeTumor	COL6A3	2	238296599	Missense_Mutation	C	T	p.G313E	215	91	0.423	0.645	3	2	1	152	collagen, type VI, alpha 3	ENST00000295550.4
Case#2-Relapse-WholeTumor	RBM44	2	238733043	Nonsense_Mutation	G	A	p.W811*	210	34	0.162	0.247	3	2	1	41	RNA binding motif protein 44	ENST00000409864.1
Case#2-Relapse-WholeTumor	CHGB	20	5903578	Missense_Mutation	C	T	p.S263F	128	24	0.188	0.286	3	2	1	81	chromogranin B (secretogranin 1)	ENST00000378961.4
Case#2-Relapse-WholeTumor	HAO1	20	7886973	Missense_Mutation	C	T	p.M183I	104	26	0.250	0.381	3	2	1	66	hydroxyacid oxidase (glycolate oxidase) 1	ENST00000378789.3
Case#2-Relapse-WholeTumor	SLX4IP	20	10603749	Nonsense_Mutation	C	T	p.R317*	146	29	0.199	0.303	3	2	1	135	SLX4 interacting protein	ENST00000334534.5
Case#2-Relapse-WholeTumor	TTLL9	20	30513896	Splice_Site	T	A		212	90	0.425	0.647	3	2	1	129	tubulin tyrosine ligase-like family, member 9	ENST00000375938.4
Case#2-Relapse-WholeTumor	GDF5	20	34022347	Missense_Mutation	G	T	p.S289Y	146	24	0.164	0.229	4	3	1	108	growth differentiation factor 5	ENST00000374372.1
Case#2-Relapse-WholeTumor	SAMHD1	20	35545391	Missense_Mutation	C	T	p.R305K	129	60	0.465	0.648	4	3	1	98	SAM domain and HD domain 1	ENST00000262878.4
Case#2-Relapse-WholeTumor	PABPC1L	20	43559255	Missense_Mutation	C	T	p.A376V	187	29	0.155	0.216	4	3	1	166	poly(A) binding protein, cytoplasmic 1-like	ENST00000217073.2
Case#2-Relapse-WholeTumor	PABPC1L	20	43566704	Missense_Mutation	G	A	p.E550K	210	126	0.600	0.836	4	3	1	152	poly(A) binding protein, cytoplasmic 1-like	ENST00000217073.2
Case#2-Relapse-WholeTumor	ZNF334	20	45133364	Nonsense_Mutation	G	A	p.Q13*	243	121	0.498	0.694	4	3	1	145	zinc finger protein 334	ENST00000347606.4
Case#2-Relapse-WholeTumor	FAM217B	20	58519207	Missense_Mutation	CC	TT	p.A70V	132	40	0.303	0.398	5	3	2	117	family with sequence similarity 217, member B	ENST00000358293.3
Case#2-Relapse-WholeTumor	USP25	21	17250160	Nonsense_Mutation	C	T	p.R949*	180	39	0.217	0.330	3	2	1	167	ubiquitin specific peptidase 25	ENST00000285679.6
Case#2-Relapse-WholeTumor	GRIK1	21	31062192	Missense_Mutation	G	A	p.R134C	148	53	0.358	0.546	3	2	1	117	glutamate receptor, ionotropic, kainate 1	ENST00000399907.1
Case#2-Relapse-WholeTumor	IFNAR2	21	34635507	Missense_Mutation	C	T	p.S417F	159	68	0.428	0.652	3	2	1	138	interferon (alpha, beta and omega) receptor 2	ENST00000342136.4
Case#2-Relapse-WholeTumor	ABCG1	21	43714725	Missense_Mutation	C	T	p.T588I	136	32	0.235	0.359	3	2	1	115	ATP-binding cassette, sub-family G (WHITE), member 1	ENST00000361802.2
Case#2-Relapse-WholeTumor	KRTAP10-11	21	46067102	Missense_Mutation	C	T	p.P243S	221	55	0.249	0.379	3	2	1	197	keratin associated protein 10-11	ENST00000334670.8
Case#2-Relapse-WholeTumor	COL18A1	21	46914475	Missense_Mutation	G	A	p.R1205Q	138	29	0.210	0.320	3	2	1	111	collagen, type XVIII, alpha 1	ENST00000359759.4
Case#2-Relapse-WholeTumor	PCNT	21	47836080	Missense_Mutation	C	T	p.S2083F	211	99	0.469	0.715	3	2	1	169	pericentrin	ENST00000359568.5
Case#2-Relapse-WholeTumor	RIMBP3	22	20456945	Missense_Mutation	G	A	p.P1453S	491	72	0.147	0.193	5	3	2	280	RIMS binding protein 3	ENST00000426804.1
Case#2-Relapse-WholeTumor	LZTR1	22	21343110	Missense_Mutation	C	T	p.T181M	203	90	0.443	0.583	5	3	2	111	leucine-zipper-like transcription regulator 1	ENST00000215739.8
Case#2-Relapse-WholeTumor	PIWIL3	22	25155951	Missense_Mutation	C	G	p.Q36H	156	50	0.321	0.421	5	4	1	110	piwi-like RNA-mediated gene silencing 3	ENST00000332271.5
Case#2-Relapse-WholeTumor	CABP7	22	30124619	Splice_Site	G	A	p.G85D	137	58	0.423	0.590	4	2	2	66	calcium binding protein 7	ENST00000216144.3
Case#2-Relapse-WholeTumor	EIF3D	22	36916707	Missense_Mutation	C	T	p.R165H	98	26	0.265	0.370	4	2	2	75	eukaryotic translation initiation factor 3, subunit D	ENST00000216190.8
Case#2-Relapse-WholeTumor	MPPED1	22	43898547	Missense_Mutation	A	G	p.K258E	126	22	0.175	0.243	4	2	2	88	metallophosphoesterase domain containing 1	ENST00000417669.2
Case#2-Relapse-WholeTumor	PARVB	22	44489874	Missense_Mutation	T	C	p.V60A	147	58	0.395	0.550	4	2	2	104	parvin, beta	ENST00000338758.7
Case#2-Relapse-WholeTumor	NUP210	3	13372082	Missense_Mutation	G	A	p.P1330S	235	105	0.447	0.681	3	2	1	199	nucleoporin 210kDa	ENST00000254508.5
Case#2-Relapse-WholeTumor	SLC4A7	3	27498171	Missense_Mutation	C	T	p.E2K	205	50	0.244	0.372	3	2	1	140	solute carrier family 4, sodium bicarbonate cotransporter, member 7	ENST00000295736.5
Case#2-Relapse-WholeTumor	SCN5A	3	38592057	Missense_Mutation	G	A	p.L1936F	129	65	0.504	0.768	3	2	1	93	sodium channel, voltage-gated, type V, alpha subunit	ENST00000333535.4
Case#2-Relapse-WholeTumor	CSRNP1	3	39185707	Missense_Mutation	C	T	p.R234Q	261	72	0.276	0.420	3	2	1	184	cysteine-serine-rich nuclear protein 1	ENST00000273153.5
Case#2-Relapse-WholeTumor	LRRC2	3	46593024	Missense_Mutation	G	A	p.R20C	182	34	0.187	0.285	3	2	1	169	leucine rich repeat containing 2	ENST00000395905.3
Case#2-Relapse-WholeTumor	SLC26A6	3	48669111	Missense_Mutation	G	A	p.P292S	104	18	0.173	0.264	3	2	1	115	solute carrier family 26 (anion exchanger), member 6	ENST00000395550.2
Case#2-Relapse-WholeTumor	UBA7	3	49847517	Missense_Mutation	AC	TT	p.V578K	112	50	0.446	0.680	3	2	1	115	ubiquitin-like modifier activating enzyme 7	ENST00000333486.3
Case#2-Relapse-WholeTumor	DOCK3	3	51127760	Missense_Mutation	G	A	p.E231K	196	69	0.352	0.536	3	2	1	158	dedicator of cytokinesis 3	ENST00000266037.9
Case#2-Relapse-WholeTumor	LRTM1	3	54961931	Splice_Site	C	G		147	74	0.503	0.767	3	2	1	153	leucine-rich repeats and transmembrane domains 1	ENST00000273286.5
Case#2-Relapse-WholeTumor	PTPRG	3	62216967	Missense_Mutation	G	A	p.R786K	49	12	0.245	0.373	3	2	1	48	protein tyrosine phosphatase, receptor type, G	ENST00000474889.1
Case#2-Relapse-WholeTumor	UBA3	3	69105214	Splice_Site	C	A	p.L395L	116	24	0.207	0.315	3	2	1	99	ubiquitin-like modifier activating enzyme 3	ENST00000361055.4
Case#2-Relapse-WholeTumor	DHFRL1	3	93779809	Missense_Mutation	A	G	p.C183R	179	88	0.492	0.749	3	2	1	165	dihydrofolate reductase-like 1	ENST00000394221.2
Case#2-Relapse-WholeTumor	SLC9C1	3	111996674	Missense_Mutation	T	G	p.N118H	180	68	0.378	0.576	3	2	1	147	solute carrier family 9, subfamily C (Na+-transporting carboxylic acid decarboxylase), member 1	ENST00000305815.5
Case#2-Relapse-WholeTumor	WDR52	3	113092257	Splice_Site	C	G		206	48	0.233	0.355	3	2	1	139		ENST00000295868.2
Case#2-Relapse-WholeTumor	SIDT1	3	113300268	Missense_Mutation	A	C	p.K242Q	167	37	0.222	0.338	3	2	1	155	SID1 transmembrane family, member 1	ENST00000264852.4
Case#2-Relapse-WholeTumor	GRAMD1C	3	113595055	Missense_Mutation	A	C	p.K136T	221	44	0.199	0.303	3	2	1	176	GRAM domain containing 1C	ENST00000358160.4
Case#2-Relapse-WholeTumor	KALRN	3	124201655	Splice_Site	G	A	p.E1396K	128	56	0.438	0.667	3	2	1	121	kalirin, RhoGEF kinase	ENST00000240874.3
Case#2-Relapse-WholeTumor	COL6A5	3	130141610	Missense_Mutation	G	A	p.G1695E	110	27	0.245	0.374	3	2	1	110	collagen, type VI, alpha 5	ENST00000432398.2
Case#2-Relapse-WholeTumor	ACKR4	3	132319698	Missense_Mutation	C	T	p.P153S	352	69	0.196	0.299	3	2	1	334	atypical chemokine receptor 4	ENST00000249887.2
Case#2-Relapse-WholeTumor	GRK7	3	141535846	Missense_Mutation	G	A	p.C539Y	117	25	0.214	0.326	3	2	1	80	G protein-coupled receptor kinase 7	ENST00000264952.2
Case#2-Relapse-WholeTumor	WDR49	3	167254723	Missense_Mutation	C	T	p.G278E	207	42	0.203	0.309	3	2	1	156	WD repeat domain 49	ENST00000308378.3
Case#2-Relapse-WholeTumor	THPO	3	184090671	Missense_Mutation	C	T	p.G231D	120	29	0.242	0.368	3	2	1	80	thrombopoietin	ENST00000204615.7
Case#2-Relapse-WholeTumor	LSG1	3	194387217	Missense_Mutation	T	G	p.H104P	108	26	0.241	0.367	3	2	1	93	large 60S subunit nuclear export GTPase 1	ENST00000265245.5
Case#2-Relapse-WholeTumor	RGS12	4	3432545	Missense_Mutation	C	T	p.A1326V	170	44	0.259	0.462	2	1	1	187	regulator of G-protein signaling 12	ENST00000344733.5
Case#2-Relapse-WholeTumor	MAN2B2	4	6611023	Nonsense_Mutation	C	G	p.Y668*	110	33	0.300	0.536	2	1	1	122	mannosidase, alpha, class 2B, member 2	ENST00000285599.3
Case#2-Relapse-WholeTumor	CD38	4	15826506	Missense_Mutation	T	G	p.I122M	201	48	0.239	0.364	3	2	1	156	CD38 molecule	ENST00000226279.3
Case#2-Relapse-WholeTumor	SLIT2	4	20619226	Missense_Mutation	C	T	p.P1434L	163	78	0.479	0.729	3	2	1	157	slit homolog 2 (Drosophila)	ENST00000504154.1
Case#2-Relapse-WholeTumor	KLHL5	4	39116817	Missense_Mutation	C	T	p.S693F	118	30	0.254	0.387	3	2	1	90	kelch-like family member 5	ENST00000504108.1
Case#2-Relapse-WholeTumor	CHRNA9	4	40351379	Missense_Mutation	T	G	p.F282L	132	32	0.242	0.369	3	2	1	140	cholinergic receptor, nicotinic, alpha 9 (neuronal)	ENST00000310169.2
Case#2-Relapse-WholeTumor	RBM47	4	40440602	Missense_Mutation	C	T	p.M103I	216	44	0.204	0.310	3	2	1	179	RNA binding motif protein 47	ENST00000381793.2
Case#2-Relapse-WholeTumor	GUF1	4	44691955	Missense_Mutation	C	T	p.P433L	128	8	0.063	0.095	3	2	1	126	GUF1 GTPase homolog (S. cerevisiae)	ENST00000281543.5
Case#2-Relapse-WholeTumor	ENAM	4	71509437	Missense_Mutation	C	T	p.S765F	165	34	0.206	0.314	3	2	1	124	enamelin	ENST00000396073.3
Case#2-Relapse-WholeTumor	KIAA1109	4	123234822	Missense_Mutation	C	T	p.T3431I	122	30	0.246	0.375	3	2	1	108	KIAA1109	ENST00000264501.4
Case#2-Relapse-WholeTumor	FREM3	4	144620448	Missense_Mutation	C	T	p.D461N	192	84	0.438	0.667	3	2	1	168	FRAS1 related extracellular matrix 3	ENST00000329798.5
Case#2-Relapse-WholeTumor	ANXA10	4	169049272	Missense_Mutation	C	T	p.P19L	106	26	0.245	0.374	3	2	1	90	annexin A10	ENST00000359299.3
Case#2-Relapse-WholeTumor	SPATA4	4	177116616	Missense_Mutation	C	T	p.R33Q	276	71	0.257	0.392	3	2	1	214	spermatogenesis associated 4	ENST00000280191.2
Case#2-Relapse-WholeTumor	TENM3	4	183714432	Missense_Mutation	G	A	p.E2203K	175	72	0.411	0.627	3	2	1	138	teneurin transmembrane protein 3	ENST00000511685.1
Case#2-Relapse-WholeTumor	WWC2	4	184171119	Missense_Mutation	G	A	p.S309N	156	29	0.186	0.283	3	2	1	129	WW and C2 domain containing 2	ENST00000403733.3
Case#2-Relapse-WholeTumor	DNAH5	5	13885322	Missense_Mutation	C	T	p.G920E	69	27	0.391	0.545	4	2	2	45	dynein, axonemal, heavy chain 5	ENST00000265104.4
Case#2-Relapse-WholeTumor	C9	5	39341716	Missense_Mutation	GG	AA	p.P90L	218	73	0.335	0.466	4	2	2	170	complement component 9	ENST00000263408.4
Case#2-Relapse-WholeTumor	CMYA5	5	79026782	Missense_Mutation	C	T	p.P732S	177	62	0.350	0.488	4	2	2	108	cardiomyopathy associated 5	ENST00000446378.2
Case#2-Relapse-WholeTumor	CMYA5	5	79033293	Missense_Mutation	G	T	p.S2902I	162	26	0.160	0.224	4	2	2	98	cardiomyopathy associated 5	ENST00000446378.2
Case#2-Relapse-WholeTumor	GPR98	5	90052415	Missense_Mutation	C	A	p.P3909T	134	25	0.187	0.260	4	2	2	88	G protein-coupled receptor 98	ENST00000405460.2
Case#2-Relapse-WholeTumor	KIF3A	5	132056301	Splice_Site	G	A	p.R206C	170	60	0.353	0.538	3	2	1	129	kinesin family member 3A	ENST00000378746.4
Case#2-Relapse-WholeTumor	PCDHA4	5	140188687	Missense_Mutation	G	A	p.E639K	486	197	0.405	0.618	3	2	1	438	protocadherin alpha 4	ENST00000530339.1
Case#2-Relapse-WholeTumor	PCDHB8	5	140558546	Missense_Mutation	G	A	p.E311K	168	29	0.173	0.263	3	2	1	162	protocadherin beta 8	ENST00000239444.2
Case#2-Relapse-WholeTumor	SPINK14	5	147549340	Missense_Mutation	G	T	p.L15F	167	84	0.503	0.766	3	2	1	103	serine peptidase inhibitor, Kazal type 14 (putative)	ENST00000356972.1
Case#2-Relapse-WholeTumor	SYNPO	5	150027783	Missense_Mutation	CC	TT	p.P227S	148	65	0.439	0.669	3	2	1	111	synaptopodin	ENST00000394243.1
Case#2-Relapse-WholeTumor	KIF4B	5	154394048	Missense_Mutation	C	T	p.S210F	231	16	0.069	0.106	3	2	1	162	kinesin family member 4B	ENST00000435029.4
Case#2-Relapse-WholeTumor	BTNL9	5	180474954	Missense_Mutation	C	T	p.P46L	130	62	0.477	0.727	3	2	1	125	butyrophilin-like 9	ENST00000327705.9
Case#2-Relapse-WholeTumor	PRSS16	6	27222499	Missense_Mutation	C	T	p.P393L	97	34	0.351	0.534	3	2	1	82	protease, serine, 16 (thymus)	ENST00000230582.3
Case#2-Relapse-WholeTumor	TREML2	6	41162493	Missense_Mutation	G	A	p.A152V	168	32	0.190	0.290	3	2	1	152	triggering receptor expressed on myeloid cells-like 2	ENST00000483722.1
Case#2-Relapse-WholeTumor	BMP5	6	55739516	Missense_Mutation	C	T	p.E50K	204	85	0.417	0.635	3	2	1	176	bone morphogenetic protein 5	ENST00000370830.3
Case#2-Relapse-WholeTumor	COL19A1	6	70866106	Missense_Mutation	G	A	p.D723N	146	26	0.178	0.271	3	2	1	150	collagen, type XIX, alpha 1	ENST00000322773.4
Case#2-Relapse-WholeTumor	NR2E1	6	108502798	Missense_Mutation	C	T	p.A313V	131	30	0.229	0.349	3	2	1	88	nuclear receptor subfamily 2, group E, member 1	ENST00000368986.4

Case#2-Relapse-WholeTumor	ASF1A	6	119222008	Missense_Mutation	G	A	p.G63S	145	66	0.455	0.694	3	2	1	174	anti-silencing function 1A histone chaperone	ENST00000229595.5
Case#2-Relapse-WholeTumor	THEMIS	6	128134071	Missense_Mutation	G	A	p.T572I	217	46	0.212	0.323	3	2	1	173	thymocyte selection associated	ENST00000368248.2
Case#2-Relapse-WholeTumor	MYB	6	135517046	Missense_Mutation	C	T	p.S370L	237	45	0.190	0.289	3	2	1	181	v-myb avian myeloblastosis viral oncogene homolog	ENST00000367814.4
Case#2-Relapse-WholeTumor	VTA1	6	142510629	Missense_Mutation	G	A	p.E160K	188	70	0.372	0.567	3	2	1	172	vesicle (multivesicular body) trafficking 1	ENST00000367630.4
Case#2-Relapse-WholeTumor	OPRM1	6	154412483	Missense_Mutation	G	A	p.R347Q	232	98	0.422	0.644	3	2	1	198	opioid receptor, mu 1	ENST00000330432.7
Case#2-Relapse-WholeTumor	LPA	6	161027508	Splice_Site	C	T		328	62	0.189	0.288	3	2	1	282	lipoprotein, Lp(a)	ENST00000316300.5
Case#2-Relapse-WholeTumor	VWDE	7	12373192	Missense_Mutation	T	A	p.I1553F	363	106	0.292	0.343	9	5	4	127	von Willebrand factor D and EGF domains	ENST00000275358.3
Case#2-Relapse-WholeTumor	SNX10	7	26400626	Missense_Mutation	GG	AA	p.R19K	325	147	0.452	0.531	9	5	4	109	sorting nexin 10	ENST00000338523.4
Case#2-Relapse-WholeTumor	FAM188B	7	30825484	Missense_Mutation	A	G	p.E180G	402	29	0.072	0.085	9	5	4	125	family with sequence similarity 188, member B	ENST00000265299.6
Case#2-Relapse-WholeTumor	ABCA13	7	48318976	Missense_Mutation	A	T	p.T2729S	369	38	0.103	0.121	9	5	4	134	ATP-binding cassette, sub-family A (ABC1), member 13	ENST00000435803.1
Case#2-Relapse-WholeTumor	ZNF716	7	57528786	Missense_Mutation	C	T	p.H207Y	614	170	0.277	NA	NA	NA	NA	256	zinc finger protein 716	ENST00000420713.1
Case#2-Relapse-WholeTumor	ABCB4	7	87101971	Missense_Mutation	G	C	p.T34R	145	8	0.055	0.070	6	6	0	93	ATP-binding cassette, sub-family B (MDR/TAP), member 4	ENST00000265723.4
Case#2-Relapse-WholeTumor	SAMD9	7	92734447	Nonsense_Mutation	G	A	p.Q322*	162	131	0.809	1.020	6	6	0	102	sterile alpha motif domain containing 9	ENST00000379958.2
Case#2-Relapse-WholeTumor	COPS6	7	99688107	Missense_Mutation	G	T	p.K140N	341	46	0.135	0.170	6	6	0	169	COP9 signalosome subunit 6	ENST00000303904.3
Case#2-Relapse-WholeTumor	CHRM2	7	136700034	Missense_Mutation	G	C	p.G141A	177	19	0.107	0.135	6	6	0	101	cholinergic receptor, muscarinic 2	ENST00000445907.2
Case#2-Relapse-WholeTumor	DGKI	7	137170128	Missense_Mutation	G	A	p.H807Y	146	11	0.075	0.095	6	6	0	65	diacylglycerol kinase, iota	ENST00000288490.5
Case#2-Relapse-WholeTumor	BRAF	7	140453145	Missense_Mutation	AG	GA	p.L597S	301	228	0.757	0.956	6	6	0	155	B-Raf proto-oncogene, serine/threonine kinase	ENST00000288602.6
Case#2-Relapse-WholeTumor	NOS3	7	150696287	Missense_Mutation	G	C	p.W322C	154	21	0.136	0.172	6	6	0	75	nitric oxide synthase 3 (endothelial cell)	ENST00000484524.1
Case#2-Relapse-WholeTumor	CSMD1	8	2800046	Missense_Mutation	G	A	p.P3496S	181	35	0.193	0.269	4	2	2	137	CUB and Sushi multiple domains 1	ENST00000520002.1
Case#2-Relapse-WholeTumor	CSMD1	8	2830815	Missense_Mutation	T	G	p.N2917T	141	49	0.348	0.484	4	2	2	105	CUB and Sushi multiple domains 1	ENST00000520002.1
Case#2-Relapse-WholeTumor	CSMD1	8	2949047	Missense_Mutation	G	A	p.R2427C	161	50	0.311	0.433	4	2	2	117	CUB and Sushi multiple domains 1	ENST00000520002.1
Case#2-Relapse-WholeTumor	RP1L1	8	10470320	Nonsense_Mutation	G	A	p.Q430*	157	53	0.338	0.470	4	2	2	145	retinitis pigmentosa 1-like 1	ENST00000382483.3
Case#2-Relapse-WholeTumor	KIF13B	8	29037719	Missense_Mutation	G	A	p.R208C	265	84	0.317	0.442	4	2	2	202	kinesin family member 13B	ENST00000524189.1
Case#2-Relapse-WholeTumor	RP1	8	55538384	Missense_Mutation	G	A	p.E648K	161	58	0.360	0.549	3	2	1	156	retinitis pigmentosa 1 (autosomal dominant)	ENST00000220676.1
Case#2-Relapse-WholeTumor	RP1	8	55538858	Missense_Mutation	G	A	p.E806K	202	36	0.178	0.272	3	2	1	152	retinitis pigmentosa 1 (autosomal dominant)	ENST00000220676.1
Case#2-Relapse-WholeTumor	RP1	8	55540103	Missense_Mutation	C	T	p.P1221S	130	43	0.331	0.504	3	2	1	139	retinitis pigmentosa 1 (autosomal dominant)	ENST00000220676.1
Case#2-Relapse-WholeTumor	SLCO5A1	8	70617305	Missense_Mutation	C	T	p.S528N	218	42	0.193	0.294	3	2	1	207	solute carrier organic anion transporter family, member 5A1	ENST00000260126.4
Case#2-Relapse-WholeTumor	OTUD6B	8	92090825	Missense_Mutation	A	G	p.Y216C	132	29	0.220	0.335	3	2	1	128	OTU domain containing 6B	ENST00000285420.4
Case#2-Relapse-WholeTumor	STK3	8	99591892	Splice_Site	C	T	p.S316S	140	69	0.493	0.751	3	2	1	117	serine/threonine kinase 3	ENST00000419617.2
Case#2-Relapse-WholeTumor	UBR5	8	103297416	Missense_Mutation	C	T	p.A1879T	80	20	0.250	0.381	3	2	1	63	ubiquitin protein ligase E3 component n-recognin 5	ENST00000520539.1
Case#2-Relapse-WholeTumor	DCSTAMP	8	105360905	Frame_Shift_Del	T	-	p.I42fs	193	42	0.218	0.332	3	2	1	111	dendrocyte expressed seven transmembrane protein	ENST00000297581.2
Case#2-Relapse-WholeTumor	RSPO2	8	108970406	Missense_Mutation	G	T	p.T173K	97	19	0.196	0.298	3	2	1	105	R-spondin 2	ENST00000276659.5
Case#2-Relapse-WholeTumor	PKHD1L1	8	110520455	Missense_Mutation	T	C	p.V3786A	122	13	0.107	0.162	3	2	1	109	polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1	ENST00000378402.5
Case#2-Relapse-WholeTumor	JAK2	9	5070054	Splice_Site	T	G		76	42	0.553	0.987	2	2	0	87	Janus kinase 2	ENST00000381652.3
Case#2-Relapse-WholeTumor	TAF1L	9	32633779	Missense_Mutation	C	T	p.R600Q	159	87	0.547	0.977	2	2	0	178	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 210kDa-like	ENST00000242310.4
Case#2-Relapse-WholeTumor	FAM205A	9	34725994	Missense_Mutation	C	A	p.G415W	162	28	0.173	0.309	2	2	0	142	family with sequence similarity 205, member A	ENST00000378788.3
Case#2-Relapse-WholeTumor	TRPM6	9	77422991	Missense_Mutation	G	A	p.H533Y	148	29	0.196	0.350	2	2	0	143	transient receptor potential cation channel, subfamily M, member 6	ENST00000360774.1
Case#2-Relapse-WholeTumor	DAPK1	9	90321284	Frame_Shift_Ins	-	T	p.M1100fs	184	45	0.245	0.437	2	2	0	208	death-associated protein kinase 1	ENST00000408954.3
Case#2-Relapse-WholeTumor	WNK2	9	95997111	Missense_Mutation	C	T	p.P366L	145	80	0.552	0.985	2	2	0	156	WNK lysine deficient protein kinase 2	ENST00000297954.4
Case#2-Relapse-WholeTumor	FBP2	9	97349720	Missense_Mutation	C	T	p.G68R	189	99	0.524	0.935	2	2	0	203	fructose-1,6-bisphosphatase 2	ENST00000375337.3
Case#2-Relapse-WholeTumor	OR13D1	9	107457064	Missense_Mutation	G	A	p.R121K	157	74	0.471	0.842	2	2	0	151	olfactory receptor, family 13, subfamily D, member 1	ENST00000318763.5
Case#2-Relapse-WholeTumor	OLFM1	9	138011716	Missense_Mutation	C	T	p.P384S	121	64	0.529	0.945	2	2	0	120	olfactomedin 1	ENST00000371793.3
Case#2-Relapse-WholeTumor	KCNT1	9	138649216	Missense_Mutation	G	A	p.E231K	161	95	0.590	1.054	2	2	0	164	potassium channel, subfamily T, member 1	ENST00000263604.3
Case#2-Relapse-WholeTumor	FAM166A	9	140139847	Missense_Mutation	C	T	p.G145E	169	87	0.515	0.919	2	2	0	188	family with sequence similarity 166, member A	ENST00000344774.4
Case#2-Relapse-WholeTumor	DCAF8L1	X	27997672	Nonsense_Mutation	G	A	p.R594*	151	99	0.656	NA	NA	NA	NA	97	DDB1 and CUL4 associated factor 8-like 1	ENST00000441525.1
Case#2-Relapse-WholeTumor	CHST7	X	46433406	Missense_Mutation	T	G	p.F14V	144	47	0.326	NA	NA	NA	NA	92	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	ENST00000276055.3
Case#2-Relapse-WholeTumor	OPHN1	X	67652784	Nonsense_Mutation	G	A	p.Q27*	90	37	0.411	NA	NA	NA	NA	65	oligophrenin 1	ENST00000355520.5
Case#2-Relapse-WholeTumor	MAGEE2	X	75003604	Missense_Mutation	C	T	p.R428Q	116	89	0.767	NA	NA	NA	NA	87	melanoma antigen family E, 2	ENST00000373359.2
Case#2-Relapse-WholeTumor	MUM1L1	X	105451316	Missense_Mutation	G	A	p.D631N	78	50	0.641	NA	NA	NA	NA	59	melanoma associated antigen (mutated) 1-like 1	ENST00000357175.2
Case#2-Relapse-WholeTumor	COL4A5	X	107909764	Missense_Mutation	G	A	p.E1165K	133	80	0.602	NA	NA	NA	NA	76	collagen, type IV, alpha 5	ENST00000361603.2
Case#2-Relapse-WholeTumor	F8	X	154130406	Missense_Mutation	G	C	p.A2012G	104	36	0.346	NA	NA	NA	NA	83	coagulation factor VIII, procoagulant component	ENST00000360256.4
Case#2-Relapse-M464	UBR4	1	19446148	Missense_Mutation	G	A	p.S3453F	230	116	0.504	0.509	4	2	2	95	ubiquitin protein ligase E3 component n-recognin 4	ENST00000375254.3
Case#2-Relapse-M464	USP48	1	22074689	Nonsense_Mutation	G	A	p.R284*	196	87	0.444	0.448	4	2	2	112	ubiquitin specific peptidase 48	ENST00000308271.9
Case#2-Relapse-M464	CSMD2	1	34158630	Missense_Mutation	C	T	p.E191K	245	132	0.539	0.544	4	2	2	153	CUB and Sushi multiple domains 2	ENST00000373380.1
Case#2-Relapse-M464	GUCA2A	1	42629134	Missense_Mutation	G	A	p.P75S	224	106	0.473	0.478	4	2	2	114	guanylate cyclase activator 2A (guanylin)	ENST00000357001.2
Case#2-Relapse-M464	YBX1	1	43162403	Missense_Mutation	C	T	p.P149S	357	168	0.471	0.475	4	2	2	256	Y box binding protein 1	ENST00000321358.7
Case#2-Relapse-M464	EIF2B3	1	45316632	Missense_Mutation	C	T	p.M450I	218	91	0.417	0.422	4	2	2	127	eukaryotic translation initiation factor 2B, subunit 3 gamma, 58kDa	ENST00000360403.2
Case#2-Relapse-M464	ZSWIM5	1	45501872	Missense_Mutation	G	A	p.A665V	199	30	0.151	0.152	4	2	2	103	zinc finger, SWIM-type containing 5	ENST00000359600.5
Case#2-Relapse-M464	TMEM69	1	46159342	Missense_Mutation	T	G	p.F170C	379	192	0.507	0.512	4	2	2	205	transmembrane protein 69	ENST00000372025.4
Case#2-Relapse-M464	SPATA6	1	48771504	Missense_Mutation	C	G	p.S414T	172	18	0.105	0.106	4	2	2	88	spermatogenesis associated 6	ENST00000371847.3
Case#2-Relapse-M464	NRD1	1	52287201	Missense_Mutation	C	T	p.V464M	190	91	0.479	0.484	4	2	2	107	nardilysin (N-arginine dibasic convertase)	ENST00000354831.7
Case#2-Relapse-M464	MROH7	1	55167778	Missense_Mutation	C	T	p.R1101C	212	89	0.420	0.424	4	2	2	115	maestro heat-like repeat family member 7	ENST00000421030.2
Case#2-Relapse-M464	C8A	1	57333319	Missense_Mutation	T	G	p.C39G	251	52	0.207	0.209	4	2	2	147	complement component 8, alpha polypeptide	ENST00000361249.3
Case#2-Relapse-M464	NFIA	1	61554113	Missense_Mutation	A	G	p.N107S	237	114	0.481	0.486	4	2	2	152	nuclear factor I/A	ENST00000403491.3
Case#2-Relapse-M464	WDR78	1	67292573	Missense_Mutation	G	A	p.P757S	337	155	0.460	0.465	4	2	2	184	WD repeat domain 78	ENST00000371026.3
Case#2-Relapse-M464	OVGP1	1	111957517	Missense_Mutation	T	C	p.S536G	120	49	0.408	0.414	3	2	1	39	oviductal glycoprotein 1, 120kDa	ENST00000369732.3
Case#2-Relapse-M464	MAGI3	1	114201725	Nonsense_Mutation	GTC	TAA	p.V885*	92	46	0.500	0.507	3	2	1	76	membrane associated guanylate kinase, WW and PDZ domain containing 3	ENST00000307546.9
Case#2-Relapse-M464	CD101	1	117554348	Missense_Mutation	C	T	p.L201F	214	111	0.519	0.526	3	2	1	141	CD101 molecule	ENST00000256652.4
Case#2-Relapse-M464	SPRR3	1	152975659	Frame_Shift_Del	GAGCCAGGCT GTACCAAGGT CCCT	-	p.E55fs	386	43	0.111	0.113	3	2	1	295	small proline-rich protein 3	ENST00000295367.4
Case#2-Relapse-M464	KCNN3	1	154744784	Missense_Mutation	A	G	p.V372A	230	45	0.196	0.198	3	2	1	132	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3	ENST00000271915.4
Case#2-Relapse-M464	FCRL5	1	157494225	Missense_Mutation	G	A	p.H695Y	260	95	0.365	0.370	3	2	1	138	Fc receptor-like 5	ENST00000361835.3
Case#2-Relapse-M464	OR10K1	1	158435851	Missense_Mutation	C	T	p.P167L	240	148	0.617	0.625	3	2	1	169	olfactory receptor, family 10, subfamily K, member 1	ENST00000289451.2
Case#2-Relapse-M464	SPTA1	1	158582643	Missense_Mutation	C	G	p.E2366D	157	89	0.567	0.575	3	2	1	112	spectrin, alpha, erythrocytic 1	ENST00000368147.4
Case#2-Relapse-M464	ADCY10	1	167830176	Missense_Mutation	C	T	p.R581Q	238	96	0.403	0.409	3	2	1	162	adenylate cyclase 10 (soluble)	ENST00000367851.4
Case#2-Relapse-M464	FMO1	1	171254450	Missense_Mutation	G	A	p.D456N	205	80	0.390	0.396	3	2	1	145	flavin containing monooxygenase 1	ENST00000354841.4
Case#2-Relapse-M464	FASLG	1	172634863	Missense_Mutation	G	A	p.E185K	177	71	0.401	0.407	3	2	1	124	Fas ligand (TNF superfamily, member 6)	ENST00000367721.2
Case#2-Relapse-M464	SLC9C2	1	173506151	Missense_Mutation	C	T	p.G529R	187	56	0.299	0.304	3	2	1	129	solute carrier family 9, member C2 (putative)	ENST00000367714.3

Case#2-Relapse-M464	LAMC2	1	183205632	Missense_Mutation	A	G	p.R832G	109	12	0.110	0.112	3	2	1	72	laminin, gamma 2	ENST00000264144.4
Case#2-Relapse-M464	CFH	1	196709900	Missense_Mutation	G	T	p.W978C	174	59	0.339	0.344	3	2	1	141	complement factor H	ENST00000367429.4
Case#2-Relapse-M464	KIF21B	1	200944701	Missense_Mutation	C	T	p.G1514R	126	50	0.397	0.402	3	2	1	85	kinesin family member 21B	ENST00000422435.2
Case#2-Relapse-M464	NUAK2	1	205272869	Missense_Mutation	GG	AA	p.P532L	102	57	0.559	0.566	3	2	1	59	NUAK family, SNF1-like kinase, 2	ENST00000367157.3
Case#2-Relapse-M464	KCNH1	1	211093144	Missense_Mutation	C	T	p.G434R	351	196	0.558	0.566	3	2	1	277	potassium voltage-gated channel, subfamily H (eag-related), member 1	ENST00000271751.4
Case#2-Relapse-M464	USH2A	1	215972377	Missense_Mutation	C	T	p.G3277E	225	92	0.409	0.414	3	2	1	204	Usher syndrome 2A (autosomal recessive, mild)	ENST00000307340.3
Case#2-Relapse-M464	USH2A	1	216061902	Missense_Mutation	C	T	p.E2697K	161	52	0.323	0.327	3	2	1	119	Usher syndrome 2A (autosomal recessive, mild)	ENST00000307340.3
Case#2-Relapse-M464	DISP1	1	223176405	Missense_Mutation	C	T	p.P556S	140	82	0.586	0.594	3	2	1	88	dispatched homolog 1 (Drosophila)	ENST00000284476.6
Case#2-Relapse-M464	SUSD4	1	223396814	Missense_Mutation	G	T	p.D407E	102	42	0.412	0.417	3	2	1	62	sushi domain containing 4	ENST00000343846.3
Case#2-Relapse-M464	SDE2	1	226180122	Missense_Mutation	C	T	p.R166H	150	61	0.407	0.412	3	2	1	91	SDE2 telomere maintenance homolog (S. pombe)	ENST00000272091.7
Case#2-Relapse-M464	OBSCN	1	228403370	Missense_Mutation	C	A	p.F645L	385	70	0.182	0.184	3	2	1	247	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	ENST00000422127.1
Case#2-Relapse-M464	OBSCN	1	228494211	Missense_Mutation	G	A	p.G3933E	115	39	0.339	0.344	3	2	1	83	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	ENST00000422127.1
Case#2-Relapse-M464	ABCB10	1	229683251	Missense_Mutation	T	A	p.M306L	301	171	0.568	0.576	3	2	1	198	ATP-binding cassette, sub-family B (MDR/TAP), member 10	ENST00000344517.4
Case#2-Relapse-M464	PCNXL2	1	233270779	Missense_Mutation	C	T	p.V1273M	276	102	0.370	0.375	3	2	1	169	pecanex-like 2 (Drosophila)	ENST00000258229.9
Case#2-Relapse-M464	OR1C1	1	247920918	Missense_Mutation	G	A	p.S264F	119	46	0.387	0.394	2	1	1	134	olfactory receptor, family 1, subfamily C, member 1	ENST00000408896.2
Case#2-Relapse-M464	DCLRE1C	10	14977485	Missense_Mutation	C	T	p.M147I	107	63	0.589	0.613	1	1	0	35	DNA cross-link repair 1C	ENST00000378278.2
Case#2-Relapse-M464	DCLRE1C	10	14977523	Missense_Mutation	C	T	p.G135R	104	57	0.548	0.570	1	1	0	35	DNA cross-link repair 1C	ENST00000378278.2
Case#2-Relapse-M464	ARHGAP22	10	49791162	Missense_Mutation	G	A	p.R24W	55	55	1.000	1.020	2	2	0	72	Rho GTPase activating protein 22	ENST00000249601.4
Case#2-Relapse-M464	DLG5	10	79580911	Missense_Mutation	G	A	p.R1111C	80	74	0.925	0.944	2	2	0	83	discs, large homolog 5 (Drosophila)	ENST00000372391.2
Case#2-Relapse-M464	LRIT1	10	85993828	Splice_Site	C	T		105	21	0.200	0.204	2	2	0	115	leucine-rich repeat, immunoglobulin-like and transmembrane domains 1	ENST00000372105.3
Case#2-Relapse-M464	DCLRE1A	10	115610037	Missense_Mutation	C	T	p.R276H	107	7	0.065	0.067	2	2	0	101	DNA cross-link repair 1A	ENST00000361384.2
Case#2-Relapse-M464	MUC6	11	1030779	Splice_Site	GC	TT	p.A229N	63	60	0.952	0.962	4	4	0	51	mucin 6, oligomeric mucus/gel-forming	ENST00000421673.2
Case#2-Relapse-M464	MUC2	11	1092926	Missense_Mutation	C	G	p.T1582R	1744	119	0.068	0.069	8	5	3	1016	mucin 2, oligomeric mucus/gel-forming	ENST00000441003.2
Case#2-Relapse-M464	TH	11	2186536	Missense_Mutation	C	G	p.Q451H	102	6	0.059	0.060	3	3	0	94	tyrosine hydroxylase	ENST00000381178.1
Case#2-Relapse-M464	OR51I1	11	5461851	Missense_Mutation	GG	AA	p.T298I	116	111	0.957	0.970	3	3	0	127	olfactory receptor, family 51, subfamily I, member 1	ENST00000380211.1
Case#2-Relapse-M464	OR5P2	11	7818171	Missense_Mutation	C	T	p.E107K	153	150	0.980	0.994	3	3	0	158	olfactory receptor, family 5, subfamily P, member 2	ENST00000329434.2
Case#2-Relapse-M464	OR4A16	11	55110683	Missense_Mutation	C	T	p.P3S	154	150	0.974	0.994	2	2	0	140	olfactory receptor, family 4, subfamily A, member 16	ENST00000314721.2
Case#2-Relapse-M464	CTNND1	11	57564280	Missense_Mutation	G	A	p.G258R	164	159	0.970	0.983	3	3	0	210	catenin (cadherin-associated protein), delta 1	ENST00000399050.4
Case#2-Relapse-M464	PCNXL3	11	65384461	Missense_Mutation	A	T	p.Q107L	74	29	0.392	0.397	3	3	0	53	pecanex-like 3 (Drosophila)	ENST00000355703.3
Case#2-Relapse-M464	IGHMBP2	11	68675723	Missense_Mutation	G	A	p.D123N	139	137	0.986	0.999	3	3	0	128	immunoglobulin mu binding protein 2	ENST00000255078.3
Case#2-Relapse-M464	B3GNT6	11	76751713	Missense_Mutation	G	A	p.S373N	192	14	0.073	0.074	3	3	0	127	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (core 3 synthase)	ENST00000533140.1
Case#2-Relapse-M464	TRIM77	11	89444610	Nonsense_Mutation	G	A	p.W148*	111	109	0.982	0.995	3	3	0	116	tripartite motif containing 77	ENST00000398290.3
Case#2-Relapse-M464	MMP20	11	102487610	Missense_Mutation	G	A	p.P103S	157	153	0.975	0.988	3	3	0	151	matrix metallopeptidase 20	ENST00000260228.2
Case#2-Relapse-M464	GRIA4	11	105789535	Missense_Mutation	A	G	p.K456R	185	81	0.438	0.444	3	3	0	150	glutamate receptor, ionotropic, AMPA 4	ENST00000530497.1
Case#2-Relapse-M464	GRAMD1B	11	123465478	Nonsense_Mutation	C	T	p.Q126*	148	146	0.986	1.000	3	3	0	98	GRAM domain containing 1B	ENST00000529750.1
Case#2-Relapse-M464	KCNJ5	11	128781214	Missense_Mutation	G	A	p.G16R	170	166	0.976	0.990	3	3	0	146	potassium inwardly-rectifying channel, subfamily J, member 5	ENST00000338350.4
Case#2-Relapse-M464	ADAMTS15	11	130339181	Missense_Mutation	G	A	p.D523N	99	96	0.970	0.983	3	3	0	74	ADAM metallopeptidase with thrombospondin type 1 motif, 15	ENST00000299164.2
Case#2-Relapse-M464	DCP1B	12	2058318	Frame_Shift_Del	G	-	p.P569fs	195	51	0.262	0.265	3	2	1	133	decapping mRNA 1B	ENST00000280665.6
Case#2-Relapse-M464	PRMT8	12	3649955	Missense_Mutation	G	A	p.E87K	205	57	0.278	0.282	3	2	1	142	protein arginine methyltransferase 8	ENST00000382622.3
Case#2-Relapse-M464	VWF	12	6103165	Missense_Mutation	A	T	p.L2154Q	174	110	0.632	0.641	3	2	1	109	von Willebrand factor	ENST00000261405.5
Case#2-Relapse-M464	CD163L1	12	7521564	Splice_Site	GA	-		120	16	0.133	0.135	3	2	1	84	CD163 molecule-like 1	ENST00000313599.3
Case#2-Relapse-M464	PRH2	12	11083425	Missense_Mutation	G	A	p.G89R	379	50	0.132	0.134	3	2	1	260	proline-rich protein HaeIII subfamily 2	ENST00000396400.3
Case#2-Relapse-M464	PIK3C2G	12	18716366	Missense_Mutation	C	T	p.S1238L	125	53	0.424	0.430	3	2	1	108	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 gamma	ENST00000266497.5
Case#2-Relapse-M464	PIK3C2G	12	18716381	Missense_Mutation	CA	AT	p.S1243Y	129	32	0.248	0.251	3	2	1	114	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 gamma	ENST00000266497.5
Case#2-Relapse-M464	SLCO1B3	12	21069126	Missense_Mutation	G	A	p.G685E	226	69	0.305	0.309	3	2	1	155	solute carrier organic anion transporter family, member 1B3	ENST00000381545.3
Case#2-Relapse-M464	KCNJ8	12	21918938	Missense_Mutation	C	T	p.E332K	203	124	0.611	0.619	3	2	1	162	potassium inwardly-rectifying channel, subfamily J, member 8	ENST00000240662.2
Case#2-Relapse-M464	SLC38A4	12	47178369	Missense_Mutation	C	T	p.G150E	90	89	0.989	1.009	2	2	0	97	solute carrier family 38, member 4	ENST00000447411.1
Case#2-Relapse-M464	ADCY6	12	49170029	Missense_Mutation	A	G	p.I547T	91	5	0.055	0.056	2	2	0	79	adenylate cyclase 6	ENST00000307885.4
Case#2-Relapse-M464	DIP2B	12	51118670	Splice_Site	G	A		130	126	0.969	0.989	2	1	1	151	DIP2 disco-interacting protein 2 homolog B (Drosophila)	ENST00000301180.5
Case#2-Relapse-M464	KRT2	12	53042832	Missense_Mutation	G	T	p.L306M	201	112	0.557	0.569	2	2	0	147	keratin 2	ENST00000309680.3
Case#2-Relapse-M464	KRT76	12	53162841	Missense_Mutation	C	T	p.V525I	178	77	0.433	0.441	2	2	0	215	keratin 76	ENST00000332411.2
Case#2-Relapse-M464	MYO1A	12	57422920	Missense_Mutation	C	T	p.E1001K	87	86	0.989	1.009	2	2	0	81	myosin IA	ENST00000442789.2
Case#2-Relapse-M464	C12orf55	12	97180611	Missense_Mutation	G	A	p.E2872K	76	74	0.974	0.994	2	2	0	106		ENST00000524981.4
Case#2-Relapse-M464	GNPTAB	12	102153816	Missense_Mutation	G	T	p.P1081T	101	96	0.950	0.970	2	2	0	136	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	ENST00000299314.7
Case#2-Relapse-M464	TDG	12	104376924	Missense_Mutation	C	T	p.R209C	105	104	0.990	1.011	2	2	0	112	thymine-DNA glycosylase	ENST00000392872.3
Case#2-Relapse-M464	CUX2	12	111757876	Missense_Mutation	C	T	p.T688I	104	99	0.952	0.971	2	2	0	108	cut-like homeobox 2	ENST00000261726.6
Case#2-Relapse-M464	ATXN2	12	111924586	Missense_Mutation	G	T	p.F921L	57	21	0.368	0.376	2	2	0	69	ataxin 2	ENST00000377617.3
Case#2-Relapse-M464	DNAH10	12	124267722	Missense_Mutation	G	A	p.E243K	183	180	0.984	1.004	2	2	0	162	dynein, axonemal, heavy chain 10	ENST00000409039.3
Case#2-Relapse-M464	BRCA2	13	32930738	Missense_Mutation	C	T	p.H2537Y	84	82	0.976	0.996	2	2	0	96	breast cancer 2, early onset	ENST00000380152.3
Case#2-Relapse-M464	NBEA	13	36124642	Missense_Mutation	G	A	p.G2205E	127	126	0.992	1.012	2	2	0	151	neurobeachin	ENST00000400445.3
Case#2-Relapse-M464	MYCBP2	13	77635403	Missense_Mutation	C	T	p.D4275N	115	9	0.078	0.080	2	2	0	157	MYC binding protein 2, E3 ubiquitin protein ligase	ENST00000544440.2
Case#2-Relapse-M464	NFKBIA	14	35871725	Missense_Mutation	G	A	p.P261S	85	82	0.965	0.984	2	2	0	93	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	ENST00000216797.5
Case#2-Relapse-M464	TTC6	14	38151975	Missense_Mutation	G	A	p.E355K	97	94	0.969	0.989	2	2	0	126	tetratricopeptide repeat domain 6	ENST00000553443.1
Case#2-Relapse-M464	SSTR1	14	38679319	Missense_Mutation	G	T	p.C242F	124	32	0.258	0.263	2	2	0	124	somatostatin receptor 1	ENST00000267377.2
Case#2-Relapse-M464	PRPF39	14	45583459	Splice_Site	G	A	p.G611R	105	23	0.219	0.224	2	2	0	134	pre-mRNA processing factor 39	ENST00000355765.6
Case#2-Relapse-M464	KCNH5	14	63453861	Missense_Mutation	G	C	p.R160G	123	123	1.000	1.020	2	2	0	142	potassium voltage-gated channel, subfamily H (eag-related), member 5	ENST00000322893.7
Case#2-Relapse-M464	MAP3K9	14	71197329	Missense_Mutation	G	C	p.T1028R	153	11	0.072	0.073	2	2	0	163	mitogen-activated protein kinase kinase kinase 9	ENST00000554752.2
Case#2-Relapse-M464	ABCD4	14	74764632	Splice_Site	C	T		171	77	0.450	0.459	2	2	0	184	ATP-binding cassette, sub-family D (ALD), member 4	ENST00000356924.4
Case#2-Relapse-M464	BEGAIN	14	101004431	Missense_Mutation	A	T	p.S553T	33	7	0.212	0.216	2	2	0	19	brain-enriched guanylate kinase-associated	ENST00000355173.2
Case#2-Relapse-M464	AHNAK2	14	105405040	Missense_Mutation	A	T	p.V5583E	105	8	0.076	0.078	2	2	0	93	AHNAK nucleoprotein 2	ENST00000333244.5
Case#2-Relapse-M464	OR4M2	15	22369306	Missense_Mutation	C	T	p.S244F	822	242	0.294	0.298	3	2	1	727	olfactory receptor, family 4, subfamily M, member 2	ENST00000332663.2
Case#2-Relapse-M464	FMN1	15	33261614	Missense_Mutation	T	C	p.E763G	173	114	0.659	0.668	3	2	1	117	formin 1	ENST00000559047.1
Case#2-Relapse-M464	SLC28A2	15	45545451	Missense_Mutation	C	T	p.S13F	180	106	0.589	0.597	3	2	1	145	solute carrier family 28 (concentrative nucleoside transporter), member 2	ENST00000347644.3
Case#2-Relapse-M464	GLDN	15	51692684	Missense_Mutation	A	T	p.E339V	209	40	0.191	0.194	3	2	1	127	gliomedin	ENST00000335449.6
Case#2-Relapse-M464	CYP1A2	15	75042116	Missense_Mutation	G	A	p.E13K	195	130	0.667	0.676	3	2	1	149	cytochrome P450, family 1, subfamily A, polypeptide 2	ENST00000343932.4
Case#2-Relapse-M464	KIAA1199	15	81188289	Nonsense_Mutation	G	A	p.W433*	255	163	0.639	0.648	3	2	1	184		ENST00000394685.3

Case#2-Relapse-M464	LRRK1	15	101606184	Missense_Mutation	C	G	p.P1848A	97	48	0.495	0.502	3	2	1	65	leucine-rich repeat kinase 1	ENST00000388948.3
Case#2-Relapse-M464	PKD1	16	2160895	Missense_Mutation	G	A	p.R1425C	491	175	0.356	0.361	3	2	1	323	polycystic kidney disease 1 (autosomal dominant)	ENST00000262304.4
Case#2-Relapse-M464	DNAH3	16	20974716	Missense_Mutation	C	T	p.G3497E	239	133	0.556	0.564	3	2	1	181	dynein, axonemal, heavy chain 3	ENST00000261383.3
Case#2-Relapse-M464	DNAH3	16	21086851	Missense_Mutation	C	T	p.E1001K	116	76	0.655	0.664	3	2	1	92	dynein, axonemal, heavy chain 3	ENST00000261383.3
Case#2-Relapse-M464	TMEM159	16	21185368	Missense_Mutation	C	G	p.C101W	172	64	0.372	0.377	3	2	1	124	transmembrane protein 159	ENST00000233047.4
Case#2-Relapse-M464	TNRC6A	16	24815560	Nonsense_Mutation	C	T	p.R1253*	125	35	0.280	0.284	3	2	1	103	trinucleotide repeat containing 6A	ENST00000395799.3
Case#2-Relapse-M464	PRR14	16	30666042	Missense_Mutation	CG	TT	p.R251F	98	25	0.255	0.259	3	2	1	79	proline rich 14	ENST00000542965.2
Case#2-Relapse-M464	STX1B	16	31004546	Missense_Mutation	G	C	p.R231G	161	40	0.248	0.252	3	2	1	121	syntaxin 1B	ENST00000215095.5
Case#2-Relapse-M464	ITGAM	16	31309065	Splice_Site	G	A		138	87	0.630	0.639	3	2	1	94	integrin, alpha M (complement component 3 receptor 3 subunit)	ENST00000287497.8
Case#2-Relapse-M464	ITGAM	16	31309202	Missense_Mutation	A	T	p.E545V	133	41	0.308	0.312	3	2	1	98	integrin, alpha M (complement component 3 receptor 3 subunit)	ENST00000287497.8
Case#2-Relapse-M464	PAPD5	16	50263084	Missense_Mutation	C	T	p.R538C	139	39	0.281	0.284	3	2	1	117	PAP associated domain containing 5	ENST00000561678.1
Case#2-Relapse-M464	OGFOD1	16	56504605	Missense_Mutation	C	T	p.P396L	102	30	0.294	0.298	3	2	1	81	2-oxoglutarate and iron-dependent oxygenase domain containing 1	ENST00000566157.1
Case#2-Relapse-M464	SLC12A3	16	56947280	Missense_Mutation	G	A	p.G1010E	363	228	0.628	0.637	3	2	1	244	solute carrier family 12 (sodium/chloride transporter), member 3	ENST00000563236.1
Case#2-Relapse-M464	NLRC5	16	57110766	Missense_Mutation	G	A	p.C1596Y	106	29	0.274	0.277	3	2	1	84	NLR family, CARD domain containing 5	ENST00000262510.6
Case#2-Relapse-M464	EXOC3L1	16	67221347	Missense_Mutation	C	T	p.G274E	121	78	0.645	0.653	3	2	1	61	exocyst complex component 3-like 1	ENST00000314586.6
Case#2-Relapse-M464	HYDIN	16	70977759	Missense_Mutation	G	A	p.L2209F	80	53	0.663	0.672	3	2	1	46	HYDIN, axonemal central pair apparatus protein	ENST00000393567.2
Case#2-Relapse-M464	HYDIN	16	71007260	Missense_Mutation	T	G	p.M1789L	444	85	0.191	0.194	3	2	1	271	HYDIN, axonemal central pair apparatus protein	ENST00000393567.2
Case#2-Relapse-M464	HYDIN	16	71009082	Missense_Mutation	C	T	p.D1577N	1113	446	0.401	0.406	3	2	1	872	HYDIN, axonemal central pair apparatus protein	ENST00000393567.2
Case#2-Relapse-M464	CHST4	16	71570816	Nonsense_Mutation	G	A	p.W79*	179	110	0.615	0.623	3	2	1	126	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4	ENST00000338482.5
Case#2-Relapse-M464	JPH3	16	87678364	Missense_Mutation	G	A	p.D295N	484	147	0.304	0.308	3	2	1	387	junctophilin 3	ENST00000284262.2
Case#2-Relapse-M464	DNAH2	17	7702025	Missense_Mutation	G	A	p.E2850K	103	49	0.476	0.485	2	1	1	125	dynein, axonemal, heavy chain 2	ENST00000572933.1
Case#2-Relapse-M464	KCNAB3	17	7827771	Missense_Mutation	A	T	p.Y225N	160	70	0.438	0.446	2	1	1	163	potassium voltage-gated channel, shaker-related subfamily, beta member 3	ENST00000303790.2
Case#2-Relapse-M464	USP43	17	9583599	Nonsense_Mutation	G	T	p.E341*	120	63	0.525	0.536	2	1	1	111	ubiquitin specific peptidase 43	ENST00000285199.7
Case#2-Relapse-M464	MYH4	17	10358940	Missense_Mutation	A	T	p.F722Y	186	85	0.457	0.466	2	1	1	213	myosin, heavy chain 4, skeletal muscle	ENST00000255381.2
Case#2-Relapse-M464	DNAH9	17	11607590	Missense_Mutation	G	A	p.G1741D	110	56	0.509	0.519	2	1	1	141	dynein, axonemal, heavy chain 9	ENST00000262442.4
Case#2-Relapse-M464	ERBB2	17	37871538	Splice_Site	G	T		94	8	0.085	0.087	2	1	1	84	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2	ENST00000269571.5
Case#2-Relapse-M464	CSF3	17	38172825	Missense_Mutation	C	A	p.P134T	229	119	0.520	0.530	2	1	1	182	colony stimulating factor 3 (granulocyte)	ENST00000225474.2
Case#2-Relapse-M464	KRTAP4-5	17	39305785	Missense_Mutation	A	T	p.C79S	446	86	0.193	0.197	2	1	1	362	keratin associated protein 4-5	ENST00000343246.4
Case#2-Relapse-M464	ZNF385C	17	40181094	Splice_Site	G	A	p.A226V	68	21	0.309	0.315	2	1	1	63	zinc finger protein 385C	ENST00000436535.3
Case#2-Relapse-M464	IGF2BP1	17	47126787	Missense_Mutation	C	T	p.A572V	146	47	0.322	0.326	3	2	1	101	insulin-like growth factor 2 mRNA binding protein 1	ENST00000290341.3
Case#2-Relapse-M464	SGCA	17	48245845	Missense_Mutation	G	A	p.E166K	242	156	0.645	0.653	3	2	1	167	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)	ENST00000262018.3
Case#2-Relapse-M464	XYLT2	17	48432324	Missense_Mutation	G	C	p.R305T	143	10	0.070	0.071	3	2	1	116	xylosyltransferase II	ENST00000017003.2
Case#2-Relapse-M464	ANKFN1	17	54431262	Missense_Mutation	C	G	p.I155M	309	56	0.181	0.184	3	2	1	216	ankyrin-repeat and fibronectin type III domain containing 1	ENST00000318698.2
Case#2-Relapse-M464	CD300A	17	72477896	Missense_Mutation	A	T	p.N233I	222	139	0.626	0.635	3	2	1	200	CD300a molecule	ENST00000360141.3
Case#2-Relapse-M464	RBFOX3	17	77100159	Missense_Mutation	G	A	p.S137F	168	115	0.685	0.694	3	2	1	105	RNA binding protein, fox-1 homolog (C. elegans) 3	ENST00000453134.2
Case#2-Relapse-M464	RNF213	17	78346865	Missense_Mutation	G	C	p.R4281P	175	17	0.097	0.098	3	2	1	139	ring finger protein 213	ENST00000582970.1
Case#2-Relapse-M464	EMILIN2	18	2891917	Missense_Mutation	G	A	p.E598K	170	57	0.335	0.340	3	2	1	112	elastin microfibril interfacer 2	ENST00000254528.3
Case#2-Relapse-M464	TMEM200C	18	5890552	Missense_Mutation	G	A	p.A504V	57	12	0.211	0.213	3	2	1	43	transmembrane protein 200C	ENST00000581347.2
Case#2-Relapse-M464	IMPACT	18	22023054	Missense_Mutation	C	T	p.P178S	131	81	0.618	0.627	3	2	1	82	impact RWD domain protein	ENST00000284202.4
Case#2-Relapse-M464	DSC1	18	28714538	Missense_Mutation	CC	TT	p.D625N	150	93	0.620	0.628	3	2	1	114	desmocollin 1	ENST00000257198.5
Case#2-Relapse-M464	ALPK2	18	56196344	Missense_Mutation	G	A	p.S1827F	182	113	0.621	0.629	3	2	1	108	alpha-kinase 2	ENST00000361673.3
Case#2-Relapse-M464	SERPINB8	18	61652436	Missense_Mutation	G	T	p.S226I	169	51	0.302	0.306	3	2	1	141	serpin peptidase inhibitor, clade B (ovalbumin), member 8	ENST00000397985.2
Case#2-Relapse-M464	CNDP1	18	72250811	Missense_Mutation	C	T	p.P442S	198	61	0.308	0.312	3	2	1	188	carnosine dipeptidase 1 (metallopeptidase M20 family)	ENST00000358821.3
Case#2-Relapse-M464	PTBP1	19	805050	Missense_Mutation	C	T	p.T252M	451	315	0.698	0.706	4	3	1	185	polypyrimidine tract binding protein 1	ENST00000349038.4
Case#2-Relapse-M464	GNG7	19	2515129	Missense_Mutation	G	A	p.S33F	252	82	0.325	0.330	3	2	1	147	guanine nucleotide binding protein (G protein), gamma 7	ENST00000382159.3
Case#2-Relapse-M464	MAP2K2	19	4110574	Missense_Mutation	G	C	p.P128R	190	114	0.600	0.608	3	2	1	162	mitogen-activated protein kinase kinase 2	ENST00000262948.5
Case#2-Relapse-M464	MUC16	19	9061537	Missense_Mutation	C	T	p.E8637K	227	146	0.643	0.652	3	2	1	158	mucin 16, cell surface associated	ENST00000397910.4
Case#2-Relapse-M464	MUC16	19	9064668	Missense_Mutation	G	C	p.S7593C	266	78	0.293	0.297	3	2	1	177	mucin 16, cell surface associated	ENST00000397910.4
Case#2-Relapse-M464	MUC16	19	9082813	Missense_Mutation	G	A	p.S3001L	243	82	0.337	0.342	3	2	1	167	mucin 16, cell surface associated	ENST00000397910.4
Case#2-Relapse-M464	MUC16	19	9085250	Missense_Mutation	C	T	p.E2189K	231	150	0.649	0.658	3	2	1	154	mucin 16, cell surface associated	ENST00000397910.4
Case#2-Relapse-M464	OR7G3	19	9236942	Missense_Mutation	G	A	p.P229S	225	81	0.360	0.365	3	2	1	168	olfactory receptor, family 7, subfamily G, member 3	ENST00000305444.2
Case#2-Relapse-M464	ZNF560	19	9577307	Missense_Mutation	C	G	p.Q772H	336	100	0.298	0.302	3	2	1	264	zinc finger protein 560	ENST00000301480.4
Case#2-Relapse-M464	ZNF563	19	12429713	Missense_Mutation	G	A	p.H376Y	484	146	0.302	0.306	3	2	1	406	zinc finger protein 563	ENST00000293725.5
Case#2-Relapse-M464	ABHD8	19	17412109	Missense_Mutation	C	T	p.G106E	27	19	0.704	0.713	3	2	1	20	abhydrolase domain containing 8	ENST00000247706.3
Case#2-Relapse-M464	TM6SF2	19	19377376	Missense_Mutation	C	T	p.A283T	195	41	0.210	0.213	3	2	1	130	transmembrane 6 superfamily member 2	ENST00000389363.4
Case#2-Relapse-M464	ZNF729	19	22497144	Missense_Mutation	G	T	p.A309S	111	8	0.072	0.073	3	2	1	74	zinc finger protein 729	ENST00000601693.1
Case#2-Relapse-M464	ARHGAP35	19	47422066	Missense_Mutation	C	T	p.P45L	253	163	0.644	0.653	3	2	1	282	Rho GTPase activating protein 35	ENST00000404338.3
Case#2-Relapse-M464	LHB	19	49519534	Missense_Mutation	G	A	p.P73S	649	181	0.279	0.283	3	2	1	386	luteinizing hormone beta polypeptide	ENST00000221421.2
Case#2-Relapse-M464	SCAF1	19	50156247	Missense_Mutation	CC	TT	p.R868C	450	265	0.589	0.597	3	2	1	339	SR-related CTD-associated factor 1	ENST00000360565.3
Case#2-Relapse-M464	LILRB5	19	54759398	Missense_Mutation	C	T	p.A235T	343	227	0.662	0.671	3	2	1	197	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5	ENST00000316219.5
Case#2-Relapse-M464	LILRA1	19	55107746	Missense_Mutation	C	T	p.P351S	275	182	0.662	0.671	3	2	1	214	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1	ENST00000251372.3
Case#2-Relapse-M464	ZNF324B	19	58966688	Missense_Mutation	CG	TT	p.P126L	262	95	0.363	0.368	3	2	1	227	zinc finger protein 324B	ENST00000336614.4
Case#2-Relapse-M464	CAD	2	27464912	Missense_Mutation	C	T	p.S1943F	165	116	0.703	0.713	3	2	1	131	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	ENST00000403525.1
Case#2-Relapse-M464	C2orf16	2	27803529	Missense_Mutation	G	A	p.A1364T	178	51	0.287	0.290	3	2	1	131	chromosome 2 open reading frame 16	ENST00000408964.2
Case#2-Relapse-M464	HEATR5B	2	37234373	Missense_Mutation	G	A	p.H1533Y	205	126	0.615	0.623	3	2	1	135	HEAT repeat containing 5B	ENST00000233099.5
Case#2-Relapse-M464	HNRNPLL	2	38809081	Missense_Mutation	T	C	p.Y259C	240	73	0.304	0.308	3	2	1	192	heterogeneous nuclear ribonucleoprotein L-like	ENST00000449105.3
Case#2-Relapse-M464	USP34	2	61633078	Missense_Mutation	T	A	p.N106I	99	70	0.707	0.717	3	2	1	96	ubiquitin specific peptidase 34	ENST00000398571.2
Case#2-Relapse-M464	DUSP11	2	73993587	Missense_Mutation	C	T	p.R298Q	255	101	0.396	0.401	3	2	1	199	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	ENST00000272444.3
Case#2-Relapse-M464	CNTNAP5	2	125175155	Missense_Mutation	G	A	p.G173R	193	114	0.591	0.599	3	2	1	148	contactin associated protein-like 5	ENST00000431078.1
Case#2-Relapse-M464	MYO7B	2	128366350	Missense_Mutation	C	T	p.S904F	462	146	0.316	0.320	3	2	1	311	myosin VIIB	ENST00000409816.2
Case#2-Relapse-M464	GPR39	2	133402871	Missense_Mutation	C	T	p.R352W	195	126	0.646	0.655	3	2	1	136	G protein-coupled receptor 39	ENST00000329321.3
Case#2-Relapse-M464	LRP1B	2	141607835	Missense_Mutation	G	A	p.P1592L	161	47	0.292	0.296	3	2	1	137	low density lipoprotein receptor-related protein 1B	ENST00000389484.3
Case#2-Relapse-M464	NEB	2	152427025	Missense_Mutation	C	T	p.E4001K	155	48	0.310	0.314	3	2	1	88	nebulin	ENST00000172853.10
Case#2-Relapse-M464	FMNL2	2	153497396	Missense_Mutation	G	A	p.G421E	202	55	0.272	0.276	3	2	1	133	formin-like 2	ENST00000475377.2
Case#2-Relapse-M464	DCAF17	2	172325510	Missense_Mutation	C	A	p.F317L	143	95	0.664	0.673	3	2	1	94	DDB1 and CUL4 associated factor 17	ENST00000375255.3
Case#2-Relapse-M464	PDE1A	2	183011865	Missense_Mutation	G	A	p.H527Y	79	32	0.405	0.411	3	2	1	69	phosphodiesterase 1A, calmodulin-dependent	ENST00000435564.1
Case#2-Relapse-M464	SLC40A1	2	190428486	Missense_Mutation	C	T	p.R409Q	243	87	0.358	0.363	3	2	1	155	solute carrier family 40 (iron-regulated transporter), member 1	ENST00000261024.2
Case#2-Relapse-M464	STAT4	2	191919251	Missense_Mutation	C	T	p.E406K	183	120	0.656	0.665	3	2	1	141	signal transducer and activator of transcription 4	ENST00000392320.2
Case#2-Relapse-M464	DNAH7	2	196762426	Missense_Mutation	G	C	p.P1538A	225	66	0.293	0.297	3	2	1	191	dynein, axonemal, heavy chain 7	ENST00000312428.6
Case#2-Relapse-M464	DNAH7	2	196799458	Missense_Mutation	C	T	p.E1110K	177	58	0.328	0.332	3	2	1	129	dynein, axonemal, heavy chain 7	ENST00000312428.6

Case#2-Relapse-M464	CRYGA	2	209025650	Missense_Mutation	C	T	p.E135K	212	136	0.642	0.650	3	2	1	173	crystallin, gamma A	ENST00000304502.4
Case#2-Relapse-M464	PTH2R	2	209302602	Missense_Mutation	G	A	p.G136E	153	45	0.294	0.298	3	2	1	111	parathyroid hormone 2 receptor	ENST00000272847.2
Case#2-Relapse-M464	ARPC2	2	219093493	Missense_Mutation	C	T	p.P48S	127	82	0.646	0.654	3	2	1	130	actin related protein 2/3 complex, subunit 2, 34kDa	ENST00000295685.10
Case#2-Relapse-M464	PNKD	2	219206288	Missense_Mutation	C	T	p.R186W	296	35	0.118	0.120	3	2	1	208	paroxysmal nonkinesigenic dyskinesia	ENST00000273077.4
Case#2-Relapse-M464	ACSL3	2	223782833	Missense_Mutation	A	G	p.N209S	123	40	0.325	0.330	3	2	1	95	acyl-CoA synthetase long-chain family member 3	ENST00000357430.3
Case#2-Relapse-M464	COL4A3	2	228109667	Splice_Site	G	A	p.G94R	219	65	0.297	0.301	3	2	1	166	collagen, type IV, alpha 3 (Goodpasture antigen)	ENST00000396578.3
Case#2-Relapse-M464	CHRNG	2	233408368	Missense_Mutation	C	T	p.R332W	146	51	0.349	0.354	3	2	1	122	cholinergic receptor, nicotinic, gamma (muscle)	ENST00000389494.3
Case#2-Relapse-M464	INPP5D	2	234112887	Missense_Mutation	C	T	p.P1019S	200	120	0.600	0.608	3	2	1	105	inositol polyphosphate-5-phosphatase, 145kDa	ENST00000359570.5
Case#2-Relapse-M464	COL6A3	2	238296599	Missense_Mutation	C	T	p.G313E	234	153	0.654	0.663	3	2	1	152	collagen, type VI, alpha 3	ENST00000295550.4
Case#2-Relapse-M464	RBM44	2	238733043	Nonsense_Mutation	G	A	p.W811*	260	84	0.323	0.327	3	2	1	41	RNA binding motif protein 44	ENST00000409864.1
Case#2-Relapse-M464	CHGB	20	5903578	Missense_Mutation	C	T	p.S263F	136	39	0.287	0.291	3	2	1	81	chromogranin B (secretogranin 1)	ENST00000378961.4
Case#2-Relapse-M464	HAO1	20	7886973	Missense_Mutation	C	T	p.M183I	102	32	0.314	0.318	3	2	1	66	hydroxyacid oxidase (glycolate oxidase) 1	ENST00000378789.3
Case#2-Relapse-M464	SLX4IP	20	10603749	Nonsense_Mutation	C	T	p.R317*	221	66	0.299	0.303	3	2	1	135	SLX4 interacting protein	ENST00000334534.5
Case#2-Relapse-M464	TTLL9	20	30513896	Splice_Site	T	A		236	141	0.597	0.606	3	2	1	129	tubulin tyrosine ligase-like family, member 9	ENST00000375938.4
Case#2-Relapse-M464	GDF5	20	34022347	Missense_Mutation	G	T	p.S289Y	146	43	0.295	0.299	3	2	1	108	growth differentiation factor 5	ENST00000374372.1
Case#2-Relapse-M464	SAMHD1	20	35545391	Missense_Mutation	C	T	p.R305K	128	80	0.625	0.634	3	2	1	98	SAM domain and HD domain 1	ENST00000262878.4
Case#2-Relapse-M464	PABPC1L	20	43559255	Missense_Mutation	C	T	p.A376V	210	74	0.352	0.357	3	2	1	166	poly(A) binding protein, cytoplasmic 1-like	ENST00000217073.2
Case#2-Relapse-M464	PABPC1L	20	43566704	Missense_Mutation	G	A	p.E550K	181	114	0.630	0.638	3	2	1	152	poly(A) binding protein, cytoplasmic 1-like	ENST00000217073.2
Case#2-Relapse-M464	ZNF334	20	45133364	Nonsense_Mutation	G	A	p.Q13*	204	118	0.578	0.586	3	2	1	145	zinc finger protein 334	ENST00000347606.4
Case#2-Relapse-M464	FAM217B	20	58519207	Missense_Mutation	CC	TT	p.A70V	152	77	0.507	0.512	4	2	2	117	family with sequence similarity 217, member B	ENST00000358293.3
Case#2-Relapse-M464	USP25	21	17250160	Nonsense_Mutation	C	T	p.R949*	171	52	0.304	0.308	3	2	1	167	ubiquitin specific peptidase 25	ENST00000285679.6
Case#2-Relapse-M464	GRIK1	21	31062192	Missense_Mutation	G	A	p.R134C	131	89	0.679	0.689	3	2	1	117	glutamate receptor, ionotropic, kainate 1	ENST00000399907.1
Case#2-Relapse-M464	IFNAR2	21	34635507	Missense_Mutation	C	T	p.S417F	187	139	0.743	0.753	3	2	1	138	interferon (alpha, beta and omega) receptor 2	ENST00000342136.4
Case#2-Relapse-M464	KCNE1	21	35821821	Missense_Mutation	T	C	p.S38G	252	13	0.052	0.052	3	2	1	174	potassium voltage-gated channel, Isk-related family, member 1	ENST00000337385.3
Case#2-Relapse-M464	ABCG1	21	43714725	Missense_Mutation	C	T	p.T588I	171	46	0.269	0.273	3	2	1	115	ATP-binding cassette, sub-family G (WHITE), member 1	ENST00000361802.2
Case#2-Relapse-M464	KRTAP10-11	21	46067102	Missense_Mutation	C	T	p.P243S	287	86	0.300	0.304	3	2	1	197	keratin associated protein 10-11	ENST00000334670.8
Case#2-Relapse-M464	COL18A1	21	46914475	Missense_Mutation	G	A	p.R1205Q	198	56	0.283	0.287	3	2	1	111	collagen, type XVIII, alpha 1	ENST00000359759.4
Case#2-Relapse-M464	PCNT	21	47836080	Missense_Mutation	C	T	p.S2083F	263	169	0.643	0.651	3	2	1	169	pericentrin	ENST00000359568.5
Case#2-Relapse-M464	RIMBP3	22	20456945	Missense_Mutation	G	A	p.P1453S	491	126	0.257	0.260	3	2	1	280	RIMS binding protein 3	ENST00000426804.1
Case#2-Relapse-M464	LZTR1	22	21343110	Missense_Mutation	C	T	p.T181M	180	91	0.506	0.511	4	2	2	111	leucine-zipper-like transcription regulator 1	ENST00000215739.8
Case#2-Relapse-M464	PIWIL3	22	25155951	Missense_Mutation	C	G	p.Q36H	169	68	0.402	0.406	4	3	1	110	piwi-like RNA-mediated gene silencing 3	ENST00000332271.5
Case#2-Relapse-M464	CABP7	22	30124619	Splice_Site	G	A	p.G85D	152	89	0.586	0.592	4	2	2	66	calcium binding protein 7	ENST00000216144.3
Case#2-Relapse-M464	EIF3D	22	36916707	Missense_Mutation	C	T	p.R165H	126	48	0.381	0.385	4	2	2	75	eukaryotic translation initiation factor 3, subunit D	ENST00000216190.8
Case#2-Relapse-M464	TRIOBP	22	38120671	Missense_Mutation	G	A	p.R703Q	563	85	0.151	0.153	4	2	2	284	TRIO and F-actin binding protein	ENST00000406386.3
Case#2-Relapse-M464	MPPED1	22	43898547	Missense_Mutation	A	G	p.K258E	170	34	0.200	0.202	4	2	2	88	metallophosphoesterase domain containing 1	ENST00000417669.2
Case#2-Relapse-M464	PARVB	22	44489874	Missense_Mutation	T	C	p.V60A	210	90	0.429	0.433	4	2	2	104	parvin, beta	ENST00000338758.7
Case#2-Relapse-M464	NUP210	3	13372082	Missense_Mutation	G	A	p.P1330S	303	191	0.630	0.639	3	2	1	199	nucleoporin 210kDa	ENST00000254508.5
Case#2-Relapse-M464	SLC4A7	3	27498171	Missense_Mutation	C	T	p.E2K	126	41	0.325	0.330	3	2	1	140	solute carrier family 4, sodium bicarbonate cotransporter, member 7	ENST00000295736.5
Case#2-Relapse-M464	SCN5A	3	38592057	Missense_Mutation	G	A	p.L1936F	172	108	0.628	0.636	3	2	1	93	sodium channel, voltage-gated, type V, alpha subunit	ENST00000333535.4
Case#2-Relapse-M464	CSRNP1	3	39185707	Missense_Mutation	C	T	p.R234Q	301	94	0.312	0.317	3	2	1	184	cysteine-serine-rich nuclear protein 1	ENST00000273153.5
Case#2-Relapse-M464	CCR1	3	46244924	Missense_Mutation	C	G	p.C294S	274	17	0.062	0.063	3	2	1	168	chemokine (C-C motif) receptor 1	ENST00000296140.3
Case#2-Relapse-M464	LRRC2	3	46593024	Missense_Mutation	G	A	p.R20C	198	57	0.288	0.292	3	2	1	169	leucine rich repeat containing 2	ENST00000395905.3
Case#2-Relapse-M464	SLC26A6	3	48669111	Missense_Mutation	G	A	p.P292S	141	53	0.376	0.381	3	2	1	115	solute carrier family 26 (anion exchanger), member 6	ENST00000395550.2
Case#2-Relapse-M464	UBA7	3	49847517	Missense_Mutation	AC	TT	p.V578K	123	77	0.626	0.635	3	2	1	115	ubiquitin-like modifier activating enzyme 7	ENST00000333486.3
Case#2-Relapse-M464	DOCK3	3	51127760	Missense_Mutation	G	A	p.E231K	156	108	0.692	0.702	3	2	1	158	dedicator of cytokinesis 3	ENST00000266037.9
Case#2-Relapse-M464	LRTM1	3	54961931	Splice_Site	C	G		159	104	0.654	0.663	3	2	1	153	leucine-rich repeats and transmembrane domains 1	ENST00000273286.5
Case#2-Relapse-M464	PTPRG	3	62216967	Missense_Mutation	G	A	p.R786K	58	20	0.345	0.350	3	2	1	48	protein tyrosine phosphatase, receptor type, G	ENST00000474889.1
Case#2-Relapse-M464	UBA3	3	69105214	Splice_Site	C	A	p.L395L	123	46	0.374	0.379	3	2	1	99	ubiquitin-like modifier activating enzyme 3	ENST00000361055.4
Case#2-Relapse-M464	PPP4R2	3	73114862	Nonsense_Mutation	G	T	p.E415*	242	39	0.161	0.163	3	2	1	195	protein phosphatase 4, regulatory subunit 2	ENST00000356692.5
Case#2-Relapse-M464	DHFRL1	3	93779809	Missense_Mutation	A	G	p.C183R	210	131	0.624	0.632	3	2	1	165	dihydrofolate reductase-like 1	ENST00000394221.2
Case#2-Relapse-M464	SLC9C1	3	111996674	Missense_Mutation	T	G	p.N118H	173	114	0.659	0.668	3	2	1	147	solute carrier family 9, subfamily C (Na+-transporting carboxylic acid decarboxylase), member 1	ENST00000305815.5
Case#2-Relapse-M464	WDR52	3	113092257	Splice_Site	C	G		201	71	0.353	0.358	3	2	1	139		ENST00000295868.2
Case#2-Relapse-M464	SIDT1	3	113300268	Missense_Mutation	A	C	p.K242Q	138	37	0.268	0.272	3	2	1	155	SID1 transmembrane family, member 1	ENST00000264852.4
Case#2-Relapse-M464	GRAMD1C	3	113595055	Missense_Mutation	A	C	p.K136T	245	56	0.229	0.232	3	2	1	176	GRAM domain containing 1C	ENST00000358160.4
Case#2-Relapse-M464	MYLK	3	123419446	Missense_Mutation	G	C	p.L957V	194	34	0.175	0.178	3	2	1	99	myosin light chain kinase	ENST00000475616.1
Case#2-Relapse-M464	KALRN	3	124201655	Splice_Site	G	A	p.E1396K	127	81	0.638	0.646	3	2	1	121	kalirin, RhoGEF kinase	ENST00000240874.3
Case#2-Relapse-M464	COL6A5	3	130141610	Missense_Mutation	G	A	p.G1695E	145	50	0.345	0.350	3	2	1	110	collagen, type VI, alpha 5	ENST00000432398.2
Case#2-Relapse-M464	ACKR4	3	132319698	Missense_Mutation	C	T	p.P153S	451	147	0.326	0.330	3	2	1	334	atypical chemokine receptor 4	ENST00000249887.2
Case#2-Relapse-M464	GRK7	3	141535846	Missense_Mutation	G	A	p.C539Y	153	58	0.379	0.384	3	2	1	80	G protein-coupled receptor kinase 7	ENST00000264952.2
Case#2-Relapse-M464	WDR49	3	167254723	Missense_Mutation	C	T	p.G278E	214	58	0.271	0.275	3	2	1	156	WD repeat domain 49	ENST00000308378.3
Case#2-Relapse-M464	THPO	3	184090671	Missense_Mutation	C	T	p.G231D	137	49	0.358	0.363	3	2	1	80	thrombopoietin	ENST00000204615.7
Case#2-Relapse-M464	LSG1	3	194387217	Missense_Mutation	T	G	p.H104P	130	43	0.331	0.335	3	2	1	93	large 60S subunit nuclear export GTPase 1	ENST00000265245.5
Case#2-Relapse-M464	ZNF595	4	59391	Nonsense_Mutation	CC	TT	p.Q25*	1546	164	0.106	0.108	2	1	1	1401	zinc finger protein 595	ENST00000509152.2
Case#2-Relapse-M464	RGS12	4	3432545	Missense_Mutation	C	T	p.A1326V	174	90	0.517	0.528	2	1	1	187	regulator of G-protein signaling 12	ENST00000344733.5
Case#2-Relapse-M464	MAN2B2	4	6611023	Nonsense_Mutation	C	G	p.Y668*	134	68	0.507	0.518	2	1	1	122	mannosidase, alpha, class 2B, member 2	ENST00000285599.3
Case#2-Relapse-M464	CD38	4	15826506	Missense_Mutation	T	G	p.I122M	233	91	0.391	0.396	3	2	1	156	CD38 molecule	ENST00000226279.3
Case#2-Relapse-M464	SLIT2	4	20619226	Missense_Mutation	C	T	p.P1434L	184	109	0.592	0.600	3	2	1	157	slit homolog 2 (Drosophila)	ENST00000504154.1
Case#2-Relapse-M464	KLHL5	4	39116817	Missense_Mutation	C	T	p.S693F	161	44	0.273	0.277	3	2	1	90	kelch-like family member 5	ENST00000504108.1
Case#2-Relapse-M464	CHRNA9	4	40351379	Missense_Mutation	T	G	p.F282L	187	55	0.294	0.298	3	2	1	140	cholinergic receptor, nicotinic, alpha 9 (neuronal)	ENST00000310169.2
Case#2-Relapse-M464	RBM47	4	40440602	Missense_Mutation	C	T	p.M103I	280	80	0.286	0.290	3	2	1	179	RNA binding motif protein 47	ENST00000381793.2
Case#2-Relapse-M464	LIMCH1	4	41648273	Missense_Mutation	C	G	p.T411S	204	19	0.093	0.094	3	2	1	128	LIM and calponin homology domains 1	ENST00000313860.7
Case#2-Relapse-M464	ENAM	4	71509437	Missense_Mutation	C	T	p.S765F	199	59	0.296	0.301	3	2	1	124	enamelin	ENST00000396073.3
Case#2-Relapse-M464	TRPC3	4	122820844	Missense_Mutation	G	T	p.L824I	75	13	0.173	0.176	3	2	1	67	transient receptor potential cation channel, subfamily C, member 3	ENST00000379645.3
Case#2-Relapse-M464	KIAA1109	4	123234822	Missense_Mutation	C	T	p.T3431I	156	63	0.404	0.409	3	2	1	108	KIAA1109	ENST00000264501.4
Case#2-Relapse-M464	FREM3	4	144620448	Missense_Mutation	C	T	p.D461N	238	129	0.542	0.549	3	2	1	168	FRAS1 related extracellular matrix 3	ENST00000329798.5
Case#2-Relapse-M464	ANXA10	4	169049272	Missense_Mutation	C	T	p.P19L	84	16	0.190	0.193	3	2	1	90	annexin A10	ENST00000359299.3
Case#2-Relapse-M464	SPATA4	4	177116616	Missense_Mutation	C	T	p.R33Q	256	83	0.324	0.329	3	2	1	214	spermatogenesis associated 4	ENST00000280191.2
Case#2-Relapse-M464	TENM3	4	183714432	Missense_Mutation	G	A	p.E2203K	185	116	0.627	0.636	3	2	1	138	teneurin transmembrane protein 3	ENST00000511685.1
Case#2-Relapse-M464	WWC2	4	184171119	Missense_Mutation	G	A	p.S309N	173	57	0.329	0.334	3	2	1	129	WW and C2 domain containing 2	ENST00000403733.3
Case#2-Relapse-M464	DNAH5	5	13885322	Missense_Mutation	C	T	p.G920E	100	54	0.540	0.546	4	2	2	64	dynein, axonemal, heavy chain 5	ENST00000265104.4
Case#2-Relapse-M464	C9	5	39341716	Missense_Mutation	GG	AA	p.P90L	266	140	0.526	0.532	4	2	2	170	complement component 9	ENST00000263408.4
Case#2-Relapse-M464	CMYA5	5	79026782	Missense_Mutation	C	T	p.P732S	210	94	0.448	0.452	4	2	2	108	cardiomyopathy associated 5	ENST00000446378.2

Case#2-Relapse-M464	CMYA5	5	79033293	Missense_Mutation	G	T	p.S2902I	160	34	0.213	0.215	4	2	2	98	cardiomyopathy associated 5	ENST00000446378.2
Case#2-Relapse-M464	GPR98	5	89985788	Missense_Mutation	T	G	p.F2201V	148	18	0.122	0.123	4	2	2	101	G protein-coupled receptor 98	ENST00000405460.2
Case#2-Relapse-M464	GPR98	5	90052415	Missense_Mutation	C	A	p.P3909T	141	37	0.262	0.265	4	2	2	88	G protein-coupled receptor 98	ENST00000405460.2
Case#2-Relapse-M464	ERAP2	5	96239260	Missense_Mutation	G	T	p.V670F	174	18	0.103	0.105	3	2	1	177	endoplasmic reticulum aminopeptidase 2	ENST00000437043.3
Case#2-Relapse-M464	KIF3A	5	132056301	Splice_Site	G	A	p.R206C	180	113	0.628	0.636	3	2	1	129	kinesin family member 3A	ENST00000378746.4
Case#2-Relapse-M464	PCDHA4	5	140188687	Missense_Mutation	G	A	p.E639K	565	345	0.611	0.619	3	2	1	438	protocadherin alpha 4	ENST00000530339.1
Case#2-Relapse-M464	PCDHB8	5	140558546	Missense_Mutation	G	A	p.E311K	231	75	0.325	0.329	3	2	1	162	protocadherin beta 8	ENST00000239444.2
Case#2-Relapse-M464	SPINK14	5	147549340	Missense_Mutation	G	T	p.L15F	150	95	0.633	0.642	3	2	1	103	serine peptidase inhibitor, Kazal type 14 (putative)	ENST00000356972.1
Case#2-Relapse-M464	SYNPO	5	150027783	Missense_Mutation	CC	TT	p.P227S	193	121	0.627	0.635	3	2	1	111	synaptopodin	ENST00000394243.1
Case#2-Relapse-M464	HAVCR1	5	156476105	Missense_Mutation	A	T	p.L242Q	262	39	0.149	0.151	3	2	1	218	hepatitis A virus cellular receptor 1	ENST00000339252.3
Case#2-Relapse-M464	BTNL9	5	180474954	Missense_Mutation	C	T	p.P46L	161	99	0.615	0.623	3	2	1	125	butyrophilin-like 9	ENST00000327705.9
Case#2-Relapse-M464	PRSS16	6	27222499	Missense_Mutation	C	T	p.P393L	100	71	0.710	0.720	3	2	1	82	protease, serine, 16 (thymus)	ENST00000230582.3
Case#2-Relapse-M464	TREML2	6	41162493	Missense_Mutation	G	A	p.A152V	246	68	0.276	0.280	3	2	1	152	triggering receptor expressed on myeloid cells-like 2	ENST00000483722.1
Case#2-Relapse-M464	BMP5	6	55739516	Missense_Mutation	C	T	p.E50K	213	146	0.685	0.695	3	2	1	176	bone morphogenetic protein 5	ENST00000370830.3
Case#2-Relapse-M464	COL19A1	6	70866106	Missense_Mutation	G	A	p.D723N	164	46	0.280	0.284	3	2	1	150	collagen, type XIX, alpha 1	ENST00000322773.4
Case#2-Relapse-M464	NR2E1	6	108502798	Missense_Mutation	C	T	p.A313V	137	46	0.336	0.340	3	2	1	88	nuclear receptor subfamily 2, group E, member 1	ENST00000368986.4
Case#2-Relapse-M464	ASF1A	6	119222008	Missense_Mutation	G	A	p.G63S	194	118	0.608	0.617	3	2	1	174	anti-silencing function 1A histone chaperone	ENST00000229595.5
Case#2-Relapse-M464	THEMIS	6	128134071	Missense_Mutation	G	A	p.T572I	207	63	0.304	0.308	3	2	1	173	thymocyte selection associated	ENST00000368248.2
Case#2-Relapse-M464	MYB	6	135517046	Missense_Mutation	C	T	p.S370L	191	54	0.283	0.287	3	2	1	181	v-myb avian myeloblastosis viral oncogene homolog	ENST00000367814.4
Case#2-Relapse-M464	VTA1	6	142510629	Missense_Mutation	G	A	p.E160K	197	130	0.660	0.669	3	2	1	172	vesicle (multivesicular body) trafficking 1	ENST00000367630.4
Case#2-Relapse-M464	OPRM1	6	154412483	Missense_Mutation	G	A	p.R347Q	248	156	0.629	0.638	3	2	1	198	opioid receptor, mu 1	ENST00000330432.7
Case#2-Relapse-M464	LPA	6	161027508	Splice_Site	C	T		433	163	0.376	0.382	3	2	1	282	lipoprotein, Lp(a)	ENST00000316300.5
Case#2-Relapse-M464	EIF3B	7	2418877	Splice_Site	G	A	p.G781R	620	34	0.055	NA	NA	NA	NA	140	eukaryotic translation initiation factor 3, subunit B	ENST00000360876.4
Case#2-Relapse-M464	VWDE	7	12373192	Missense_Mutation	T	A	p.I1553F	430	105	0.244	0.245	8	5	3	127	von Willebrand factor D and EGF domains	ENST00000275358.3
Case#2-Relapse-M464	SNX10	7	26400626	Missense_Mutation	GG	AA	p.R19K	372	226	0.608	0.611	8	5	3	109	sorting nexin 10	ENST00000338523.4
Case#2-Relapse-M464	FAM188B	7	30825484	Missense_Mutation	A	G	p.E180G	554	57	0.103	0.103	8	5	3	125	family with sequence similarity 188, member B	ENST00000265299.6
Case#2-Relapse-M464	ZNF716	7	57528786	Missense_Mutation	C	T	p.H207Y	887	249	0.281	NA	NA	NA	NA	256	zinc finger protein 716	ENST00000420713.1
Case#2-Relapse-M464	SAMD9	7	92734447	Nonsense_Mutation	G	A	p.Q322*	216	216	1.000	1.007	6	6	0	102	sterile alpha motif domain containing 9	ENST00000379958.2
Case#2-Relapse-M464	COPS6	7	99688107	Missense_Mutation	G	T	p.K140N	420	70	0.167	0.168	6	6	0	169	COP9 signalosome subunit 6	ENST00000303904.3
Case#2-Relapse-M464	LRCH4	7	100175313	Missense_Mutation	C	G	p.E364Q	423	33	0.078	0.079	6	6	0	134	leucine-rich repeats and calponin homology (CH) domain containing 4	ENST00000310300.6
Case#2-Relapse-M464	FEZF1	7	121944058	Missense_Mutation	C	A	p.R145M	329	17	0.052	0.052	6	6	0	119	FEZ family zinc finger 1	ENST00000442488.2
Case#2-Relapse-M464	CHRM2	7	136700034	Missense_Mutation	G	C	p.G141A	244	37	0.152	0.153	6	6	0	101	cholinergic receptor, muscarinic 2	ENST00000445907.2
Case#2-Relapse-M464	DGKI	7	137170128	Missense_Mutation	G	A	p.H807Y	142	24	0.169	0.170	6	6	0	65	diacylglycerol kinase, iota	ENST00000288490.5
Case#2-Relapse-M464	BRAF	7	140453145	Missense_Mutation	AG	GA	p.L597S	375	374	0.997	1.004	6	6	0	155	B-Raf proto-oncogene, serine/threonine kinase	ENST00000288602.6
Case#2-Relapse-M464	CTAGE15	7	143270172	Missense_Mutation	A	G	p.E421G	28	6	0.214	0.216	5	3	2	43	CTAGE family, member 15	ENST00000420911.2
Case#2-Relapse-M464	NOS3	7	150696287	Missense_Mutation	G	C	p.W322C	316	52	0.165	0.166	6	6	0	75	nitric oxide synthase 3 (endothelial cell)	ENST00000484524.1
Case#2-Relapse-M464	CSMD1	8	2800046	Missense_Mutation	G	A	p.P3496S	199	43	0.216	0.218	4	2	2	137	CUB and Sushi multiple domains 1	ENST00000520002.1
Case#2-Relapse-M464	CSMD1	8	2830815	Missense_Mutation	T	G	p.N2917T	157	66	0.420	0.425	4	2	2	105	CUB and Sushi multiple domains 1	ENST00000520002.1
Case#2-Relapse-M464	CSMD1	8	2949047	Missense_Mutation	G	A	p.R2427C	164	71	0.433	0.437	4	2	2	117	CUB and Sushi multiple domains 1	ENST00000520002.1
Case#2-Relapse-M464	RP1L1	8	10470320	Nonsense_Mutation	G	A	p.Q430*	216	110	0.509	0.514	4	2	2	145	retinitis pigmentosa 1-like 1	ENST00000382483.3
Case#2-Relapse-M464	KIF13B	8	29037719	Missense_Mutation	G	A	p.R208C	247	105	0.425	0.429	4	2	2	202	kinesin family member 13B	ENST00000524189.1
Case#2-Relapse-M464	RP1	8	55538384	Missense_Mutation	G	A	p.E648K	182	115	0.632	0.640	3	2	1	156	retinitis pigmentosa 1 (autosomal dominant)	ENST00000220676.1
Case#2-Relapse-M464	RP1	8	55538858	Missense_Mutation	G	A	p.E806K	170	49	0.288	0.292	3	2	1	152	retinitis pigmentosa 1 (autosomal dominant)	ENST00000220676.1
Case#2-Relapse-M464	RP1	8	55540103	Missense_Mutation	C	T	p.P1221S	156	96	0.615	0.624	3	2	1	139	retinitis pigmentosa 1 (autosomal dominant)	ENST00000220676.1
Case#2-Relapse-M464	SLCO5A1	8	70617305	Missense_Mutation	C	T	p.S528N	244	94	0.385	0.390	3	2	1	207	solute carrier organic anion transporter family, member 5A1	ENST00000260126.4
Case#2-Relapse-M464	OTUD6B	8	92090825	Missense_Mutation	A	G	p.Y216C	167	50	0.299	0.303	3	2	1	128	OTU domain containing 6B	ENST00000285420.4
Case#2-Relapse-M464	STK3	8	99591892	Splice_Site	C	T	p.S316S	185	115	0.622	0.630	3	2	1	117	serine/threonine kinase 3	ENST00000419617.2
Case#2-Relapse-M464	UBR5	8	103297416	Missense_Mutation	C	T	p.A1879T	81	28	0.346	0.350	3	2	1	63	ubiquitin protein ligase E3 component n-recognin 5	ENST00000520539.1
Case#2-Relapse-M464	DCSTAMP	8	105360905	Frame_Shift_Del	T	-	p.I42fs	201	60	0.299	0.303	3	2	1	111	dendrocyte expressed seven transmembrane protein	ENST00000297581.2
Case#2-Relapse-M464	RSPO2	8	108970406	Missense_Mutation	G	T	p.T173K	109	34	0.312	0.316	3	2	1	105	R-spondin 2	ENST00000276659.5
Case#2-Relapse-M464	JAK2	9	5070054	Splice_Site	T	G		86	86	1.000	1.020	2	2	0	87	Janus kinase 2	ENST00000381652.3
Case#2-Relapse-M464	TAF1L	9	32633779	Missense_Mutation	C	T	p.R600Q	150	147	0.980	1.000	2	2	0	178	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 210kDa-like	ENST00000242310.4
Case#2-Relapse-M464	FAM205A	9	34725994	Missense_Mutation	C	A	p.G415W	150	61	0.407	0.415	2	2	0	142	family with sequence similarity 205, member A	ENST00000378788.3
Case#2-Relapse-M464	TRPM6	9	77422991	Missense_Mutation	G	A	p.H533Y	108	51	0.472	0.482	2	2	0	143	transient receptor potential cation channel, subfamily M, member 6	ENST00000360774.1
Case#2-Relapse-M464	DAPK1	9	90321284	Frame_Shift_Ins	-	T	p.M1100fs	172	63	0.366	0.374	2	2	0	208	death-associated protein kinase 1	ENST00000408954.3
Case#2-Relapse-M464	WNK2	9	95997111	Missense_Mutation	C	T	p.P366L	159	153	0.962	0.982	2	2	0	156	WNK lysine deficient protein kinase 2	ENST00000297954.4
Case#2-Relapse-M464	FBP2	9	97349720	Missense_Mutation	C	T	p.G68R	135	132	0.978	0.998	2	2	0	203	fructose-1,6-bisphosphatase 2	ENST00000375337.3
Case#2-Relapse-M464	OR13D1	9	107457064	Missense_Mutation	G	A	p.R121K	139	136	0.978	0.998	2	2	0	151	olfactory receptor, family 13, subfamily D, member 1	ENST00000318763.5
Case#2-Relapse-M464	OLFM1	9	138011716	Missense_Mutation	C	T	p.P384S	110	106	0.964	0.983	2	2	0	120	olfactomedin 1	ENST00000371793.3
Case#2-Relapse-M464	KCNT1	9	138649216	Missense_Mutation	G	A	p.E231K	143	137	0.958	0.978	2	2	0	164	potassium channel, subfamily T, member 1	ENST00000263604.3
Case#2-Relapse-M464	FAM166A	9	140139847	Missense_Mutation	C	T	p.G145E	175	171	0.977	0.997	2	2	0	188	family with sequence similarity 166, member A	ENST00000344774.4
Case#2-Relapse-M464	DCAF8L1	X	27997672	Nonsense_Mutation	G	A	p.R594*	119	118	0.992	NA	NA	NA	NA	97	DDB1 and CUL4 associated factor 8-like 1	ENST00000441525.1
Case#2-Relapse-M464	CHST7	X	46433406	Missense_Mutation	T	G	p.F14V	125	78	0.624	NA	NA	NA	NA	92	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	ENST00000276055.3
Case#2-Relapse-M464	OPHN1	X	67652784	Nonsense_Mutation	G	A	p.Q27*	83	49	0.590	NA	NA	NA	NA	65	oligophrenin 1	ENST00000355520.5
Case#2-Relapse-M464	MAGEE2	X	75003604	Missense_Mutation	C	T	p.R428Q	101	100	0.990	NA	NA	NA	NA	87	melanoma antigen family E, 2	ENST00000373359.2
Case#2-Relapse-M464	MUM1L1	X	105451316	Missense_Mutation	G	A	p.D631N	72	71	0.986	NA	NA	NA	NA	59	melanoma associated antigen (mutated) 1-like 1	ENST00000357175.2
Case#2-Relapse-M464	COL4A5	X	107909764	Missense_Mutation	G	A	p.E1165K	86	83	0.965	NA	NA	NA	NA	76	collagen, type IV, alpha 5	ENST00000361603.2
Case#2-Relapse-M464	PLXNB3	X	153039502	Missense_Mutation	G	C	p.E1156D	104	6	0.058	NA	NA	NA	NA	63	plexin B3	ENST00000361971.5
Case#2-Relapse-M464	F8	X	154130406	Missense_Mutation	G	C	p.A2012G	88	46	0.523	NA	NA	NA	NA	83	coagulation factor VIII, procoagulant component	ENST00000360256.4
Case#3-Relapse-WholeTumor	TTC34	1	2704108	Missense_Mutation	G	A	p.P85S	167	46	0.275	0.482	4	2	2	113	tetratricopeptide repeat domain 34	ENST00000401095.3
Case#3-Relapse-WholeTumor	WRAP73	1	3548848	Missense_Mutation	C	T	p.R326K	270	66	0.244	0.428	4	2	2	201	WD repeat containing, antisense to TP73	ENST00000270708.7
Case#3-Relapse-WholeTumor	GPR153	1	6311591	Splice_Site	C	A		109	39	0.358	0.626	4	2	2	87	G protein-coupled receptor 153	ENST00000377893.2
Case#3-Relapse-WholeTumor	CLSTN1	1	9809822	Splice_Site	C	A	p.G267*	270	74	0.274	0.480	4	2	2	169	calsyntenin 1	ENST00000377298.4
Case#3-Relapse-WholeTumor	SPEN	1	16263724	Frame_Shift_Ins	-	CTGCA	p.-3366fs	121	27	0.223	0.390	4	2	2	95	spen family transcriptional repressor	ENST00000375759.3
Case#3-Relapse-WholeTumor	CROCC	1	17292248	Missense_Mutation	CC	TT	p.T1479I	157	45	0.287	NA	NA	NA	NA	130	ciliary rootlet coiled-coil, rootletin	ENST00000375541.5
Case#3-Relapse-WholeTumor	PADI3	1	17601157	Missense_Mutation	G	A	p.E395K	273	77	0.282	0.494	4	2	2	207	peptidyl arginine deiminase, type III	ENST00000375460.3
Case#3-Relapse-WholeTumor	CELA3A	1	22333956	Missense_Mutation	C	T	p.T197I	196	59	0.301	0.527	4	2	2	141	chymotrypsin-like elastase family, member 3A	ENST00000290122.3
Case#3-Relapse-WholeTumor	MYOM3	1	24384118	Splice_Site	C	T		263	79	0.300	0.526	4	2	2	178	myomesin 3	ENST00000374434.3
Case#3-Relapse-WholeTumor	MATN1	1	31189129	Missense_Mutation	GA	AT	p.F278Y	194	53	0.273	0.478	4	2	2	125	matrilin 1, cartilage matrix protein	ENST00000373765.4
Case#3-Relapse-WholeTumor	LCK	1	32741652	Missense_Mutation	C	T	p.R207C	213	54	0.254	0.444	4	2	2	127	LCK proto-oncogene, Src family tyrosine kinase	ENST00000336890.5
Case#3-Relapse-WholeTumor	ADC	1	33583660	Missense_Mutation	C	T	p.S396F	290	78	0.269	0.471	4	2	2	191		ENST00000294517.6
Case#3-Relapse-WholeTumor	COL8A2	1	36564404	Missense_Mutation	C	T	p.G293D	94	23	0.245	0.428	4	2	2	66	collagen, type VIII, alpha 2	ENST00000397799.1

Case#3-Relapse-WholeTumor	CSF3R	1	36932118	Missense_Mutation	G	A	p.P784L	136	48	0.353	0.618	4	2	2	109	colony stimulating factor 3 receptor (granulocyte)	ENST00000373106.1
Case#3-Relapse-WholeTumor	COL9A2	1	40777362	Missense_Mutation	G	A	p.S148L	154	41	0.266	0.466	4	2	2	113	collagen, type IX, alpha 2	ENST00000372748.3
Case#3-Relapse-WholeTumor	DPH2	1	44437416	Missense_Mutation	C	T	p.A281V	151	44	0.291	0.510	4	2	2	95	DPH2 homolog (S. cerevisiae)	ENST00000255108.3
Case#3-Relapse-WholeTumor	C1orf173	1	75078442	Missense_Mutation	G	A	p.T351I	278	74	0.266	0.466	4	2	2	183		ENST00000326665.5
Case#3-Relapse-WholeTumor	COL11A1	1	103345336	Missense_Mutation	C	T	p.G1726E	269	73	0.271	0.475	4	2	2	205	collagen, type XI, alpha 1	ENST00000370096.3
Case#3-Relapse-WholeTumor	COL11A1	1	103467995	Missense_Mutation	G	A	p.P696S	137	37	0.270	0.473	4	2	2	91	collagen, type XI, alpha 1	ENST00000370096.3
Case#3-Relapse-WholeTumor	GNAI3	1	110128916	Missense_Mutation	C	A	p.F223L	238	62	0.261	0.456	4	2	2	165	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3	ENST00000369851.4
Case#3-Relapse-WholeTumor	GNAT2	1	110148621	Missense_Mutation	C	T	p.D231N	234	62	0.265	0.464	4	2	2	142	guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 2	ENST00000351050.3
Case#3-Relapse-WholeTumor	KCND3	1	112319738	Missense_Mutation	T	A	p.N559I	304	75	0.247	0.432	4	2	2	258	potassium voltage-gated channel, Shal-related subfamily, member 3	ENST00000315987.2
Case#3-Relapse-WholeTumor	NRAS	1	115256530	Missense_Mutation	G	T	p.Q61K	189	54	0.286	0.500	4	2	2	113	neuroblastoma RAS viral (v-ras) oncogene homolog	ENST00000369535.4
Case#3-Relapse-WholeTumor	KPRP	1	152732182	Missense_Mutation	C	T	p.P40S	293	93	0.317	0.555	4	2	2	234	keratinocyte proline-rich protein	ENST00000606109.1
Case#3-Relapse-WholeTumor	INSRR	1	156812030	Missense_Mutation	C	T	p.E1091K	174	46	0.264	0.463	4	2	2	133	insulin receptor-related receptor	ENST00000368195.3
Case#3-Relapse-WholeTumor	MNDA	1	158813785	Missense_Mutation	G	A	p.R148K	245	62	0.253	0.443	4	2	2	154	myeloid cell nuclear differentiation antigen	ENST00000368141.4
Case#3-Relapse-WholeTumor	CCDC19	1	159842813	Missense_Mutation	C	T	p.G500S	127	48	0.378	0.661	4	2	2	90		ENST00000368099.4
Case#3-Relapse-WholeTumor	SLAMF7	1	160719693	Missense_Mutation	G	A	p.M153I	195	53	0.272	0.476	4	2	2	164	SLAM family member 7	ENST00000368043.3
Case#3-Relapse-WholeTumor	CD244	1	160801172	Missense_Mutation	G	A	p.R360C	134	44	0.328	0.575	4	2	2	108	CD244 molecule, natural killer cell receptor 2B4	ENST00000368033.3
Case#3-Relapse-WholeTumor	HSPA6	1	161495026	Missense_Mutation	G	A	p.G193E	297	70	0.236	0.412	4	3	1	208	heat shock 70kDa protein 6 (HSP70B')	ENST00000309758.4
Case#3-Relapse-WholeTumor	DPT	1	168665821	Missense_Mutation	A	C	p.M191R	331	82	0.248	0.434	4	2	2	215	dermatopontin	ENST00000367817.3
Case#3-Relapse-WholeTumor	F5	1	169515815	Missense_Mutation	C	T	p.E543K	231	55	0.238	0.417	4	2	2	170	coagulation factor V (proaccelerin, labile factor)	ENST00000367797.3
Case#3-Relapse-WholeTumor	FMO1	1	171236697	Missense_Mutation	G	A	p.G50S	228	61	0.268	0.468	4	2	2	159	flavin containing monooxygenase 1	ENST00000354841.4
Case#3-Relapse-WholeTumor	MYOC	1	171621173	Missense_Mutation	CC	TT	p.R193Q	136	36	0.265	0.463	4	2	2	70	myocilin, trabecular meshwork inducible glucocorticoid response	ENST00000037502.6
Case#3-Relapse-WholeTumor	TNN	1	175067690	Missense_Mutation	G	A	p.G693E	386	118	0.306	0.535	4	2	2	284	tenascin N	ENST00000239462.4
Case#3-Relapse-WholeTumor	RASAL2	1	178411936	Nonsense_Mutation	A	T	p.K204*	259	58	0.224	0.392	4	2	2	153	RAS protein activator like 2	ENST00000462775.1
Case#3-Relapse-WholeTumor	KIF14	1	200587142	Missense_Mutation	G	A	p.T237M	140	42	0.300	0.525	4	2	2	91	kinesin family member 14	ENST00000367350.4
Case#3-Relapse-WholeTumor	CACNA1S	1	201029884	Missense_Mutation	G	A	p.P1106S	247	72	0.291	0.510	4	2	2	179	calcium channel, voltage-dependent, L type, alpha 1S subunit	ENST00000362061.3
Case#3-Relapse-WholeTumor	IGFN1	1	201196190	Missense_Mutation	G	A	p.G3656E	293	70	0.239	0.418	4	2	2	244	immunoglobulin-like and fibronectin type III domain containing 1	ENST00000335211.4
Case#3-Relapse-WholeTumor	CHI3L1	1	203152860	Missense_Mutation	G	A	p.P125L	328	104	0.317	0.555	4	2	2	264	chitinase 3-like 1 (cartilage glycoprotein-39)	ENST00000255409.3
Case#3-Relapse-WholeTumor	C1orf116	1	207196283	Missense_Mutation	C	T	p.E276K	104	33	0.317	0.555	4	2	2	89	chromosome 1 open reading frame 116	ENST00000359470.5
Case#3-Relapse-WholeTumor	HHIPL2	1	222717359	Missense_Mutation	C	T	p.G165D	252	67	0.266	0.465	4	2	2	190	HHIP-like 2	ENST00000343410.6
Case#3-Relapse-WholeTumor	ITPKB	1	226835055	Missense_Mutation	T	C	p.R687G	190	54	0.284	0.497	4	2	2	191	inositol-trisphosphate 3-kinase B	ENST00000272117.3
Case#3-Relapse-WholeTumor	CDC42BPA	1	227181974	Missense_Mutation	G	A	p.P1719S	154	44	0.286	0.500	4	2	2	107	CDC42 binding protein kinase alpha (DMPK-like)	ENST00000366769.3
Case#3-Relapse-WholeTumor	OBSCN	1	228504591	Missense_Mutation	C	A	p.H4489Q	40	5	0.125	0.219	4	2	2	41	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	ENST00000422127.1
Case#3-Relapse-WholeTumor	OBSCN	1	228504670	Missense_Mutation	C	T	p.R4516W	14	4	0.286	0.500	4	2	2	30	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	ENST00000422127.1
Case#3-Relapse-WholeTumor	OBSCN	1	228509823	Missense_Mutation	G	A	p.G5094E	147	45	0.306	0.536	4	2	2	90	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	ENST00000422127.1
Case#3-Relapse-WholeTumor	TTC13	1	231042719	Missense_Mutation	G	A	p.P839S	316	95	0.301	0.526	4	2	2	192	tetratricopeptide repeat domain 13	ENST00000366661.4
Case#3-Relapse-WholeTumor	ACTN2	1	236917278	Missense_Mutation	C	T	p.S624F	133	32	0.241	0.421	4	2	2	115	actinin, alpha 2	ENST00000366578.4
Case#3-Relapse-WholeTumor	FMN2	1	240371804	Missense_Mutation	G	A	p.G1231E	127	23	0.181	0.317	4	2	2	82	formin 2	ENST00000319653.9
Case#3-Relapse-WholeTumor	NLRP3	1	247588522	Missense_Mutation	G	A	p.E593K	196	50	0.255	0.446	4	2	2	135	NLR family, pyrin domain containing 3	ENST00000336119.3
Case#3-Relapse-WholeTumor	OR2G2	1	247752288	Missense_Mutation	CC	TT	p.L210F	334	81	0.243	0.424	4	2	2	232	olfactory receptor, family 2, subfamily G, member 2	ENST00000320065.1
Case#3-Relapse-WholeTumor	OR14A2	1	247887074	Missense_Mutation	G	A	p.S91F	420	105	0.250	0.438	4	2	2	332	olfactory receptor, family 14, subfamily A, member 2	ENST00000366485.1
Case#3-Relapse-WholeTumor	C10orf68	10	33136793	Missense_Mutation	G	A	p.G443S	248	106	0.427	1.069	2	2	0	227		ENST00000375030.2
Case#3-Relapse-WholeTumor	NRP1	10	33502507	Missense_Mutation	G	A	p.P474L	290	98	0.338	0.845	2	2	0	289	neuropilin 1	ENST00000265371.4
Case#3-Relapse-WholeTumor	OR13A1	10	45799119	Missense_Mutation	C	T	p.G251E	122	48	0.393	0.984	2	2	0	86	olfactory receptor, family 13, subfamily A, member 1	ENST00000553795.1
Case#3-Relapse-WholeTumor	ALOX5	10	45907693	Missense_Mutation	GG	AA	p.D163N	156	49	0.314	0.785	2	2	0	187	arachidonate 5-lipoxygenase	ENST00000374391.2
Case#3-Relapse-WholeTumor	FAM21C	10	46235637	Missense_Mutation	CT	TA	p.S158T	520	96	0.185	0.462	2	2	0	490	family with sequence similarity 21, member C	ENST00000336378.4
Case#3-Relapse-WholeTumor	GPRIN2	10	47000217	Missense_Mutation	G	A	p.R446H	71	4	0.056	0.141	2	2	0	132	G protein regulated inducer of neurite outgrowth 2	ENST00000374317.1
Case#3-Relapse-WholeTumor	COL13A1	10	71697406	Missense_Mutation	G	A	p.D594N	189	67	0.354	0.886	2	2	0	187	collagen, type XIII, alpha 1	ENST00000398978.3
Case#3-Relapse-WholeTumor	SPOCK2	10	73826708	Missense_Mutation	C	T	p.D294N	151	62	0.411	1.026	2	2	0	123	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	ENST00000373109.2
Case#3-Relapse-WholeTumor	DLG5	10	79584164	Missense_Mutation	G	A	p.S787F	103	37	0.359	0.898	2	2	0	102	discs, large homolog 5 (Drosophila)	ENST00000372391.2
Case#3-Relapse-WholeTumor	GRID1	10	87487637	Missense_Mutation	C	T	p.G503E	77	31	0.403	1.006	2	2	0	73	glutamate receptor, ionotropic, delta 1	ENST00000327946.7
Case#3-Relapse-WholeTumor	FAM25A	10	88780148	Missense_Mutation	G	A	p.G23R	439	166	0.378	0.945	2	2	0	513	family with sequence similarity 25, member A	ENST00000343959.4
Case#3-Relapse-WholeTumor	PTEN	10	89720649	Splice_Site	A	T		42	7	0.167	0.417	2	2	0	43	phosphatase and tensin homolog	ENST00000371953.3
Case#3-Relapse-WholeTumor	CEP55	10	95259816	Missense_Mutation	C	T	p.S3F	133	44	0.331	0.827	2	2	0	122	centrosomal protein 55kDa	ENST00000371485.3
Case#3-Relapse-WholeTumor	ENTPD1	10	97604267	Missense_Mutation	G	A	p.D150N	181	76	0.420	1.050	2	2	0	173	ectonucleoside triphosphate diphosphohydrolase 1	ENST00000371205.4
Case#3-Relapse-WholeTumor	SORCS3	10	106960963	Missense_Mutation	G	A	p.G738E	165	63	0.382	0.955	2	2	0	164	sortilin-related VPS10 domain containing receptor 3	ENST00000369701.3
Case#3-Relapse-WholeTumor	DMBT1	10	124377802	Missense_Mutation	G	A	p.G1592S	429	158	0.368	0.921	2	2	0	474	deleted in malignant brain tumors 1	ENST00000338354.3
Case#3-Relapse-WholeTumor	MUC5B	11	1272226	Missense_Mutation	A	C	p.T4706P	369	28	0.076	0.190	2	2	0	439	mucin 5B, oligomeric mucus/gel-forming	ENST00000529681.1
Case#3-Relapse-WholeTumor	OR52E8	11	5878793	Missense_Mutation	C	T	p.G47E	232	86	0.371	0.927	2	2	0	228	olfactory receptor, family 52, subfamily E, member 8	ENST00000537935.1
Case#3-Relapse-WholeTumor	OR4C11	11	55371179	Missense_Mutation	C	T	p.R224K	148	65	0.439	1.098	2	2	0	140	olfactory receptor, family 4, subfamily C, member 11	ENST00000302231.4
Case#3-Relapse-WholeTumor	OR8K5	11	55926983	Missense_Mutation	C	T	p.D271N	155	55	0.355	0.887	2	2	0	117	olfactory receptor, family 8, subfamily K, member 5	ENST00000313447.1
Case#3-Relapse-WholeTumor	OR5J2	11	55944743	Missense_Mutation	C	T	p.S217F	239	82	0.343	0.858	2	2	0	243	olfactory receptor, family 5, subfamily J, member 2	ENST00000312298.1
Case#3-Relapse-WholeTumor	PLCB3	11	64034876	Nonsense_Mutation	C	T	p.Q1185*	94	37	0.394	0.984	2	2	0	94	phospholipase C, beta 3 (phosphatidylinositol-specific)	ENST00000540288.1
Case#3-Relapse-WholeTumor	SHANK2	11	70333304	Missense_Mutation	G	A	p.P653S	139	59	0.424	1.061	2	2	0	174	SH3 and multiple ankyrin repeat domains 2	ENST00000423696.2
Case#3-Relapse-WholeTumor	LRRC32	11	76371798	Missense_Mutation	GG	AA	p.P280F	140	57	0.407	1.018	2	2	0	163	leucine rich repeat containing 32	ENST00000407242.2
Case#3-Relapse-WholeTumor	OR8B3	11	124266391	Missense_Mutation	G	A	p.P286L	148	51	0.345	0.861	2	2	0	134	olfactory receptor, family 8, subfamily B, member 3	ENST00000354597.3
Case#3-Relapse-WholeTumor	CACNA1C	12	2797799	Missense_Mutation	C	T	p.H2039Y	234	94	0.402	1.004	2	2	0	262	calcium channel, voltage-dependent, L type, alpha 1C subunit	ENST00000347598.4
Case#3-Relapse-WholeTumor	GRIN2B	12	13717537	Missense_Mutation	C	T	p.E879K	108	45	0.417	1.042	2	2	0	99	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	ENST00000609686.1
Case#3-Relapse-WholeTumor	ARID2	12	46243857	Nonsense_Mutation	C	T	p.Q651*	105	43	0.410	1.024	2	2	0	102	AT rich interactive domain 2 (ARID, RFX-like)	ENST00000334344.6
Case#3-Relapse-WholeTumor	OR10AD1	12	48596927	Missense_Mutation	G	A	p.S50F	241	105	0.436	1.089	2	2	0	212	olfactory receptor, family 10, subfamily AD, member 1	ENST00000310248.2
Case#3-Relapse-WholeTumor	GALNT6	12	51758017	Nonsense_Mutation	GG	AA	p.Q313*	179	65	0.363	0.908	2	2	0	202	polypeptide N-acetylgalactosaminyltransferase 6	ENST00000543196.2
Case#3-Relapse-WholeTumor	ORMDL2	12	56214160	Missense_Mutation	T	C	p.F148S	163	68	0.417	1.043	2	2	0	54	ORMDL sphingolipid biosynthesis regulator 2	ENST00000243045.5
Case#3-Relapse-WholeTumor	HELB	12	66731841	Missense_Mutation	C	T	p.P1075S	86	33	0.384	0.959	2	2	0	62	helicase (DNA) B	ENST00000247815.4
Case#3-Relapse-WholeTumor	STAB2	12	104054483	Missense_Mutation	C	T	p.S604F	136	59	0.434	1.085	2	2	0	132	stabilin 2	ENST00000388887.2
Case#3-Relapse-WholeTumor	STAB2	12	104118771	Missense_Mutation	G	A	p.E1568K	128	58	0.453	1.133	2	2	0	110	stabilin 2	ENST00000388887.2
Case#3-Relapse-WholeTumor	PARP4	13	25009317	Missense_Mutation	GG	AA	p.P1321L	308	84	0.273	0.477	4	2	2	183	poly (ADP-ribose) polymerase family, member 4	ENST00000381989.3
Case#3-Relapse-WholeTumor	FREM2	13	39262018	Missense_Mutation	GG	AA	p.E180K	197	38	0.193	0.338	4	2	2	277	FRAS1 related extracellular matrix protein 2	ENST00000280481.7
Case#3-Relapse-WholeTumor	MED4	13	48664557	Splice_Site	A	-		219	20	0.091	0.160	4	2	2	139	mediator complex subunit 4	ENST00000258648.2
Case#3-Relapse-WholeTumor	LMO7	13	76287354	Nonsense_Mutation	C	T	p.R88*	464	134	0.289	0.505	4	2	2	265	LIM domain 7	ENST00000341547.4
Case#3-Relapse-WholeTumor	CLYBL	13	100425124	Missense_Mutation	T	G	p.S37A	270	73	0.270	0.473	4	2	2	182	citrate lyase beta like	ENST00000376360.1
Case#3-Relapse-WholeTumor	ITGBL1	13	102367919	Missense_Mutation	G	A	p.G467E	153	42	0.275	0.480	4	2	2	105	integrin, beta-like 1 (with EGF-like repeat domains)	ENST00000376180.3

Case#3-Relapse-WholeTumor	F7	13	113772987	Missense_Mutation	G	A	p.E356K	305	78	0.256	0.448	4	2	2	233	coagulation factor VII (serum prothrombin conversion accelerator)	ENST00000375581.3
Case#3-Relapse-WholeTumor	CHAMP1	13	115090674	Missense_Mutation	CC	TT	p.P453F	184	48	0.261	NA	NA	NA	NA	154	chromosome alignment maintaining phosphoprotein 1	ENST00000361283.1
Case#3-Relapse-WholeTumor	POTEG	14	19574200	Missense_Mutation	G	A	p.M419I	1282	152	0.119	0.474	1	1	0	1335	POTE ankyrin domain family, member G	ENST00000409832.3
Case#3-Relapse-WholeTumor	POTEM	14	20002247	Missense_Mutation	C	T	p.G392E	1910	149	0.078	0.312	1	1	0	1730	POTE ankyrin domain family, member M	ENST00000551509.1
Case#3-Relapse-WholeTumor	OR5AU1	14	21623343	Missense_Mutation	G	A	p.S281L	200	97	0.485	1.213	2	2	0	201	olfactory receptor, family 5, subfamily AU, member 1	ENST00000304418.3
Case#3-Relapse-WholeTumor	OR10G2	14	22102188	Missense_Mutation	C	T	p.D271N	172	40	0.233	0.581	2	2	0	179	olfactory receptor, family 10, subfamily G, member 2	ENST00000542433.1
Case#3-Relapse-WholeTumor	ZFHX2	14	23994870	Missense_Mutation	GG	AA	p.P1427L	46	20	0.435	1.087	2	2	0	52	zinc finger homeobox 2	ENST00000419474.3
Case#3-Relapse-WholeTumor	DHRS4-AS1	14	24408806	Missense_Mutation	G	A	p.E25K	70	30	0.429	1.071	2	2	0	55	DHRS4 antisense RNA 1	ENST00000354854.1
Case#3-Relapse-WholeTumor	SYNE2	14	64465727	Missense_Mutation	C	T	p.S1150F	99	38	0.384	0.960	2	2	0	122	spectrin repeat containing, nuclear envelope 2	ENST00000344113.4
Case#3-Relapse-WholeTumor	PAPLN	14	73716803	Missense_Mutation	G	A	p.C149Y	168	70	0.417	1.042	2	2	0	143	papilin, proteoglycan-like sulfated glycoprotein	ENST00000554301.1
Case#3-Relapse-WholeTumor	EIF5	14	103806121	Missense_Mutation	T	C	p.I351T	200	81	0.405	1.013	2	2	0	189	eukaryotic translation initiation factor 5	ENST00000216554.3
Case#3-Relapse-WholeTumor	B2M	15	45003786	Frame_Shift_Del	TCTT	-	p.S14fs	90	40	0.444	1.111	2	2	0	84	beta-2-microglobulin	ENST00000558401.1
Case#3-Relapse-WholeTumor	CGNL1	15	57731599	Missense_Mutation	G	A	p.G468R	224	82	0.366	0.915	2	2	0	198	cingulin-like 1	ENST00000281282.5
Case#3-Relapse-WholeTumor	HERC1	15	63932569	Missense_Mutation	G	A	p.H3895Y	154	58	0.377	0.942	2	2	0	160	HECT and RLD domain containing E3 ubiquitin protein ligase family member 1	ENST00000443617.2
Case#3-Relapse-WholeTumor	ZNF609	15	64966930	Missense_Mutation	C	T	p.S626F	83	35	0.422	1.054	2	2	0	73	zinc finger protein 609	ENST00000326648.3
Case#3-Relapse-WholeTumor	MEGF11	15	66386745	Missense_Mutation	G	A	p.S130F	228	86	0.377	0.943	2	2	0	245	multiple EGF-like-domains 11	ENST00000409699.2
Case#3-Relapse-WholeTumor	SH2D7	15	78390783	Missense_Mutation	G	A	p.D164N	241	113	0.469	1.172	2	2	0	211	SH2 domain containing 7	ENST00000328828.5
Case#3-Relapse-WholeTumor	KIAA1199	15	81239357	Nonsense_Mutation	G	A	p.W1303*	140	52	0.371	0.929	2	2	0	124		ENST00000394685.3
Case#3-Relapse-WholeTumor	PKD1	16	2164850	Missense_Mutation	G	A	p.A725V	191	40	0.209	0.419	3	2	1	286	polycystic kidney disease 1 (autosomal dominant)	ENST00000262304.4
Case#3-Relapse-WholeTumor	PRSS33	16	2835130	Missense_Mutation	G	A	p.P186L	52	11	0.212	0.423	3	2	1	40	protease, serine, 33	ENST00000293851.5
Case#3-Relapse-WholeTumor	RBFOX1	16	7657301	Missense_Mutation	C	T	p.P213S	168	42	0.250	0.500	3	2	1	109	RNA binding protein, fox-1 homolog (C. elegans) 1	ENST00000550418.1
Case#3-Relapse-WholeTumor	GRIN2A	16	9857865	Missense_Mutation	G	A	p.S1179F	175	49	0.280	0.560	3	2	1	145	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	ENST00000396573.2
Case#3-Relapse-WholeTumor	CIITA	16	11001583	Missense_Mutation	G	A	p.R745K	117	30	0.256	0.513	3	2	1	134	class II, major histocompatibility complex, transactivator	ENST00000324288.8
Case#3-Relapse-WholeTumor	ZP2	16	21213516	Missense_Mutation	C	T	p.G399E	159	40	0.252	0.503	3	2	1	115	zona pellucida glycoprotein 2 (sperm receptor)	ENST00000574002.1
Case#3-Relapse-WholeTumor	SETD1A	16	30972725	Missense_Mutation	CC	TT	p.P129S	270	91	0.337	0.674	3	2	1	202	SET domain containing 1A	ENST00000262519.8
Case#3-Relapse-WholeTumor	KAT8	16	31139429	Missense_Mutation	C	T	p.S247F	133	32	0.241	0.481	3	2	1	95	K(lysine) acetyltransferase 8	ENST00000543774.2
Case#3-Relapse-WholeTumor	ABCC12	16	48120720	Missense_Mutation	C	T	p.D1216N	222	48	0.216	0.432	3	2	1	166	ATP-binding cassette, sub-family C (CFTR/MRP), member 12	ENST00000311303.3
Case#3-Relapse-WholeTumor	C16orf80	16	58150028	Missense_Mutation	GG	AA	p.P65S	152	40	0.263	0.526	3	2	1	105		ENST00000262498.3
Case#3-Relapse-WholeTumor	SLC12A4	16	67978823	Missense_Mutation	GG	AA	p.L1060F	179	41	0.229	0.458	3	2	1	121	solute carrier family 12 (potassium/chloride transporter), member 4	ENST00000316341.3
Case#3-Relapse-WholeTumor	PHLPP2	16	71715720	Missense_Mutation	G	A	p.T275I	221	42	0.190	0.380	3	2	1	127	PH domain and leucine rich repeat protein phosphatase 2	ENST00000568954.1
Case#3-Relapse-WholeTumor	ZNF469	16	88502825	Missense_Mutation	C	T	p.R2955W	249	50	0.201	0.402	3	2	1	191	zinc finger protein 469	ENST00000437464.1
Case#3-Relapse-WholeTumor	RPH3AL	17	65450	Missense_Mutation	CC	TT	p.A291T	119	41	0.345	0.861	2	2	0	131	rabphilin 3A-like (without C2 domains)	ENST00000331302.7
Case#3-Relapse-WholeTumor	USP6	17	5072287	Missense_Mutation	G	A	p.E1152K	331	132	0.399	0.997	2	2	0	313	ubiquitin specific peptidase 6	ENST00000574788.1
Case#3-Relapse-WholeTumor	TP53	17	7578212	Nonsense_Mutation	G	A	p.R213*	179	76	0.425	1.061	2	2	0	129	tumor protein p53	ENST00000269305.4
Case#3-Relapse-WholeTumor	DNAH9	17	11631201	Nonsense_Mutation	C	T	p.R1926*	151	45	0.298	0.745	2	2	0	151	dynein, axonemal, heavy chain 9	ENST00000262442.4
Case#3-Relapse-WholeTumor	MYOCD	17	12649381	Missense_Mutation	G	A	p.D373N	174	63	0.362	0.905	2	2	0	160	myocardin	ENST00000343344.4
Case#3-Relapse-WholeTumor	TRIM16	17	15539436	Missense_Mutation	GG	AT	p.H254Q	249	78	0.313	0.783	2	2	0	267	tripartite motif containing 16	ENST00000578237.1
Case#3-Relapse-WholeTumor	TAOK1	17	27861294	Missense_Mutation	CC	TT	p.R841W	124	51	0.411	1.028	2	2	0	94	TAO kinase 1	ENST00000261716.3
Case#3-Relapse-WholeTumor	MYO1D	17	31075981	Missense_Mutation	C	T	p.R504Q	139	44	0.317	0.791	2	2	0	124	myosin ID	ENST00000318217.5
Case#3-Relapse-WholeTumor	DDX52	17	35988719	Splice_Site	A	-		26	4	0.154	0.385	2	2	0	25	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	ENST00000349699.2
Case#3-Relapse-WholeTumor	TUBG1	17	40765003	Missense_Mutation	C	T	p.P173L	166	65	0.392	0.979	2	2	0	163	tubulin, gamma 1	ENST00000251413.3
Case#3-Relapse-WholeTumor	EZH1	17	40879733	Missense_Mutation	G	A	p.L56F	101	38	0.376	0.941	2	2	0	91	enhancer of zeste 1 polycomb repressive complex 2 subunit	ENST00000428826.2
Case#3-Relapse-WholeTumor	MED13	17	60059588	Missense_Mutation	G	A	p.S1259L	152	59	0.388	0.970	2	2	0	130	mediator complex subunit 13	ENST00000397786.2
Case#3-Relapse-WholeTumor	TLK2	17	60601646	Missense_Mutation	C	T	p.P106L	179	65	0.363	0.908	2	2	0	139	tousled-like kinase 2	ENST00000326270.9
Case#3-Relapse-WholeTumor	ABCA8	17	66899001	Missense_Mutation	C	T	p.G833R	236	92	0.390	0.975	2	2	0	208	ATP-binding cassette, sub-family A (ABC1), member 8	ENST00000269080.2
Case#3-Relapse-WholeTumor	SLC16A5	17	73096288	Missense_Mutation	G	A	p.G177E	188	81	0.431	1.077	2	2	0	180	solute carrier family 16 (monocarboxylate transporter), member 5	ENST00000450736.2
Case#3-Relapse-WholeTumor	RP11-1055B8.7	17	79428645	Missense_Mutation	C	T	p.S2319F	138	50	0.362	0.906	2	2	0	292		ENST00000307745.7
Case#3-Relapse-WholeTumor	ZBTB14	18	5291177	Missense_Mutation	G	A	p.R344C	144	40	0.278	0.486	4	2	2	122	zinc finger and BTB domain containing 14	ENST00000357006.4
Case#3-Relapse-WholeTumor	DSG1	18	28926010	Missense_Mutation	G	A	p.R650K	167	10	0.060	0.150	2	2	0	125	desmoglein 1	ENST00000257192.4
Case#3-Relapse-WholeTumor	SLC14A2	18	43221220	Nonsense_Mutation	G	A	p.W346*	181	12	0.066	0.166	2	2	0	151	solute carrier family 14 (urea transporter), member 2	ENST00000255226.6
Case#3-Relapse-WholeTumor	SMAD7	18	46474786	Missense_Mutation	G	A	p.S212F	66	25	0.379	0.947	2	2	0	87	SMAD family member 7	ENST00000262158.2
Case#3-Relapse-WholeTumor	DCC	18	51025778	Nonsense_Mutation	C	T	p.R1337*	302	90	0.298	0.745	2	2	0	265	DCC netrin 1 receptor	ENST00000442544.2
Case#3-Relapse-WholeTumor	MALT1	18	56412976	Missense_Mutation	C	T	p.P664S	160	66	0.413	1.031	2	2	0	91	mucosa associated lymphoid tissue lymphoma translocation gene 1	ENST00000348428.3
Case#3-Relapse-WholeTumor	SERPINB2	18	61570441	Missense_Mutation	G	A	p.G384R	207	61	0.295	0.737	2	2	0	173	serpin peptidase inhibitor, clade B (ovalbumin), member 2	ENST00000299502.4
Case#3-Relapse-WholeTumor	TSHZ1	18	73000585	Missense_Mutation	G	C	p.E1075Q	163	12	0.074	0.184	2	2	0	176	teashirt zinc finger homeobox 1	ENST00000580243.1
Case#3-Relapse-WholeTumor	MIER2	19	326549	Missense_Mutation	GG	AA	p.S181F	160	61	0.381	0.667	4	2	2	133	mesoderm induction early response 1, family member 2	ENST00000264819.4
Case#3-Relapse-WholeTumor	DOT1L	19	2226676	Missense_Mutation	G	A	p.G1386S	28	5	0.179	0.313	4	2	2	86	DOT1-like histone H3K79 methyltransferase	ENST00000398665.3
Case#3-Relapse-WholeTumor	LRG1	19	4538370	Missense_Mutation	C	T	p.R209K	203	42	0.207	0.362	4	2	2	165	leucine-rich alpha-2-glycoprotein 1	ENST00000306390.6
Case#3-Relapse-WholeTumor	SH2D3A	19	6760941	Missense_Mutation	G	A	p.R43C	224	64	0.286	0.500	4	2	2	138	SH2 domain containing 3A	ENST00000245908.6
Case#3-Relapse-WholeTumor	MUC16	19	9075262	Missense_Mutation	G	A	p.L4062F	291	85	0.292	0.511	4	2	2	199	mucin 16, cell surface associated	ENST00000397910.4
Case#3-Relapse-WholeTumor	OR7G2	19	9213712	Missense_Mutation	C	T	p.D91N	357	81	0.227	0.397	4	2	2	230	olfactory receptor, family 7, subfamily G, member 2	ENST00000305456.2
Case#3-Relapse-WholeTumor	ZNF559	19	9452789	Missense_Mutation	C	T	p.T221I	257	63	0.245	0.429	4	2	2	142	zinc finger protein 559	ENST00000393883.2
Case#3-Relapse-WholeTumor	ZNF812	19	9801529	Missense_Mutation	C	T	p.G217E	244	54	0.221	0.387	4	2	2	175	zinc finger protein 812	ENST00000457674.2
Case#3-Relapse-WholeTumor	RDH8	19	10131432	Missense_Mutation	G	A	p.G164R	78	18	0.231	0.404	4	2	2	58	retinol dehydrogenase 8 (all-trans)	ENST00000171214.1
Case#3-Relapse-WholeTumor	RGL3	19	11510969	Missense_Mutation	G	A	p.R497W	82	23	0.280	0.491	4	2	2	33	ral guanine nucleotide dissociation stimulator-like 3	ENST00000380456.3
Case#3-Relapse-WholeTumor	ZNF491	19	11916814	Missense_Mutation	G	C	p.E16Q	108	29	0.269	0.470	4	2	2	74	zinc finger protein 491	ENST00000323169.5
Case#3-Relapse-WholeTumor	RAD23A	19	13059521	Missense_Mutation	C	T	p.T165M	159	44	0.277	0.484	4	2	2	108	RAD23 homolog A (S. cerevisiae)	ENST00000586534.1
Case#3-Relapse-WholeTumor	ZNF493	19	21607009	Missense_Mutation	CT	TC	p.Y389H	174	40	0.230	0.402	4	2	2	101	zinc finger protein 493	ENST00000355504.4
Case#3-Relapse-WholeTumor	KLK5	19	51452217	Missense_Mutation	G	A	p.R164C	76	29	0.382	0.954	2	2	0	70	kallikrein-related peptidase 5	ENST00000336334.3
Case#3-Relapse-WholeTumor	CACNG7	19	54417812	Missense_Mutation	GG	AA	p.V86M	75	31	0.413	1.033	2	2	0	80	calcium channel, voltage-dependent, gamma subunit 7	ENST00000391767.1
Case#3-Relapse-WholeTumor	LILRA6	19	54744887	Missense_Mutation	C	T	p.E259K	674	80	0.119	0.297	2	2	0	623	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 6	ENST00000396365.2
Case#3-Relapse-WholeTumor	LILRA4	19	54848803	Missense_Mutation	C	T	p.G274R	292	109	0.373	0.933	2	2	0	263	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 4	ENST00000291759.4
Case#3-Relapse-WholeTumor	NLRP8	19	56466053	Missense_Mutation	G	A	p.G210E	205	89	0.434	1.085	2	2	0	187	NLR family, pyrin domain containing 8	ENST00000291971.3
Case#3-Relapse-WholeTumor	ZNF835	19	57175578	Missense_Mutation	C	T	p.G330D	64	10	0.156	0.391	2	2	0	220	zinc finger protein 835	ENST00000537055.2
Case#3-Relapse-WholeTumor	ZIM3	19	57647454	Missense_Mutation	C	T	p.G84E	173	68	0.393	0.983	2	2	0	136	zinc finger, imprinted 3	ENST00000269834.1
Case#3-Relapse-WholeTumor	ZNF805	19	57764450	Missense_Mutation	G	A	p.G88E	124	43	0.347	0.867	2	2	0	135	zinc finger protein 805	ENST00000414468.2
Case#3-Relapse-WholeTumor	RAD51AP2	2	17699133	Missense_Mutation	C	T	p.D184N	175	37	0.211	0.370	4	2	2	99	RAD51 associated protein 2	ENST00000399080.2
Case#3-Relapse-WholeTumor	HS1BP3	2	20824519	Missense_Mutation	G	A	p.P253S	147	41	0.279	0.488	4	2	2	114	HCLS1 binding protein 3	ENST00000304031.3

Case#3-Relapse-WholeTumor	ATAD2B	2	24110824	Missense_Mutation	C	G	p.K150N	302	87	0.288	0.504	4	2	2	138	ATPase family, AAA domain containing 2B	ENST00000238789.5
Case#3-Relapse-WholeTumor	GAREML	2	26410435	Missense_Mutation	C	T	p.A645V	252	71	0.282	0.493	4	2	2	200	GRB2 associated, regulator of MAPK1-like	ENST00000401533.2
Case#3-Relapse-WholeTumor	CAPN13	2	30987042	Missense_Mutation	C	T	p.A219T	196	59	0.301	0.527	4	2	2	150	calpain 13	ENST00000295055.8
Case#3-Relapse-WholeTumor	NLRC4	2	32449780	Missense_Mutation	C	T	p.G946E	177	35	0.198	0.346	4	2	2	104	NLR family, CARD domain containing 4	ENST00000404025.2
Case#3-Relapse-WholeTumor	TMEM178A	2	39944333	Missense_Mutation	C	T	p.P279L	200	53	0.265	0.464	4	2	2	112	transmembrane protein 178A	ENST00000281961.2
Case#3-Relapse-WholeTumor	SLC3A1	2	44502865	Missense_Mutation	C	T	p.P64L	240	67	0.279	0.489	4	2	2	164	solute carrier family 3 (amino acid transporter heavy chain), member 1	ENST00000260649.6
Case#3-Relapse-WholeTumor	SEMA4F	2	74906438	Missense_Mutation	C	T	p.S560F	201	64	0.318	0.557	4	2	2	148	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F	ENST00000357877.2
Case#3-Relapse-WholeTumor	LRRTM4	2	76976028	Missense_Mutation	C	T	p.M522I	168	46	0.274	0.479	4	2	2	140	leucine rich repeat transmembrane neuronal 4	ENST00000409093.1
Case#3-Relapse-WholeTumor	DNAH6	2	84899586	Missense_Mutation	A	C	p.K2197T	156	38	0.244	0.426	4	2	2	97	dynein, axonemal, heavy chain 6	ENST00000237449.6
Case#3-Relapse-WholeTumor	DNAH6	2	84936603	Missense_Mutation	C	T	p.S3062L	175	44	0.251	0.440	4	2	2	132	dynein, axonemal, heavy chain 6	ENST00000237449.6
Case#3-Relapse-WholeTumor	ANKRD36C	2	96589416	Missense_Mutation	G	A	p.P688L	439	114	0.260	0.454	4	2	2	259	ankyrin repeat domain 36C	ENST00000456556.1
Case#3-Relapse-WholeTumor	SNRNP200	2	96952155	Missense_Mutation	GG	AA	p.T1299I	125	39	0.312	0.546	4	3	1	97	small nuclear ribonucleoprotein 200kDa (U5)	ENST00000323853.5
Case#3-Relapse-WholeTumor	KANSL3	2	97276608	Missense_Mutation	G	A	p.P392S	216	68	0.315	0.551	4	3	1	180	KAT8 regulatory NSL complex subunit 3	ENST00000431828.1
Case#3-Relapse-WholeTumor	TSGA10	2	99725886	Missense_Mutation	G	A	p.S6F	202	57	0.282	0.494	4	2	2	90	testis specific, 10	ENST00000393483.3
Case#3-Relapse-WholeTumor	IL18RAP	2	103067316	Missense_Mutation	G	A	p.D407N	155	46	0.297	0.519	4	2	2	93	interleukin 18 receptor accessory protein	ENST00000264260.2
Case#3-Relapse-WholeTumor	RGPD8	2	113191010	Missense_Mutation	A	C	p.D7E	204	13	0.064	0.112	4	2	2	197	RANBP2-like and GRIP domain containing 8	ENST00000302558.3
Case#3-Relapse-WholeTumor	SAP130	2	128712815	Missense_Mutation	GG	AA	p.P714S	117	36	0.308	0.538	4	2	2	84	Sin3A-associated protein, 130kDa	ENST00000259235.3
Case#3-Relapse-WholeTumor	POTEI	2	131220643	Missense_Mutation	C	T	p.D992N	680	60	0.088	0.176	3	2	1	616	POTE ankyrin domain family, member I	ENST00000451531.2
Case#3-Relapse-WholeTumor	NCKAP5	2	133542604	Missense_Mutation	C	T	p.E594K	109	27	0.248	0.433	4	2	2	95	NCK-associated protein 5	ENST00000409261.1
Case#3-Relapse-WholeTumor	THSD7B	2	138400156	Missense_Mutation	C	T	p.P1300S	142	43	0.303	0.530	4	2	2	99	thrombospondin, type I, domain containing 7B	ENST00000409968.1
Case#3-Relapse-WholeTumor	CACNB4	2	152728990	Missense_Mutation	G	A	p.S180F	201	43	0.214	0.374	4	2	2	114	calcium channel, voltage-dependent, beta 4 subunit	ENST00000539935.1
Case#3-Relapse-WholeTumor	SCN1A	2	166892697	Missense_Mutation	A	C	p.I1097S	386	119	0.308	0.540	4	2	2	220	sodium channel, voltage-gated, type I, alpha subunit	ENST00000303395.4
Case#3-Relapse-WholeTumor	LRP2	2	169989179	Missense_Mutation	C	T	p.E4545K	210	47	0.224	0.392	4	2	2	121	low density lipoprotein receptor-related protein 2	ENST00000263816.3
Case#3-Relapse-WholeTumor	LRP2	2	170027117	Missense_Mutation	C	T	p.R3775Q	248	65	0.262	0.459	4	2	2	166	low density lipoprotein receptor-related protein 2	ENST00000263816.3
Case#3-Relapse-WholeTumor	TTN	2	179542597	Missense_Mutation	C	T	p.E11031K	240	62	0.258	0.452	4	2	2	161	titin	ENST00000591111.1
Case#3-Relapse-WholeTumor	TTN	2	179638013	Missense_Mutation	C	T	p.G2560R	174	63	0.362	0.634	4	2	2	115	titin	ENST00000591111.1
Case#3-Relapse-WholeTumor	ITGA4	2	182347248	Missense_Mutation	C	T	p.S304L	290	88	0.303	0.531	4	2	2	197	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	ENST00000397033.2
Case#3-Relapse-WholeTumor	FSIP2	2	186665668	Missense_Mutation	G	A	p.E3879K	161	43	0.267	0.467	4	2	2	113	fibrous sheath interacting protein 2	ENST00000424728.1
Case#3-Relapse-WholeTumor	STAT4	2	191894582	Missense_Mutation	G	A	p.P744L	111	27	0.243	0.426	4	2	2	91	signal transducer and activator of transcription 4	ENST00000392320.2
Case#3-Relapse-WholeTumor	ZNF142	2	219507517	Missense_Mutation	G	A	p.S1241L	255	68	0.267	0.467	4	2	2	181	zinc finger protein 142	ENST00000449707.1
Case#3-Relapse-WholeTumor	NYAP2	2	226446941	Missense_Mutation	G	A	p.E270K	247	62	0.251	0.439	4	2	2	177	neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adaptor 2	ENST00000272907.6
Case#3-Relapse-WholeTumor	COL4A4	2	227954646	Missense_Mutation	CC	TT	p.G466K	132	42	0.318	0.557	4	2	2	98	collagen, type IV, alpha 4	ENST00000396625.3
Case#3-Relapse-WholeTumor	C2orf83	2	228476118	Missense_Mutation	C	T	p.G149R	210	61	0.290	0.508	4	2	2	156	chromosome 2 open reading frame 83	ENST00000264387.4
Case#3-Relapse-WholeTumor	HTR2B	2	231973845	Missense_Mutation	G	A	p.P278S	400	123	0.308	0.538	4	2	2	267	5-hydroxytryptamine (serotonin) receptor 2B, G protein-coupled	ENST00000258400.3
Case#3-Relapse-WholeTumor	SAG	2	234235774	Missense_Mutation	G	A	p.G148E	174	42	0.241	0.422	4	2	2	112	S-antigen; retina and pineal gland (arrestin)	ENST00000409110.1
Case#3-Relapse-WholeTumor	KLHL30	2	239050033	Missense_Mutation	C	T	p.A213V	53	7	0.132	0.231	4	2	2	38	kelch-like family member 30	ENST00000409223.1
Case#3-Relapse-WholeTumor	ARHGAP40	20	37272501	Missense_Mutation	G	A	p.G453E	195	49	0.251	0.440	4	2	2	138	Rho GTPase activating protein 40	ENST00000373345.4
Case#3-Relapse-WholeTumor	EMILIN3	20	39989988	Missense_Mutation	C	T	p.D741N	268	77	0.287	0.503	4	2	2	177	elastin microfibril interfacer 3	ENST00000332312.3
Case#3-Relapse-WholeTumor	PTPRT	20	40727140	Missense_Mutation	G	A	p.T1256I	339	82	0.242	0.423	4	2	2	246	protein tyrosine phosphatase, receptor type, T	ENST00000373187.1
Case#3-Relapse-WholeTumor	L3MBTL1	20	42162925	Splice_Site	G	A	p.R512Q	162	41	0.253	0.443	4	2	2	147	l(3)mbt-like 1 (Drosophila)	ENST00000427442.2
Case#3-Relapse-WholeTumor	SEMG1	20	43837235	Missense_Mutation	G	A	p.G433R	246	84	0.341	0.598	4	2	2	142	semenogelin I	ENST00000372781.3
Case#3-Relapse-WholeTumor	ELMO2	20	45014770	Missense_Mutation	G	A	p.L224F	163	44	0.270	0.472	4	2	2	96	engulfment and cell motility 2	ENST00000290246.6
Case#3-Relapse-WholeTumor	OCSTAMP	20	45174451	Missense_Mutation	C	T	p.E188K	197	44	0.223	0.391	4	2	2	144	osteoclast stimulatory transmembrane protein	ENST00000279028.2
Case#3-Relapse-WholeTumor	ZNF831	20	57829425	Missense_Mutation	C	T	p.S1554L	150	44	0.293	0.513	4	2	2	96	zinc finger protein 831	ENST00000371030.2
Case#3-Relapse-WholeTumor	ADRM1	20	60882680	Missense_Mutation	CC	TT	p.P218L	153	44	0.288	0.503	4	2	2	82	adhesion regulating molecule 1	ENST00000253003.2
Case#3-Relapse-WholeTumor	TPTE	21	10906910	Missense_Mutation	C	T	p.D551N	533	41	0.077	0.154	3	2	1	360	transmembrane phosphatase with tensin homology	ENST00000361285.4
Case#3-Relapse-WholeTumor	LIPI	21	15537711	Splice_Site	C	T	p.G245E	91	20	0.220	0.385	4	2	2	65	lipase, member I	ENST00000536861.1
Case#3-Relapse-WholeTumor	LTN1	21	30365209	Missense_Mutation	G	A	p.S19F	137	28	0.204	0.358	4	2	2	113	listerin E3 ubiquitin protein ligase 1	ENST00000389195.2
Case#3-Relapse-WholeTumor	SYNJ1	21	34045776	Nonsense_Mutation	G	A	p.R534*	192	42	0.219	0.383	4	2	2	102	synaptojanin 1	ENST00000322229.7
Case#3-Relapse-WholeTumor	RRP1B	21	45113233	Missense_Mutation	G	A	p.R749K	247	78	0.316	0.553	4	2	2	175	ribosomal RNA processing 1B	ENST00000340648.4
Case#3-Relapse-WholeTumor	DNMT3L	21	45679432	Splice_Site	C	T	p.D78N	203	46	0.227	0.397	4	2	2	152	DNA (cytosine-5-)-methyltransferase 3-like	ENST00000418993.1
Case#3-Relapse-WholeTumor	KRTAP10-4	21	45993684	Missense_Mutation	C	T	p.P17S	349	93	0.266	0.466	4	2	2	317	keratin associated protein 10-4	ENST00000400374.3
Case#3-Relapse-WholeTumor	ITGB2	21	46309893	Splice_Site	C	T	p.G553R	334	88	0.263	0.461	4	2	2	276	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	ENST00000397850.2
Case#3-Relapse-WholeTumor	POTEH	22	16275210	Missense_Mutation	G	A	p.P412S	702	90	0.128	0.513	1	1	0	577	POTE ankyrin domain family, member H	ENST00000343518.6
Case#3-Relapse-WholeTumor	OR11H1	22	16449062	Missense_Mutation	CC	TT	p.G248K	564	120	0.213	0.372	4	3	1	459	olfactory receptor, family 11, subfamily H, member 1	ENST00000252835.4
Case#3-Relapse-WholeTumor	CCT8L2	22	17073167	Missense_Mutation	C	T	p.E92K	307	73	0.238	0.416	4	3	1	232	chaperonin containing TCP1, subunit 8 (theta)-like 2	ENST00000359963.3
Case#3-Relapse-WholeTumor	ZNF74	22	20760975	Missense_Mutation	C	T	p.S551F	256	77	0.301	0.526	4	3	1	190	zinc finger protein 74	ENST00000400451.2
Case#3-Relapse-WholeTumor	CCDC116	22	21989439	Missense_Mutation	T	A	p.Y363N	354	100	0.282	0.494	4	3	1	234	coiled-coil domain containing 116	ENST00000292779.3
Case#3-Relapse-WholeTumor	C22orf43	22	23959845	Splice_Site	C	T		376	106	0.282	0.493	4	2	2	260		ENST00000317749.5
Case#3-Relapse-WholeTumor	MYO18B	22	26388328	Splice_Site	GG	AA	p.E2054K	262	68	0.260	0.454	4	2	2	181	myosin XVIIIB	ENST00000407587.2
Case#3-Relapse-WholeTumor	HPS4	22	26854495	Missense_Mutation	C	T	p.E588K	103	24	0.233	0.408	4	2	2	56	Hermansky-Pudlak syndrome 4	ENST00000398145.2
Case#3-Relapse-WholeTumor	C22orf42	22	32555199	Missense_Mutation	C	T	p.G2R	150	44	0.293	0.513	4	2	2	102	chromosome 22 open reading frame 42	ENST00000382097.3
Case#3-Relapse-WholeTumor	CSF2RB	22	37328885	Missense_Mutation	G	A	p.R364Q	192	48	0.250	0.438	4	2	2	136	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	ENST00000403662.3
Case#3-Relapse-WholeTumor	MGAT3	22	39883568	Missense_Mutation	CC	AT	p.P73S	136	33	0.243	0.425	4	2	2	107	mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	ENST00000341184.6
Case#3-Relapse-WholeTumor	SCUBE1	22	43634939	Nonsense_Mutation	CC	TA	p.G250*	268	69	0.257	0.451	4	2	2	215	signal peptide, CUB domain, EGF-like 1	ENST00000360835.4
Case#3-Relapse-WholeTumor	ALG12	22	50297882	Missense_Mutation	C	A	p.V395L	444	125	0.282	0.493	4	2	2	346	ALG12, alpha-1,6-mannosyltransferase	ENST00000330817.6
Case#3-Relapse-WholeTumor	SLC22A13	3	38307716	Missense_Mutation	C	T	p.S122F	46	17	0.370	0.924	2	2	0	66	solute carrier family 22 (organic anion/urate transporter), member 13	ENST00000311856.4
Case#3-Relapse-WholeTumor	ULK4	3	41607542	Missense_Mutation	G	A	p.S1067L	191	71	0.372	0.929	2	2	0	158	unc-51 like kinase 4	ENST00000301831.4
Case#3-Relapse-WholeTumor	ELP6	3	47537655	Missense_Mutation	GG	AA	p.P235L	106	45	0.425	1.061	2	2	0	125	elongator acetyltransferase complex subunit 6	ENST00000296149.4
Case#3-Relapse-WholeTumor	TMEM89	3	48658426	Nonsense_Mutation	C	T	p.W110*	188	72	0.383	0.957	2	2	0	132	transmembrane protein 89	ENST00000330862.3
Case#3-Relapse-WholeTumor	ITIH1	3	52823792	Missense_Mutation	C	A	p.P748H	181	11	0.061	0.152	2	2	0	198	inter-alpha-trypsin inhibitor heavy chain 1	ENST00000273283.2
Case#3-Relapse-WholeTumor	ROBO1	3	78719412	Missense_Mutation	G	A	p.P461L	279	76	0.272	0.477	4	2	2	165	roundabout, axon guidance receptor, homolog 1 (Drosophila)	ENST00000464233.1
Case#3-Relapse-WholeTumor	OR5K4	3	98072744	Missense_Mutation	G	A	p.G16E	223	56	0.251	0.439	4	2	2	113	olfactory receptor, family 5, subfamily K, member 4	ENST00000354924.2
Case#3-Relapse-WholeTumor	WDR52	3	113120468	Missense_Mutation	TT	AA	p.K430L	194	51	0.263	0.460	4	2	2	123		ENST00000295868.2
Case#3-Relapse-WholeTumor	SIDT1	3	113342480	Missense_Mutation	C	T	p.S736F	120	36	0.300	0.525	4	2	2	84	SID1 transmembrane family, member 1	ENST00000264852.4

Case#3-Relapse-WholeTumor	SEMA5B	3	122629695	Missense_Mutation	C	T	p.E1097K	66	19	0.288	0.504	4	2	2	38	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5B	ENST00000357599.3
Case#3-Relapse-WholeTumor	MCM2	3	127335939	Missense_Mutation	GT	TA	p.C584L	170	37	0.218	0.381	4	2	2	114	minichromosome maintenance complex component 2	ENST00000265056.7
Case#3-Relapse-WholeTumor	PODXL2	3	127387359	Missense_Mutation	C	T	p.H428Y	169	43	0.254	0.445	4	2	2	96	podocalyxin-like 2	ENST00000342480.6
Case#3-Relapse-WholeTumor	DNAJB8	3	128181545	Missense_Mutation	C	T	p.V182M	316	84	0.266	0.465	4	2	2	231	DnaJ (Hsp40) homolog, subfamily B, member 8	ENST00000469083.1
Case#3-Relapse-WholeTumor	HMCES	3	129020881	Missense_Mutation	C	T	p.H242Y	229	76	0.332	0.581	4	2	2	173	5-hydroxymethylcytosine (hmC) binding, ES cell-specific	ENST00000383463.4
Case#3-Relapse-WholeTumor	MBD4	3	129155946	Nonsense_Mutation	G	A	p.R181*	139	42	0.302	0.529	4	2	2	89	methyl-CpG binding domain protein 4	ENST00000249910.1
Case#3-Relapse-WholeTumor	SI	3	164785192	Missense_Mutation	C	T	p.D191N	326	85	0.261	0.456	4	2	2	190	sucrase-isomaltase (alpha-glucosidase)	ENST00000264382.3
Case#3-Relapse-WholeTumor	MYNN	3	169496854	Missense_Mutation	C	T	p.P189S	242	63	0.260	0.456	4	2	2	147	myoneurin	ENST00000349841.5
Case#3-Relapse-WholeTumor	EHHADH	3	184922263	Missense_Mutation	G	A	p.P284L	249	81	0.325	0.569	4	2	2	136	enoyl-CoA, hydratase/3-hydroxyacyl CoA dehydrogenase	ENST00000231887.3
Case#3-Relapse-WholeTumor	KCTD8	4	44177097	Missense_Mutation	G	T	p.Q378K	120	58	0.483	1.208	2	2	0	123	potassium channel tetramerization domain containing 8	ENST00000360029.3
Case#3-Relapse-WholeTumor	ALB	4	74275082	Missense_Mutation	G	A	p.E15K	111	36	0.324	0.811	2	2	0	92	albumin	ENST00000503124.1
Case#3-Relapse-WholeTumor	FRAS1	4	78987156	Missense_Mutation	G	A	p.D32N	143	56	0.392	0.979	2	2	0	140	Fraser extracellular matrix complex subunit 1	ENST00000325942.6
Case#3-Relapse-WholeTumor	FAM13A	4	89950703	Missense_Mutation	C	A	p.G42V	137	54	0.394	0.985	2	2	0	120	family with sequence similarity 13, member A	ENST00000264344.5
Case#3-Relapse-WholeTumor	RP11-766F14.2	4	100570579	Missense_Mutation	G	A	p.P1743S	131	69	0.527	1.317	2	2	0	134		ENST00000511828.1
Case#3-Relapse-WholeTumor	DCHS2	4	155219419	Missense_Mutation	C	T	p.G1561D	139	69	0.496	1.241	2	2	0	150	dachsous cadherin-related 2	ENST00000357232.4
Case#3-Relapse-WholeTumor	TLR3	4	187004899	Missense_Mutation	C	T	p.P687S	133	51	0.383	0.959	2	2	0	117	toll-like receptor 3	ENST00000296795.3
Case#3-Relapse-WholeTumor	PLEKHG4B	5	163077	Missense_Mutation	G	A	p.D608N	284	65	0.229	0.401	4	2	2	218	pleckstrin homology domain containing, family G (with RhoGef domain) member 4B	ENST00000283426.6
Case#3-Relapse-WholeTumor	DROSHA	5	31508735	Missense_Mutation	G	A	p.P527L	222	56	0.252	0.441	4	2	2	163	drosha, ribonuclease type III	ENST00000511367.2
Case#3-Relapse-WholeTumor	AGXT2	5	35047922	Missense_Mutation	G	A	p.P26S	199	46	0.231	0.405	4	2	2	143	alanine--glyoxylate aminotransferase 2	ENST00000231420.6
Case#3-Relapse-WholeTumor	LMBRD2	5	36117895	Missense_Mutation	G	A	p.S415F	177	50	0.282	0.494	4	2	2	110	LMBR1 domain containing 2	ENST00000296603.4
Case#3-Relapse-WholeTumor	MROH2B	5	41009457	Missense_Mutation	CC	TT	p.G1115E	184	46	0.250	0.438	4	2	2	143	maestro heat-like repeat family member 2B	ENST00000399564.4
Case#3-Relapse-WholeTumor	AFF4	5	132223577	Missense_Mutation	G	A	p.S965F	108	48	0.444	1.111	2	2	0	103	AF4/FMR2 family, member 4	ENST00000265343.5
Case#3-Relapse-WholeTumor	PCDHB3	5	140482430	Missense_Mutation	C	T	p.P733S	293	80	0.273	0.683	2	2	0	310	protocadherin beta 3	ENST00000231130.2
Case#3-Relapse-WholeTumor	PCDHB13	5	140595625	Missense_Mutation	G	A	p.V644I	132	14	0.106	0.265	2	2	0	377	protocadherin beta 13	ENST00000341948.4
Case#3-Relapse-WholeTumor	FAT2	5	150948044	Missense_Mutation	G	A	p.P150L	112	43	0.384	0.960	2	2	0	107	FAT atypical cadherin 2	ENST00000261800.5
Case#3-Relapse-WholeTumor	BTNL9	5	180474965	Missense_Mutation	C	T	p.L50F	115	40	0.348	0.870	2	2	0	112	butyrophilin-like 9	ENST00000327705.9
Case#3-Relapse-WholeTumor	HUS1B	6	656555	Missense_Mutation	G	T	p.H130Q	17	3	0.176	0.441	2	2	0	74	HUS1 checkpoint homolog b (S. pombe)	ENST00000380907.2
Case#3-Relapse-WholeTumor	TULP1	6	35467812	Missense_Mutation	C	T	p.G481S	119	53	0.445	1.113	2	2	0	115	tubby like protein 1	ENST00000229771.6
Case#3-Relapse-WholeTumor	GLTSCR1L	6	42797699	Missense_Mutation	T	G	p.V543G	138	10	0.072	0.181	2	2	0	140	GLTSCR1-like	ENST00000314073.5
Case#3-Relapse-WholeTumor	TMEM63B	6	44117624	Missense_Mutation	C	T	p.T481I	129	50	0.388	0.969	2	2	0	130	transmembrane protein 63B	ENST00000259746.9
Case#3-Relapse-WholeTumor	NFKBIE	6	44227856	Missense_Mutation	G	A	p.S454F	163	69	0.423	1.058	2	2	0	149	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	ENST00000275015.5
Case#3-Relapse-WholeTumor	TCTE1	6	44250280	Missense_Mutation	C	T	p.R288Q	49	22	0.449	1.122	2	2	0	53	t-complex-associated-testis-expressed 1	ENST00000371505.4
Case#3-Relapse-WholeTumor	PGK2	6	49754689	Missense_Mutation	G	A	p.P71L	166	57	0.343	0.858	2	2	0	207	phosphoglycerate kinase 2	ENST00000304801.3
Case#3-Relapse-WholeTumor	FAM83B	6	54804992	Missense_Mutation	G	A	p.R408K	95	32	0.337	0.842	2	2	0	105	family with sequence similarity 83, member B	ENST00000306858.7
Case#3-Relapse-WholeTumor	COL9A1	6	70963105	Missense_Mutation	C	T	p.G583S	173	75	0.434	1.084	2	2	0	168	collagen, type IX, alpha 1	ENST00000357250.6
Case#3-Relapse-WholeTumor	IMPG1	6	76660307	Missense_Mutation	C	T	p.R599Q	143	60	0.420	1.049	2	2	0	125	interphotoreceptor matrix proteoglycan 1	ENST00000369950.3
Case#3-Relapse-WholeTumor	TRDN	6	123658781	Missense_Mutation	G	A	p.S468L	114	54	0.474	1.184	2	2	0	82	triadin	ENST00000398178.3
Case#3-Relapse-WholeTumor	ENPP1	6	132196928	Missense_Mutation	G	A	p.G550S	185	78	0.422	1.054	2	2	0	123	ectonucleotide pyrophosphatase/phosphodiesterase 1	ENST00000360971.2
Case#3-Relapse-WholeTumor	LPA	6	161020680	Missense_Mutation	C	T	p.E1047K	375	140	0.373	0.933	2	2	0	371	lipoprotein, Lp(a)	ENST00000316300.5
Case#3-Relapse-WholeTumor	LFNG	7	2552914	Nonsense_Mutation	G	A	p.W57*	269	69	0.257	0.449	4	2	2	184	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	ENST00000402506.1
Case#3-Relapse-WholeTumor	ABCA13	7	48550794	Splice_Site	GG	AA	p.G4547K	216	65	0.301	0.527	4	2	2	140	ATP-binding cassette, sub-family A (ABC1), member 13	ENST00000435803.1
Case#3-Relapse-WholeTumor	ABCA13	7	48626876	Missense_Mutation	C	T	p.L4878F	147	43	0.293	0.512	4	2	2	98	ATP-binding cassette, sub-family A (ABC1), member 13	ENST00000435803.1
Case#3-Relapse-WholeTumor	ABCA13	7	48634326	Missense_Mutation	G	A	p.M4887I	262	67	0.256	0.448	4	2	2	161	ATP-binding cassette, sub-family A (ABC1), member 13	ENST00000435803.1
Case#3-Relapse-WholeTumor	IKZF1	7	50450237	Splice_Site	G	A		215	72	0.335	0.586	4	2	2	184	IKAROS family zinc finger 1 (Ikaros)	ENST00000331340.3
Case#3-Relapse-WholeTumor	GRB10	7	50737450	Missense_Mutation	G	A	p.S158F	269	73	0.271	0.475	4	2	2	222	growth factor receptor-bound protein 10	ENST00000401949.1
Case#3-Relapse-WholeTumor	ZNF117	7	64439738	Nonsense_Mutation	G	A	p.Q71*	171	24	0.140	0.351	2	1	1	147	zinc finger protein 117	ENST00000282869.6
Case#3-Relapse-WholeTumor	LIMK1	7	73521416	Missense_Mutation	C	T	p.R320C	454	120	0.264	0.463	4	2	2	312	LIM domain kinase 1	ENST00000336180.2
Case#3-Relapse-WholeTumor	PRKRIP1	7	102040046	Missense_Mutation	G	A	p.R86H	85	26	0.306	0.535	4	3	1	67	PRKR interacting protein 1 (IL11 inducible)	ENST00000496391.1
Case#3-Relapse-WholeTumor	MET	7	116418969	Missense_Mutation	G	A	p.M1178I	241	70	0.290	0.508	4	2	2	135	MET proto-oncogene, receptor tyrosine kinase	ENST00000318493.6
Case#3-Relapse-WholeTumor	CFTR	7	117144383	Missense_Mutation	G	A	p.D44N	99	25	0.253	0.442	4	2	2	57	cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C, member 7)	ENST00000003084.6
Case#3-Relapse-WholeTumor	FLNC	7	128486089	Missense_Mutation	C	T	p.S1279F	218	71	0.326	0.570	4	2	2	144	filamin C, gamma	ENST00000325888.8
Case#3-Relapse-WholeTumor	CPA4	7	129950718	Nonsense_Mutation	CC	TT	p.Q296*	253	74	0.292	0.512	4	2	2	183	carboxypeptidase A4	ENST00000222482.4
Case#3-Relapse-WholeTumor	AGBL3	7	134800245	Missense_Mutation	G	A	p.V742I	229	67	0.293	0.512	4	2	2	119	ATP/GTP binding protein-like 3	ENST00000436302.2
Case#3-Relapse-WholeTumor	MGAM	7	141750536	Missense_Mutation	G	A	p.D893N	280	72	0.257	0.450	4	2	2	199	maltase-glucoamylase (alpha-glucosidase)	ENST00000549489.2
Case#3-Relapse-WholeTumor	MGAM	7	141754666	Missense_Mutation	C	T	p.P1091L	367	113	0.308	0.539	4	2	2	293	maltase-glucoamylase (alpha-glucosidase)	ENST00000549489.2
Case#3-Relapse-WholeTumor	RP11-1220K2.2	7	141884914	Missense_Mutation	C	T	p.S1321F	191	48	0.251	0.440	4	2	2	136		ENST00000477922.3
Case#3-Relapse-WholeTumor	KEL	7	142655488	Missense_Mutation	G	A	p.S143F	174	45	0.259	0.517	3	2	1	111	Kell blood group, metallo-endopeptidase	ENST00000355265.2
Case#3-Relapse-WholeTumor	RP1L1	8	10469030	Missense_Mutation	G	A	p.R860W	54	5	0.093	0.231	2	2	0	84	retinitis pigmentosa 1-like 1	ENST00000382483.3
Case#3-Relapse-WholeTumor	TACC1	8	38677979	Missense_Mutation	C	T	p.S406F	158	67	0.424	1.060	2	2	0	168	transforming, acidic coiled-coil containing protein 1	ENST00000317827.4
Case#3-Relapse-WholeTumor	RP1	8	55533815	Missense_Mutation	G	A	p.E97K	138	45	0.326	0.815	2	2	0	136	retinitis pigmentosa 1 (autosomal dominant)	ENST00000220676.1
Case#3-Relapse-WholeTumor	PREX2	8	68968209	Splice_Site	G	A	p.S413N	194	87	0.448	1.121	2	2	0	173	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2	ENST00000288368.4
Case#3-Relapse-WholeTumor	POP1	8	99135603	Missense_Mutation	T	A	p.M13K	148	63	0.426	1.064	2	2	0	146	processing of precursor 1, ribonuclease P/MRP subunit (S. cerevisiae)	ENST00000401707.2
Case#3-Relapse-WholeTumor	NFIB	9	14179774	Missense_Mutation	C	T	p.G190R	84	37	0.440	1.101	2	2	0	70	nuclear factor I/B	ENST00000380959.3
Case#3-Relapse-WholeTumor	VPS13A	9	79938016	Missense_Mutation	C	T	p.P1955L	192	78	0.406	1.016	2	2	0	141	vacuolar protein sorting 13 homolog A (S. cerevisiae)	ENST00000360280.3
Case#3-Relapse-WholeTumor	NXNL2	9	91159394	Missense_Mutation	G	A	p.E135K	92	30	0.326	0.815	2	2	0	92	nucleoredoxin-like 2	ENST00000375854.3
Case#3-Relapse-WholeTumor	CYLC2	9	105767601	Missense_Mutation	T	A	p.S230T	144	8	0.056	0.139	2	2	0	162	cylicin, basic protein of sperm head cytoskeleton 2	ENST00000374798.3
Case#3-Relapse-WholeTumor	OR13C2	9	107367788	Missense_Mutation	C	T	p.G41R	440	115	0.261	0.653	2	2	0	447	olfactory receptor, family 13, subfamily C, member 2	ENST00000542196.1
Case#3-Relapse-WholeTumor	PAPPA	9	118949983	Missense_Mutation	GG	TC	p.E323Q	127	52	0.409	1.024	2	2	0	156	pregnancy-associated plasma protein A, pappalysin 1	ENST00000328252.3
Case#3-Relapse-WholeTumor	OR1Q1	9	125377645	Missense_Mutation	C	T	p.A210V	199	84	0.422	1.055	2	2	0	151	olfactory receptor, family 1, subfamily Q, member 1	ENST00000297913.2
Case#3-Relapse-WholeTumor	PNPLA7	9	140409917	Missense_Mutation	G	A	p.S355F	173	85	0.491	1.228	2	2	0	139	patatin-like phospholipase domain containing 7	ENST00000277531.4
Case#3-Relapse-WholeTumor	ARSF	X	3007595	Missense_Mutation	C	T	p.P297S	173	93	0.538	1.075	3	3	0	95	arylsulfatase F	ENST00000381127.1
Case#3-Relapse-WholeTumor	CYBB	X	37663372	Nonsense_Mutation	G	A	p.W380*	174	101	0.580	1.016	4	4	0	93	cytochrome b-245, beta polypeptide	ENST00000378588.4
Case#3-Relapse-WholeTumor	HEPH	X	65474933	Missense_Mutation	G	A	p.D874N	64	32	0.500	0.875	4	3	1	41	hephaestin	ENST00000343002.2
Case#3-Relapse-WholeTumor	BHLHB9	X	102004491	Missense_Mutation	C	T	p.P190S	228	116	0.509	0.890	4	3	1	150	basic helix-loop-helix domain containing, class B, 9	ENST00000372735.1
Case#3-Relapse-WholeTumor	NRK	X	105187944	Missense_Mutation	G	A	p.E1324K	105	56	0.533	0.933	4	3	1	66	Nik related kinase	ENST00000243300.9
Case#3-Relapse-WholeTumor	KCNE1L	X	108868108	Missense_Mutation	C	T	p.G48S	42	23	0.548	0.958	4	3	1	50	KCNE1-like	ENST00000372101.2
Case#3-Relapse-WholeTumor	TENM1	X	123637409	Splice_Site	CC	TT	p.G1149K	139	82	0.590	1.032	4	3	1	93	teneurin transmembrane protein 1	ENST00000371130.3
Case#3-Relapse-WholeTumor	ARHGAP36	X	130218204	Missense_Mutation	G	A	p.D191N	90	53	0.589	1.031	4	3	1	48	Rho GTPase activating protein 36	ENST00000276211.5

Case#3-Relapse-WholeTumor	GPC4	X	132458528	Missense_Mutation	G	A	p.S119F	26	12	0.462	0.808	4	3	1	21	glypican 4	ENST00000370828.3
Case#3-Relapse-WholeTumor	PASD1	X	150832597	Missense_Mutation	C	T	p.S283F	93	42	0.452	0.903	3	2	1	74	PAS domain containing 1	ENST00000370357.4
Case#3-Relapse-WholeTumor	PLXNA3	X	153689479	Missense_Mutation	C	T	p.P212L	129	77	0.597	1.194	3	2	1	98	plexin A3	ENST00000369682.3
Case#3-Relapse-WholeTumor	F8	X	154065973	Missense_Mutation	G	A	p.P2319S	184	98	0.533	1.065	3	2	1	142	coagulation factor VIII, procoagulant component	ENST00000360256.4
Case#3-Baseline-M437	ATAD3B	1	1431165	Missense_Mutation	C	T	p.P639S	132	13	0.098	0.102	3	2	1	132	ATPase family, AAA domain containing 3B	ENST00000308647.7
Case#3-Baseline-M437	TTC34	1	2704108	Missense_Mutation	G	A	p.P85S	88	25	0.284	0.294	3	2	1	113	tetratricopeptide repeat domain 34	ENST00000401095.3
Case#3-Baseline-M437	WRAP73	1	3548848	Missense_Mutation	C	T	p.R326K	185	121	0.654	0.677	3	2	1	201	WD repeat containing, antisense to TP73	ENST00000270708.7
Case#3-Baseline-M437	GPR153	1	6311591	Splice_Site	C	A		42	25	0.595	0.616	3	2	1	87	G protein-coupled receptor 153	ENST00000377893.2
Case#3-Baseline-M437	CLSTN1	1	9809822	Splice_Site	C	A	p.G267*	205	59	0.288	0.298	3	2	1	169	calsyntenin 1	ENST00000377298.4
Case#3-Baseline-M437	PRAMEF17	1	13718514	Missense_Mutation	A	G	p.H326R	181	12	0.066	0.069	3	2	1	185	PRAME family member 17	ENST00000376098.4
Case#3-Baseline-M437	SPEN	1	16263724	Frame_Shift_Ins	-	CTGCA	p.-3366fs	75	31	0.413	0.428	3	2	1	95	spen family transcriptional repressor	ENST00000375759.3
Case#3-Baseline-M437	CROCC	1	17292248	Missense_Mutation	CC	TT	p.T1479I	105	29	0.276	0.286	3	2	1	130	ciliary rootlet coiled-coil, rootletin	ENST00000375541.5
Case#3-Baseline-M437	PADI3	1	17601157	Missense_Mutation	G	A	p.E395K	165	106	0.642	0.665	3	2	1	207	peptidyl arginine deiminase, type III	ENST00000375460.3
Case#3-Baseline-M437	TAS1R2	1	19180962	Missense_Mutation	GC	TT	p.G334E	114	9	0.079	0.082	3	2	1	148	taste receptor, type 1, member 2	ENST00000375371.3
Case#3-Baseline-M437	CELA3A	1	22333956	Missense_Mutation	C	T	p.T197I	168	102	0.607	0.628	3	2	1	141	chymotrypsin-like elastase family, member 3A	ENST00000290122.3
Case#3-Baseline-M437	MYOM3	1	24384118	Splice_Site	C	T		161	100	0.621	0.643	3	2	1	178	myomesin 3	ENST00000374434.3
Case#3-Baseline-M437	MATN1	1	31189129	Missense_Mutation	GA	AT	p.F278Y	80	22	0.275	0.285	3	2	1	125	matrilin 1, cartilage matrix protein	ENST00000373765.4
Case#3-Baseline-M437	LCK	1	32741652	Missense_Mutation	C	T	p.R207C	146	41	0.281	0.291	3	2	1	127	LCK proto-oncogene, Src family tyrosine kinase	ENST00000336890.5
Case#3-Baseline-M437	ADC	1	33583660	Missense_Mutation	C	T	p.S396F	138	41	0.297	0.308	3	2	1	191		ENST00000294517.6
Case#3-Baseline-M437	COL8A2	1	36564404	Missense_Mutation	C	T	p.G293D	58	20	0.345	0.357	3	2	1	66	collagen, type VIII, alpha 2	ENST00000397799.1
Case#3-Baseline-M437	CSF3R	1	36932118	Missense_Mutation	G	A	p.P784L	97	26	0.268	0.277	3	2	1	109	colony stimulating factor 3 receptor (granulocyte)	ENST00000373106.1
Case#3-Baseline-M437	COL9A2	1	40777362	Missense_Mutation	G	A	p.S148L	102	33	0.324	0.335	3	2	1	113	collagen, type IX, alpha 2	ENST00000372748.3
Case#3-Baseline-M437	DPH2	1	44437416	Missense_Mutation	C	T	p.A281V	119	44	0.370	0.383	3	2	1	95	DPH2 homolog (S. cerevisiae)	ENST00000255108.3
Case#3-Baseline-M437	C1orf173	1	75078442	Missense_Mutation	G	A	p.T351I	117	73	0.624	0.646	3	2	1	183		ENST00000326665.5
Case#3-Baseline-M437	COL11A1	1	103345336	Missense_Mutation	C	T	p.G1726E	133	82	0.617	0.638	3	2	1	205	collagen, type XI, alpha 1	ENST00000370096.3
Case#3-Baseline-M437	COL11A1	1	103467995	Missense_Mutation	G	A	p.P696S	104	31	0.298	0.309	3	2	1	91	collagen, type XI, alpha 1	ENST00000370096.3
Case#3-Baseline-M437	GNAI3	1	110128916	Missense_Mutation	C	A	p.F223L	145	46	0.317	0.328	3	2	1	165	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3	ENST00000369851.4
Case#3-Baseline-M437	GNAT2	1	110148621	Missense_Mutation	C	T	p.D231N	156	38	0.244	0.252	3	2	1	142	guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 2	ENST00000351050.3
Case#3-Baseline-M437	KCND3	1	112319738	Missense_Mutation	T	A	p.N559I	186	61	0.328	0.339	3	2	1	258	potassium voltage-gated channel, Shal-related subfamily, member 3	ENST00000315987.2
Case#3-Baseline-M437	NRAS	1	115256530	Missense_Mutation	G	T	p.Q61K	107	63	0.589	0.609	3	2	1	113	neuroblastoma RAS viral (v-ras) oncogene homolog	ENST00000369535.4
Case#3-Baseline-M437	TRIM45	1	117659298	Missense_Mutation	A	G	p.I431T	116	15	0.129	0.134	3	2	1	104	tripartite motif containing 45	ENST00000256649.4
Case#3-Baseline-M437	KPRP	1	152732182	Missense_Mutation	C	T	p.P40S	160	51	0.319	0.330	3	2	1	234	keratinocyte proline-rich protein	ENST00000606109.1
Case#3-Baseline-M437	SPRR2E	1	153066106	Missense_Mutation	C	A	p.C41F	205	47	0.229	0.237	3	2	1	277	small proline-rich protein 2E	ENST00000368751.1
Case#3-Baseline-M437	INSRR	1	156812030	Missense_Mutation	C	T	p.E1091K	84	47	0.560	0.579	3	2	1	133	insulin receptor-related receptor	ENST00000368195.3
Case#3-Baseline-M437	MNDA	1	158813785	Missense_Mutation	G	A	p.R148K	111	71	0.640	0.662	3	2	1	154	myeloid cell nuclear differentiation antigen	ENST00000368141.4
Case#3-Baseline-M437	CCDC19	1	159842813	Missense_Mutation	C	T	p.G500S	105	28	0.267	0.276	3	2	1	90		ENST00000368099.4
Case#3-Baseline-M437	SLAMF7	1	160719693	Missense_Mutation	G	A	p.M153I	110	65	0.591	0.612	3	2	1	164	SLAM family member 7	ENST00000368043.3
Case#3-Baseline-M437	CD244	1	160801172	Missense_Mutation	G	A	p.R360C	101	32	0.317	0.328	3	2	1	108	CD244 molecule, natural killer cell receptor 2B4	ENST00000368033.3
Case#3-Baseline-M437	HSPA6	1	161495026	Missense_Mutation	G	A	p.G193E	94	19	0.202	0.209	3	2	1	208	heat shock 70kDa protein 6 (HSP70B')	ENST00000309758.4
Case#3-Baseline-M437	DPT	1	168665821	Missense_Mutation	A	C	p.M191R	238	75	0.315	0.326	3	2	1	215	dermatopontin	ENST00000367817.3
Case#3-Baseline-M437	BLZF1	1	169345963	Nonsense_Mutation	A	T	p.K72*	103	13	0.126	0.131	3	2	1	169	basic leucine zipper nuclear factor 1	ENST00000367808.3
Case#3-Baseline-M437	F5	1	169515815	Missense_Mutation	C	T	p.E543K	120	72	0.600	0.621	3	2	1	170	coagulation factor V (proaccelerin, labile factor)	ENST00000367797.3
Case#3-Baseline-M437	FMO1	1	171236697	Missense_Mutation	G	A	p.G50S	137	86	0.628	0.650	3	2	1	159	flavin containing monooxygenase 1	ENST00000354841.4
Case#3-Baseline-M437	MYOC	1	171621173	Missense_Mutation	CC	TT	p.R193Q	76	16	0.211	0.218	3	2	1	70	myocilin, trabecular meshwork inducible glucocorticoid response	ENST00000037502.6
Case#3-Baseline-M437	TNN	1	175067690	Missense_Mutation	G	A	p.G693E	178	66	0.371	0.384	3	2	1	284	tenascin N	ENST00000239462.4
Case#3-Baseline-M437	RASAL2	1	178411936	Nonsense_Mutation	A	T	p.K204*	175	53	0.303	0.313	3	2	1	153	RAS protein activator like 2	ENST00000462775.1
Case#3-Baseline-M437	KIF14	1	200587142	Missense_Mutation	G	A	p.T237M	134	42	0.313	0.324	3	2	1	91	kinesin family member 14	ENST00000367350.4
Case#3-Baseline-M437	KIF14	1	200587679	Missense_Mutation	C	T	p.G58D	135	11	0.081	0.084	3	2	1	100	kinesin family member 14	ENST00000367350.4
Case#3-Baseline-M437	CACNA1S	1	201029884	Missense_Mutation	G	A	p.P1106S	176	56	0.318	0.329	3	2	1	179	calcium channel, voltage-dependent, L type, alpha 1S subunit	ENST00000362061.3
Case#3-Baseline-M437	IGFN1	1	201196190	Missense_Mutation	G	A	p.G3656E	133	81	0.609	0.630	3	2	1	244	immunoglobulin-like and fibronectin type III domain containing 1	ENST00000335211.4
Case#3-Baseline-M437	CHI3L1	1	203152860	Missense_Mutation	G	A	p.P125L	209	62	0.297	0.307	3	2	1	264	chitinase 3-like 1 (cartilage glycoprotein-39)	ENST00000255409.3
Case#3-Baseline-M437	C1orf116	1	207196283	Missense_Mutation	C	T	p.E276K	108	60	0.556	0.575	3	2	1	89	chromosome 1 open reading frame 116	ENST00000359470.5
Case#3-Baseline-M437	HHIPL2	1	222717003	Missense_Mutation	G	A	p.R284C	114	35	0.307	0.318	3	2	1	106	HHIP-like 2	ENST00000343410.6
Case#3-Baseline-M437	HHIPL2	1	222717359	Missense_Mutation	C	T	p.G165D	122	78	0.639	0.662	3	2	1	190	HHIP-like 2	ENST00000343410.6
Case#3-Baseline-M437	ITPKB	1	226835055	Missense_Mutation	T	C	p.R687G	113	39	0.345	0.357	3	2	1	191	inositol-trisphosphate 3-kinase B	ENST00000272117.3
Case#3-Baseline-M437	CDC42BPA	1	227181974	Missense_Mutation	G	A	p.P1719S	78	51	0.654	0.677	3	2	1	107	CDC42 binding protein kinase alpha (DMPK-like)	ENST00000366769.3
Case#3-Baseline-M437	OBSCN	1	228412227	Missense_Mutation	TG	CA	p.A908T	149	13	0.087	0.090	3	2	1	342	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	ENST00000422127.1
Case#3-Baseline-M437	OBSCN	1	228481143	Missense_Mutation	G	C	p.A3653P	132	29	0.220	0.227	3	2	1	166	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	ENST00000422127.1
Case#3-Baseline-M437	OBSCN	1	228509823	Missense_Mutation	G	A	p.G5094E	100	63	0.630	0.652	3	2	1	90	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	ENST00000422127.1
Case#3-Baseline-M437	TTC13	1	231042719	Missense_Mutation	G	A	p.P839S	173	52	0.301	0.311	3	2	1	192	tetratricopeptide repeat domain 13	ENST00000366661.4
Case#3-Baseline-M437	ACTN2	1	236917278	Missense_Mutation	C	T	p.S624F	97	24	0.247	0.256	3	2	1	115	actinin, alpha 2	ENST00000366578.4
Case#3-Baseline-M437	FMN2	1	240371804	Missense_Mutation	G	A	p.G1231E	77	37	0.481	0.497	3	2	1	82	formin 2	ENST00000319653.9
Case#3-Baseline-M437	NLRP3	1	247588522	Missense_Mutation	G	A	p.E593K	143	40	0.280	0.290	3	2	1	135	NLR family, pyrin domain containing 3	ENST00000336119.3
Case#3-Baseline-M437	OR2G2	1	247752288	Missense_Mutation	CC	TT	p.L210F	178	55	0.309	NA	NA	NA	NA	232	olfactory receptor, family 2, subfamily G, member 2	ENST00000320065.1
Case#3-Baseline-M437	OR14A2	1	247887074	Missense_Mutation	G	A	p.S91F	216	140	0.648	0.671	3	2	1	332	olfactory receptor, family 14, subfamily A, member 2	ENST00000366485.1
Case#3-Baseline-M437	C10orf68	10	33136793	Missense_Mutation	G	A	p.G443S	123	118	0.959	1.010	2	2	0	227		ENST00000375030.2
Case#3-Baseline-M437	NRP1	10	33475282	Missense_Mutation	C	T	p.V733I	82	5	0.061	0.064	2	2	0	153	neuropilin 1	ENST00000265371.4
Case#3-Baseline-M437	NRP1	10	33502507	Missense_Mutation	G	A	p.P474L	144	136	0.944	0.994	2	2	0	289	neuropilin 1	ENST00000265371.4
Case#3-Baseline-M437	OR13A1	10	45799119	Missense_Mutation	C	T	p.G251E	53	50	0.943	0.993	2	2	0	86	olfactory receptor, family 13, subfamily A, member 1	ENST00000553795.1
Case#3-Baseline-M437	ALOX5	10	45907693	Missense_Mutation	GG	AA	p.D163N	127	122	0.961	1.011	2	2	0	187	arachidonate 5-lipoxygenase	ENST00000374391.2
Case#3-Baseline-M437	FAM21C	10	46235637	Missense_Mutation	CT	TA	p.S158T	264	145	0.549	0.578	2	2	0	490	family with sequence similarity 21, member C	ENST00000336378.4
Case#3-Baseline-M437	COL13A1	10	71697406	Missense_Mutation	G	A	p.D594N	63	60	0.952	1.003	2	2	0	187	collagen, type XIII, alpha 1	ENST00000398978.3
Case#3-Baseline-M437	SPOCK2	10	73826708	Missense_Mutation	C	T	p.D294N	117	107	0.915	0.963	2	2	0	123	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	ENST00000373109.2
Case#3-Baseline-M437	DLG5	10	79584164	Missense_Mutation	G	A	p.S787F	79	78	0.987	1.039	2	2	0	34	discs, large homolog 5 (Drosophila)	ENST00000372391.2
Case#3-Baseline-M437	GRID1	10	87487637	Missense_Mutation	C	T	p.G503E	67	66	0.985	1.037	2	2	0	73	glutamate receptor, ionotropic, delta 1	ENST00000327946.7
Case#3-Baseline-M437	FAM25A	10	88780148	Missense_Mutation	G	A	p.G23R	172	155	0.901	0.949	2	2	0	513	family with sequence similarity 25, member A	ENST00000343959.4
Case#3-Baseline-M437	CEP55	10	95259816	Missense_Mutation	C	T	p.S3F	75	71	0.947	0.996	2	2	0	122	centrosomal protein 55kDa	ENST00000371485.3
Case#3-Baseline-M437	ENTPD1	10	97604267	Missense_Mutation	G	A	p.D150N	96	92	0.958	1.009	2	2	0	173	ectonucleoside triphosphate diphosphohydrolase 1	ENST00000371205.4
Case#3-Baseline-M437	PDZD7	10	102783697	Missense_Mutation	C	T	p.G119S	70	27	0.386	0.406	2	2	0	98	PDZ domain containing 7	ENST00000370215.3
Case#3-Baseline-M437	GSTO2	10	106039185	Missense_Mutation	A	G	p.N142D	90	6	0.067	0.070	2	2	0	125	glutathione S-transferase omega 2	ENST00000338595.2
Case#3-Baseline-M437	SORCS3	10	106960963	Missense_Mutation	G	A	p.G738E	118	108	0.915	0.963	2	2	0	164	sortilin-related VPS10 domain containing receptor 3	ENST00000369701.3

Case#3-Baseline-M437	DMBT1	10	124377802	Missense_Mutation	G	A	p.G1592S	237	214	0.903	0.950	2	2	0	474	deleted in malignant brain tumors 1	ENST00000338354.3
Case#3-Baseline-M437	OR52E6	11	5862653	Missense_Mutation	T	C	p.I159V	122	7	0.057	0.060	2	2	0	213	olfactory receptor, family 52, subfamily E, member 6	ENST00000329322.5
Case#3-Baseline-M437	OR52E8	11	5878793	Missense_Mutation	C	T	p.G47E	82	77	0.939	0.988	2	2	0	228	olfactory receptor, family 52, subfamily E, member 8	ENST00000537935.1
Case#3-Baseline-M437	ZNF214	11	7022717	Missense_Mutation	T	C	p.Y66C	71	4	0.056	0.059	2	2	0	103	zinc finger protein 214	ENST00000278314.4
Case#3-Baseline-M437	OR4C11	11	55371179	Missense_Mutation	C	T	p.R224K	91	88	0.967	1.018	2	2	0	140	olfactory receptor, family 4, subfamily C, member 11	ENST00000302231.4
Case#3-Baseline-M437	OR8K5	11	55926983	Missense_Mutation	C	T	p.D271N	78	75	0.962	1.012	2	2	0	117	olfactory receptor, family 8, subfamily K, member 5	ENST00000313447.1
Case#3-Baseline-M437	OR5J2	11	55944743	Missense_Mutation	C	T	p.S217F	123	112	0.911	0.958	2	2	0	243	olfactory receptor, family 5, subfamily J, member 2	ENST00000312298.1
Case#3-Baseline-M437	PLCB3	11	64034876	Nonsense_Mutation	C	T	p.Q1185*	39	36	0.923	0.972	2	2	0	94	phospholipase C, beta 3 (phosphatidylinositol-specific)	ENST00000540288.1
Case#3-Baseline-M437	SPTBN2	11	66461656	Missense_Mutation	G	T	p.A1486D	60	5	0.083	0.088	2	2	0	85	spectrin, beta, non-erythrocytic 2	ENST00000533211.1
Case#3-Baseline-M437	SHANK2	11	70333304	Missense_Mutation	G	A	p.P653S	96	88	0.917	0.965	2	2	0	174	SH3 and multiple ankyrin repeat domains 2	ENST00000423696.2
Case#3-Baseline-M437	LRRC32	11	76371798	Missense_Mutation	GG	AA	p.P280F	93	85	0.914	0.962	2	2	0	163	leucine rich repeat containing 32	ENST00000407242.2
Case#3-Baseline-M437	TENM4	11	78423682	Missense_Mutation	C	T	p.R1300Q	114	64	0.561	0.591	2	2	0	155	teneurin transmembrane protein 4	ENST00000278550.7
Case#3-Baseline-M437	OR8B3	11	124266391	Missense_Mutation	G	A	p.P286L	82	78	0.951	1.001	2	2	0	134	olfactory receptor, family 8, subfamily B, member 3	ENST00000354597.3
Case#3-Baseline-M437	IGSF9B	11	133800880	Splice_Site	G	A	p.I506I	71	4	0.056	0.059	2	2	0	83	immunoglobulin superfamily, member 9B	ENST00000321016.8
Case#3-Baseline-M437	CACNA1C	12	2797799	Missense_Mutation	C	T	p.H2039Y	144	130	0.903	0.950	2	2	0	262	calcium channel, voltage-dependent, L type, alpha 1C subunit	ENST00000347598.4
Case#3-Baseline-M437	PRB4	12	11461549	Missense_Mutation	G	C	p.P123R	73	13	0.178	0.187	2	2	0	56	proline-rich protein BstNI subfamily 4	ENST00000535904.1
Case#3-Baseline-M437	PRB4	12	11461570	Missense_Mutation	G	T	p.P116H	80	35	0.438	0.461	2	2	0	65	proline-rich protein BstNI subfamily 4	ENST00000535904.1
Case#3-Baseline-M437	PRB4	12	11461706	Missense_Mutation	G	T	p.P71T	133	31	0.233	0.245	2	2	0	45	proline-rich protein BstNI subfamily 4	ENST00000535904.1
Case#3-Baseline-M437	GRIN2B	12	13717537	Missense_Mutation	C	T	p.E879K	73	69	0.945	0.995	2	2	0	99	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	ENST00000609686.1
Case#3-Baseline-M437	TMTC1	12	29904620	Missense_Mutation	C	T	p.R306Q	58	49	0.845	0.889	2	2	0	157	transmembrane and tetratricopeptide repeat containing 1	ENST00000539277.1
Case#3-Baseline-M437	ARID2	12	46243857	Nonsense_Mutation	C	T	p.Q651*	52	51	0.981	1.032	2	2	0	102	AT rich interactive domain 2 (ARID, RFX-like)	ENST00000334344.6
Case#3-Baseline-M437	OR10AD1	12	48596927	Missense_Mutation	G	A	p.S50F	124	111	0.895	0.942	2	2	0	212	olfactory receptor, family 10, subfamily AD, member 1	ENST00000310248.2
Case#3-Baseline-M437	C12orf54	12	48888594	Missense_Mutation	C	T	p.P86S	105	6	0.057	0.060	2	2	0	135	chromosome 12 open reading frame 54	ENST00000548364.1
Case#3-Baseline-M437	OR8S1	12	48919796	Missense_Mutation	C	T	p.R128C	131	13	0.099	0.104	2	2	0	138	olfactory receptor, family 8, subfamily S, member 1	ENST00000310194.1
Case#3-Baseline-M437	TUBA1B	12	49523385	Missense_Mutation	T	C	p.I42V	150	27	0.180	0.189	2	2	0	316	tubulin, alpha 1b	ENST00000336023.5
Case#3-Baseline-M437	FAM186A	12	50745821	Missense_Mutation	TT	AG	p.E1598A	172	11	0.064	0.066	4	3	1	246	family with sequence similarity 186, member A	ENST00000327337.5
Case#3-Baseline-M437	GALNT6	12	51758017	Nonsense_Mutation	GG	AA	p.Q313*	113	107	0.947	0.997	2	2	0	202	polypeptide N-acetylgalactosaminyltransferase 6	ENST00000543196.2
Case#3-Baseline-M437	KRT72	12	52992812	Missense_Mutation	T	C	p.N171D	101	8	0.079	0.083	2	2	0	155	keratin 72	ENST00000537672.2
Case#3-Baseline-M437	ORMDL2	12	56214160	Missense_Mutation	T	C	p.F148S	76	74	0.974	1.025	2	2	0	54	ORMDL sphingolipid biosynthesis regulator 2	ENST00000243045.5
Case#3-Baseline-M437	HELB	12	66731841	Missense_Mutation	C	T	p.P1075S	53	53	1.000	1.053	2	2	0	62	helicase (DNA) B	ENST00000247815.4
Case#3-Baseline-M437	MDM1	12	68707287	Missense_Mutation	G	A	p.P552L	87	5	0.057	0.060	2	2	0	102	Mdm1 nuclear protein homolog (mouse)	ENST00000303145.7
Case#3-Baseline-M437	C12orf42	12	103696182	Missense_Mutation	T	G	p.S263R	58	7	0.121	0.127	2	2	0	145	chromosome 12 open reading frame 42	ENST00000378113.2
Case#3-Baseline-M437	STAB2	12	104054483	Missense_Mutation	C	T	p.S604F	80	76	0.950	1.000	2	2	0	132	stabilin 2	ENST00000388887.2
Case#3-Baseline-M437	STAB2	12	104118771	Missense_Mutation	G	A	p.E1568K	65	62	0.954	1.004	2	2	0	110	stabilin 2	ENST00000388887.2
Case#3-Baseline-M437	MVK	12	110013879	Missense_Mutation	G	A	p.S52N	114	7	0.061	0.065	2	2	0	168	mevalonate kinase	ENST00000228510.3
Case#3-Baseline-M437	HNF1A	12	121434359	Missense_Mutation	G	C	p.G375R	93	7	0.075	0.079	2	2	0	143	HNF1 homeobox A	ENST00000257555.6
Case#3-Baseline-M437	PARP4	13	25009317	Missense_Mutation	GG	AA	p.P1321L	213	106	0.498	0.511	4	2	2	183	poly (ADP-ribose) polymerase family, member 4	ENST00000381989.3
Case#3-Baseline-M437	SLC46A3	13	29278221	Missense_Mutation	C	T	p.C387Y	117	31	0.265	0.272	4	2	2	156	solute carrier family 46, member 3	ENST00000266943.6
Case#3-Baseline-M437	FREM2	13	39262018	Missense_Mutation	GG	AA	p.E180K	204	99	0.485	0.498	4	2	2	277	FRAS1 related extracellular matrix protein 2	ENST00000280481.7
Case#3-Baseline-M437	MED4	13	48664557	Splice_Site	A	-		154	16	0.104	0.107	4	2	2	139	mediator complex subunit 4	ENST00000258648.2
Case#3-Baseline-M437	LMO7	13	76287354	Nonsense_Mutation	C	T	p.R88*	262	152	0.580	0.595	4	2	2	265	LIM domain 7	ENST00000341547.4
Case#3-Baseline-M437	CLYBL	13	100425124	Missense_Mutation	T	G	p.S37A	215	95	0.442	0.453	4	2	2	182	citrate lyase beta like	ENST00000376360.1
Case#3-Baseline-M437	ITGBL1	13	102367919	Missense_Mutation	G	A	p.G467E	162	63	0.389	0.399	4	2	2	80	integrin, beta-like 1 (with EGF-like repeat domains)	ENST00000376180.3
Case#3-Baseline-M437	F7	13	113772987	Missense_Mutation	G	A	p.E356K	185	82	0.443	0.455	4	2	2	233	coagulation factor VII (serum prothrombin conversion accelerator)	ENST00000375581.3
Case#3-Baseline-M437	CHAMP1	13	115090674	Missense_Mutation	CC	TT	p.P453F	113	54	0.478	NA	NA	NA	NA	154	chromosome alignment maintaining phosphoprotein 1	ENST00000361283.1
Case#3-Baseline-M437	POTEG	14	19574200	Missense_Mutation	G	A	p.M419I	647	84	0.130	0.137	2	1	1	1335	POTE ankyrin domain family, member G	ENST00000409832.3
Case#3-Baseline-M437	OR4Q3	14	20215708	Missense_Mutation	G	A	p.G41E	326	59	0.181	0.191	2	1	1	356	olfactory receptor, family 4, subfamily Q, member 3	ENST00000331723.1
Case#3-Baseline-M437	OR4M1	14	20248980	Missense_Mutation	C	T	p.P167S	494	74	0.150	0.158	2	1	1	802	olfactory receptor, family 4, subfamily M, member 1	ENST00000315957.4
Case#3-Baseline-M437	OR4K2	14	20344897	Missense_Mutation	G	A	p.M157I	313	45	0.144	0.151	2	1	1	463	olfactory receptor, family 4, subfamily K, member 2	ENST00000298642.2
Case#3-Baseline-M437	RNASE6	14	21250124	Missense_Mutation	G	A	p.R89Q	110	7	0.064	0.067	2	1	1	161	ribonuclease, RNase A family, k6	ENST00000304677.2
Case#3-Baseline-M437	OR5AU1	14	21623343	Missense_Mutation	G	A	p.S281L	125	59	0.472	0.497	2	1	1	201	olfactory receptor, family 5, subfamily AU, member 1	ENST00000304418.3
Case#3-Baseline-M437	ZFHX2	14	23994870	Missense_Mutation	GG	AA	p.P1427L	31	13	0.419	0.441	2	1	1	52	zinc finger homeobox 2	ENST00000419474.3
Case#3-Baseline-M437	DHRS2	14	24109099	Missense_Mutation	G	A	p.D139N	52	16	0.308	0.324	2	1	1	64	dehydrogenase/reductase (SDR family) member 2	ENST00000250383.6
Case#3-Baseline-M437	DHRS4-AS1	14	24408806	Missense_Mutation	G	A	p.E25K	48	20	0.417	0.439	2	1	1	55	DHRS4 antisense RNA 1	ENST00000354854.1
Case#3-Baseline-M437	IPO4	14	24655161	Nonsense_Mutation	C	A	p.E359*	71	29	0.408	0.430	2	1	1	132	importin 4	ENST00000354464.6
Case#3-Baseline-M437	RTN1	14	60193697	Missense_Mutation	C	T	p.G569S	82	41	0.500	0.526	2	1	1	133	reticulon 1	ENST00000267484.5
Case#3-Baseline-M437	SYNE2	14	64465727	Missense_Mutation	C	T	p.S1150F	65	29	0.446	0.470	2	1	1	122	spectrin repeat containing, nuclear envelope 2	ENST00000344113.4
Case#3-Baseline-M437	PAPLN	14	73716803	Missense_Mutation	G	A	p.C149Y	107	43	0.402	0.423	2	1	1	143	papilin, proteoglycan-like sulfated glycoprotein	ENST00000554301.1
Case#3-Baseline-M437	CCDC88C	14	91792319	Missense_Mutation	C	T	p.D378N	71	36	0.507	0.534	2	1	1	76	coiled-coil domain containing 88C	ENST00000389857.6
Case#3-Baseline-M437	FBLN5	14	92403347	Missense_Mutation	G	A	p.S108F	99	49	0.495	0.521	2	1	1	161	fibulin 5	ENST00000342058.4
Case#3-Baseline-M437	SLC25A47	14	100795139	Missense_Mutation	G	T	p.R135L	97	11	0.113	0.119	2	1	1	262	solute carrier family 25, member 47	ENST00000361529.3
Case#3-Baseline-M437	EIF5	14	103806121	Missense_Mutation	T	C	p.I351T	121	58	0.479	0.505	2	1	1	189	eukaryotic translation initiation factor 5	ENST00000216554.3
Case#3-Baseline-M437	AHNAK2	14	105409228	Missense_Mutation	G	A	p.S4187F	146	70	0.479	0.505	2	1	1	239	AHNAK nucleoprotein 2	ENST00000333244.5
Case#3-Baseline-M437	AHNAK2	14	105420164	Missense_Mutation	C	T	p.E542K	102	44	0.431	0.454	2	1	1	115	AHNAK nucleoprotein 2	ENST00000333244.5
Case#3-Baseline-M437	MAPKBP1	15	42105918	Missense_Mutation	C	G	p.L313V	59	5	0.085	0.089	2	2	0	113	mitogen-activated protein kinase binding protein 1	ENST00000456763.2
Case#3-Baseline-M437	CAPN3	15	42693849	Missense_Mutation	G	T	p.W455C	85	26	0.306	0.322	2	2	0	130	calpain 3, (p94)	ENST00000397163.3
Case#3-Baseline-M437	CGNL1	15	57731599	Missense_Mutation	G	A	p.G468R	92	87	0.946	0.995	2	2	0	198	cingulin-like 1	ENST00000281282.5
Case#3-Baseline-M437	HERC1	15	63932569	Missense_Mutation	G	A	p.H3895Y	77	71	0.922	0.971	2	2	0	160	HECT and RLD domain containing E3 ubiquitin protein ligase family member 1	ENST00000443617.2
Case#3-Baseline-M437	ZNF609	15	64966930	Missense_Mutation	C	T	p.S626F	62	59	0.952	1.002	2	2	0	73	zinc finger protein 609	ENST00000326648.3
Case#3-Baseline-M437	MEGF11	15	66386745	Missense_Mutation	G	A	p.S130F	69	66	0.957	1.007	2	2	0	245	multiple EGF-like-domains 11	ENST00000409699.2
Case#3-Baseline-M437	SH2D7	15	78390783	Missense_Mutation	G	A	p.D164N	100	90	0.900	NA	NA	NA	NA	211	SH2 domain containing 7	ENST00000328828.5
Case#3-Baseline-M437	KIAA1199	15	81239357	Nonsense_Mutation	G	A	p.W1303*	79	74	0.937	0.986	2	2	0	124		ENST00000394685.3
Case#3-Baseline-M437	AKAP13	15	86122395	Missense_Mutation	G	A	p.D366N	86	39	0.453	0.477	2	2	0	124	A kinase (PRKA) anchor protein 13	ENST00000394518.2
Case#3-Baseline-M437	PKD1	16	2164850	Missense_Mutation	G	A	p.A725V	167	93	0.557	0.576	3	2	1	286	polycystic kidney disease 1 (autosomal dominant)	ENST00000262304.4
Case#3-Baseline-M437	PRSS33	16	2835130	Missense_Mutation	G	A	p.P186L	59	22	0.373	0.386	3	2	1	40	protease, serine, 33	ENST00000293851.5
Case#3-Baseline-M437	CLDN6	16	3065596	Missense_Mutation	T	C	p.I143V	112	7	0.063	0.065	3	2	1	177	claudin 6	ENST00000396925.1
Case#3-Baseline-M437	RBFOX1	16	7657301	Missense_Mutation	C	T	p.P213S	130	84	0.646	0.669	3	2	1	109	RNA binding protein, fox-1 homolog (C. elegans) 1	ENST00000550418.1
Case#3-Baseline-M437	GRIN2A	16	9857865	Missense_Mutation	G	A	p.S1179F	114	31	0.272	0.281	3	2	1	145	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	ENST00000396573.2
Case#3-Baseline-M437	CIITA	16	11001583	Missense_Mutation	G	A	p.R745K	96	19	0.198	0.205	3	2	1	134	class II, major histocompatibility complex, transactivator	ENST00000324288.8
Case#3-Baseline-M437	ZP2	16	21213516	Missense_Mutation	C	T	p.G399E	104	59	0.567	0.587	3	2	1	115	zona pellucida glycoprotein 2 (sperm receptor)	ENST00000574002.1
Case#3-Baseline-M437	SETD1A	16	30972725	Missense_Mutation	CC	TT	p.P129S	166	56	0.337	0.349	3	2	1	202	SET domain containing 1A	ENST00000262519.8
Case#3-Baseline-M437	KAT8	16	31139429	Missense_Mutation	C	T	p.S247F	68	35	0.515	0.533	3	2	1	95	K(lysine) acetyltransferase 8	ENST00000543774.2
Case#3-Baseline-M437	ABCC12	16	48120720	Missense_Mutation	C	T	p.D1216N	104	63	0.606	0.627	3	2	1	166	ATP-binding cassette, sub-family C (CFTR/MRP), member 12	ENST00000311303.3

Case#3-Baseline-M437	C16orf80	16	58150028	Missense_Mutation	GG	AA	p.P65S	107	55	0.514	0.532	3	2	1	105		ENST00000262498.3
Case#3-Baseline-M437	SLC12A4	16	67978823	Missense_Mutation	GG	AA	p.L1060F	69	38	0.551	0.570	3	2	1	121	solute carrier family 12 (potassium/chloride transporter), member 4	ENST00000316341.3
Case#3-Baseline-M437	FUK	16	70508588	Missense_Mutation	G	C	p.D716H	106	36	0.340	0.352	3	2	1	122	fucokinase	ENST00000288078.6
Case#3-Baseline-M437	PHLPP2	16	71715720	Missense_Mutation	G	A	p.T275I	146	85	0.582	0.603	3	2	1	127	PH domain and leucine rich repeat protein phosphatase 2	ENST00000568954.1
Case#3-Baseline-M437	ZNF469	16	88502825	Missense_Mutation	C	T	p.R2955W	171	106	0.620	0.642	3	2	1	191	zinc finger protein 469	ENST00000437464.1
Case#3-Baseline-M437	RPH3AL	17	65450	Missense_Mutation	CC	TT	p.A291T	69	62	0.899	0.946	2	2	0	131	rabphilin 3A-like (without C2 domains)	ENST00000331302.7
Case#3-Baseline-M437	OR1D5	17	2966391	Missense_Mutation	G	T	p.P171T	312	80	0.256	NA	NA	NA	NA	569	olfactory receptor, family 1, subfamily D, member 5	ENST00000575751.1
Case#3-Baseline-M437	USP6	17	5072287	Missense_Mutation	G	A	p.E1152K	170	158	0.929	0.978	2	2	0	313	ubiquitin specific peptidase 6	ENST00000574788.1
Case#3-Baseline-M437	TP53	17	7578212	Nonsense_Mutation	G	A	p.R213*	102	97	0.951	1.001	2	2	0	129	tumor protein p53	ENST00000269305.4
Case#3-Baseline-M437	WRAP53	17	7606722	Missense_Mutation	C	G	p.A522G	56	5	0.089	0.094	2	2	0	110	WD repeat containing, antisense to TP53	ENST00000316024.5
Case#3-Baseline-M437	ALOX15B	17	7951819	Missense_Mutation	A	G	p.Q656R	82	5	0.061	0.064	2	2	0	119	arachidonate 15-lipoxygenase, type B	ENST00000380183.4
Case#3-Baseline-M437	C17orf59	17	8092453	Missense_Mutation	G	C	p.Q336E	70	35	0.500	0.526	2	2	0	204	chromosome 17 open reading frame 59	ENST00000389017.4
Case#3-Baseline-M437	DNAH9	17	11631201	Nonsense_Mutation	C	T	p.R1926*	115	107	0.930	0.979	2	2	0	151	dynein, axonemal, heavy chain 9	ENST00000262442.4
Case#3-Baseline-M437	MYOCD	17	12649381	Missense_Mutation	G	A	p.D373N	94	85	0.904	0.952	2	2	0	160	myocardin	ENST00000343344.4
Case#3-Baseline-M437	TRIM16	17	15539436	Missense_Mutation	GG	AT	p.H254Q	146	130	0.890	0.937	2	1	1	267	tripartite motif containing 16	ENST00000578237.1
Case#3-Baseline-M437	TAOK1	17	27861294	Missense_Mutation	CC	TT	p.R841W	61	58	0.951	1.001	2	2	0	94	TAO kinase 1	ENST00000261716.3
Case#3-Baseline-M437	MYO1D	17	31075981	Missense_Mutation	C	T	p.R504Q	79	76	0.962	1.013	2	2	0	124	myosin ID	ENST00000318217.5
Case#3-Baseline-M437	KRTAP9-1	17	39346518	Missense_Mutation	T	C	p.I127T	136	15	0.110	0.116	2	2	0	281	keratin associated protein 9-1	ENST00000398470.1
Case#3-Baseline-M437	TUBG1	17	40765003	Missense_Mutation	C	T	p.P173L	84	79	0.940	0.990	2	2	0	163	tubulin, gamma 1	ENST00000251413.3
Case#3-Baseline-M437	EZH1	17	40879733	Missense_Mutation	G	A	p.L56F	39	39	1.000	1.053	2	2	0	91	enhancer of zeste 1 polycomb repressive complex 2 subunit	ENST00000428826.2
Case#3-Baseline-M437	BRCA1	17	41244936	Missense_Mutation	G	A	p.P871L	129	9	0.070	0.073	2	2	0	128	breast cancer 1, early onset	ENST00000357654.3
Case#3-Baseline-M437	MED13	17	60059588	Missense_Mutation	G	A	p.S1259L	68	65	0.956	1.006	2	2	0	130	mediator complex subunit 13	ENST00000397786.2
Case#3-Baseline-M437	TLK2	17	60601646	Missense_Mutation	C	T	p.P106L	99	85	0.859	0.904	2	2	0	139	tousled-like kinase 2	ENST00000326270.9
Case#3-Baseline-M437	ABCA8	17	66899001	Missense_Mutation	C	T	p.G833R	115	104	0.904	0.952	2	2	0	208	ATP-binding cassette, sub-family A (ABC1), member 8	ENST00000269080.2
Case#3-Baseline-M437	TTYH2	17	72240177	Missense_Mutation	T	G	p.S265A	48	5	0.104	0.110	2	2	0	68	tweety family member 2	ENST00000269346.4
Case#3-Baseline-M437	SLC16A5	17	73096288	Missense_Mutation	G	A	p.G177E	106	96	0.906	0.953	2	2	0	180	solute carrier family 16 (monocarboxylate transporter), member 5	ENST00000450736.2
Case#3-Baseline-M437	MGAT5B	17	74878259	Missense_Mutation	G	A	p.V70I	110	13	0.118	0.124	2	2	0	247	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase, isozyme B	ENST00000569840.2
Case#3-Baseline-M437	RP11-1055B8.7	17	79428645	Missense_Mutation	C	T	p.S2319F	124	108	0.871	0.917	2	2	0	292		ENST00000307745.7
Case#3-Baseline-M437	ZNF750	17	80789468	Missense_Mutation	G	A	p.P288L	161	10	0.062	0.065	2	2	0	220	zinc finger protein 750	ENST00000269394.3
Case#3-Baseline-M437	ZBTB14	18	5291177	Missense_Mutation	G	A	p.R344C	144	72	0.500	0.513	4	2	2	122	zinc finger and BTB domain containing 14	ENST00000357006.4
Case#3-Baseline-M437	DSG1	18	28926010	Missense_Mutation	G	A	p.R650K	128	33	0.258	0.265	4	3	1	125	desmoglein 1	ENST00000257192.4
Case#3-Baseline-M437	SETBP1	18	42533090	Missense_Mutation	G	A	p.R1262K	100	27	0.270	0.277	4	3	1	133	SET binding protein 1	ENST00000282030.5
Case#3-Baseline-M437	SLC14A2	18	43221220	Nonsense_Mutation	G	A	p.W346*	210	52	0.248	0.254	4	3	1	151	solute carrier family 14 (urea transporter), member 2	ENST00000255226.6
Case#3-Baseline-M437	SMAD7	18	46474786	Missense_Mutation	G	A	p.S212F	106	75	0.708	0.726	4	3	1	87	SMAD family member 7	ENST00000262158.2
Case#3-Baseline-M437	DCC	18	51025778	Nonsense_Mutation	C	T	p.R1337*	229	176	0.769	0.789	4	3	1	265	DCC netrin 1 receptor	ENST00000442544.2
Case#3-Baseline-M437	MALT1	18	56412976	Missense_Mutation	C	T	p.P664S	155	120	0.774	0.795	4	3	1	91	mucosa associated lymphoid tissue lymphoma translocation gene 1	ENST00000348428.3
Case#3-Baseline-M437	SERPINB2	18	61570441	Missense_Mutation	G	A	p.G384R	180	132	0.733	0.753	4	3	1	173	serpin peptidase inhibitor, clade B (ovalbumin), member 2	ENST00000299502.4
Case#3-Baseline-M437	TSHZ1	18	73000585	Missense_Mutation	G	C	p.E1075Q	182	49	0.269	0.276	4	3	1	176	teashirt zinc finger homeobox 1	ENST00000580243.1
Case#3-Baseline-M437	MIER2	19	326549	Missense_Mutation	GG	AA	p.S181F	131	82	0.626	0.648	3	2	1	133	mesoderm induction early response 1, family member 2	ENST00000264819.4
Case#3-Baseline-M437	ZNF77	19	2934701	Missense_Mutation	A	G	p.S142P	173	30	0.173	0.179	3	2	1	140	zinc finger protein 77	ENST00000314531.4
Case#3-Baseline-M437	LRG1	19	4538370	Missense_Mutation	C	T	p.R209K	210	89	0.424	0.439	3	2	1	165	leucine-rich alpha-2-glycoprotein 1	ENST00000306390.6
Case#3-Baseline-M437	SH2D3A	19	6760941	Missense_Mutation	G	A	p.R43C	106	66	0.623	0.644	3	2	1	138	SH2 domain containing 3A	ENST00000245908.6
Case#3-Baseline-M437	MUC16	19	9075262	Missense_Mutation	G	A	p.L4062F	223	142	0.637	0.659	3	2	1	199	mucin 16, cell surface associated	ENST00000397910.4
Case#3-Baseline-M437	OR7G2	19	9213712	Missense_Mutation	C	T	p.D91N	198	125	0.631	0.653	3	2	1	230	olfactory receptor, family 7, subfamily G, member 2	ENST00000305456.2
Case#3-Baseline-M437	OR7G1	19	9225341	Missense_Mutation	C	T	p.R312Q	27	12	0.444	0.460	3	2	1	18	olfactory receptor, family 7, subfamily G, member 1	ENST00000293614.1
Case#3-Baseline-M437	ZNF559	19	9452789	Missense_Mutation	C	T	p.T221I	134	46	0.343	0.355	3	2	1	142	zinc finger protein 559	ENST00000393883.2
Case#3-Baseline-M437	ZNF812	19	9801529	Missense_Mutation	C	T	p.G217E	193	118	0.611	0.633	3	2	1	175	zinc finger protein 812	ENST00000457674.2
Case#3-Baseline-M437	RDH8	19	10131432	Missense_Mutation	G	A	p.G164R	46	26	0.565	0.585	3	2	1	58	retinol dehydrogenase 8 (all-trans)	ENST00000171214.1
Case#3-Baseline-M437	RGL3	19	11510969	Missense_Mutation	G	A	p.R497W	53	21	0.396	0.410	3	2	1	33	ral guanine nucleotide dissociation stimulator-like 3	ENST00000380456.3
Case#3-Baseline-M437	RAD23A	19	13059521	Missense_Mutation	C	T	p.T165M	126	82	0.651	0.674	3	2	1	108	RAD23 homolog A (S. cerevisiae)	ENST00000586534.1
Case#3-Baseline-M437	ZNF493	19	21607009	Missense_Mutation	CT	TC	p.Y389H	90	19	0.211	0.219	3	2	1	101	zinc finger protein 493	ENST00000355504.4
Case#3-Baseline-M437	ZNF781	19	38160347	Missense_Mutation	C	G	p.G235R	115	8	0.070	0.073	2	2	0	191	zinc finger protein 781	ENST00000590008.1
Case#3-Baseline-M437	PRX	19	40902757	Missense_Mutation	T	A	p.E501V	123	113	0.919	0.967	2	2	0	183	periaxin	ENST00000324001.7
Case#3-Baseline-M437	PSG4	19	43699336	Missense_Mutation	T	C	p.K267E	288	32	0.111	0.117	2	2	0	652	pregnancy specific beta-1-glycoprotein 4	ENST00000405312.3
Case#3-Baseline-M437	KLK5	19	51452217	Missense_Mutation	G	A	p.R164C	70	64	0.914	0.962	2	2	0	70	kallikrein-related peptidase 5	ENST00000336334.3
Case#3-Baseline-M437	CD33	19	51728641	Missense_Mutation	A	G	p.R69G	116	7	0.060	0.064	2	2	0	186	CD33 molecule	ENST00000262262.4
Case#3-Baseline-M437	CACNG7	19	54417812	Missense_Mutation	GG	AA	p.V86M	45	43	0.956	1.006	2	2	0	80	calcium channel, voltage-dependent, gamma subunit 7	ENST00000391767.1
Case#3-Baseline-M437	LILRA6	19	54744887	Missense_Mutation	C	T	p.E259K	352	108	0.307	0.318	3	2	1	623	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 6	ENST00000396365.2
Case#3-Baseline-M437	LILRA4	19	54848803	Missense_Mutation	C	T	p.G274R	111	100	0.901	0.948	2	2	0	263	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 4	ENST00000291759.4
Case#3-Baseline-M437	KIR3DL3	19	55239168	Missense_Mutation	G	T	p.R149S	77	6	0.078	0.082	2	2	0	212	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 3	ENST00000291860.1
Case#3-Baseline-M437	KIR3DL1	19	55340906	Missense_Mutation	G	A	p.C364Y	15	4	0.267	0.281	2	2	0	44	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1	ENST00000391728.4
Case#3-Baseline-M437	KIR3DL1	19	55341575	Missense_Mutation	G	C	p.E394Q	20	11	0.550	0.579	2	2	0	55	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1	ENST00000391728.4
Case#3-Baseline-M437	NLRP8	19	56466053	Missense_Mutation	G	A	p.G210E	118	107	0.907	0.955	2	2	0	187	NLR family, pyrin domain containing 8	ENST00000291971.3
Case#3-Baseline-M437	ZFP28	19	57058998	Missense_Mutation	C	G	p.S141W	99	5	0.051	0.053	2	2	0	160	ZFP28 zinc finger protein	ENST00000301318.3
Case#3-Baseline-M437	ZIM3	19	57647454	Missense_Mutation	C	T	p.G84E	98	92	0.939	0.988	2	2	0	136	zinc finger, imprinted 3	ENST00000269834.1
Case#3-Baseline-M437	ZNF805	19	57764450	Missense_Mutation	G	A	p.G88E	77	74	0.961	1.012	2	2	0	135	zinc finger protein 805	ENST00000414468.2
Case#3-Baseline-M437	RAD51AP2	2	17699133	Missense_Mutation	C	T	p.D184N	101	64	0.634	0.656	3	2	1	99	RAD51 associated protein 2	ENST00000399080.2
Case#3-Baseline-M437	HS1BP3	2	20824519	Missense_Mutation	G	A	p.P253S	94	57	0.606	0.628	3	2	1	114	HCLS1 binding protein 3	ENST00000304031.3
Case#3-Baseline-M437	GAREML	2	26410435	Missense_Mutation	C	T	p.A645V	160	55	0.344	0.356	3	2	1	200	GRB2 associated, regulator of MAPK1-like	ENST00000401533.2
Case#3-Baseline-M437	CAPN13	2	30987042	Missense_Mutation	C	T	p.A219T	157	99	0.631	0.653	3	2	1	150	calpain 13	ENST00000295055.8
Case#3-Baseline-M437	NLRC4	2	32449780	Missense_Mutation	C	T	p.G946E	83	52	0.627	0.648	3	2	1	104	NLR family, CARD domain containing 4	ENST00000404025.2
Case#3-Baseline-M437	TMEM178A	2	39944333	Missense_Mutation	C	T	p.P279L	110	32	0.291	0.301	3	2	1	112	transmembrane protein 178A	ENST00000281961.2
Case#3-Baseline-M437	SLC3A1	2	44502865	Missense_Mutation	C	T	p.P64L	111	71	0.640	0.662	3	2	1	164	solute carrier family 3 (amino acid transporter heavy chain), member 1	ENST00000260649.6
Case#3-Baseline-M437	SEMA4F	2	74906438	Missense_Mutation	C	T	p.S560F	257	96	0.374	0.387	3	2	1	148	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F	ENST00000357877.2

Case#3-Baseline-M437	LRRTM4	2	76976028	Missense_Mutation	C	T	p.M522I	88	56	0.636	0.659	3	2	1	140	leucine rich repeat transmembrane neuronal 4	ENST00000409093.1
Case#3-Baseline-M437	DNAH6	2	84899586	Missense_Mutation	A	C	p.K2197T	107	33	0.308	0.319	3	2	1	97	dynein, axonemal, heavy chain 6	ENST00000237449.6
Case#3-Baseline-M437	DNAH6	2	84936603	Missense_Mutation	C	T	p.S3062L	105	67	0.638	0.660	3	2	1	132	dynein, axonemal, heavy chain 6	ENST00000237449.6
Case#3-Baseline-M437	ANKRD36C	2	96589416	Missense_Mutation	G	A	p.P688L	210	76	0.362	0.375	3	2	1	259	ankyrin repeat domain 36C	ENST00000456556.1
Case#3-Baseline-M437	SNRNP200	2	96952155	Missense_Mutation	GG	AA	p.T1299I	97	27	0.278	0.288	3	2	1	97	small nuclear ribonucleoprotein 200kDa (U5)	ENST00000323853.5
Case#3-Baseline-M437	KANSL3	2	97276608	Missense_Mutation	G	A	p.P392S	147	94	0.639	0.662	3	2	1	180	KAT8 regulatory NSL complex subunit 3	ENST00000431828.1
Case#3-Baseline-M437	TSGA10	2	99725886	Missense_Mutation	G	A	p.S6F	137	91	0.664	0.688	3	2	1	90	testis specific, 10	ENST00000393483.3
Case#3-Baseline-M437	NPAS2	2	101609910	Missense_Mutation	A	C	p.H738P	71	8	0.113	0.117	3	2	1	120	neuronal PAS domain protein 2	ENST00000335681.5
Case#3-Baseline-M437	IL18RAP	2	103067316	Missense_Mutation	G	A	p.D407N	104	25	0.240	0.249	3	2	1	93	interleukin 18 receptor accessory protein	ENST00000264260.2
Case#3-Baseline-M437	SAP130	2	128712815	Missense_Mutation	GG	AA	p.P714S	75	44	0.587	0.607	3	2	1	84	Sin3A-associated protein, 130kDa	ENST00000259235.3
Case#3-Baseline-M437	POTEI	2	131220643	Missense_Mutation	C	T	p.D992N	329	76	0.231	0.239	3	2	1	616	POTE ankyrin domain family, member I	ENST00000451531.2
Case#3-Baseline-M437	NCKAP5	2	133542604	Missense_Mutation	C	T	p.E594K	99	54	0.545	0.565	3	2	1	95	NCK-associated protein 5	ENST00000409261.1
Case#3-Baseline-M437	THSD7B	2	138400156	Missense_Mutation	C	T	p.P1300S	71	36	0.507	0.525	3	2	1	99	thrombospondin, type I, domain containing 7B	ENST00000409968.1
Case#3-Baseline-M437	CACNB4	2	152728990	Missense_Mutation	G	A	p.S180F	141	38	0.270	0.279	3	2	1	114	calcium channel, voltage-dependent, beta 4 subunit	ENST00000539935.1
Case#3-Baseline-M437	SCN1A	2	166892697	Missense_Mutation	A	C	p.I1097S	173	109	0.630	0.652	3	2	1	220	sodium channel, voltage-gated, type I, alpha subunit	ENST00000303395.4
Case#3-Baseline-M437	LRP2	2	169989179	Missense_Mutation	C	T	p.E4545K	125	80	0.640	0.662	3	2	1	121	low density lipoprotein receptor-related protein 2	ENST00000263816.3
Case#3-Baseline-M437	LRP2	2	170027117	Missense_Mutation	C	T	p.R3775Q	156	49	0.314	0.325	3	2	1	166	low density lipoprotein receptor-related protein 2	ENST00000263816.3
Case#3-Baseline-M437	TTN	2	179542597	Missense_Mutation	C	T	p.E11031K	148	33	0.223	0.231	3	2	1	161	titin	ENST00000591111.1
Case#3-Baseline-M437	TTN	2	179638013	Missense_Mutation	C	T	p.G2560R	139	44	0.317	0.328	3	2	1	115	titin	ENST00000591111.1
Case#3-Baseline-M437	ITGA4	2	182347248	Missense_Mutation	C	T	p.S304L	155	99	0.639	0.661	3	2	1	197	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	ENST00000397033.2
Case#3-Baseline-M437	FSIP2	2	186665668	Missense_Mutation	G	A	p.E3879K	89	27	0.303	0.314	3	2	1	113	fibrous sheath interacting protein 2	ENST00000424728.1
Case#3-Baseline-M437	STAT4	2	191894582	Missense_Mutation	G	A	p.P744L	97	25	0.258	0.267	3	2	1	91	signal transducer and activator of transcription 4	ENST00000392320.2
Case#3-Baseline-M437	ZNF142	2	219507517	Missense_Mutation	G	A	p.S1241L	170	61	0.359	0.371	3	2	1	181	zinc finger protein 142	ENST00000449707.1
Case#3-Baseline-M437	DOCK10	2	225652038	Missense_Mutation	A	G	p.V1832A	100	6	0.060	0.062	3	2	1	68	dedicator of cytokinesis 10	ENST00000258390.7
Case#3-Baseline-M437	NYAP2	2	226446941	Missense_Mutation	G	A	p.E270K	127	38	0.299	0.310	3	2	1	177	neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adaptor 2	ENST00000272907.6
Case#3-Baseline-M437	COL4A4	2	227954599	Missense_Mutation	G	A	p.P482S	138	9	0.065	0.068	3	2	1	134	collagen, type IV, alpha 4	ENST00000396625.3
Case#3-Baseline-M437	COL4A4	2	227954646	Missense_Mutation	CC	TT	p.G466K	111	67	0.604	0.625	3	2	1	98	collagen, type IV, alpha 4	ENST00000396625.3
Case#3-Baseline-M437	C2orf83	2	228476118	Missense_Mutation	C	T	p.G149R	129	75	0.581	0.602	3	2	1	156	chromosome 2 open reading frame 83	ENST00000264387.4
Case#3-Baseline-M437	HTR2B	2	231973845	Missense_Mutation	G	A	p.P278S	173	114	0.659	0.682	3	2	1	267	5-hydroxytryptamine (serotonin) receptor 2B, G protein-coupled	ENST00000258400.3
Case#3-Baseline-M437	SAG	2	234235774	Missense_Mutation	G	A	p.G148E	85	49	0.576	0.597	3	2	1	112	S-antigen; retina and pineal gland (arrestin)	ENST00000409110.1
Case#3-Baseline-M437	DEFB129	20	207945	Missense_Mutation	C	T	p.P6S	98	42	0.429	0.444	3	2	1	164	defensin, beta 129	ENST00000246105.4
Case#3-Baseline-M437	SIRPB1	20	1552521	Missense_Mutation	G	A	p.P199L	442	164	0.371	0.384	3	2	1	566	signal-regulatory protein beta 1	ENST00000381605.4
Case#3-Baseline-M437	TGM3	20	2293636	Missense_Mutation	T	G	p.N211K	94	41	0.436	0.451	3	2	1	93	transglutaminase 3	ENST00000381458.5
Case#3-Baseline-M437	CDC25B	20	3781454	Missense_Mutation	G	A	p.R175Q	120	41	0.342	0.354	3	2	1	164	cell division cycle 25B	ENST00000245960.5
Case#3-Baseline-M437	HAO1	20	7921011	Missense_Mutation	G	A	p.P20L	127	49	0.386	0.399	3	2	1	121	hydroxyacid oxidase (glycolate oxidase) 1	ENST00000378789.3
Case#3-Baseline-M437	THBD	20	23028724	Missense_Mutation	G	A	p.A473V	159	10	0.063	0.065	3	2	1	204	thrombomodulin	ENST00000377103.2
Case#3-Baseline-M437	ARHGAP40	20	37272501	Missense_Mutation	G	A	p.G453E	152	84	0.553	0.567	4	2	2	138	Rho GTPase activating protein 40	ENST00000373345.4
Case#3-Baseline-M437	EMILIN3	20	39989988	Missense_Mutation	C	T	p.D741N	168	43	0.256	0.263	4	2	2	177	elastin microfibril interfacer 3	ENST00000332312.3
Case#3-Baseline-M437	PTPRT	20	40727140	Missense_Mutation	G	A	p.T1256I	290	122	0.421	0.432	4	2	2	246	protein tyrosine phosphatase, receptor type, T	ENST00000373187.1
Case#3-Baseline-M437	L3MBTL1	20	42162925	Splice_Site	G	A	p.R512Q	137	54	0.394	0.405	4	2	2	147	l(3)mbt-like 1 (Drosophila)	ENST00000427442.2
Case#3-Baseline-M437	SEMG1	20	43837235	Missense_Mutation	G	A	p.G433R	176	90	0.511	0.525	4	2	2	142	semenogelin I	ENST00000372781.3
Case#3-Baseline-M437	ELMO2	20	45014770	Missense_Mutation	G	A	p.L224F	139	63	0.453	0.465	4	2	2	96	engulfment and cell motility 2	ENST00000290246.6
Case#3-Baseline-M437	OCSTAMP	20	45174451	Missense_Mutation	C	T	p.E188K	112	55	0.491	0.504	4	2	2	144	osteoclast stimulatory transmembrane protein	ENST00000279028.2
Case#3-Baseline-M437	ZNF831	20	57829425	Missense_Mutation	C	T	p.S1554L	103	47	0.456	0.468	4	2	2	96	zinc finger protein 831	ENST00000371030.2
Case#3-Baseline-M437	ADRM1	20	60882680	Missense_Mutation	CC	TT	p.P218L	115	63	0.548	0.562	4	2	2	82	adhesion regulating molecule 1	ENST00000253003.2
Case#3-Baseline-M437	GATA5	20	61041528	Missense_Mutation	C	T	p.G260E	190	58	0.305	0.313	4	2	2	209	GATA binding protein 5	ENST00000252997.2
Case#3-Baseline-M437	KCNQ2	20	62055543	Missense_Mutation	CC	TT	p.E412K	151	71	0.470	0.483	4	2	2	107	potassium voltage-gated channel, KQT-like subfamily, member 2	ENST00000359125.2
Case#3-Baseline-M437	LIPI	21	15537711	Splice_Site	C	T	p.G245E	50	20	0.400	0.421	2	1	1	65	lipase, member I	ENST00000536861.1
Case#3-Baseline-M437	LTN1	21	30365209	Missense_Mutation	G	A	p.S19F	64	18	0.281	0.296	2	1	1	113	listerin E3 ubiquitin protein ligase 1	ENST00000389195.2
Case#3-Baseline-M437	SYNJ1	21	34045776	Nonsense_Mutation	G	A	p.R534*	92	32	0.348	0.366	2	1	1	102	synaptojanin 1	ENST00000322229.7
Case#3-Baseline-M437	RRP1B	21	45113233	Missense_Mutation	G	A	p.R749K	61	23	0.377	0.397	2	1	1	175	ribosomal RNA processing 1B	ENST00000340648.4
Case#3-Baseline-M437	DNMT3L	21	45679432	Splice_Site	C	T	p.D78N	91	36	0.396	0.416	2	1	1	152	DNA (cytosine-5-)-methyltransferase 3-like	ENST00000418993.1
Case#3-Baseline-M437	KRTAP10-4	21	45993684	Missense_Mutation	C	T	p.P17S	97	32	0.330	0.347	2	1	1	317	keratin associated protein 10-4	ENST00000400374.3
Case#3-Baseline-M437	ITGB2	21	46309893	Splice_Site	C	T	p.G553R	143	63	0.441	0.464	2	1	1	276	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	ENST00000397850.2
Case#3-Baseline-M437	POTEH	22	16275210	Missense_Mutation	G	A	p.P412S	407	69	0.170	0.175	3	2	1	577	POTE ankyrin domain family, member H	ENST00000343518.6
Case#3-Baseline-M437	OR11H1	22	16449062	Missense_Mutation	CC	TT	p.G248K	286	142	0.497	0.514	3	2	1	459	olfactory receptor, family 11, subfamily H, member 1	ENST00000252835.4
Case#3-Baseline-M437	CCT8L2	22	17073167	Missense_Mutation	C	T	p.E92K	181	47	0.260	0.269	3	2	1	232	chaperonin containing TCP1, subunit 8 (theta)-like 2	ENST00000359963.3
Case#3-Baseline-M437	ZNF74	22	20760975	Missense_Mutation	C	T	p.S551F	163	49	0.301	0.311	3	2	1	190	zinc finger protein 74	ENST00000400451.2
Case#3-Baseline-M437	CCDC116	22	21989439	Missense_Mutation	T	A	p.Y363N	129	81	0.628	0.650	3	2	1	234	coiled-coil domain containing 116	ENST00000292779.3
Case#3-Baseline-M437	C22orf43	22	23959845	Splice_Site	C	T		230	73	0.317	0.329	3	2	1	260		ENST00000317749.5
Case#3-Baseline-M437	MYO18B	22	26388328	Splice_Site	GG	AA	p.E2054K	176	45	0.256	0.265	3	2	1	181	myosin XVIIIB	ENST00000407587.2
Case#3-Baseline-M437	HPS4	22	26854495	Missense_Mutation	C	T	p.E588K	48	35	0.729	0.755	3	2	1	56	Hermansky-Pudlak syndrome 4	ENST00000398145.2
Case#3-Baseline-M437	SEC14L3	22	30860830	Missense_Mutation	C	T	p.R214H	154	8	0.052	0.054	3	2	1	157	SEC14-like 3 (S. cerevisiae)	ENST00000215812.4
Case#3-Baseline-M437	C22orf42	22	32555199	Missense_Mutation	C	T	p.G2R	101	32	0.317	0.328	3	2	1	102	chromosome 22 open reading frame 42	ENST00000382097.3
Case#3-Baseline-M437	CSF2RB	22	37328885	Missense_Mutation	G	A	p.R364Q	127	39	0.307	0.318	3	2	1	136	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	ENST00000403662.3
Case#3-Baseline-M437	MGAT3	22	39883568	Missense_Mutation	CC	AT	p.P73S	65	36	0.554	0.573	3	2	1	107	mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	ENST00000341184.6
Case#3-Baseline-M437	MKL1	22	40814500	Missense_Mutation	T	C	p.S648G	72	5	0.069	0.072	3	2	1	78	megakaryoblastic leukemia (translocation) 1	ENST00000355630.3
Case#3-Baseline-M437	SCUBE1	22	43634939	Nonsense_Mutation	CC	TA	p.G250*	155	96	0.619	0.641	3	2	1	215	signal peptide, CUB domain, EGF-like 1	ENST00000360835.4
Case#3-Baseline-M437	ALG12	22	50297882	Missense_Mutation	C	A	p.V395L	226	135	0.597	0.618	3	2	1	346	ALG12, alpha-1,6-mannosyltransferase	ENST00000330817.6
Case#3-Baseline-M437	PLCL2	3	17052750	Nonsense_Mutation	C	T	p.Q512*	93	47	0.505	0.532	2	1	1	134	phospholipase C-like 2	ENST00000418129.2
Case#3-Baseline-M437	TRANK1	3	36874140	Missense_Mutation	G	A	p.H2268Y	76	37	0.487	0.512	2	1	1	105	tetratricopeptide repeat and ankyrin repeat containing 1	ENST00000429976.2
Case#3-Baseline-M437	ITGA9	3	37818898	Missense_Mutation	G	A	p.G853R	98	55	0.561	0.591	2	1	1	154	integrin, alpha 9	ENST00000264741.5
Case#3-Baseline-M437	SLC22A13	3	38307716	Missense_Mutation	C	T	p.S122F	32	8	0.250	0.263	2	1	1	66	solute carrier family 22 (organic anion/urate transporter), member 13	ENST00000311856.4
Case#3-Baseline-M437	MYRIP	3	40231388	Nonsense_Mutation	C	T	p.R367*	54	22	0.407	0.429	2	1	1	92	myosin VIIA and Rab interacting protein	ENST00000302541.6
Case#3-Baseline-M437	ULK4	3	41607542	Missense_Mutation	G	A	p.S1067L	118	54	0.458	0.482	2	1	1	158	unc-51 like kinase 4	ENST00000301831.4
Case#3-Baseline-M437	HIGD1A	3	42835700	Nonsense_Mutation	G	A	p.Q16*	98	47	0.480	0.505	2	1	1	153	HIG1 hypoxia inducible domain family, member 1A	ENST00000321331.7
Case#3-Baseline-M437	CCR9	3	45942593	Missense_Mutation	G	A	p.A105T	163	85	0.521	0.549	2	1	1	297	chemokine (C-C motif) receptor 9	ENST00000357632.2
Case#3-Baseline-M437	NBEAL2	3	47046766	Missense_Mutation	GC	AA	p.R2172Q	90	47	0.522	0.550	2	1	1	176	neurobeachin-like 2	ENST00000450053.3
Case#3-Baseline-M437	ELP6	3	47537655	Missense_Mutation	GG	AA	p.P235L	78	31	0.397	0.418	2	1	1	125	elongator acetyltransferase complex subunit 6	ENST00000296149.4

Case#3-Baseline-M437	FBXW12	3	48420005	Missense_Mutation	C	T	p.P202S	122	59	0.484	0.509	2	1	1	115	F-box and WD repeat domain containing 12	ENST00000296438.5
Case#3-Baseline-M437	TMEM89	3	48658426	Nonsense_Mutation	C	T	p.W110*	127	45	0.354	0.373	2	1	1	132	transmembrane protein 89	ENST00000330862.3
Case#3-Baseline-M437	FAM3D	3	58639419	Missense_Mutation	G	A	p.R35C	80	44	0.550	0.579	2	1	1	136	family with sequence similarity 3, member D	ENST00000358781.2
Case#3-Baseline-M437	PTPRG	3	62189189	Missense_Mutation	G	A	p.G574S	52	4	0.077	0.081	2	1	1	183	protein tyrosine phosphatase, receptor type, G	ENST00000474889.1
Case#3-Baseline-M437	ROBO1	3	78719412	Missense_Mutation	G	A	p.P461L	82	45	0.549	0.578	2	1	1	165	roundabout, axon guidance receptor, homolog 1 (Drosophila)	ENST00000464233.1
Case#3-Baseline-M437	EPHA3	3	89521664	Missense_Mutation	G	A	p.R914H	82	6	0.073	0.077	2	1	1	199	EPH receptor A3	ENST00000336596.2
Case#3-Baseline-M437	OR5K4	3	98072744	Missense_Mutation	G	A	p.G16E	165	58	0.352	0.364	3	2	1	113	olfactory receptor, family 5, subfamily K, member 4	ENST00000354924.2
Case#3-Baseline-M437	WDR52	3	113120468	Missense_Mutation	TT	AA	p.K430L	120	39	0.325	0.336	3	2	1	123		ENST00000295868.2
Case#3-Baseline-M437	SIDT1	3	113342480	Missense_Mutation	C	T	p.S736F	98	62	0.633	0.655	3	2	1	84	SID1 transmembrane family, member 1	ENST00000264852.4
Case#3-Baseline-M437	SEMA5B	3	122629695	Missense_Mutation	C	T	p.E1097K	33	20	0.606	0.627	3	2	1	38	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5B	ENST00000357599.3
Case#3-Baseline-M437	MCM2	3	127335939	Missense_Mutation	GT	TA	p.C584L	151	87	0.576	0.596	3	2	1	114	minichromosome maintenance complex component 2	ENST00000265056.7
Case#3-Baseline-M437	PODXL2	3	127387359	Missense_Mutation	C	T	p.H428Y	108	39	0.361	0.374	3	2	1	96	podocalyxin-like 2	ENST00000342480.6
Case#3-Baseline-M437	DNAJB8	3	128181545	Missense_Mutation	C	T	p.V182M	215	133	0.619	0.640	3	2	1	231	DnaJ (Hsp40) homolog, subfamily B, member 8	ENST00000469083.1
Case#3-Baseline-M437	HMCES	3	129020881	Missense_Mutation	C	T	p.H242Y	171	100	0.585	0.605	3	2	1	173	5-hydroxymethylcytosine (hmC) binding, ES cell-specific	ENST00000383463.4
Case#3-Baseline-M437	MBD4	3	129155946	Nonsense_Mutation	G	A	p.R181*	126	71	0.563	0.583	3	2	1	89	methyl-CpG binding domain protein 4	ENST00000249910.1
Case#3-Baseline-M437	SI	3	164785192	Missense_Mutation	C	T	p.D191N	148	82	0.554	0.573	3	2	1	190	sucrase-isomaltase (alpha-glucosidase)	ENST00000264382.3
Case#3-Baseline-M437	MYNN	3	169496854	Missense_Mutation	C	T	p.P189S	107	63	0.589	0.609	3	2	1	147	myoneurin	ENST00000349841.5
Case#3-Baseline-M437	EHHADH	3	184922263	Missense_Mutation	G	A	p.P284L	140	49	0.350	0.362	3	2	1	136	enoyl-CoA, hydratase/3-hydroxyacyl CoA dehydrogenase	ENST00000231887.3
Case#3-Baseline-M437	ATP13A4	3	193171893	Missense_Mutation	G	A	p.T675M	179	105	0.587	0.607	3	2	1	176	ATPase type 13A4	ENST00000342695.4
Case#3-Baseline-M437	NOP14	4	2943361	Missense_Mutation	T	C	p.Q716R	56	5	0.089	0.094	2	2	0	116	NOP14 nucleolar protein	ENST00000314262.6
Case#3-Baseline-M437	GRK4	4	2990499	Missense_Mutation	G	T	p.R65L	123	9	0.073	0.077	2	2	0	153	G protein-coupled receptor kinase 4	ENST00000398052.4
Case#3-Baseline-M437	NCAPG	4	17818885	Splice_Site	T	C	p.D259D	71	6	0.085	0.089	2	2	0	111	non-SMC condensin I complex, subunit G	ENST00000251496.2
Case#3-Baseline-M437	KCTD8	4	44177097	Missense_Mutation	G	T	p.Q378K	110	103	0.936	0.986	2	2	0	123	potassium channel tetramerization domain containing 8	ENST00000360029.3
Case#3-Baseline-M437	CWH43	4	49063872	Missense_Mutation	C	A	p.H689N	130	7	0.054	NA	NA	NA	NA	155	cell wall biogenesis 43 C-terminal homolog (S. cerevisiae)	ENST00000226432.4
Case#3-Baseline-M437	UGT2A1	4	70455302	Missense_Mutation	C	T	p.A458T	177	9	0.051	0.054	2	2	0	344	UDP glucuronosyltransferase 2 family, polypeptide A1, complex locus	ENST00000503640.1
Case#3-Baseline-M437	ANKRD17	4	74124097	Missense_Mutation	C	A	p.G97C	88	45	0.511	0.538	2	2	0	197	ankyrin repeat domain 17	ENST00000358602.4
Case#3-Baseline-M437	ALB	4	74275082	Missense_Mutation	G	A	p.E15K	75	72	0.960	1.011	2	2	0	92	albumin	ENST00000503124.1
Case#3-Baseline-M437	SHROOM3	4	77675505	Missense_Mutation	C	T	p.P1290L	59	6	0.102	0.107	2	2	0	78	shroom family member 3	ENST00000296043.6
Case#3-Baseline-M437	FRAS1	4	78987156	Missense_Mutation	G	A	p.D32N	122	118	0.967	1.018	2	2	0	140	Fraser extracellular matrix complex subunit 1	ENST00000325942.6
Case#3-Baseline-M437	FRAS1	4	79284694	Missense_Mutation	C	T	p.A817V	61	5	0.082	0.086	2	2	0	104	Fraser extracellular matrix complex subunit 1	ENST00000325942.6
Case#3-Baseline-M437	FAM13A	4	89950703	Missense_Mutation	C	A	p.G42V	90	85	0.944	0.994	2	2	0	120	family with sequence similarity 13, member A	ENST00000264344.5
Case#3-Baseline-M437	RP11-766F14.4	4	100570579	Missense_Mutation	G	A	p.P1743S	84	78	0.929	0.977	2	2	0	134		ENST00000511828.1
Case#3-Baseline-M437	SCOC	4	141294756	Missense_Mutation	C	G	p.F22L	88	6	0.068	0.072	2	2	0	154	short coiled-coil protein	ENST00000608372.1
Case#3-Baseline-M437	DCHS2	4	155219419	Missense_Mutation	C	T	p.G1561D	104	100	0.962	1.012	2	2	0	150	dachsous cadherin-related 2	ENST00000357232.4
Case#3-Baseline-M437	NPY1R	4	164247381	Missense_Mutation	C	T	p.G109D	95	6	0.063	0.066	2	2	0	165	neuropeptide Y receptor Y1	ENST00000296533.2
Case#3-Baseline-M437	TLR3	4	187004899	Missense_Mutation	C	T	p.P687S	89	82	0.921	0.970	2	2	0	117	toll-like receptor 3	ENST00000296795.3
Case#3-Baseline-M437	PLEKHG4B	5	163077	Missense_Mutation	G	A	p.D608N	140	94	0.671	0.695	3	2	1	218	pleckstrin homology domain containing, family G (with RhoGef domain) member 4B	ENST00000283426.6
Case#3-Baseline-M437	DROSHA	5	31508735	Missense_Mutation	G	A	p.P527L	125	82	0.656	0.679	3	2	1	163	drosha, ribonuclease type III	ENST00000511367.2
Case#3-Baseline-M437	RXFP3	5	33937020	Missense_Mutation	G	A	p.G59S	117	27	0.231	0.239	3	2	1	142	relaxin/insulin-like family peptide receptor 3	ENST00000330120.3
Case#3-Baseline-M437	AGXT2	5	35047922	Missense_Mutation	G	A	p.P26S	94	58	0.617	0.639	3	2	1	143	alanine--glyoxylate aminotransferase 2	ENST00000231420.6
Case#3-Baseline-M437	LMBRD2	5	36117895	Missense_Mutation	G	A	p.S415F	89	58	0.652	0.675	3	2	1	110	LMBR1 domain containing 2	ENST00000296603.4
Case#3-Baseline-M437	MROH2B	5	41009457	Missense_Mutation	CC	TT	p.G1115E	108	29	0.269	0.278	3	2	1	143	maestro heat-like repeat family member 2B	ENST00000399564.4
Case#3-Baseline-M437	BDP1	5	70751818	Missense_Mutation	T	G	p.D38E	45	6	0.133	0.138	3	2	1	44	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	ENST00000358731.4
Case#3-Baseline-M437	TMEM171	5	72419456	Missense_Mutation	C	G	p.R86G	87	9	0.103	0.107	3	2	1	95	transmembrane protein 171	ENST00000454765.2
Case#3-Baseline-M437	ANKRA2	5	72850174	Missense_Mutation	G	A	p.H260Y	151	93	0.616	0.638	3	2	1	177	ankyrin repeat, family A (RFXANK-like), 2	ENST00000296785.3
Case#3-Baseline-M437	MEGF10	5	126769142	Frame_Shift_Del	C	-	p.S594fs	114	30	0.263	0.272	3	2	1	110	multiple EGF-like-domains 10	ENST00000274473.6
Case#3-Baseline-M437	AFF4	5	132223577	Missense_Mutation	G	A	p.S965F	77	22	0.286	0.296	3	2	1	103	AF4/FMR2 family, member 4	ENST00000265343.5
Case#3-Baseline-M437	PCDHB3	5	140482430	Missense_Mutation	C	T	p.P733S	216	62	0.287	0.297	3	2	1	310	protocadherin beta 3	ENST00000231130.2
Case#3-Baseline-M437	PCDHB17	5	140536603	Missense_Mutation	G	A	p.D343N	112	69	0.616	0.638	3	2	1	104	protocadherin beta 17 pseudogene	ENST00000539533.1
Case#3-Baseline-M437	PCDHB11	5	140581458	Missense_Mutation	C	T	p.S704L	192	111	0.578	0.598	3	2	1	336	protocadherin beta 11	ENST00000354757.3
Case#3-Baseline-M437	FAT2	5	150948044	Missense_Mutation	G	A	p.P150L	150	49	0.327	0.338	3	2	1	107	FAT atypical cadherin 2	ENST00000261800.5
Case#3-Baseline-M437	GLRA1	5	151239530	Missense_Mutation	C	T	p.D98N	169	95	0.562	0.582	3	2	1	199	glycine receptor, alpha 1	ENST00000455880.2
Case#3-Baseline-M437	GRIA1	5	153190585	Splice_Site	G	A	p.G841S	144	75	0.521	0.539	3	2	1	165	glutamate receptor, ionotropic, AMPA 1	ENST00000285900.5
Case#3-Baseline-M437	GEMIN5	5	154311745	Missense_Mutation	C	T	p.R192Q	102	56	0.549	0.568	3	2	1	100	gem (nuclear organelle) associated protein 5	ENST00000285873.7
Case#3-Baseline-M437	HAVCR1	5	156479444	Frame_Shift_Del	TTG	-	p.Q201fs	290	19	0.066	0.068	3	2	1	434	hepatitis A virus cellular receptor 1	ENST00000339252.3
Case#3-Baseline-M437	COL23A1	5	177666176	Missense_Mutation	G	A	p.P529L	89	71	0.798	0.826	3	2	1	136	collagen, type XXIII, alpha 1	ENST00000390654.3
Case#3-Baseline-M437	OR2Y1	5	180166561	Missense_Mutation	C	G	p.M166I	70	11	0.157	0.163	3	2	1	153	olfactory receptor, family 2, subfamily Y, member 1	ENST00000307832.2
Case#3-Baseline-M437	BTNL9	5	180474965	Missense_Mutation	C	T	p.L50F	106	35	0.330	0.342	3	2	1	112	butyrophilin-like 9	ENST00000327705.9
Case#3-Baseline-M437	TRIM41	5	180651693	Missense_Mutation	G	A	p.E232K	77	55	0.714	0.739	3	2	1	116	tripartite motif containing 41	ENST00000315073.5
Case#3-Baseline-M437	DSP	6	7580550	Missense_Mutation	CC	TT	p.T1376I	108	48	0.444	0.456	4	2	2	169	desmoplakin	ENST00000379802.3
Case#3-Baseline-M437	IP6K3	6	33690912	Missense_Mutation	C	T	p.R273K	122	59	0.484	0.496	4	2	2	91	inositol hexakisphosphate kinase 3	ENST00000293756.4
Case#3-Baseline-M437	TULP1	6	35467812	Missense_Mutation	C	T	p.G481S	131	63	0.481	0.494	4	2	2	115	tubby like protein 1	ENST00000229771.6
Case#3-Baseline-M437	CUL9	6	43152092	Missense_Mutation	G	A	p.G15E	120	59	0.492	0.505	4	2	2	87	cullin 9	ENST00000252050.4
Case#3-Baseline-M437	CRIP3	6	43273795	Missense_Mutation	GG	AA	p.P188F	126	63	0.500	0.513	4	2	2	88	cysteine-rich protein 3	ENST00000274990.4
Case#3-Baseline-M437	TMEM63B	6	44117624	Missense_Mutation	C	T	p.T481I	161	83	0.516	0.529	4	2	2	130	transmembrane protein 63B	ENST00000259746.9
Case#3-Baseline-M437	NFKBIE	6	44227856	Missense_Mutation	G	A	p.S454F	125	72	0.576	0.591	4	2	2	149	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	ENST00000275015.5
Case#3-Baseline-M437	TCTE1	6	44250280	Missense_Mutation	C	T	p.R288Q	56	26	0.464	0.477	4	2	2	53	t-complex-associated-testis-expressed 1	ENST00000371505.4
Case#3-Baseline-M437	GPR115	6	47681990	Missense_Mutation	G	A	p.E337K	115	66	0.574	0.589	4	2	2	103	G protein-coupled receptor 115	ENST00000283303.2
Case#3-Baseline-M437	PGK2	6	49754689	Missense_Mutation	G	A	p.P71L	215	94	0.437	0.449	4	2	2	207	phosphoglycerate kinase 2	ENST00000304801.3
Case#3-Baseline-M437	FAM83B	6	54804992	Missense_Mutation	G	A	p.R408K	97	42	0.433	0.444	4	2	2	105	family with sequence similarity 83, member B	ENST00000306858.7
Case#3-Baseline-M437	COL9A1	6	70963105	Missense_Mutation	C	T	p.G583S	76	73	0.961	1.011	2	2	0	33	collagen, type IX, alpha 1	ENST00000357250.6
Case#3-Baseline-M437	IMPG1	6	76660307	Missense_Mutation	C	T	p.R599Q	78	77	0.987	1.039	2	2	0	125	interphotoreceptor matrix proteoglycan 1	ENST00000369950.3
Case#3-Baseline-M437	FAM162B	6	117086378	Missense_Mutation	C	A	p.Q71H	116	6	0.052	0.054	2	2	0	192	family with sequence similarity 162, member B	ENST00000368557.4
Case#3-Baseline-M437	TRDN	6	123658781	Missense_Mutation	G	A	p.S468L	49	48	0.980	1.031	2	2	0	43	triadin	ENST00000398178.3
Case#3-Baseline-M437	ENPP1	6	132196928	Missense_Mutation	G	A	p.G550S	85	82	0.965	1.015	2	2	0	123	ectonucleotide pyrophosphatase/phosphodiesterase 1	ENST00000360971.2
Case#3-Baseline-M437	LPA	6	161020680	Missense_Mutation	C	T	p.E1047K	200	185	0.925	0.974	2	2	0	371	lipoprotein, Lp(a)	ENST00000316300.5
Case#3-Baseline-M437	LFNG	7	2552914	Nonsense_Mutation	G	A	p.W57*	199	106	0.533	0.547	4	2	2	184	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	ENST00000402506.1
Case#3-Baseline-M437	FOXK1	7	4798947	Missense_Mutation	C	T	p.P473S	64	14	0.219	0.225	4	2	2	34	forkhead box K1	ENST00000328914.4
Case#3-Baseline-M437	ETV1	7	13978809	Missense_Mutation	T	C	p.S100G	96	5	0.052	0.053	4	2	2	87	ets variant 1	ENST00000430479.1

Case#3-Baseline-M437	ABCA13	7	48313481	Missense_Mutation	G	C	p.L1406F	164	16	0.098	0.100	4	2	2	120	ATP-binding cassette, sub-family A (ABC1), member 13	ENST00000435803.1
Case#3-Baseline-M437	ABCA13	7	48550794	Splice_Site	GG	AA	p.G4547K	204	96	0.471	0.483	4	2	2	140	ATP-binding cassette, sub-family A (ABC1), member 13	ENST00000435803.1
Case#3-Baseline-M437	ABCA13	7	48626876	Missense_Mutation	C	T	p.L4878F	97	42	0.433	0.444	4	2	2	98	ATP-binding cassette, sub-family A (ABC1), member 13	ENST00000435803.1
Case#3-Baseline-M437	ABCA13	7	48634326	Missense_Mutation	G	A	p.M4887I	214	104	0.486	0.499	4	2	2	161	ATP-binding cassette, sub-family A (ABC1), member 13	ENST00000435803.1
Case#3-Baseline-M437	IKZF1	7	50450237	Splice_Site	G	A		156	66	0.423	0.434	4	2	2	184	IKAROS family zinc finger 1 (Ikaros)	ENST00000331340.3
Case#3-Baseline-M437	GRB10	7	50737450	Missense_Mutation	G	A	p.S158F	143	69	0.483	0.495	4	2	2	222	growth factor receptor-bound protein 10	ENST00000401949.1
Case#3-Baseline-M437	ZNF117	7	64439738	Nonsense_Mutation	G	A	p.Q71*	201	97	0.483	NA	NA	NA	NA	147	zinc finger protein 117	ENST00000282869.6
Case#3-Baseline-M437	LIMK1	7	73521416	Missense_Mutation	C	T	p.R320C	250	110	0.440	0.452	4	2	2	312	LIM domain kinase 1	ENST00000336180.2
Case#3-Baseline-M437	SEMA3C	7	80434967	Missense_Mutation	T	C	p.K216E	249	61	0.245	0.251	4	2	2	180	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	ENST00000265361.3
Case#3-Baseline-M437	FZD1	7	90894449	Missense_Mutation	C	T	p.P85L	21	8	0.381	0.391	4	2	2	34	frizzled class receptor 1	ENST00000287934.2
Case#3-Baseline-M437	AZGP1	7	99564848	Nonsense_Mutation	G	T	p.C225*	183	43	0.235	0.241	4	2	2	175	alpha-2-glycoprotein 1, zinc-binding	ENST00000292401.4
Case#3-Baseline-M437	PRKRIP1	7	102040046	Missense_Mutation	G	A	p.R86H	89	42	0.472	0.488	3	2	1	67	PRKR interacting protein 1 (IL11 inducible)	ENST00000496391.1
Case#3-Baseline-M437	MET	7	116418969	Missense_Mutation	G	A	p.M1178I	162	78	0.481	0.494	4	2	2	135	MET proto-oncogene, receptor tyrosine kinase	ENST00000318493.6
Case#3-Baseline-M437	CFTR	7	117144383	Missense_Mutation	G	A	p.D44N	95	39	0.411	0.421	4	2	2	57	cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C, member 7)	ENST00000003084.6
Case#3-Baseline-M437	FLNC	7	128486089	Missense_Mutation	C	T	p.S1279F	146	71	0.486	0.499	4	2	2	144	filamin C, gamma	ENST00000325888.8
Case#3-Baseline-M437	CPA4	7	129950718	Nonsense_Mutation	CC	TT	p.Q296*	207	96	0.464	0.476	4	2	2	183	carboxypeptidase A4	ENST00000222482.4
Case#3-Baseline-M437	MGAM	7	141750536	Missense_Mutation	G	A	p.D893N	217	92	0.424	0.435	4	2	2	199	maltase-glucoamylase (alpha-glucosidase)	ENST00000549489.2
Case#3-Baseline-M437	MGAM	7	141754666	Missense_Mutation	C	T	p.P1091L	341	173	0.507	0.521	4	2	2	293	maltase-glucoamylase (alpha-glucosidase)	ENST00000549489.2
Case#3-Baseline-M437	RP11-1220K2.2	7	141884914	Missense_Mutation	C	T	p.S1321F	227	109	0.480	0.493	4	2	2	136		ENST00000477922.3
Case#3-Baseline-M437	KEL	7	142655488	Missense_Mutation	G	A	p.S143F	146	64	0.438	0.450	4	2	2	111	Kell blood group, metallo-endopeptidase	ENST00000355265.2
Case#3-Baseline-M437	CSMD1	8	3205615	Missense_Mutation	C	T	p.D1126N	85	49	0.576	0.597	3	2	1	63	CUB and Sushi multiple domains 1	ENST00000520002.1
Case#3-Baseline-M437	RP1L1	8	10464515	Missense_Mutation	C	T	p.G2365R	84	54	0.643	0.665	3	2	1	89	retinitis pigmentosa 1-like 1	ENST00000382483.3
Case#3-Baseline-M437	TACC1	8	38677979	Missense_Mutation	C	T	p.S406F	114	44	0.386	0.400	3	2	1	168	transforming, acidic coiled-coil containing protein 1	ENST00000317827.4
Case#3-Baseline-M437	RP1	8	55533815	Missense_Mutation	G	A	p.E97K	93	32	0.344	0.356	3	2	1	136	retinitis pigmentosa 1 (autosomal dominant)	ENST00000220676.1
Case#3-Baseline-M437	TOX	8	59872518	Missense_Mutation	T	C	p.Y51C	156	105	0.673	0.697	3	2	1	137	thymocyte selection-associated high mobility group box	ENST00000361421.1
Case#3-Baseline-M437	PREX2	8	68968209	Splice_Site	G	A	p.S413N	180	64	0.356	0.368	3	2	1	173	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2	ENST00000288368.4
Case#3-Baseline-M437	CNGB3	8	87679259	Missense_Mutation	T	C	p.N249S	152	83	0.546	0.565	3	2	1	215	cyclic nucleotide gated channel beta 3	ENST00000320005.5
Case#3-Baseline-M437	POP1	8	99135603	Missense_Mutation	T	A	p.M13K	99	34	0.343	0.355	3	2	1	146	processing of precursor 1, ribonuclease P/MRP subunit (S. cerevisiae)	ENST00000401707.2
Case#3-Baseline-M437	ZFPM2	8	106814964	Missense_Mutation	A	G	p.N885S	106	74	0.698	0.723	3	2	1	98	zinc finger protein, FOG family member 2	ENST00000407775.2
Case#3-Baseline-M437	COL14A1	8	121170482	Missense_Mutation	T	G	p.S68A	170	28	0.165	0.170	3	2	1	155	collagen, type XIV, alpha 1	ENST00000297848.3
Case#3-Baseline-M437	NFIB	9	14179774	Missense_Mutation	C	T	p.G190R	41	39	0.951	1.001	2	2	0	70	nuclear factor I/B	ENST00000380959.3
Case#3-Baseline-M437	TTC39B	9	15188106	Missense_Mutation	T	C	p.I420V	116	13	0.112	0.118	2	2	0	175	tetratricopeptide repeat domain 39B	ENST00000512701.2
Case#3-Baseline-M437	FAM214B	9	35108261	Missense_Mutation	A	T	p.V4E	36	4	0.111	0.117	2	2	0	55	family with sequence similarity 214, member B	ENST00000378561.1
Case#3-Baseline-M437	PAX5	9	36923406	Missense_Mutation	G	A	p.P286S	69	36	0.522	0.549	2	2	0	114	paired box 5	ENST00000358127.4
Case#3-Baseline-M437	SPATA31A6	9	43624907	Nonsense_Mutation	A	C	p.Y1260*	23	5	0.217	0.229	2	1	1	288	SPATA31 subfamily A, member 6	ENST00000332857.6
Case#3-Baseline-M437	PRUNE2	9	79324179	Missense_Mutation	G	A	p.T1004M	170	15	0.088	0.093	2	2	0	233	prune homolog 2 (Drosophila)	ENST00000376718.3
Case#3-Baseline-M437	PRUNE2	9	79324741	Missense_Mutation	T	C	p.N817D	118	8	0.068	0.071	2	2	0	171	prune homolog 2 (Drosophila)	ENST00000376718.3
Case#3-Baseline-M437	VPS13A	9	79938016	Missense_Mutation	C	T	p.P1955L	116	113	0.974	1.025	2	2	0	141	vacuolar protein sorting 13 homolog A (S. cerevisiae)	ENST00000360280.3
Case#3-Baseline-M437	NXNL2	9	91159394	Missense_Mutation	G	A	p.E135K	63	59	0.937	0.986	2	2	0	92	nucleoredoxin-like 2	ENST00000375854.3
Case#3-Baseline-M437	OR13C2	9	107367788	Missense_Mutation	C	T	p.G41R	190	147	0.774	0.814	2	2	0	447	olfactory receptor, family 13, subfamily C, member 2	ENST00000542196.1
Case#3-Baseline-M437	PAPPA	9	118949983	Missense_Mutation	GG	TC	p.E323Q	65	57	0.877	0.923	2	2	0	156	pregnancy-associated plasma protein A, pappalysin 1	ENST00000328252.3
Case#3-Baseline-M437	OR1Q1	9	125377645	Missense_Mutation	C	T	p.A210V	101	95	0.941	0.990	2	2	0	151	olfactory receptor, family 1, subfamily Q, member 1	ENST00000297913.2
Case#3-Baseline-M437	AL590708.2	9	130891060	Missense_Mutation	G	A	p.G92E	145	11	0.076	NA	NA	NA	NA	223		ENST00000443493.1
Case#3-Baseline-M437	NOXA1	9	140327663	Missense_Mutation	C	T	p.P286L	40	5	0.125	0.132	2	2	0	101	NADPH oxidase activator 1	ENST00000341349.2
Case#3-Baseline-M437	PNPLA7	9	140409917	Missense_Mutation	G	A	p.S355F	125	112	0.896	0.943	2	2	0	139	patatin-like phospholipase domain containing 7	ENST00000277531.4
Case#3-Baseline-M437	ARSF	X	3007595	Missense_Mutation	C	T	p.P297S	45	43	0.956	1.006	2	2	0	95	arylsulfatase F	ENST00000381127.1
Case#3-Baseline-M437	CYBB	X	37663372	Nonsense_Mutation	G	A	p.W380*	61	56	0.918	0.966	2	1	1	93	cytochrome b-245, beta polypeptide	ENST00000378588.4
Case#3-Baseline-M437	HEPH	X	65474933	Missense_Mutation	G	A	p.D874N	40	37	0.925	0.974	2	1	1	41	hephaestin	ENST00000343002.2
Case#3-Baseline-M437	POF1B	X	84563135	Missense_Mutation	T	A	p.M349L	74	9	0.122	0.128	2	1	1	140	premature ovarian failure, 1B	ENST00000262753.4
Case#3-Baseline-M437	BHLHB9	X	102004491	Missense_Mutation	C	T	p.P190S	100	94	0.940	0.989	2	1	1	150	basic helix-loop-helix domain containing, class B, 9	ENST00000372735.1
Case#3-Baseline-M437	H2BFM	X	103268333	Missense_Mutation	G	A	p.R22H	70	5	0.071	0.075	2	1	1	149	H2B histone family, member M	ENST00000243297.5
Case#3-Baseline-M437	NRK	X	105187944	Missense_Mutation	G	A	p.E1324K	59	54	0.915	0.963	2	1	1	66	Nik related kinase	ENST00000243300.9
Case#3-Baseline-M437	KCNE1L	X	108868108	Missense_Mutation	C	T	p.G48S	22	19	0.864	0.909	2	1	1	50	KCNE1-like	ENST00000372101.2
Case#3-Baseline-M437	TENM1	X	123637409	Splice_Site	CC	TT	p.G1149K	55	52	0.945	0.995	2	1	1	93	teneurin transmembrane protein 1	ENST00000371130.3
Case#3-Baseline-M437	ARHGAP36	X	130218204	Missense_Mutation	G	A	p.D191N	55	54	0.982	1.033	2	1	1	48	Rho GTPase activating protein 36	ENST00000276211.5
Case#3-Baseline-M437	GPR112	X	135426693	Missense_Mutation	A	G	p.I276M	56	5	0.089	0.094	2	1	1	94	G protein-coupled receptor 112	ENST00000394143.1
Case#3-Baseline-M437	PASD1	X	150832597	Missense_Mutation	C	T	p.S283F	43	37	0.860	0.906	2	1	1	74	PAS domain containing 1	ENST00000370357.4
Case#3-Baseline-M437	BGN	X	152770714	Missense_Mutation	A	G	p.K86R	96	6	0.063	0.066	2	1	1	81	biglycan	ENST00000331595.4
Case#3-Baseline-M437	PLXNB3	X	153039502	Missense_Mutation	G	C	p.E1156D	20	4	0.200	0.211	2	1	1	59	plexin B3	ENST00000361971.5
Case#3-Baseline-M437	PLXNA3	X	153689479	Missense_Mutation	C	T	p.P212L	55	50	0.909	0.957	2	1	1	98	plexin A3	ENST00000369682.3
Case#3-Baseline-M437	F8	X	154065973	Missense_Mutation	G	A	p.P2319S	73	66	0.904	0.952	2	1	1	142	coagulation factor VIII, procoagulant component	ENST00000360256.4

Supplementary Table S5: Non-synonymous mutation differences between baseline and relapse

Mutations are sorted according to the following criteria:

1. Case 1-4
2. Relapse Only, Het->Homozygous, Baseline Only
3. Homozygous (Adj VAF > 0.85), Heterozygous (Adj VAF < 0.85)
4. Chromosome, Start_position

VAF = Variant Allele Frequency
CN = Copy Number

									Baseline			Relapse			
Sample	Baseline_vs_Relapse	Hugo_Symbol	Chromosome	Start_position	Variant_Classification	Reference Allele	Mutant Allele	Protein_Change	Coverage	Raw_VAF	Adjusted_VAF	Coverage	Raw_VAF	Adjusted_VAF	Description
Case#1	Relapse Only	JAK1	1	65321333	Nonsense_Mutation	G	A	p.Q503*	NA	NA	NA	83	0.530	1.178	Janus kinase 1
Case#1	Relapse Only	HIST1H1E	6	26156625	Nonsense_Mutation	G	T	p.E3*	NA	NA	NA	43	0.395	0.879	histone cluster 1, H1e
Case#1	Relapse Only	MIIP	1	12090096	Missense_Mutation	C	A	p.P286Q	NA	NA	NA	102	0.059	0.131	migration and invasion inhibitory protein
Case#1	Relapse Only	SEMA6C	1	151109476	Missense_Mutation	C	G	p.W277C	NA	NA	NA	190	0.100	0.181	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C
Case#1	Relapse Only	FLG2	1	152329859	Missense_Mutation	T	A	p.S135C	NA	NA	NA	323	0.056	0.101	filaggrin family member 2
Case#1	Relapse Only	CD48	1	160650992	Splice_Site	C	T	p.A218T	NA	NA	NA	152	0.072	0.131	CD48 molecule
Case#1	Relapse Only	NID1	1	236175223	Missense_Mutation	C	T	p.G842E	NA	NA	NA	130	0.138	0.251	nidogen 1
Case#1	Relapse Only	OR13G1	1	247836148	Missense_Mutation	C	T	p.V66M	NA	NA	NA	130	0.123	0.223	olfactory receptor, family 13, subfamily G, member 1
Case#1	Relapse Only	IL15RA	10	6008182	Missense_Mutation	G	A	p.S70F	NA	NA	NA	130	0.269	0.598	interleukin 15 receptor, alpha
Case#1	Relapse Only	ITIH5	10	7611648	Missense_Mutation	G	A	p.S711F	NA	NA	NA	118	0.288	0.640	inter-alpha-trypsin inhibitor heavy chain family, member 5
Case#1	Relapse Only	GATA3	10	8115931	Missense_Mutation	C	T	p.S426F	NA	NA	NA	61	0.180	0.401	GATA binding protein 3
Case#1	Relapse Only	FAM171A1	10	15256377	Missense_Mutation	G	A	p.P404S	NA	NA	NA	84	0.143	0.317	family with sequence similarity 171, member A1
Case#1	Relapse Only	C10orf112	10	19787440	Missense_Mutation	T	G	p.C1095G	NA	NA	NA	127	0.173	0.385	
Case#1	Relapse Only	RET	10	43609005	Splice_Site	G	A	p.R587R	NA	NA	NA	45	0.333	0.741	ret proto-oncogene
Case#1	Relapse Only	ANK3	10	61830674	Missense_Mutation	G	A	p.S3322F	NA	NA	NA	49	0.204	0.454	ankyrin 3, node of Ranvier (ankyrin G)
Case#1	Relapse Only	DOCK1	10	129207624	Missense_Mutation	T	G	p.F1417V	NA	NA	NA	109	0.083	0.183	dedicator of cytokinesis 1
Case#1	Relapse Only	OR5AK2	11	56756984	Missense_Mutation	T	G	p.L199R	NA	NA	NA	340	0.082	0.183	olfactory receptor, family 5, subfamily AK, member 2
Case#1	Relapse Only	HTR3B	11	113803745	Missense_Mutation	T	C	p.L209P	NA	NA	NA	163	0.135	0.300	5-hydroxytryptamine (serotonin) receptor 3B, ionotropic
Case#1	Relapse Only	TUBGCP3	13	113210479	Missense_Mutation	A	C	p.L203R	NA	NA	NA	264	0.102	0.165	tubulin, gamma complex associated protein 3
Case#1	Relapse Only	NSMCE1	16	27237115	Missense_Mutation	T	C	p.K218R	NA	NA	NA	133	0.128	0.232	non-SMC element 1 homolog (S. cerevisiae)
Case#1	Relapse Only	OR10H1	19	15918210	Missense_Mutation	A	G	p.L213P	NA	NA	NA	265	0.091	0.201	olfactory receptor, family 10, subfamily H, member 1
Case#1	Relapse Only	USP29	19	57640723	Missense_Mutation	C	T	p.S227L	NA	NA	NA	50	0.240	0.533	ubiquitin specific peptidase 29
Case#1	Relapse Only	PUS10	2	61235910	Missense_Mutation	C	G	p.D123H	NA	NA	NA	63	0.254	0.564	pseudouridylate synthase 10
Case#1	Relapse Only	C2orf74	2	61391520	Missense_Mutation	T	C	p.V148A	NA	NA	NA	102	0.069	0.153	chromosome 2 open reading frame 74
Case#1	Relapse Only	DNAH6	2	84880610	Missense_Mutation	T	G	p.V1749G	NA	NA	NA	170	0.071	0.157	dynein, axonemal, heavy chain 6
Case#1	Relapse Only	TFCP2L1	2	121991768	Missense_Mutation	T	A	p.N366I	NA	NA	NA	82	0.232	0.515	transcription factor CP2-like 1
Case#1	Relapse Only	CWC22	2	180837922	Missense_Mutation	C	T	p.V268M	NA	NA	NA	97	0.072	0.131	CWC22 spliceosome-associated protein
Case#1	Relapse Only	FAM83D	20	37576624	Missense_Mutation	G	A	p.V283M	NA	NA	NA	202	0.168	0.374	family with sequence similarity 83, member D
Case#1	Relapse Only	SLC5A3	21	35468687	Missense_Mutation	T	A	p.L397H	NA	NA	NA	105	0.114	0.254	solute carrier family 5 (sodium/myo-inositol cotransporter), member 3
Case#1	Relapse Only	MED15	22	20920814	Frame_Shift_Del	CAG	-	p.Q262fs	NA	NA	NA	61	0.098	0.219	mediator complex subunit 15
Case#1	Relapse Only	C22orf46	22	42089609	Missense_Mutation	G	T	p.S120I	NA	NA	NA	140	0.443	0.713	chromosome 22 open reading frame 46
Case#1	Relapse Only	PPARGC1A	4	23816051	Missense_Mutation	G	A	p.S352F	NA	NA	NA	73	0.205	0.457	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
Case#1	Relapse Only	ADAMTS12	5	33637846	Missense_Mutation	T	G	p.K575T	NA	NA	NA	147	0.109	0.242	ADAM metallopeptidase with thrombospondin type 1 motif, 12
Case#1	Relapse Only	PARP8	5	50091115	Missense_Mutation	A	G	p.K431R	NA	NA	NA	82	0.110	0.244	poly (ADP-ribose) polymerase family, member 8
Case#1	Relapse Only	GFOD1	6	13365771	Missense_Mutation	G	A	p.P126L	NA	NA	NA	121	0.355	0.645	glucose-fructose oxidoreductase domain containing 1
Case#1	Relapse Only	ZKSCAN3	6	28333706	Missense_Mutation	A	G	p.T421A	NA	NA	NA	97	0.072	0.160	zinc finger with KRAB and SCAN domains 3
Case#1	Relapse Only	FKBP1C	6	63921759	Missense_Mutation	T	G	p.F100V	NA	NA	NA	180	0.139	0.309	FK506 binding protein 1C
Case#1	Relapse Only	LGSN	6	63990777	Missense_Mutation	G	A	p.P227S	NA	NA	NA	28	0.321	0.714	lengsin, lens protein with glutamine synthetase domain
Case#1	Relapse Only	ORC3	6	88331115	Missense_Mutation	T	C	p.L344P	NA	NA	NA	125	0.200	0.444	origin recognition complex, subunit 3
Case#1	Relapse Only	CLVS2	6	123377038	Missense_Mutation	C	T	p.P255S	NA	NA	NA	97	0.062	0.137	clavesin 2
Case#1	Relapse Only	RPS6KA2	6	166827406	Missense_Mutation	T	G	p.K651T	NA	NA	NA	77	0.065	0.144	ribosomal protein S6 kinase, 90kDa, polypeptide 2
Case#1	Relapse Only	NPC1L1	7	44553240	Missense_Mutation	C	T	p.V1296I	NA	NA	NA	105	0.219	0.326	NPC1-like 1
Case#1	Relapse Only	NACAD	7	45125328	Missense_Mutation	G	A	p.P151S	NA	NA	NA	38	0.316	0.470	NAC alpha domain containing
Case#1	Relapse Only	SPDYE3	7	99910811	Missense_Mutation	G	A	p.R271K	NA	NA	NA	1205	0.105	0.168	speedy/RINGO cell cycle regulator family member E3
Case#1	Relapse Only	PNPLA8	7	108119753	Missense_Mutation	A	G	p.V650A	NA	NA	NA	161	0.093	0.169	patatin-like phospholipase domain containing 8
Case#1	Relapse Only	TRPV6	7	142571199	Splice_Site	A	G		NA	NA	NA	158	0.063	0.115	transient receptor potential cation channel, subfamily V, member 6
Case#1	Relapse Only	PKHD1L1	8	110477423	Missense_Mutation	T	G	p.F2788V	NA	NA	NA	148	0.115	0.208	polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1
Case#1	Relapse Only	KCNV2	9	2717824	Missense_Mutation	A	G	p.S29G	NA	NA	NA	85	0.071	0.157	potassium channel, subfamily V, member 2
Case#1	Relapse Only	NPR2	9	35808639	Missense_Mutation	G	C	p.R949P	NA	NA	NA	93	0.065	0.143	natriuretic peptide receptor 2
Case#1	Relapse Only	PCSK5	9	78601062	Missense_Mutation	A	C	p.Q104H	NA	NA	NA	116	0.052	0.115	proprotein convertase subtilisin/kexin type 5
Case#1	Relapse Only	SYK	9	93641149	Missense_Mutation	A	C	p.N499H	NA	NA	NA	138	0.109	0.242	spleen tyrosine kinase
Case#1	Relapse Only	TAF7L	X	100531091	Missense_Mutation	A	G	p.I394T	NA	NA	NA	36	0.333	NA	TAF7-like RNA polymerase II, TATA box binding protein (TBP)-associated factor, 50kDa
Case#1	Relapse Only	ESX1	X	103499146	Missense_Mutation	CC	AT	p.G65D	NA	NA	NA	24	0.458	NA	ESX homeobox 1
Case#1	Het->Homozygous	UBR4	1	19411143	Nonsense_Mutation	G	A	p.Q4955*	91	0.308	0.389	117	0.462	1.026	ubiquitin protein ligase E3 component n-recognin 4
Case#1	Het->Homozygous	YTHDF2	1	29070382	Missense_Mutation	C	G	p.L534V	127	0.346	0.439	192	0.443	0.984	YTH domain family, member 2
Case#1	Het->Homozygous	CSMD2	1	34128655	Missense_Mutation	C	T	p.D237N	43	0.465	0.589	56	0.429	0.952	CUB and Sushi multiple domains 2
Case#1	Het->Homozygous	MACF1	1	39823309	Missense_Mutation	C	T	p.S3901F	75	0.413	0.523	77	0.429	0.952	microtubule-actin crosslinking factor 1
Case#1	Het->Homozygous	C1orf50	1	43240949	Missense_Mutation	C	T	p.P162S	66	0.364	0.460	80	0.500	1.111	chromosome 1 open reading frame 50
Case#1	Het->Homozygous	SLC5A9	1	48694988	Missense_Mutation	C	T	p.L121F	66	0.424	0.537	102	0.461	1.024	solute carrier family 5 (sodium/sugar cotransporter), member 9
Case#1	Het->Homozygous	PODN	1	53543414	Missense_Mutation	G	A	p.E314K	65	0.415	0.526	59	0.441	0.979	podocan

Case#1	Het->Homozygous	FAM151A	1	55088975	Missense_Mutation	G	A	p.L32F	150	0.280	0.354	176	0.528	1.174	family with sequence similarity 151, member A
Case#1	Het->Homozygous	C1orf168	1	57219580	Missense_Mutation	C	T	p.E387K	94	0.277	0.350	166	0.488	1.084	chromosome 1 open reading frame 168
Case#1	Het->Homozygous	C1orf168	1	57257903	Missense_Mutation	G	A	p.P195S	49	0.184	0.232	93	0.484	1.075	chromosome 1 open reading frame 168
Case#1	Het->Homozygous	FGGY	1	60139762	Missense_Mutation	C	T	p.A490V	101	0.475	0.602	152	0.480	1.067	FGGY carbohydrate kinase domain containing
Case#1	Het->Homozygous	DEPDC1	1	68944934	Missense_Mutation	C	T	p.G669R	70	0.386	0.488	74	0.419	0.931	DEP domain containing 1
Case#1	Het->Homozygous	SLC44A5	1	75708615	Missense_Mutation	C	T	p.E143K	61	0.262	0.332	102	0.402	0.893	solute carrier family 44, member 5
Case#1	Het->Homozygous	GIPC2	1	78560732	Missense_Mutation	C	T	p.H175Y	93	0.387	0.490	146	0.466	1.035	GIPC PDZ domain containing family, member 2
Case#1	Het->Homozygous	MYBPHL	1	109839414	Nonsense_Mutation	G	A	p.Q241*	125	0.464	0.587	158	0.430	0.956	myosin binding protein H-like
Case#1	Het->Homozygous	LRIG2	1	113666581	Missense_Mutation	C	T	p.S1019L	74	0.351	0.445	106	0.415	0.922	leucine-rich repeats and immunoglobulin-like domains 2
Case#1	Het->Homozygous	SYCP1	1	115487554	Missense_Mutation	G	A	p.R702Q	93	0.409	0.517	118	0.508	1.130	synaptonemal complex protein 1
Case#1	Het->Homozygous	NGF	1	115829131	Missense_Mutation	C	T	p.E96K	68	0.294	0.372	59	0.407	0.904	nerve growth factor (beta polypeptide)
Case#1	Het->Homozygous	HSD3B2	1	119964548	Missense_Mutation	G	A	p.E142K	89	0.315	0.398	145	0.497	1.103	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2
Case#1	Het->Homozygous	HSD3B2	1	119965208	Missense_Mutation	C	T	p.R362W	79	0.380	0.481	149	0.497	1.104	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2
Case#1	Het->Homozygous	RND1	12	49254905	Missense_Mutation	C	T	p.E110K	17	0.235	0.298	33	0.394	0.875	Rho family GTPase 1
Case#1	Het->Homozygous	FRY	13	32776086	Missense_Mutation	C	T	p.P1252L	76	0.289	0.341	102	0.529	0.853	furry homolog (Drosophila)
Case#1	Het->Homozygous	RAB11FIP3	16	476583	Missense_Mutation	C	T	p.L193F	37	0.405	0.513	33	0.333	1.148	RAB11 family interacting protein 3 (class II)
Case#1	Het->Homozygous	TSC2	16	2111962	Nonsense_Mutation	C	T	p.Q404*	149	0.463	0.586	154	0.539	0.978	tuberous sclerosis 2
Case#1	Het->Homozygous	TIGD7	16	3349540	Missense_Mutation	C	T	p.D359N	34	0.441	0.558	43	0.605	1.097	tigger transposable element derived 7
Case#1	Het->Homozygous	CLUAP1	16	3554779	Missense_Mutation	C	T	p.R28C	114	0.412	0.522	139	0.590	1.071	clusterin associated protein 1
Case#1	Het->Homozygous	ZNF500	16	4802975	Missense_Mutation	C	T	p.R282Q	97	0.454	0.574	101	0.624	1.132	zinc finger protein 500
Case#1	Het->Homozygous	RBFOX1	16	7759066	Missense_Mutation	G	A	p.R335Q	102	0.363	0.459	165	0.509	0.924	RNA binding protein, fox-1 homolog (C. elegans) 1
Case#1	Het->Homozygous	ACSM2A	16	20476954	Missense_Mutation	C	T	p.S98L	137	0.255	0.323	201	0.502	0.912	acyl-CoA synthetase medium-chain family member 2A
Case#1	Het->Homozygous	GATSL3	22	30682360	Missense_Mutation	G	A	p.P212L	51	0.392	0.496	88	0.398	0.884	GATS protein-like 3
Case#1	Het->Homozygous	SPON2	4	1164876	Missense_Mutation	C	T	p.D183N	17	0.353	0.447	14	0.500	1.111	spondin 2, extracellular matrix protein
Case#1	Baseline Only	KIAA1984	9	139694569	Missense_Mutation	A	C	p.D129A	10	1.000	1.266	NA	NA	NA	
Case#1	Baseline Only	PRDM16	1	3321331	Missense_Mutation	G	A	p.E305K	86	0.326	0.412	NA	NA	NA	PR domain containing 16
Case#1	Baseline Only	EXOSC10	1	11158126	Missense_Mutation	G	A	p.P67S	69	0.435	0.550	NA	NA	NA	exosome component 10
Case#1	Baseline Only	PLOD1	1	12017971	Missense_Mutation	G	A	p.E272K	121	0.430	0.544	NA	NA	NA	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1
Case#1	Baseline Only	PRAMEF4	1	12941719	Missense_Mutation	C	T	p.M277I	559	0.188	0.238	NA	NA	NA	PRAME family member 4
Case#1	Baseline Only	RSC1A1	1	15987133	Missense_Mutation	C	T	p.S257F	35	0.400	0.506	NA	NA	NA	regulatory solute carrier protein, family 1, member 1
Case#1	Baseline Only	FAM131C	1	16385124	Missense_Mutation	GG	AA	p.S217F	142	0.141	0.178	NA	NA	NA	family with sequence similarity 131, member C
Case#1	Baseline Only	FBXO42	1	16577779	Missense_Mutation	G	A	p.P514S	62	0.339	0.429	NA	NA	NA	F-box protein 42
Case#1	Baseline Only	NBPF1	1	16892277	Missense_Mutation	G	A	p.A972V	133	0.083	0.105	NA	NA	NA	neuroblastoma breakpoint family, member 1
Case#1	Baseline Only	NBPF1	1	16895613	Missense_Mutation	G	A	p.H857Y	1129	0.097	0.122	NA	NA	NA	neuroblastoma breakpoint family, member 1
Case#1	Baseline Only	IL22RA1	1	24447965	Missense_Mutation	G	A	p.A352V	97	0.412	0.522	NA	NA	NA	interleukin 22 receptor, alpha 1
Case#1	Baseline Only	CSMD2	1	34037163	Nonsense_Mutation	C	T	p.W2642*	81	0.333	0.422	NA	NA	NA	CUB and Sushi multiple domains 2
Case#1	Baseline Only	CSMD2	1	34401378	Missense_Mutation	G	A	p.P232L	28	0.286	0.362	NA	NA	NA	CUB and Sushi multiple domains 2
Case#1	Baseline Only	NFYC	1	41236181	Frame_Shift_Ins	-	C	p.HP353fs	71	0.380	0.481	NA	NA	NA	nuclear transcription factor Y, gamma
Case#1	Baseline Only	KLF17	1	44595265	Missense_Mutation	C	T	p.P108S	61	0.328	0.415	NA	NA	NA	Kruppel-like factor 17
Case#1	Baseline Only	PTCH2	1	45297861	Missense_Mutation	GG	AA	p.L140F	78	0.385	0.487	NA	NA	NA	patched 2
Case#1	Baseline Only	ECHDC2	1	53370732	Missense_Mutation	G	A	p.T163I	93	0.462	0.585	NA	NA	NA	enoyl CoA hydratase domain containing 2
Case#1	Baseline Only	C1orf168	1	57257998	Missense_Mutation	C	T	p.G163E	60	0.317	0.401	NA	NA	NA	chromosome 1 open reading frame 168
Case#1	Baseline Only	C8B	1	57417854	Splice_Site	C	T		81	0.457	0.578	NA	NA	NA	complement component 8, beta polypeptide
Case#1	Baseline Only	L1TD1	1	62676451	Nonsense_Mutation	C	T	p.Q669*	36	0.389	0.492	NA	NA	NA	LINE-1 type transposase domain containing 1
Case#1	Baseline Only	PGM1	1	64125279	Missense_Mutation	C	T	p.S541F	46	0.370	0.468	NA	NA	NA	phosphoglucomutase 1
Case#1	Baseline Only	CACHD1	1	65131810	Missense_Mutation	G	A	p.G783S	72	0.417	0.527	NA	NA	NA	cache domain containing 1
Case#1	Baseline Only	TCTEX1D1	1	67242961	Missense_Mutation	A	C	p.M122L	67	0.448	0.567	NA	NA	NA	Tctex1 domain containing 1
Case#1	Baseline Only	CLCA2	1	86913369	Missense_Mutation	G	A	p.G631E	80	0.400	0.506	NA	NA	NA	chloride channel accessory 2
Case#1	Baseline Only	LRRC8B	1	90048448	Missense_Mutation	CC	TT	p.S80F	44	0.295	0.374	NA	NA	NA	leucine rich repeat containing 8 family, member B
Case#1	Baseline Only	F3	1	95005853	Missense_Mutation	C	T	p.E58K	103	0.427	0.541	NA	NA	NA	coagulation factor III (thromboplastin, tissue factor)
Case#1	Baseline Only	DPYD	1	98293682	Missense_Mutation	C	T	p.R74Q	38	0.316	0.400	NA	NA	NA	dihydropyrimidine dehydrogenase
Case#1	Baseline Only	COL11A1	1	103364320	Missense_Mutation	C	T	p.G1384S	113	0.319	0.403	NA	NA	NA	collagen, type XI, alpha 1
Case#1	Baseline Only	COL11A1	1	103463909	Missense_Mutation	C	T	p.G718E	77	0.312	0.395	NA	NA	NA	collagen, type XI, alpha 1
Case#1	Baseline Only	CELSR2	1	109813876	Missense_Mutation	C	T	p.S2545F	65	0.400	0.506	NA	NA	NA	cadherin, EGF LAG seven-pass G-type receptor 2
Case#1	Baseline Only	AHCYL1	1	110527681	Frame_Shift_Ins	-	TGCC	p.-4fs	97	0.320	0.405	NA	NA	NA	adenosylhomocysteinase-like 1
Case#1	Baseline Only	DENND2C	1	115164674	Missense_Mutation	G	A	p.P357S	126	0.397	0.502	NA	NA	NA	DENN/MADD domain containing 2C
Case#1	Baseline Only	IGSF3	1	117142910	Missense_Mutation	G	A	p.S561F	68	0.338	0.428	NA	NA	NA	immunoglobulin superfamily, member 3
Case#1	Baseline Only	WDR3	1	118481139	Missense_Mutation	T	A	p.D179E	76	0.382	0.483	NA	NA	NA	WD repeat domain 3
Case#1	Baseline Only	SPAG17	1	118624140	Missense_Mutation	C	T	p.E630K	60	0.267	0.338	NA	NA	NA	sperm associated antigen 17
Case#1	Baseline Only	CRNN	1	152382120	Missense_Mutation	C	T	p.G480S	121	0.066	0.078	NA	NA	NA	cornulin
Case#1	Baseline Only	CHRM3	1	240071811	Missense_Mutation	G	A	p.E354K	21	0.619	0.729	NA	NA	NA	cholinergic receptor, muscarinic 3
Case#1	Baseline Only	FRMPD2	10	49446153	Missense_Mutation	C	G	p.A268P	57	0.158	0.200	NA	NA	NA	FERM and PDZ domain containing 2
Case#1	Baseline Only	PCDH15	10	55582166	Missense_Mutation	A	T	p.F1774I	14	0.214	0.271	NA	NA	NA	protocadherin-related 15
Case#1	Baseline Only	ARID5B	10	63850676	Missense_Mutation	C	T	p.P485L	34	0.353	0.447	NA	NA	NA	AT rich interactive domain 5B (MRF1-like)
Case#1	Baseline Only	RUFY2	10	70139242	Missense_Mutation	T	C	p.I382V	35	0.171	0.217	NA	NA	NA	RUN and FYVE domain containing 2
Case#1	Baseline Only	OR4C5	11	48387693	Frame_Shift_Del	C	-	p.E109fs	42	0.262	0.332	NA	NA	NA	olfactory receptor, family 4, subfamily C, member 5
Case#1	Baseline Only	CWF19L2	11	107309831	Missense_Mutation	A	G	p.S217P	104	0.144	0.183	NA	NA	NA	CWF19-like 2, cell cycle control (S. pombe)
Case#1	Baseline Only	CEP164	11	117234205	Missense_Mutation	G	A	p.G250S	143	0.063	0.080	NA	NA	NA	centrosomal protein 164kDa
Case#1	Baseline Only	PRB3	12	11420444	Missense_Mutation	C	G	p.E247Q	65	0.062	0.078	NA	NA	NA	proline-rich protein BstNI subfamily 3
Case#1	Baseline Only	CAPRIN2	12	30882208	Missense_Mutation	C	T	p.E386K	24	0.375	0.475	NA	NA	NA	caprin family member 2
Case#1	Baseline Only	MUC19	12	40821867	Missense_Mutation	G	A	p.V206I	143	0.070	0.089	NA	NA	NA	mucin 19, oligomeric
Case#1	Baseline Only	TMCC3	12	94976130	Missense_Mutation	G	A	p.S88L	62	0.306	0.388	NA	NA	NA	transmembrane and coiled-coil domain family 3
Case#1	Baseline Only	APAF1	12	99060110	Missense_Mutation	C	A	p.T446K	62	0.113	0.143	NA	NA	NA	apoptotic peptidase activating factor 1
Case#1	Baseline Only	GJA3	13	20716277	Missense_Mutation	C	T	p.G384E	24	0.500	0.633	NA	NA	NA	gap junction protein, alpha 3, 46kDa
Case#1	Baseline Only	PCDH17	13	58208790	Missense_Mutation	A	C	p.M704L	64	0.203	0.239	NA	NA	NA	protocadherin 17
Case#1	Baseline Only	OR4N4	15	22382897	Missense_Mutation	A	G	p.Y142C	27	0.185	0.234	NA	NA	NA	olfactory receptor, family 4, subfamily N, member 4
Case#1	Baseline Only	RP11-467N20.5	15	23407013	Missense_Mutation	C	T	p.R608K	221	0.063	0.080	NA	NA	NA	

Case#1	Baseline Only	UBE2I	16	1364309	Missense_Mutation	C	T	p.P28S	173	0.382	0.483	NA	NA	NA	ubiquitin-conjugating enzyme E2I
Case#1	Baseline Only	E4F1	16	2283990	Splice_Site	C	T	p.T458T	104	0.404	0.511	NA	NA	NA	E4F transcription factor 1
Case#1	Baseline Only	ABCA3	16	2328371	Missense_Mutation	C	T	p.D1546N	81	0.370	0.469	NA	NA	NA	ATP-binding cassette, sub-family A (ABC1), member 3
Case#1	Baseline Only	C16orf96	16	4625472	Missense_Mutation	G	A	p.G331R	79	0.329	0.417	NA	NA	NA	chromosome 16 open reading frame 96
Case#1	Baseline Only	ACSM2B	16	20570685	Missense_Mutation	C	T	p.E88K	35	0.314	0.398	NA	NA	NA	acyl-CoA synthetase medium-chain family member 2B
Case#1	Baseline Only	ACSM1	16	20693784	Splice_Site	C	T	p.G135G	171	0.246	0.311	NA	NA	NA	acyl-CoA synthetase medium-chain family member 1
Case#1	Baseline Only	WWP2	16	69969798	Missense_Mutation	C	T	p.P629S	53	0.377	0.478	NA	NA	NA	WW domain containing E3 ubiquitin protein ligase 2
Case#1	Baseline Only	SYNRG	17	35880726	Missense_Mutation	G	A	p.S1231F	52	0.327	0.414	NA	NA	NA	synergin, gamma
Case#1	Baseline Only	TBC1D3F	17	36288299	Nonsense_Mutation	C	T	p.Q129*	702	0.087	0.110	NA	NA	NA	TBC1 domain family, member 3F
Case#1	Baseline Only	MUC16	19	9017469	Missense_Mutation	GG	AA	p.R12619C	202	0.109	0.138	NA	NA	NA	mucin 16, cell surface associated
Case#1	Baseline Only	DNMT1	19	10305571	Missense_Mutation	G	A	p.P2L	36	0.417	0.527	NA	NA	NA	DNA (cytosine-5-)-methyltransferase 1
Case#1	Baseline Only	AC007204.1	19	20048638	Missense_Mutation	C	T	p.G1E	120	0.367	0.464	NA	NA	NA	
Case#1	Baseline Only	WDR87	19	38376099	Missense_Mutation	C	T	p.D2699N	41	0.390	0.494	NA	NA	NA	WD repeat domain 87
Case#1	Baseline Only	AC011500.1	19	39930255	Missense_Mutation	C	T	p.P15L	29	0.483	0.611	NA	NA	NA	
Case#1	Baseline Only	POLD1	19	50906324	Missense_Mutation	C	T	p.P329S	37	0.405	0.513	NA	NA	NA	polymerase (DNA directed), delta 1, catalytic subunit
Case#1	Baseline Only	SHANK1	19	51172351	Missense_Mutation	G	A	p.P956S	17	0.235	0.298	NA	NA	NA	SH3 and multiple ankyrin repeat domains 1
Case#1	Baseline Only	C2orf78	2	74043397	Missense_Mutation	G	A	p.G683S	19	0.421	0.533	NA	NA	NA	chromosome 2 open reading frame 78
Case#1	Baseline Only	IWS1	2	128263292	Nonsense_Mutation	C	A	p.G63*	31	0.129	0.163	NA	NA	NA	IWS1 homolog (S. cerevisiae)
Case#1	Baseline Only	SOGA1	20	35431407	Missense_Mutation	G	A	p.S826F	43	0.302	0.383	NA	NA	NA	suppressor of glucose, autophagy associated 1
Case#1	Baseline Only	C20orf62	20	43090908	Missense_Mutation	C	T	p.D44N	30	0.400	0.506	NA	NA	NA	chromosome 20 open reading frame 62
Case#1	Baseline Only	SCN11A	3	38889189	Missense_Mutation	GG	AA	p.P1458S	36	0.528	0.621	NA	NA	NA	sodium channel, voltage-gated, type XI, alpha subunit
Case#1	Baseline Only	BMP2K	4	79792083	Frame_Shift_Del	CAG	-	p.Q486fs	90	0.078	0.098	NA	NA	NA	BMP2 inducible kinase
Case#1	Baseline Only	SLC9B1	4	103822321	Missense_Mutation	C	T	p.D501N	595	0.052	0.066	NA	NA	NA	solute carrier family 9, subfamily B (NHA1, cation proton antiporter 1), member 1
Case#1	Baseline Only	PCDHB7	5	140554769	Missense_Mutation	C	T	p.R785C	343	0.149	0.188	NA	NA	NA	protocadherin beta 7
Case#1	Baseline Only	KIAA1009	6	84884944	Missense_Mutation	G	T	p.Q596K	26	0.192	0.295	NA	NA	NA	
Case#1	Baseline Only	RHOBTB2	8	22864490	Missense_Mutation	GG	AA	p.V245M	23	0.348	0.440	NA	NA	NA	Rho-related BTB domain containing 2
Case#1	Baseline Only	PREX2	8	69104673	Missense_Mutation	C	T	p.S1506F	63	0.270	0.318	NA	NA	NA	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2
Case#1	Baseline Only	CR769776.1	9	69380339	Missense_Mutation	G	A	p.S31L	556	0.054	0.068	NA	NA	NA	
Case#1	Baseline Only	PRUNE2	9	79244209	Splice_Site	A	-		24	0.292	0.369	NA	NA	NA	prune homolog 2 (Drosophila)
Case#1	Baseline Only	ABCA2	9	139915386	Missense_Mutation	G	A	p.A341V	27	0.370	0.469	NA	NA	NA	ATP-binding cassette, sub-family A (ABC1), member 2
Case#1	Baseline Only	FAM9A	X	8763346	Frame_Shift_Del	CTG	-	p.Q202fs	32	0.188	0.237	NA	NA	NA	family with sequence similarity 9, member A
Case#1	Baseline Only	WWC3	X	10093137	Missense_Mutation	G	A	p.E634K	94	0.255	0.323	NA	NA	NA	WWC family member 3
Case#1	Baseline Only	CTBP2	10	126691950	Missense_Mutation	A	G	p.V57A	143	0.126	NA	NA	NA	NA	C-terminal binding protein 2
Case#2	Relapse Only	JAK2	9	5070054	Splice_Site	T	G		NA	NA	NA	76	0.553	0.987	Janus kinase 2
Case#2	Relapse Only	CD164L2	1	27708822	Nonsense_Mutation	A	T	p.C108*	NA	NA	NA	210	0.057	0.080	CD164 sialomucin-like 2
Case#2	Relapse Only	ZSWIM5	1	45501872	Missense_Mutation	G	A	p.A665V	NA	NA	NA	145	0.083	0.115	zinc finger, SWIM-type containing 5
Case#2	Relapse Only	C8A	1	57333319	Missense_Mutation	T	G	p.C39G	NA	NA	NA	200	0.135	0.188	complement component 8, alpha polypeptide
Case#2	Relapse Only	FCAMR	1	207140983	Missense_Mutation	C	T	p.R18K	NA	NA	NA	241	0.062	0.095	Fc receptor, IgA, IgM, high affinity
Case#2	Relapse Only	SDE2	1	226180122	Missense_Mutation	C	T	p.R166H	NA	NA	NA	135	0.170	0.260	SDE2 telomere maintenance homolog (S. pombe)
Case#2	Relapse Only	DCLRE1C	10	14977485	Missense_Mutation	C	T	p.M147I	NA	NA	NA	121	0.388	0.694	DNA cross-link repair 1C
Case#2	Relapse Only	DCLRE1C	10	14977523	Missense_Mutation	C	T	p.G135R	NA	NA	NA	113	0.407	0.727	DNA cross-link repair 1C
Case#2	Relapse Only	LRIT1	10	85993828	Splice_Site	C	T		NA	NA	NA	98	0.143	0.255	leucine-rich repeat, immunoglobulin-like and transmembrane domains 1
Case#2	Relapse Only	PCNXL3	11	65384461	Missense_Mutation	A	T	p.Q107L	NA	NA	NA	60	0.433	0.774	pecanex-like 3 (Drosophila)
Case#2	Relapse Only	GRIA4	11	105789535	Missense_Mutation	A	G	p.K456R	NA	NA	NA	165	0.267	0.476	glutamate receptor, ionotropic, AMPA 4
Case#2	Relapse Only	DCP1B	12	2058318	Frame_Shift_Del	G	-	p.P569fs	NA	NA	NA	167	0.246	0.374	decapping mRNA 1B
Case#2	Relapse Only	PRH2	12	11083425	Missense_Mutation	G	A	p.G89R	NA	NA	NA	332	0.111	0.170	proline-rich protein HaeIII subfamily 2
Case#2	Relapse Only	PIK3C2G	12	18716381	Missense_Mutation	CA	AT	p.S1243Y	NA	NA	NA	147	0.190	0.290	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 gamma
Case#2	Relapse Only	KRT2	12	53042832	Missense_Mutation	G	T	p.L306M	NA	NA	NA	151	0.311	0.556	keratin 2
Case#2	Relapse Only	KRT76	12	53162841	Missense_Mutation	C	T	p.V525I	NA	NA	NA	181	0.260	0.464	keratin 76
Case#2	Relapse Only	ATXN2	12	111924586	Missense_Mutation	G	T	p.F921L	NA	NA	NA	68	0.235	0.420	ataxin 2
Case#2	Relapse Only	LRRK1	15	101606184	Missense_Mutation	C	G	p.P1848A	NA	NA	NA	76	0.224	0.341	leucine-rich repeat kinase 1
Case#2	Relapse Only	TMEM159	16	21185368	Missense_Mutation	C	G	p.C101W	NA	NA	NA	127	0.205	0.312	transmembrane protein 159
Case#2	Relapse Only	SCNN1G	16	23223460	Missense_Mutation	C	A	p.H428N	NA	NA	NA	137	0.073	0.111	sodium channel, non-voltage-gated 1, gamma subunit
Case#2	Relapse Only	PRR14	16	30666042	Missense_Mutation	CG	TT	p.R251F	NA	NA	NA	97	0.165	0.251	proline rich 14
Case#2	Relapse Only	NLRC5	16	57110766	Missense_Mutation	G	A	p.C1596Y	NA	NA	NA	89	0.292	0.445	NLR family, CARD domain containing 5
Case#2	Relapse Only	HYDIN	16	71007260	Missense_Mutation	T	G	p.M1789L	NA	NA	NA	316	0.114	0.174	HYDIN, axonemal central pair apparatus protein
Case#2	Relapse Only	PHLPP2	16	71683269	Missense_Mutation	C	T	p.E1166K	NA	NA	NA	206	0.112	0.170	PH domain and leucine rich repeat protein phosphatase 2
Case#2	Relapse Only	KCNAB3	17	7827771	Missense_Mutation	A	T	p.Y225N	NA	NA	NA	155	0.271	0.484	potassium voltage-gated channel, shaker-related subfamily, beta member 3
Case#2	Relapse Only	USP43	17	9583599	Nonsense_Mutation	G	T	p.E341*	NA	NA	NA	115	0.209	0.373	ubiquitin specific peptidase 43
Case#2	Relapse Only	CSF3	17	38172825	Missense_Mutation	C	A	p.P134T	NA	NA	NA	172	0.267	0.478	colony stimulating factor 3 (granulocyte)
Case#2	Relapse Only	RNF213	17	78346865	Missense_Mutation	G	C	p.R4281P	NA	NA	NA	194	0.093	0.141	ring finger protein 213
Case#2	Relapse Only	TMEM200C	18	5890552	Missense_Mutation	G	A	p.A504V	NA	NA	NA	57	0.298	0.454	transmembrane protein 200C
Case#2	Relapse Only	MUC16	19	9064668	Missense_Mutation	G	C	p.S7593C	NA	NA	NA	228	0.193	0.294	mucin 16, cell surface associated
Case#2	Relapse Only	LHB	19	49519534	Missense_Mutation	G	A	p.P73S	NA	NA	NA	463	0.177	0.270	luteinizing hormone beta polypeptide
Case#2	Relapse Only	ZNF324B	19	58966688	Missense_Mutation	CG	TT	p.P126L	NA	NA	NA	246	0.199	0.304	zinc finger protein 324B
Case#2	Relapse Only	C2orf16	2	27803529	Missense_Mutation	G	A	p.A1364T	NA	NA	NA	142	0.239	0.365	chromosome 2 open reading frame 16
Case#2	Relapse Only	HNRNPLL	2	38809081	Missense_Mutation	T	C	p.Y259C	NA	NA	NA	204	0.216	0.329	heterogeneous nuclear ribonucleoprotein L-like
Case#2	Relapse Only	DUSP11	2	73993587	Missense_Mutation	C	T	p.R298Q	NA	NA	NA	234	0.209	0.319	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)
Case#2	Relapse Only	FAM178B	2	97613588	Missense_Mutation	C	T	p.D497N	NA	NA	NA	124	0.492	0.750	family with sequence similarity 178, member B
Case#2	Relapse Only	MYO7B	2	128366350	Missense_Mutation	C	T	p.S904F	NA	NA	NA	358	0.159	0.243	myosin VIIB
Case#2	Relapse Only	DNAH7	2	196762426	Missense_Mutation	G	C	p.P1538A	NA	NA	NA	239	0.188	0.287	dynein, axonemal, heavy chain 7
Case#2	Relapse Only	PNKD	2	219206288	Missense_Mutation	C	T	p.R186W	NA	NA	NA	261	0.061	0.093	paroxysmal nonkinesigenic dyskinesia
Case#2	Relapse Only	CHRNG	2	233408368	Missense_Mutation	C	T	p.R332W	NA	NA	NA	167	0.228	0.347	cholinergic receptor, nicotinic, gamma (muscle)
Case#2	Relapse Only	GDF5	20	34022347	Missense_Mutation	G	T	p.S289Y	NA	NA	NA	146	0.164	0.229	growth differentiation factor 5
Case#2	Relapse Only	MPPED1	22	43898547	Missense_Mutation	A	G	p.K258E	NA	NA	NA	126	0.175	0.243	metallophosphoesterase domain containing 1
Case#2	Relapse Only	SLC26A6	3	48669111	Missense_Mutation	G	A	p.P292S	NA	NA	NA	104	0.173	0.264	solute carrier family 26 (anion exchanger), member 6
Case#2	Relapse Only	UBA3	3	69105214	Splice_Site	C	A	p.L395L	NA	NA	NA	116	0.207	0.315	ubiquitin-like modifier activating enzyme 3

Case#2	Relapse Only	WDR52	3	113092257	Splice_Site	C	G		NA	NA	NA	206	0.233	0.355	
Case#2	Relapse Only	SIDT1	3	113300268	Missense_Mutation	A	C	p.K242Q	NA	NA	NA	167	0.222	0.338	SID1 transmembrane family, member 1
Case#2	Relapse Only	GRAMD1C	3	113595055	Missense_Mutation	A	C	p.K136T	NA	NA	NA	221	0.199	0.303	GRAM domain containing 1C
Case#2	Relapse Only	GRK7	3	141535846	Missense_Mutation	G	A	p.C539Y	NA	NA	NA	117	0.214	0.326	G protein-coupled receptor kinase 7
Case#2	Relapse Only	THPO	3	184090671	Missense_Mutation	C	T	p.G231D	NA	NA	NA	120	0.242	0.368	thrombopoietin
Case#2	Relapse Only	LSG1	3	194387217	Missense_Mutation	T	G	p.H104P	NA	NA	NA	108	0.241	0.367	large 60S subunit nuclear export GTPase 1
Case#2	Relapse Only	MAN2B2	4	6611023	Nonsense_Mutation	C	G	p.Y668*	NA	NA	NA	110	0.300	0.536	mannosidase, alpha, class 2B, member 2
Case#2	Relapse Only	CD38	4	15826506	Missense_Mutation	T	G	p.I122M	NA	NA	NA	201	0.239	0.364	CD38 molecule
Case#2	Relapse Only	CHRNA9	4	40351379	Missense_Mutation	T	G	p.F282L	NA	NA	NA	132	0.242	0.369	cholinergic receptor, nicotinic, alpha 9 (neuronal)
Case#2	Relapse Only	GUF1	4	44691955	Missense_Mutation	C	T	p.P433L	NA	NA	NA	128	0.063	0.095	GUF1 GTPase homolog (S. cerevisiae)
Case#2	Relapse Only	KIAA1109	4	123234822	Missense_Mutation	C	T	p.T3431I	NA	NA	NA	122	0.246	0.375	KIAA1109
Case#2	Relapse Only	WWC2	4	184171119	Missense_Mutation	G	A	p.S309N	NA	NA	NA	156	0.186	0.283	WW and C2 domain containing 2
Case#2	Relapse Only	CMYA5	5	79033293	Missense_Mutation	G	T	p.S2902I	NA	NA	NA	162	0.160	0.224	cardiomyopathy associated 5
Case#2	Relapse Only	GPR98	5	90052415	Missense_Mutation	C	A	p.P3909T	NA	NA	NA	134	0.187	0.260	G protein-coupled receptor 98
Case#2	Relapse Only	KIF4B	5	154394048	Missense_Mutation	C	T	p.S210F	NA	NA	NA	231	0.069	0.106	kinesin family member 4B
Case#2	Relapse Only	FAM188B	7	30825484	Missense_Mutation	A	G	p.E180G	NA	NA	NA	402	0.072	0.085	family with sequence similarity 188, member B
Case#2	Relapse Only	ABCA13	7	48318976	Missense_Mutation	A	T	p.T2729S	NA	NA	NA	369	0.103	0.121	ATP-binding cassette, sub-family A (ABC1), member 13
Case#2	Relapse Only	ABCB4	7	87101971	Missense_Mutation	G	C	p.T34R	NA	NA	NA	145	0.055	0.070	ATP-binding cassette, sub-family B (MDR/TAP), member 4
Case#2	Relapse Only	COPS6	7	99688107	Missense_Mutation	G	T	p.K140N	NA	NA	NA	341	0.135	0.170	COP9 signalosome subunit 6
Case#2	Relapse Only	CHRM2	7	136700034	Missense_Mutation	G	C	p.G141A	NA	NA	NA	177	0.107	0.135	cholinergic receptor, muscarinic 2
Case#2	Relapse Only	DGKI	7	137170128	Missense_Mutation	G	A	p.H807Y	NA	NA	NA	146	0.075	0.095	diacylglycerol kinase, iota
Case#2	Relapse Only	NOS3	7	150696287	Missense_Mutation	G	C	p.W322C	NA	NA	NA	154	0.136	0.172	nitric oxide synthase 3 (endothelial cell)
Case#2	Relapse Only	CSMD1	8	2800046	Missense_Mutation	G	A	p.P3496S	NA	NA	NA	181	0.193	0.269	CUB and Sushi multiple domains 1
Case#2	Relapse Only	DCSTAMP	8	105360905	Frame_Shift_Del	T	-	p.I42fs	NA	NA	NA	193	0.218	0.332	dendrocyte expressed seven transmembrane protein
Case#2	Relapse Only	RSPO2	8	108970406	Missense_Mutation	G	T	p.T173K	NA	NA	NA	97	0.196	0.298	R-spondin 2
Case#2	Relapse Only	PKHD1L1	8	110520455	Missense_Mutation	T	C	p.V3786A	NA	NA	NA	122	0.107	0.162	polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1
Case#2	Relapse Only	FAM205A	9	34725994	Missense_Mutation	C	A	p.G415W	NA	NA	NA	162	0.173	0.309	family with sequence similarity 205, member A
Case#2	Relapse Only	TRPM6	9	77422991	Missense_Mutation	G	A	p.H533Y	NA	NA	NA	148	0.196	0.350	transient receptor potential cation channel, subfamily M, member 6
Case#2	Relapse Only	DAPK1	9	90321284	Frame_Shift_Ins	-	T	p.M1100fs	NA	NA	NA	184	0.245	0.437	death-associated protein kinase 1
Case#2	Relapse Only	CHST7	X	46433406	Missense_Mutation	T	G	p.F14V	NA	NA	NA	144	0.326	NA	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7
Case#2	Relapse Only	OPHN1	X	67652784	Nonsense_Mutation	G	A	p.Q27*	NA	NA	NA	90	0.411	NA	oligophrenin 1
Case#2	Relapse Only	F8	X	154130406	Missense_Mutation	G	C	p.A2012G	NA	NA	NA	104	0.346	NA	coagulation factor VIII, procoagulant component
Case#2	Het->Homozygous	TAF1L	9	32633779	Missense_Mutation	C	T	p.R600Q	199	0.482	0.495	159	0.547	0.977	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 210kDa-like
Case#2	Het->Homozygous	FBP2	9	97349720	Missense_Mutation	C	T	p.G68R	142	0.556	0.576	189	0.524	0.935	fructose-1,6-bisphosphatase 2
Case#2	Het->Homozygous	OLFM1	9	138011716	Missense_Mutation	C	T	p.P384S	101	0.554	0.574	121	0.529	0.945	olfactomedin 1
Case#2	Het->Homozygous	KCNT1	9	138649216	Missense_Mutation	G	A	p.E231K	121	0.636	0.659	161	0.590	1.054	potassium channel, subfamily T, member 1
Case#2	Baseline Only	KRTAP4-5	17	39305785	Missense_Mutation	A	T	p.C79S	384	0.214	0.221	NA	NA	NA	keratin associated protein 4-5
Case#2	Baseline Only	CDC27	17	45234357	Missense_Mutation	G	A	p.S255F	131	0.053	0.055	NA	NA	NA	cell division cycle 27
Case#2	Baseline Only	EMR3	19	14769339	Missense_Mutation	C	G	p.E127Q	52	0.077	0.079	NA	NA	NA	egf-like module containing, mucin-like, hormone receptor-like 3
Case#2	Baseline Only	TAF1L	9	32632916	Missense_Mutation	G	A	p.R888C	275	0.440	0.452	NA	NA	NA	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 210kDa-like
Case#2	Baseline Only	PCSK5	9	78936451	Missense_Mutation	G	A	p.G1306E	118	0.339	0.351	NA	NA	NA	proprotein convertase subtilisin/kexin type 5
Case#2	Baseline Only	UBQLN1	9	86300989	Nonsense_Mutation	G	A	p.Q88*	81	0.272	0.281	NA	NA	NA	ubiquilin 1
Case#2	Baseline Only	CYLC2	9	105767002	Missense_Mutation	G	A	p.G69E	73	0.356	0.369	NA	NA	NA	cylicin, basic protein of sperm head cytoskeleton 2
Case#2	Baseline Only	AMBP	9	116825001	Missense_Mutation	C	T	p.G214E	150	0.473	0.486	NA	NA	NA	alpha-1-microglobulin/bikunin precursor
Case#2	Baseline Only	COL27A1	9	116958238	Splice_Site	G	A		163	0.454	0.466	NA	NA	NA	collagen, type XXVII, alpha 1
Case#2	Baseline Only	OR1N1	9	125289493	Missense_Mutation	C	T	p.G27E	178	0.494	0.507	NA	NA	NA	olfactory receptor, family 1, subfamily N, member 1
Case#2	Baseline Only	RPL7A	9	136217582	Splice_Site	C	T	p.S209L	131	0.244	0.253	NA	NA	NA	ribosomal protein L7a
Case#3	Relapse Only	B2M	15	45003786	Frame_Shift_Del	TCTT	-	p.S14fs	NA	NA	NA	90	0.444	1.111	beta-2-microglobulin
Case#3	Relapse Only	OBSCN	1	228504591	Missense_Mutation	C	A	p.H4489Q	NA	NA	NA	40	0.125	0.219	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
Case#3	Relapse Only	OBSCN	1	228504670	Missense_Mutation	C	T	p.R4516W	NA	NA	NA	14	0.286	0.500	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
Case#3	Relapse Only	GPRIN2	10	47000217	Missense_Mutation	G	A	p.R446H	NA	NA	NA	71	0.056	0.141	G protein regulated inducer of neurite outgrowth 2
Case#3	Relapse Only	PTEN	10	89720649	Splice_Site	A	T		NA	NA	NA	42	0.167	0.417	phosphatase and tensin homolog
Case#3	Relapse Only	MUC5B	11	1272226	Missense_Mutation	A	C	p.T4706P	NA	NA	NA	369	0.076	0.190	mucin 5B, oligomeric mucus/gel-forming
Case#3	Relapse Only	POTEM	14	20002247	Missense_Mutation	C	T	p.G392E	NA	NA	NA	1910	0.078	0.312	POTE ankyrin domain family, member M
Case#3	Relapse Only	OR10G2	14	22102188	Missense_Mutation	C	T	p.D271N	NA	NA	NA	172	0.233	0.581	olfactory receptor, family 10, subfamily G, member 2
Case#3	Relapse Only	DDX52	17	35988719	Splice_Site	A	-		NA	NA	NA	26	0.154	0.385	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52
Case#3	Relapse Only	DOT1L	19	2226676	Missense_Mutation	G	A	p.G1386S	NA	NA	NA	28	0.179	0.313	DOT1-like histone H3K79 methyltransferase
Case#3	Relapse Only	ZNF491	19	11916814	Missense_Mutation	G	C	p.E16Q	NA	NA	NA	108	0.269	0.470	zinc finger protein 491
Case#3	Relapse Only	ZNF835	19	57175578	Missense_Mutation	C	T	p.G330D	NA	NA	NA	64	0.156	0.391	zinc finger protein 835
Case#3	Relapse Only	ATAD2B	2	24110824	Missense_Mutation	C	G	p.K150N	NA	NA	NA	302	0.288	0.504	ATPase family, AAA domain containing 2B
Case#3	Relapse Only	RGPD8	2	113191010	Missense_Mutation	A	C	p.D7E	NA	NA	NA	204	0.064	0.112	RANBP2-like and GRIP domain containing 8
Case#3	Relapse Only	KLHL30	2	239050033	Missense_Mutation	C	T	p.A213V	NA	NA	NA	53	0.132	0.231	kelch-like family member 30
Case#3	Relapse Only	TPTE	21	10906910	Missense_Mutation	C	T	p.D551N	NA	NA	NA	533	0.077	0.154	transmembrane phosphatase with tensin homology
Case#3	Relapse Only	ITIH1	3	52823792	Missense_Mutation	C	A	p.P748H	NA	NA	NA	181	0.061	0.152	inter-alpha-trypsin inhibitor heavy chain 1
Case#3	Relapse Only	PCDHB13	5	140595625	Missense_Mutation	G	A	p.V644I	NA	NA	NA	132	0.106	0.265	protocadherin beta 13
Case#3	Relapse Only	HUS1B	6	656555	Missense_Mutation	G	T	p.H130Q	NA	NA	NA	17	0.176	0.441	HUS1 checkpoint homolog b (S. pombe)
Case#3	Relapse Only	GLTSCR1L	6	42797699	Missense_Mutation	T	G	p.V543G	NA	NA	NA	138	0.072	0.181	GLTSCR1-like
Case#3	Relapse Only	AGBL3	7	134800245	Missense_Mutation	G	A	p.V742I	NA	NA	NA	229	0.293	0.512	ATP/GTP binding protein-like 3
Case#3	Relapse Only	RP1L1	8	10469030	Missense_Mutation	G	A	p.R860W	NA	NA	NA	54	0.093	0.231	retinitis pigmentosa 1-like 1
Case#3	Relapse Only	CYLC2	9	105767601	Missense_Mutation	T	A	p.S230T	NA	NA	NA	144	0.056	0.139	cylicin, basic protein of sperm head cytoskeleton 2
Case#3	Relapse Only	GPC4	X	132458528	Missense_Mutation	G	A	p.S119F	NA	NA	NA	26	0.462	0.808	glypican 4
Case#3	Het->Homozygous	OR5AU1	14	21623343	Missense_Mutation	G	A	p.S281L	125	0.472	0.497	200	0.485	1.213	olfactory receptor, family 5, subfamily AU, member 1
Case#3	Het->Homozygous	ZFHX2	14	23994870	Missense_Mutation	GG	AA	p.P1427L	31	0.419	0.441	46	0.435	1.087	zinc finger homeobox 2
Case#3	Het->Homozygous	DHRS4-AS1	14	24408806	Missense_Mutation	G	A	p.E25K	48	0.417	0.439	70	0.429	1.071	DHRS4 antisense RNA 1
Case#3	Het->Homozygous	SYNE2	14	64465727	Missense_Mutation	C	T	p.S1150F	65	0.446	0.470	99	0.384	0.960	spectrin repeat containing, nuclear envelope 2
Case#3	Het->Homozygous	PAPLN	14	73716803	Missense_Mutation	G	A	p.C149Y	107	0.402	0.423	168	0.417	1.042	papilin, proteoglycan-like sulfated glycoprotein
Case#3	Het->Homozygous	EIF5	14	103806121	Missense_Mutation	T	C	p.I351T	121	0.479	0.505	200	0.405	1.013	eukaryotic translation initiation factor 5

Case#3	Het->Homozygous	SLC22A13	3	38307716	Missense_Mutation	C	T	p.S122F	32	0.250	0.263	46	0.370	0.924	solute carrier family 22 (organic anion/urate transporter), member 13
Case#3	Het->Homozygous	ULK4	3	41607542	Missense_Mutation	G	A	p.S1067L	118	0.458	0.482	191	0.372	0.929	unc-51 like kinase 4
Case#3	Het->Homozygous	ELP6	3	47537655	Missense_Mutation	GG	AA	p.P235L	78	0.397	0.418	106	0.425	1.061	elongator acetyltransferase complex subunit 6
Case#3	Het->Homozygous	TMEM89	3	48658426	Nonsense_Mutation	C	T	p.W110*	127	0.354	0.373	188	0.383	0.957	transmembrane protein 89
Case#3	Het->Homozygous	AFF4	5	132223577	Missense_Mutation	G	A	p.S965F	77	0.286	0.296	108	0.444	1.111	AF4/FMR2 family, member 4
Case#3	Het->Homozygous	FAT2	5	150948044	Missense_Mutation	G	A	p.P150L	150	0.327	0.338	112	0.384	0.960	FAT atypical cadherin 2
Case#3	Het->Homozygous	BTNL9	5	180474965	Missense_Mutation	C	T	p.L50F	106	0.330	0.342	115	0.348	0.870	butyrophilin-like 9
Case#3	Het->Homozygous	TULP1	6	35467812	Missense_Mutation	C	T	p.G481S	131	0.481	0.494	119	0.445	1.113	tubby like protein 1
Case#3	Het->Homozygous	TMEM63B	6	44117624	Missense_Mutation	C	T	p.T481I	161	0.516	0.529	129	0.388	0.969	transmembrane protein 63B
Case#3	Het->Homozygous	NFKBIE	6	44227856	Missense_Mutation	G	A	p.S454F	125	0.576	0.591	163	0.423	1.058	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon
Case#3	Het->Homozygous	TCTE1	6	44250280	Missense_Mutation	C	T	p.R288Q	56	0.464	0.477	49	0.449	1.122	t-complex-associated-testis-expressed 1
Case#3	Het->Homozygous	PGK2	6	49754689	Missense_Mutation	G	A	p.P71L	215	0.437	0.449	166	0.343	0.858	phosphoglycerate kinase 2
Case#3	Het->Homozygous	TACC1	8	38677979	Missense_Mutation	C	T	p.S406F	114	0.386	0.400	158	0.424	1.060	transforming, acidic coiled-coil containing protein 1
Case#3	Het->Homozygous	PREX2	8	68968209	Splice_Site	G	A	p.S413N	180	0.356	0.368	194	0.448	1.121	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2
Case#3	Het->Homozygous	POP1	8	99135603	Missense_Mutation	T	A	p.M13K	99	0.343	0.355	148	0.426	1.064	processing of precursor 1, ribonuclease P/MRP subunit (S. cerevisiae)
Case#3	Baseline Only	TMTC1	12	29904620	Missense_Mutation	C	T	p.R306Q	58	0.845	0.889	NA	NA	NA	transmembrane and tetratricopeptide repeat containing 1
Case#3	Baseline Only	PRX	19	40902757	Missense_Mutation	T	A	p.E501V	123	0.919	0.967	NA	NA	NA	periaxin
Case#3	Baseline Only	ATAD3B	1	1431165	Missense_Mutation	C	T	p.P639S	132	0.098	0.102	NA	NA	NA	ATPase family, AAA domain containing 3B
Case#3	Baseline Only	PRAMEF17	1	13718514	Missense_Mutation	A	G	p.H326R	181	0.066	0.069	NA	NA	NA	PRAME family member 17
Case#3	Baseline Only	TAS1R2	1	19180962	Missense_Mutation	GC	TT	p.G334E	114	0.079	0.082	NA	NA	NA	taste receptor, type 1, member 2
Case#3	Baseline Only	TRIM45	1	117659298	Missense_Mutation	A	G	p.I431T	116	0.129	0.134	NA	NA	NA	tripartite motif containing 45
Case#3	Baseline Only	SPRR2E	1	153066106	Missense_Mutation	C	A	p.C41F	205	0.229	0.237	NA	NA	NA	small proline-rich protein 2E
Case#3	Baseline Only	BLZF1	1	169345963	Nonsense_Mutation	A	T	p.K72*	103	0.126	0.131	NA	NA	NA	basic leucine zipper nuclear factor 1
Case#3	Baseline Only	KIF14	1	200587679	Missense_Mutation	C	T	p.G58D	135	0.081	0.084	NA	NA	NA	kinesin family member 14
Case#3	Baseline Only	HHIPL2	1	222717003	Missense_Mutation	G	A	p.R284C	114	0.307	0.318	NA	NA	NA	HHIP-like 2
Case#3	Baseline Only	OBSCN	1	228412227	Missense_Mutation	TG	CA	p.A908T	149	0.087	0.090	NA	NA	NA	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
Case#3	Baseline Only	OBSCN	1	228481143	Missense_Mutation	G	C	p.A3653P	132	0.220	0.227	NA	NA	NA	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
Case#3	Baseline Only	NRP1	10	33475282	Missense_Mutation	C	T	p.V733I	82	0.061	0.064	NA	NA	NA	neuropilin 1
Case#3	Baseline Only	PDZD7	10	102783697	Missense_Mutation	C	T	p.G119S	70	0.386	0.406	NA	NA	NA	PDZ domain containing 7
Case#3	Baseline Only	GSTO2	10	106039185	Missense_Mutation	A	G	p.N142D	90	0.067	0.070	NA	NA	NA	glutathione S-transferase omega 2
Case#3	Baseline Only	OR52E6	11	5862653	Missense_Mutation	T	C	p.I159V	122	0.057	0.060	NA	NA	NA	olfactory receptor, family 52, subfamily E, member 6
Case#3	Baseline Only	ZNF214	11	7022717	Missense_Mutation	T	C	p.Y66C	71	0.056	0.059	NA	NA	NA	zinc finger protein 214
Case#3	Baseline Only	SPTBN2	11	66461656	Missense_Mutation	G	T	p.A1486D	60	0.083	0.088	NA	NA	NA	spectrin, beta, non-erythrocytic 2
Case#3	Baseline Only	TENM4	11	78423682	Missense_Mutation	C	T	p.R1300Q	114	0.561	0.591	NA	NA	NA	teneurin transmembrane protein 4
Case#3	Baseline Only	IGSF9B	11	133800880	Splice_Site	G	A	p.I506I	71	0.056	0.059	NA	NA	NA	immunoglobulin superfamily, member 9B
Case#3	Baseline Only	PRB4	12	11461549	Missense_Mutation	G	C	p.P123R	73	0.178	0.187	NA	NA	NA	proline-rich protein BstNI subfamily 4
Case#3	Baseline Only	PRB4	12	11461570	Missense_Mutation	G	T	p.P116H	80	0.438	0.461	NA	NA	NA	proline-rich protein BstNI subfamily 4
Case#3	Baseline Only	PRB4	12	11461706	Missense_Mutation	G	T	p.P71T	133	0.233	0.245	NA	NA	NA	proline-rich protein BstNI subfamily 4
Case#3	Baseline Only	C12orf54	12	48888594	Missense_Mutation	C	T	p.P86S	105	0.057	0.060	NA	NA	NA	chromosome 12 open reading frame 54
Case#3	Baseline Only	OR8S1	12	48919796	Missense_Mutation	C	T	p.R128C	131	0.099	0.104	NA	NA	NA	olfactory receptor, family 8, subfamily S, member 1
Case#3	Baseline Only	TUBA1B	12	49523385	Missense_Mutation	T	C	p.I42V	150	0.180	0.189	NA	NA	NA	tubulin, alpha 1b
Case#3	Baseline Only	FAM186A	12	50745821	Missense_Mutation	TT	AG	p.E1598A	172	0.064	0.066	NA	NA	NA	family with sequence similarity 186, member A
Case#3	Baseline Only	KRT72	12	52992812	Missense_Mutation	T	C	p.N171D	101	0.079	0.083	NA	NA	NA	keratin 72
Case#3	Baseline Only	MDM1	12	68707287	Missense_Mutation	G	A	p.P552L	87	0.057	0.060	NA	NA	NA	Mdm1 nuclear protein homolog (mouse)
Case#3	Baseline Only	C12orf42	12	103696182	Missense_Mutation	T	G	p.S263R	58	0.121	0.127	NA	NA	NA	chromosome 12 open reading frame 42
Case#3	Baseline Only	MVK	12	110013879	Missense_Mutation	G	A	p.S52N	114	0.061	0.065	NA	NA	NA	mevalonate kinase
Case#3	Baseline Only	HNF1A	12	121434359	Missense_Mutation	G	C	p.G375R	93	0.075	0.079	NA	NA	NA	HNF1 homeobox A
Case#3	Baseline Only	SLC46A3	13	29278221	Missense_Mutation	C	T	p.C387Y	117	0.265	0.272	NA	NA	NA	solute carrier family 46, member 3
Case#3	Baseline Only	OR4Q3	14	20215708	Missense_Mutation	G	A	p.G41E	326	0.181	0.191	NA	NA	NA	olfactory receptor, family 4, subfamily Q, member 3
Case#3	Baseline Only	OR4M1	14	20248980	Missense_Mutation	C	T	p.P167S	494	0.150	0.158	NA	NA	NA	olfactory receptor, family 4, subfamily M, member 1
Case#3	Baseline Only	OR4K2	14	20344897	Missense_Mutation	G	A	p.M157I	313	0.144	0.151	NA	NA	NA	olfactory receptor, family 4, subfamily K, member 2
Case#3	Baseline Only	RNASE6	14	21250124	Missense_Mutation	G	A	p.R89Q	110	0.064	0.067	NA	NA	NA	ribonuclease, RNase A family, k6
Case#3	Baseline Only	DHRS2	14	24109099	Missense_Mutation	G	A	p.D139N	52	0.308	0.324	NA	NA	NA	dehydrogenase/reductase (SDR family) member 2
Case#3	Baseline Only	IPO4	14	24655161	Nonsense_Mutation	C	A	p.E359*	71	0.408	0.430	NA	NA	NA	importin 4
Case#3	Baseline Only	RTN1	14	60193697	Missense_Mutation	C	T	p.G569S	82	0.500	0.526	NA	NA	NA	reticulon 1
Case#3	Baseline Only	CCDC88C	14	91792319	Missense_Mutation	C	T	p.D378N	71	0.507	0.534	NA	NA	NA	coiled-coil domain containing 88C
Case#3	Baseline Only	FBLN5	14	92403347	Missense_Mutation	G	A	p.S108F	99	0.495	0.521	NA	NA	NA	fibulin 5
Case#3	Baseline Only	SLC25A47	14	100795139	Missense_Mutation	G	T	p.R135L	97	0.113	0.119	NA	NA	NA	solute carrier family 25, member 47
Case#3	Baseline Only	AHNAK2	14	105409228	Missense_Mutation	G	A	p.S4187F	146	0.479	0.505	NA	NA	NA	AHNAK nucleoprotein 2
Case#3	Baseline Only	AHNAK2	14	105420164	Missense_Mutation	C	T	p.E542K	102	0.431	0.454	NA	NA	NA	AHNAK nucleoprotein 2
Case#3	Baseline Only	MAPKBP1	15	42105918	Missense_Mutation	C	G	p.L313V	59	0.085	0.089	NA	NA	NA	mitogen-activated protein kinase binding protein 1
Case#3	Baseline Only	CAPN3	15	42693849	Missense_Mutation	G	T	p.W455C	85	0.306	0.322	NA	NA	NA	calpain 3, (p94)
Case#3	Baseline Only	AKAP13	15	86122395	Missense_Mutation	G	A	p.D366N	86	0.453	0.477	NA	NA	NA	A kinase (PRKA) anchor protein 13
Case#3	Baseline Only	CLDN6	16	3065596	Missense_Mutation	T	C	p.I143V	112	0.063	0.065	NA	NA	NA	claudin 6
Case#3	Baseline Only	FUK	16	70508588	Missense_Mutation	G	C	p.D716H	106	0.340	0.352	NA	NA	NA	fucokinase
Case#3	Baseline Only	WRAP53	17	7606722	Missense_Mutation	C	G	p.A522G	56	0.089	0.094	NA	NA	NA	WD repeat containing, antisense to TP53
Case#3	Baseline Only	ALOX15B	17	7951819	Missense_Mutation	A	G	p.Q656R	82	0.061	0.064	NA	NA	NA	arachidonate 15-lipoxygenase, type B
Case#3	Baseline Only	C17orf59	17	8092453	Missense_Mutation	G	C	p.Q336E	70	0.500	0.526	NA	NA	NA	chromosome 17 open reading frame 59
Case#3	Baseline Only	KRTAP9-1	17	39346518	Missense_Mutation	T	C	p.I127T	136	0.110	0.116	NA	NA	NA	keratin associated protein 9-1
Case#3	Baseline Only	BRCA1	17	41244936	Missense_Mutation	G	A	p.P871L	129	0.070	0.073	NA	NA	NA	breast cancer 1, early onset
Case#3	Baseline Only	TTYH2	17	72240177	Missense_Mutation	T	G	p.S265A	48	0.104	0.110	NA	NA	NA	tweety family member 2
Case#3	Baseline Only	MGAT5B	17	74878259	Missense_Mutation	G	A	p.V70I	110	0.118	0.124	NA	NA	NA	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase, isozyme B
Case#3	Baseline Only	ZNF750	17	80789468	Missense_Mutation	G	A	p.P288L	161	0.062	0.065	NA	NA	NA	zinc finger protein 750
Case#3	Baseline Only	SETBP1	18	42533090	Missense_Mutation	G	A	p.R1262K	100	0.270	0.277	NA	NA	NA	SET binding protein 1
Case#3	Baseline Only	ZNF77	19	2934701	Missense_Mutation	A	G	p.S142P	173	0.173	0.179	NA	NA	NA	zinc finger protein 77
Case#3	Baseline Only	OR7G1	19	9225341	Missense_Mutation	C	T	p.R312Q	27	0.444	0.460	NA	NA	NA	olfactory receptor, family 7, subfamily G, member 1
Case#3	Baseline Only	ZNF781	19	38160347	Missense_Mutation	C	G	p.G235R	115	0.070	0.073	NA	NA	NA	zinc finger protein 781

Case#3	Baseline Only	PSG4	19	43699336	Missense_Mutation	T	C	p.K267E	288	0.111	0.117	NA	NA	NA	pregnancy specific beta-1-glycoprotein 4
Case#3	Baseline Only	CD33	19	51728641	Missense_Mutation	A	G	p.R69G	116	0.060	0.064	NA	NA	NA	CD33 molecule
Case#3	Baseline Only	KIR3DL3	19	55239168	Missense_Mutation	G	T	p.R149S	77	0.078	0.082	NA	NA	NA	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 3
Case#3	Baseline Only	KIR3DL1	19	55340906	Missense_Mutation	G	A	p.C364Y	15	0.267	0.281	NA	NA	NA	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1
Case#3	Baseline Only	KIR3DL1	19	55341575	Missense_Mutation	G	C	p.E394Q	20	0.550	0.579	NA	NA	NA	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1
Case#3	Baseline Only	ZFP28	19	57058998	Missense_Mutation	C	G	p.S141W	99	0.051	0.053	NA	NA	NA	ZFP28 zinc finger protein
Case#3	Baseline Only	NPAS2	2	101609910	Missense_Mutation	A	C	p.H738P	71	0.113	0.117	NA	NA	NA	neuronal PAS domain protein 2
Case#3	Baseline Only	DOCK10	2	225652038	Missense_Mutation	A	G	p.V1832A	100	0.060	0.062	NA	NA	NA	dedicator of cytokinesis 10
Case#3	Baseline Only	COL4A4	2	227954599	Missense_Mutation	G	A	p.P482S	138	0.065	0.068	NA	NA	NA	collagen, type IV, alpha 4
Case#3	Baseline Only	DEFB129	20	207945	Missense_Mutation	C	T	p.P6S	98	0.429	0.444	NA	NA	NA	defensin, beta 129
Case#3	Baseline Only	SIRPB1	20	1552521	Missense_Mutation	G	A	p.P199L	442	0.371	0.384	NA	NA	NA	signal-regulatory protein beta 1
Case#3	Baseline Only	TGM3	20	2293636	Missense_Mutation	T	G	p.N211K	94	0.436	0.451	NA	NA	NA	transglutaminase 3
Case#3	Baseline Only	CDC25B	20	3781454	Missense_Mutation	G	A	p.R175Q	120	0.342	0.354	NA	NA	NA	cell division cycle 25B
Case#3	Baseline Only	HAO1	20	7921011	Missense_Mutation	G	A	p.P20L	127	0.386	0.399	NA	NA	NA	hydroxyacid oxidase (glycolate oxidase) 1
Case#3	Baseline Only	THBD	20	23028724	Missense_Mutation	G	A	p.A473V	159	0.063	0.065	NA	NA	NA	thrombomodulin
Case#3	Baseline Only	GATA5	20	61041528	Missense_Mutation	C	T	p.G260E	190	0.305	0.313	NA	NA	NA	GATA binding protein 5
Case#3	Baseline Only	KCNQ2	20	62055543	Missense_Mutation	CC	TT	p.E412K	151	0.470	0.483	NA	NA	NA	potassium voltage-gated channel, KQT-like subfamily, member 2
Case#3	Baseline Only	SEC14L3	22	30860830	Missense_Mutation	C	T	p.R214H	154	0.052	0.054	NA	NA	NA	SEC14-like 3 (S. cerevisiae)
Case#3	Baseline Only	MKL1	22	40814500	Missense_Mutation	T	C	p.S648G	72	0.069	0.072	NA	NA	NA	megakaryoblastic leukemia (translocation) 1
Case#3	Baseline Only	PLCL2	3	17052750	Nonsense_Mutation	C	T	p.Q512*	93	0.505	0.532	NA	NA	NA	phospholipase C-like 2
Case#3	Baseline Only	TRANK1	3	36874140	Missense_Mutation	G	A	p.H2268Y	76	0.487	0.512	NA	NA	NA	tetratricopeptide repeat and ankyrin repeat containing 1
Case#3	Baseline Only	ITGA9	3	37818898	Missense_Mutation	G	A	p.G853R	98	0.561	0.591	NA	NA	NA	integrin, alpha 9
Case#3	Baseline Only	MYRIP	3	40231388	Nonsense_Mutation	C	T	p.R367*	54	0.407	0.429	NA	NA	NA	myosin VIIA and Rab interacting protein
Case#3	Baseline Only	HIGD1A	3	42835700	Nonsense_Mutation	G	A	p.Q16*	98	0.480	0.505	NA	NA	NA	HIG1 hypoxia inducible domain family, member 1A
Case#3	Baseline Only	CCR9	3	45942593	Missense_Mutation	G	A	p.A105T	163	0.521	0.549	NA	NA	NA	chemokine (C-C motif) receptor 9
Case#3	Baseline Only	NBEAL2	3	47046766	Missense_Mutation	GC	AA	p.R2172Q	90	0.522	0.550	NA	NA	NA	neurobeachin-like 2
Case#3	Baseline Only	FBXW12	3	48420005	Missense_Mutation	C	T	p.P202S	122	0.484	0.509	NA	NA	NA	F-box and WD repeat domain containing 12
Case#3	Baseline Only	FAM3D	3	58639419	Missense_Mutation	G	A	p.R35C	80	0.550	0.579	NA	NA	NA	family with sequence similarity 3, member D
Case#3	Baseline Only	PTPRG	3	62189189	Missense_Mutation	G	A	p.G574S	52	0.077	0.081	NA	NA	NA	protein tyrosine phosphatase, receptor type, G
Case#3	Baseline Only	EPHA3	3	89521664	Missense_Mutation	G	A	p.R914H	82	0.073	0.077	NA	NA	NA	EPH receptor A3
Case#3	Baseline Only	ATP13A4	3	193171893	Missense_Mutation	G	A	p.T675M	179	0.587	0.607	NA	NA	NA	ATPase type 13A4
Case#3	Baseline Only	NOP14	4	2943361	Missense_Mutation	T	C	p.Q716R	56	0.089	0.094	NA	NA	NA	NOP14 nucleolar protein
Case#3	Baseline Only	GRK4	4	2990499	Missense_Mutation	G	T	p.R65L	123	0.073	0.077	NA	NA	NA	G protein-coupled receptor kinase 4
Case#3	Baseline Only	NCAPG	4	17818885	Splice_Site	T	C	p.D259D	71	0.085	0.089	NA	NA	NA	non-SMC condensin I complex, subunit G
Case#3	Baseline Only	UGT2A1	4	70455302	Missense_Mutation	C	T	p.A458T	177	0.051	0.054	NA	NA	NA	UDP glucuronosyltransferase 2 family, polypeptide A1, complex locus
Case#3	Baseline Only	ANKRD17	4	74124097	Missense_Mutation	C	A	p.G97C	88	0.511	0.538	NA	NA	NA	ankyrin repeat domain 17
Case#3	Baseline Only	SHROOM3	4	77675505	Missense_Mutation	C	T	p.P1290L	59	0.102	0.107	NA	NA	NA	shroom family member 3
Case#3	Baseline Only	FRAS1	4	79284694	Missense_Mutation	C	T	p.A817V	61	0.082	0.086	NA	NA	NA	Fraser extracellular matrix complex subunit 1
Case#3	Baseline Only	SCOC	4	141294756	Missense_Mutation	C	G	p.F22L	88	0.068	0.072	NA	NA	NA	short coiled-coil protein
Case#3	Baseline Only	NPY1R	4	164247381	Missense_Mutation	C	T	p.G109D	95	0.063	0.066	NA	NA	NA	neuropeptide Y receptor Y1
Case#3	Baseline Only	RXFP3	5	33937020	Missense_Mutation	G	A	p.G59S	117	0.231	0.239	NA	NA	NA	relaxin/insulin-like family peptide receptor 3
Case#3	Baseline Only	BDP1	5	70751818	Missense_Mutation	T	G	p.D38E	45	0.133	0.138	NA	NA	NA	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB
Case#3	Baseline Only	TMEM171	5	72419456	Missense_Mutation	C	G	p.R86G	87	0.103	0.107	NA	NA	NA	transmembrane protein 171
Case#3	Baseline Only	ANKRA2	5	72850174	Missense_Mutation	G	A	p.H260Y	151	0.616	0.638	NA	NA	NA	ankyrin repeat, family A (RFXANK-like), 2
Case#3	Baseline Only	MEGF10	5	126769142	Frame_Shift_Del	C	-	p.S594fs	114	0.263	0.272	NA	NA	NA	multiple EGF-like-domains 10
Case#3	Baseline Only	PCDHB17	5	140536603	Missense_Mutation	G	A	p.D343N	112	0.616	0.638	NA	NA	NA	protocadherin beta 17 pseudogene
Case#3	Baseline Only	PCDHB11	5	140581458	Missense_Mutation	C	T	p.S704L	192	0.578	0.598	NA	NA	NA	protocadherin beta 11
Case#3	Baseline Only	GLRA1	5	151239530	Missense_Mutation	C	T	p.D98N	169	0.562	0.582	NA	NA	NA	glycine receptor, alpha 1
Case#3	Baseline Only	GRIA1	5	153190585	Splice_Site	G	A	p.G841S	144	0.521	0.539	NA	NA	NA	glutamate receptor, ionotropic, AMPA 1
Case#3	Baseline Only	GEMIN5	5	154311745	Missense_Mutation	C	T	p.R192Q	102	0.549	0.568	NA	NA	NA	gem (nuclear organelle) associated protein 5
Case#3	Baseline Only	HAVCR1	5	156479444	Frame_Shift_Del	TTG	-	p.Q201fs	290	0.066	0.068	NA	NA	NA	hepatitis A virus cellular receptor 1
Case#3	Baseline Only	COL23A1	5	177666176	Missense_Mutation	G	A	p.P529L	89	0.798	0.826	NA	NA	NA	collagen, type XXIII, alpha 1
Case#3	Baseline Only	OR2Y1	5	180166561	Missense_Mutation	C	G	p.M166I	70	0.157	0.163	NA	NA	NA	olfactory receptor, family 2, subfamily Y, member 1
Case#3	Baseline Only	TRIM41	5	180651693	Missense_Mutation	G	A	p.E232K	77	0.714	0.739	NA	NA	NA	tripartite motif containing 41
Case#3	Baseline Only	DSP	6	7580550	Missense_Mutation	CC	TT	p.T1376I	108	0.444	0.456	NA	NA	NA	desmoplakin
Case#3	Baseline Only	IP6K3	6	33690912	Missense_Mutation	C	T	p.R273K	122	0.484	0.496	NA	NA	NA	inositol hexakisphosphate kinase 3
Case#3	Baseline Only	CUL9	6	43152092	Missense_Mutation	G	A	p.G15E	120	0.492	0.505	NA	NA	NA	cullin 9
Case#3	Baseline Only	CRIP3	6	43273795	Missense_Mutation	GG	AA	p.P188F	126	0.500	0.513	NA	NA	NA	cysteine-rich protein 3
Case#3	Baseline Only	GPR115	6	47681990	Missense_Mutation	G	A	p.E337K	115	0.574	0.589	NA	NA	NA	G protein-coupled receptor 115
Case#3	Baseline Only	FAM162B	6	117086378	Missense_Mutation	C	A	p.Q71H	116	0.052	0.054	NA	NA	NA	family with sequence similarity 162, member B
Case#3	Baseline Only	FOXK1	7	4798947	Missense_Mutation	C	T	p.P473S	64	0.219	0.225	NA	NA	NA	forkhead box K1
Case#3	Baseline Only	ETV1	7	13978809	Missense_Mutation	T	C	p.S100G	96	0.052	0.053	NA	NA	NA	ets variant 1
Case#3	Baseline Only	ABCA13	7	48313481	Missense_Mutation	G	C	p.L1406F	164	0.098	0.100	NA	NA	NA	ATP-binding cassette, sub-family A (ABC1), member 13
Case#3	Baseline Only	SEMA3C	7	80434967	Missense_Mutation	T	C	p.K216E	249	0.245	0.251	NA	NA	NA	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C
Case#3	Baseline Only	FZD1	7	90894449	Missense_Mutation	C	T	p.P85L	21	0.381	0.391	NA	NA	NA	frizzled class receptor 1
Case#3	Baseline Only	AZGP1	7	99564848	Nonsense_Mutation	G	T	p.C225*	183	0.235	0.241	NA	NA	NA	alpha-2-glycoprotein 1, zinc-binding
Case#3	Baseline Only	CSMD1	8	3205615	Missense_Mutation	C	T	p.D1126N	85	0.576	0.597	NA	NA	NA	CUB and Sushi multiple domains 1
Case#3	Baseline Only	RP1L1	8	10464515	Missense_Mutation	C	T	p.G2365R	84	0.643	0.665	NA	NA	NA	retinitis pigmentosa 1-like 1
Case#3	Baseline Only	TOX	8	59872518	Missense_Mutation	T	C	p.Y51C	156	0.673	0.697	NA	NA	NA	thymocyte selection-associated high mobility group box
Case#3	Baseline Only	CNGB3	8	87679259	Missense_Mutation	T	C	p.N249S	152	0.546	0.565	NA	NA	NA	cyclic nucleotide gated channel beta 3
Case#3	Baseline Only	ZFPM2	8	106814964	Missense_Mutation	A	G	p.N885S	106	0.698	0.723	NA	NA	NA	zinc finger protein, FOG family member 2
Case#3	Baseline Only	COL14A1	8	121170482	Missense_Mutation	T	G	p.S68A	170	0.165	0.170	NA	NA	NA	collagen, type XIV, alpha 1
Case#3	Baseline Only	TTC39B	9	15188106	Missense_Mutation	T	C	p.I420V	116	0.112	0.118	NA	NA	NA	tetratricopeptide repeat domain 39B
Case#3	Baseline Only	FAM214B	9	35108261	Missense_Mutation	A	T	p.V4E	36	0.111	0.117	NA	NA	NA	family with sequence similarity 214, member B
Case#3	Baseline Only	PAX5	9	36923406	Missense_Mutation	G	A	p.P286S	69	0.522	0.549	NA	NA	NA	paired box 5
Case#3	Baseline Only	SPATA31A6	9	43624907	Nonsense_Mutation	A	C	p.Y1260*	23	0.217	0.229	NA	NA	NA	SPATA31 subfamily A, member 6
Case#3	Baseline Only	PRUNE2	9	79324179	Missense_Mutation	G	A	p.T1004M	170	0.088	0.093	NA	NA	NA	prune homolog 2 (Drosophila)

Case#3	Baseline Only	PRUNE2	9	79324741	Missense_Mutation	T	C	p.N817D	118	0.068	0.071	NA	NA	NA	prune homolog 2 (Drosophila)
Case#3	Baseline Only	NOXA1	9	140327663	Missense_Mutation	C	T	p.P286L	40	0.125	0.132	NA	NA	NA	NADPH oxidase activator 1
Case#3	Baseline Only	POF1B	X	84563135	Missense_Mutation	T	A	p.M349L	74	0.122	0.128	NA	NA	NA	premature ovarian failure, 1B
Case#3	Baseline Only	H2BFM	X	103268333	Missense_Mutation	G	A	p.R22H	70	0.071	0.075	NA	NA	NA	H2B histone family, member M
Case#3	Baseline Only	GPR112	X	135426693	Missense_Mutation	A	G	p.I276M	56	0.089	0.094	NA	NA	NA	G protein-coupled receptor 112
Case#3	Baseline Only	BGN	X	152770714	Missense_Mutation	A	G	p.K86R	96	0.063	0.066	NA	NA	NA	biglycan
Case#3	Baseline Only	PLXNB3	X	153039502	Missense_Mutation	G	C	p.E1156D	20	0.200	0.211	NA	NA	NA	plexin B3
Case#3	Baseline Only	OR1D5	17	2966391	Missense_Mutation	G	T	p.P171T	312	0.256	NA	NA	NA	NA	olfactory receptor, family 1, subfamily D, member 5
Case#3	Baseline Only	CWH43	4	49063872	Missense_Mutation	C	A	p.H689N	130	0.054	NA	NA	NA	NA	cell wall biogenesis 43 C-terminal homolog (S. cerevisiae)
Case#3	Baseline Only	AL590708.2	9	130891060	Missense_Mutation	G	A	p.G92E	145	0.076	NA	NA	NA	NA	
Case#4	Relapse Only	AK3	9	4740973	Missense_Mutation	C	T	p.G39R	NA	NA	NA	54	0.685	0.926	adenylate kinase 3
Case#4	Relapse Only	NADK	1	1696717	Missense_Mutation	C	A	p.K43N	NA	NA	NA	137	0.212	0.261	NAD kinase
Case#4	Relapse Only	MORN1	1	2252916	Missense_Mutation	C	T	p.G467D	NA	NA	NA	24	0.167	0.206	MORN repeat containing 1
Case#4	Relapse Only	ALDH4A1	1	19200985	Missense_Mutation	C	A	p.Q517H	NA	NA	NA	243	0.198	0.244	aldehyde dehydrogenase 4 family, member A1
Case#4	Relapse Only	VWA5B1	1	20656824	Missense_Mutation	A	G	p.N469S	NA	NA	NA	98	0.051	0.063	von Willebrand factor A domain containing 5B1
Case#4	Relapse Only	TOE1	1	45806991	Missense_Mutation	G	A	p.G71E	NA	NA	NA	133	0.263	0.325	target of EGR1, member 1 (nuclear)
Case#4	Relapse Only	CDCP2	1	54606804	Missense_Mutation	C	T	p.G244R	NA	NA	NA	183	0.115	0.142	CUB domain containing protein 2
Case#4	Relapse Only	TBX15	1	119427467	Missense_Mutation	A	C	p.M566R	NA	NA	NA	118	0.059	0.073	T-box 15
Case#4	Relapse Only	ZNF687	1	151260293	Missense_Mutation	A	G	p.N509S	NA	NA	NA	114	0.219	0.258	zinc finger protein 687
Case#4	Relapse Only	HDGF	1	156713558	Missense_Mutation	G	A	p.P201L	NA	NA	NA	86	0.070	0.082	hepatoma-derived growth factor
Case#4	Relapse Only	SH2D2A	1	156784085	Splice_Site	C	A	p.E104*	NA	NA	NA	121	0.198	0.233	SH2 domain containing 2A
Case#4	Relapse Only	FCRLA	1	161683136	Missense_Mutation	G	A	p.R366Q	NA	NA	NA	124	0.073	0.085	Fc receptor-like A
Case#4	Relapse Only	PLXNA2	1	208390113	Missense_Mutation	C	A	p.W385C	NA	NA	NA	72	0.208	0.245	plexin A2
Case#4	Relapse Only	DNAH14	1	225268433	Missense_Mutation	T	A	p.I974N	NA	NA	NA	166	0.187	0.220	dynein, axonemal, heavy chain 14
Case#4	Relapse Only	AGT	1	230845977	Missense_Mutation	G	A	p.T207M	NA	NA	NA	58	0.086	0.101	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
Case#4	Relapse Only	GREM2	1	240656550	Missense_Mutation	G	C	p.Q76E	NA	NA	NA	197	0.051	0.060	gremlin 2, DAN family BMP antagonist
Case#4	Relapse Only	OR2L2	1	248202474	Missense_Mutation	A	G	p.Q302R	NA	NA	NA	385	0.171	0.202	olfactory receptor, family 2, subfamily L, member 2
Case#4	Relapse Only	PITRM1	10	3191823	Missense_Mutation	C	T	p.V621I	NA	NA	NA	99	0.071	0.087	pitrilysin metallopeptidase 1
Case#4	Relapse Only	MTPAP	10	30602756	Missense_Mutation	G	C	p.Q511E	NA	NA	NA	164	0.268	0.331	mitochondrial poly(A) polymerase
Case#4	Relapse Only	SEC24C	10	75519952	Missense_Mutation	G	T	p.G220C	NA	NA	NA	36	0.278	0.343	SEC24 family member C
Case#4	Relapse Only	TTC40	10	134647622	Missense_Mutation	T	A	p.Q2291L	NA	NA	NA	57	0.333	0.411	
Case#4	Relapse Only	METTL12	11	62434173	Missense_Mutation	G	A	p.G125S	NA	NA	NA	77	0.065	0.080	methyltransferase like 12
Case#4	Relapse Only	MYO7A	11	76853783	Missense_Mutation	T	C	p.L16S	NA	NA	NA	115	0.078	0.097	myosin VIIA
Case#4	Relapse Only	ANO2	12	6030405	Missense_Mutation	A	G	p.V108A	NA	NA	NA	133	0.060	0.074	anoctamin 2, calcium activated chloride channel
Case#4	Relapse Only	GPR162	12	6936122	Missense_Mutation	C	T	p.T507I	NA	NA	NA	90	0.233	0.288	G protein-coupled receptor 162
Case#4	Relapse Only	PRB4	12	11461549	Missense_Mutation	G	C	p.P123R	NA	NA	NA	113	0.283	0.350	proline-rich protein BstNI subfamily 4
Case#4	Relapse Only	PRB4	12	11461706	Missense_Mutation	G	T	p.P71T	NA	NA	NA	203	0.227	0.280	proline-rich protein BstNI subfamily 4
Case#4	Relapse Only	KRT78	12	53242440	Missense_Mutation	A	G	p.L92P	NA	NA	NA	159	0.082	0.101	keratin 78
Case#4	Relapse Only	ARHGAP9	12	57869131	Missense_Mutation	G	A	p.R518W	NA	NA	NA	36	0.278	0.343	Rho GTPase activating protein 9
Case#4	Relapse Only	ATXN7L3B	12	74932048	Missense_Mutation	G	C	p.E52D	NA	NA	NA	164	0.274	0.339	ataxin 7-like 3B
Case#4	Relapse Only	C12orf50	12	88390205	Missense_Mutation	T	C	p.T143A	NA	NA	NA	118	0.212	0.261	chromosome 12 open reading frame 50
Case#4	Relapse Only	RBM19	12	114374887	Missense_Mutation	T	C	p.T665A	NA	NA	NA	126	0.071	0.097	RNA binding motif protein 19
Case#4	Relapse Only	PCDH9	13	66879162	Splice_Site	T	G		NA	NA	NA	86	0.244	0.279	protocadherin 9
Case#4	Relapse Only	UGGT2	13	96589308	Missense_Mutation	C	A	p.G616V	NA	NA	NA	276	0.199	0.227	UDP-glucose glycoprotein glucosyltransferase 2
Case#4	Relapse Only	COL4A1	13	110838794	Missense_Mutation	C	A	p.G612V	NA	NA	NA	72	0.208	0.238	collagen, type IV, alpha 1
Case#4	Relapse Only	C14orf39	14	60932752	Missense_Mutation	G	A	p.A306V	NA	NA	NA	117	0.060	0.074	chromosome 14 open reading frame 39
Case#4	Relapse Only	ZFYVE21	14	104199095	Missense_Mutation	A	C	p.H222P	NA	NA	NA	83	0.181	0.223	zinc finger, FYVE domain containing 21
Case#4	Relapse Only	CCDC33	15	74622678	Missense_Mutation	G	A	p.S480N	NA	NA	NA	118	0.076	0.090	coiled-coil domain containing 33
Case#4	Relapse Only	WDR24	16	736857	Missense_Mutation	C	T	p.G537S	NA	NA	NA	83	0.241	0.283	WD repeat domain 24
Case#4	Relapse Only	PELP1	17	4578435	Missense_Mutation	C	G	p.V405L	NA	NA	NA	90	0.256	0.315	proline, glutamate and leucine rich protein 1
Case#4	Relapse Only	NEURL4	17	7229766	Missense_Mutation	G	T	p.N398K	NA	NA	NA	139	0.237	0.293	neuralized E3 ubiquitin protein ligase 4
Case#4	Relapse Only	TBC1D29	17	28890301	Missense_Mutation	G	A	p.S104N	NA	NA	NA	60	0.100	0.123	TBC1 domain family, member 29
Case#4	Relapse Only	SLFN12	17	33749919	Missense_Mutation	A	C	p.S43R	NA	NA	NA	132	0.053	0.065	schlafen family member 12
Case#4	Relapse Only	SLFN12L	17	33806164	Nonsense_Mutation	C	T	p.W355*	NA	NA	NA	162	0.216	0.267	schlafen family member 12-like
Case#4	Relapse Only	C17orf98	17	36997503	Missense_Mutation	T	C	p.Q47R	NA	NA	NA	117	0.051	0.063	chromosome 17 open reading frame 98
Case#4	Relapse Only	KRT36	17	39643646	Missense_Mutation	G	A	p.T315M	NA	NA	NA	91	0.110	0.136	keratin 36
Case#4	Relapse Only	TTYH2	17	72240177	Missense_Mutation	T	G	p.S265A	NA	NA	NA	112	0.089	0.110	tweety family member 2
Case#4	Relapse Only	NDUFS7	19	1388538	Missense_Mutation	C	T	p.P23L	NA	NA	NA	115	0.061	0.072	NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)
Case#4	Relapse Only	MKNK2	19	2039727	Missense_Mutation	C	T	p.R428Q	NA	NA	NA	56	0.071	0.084	MAP kinase interacting serine/threonine kinase 2
Case#4	Relapse Only	MUC16	19	8962010	Missense_Mutation	A	T	p.I14456N	NA	NA	NA	140	0.236	0.277	mucin 16, cell surface associated
Case#4	Relapse Only	ZNF844	19	12184876	Missense_Mutation	A	C	p.N12H	NA	NA	NA	631	0.198	0.233	zinc finger protein 844
Case#4	Relapse Only	hsa-mir-1199	19	14185226	Missense_Mutation	T	C	p.V198A	NA	NA	NA	144	0.069	0.082	
Case#4	Relapse Only	NWD1	19	16855265	Missense_Mutation	A	G	p.I78V	NA	NA	NA	213	0.070	0.083	NACHT and WD repeat domain containing 1
Case#4	Relapse Only	CARD8	19	48737706	Nonsense_Mutation	A	T	p.C10*	NA	NA	NA	173	0.058	0.068	caspase recruitment domain family, member 8
Case#4	Relapse Only	FUT2	19	49206674	Nonsense_Mutation	G	A	p.W154*	NA	NA	NA	134	0.082	0.097	fucosyltransferase 2 (secretor status included)
Case#4	Relapse Only	FSHR	2	49189921	Missense_Mutation	C	T	p.S680N	NA	NA	NA	123	0.057	0.077	follicle stimulating hormone receptor
Case#4	Relapse Only	GPAT2	2	96688929	Missense_Mutation	G	A	p.R692C	NA	NA	NA	96	0.250	0.309	glycerol-3-phosphate acyltransferase 2, mitochondrial
Case#4	Relapse Only	INPP4A	2	99172244	Missense_Mutation	A	G	p.T604A	NA	NA	NA	117	0.051	0.060	inositol polyphosphate-4-phosphatase, type I, 107kDa
Case#4	Relapse Only	POLR1B	2	113309473	Missense_Mutation	C	T	p.S295L	NA	NA	NA	267	0.060	0.070	polymerase (RNA) I polypeptide B, 128kDa
Case#4	Relapse Only	KLHL41	2	170366728	Missense_Mutation	G	C	p.C147S	NA	NA	NA	172	0.180	0.212	kelch-like family member 41
Case#4	Relapse Only	SCRN3	2	175268898	Missense_Mutation	G	A	p.M203I	NA	NA	NA	154	0.299	0.351	secernin 3
Case#4	Relapse Only	CUL3	2	225400319	Missense_Mutation	G	T	p.L102I	NA	NA	NA	161	0.137	0.161	cullin 3
Case#4	Relapse Only	ZSWIM1	20	44512136	Missense_Mutation	C	T	p.A302V	NA	NA	NA	92	0.272	0.319	zinc finger, SWIM-type containing 1
Case#4	Relapse Only	ETS2	21	40188935	Missense_Mutation	A	T	p.N170I	NA	NA	NA	194	0.175	0.206	v-ets avian erythroblastosis virus E26 oncogene homolog 2
Case#4	Relapse Only	FAM230A	22	20710213	Missense_Mutation	A	T	p.T649S	NA	NA	NA	428	0.091	0.096	family with sequence similarity 230, member A
Case#4	Relapse Only	PLXNB2	22	50721492	Missense_Mutation	C	T	p.V935I	NA	NA	NA	93	0.075	0.088	plexin B2
Case#4	Relapse Only	SHANK3	22	51117034	Missense_Mutation	G	T	p.D121Y	NA	NA	NA	167	0.198	0.232	SH3 and multiple ankyrin repeat domains 3

Case#4	Relapse Only	FAM198A	3	43074831	Missense_Mutation	G	A	p.R359Q	NA	NA	NA	110	0.064	0.079	family with sequence similarity 198, member A
Case#4	Relapse Only	RAD54L2	3	51668017	Missense_Mutation	T	A	p.F370I	NA	NA	NA	93	0.075	0.093	RAD54-like 2 (S. cerevisiae)
Case#4	Relapse Only	DNAH1	3	52430526	Missense_Mutation	G	A	p.G3801D	NA	NA	NA	103	0.058	0.072	dynein, axonemal, heavy chain 1
Case#4	Relapse Only	DHX15	4	24531266	Missense_Mutation	G	A	p.T743I	NA	NA	NA	223	0.170	0.200	DEAH (Asp-Glu-Ala-His) box helicase 15
Case#4	Relapse Only	GRID2	4	94138027	Missense_Mutation	T	C	p.C310R	NA	NA	NA	259	0.212	0.250	glutamate receptor, ionotropic, delta 2
Case#4	Relapse Only	BANK1	4	102839287	Missense_Mutation	G	A	p.A383T	NA	NA	NA	106	0.066	0.078	B-cell scaffold protein with ankyrin repeats 1
Case#4	Relapse Only	INPP4B	4	143094937	Missense_Mutation	A	G	p.S403P	NA	NA	NA	150	0.200	0.235	inositol polyphosphate-4-phosphatase, type II, 105kDa
Case#4	Relapse Only	RPS3A	4	152024138	Missense_Mutation	A	C	p.Q38P	NA	NA	NA	206	0.053	0.063	ribosomal protein S3A
Case#4	Relapse Only	AGGF1	5	76332468	Missense_Mutation	G	T	p.V202L	NA	NA	NA	116	0.069	0.085	angiogenic factor with G patch and FHA domains 1
Case#4	Relapse Only	PCDHGB3	5	140750285	Missense_Mutation	G	T	p.M108I	NA	NA	NA	170	0.288	0.356	protocadherin gamma subfamily B, 3
Case#4	Relapse Only	STK10	5	171532741	Splice_Site	C	A	p.W263C	NA	NA	NA	75	0.213	0.263	serine/threonine kinase 10
Case#4	Relapse Only	KHDC3L	6	74073531	Missense_Mutation	C	G	p.A201G	NA	NA	NA	77	0.130	0.176	KH domain containing 3-like, subcortical maternal complex member
Case#4	Relapse Only	BCLAF1	6	136593183	Missense_Mutation	G	C	p.H665D	NA	NA	NA	228	0.088	0.103	BCL2-associated transcription factor 1
Case#4	Relapse Only	NOX3	6	155761246	Missense_Mutation	G	T	p.T171K	NA	NA	NA	60	0.083	0.113	NADPH oxidase 3
Case#4	Relapse Only	SUN1	7	881668	Missense_Mutation	C	T	p.H118Y	NA	NA	NA	85	0.082	0.111	Sad1 and UNC84 domain containing 1
Case#4	Relapse Only	CCZ1B	7	6844574	Missense_Mutation	C	G	p.M367I	NA	NA	NA	130	0.092	0.125	CCZ1 vacuolar protein trafficking and biogenesis associated homolog B (S. cerevisiae)
Case#4	Relapse Only	VWDE	7	12396999	Missense_Mutation	A	T	p.S1139R	NA	NA	NA	85	0.329	0.445	von Willebrand factor D and EGF domains
Case#4	Relapse Only	C7orf31	7	25181912	Missense_Mutation	T	C	p.H300R	NA	NA	NA	108	0.065	0.088	chromosome 7 open reading frame 31
Case#4	Relapse Only	SH2B2	7	101928495	Missense_Mutation	G	C	p.A16P	NA	NA	NA	72	0.069	0.094	SH2B adaptor protein 2
Case#4	Relapse Only	POT1	7	124503424	Missense_Mutation	C	T	p.G176R	NA	NA	NA	102	0.441	0.596	protection of telomeres 1
Case#4	Relapse Only	LRGUK	7	133932357	Missense_Mutation	T	C	p.M678T	NA	NA	NA	116	0.069	0.093	leucine-rich repeats and guanylate kinase domain containing
Case#4	Relapse Only	CTAGE15	7	143270172	Missense_Mutation	A	G	p.E421G	NA	NA	NA	105	0.086	0.116	CTAGE family, member 15
Case#4	Relapse Only	LRRC61	7	150034378	Missense_Mutation	A	G	p.N143S	NA	NA	NA	21	0.190	0.257	leucine rich repeat containing 61
Case#4	Relapse Only	PCM1	8	17817553	Missense_Mutation	G	T	p.A691S	NA	NA	NA	117	0.051	0.063	pericentriolar material 1
Case#4	Relapse Only	ERCC6L2	9	98638288	Start_Codon_SNP	A	G	p.M1V	NA	NA	NA	80	0.100	0.135	excision repair cross-complementation group 6-like 2
Case#4	Relapse Only	CTNNAL1	9	111727670	Missense_Mutation	C	G	p.E527Q	NA	NA	NA	117	0.060	0.081	catenin (cadherin-associated protein), alpha-like 1
Case#4	Relapse Only	EPB41L4B	9	111945049	Missense_Mutation	T	G	p.N816T	NA	NA	NA	154	0.071	0.097	erythrocyte membrane protein band 4.1 like 4B
Case#4	Relapse Only	DNLZ	9	139256468	Missense_Mutation	C	G	p.S178T	NA	NA	NA	35	0.171	0.232	DNL-type zinc finger
Case#4	Relapse Only	EXD3	9	140243844	Missense_Mutation	C	T	p.C545Y	NA	NA	NA	27	0.148	0.200	exonuclease 3'-5' domain containing 3
Case#4	Relapse Only	MAOB	X	43656509	Missense_Mutation	C	A	p.A161S	NA	NA	NA	59	0.102	NA	monoamine oxidase B
Case#4	Relapse Only	STARD8	X	67937976	Missense_Mutation	G	A	p.R327Q	NA	NA	NA	100	0.060	NA	StAR-related lipid transfer (START) domain containing 8
Case#4	Relapse Only	MAGEE1	X	75648447	Missense_Mutation	G	T	p.G42C	NA	NA	NA	113	0.381	NA	melanoma antigen family E, 1
Case#4	Relapse Only	ABCD1	X	153002661	Missense_Mutation	G	C	p.V482L	NA	NA	NA	134	0.276	NA	ATP-binding cassette, sub-family D (ALD), member 1
Case#4	Het->Homozygous	SETBP1	18	42531243	Missense_Mutation	G	A	p.M646I	25	0.520	0.563	22	0.864	1.167	SET binding protein 1
Case#4	Baseline Only	NADK	1	1686040	Missense_Mutation	G	T	p.N262K	57	0.123	0.133	NA	NA	NA	NAD kinase
Case#4	Baseline Only	PRAMEF15	1	13645819	Missense_Mutation	G	A	p.V117I	345	0.270	0.292	NA	NA	NA	PRAME family member 15
Case#4	Baseline Only	LGALS8	1	236700836	Missense_Mutation	C	T	p.P29S	181	0.459	0.487	NA	NA	NA	lectin, galactoside-binding, soluble, 8
Case#4	Baseline Only	NEBL	10	21120508	Missense_Mutation	T	A	p.D485V	48	0.292	0.316	NA	NA	NA	nebulette
Case#4	Baseline Only	SVIL	10	29769741	Splice_Site	T	G	p.E1701A	65	0.062	0.067	NA	NA	NA	supervillin
Case#4	Baseline Only	NUMA1	11	71732302	Missense_Mutation	G	T	p.D136E	125	0.312	0.338	NA	NA	NA	nuclear mitotic apparatus protein 1
Case#4	Baseline Only	SYTL2	11	85432002	Splice_Site	C	T	p.G487D	49	0.265	0.287	NA	NA	NA	synaptotagmin-like 2
Case#4	Baseline Only	NR2C1	12	95456418	Missense_Mutation	C	T	p.G51S	97	0.052	0.056	NA	NA	NA	nuclear receptor subfamily 2, group C, member 1
Case#4	Baseline Only	ADCK1	14	78392234	Missense_Mutation	G	C	p.C379S	98	0.296	0.320	NA	NA	NA	aarF domain containing kinase 1
Case#4	Baseline Only	RPL13	16	89628073	Missense_Mutation	G	A	p.A112T	80	0.088	0.093	NA	NA	NA	ribosomal protein L13
Case#4	Baseline Only	RTN4RL1	17	1841037	Missense_Mutation	G	A	p.R27W	73	0.068	0.074	NA	NA	NA	reticulon 4 receptor-like 1
Case#4	Baseline Only	SHISA6	17	11461607	Missense_Mutation	G	A	p.E497K	23	0.348	0.376	NA	NA	NA	shisa family member 6
Case#4	Baseline Only	KRTAP9-1	17	39346139	Splice_Site	A	G	p.M1V	149	0.060	0.065	NA	NA	NA	keratin associated protein 9-1
Case#4	Baseline Only	EMILIN2	18	2891737	Missense_Mutation	G	A	p.E538K	67	0.209	0.226	NA	NA	NA	elastin microfibril interfacer 2
Case#4	Baseline Only	MRO	18	48333099	Missense_Mutation	GT	AA	p.T74F	117	0.299	0.324	NA	NA	NA	maestro
Case#4	Baseline Only	PPP1R15A	19	49377424	Missense_Mutation	G	A	p.G312S	68	0.103	0.111	NA	NA	NA	protein phosphatase 1, regulatory subunit 15A
Case#4	Baseline Only	PPP1R15A	19	49377436	Missense_Mutation	G	C	p.A316P	77	0.104	0.112	NA	NA	NA	protein phosphatase 1, regulatory subunit 15A
Case#4	Baseline Only	C2orf44	2	24261224	Nonsense_Mutation	G	A	p.R381*	95	0.326	0.353	NA	NA	NA	chromosome 2 open reading frame 44
Case#4	Baseline Only	C2orf16	2	27800620	Missense_Mutation	G	A	p.G394E	63	0.254	0.275	NA	NA	NA	chromosome 2 open reading frame 16
Case#4	Baseline Only	LTBP1	2	33589369	Missense_Mutation	C	T	p.P1496S	142	0.282	0.305	NA	NA	NA	latent transforming growth factor beta binding protein 1
Case#4	Baseline Only	RGPD2	2	88125212	Missense_Mutation	C	G	p.A13P	89	0.056	0.061	NA	NA	NA	RANBP2-like and GRIP domain containing 2
Case#4	Baseline Only	RGPD8	2	113190990	Nonsense_Mutation	G	T	p.S14*	56	0.107	0.116	NA	NA	NA	RANBP2-like and GRIP domain containing 8
Case#4	Baseline Only	PTH2R	2	209309571	Missense_Mutation	C	T	p.S271L	136	0.059	0.064	NA	NA	NA	parathyroid hormone 2 receptor
Case#4	Baseline Only	TNS1	2	218669225	Missense_Mutation	T	C	p.N1722S	68	0.103	0.111	NA	NA	NA	tensin 1
Case#4	Baseline Only	ALPP	2	233244930	Missense_Mutation	G	C	p.R231P	183	0.093	0.101	NA	NA	NA	alkaline phosphatase, placental
Case#4	Baseline Only	LRRFIP1	2	238668783	Missense_Mutation	A	G	p.Q275R	136	0.059	0.064	NA	NA	NA	leucine rich repeat (in FLII) interacting protein 1
Case#4	Baseline Only	DOPEY2	21	37603196	Missense_Mutation	C	T	p.S705F	86	0.058	0.062	NA	NA	NA	dopey family member 2
Case#4	Baseline Only	TXNRD2	22	19907099	Missense_Mutation	C	A	p.A66S	103	0.078	0.082	NA	NA	NA	thioredoxin reductase 2
Case#4	Baseline Only	FANCD2OS	3	10146268	Missense_Mutation	A	G	p.L64P	186	0.065	0.070	NA	NA	NA	FANCD2 opposite strand
Case#4	Baseline Only	ZDHHC23	3	113673125	Missense_Mutation	A	G	p.K247R	69	0.058	0.063	NA	NA	NA	zinc finger, DHHC-type containing 23
Case#4	Baseline Only	GFRAL	6	55196568	Nonsense_Mutation	T	G	p.Y26*	256	0.125	0.129	NA	NA	NA	GDNF family receptor alpha like
Case#4	Baseline Only	GPR146	7	1097183	Missense_Mutation	G	A	p.G11E	107	0.103	0.116	NA	NA	NA	G protein-coupled receptor 146
Case#4	Baseline Only	CPVL	7	29160604	Missense_Mutation	C	T	p.R25H	59	0.085	0.095	NA	NA	NA	carboxypeptidase, vitellogenic-like
Case#4	Baseline Only	SPDYE1	7	44047066	Missense_Mutation	T	C	p.C278R	280	0.089	0.100	NA	NA	NA	speedy/RINGO cell cycle regulator family member E1
Case#4	Baseline Only	C7orf72	7	50180972	Missense_Mutation	C	T	p.T358I	45	0.133	0.150	NA	NA	NA	chromosome 7 open reading frame 72
Case#4	Baseline Only	CSMD1	8	3263699	Nonsense_Mutation	C	A	p.G707*	51	0.373	0.403	NA	NA	NA	CUB and Sushi multiple domains 1
Case#4	Baseline Only	EPPK1	8	144940260	Missense_Mutation	C	T	p.D2388N	206	0.053	0.058	NA	NA	NA	epiplakin 1
Case#4	Baseline Only	SLC39A4	8	145639726	Missense_Mutation	T	C	p.T357A	111	0.081	0.088	NA	NA	NA	solute carrier family 39 (zinc transporter), member 4
Case#4	Baseline Only	ANKRD18A	9	38571130	Missense_Mutation	C	A	p.A183S	75	0.067	0.075	NA	NA	NA	ankyrin repeat domain 18A
Case#4	Baseline Only	GOLGA1	9	127661645	Missense_Mutation	G	A	p.T425M	29	0.138	0.155	NA	NA	NA	golgin A1
Case#4	Baseline Only	PNPLA7	9	140358581	Missense_Mutation	C	T	p.D1050N	41	0.146	0.164	NA	NA	NA	patatin-like phospholipase domain containing 7

Supplementary Table S6 - List of gene transcripts studied in the Nanostring panel.

List of genes chosen for the nCounter analysis including housekeeping genes used for normalization, positive and negatives controls. *Indicates part of custom gene list

Number	Gene Name	Accession#	Class name
1	A2M	NM_000014.4	Endogenous
2	ABCB1	NM_000927.3	Endogenous
3	ABL1	NM_005157.3	Endogenous
4	ADA	NM_000022.2	Endogenous
5	ADORA2A	NM_000675.3	Endogenous
6	AICDA	NM_020661.1	Endogenous
7	AIRE	NM_000383.2	Endogenous
8	AKT1*	NM_005163.2	Endogenous
9	AKT3	NM_181690.1	Endogenous
10	ALCAM	NM_001627.3	Endogenous
11	AMBP	NM_001633.3	Endogenous
12	AMICA1	NM_153206.2	Endogenous
13	ANP32B	NM_006401.2	Endogenous
14	ANXA1	NM_000700.1	Endogenous
15	APOE	NM_000041.2	Endogenous
16	APP	NM_000484.3	Endogenous
17	ARG1	NM_000045.2	Endogenous
18	ARG2	NM_001172.3	Endogenous
19	ATF1	NM_005171.2	Endogenous
20	ATF2	NM_001256090.1	Endogenous
21	ATG10	NM_001131028.1	Endogenous
22	ATG12	NM_004707.2	Endogenous
23	ATG16L1	NM_198890.2	Endogenous
24	ATG5	NM_004849.2	Endogenous
25	ATG7	NM_001136031.2	Endogenous
26	ATM	NM_000051.3	Endogenous
27	AXL	NM_021913.2	Endogenous
28	BAGE	NM_001187.1	Endogenous
29	BATF	NM_006399.3	Endogenous
30	BAX	NM_138761.3	Endogenous
31	BCL10	NM_003921.2	Endogenous
32	BCL2	NM_000657.2	Endogenous
33	BCL2L1	NM_001191.2	Endogenous
34	BCL6	NM_001706.2	Endogenous
35	BID	NM_001196.2	Endogenous
36	BIRC5	NM_001168.2	Endogenous
37	BLK	NM_001715.2	Endogenous
38	BLNK	NM_013314.2	Endogenous
39	BMI1	NM_005180.5	Endogenous
40	BST1	NM_004334.2	Endogenous
41	BST2	NM_004335.2	Endogenous
42	BTK	NM_000061.1	Endogenous
43	BTLA	NM_181780.2	Endogenous
44	C1QA	NM_015991.2	Endogenous

45	C1QB	NM_000491.3	Endogenous
46	C1QBP	NM_001212.3	Endogenous
47	C1R	NM_001733.4	Endogenous
48	C1S	NM_001734.2	Endogenous
49	C2	NM_000063.3	Endogenous
50	C3	NM_000064.2	Endogenous
51	C3AR1	NM_004054.2	Endogenous
52	C4B	NM_001002029.3	Endogenous
53	C4BPA	NM_000715.3	Endogenous
54	C5	NM_001735.2	Endogenous
55	C6	NM_000065.2	Endogenous
56	C7	NM_000587.2	Endogenous
57	C8A	NM_000562.2	Endogenous
58	C8B	NM_000066.2	Endogenous
59	C8G	NM_000606.2	Endogenous
60	C9	NM_001737.3	Endogenous
61	CAMP	NM_004345.3	Endogenous
62	CARD11	NM_032415.2	Endogenous
63	CARD9	NM_052813.4	Endogenous
64	CASP1	NM_001223.3	Endogenous
65	CASP10	NM_032977.3	Endogenous
66	CASP3	NM_032991.2	Endogenous
67	CASP8	NM_001228.4	Endogenous
68	CCL1	NM_002981.1	Endogenous
69	CCL11	NM_002986.2	Endogenous
70	CCL13	NM_005408.2	Endogenous
71	CCL14	NM_032963.3	Endogenous
72	CCL15	NM_032965.3	Endogenous
73	CCL16	NM_004590.2	Endogenous
74	CCL17	NM_002987.2	Endogenous
75	CCL18	NM_002988.2	Endogenous
76	CCL19	NM_006274.2	Endogenous
77	CCL2	NM_002982.3	Endogenous
78	CCL20	NM_004591.1	Endogenous
79	CCL21	NM_002989.2	Endogenous
80	CCL22	NM_002990.3	Endogenous
81	CCL23	NM_145898.1	Endogenous
82	CCL24	NM_002991.2	Endogenous
83	CCL25	NM_005624.2	Endogenous
84	CCL26	NM_006072.4	Endogenous
85	CCL27	NM_006664.2	Endogenous
86	CCL28	NM_148672.2	Endogenous
87	CCL3	NM_002983.2	Endogenous
88	CCL3L1	NM_021006.4	Endogenous
89	CCL4	NM_002984.2	Endogenous
90	CCL5	NM_002985.2	Endogenous
91	CCL7	NM_006273.2	Endogenous
92	CCL8	NM_005623.2	Endogenous
93	CCND3	NM_001760.2	Endogenous
94	CCR1	NM_001295.2	Endogenous

95	CCR2	NM_001123041.2	Endogenous
96	CCR3	NM_001837.2	Endogenous
97	CCR4	NM_005508.4	Endogenous
98	CCR5	NM_000579.1	Endogenous
99	CCR6	NM_031409.2	Endogenous
100	CCR7	NM_001838.2	Endogenous
101	CCR9	NM_031200.1	Endogenous
102	CCRL2	NM_003965.4	Endogenous
103	CD14	NM_000591.2	Endogenous
104	CD160	NM_007053.2	Endogenous
105	CD163	NM_004244.4	Endogenous
106	CD164	NM_006016.4	Endogenous
107	CD180	NM_005582.2	Endogenous
108	CD19	NM_001770.4	Endogenous
109	CD1A	NM_001763.2	Endogenous
110	CD1B	NM_001764.2	Endogenous
111	CD1C	NM_001765.2	Endogenous
112	CD1D	NM_001766.3	Endogenous
113	CD1E	NM_001042583.1	Endogenous
114	CD2	NM_001767.3	Endogenous
115	CD200	NM_005944.5	Endogenous
116	CD207	NM_015717.2	Endogenous
117	CD209	NM_021155.2	Endogenous
118	CD22	NM_001771.2	Endogenous
119	CD24	NM_013230.2	Endogenous
120	CD244	NM_016382.2	Endogenous
121	CD247	NM_198053.1	Endogenous
122	CD27	NM_001242.4	Endogenous
123	CD274	NM_014143.3	Endogenous
124	CD276	NM_001024736.1	Endogenous
125	CD28	NM_001243078.1	Endogenous
126	CD33	NM_001177608.1	Endogenous
127	CD34	NM_001025109.1	Endogenous
128	CD36	NM_001001548.2	Endogenous
129	CD37	NM_001774.2	Endogenous
130	CD38	NM_001775.2	Endogenous
131	CD3D	NM_000732.4	Endogenous
132	CD3E	NM_000733.2	Endogenous
133	CD3EAP	NM_012099.1	Endogenous
134	CD3G	NM_000073.2	Endogenous
135	CD4	NM_000616.4	Endogenous
136	CD40	NM_001250.4	Endogenous
137	CD40LG	NM_000074.2	Endogenous
138	CD44	NM_001001392.1	Endogenous
139	CD46	NM_172350.1	Endogenous
140	CD47	NM_001777.3	Endogenous
141	CD48	NM_001778.2	Endogenous
142	CD5	NM_014207.2	Endogenous
143	CD53	NM_001040033.1	Endogenous
144	CD55	NM_000574.3	Endogenous

145	CD58	NM_001779.2	Endogenous
146	CD59	NM_000611.4	Endogenous
147	CD6	NM_006725.3	Endogenous
148	CD63	NM_001780.4	Endogenous
149	CD68	NM_001251.2	Endogenous
150	CD7	NM_006137.6	Endogenous
151	CD70	NM_001252.2	Endogenous
152	CD74	NM_001025159.1	Endogenous
153	CD79A	NM_001783.3	Endogenous
154	CD79B	NM_021602.2	Endogenous
155	CD80	NM_005191.3	Endogenous
156	CD81	NM_004356.3	Endogenous
157	CD83	NM_004233.3	Endogenous
158	CD84	NM_001184879.1	Endogenous
159	CD86	NM_175862.3	Endogenous
160	CD8A	NM_001768.5	Endogenous
161	CD8B	NM_004931.3	Endogenous
162	CD9	NM_001769.2	Endogenous
163	CD96	NM_005816.4	Endogenous
164	CD97	NM_078481.2	Endogenous
165	CD99	NM_002414.3	Endogenous
166	CDH1	NM_004360.2	Endogenous
167	CDH5	NM_001795.3	Endogenous
168	CDK1	NM_001786.4	Endogenous
169	CDKN1A	NM_000389.2	Endogenous
170	CEACAM1	NM_001712.3	Endogenous
171	CEACAM6	NM_002483.4	Endogenous
172	CEACAM8	NM_001816.3	Endogenous
173	CEBPB	NM_005194.2	Endogenous
174	CFB	NM_001710.5	Endogenous
175	CFD	NM_001928.2	Endogenous
176	CFI	NM_000204.3	Endogenous
177	CFP	NM_002621.2	Endogenous
178	CHIT1	NM_003465.2	Endogenous
179	CHUK	NM_001278.3	Endogenous
180	CKLF	NM_181640.2	Endogenous
181	CLEC4A	NM_194448.2	Endogenous
182	CLEC4C	NM_203503.1	Endogenous
183	CLEC5A	NM_013252.2	Endogenous
184	CLEC6A	NM_001007033.1	Endogenous
185	CLEC7A	NM_197954.2	Endogenous
186	CLU	NM_001831.2	Endogenous
187	CMA1	NM_001836.2	Endogenous
188	CMKLR1	NM_004072.1	Endogenous
189	COL3A1	NM_000090.3	Endogenous
190	COLEC12	NM_130386.2	Endogenous
191	CR1	NM_000651.4	Endogenous
192	CR2	NM_001006658.1	Endogenous
193	CREB1	NM_004379.3	Endogenous
194	CREB5	NM_182898.2	Endogenous

195	CREBBP	NM_004380.2	Endogenous
196	CRK*	NM_016823.2	Endogenous
197	CRKL*	NM_005207.3	Endogenous
198	CRP	NM_000567.2	Endogenous
199	CSF1	NM_000757.4	Endogenous
200	CSF1R	NM_005211.2	Endogenous
201	CSF2	NM_000758.2	Endogenous
202	CSF2RB	NM_000395.2	Endogenous
203	CSF3	NM_000759.3	Endogenous
204	CSF3R	NM_156038.2	Endogenous
205	CT45A1	NM_001017417.1	Endogenous
206	CTAG1B	NM_001327.2	Endogenous
207	CTAGE1	NM_172241.2	Endogenous
208	CTCFL	NM_001269042.1	Endogenous
209	CTLA4	NM_005214.3	Endogenous
210	CTSG	NM_001911.2	Endogenous
211	CTSH	NM_004390.3	Endogenous
212	CTSL	NM_001912.4	Endogenous
213	CTSS	NM_004079.3	Endogenous
214	CTSW	NM_001335.3	Endogenous
215	CX3CL1	NM_002996.3	Endogenous
216	CX3CR1	NM_001337.3	Endogenous
217	CXCL1	NM_001511.1	Endogenous
218	CXCL10	NM_001565.1	Endogenous
219	CXCL11	NM_005409.4	Endogenous
220	CXCL12	NM_000609.5	Endogenous
221	CXCL13	NM_006419.2	Endogenous
222	CXCL14	NM_004887.4	Endogenous
223	CXCL16	NM_001100812.1	Endogenous
224	CXCL2	NM_002089.3	Endogenous
225	CXCL3	NM_002090.2	Endogenous
226	CXCL5	NM_002994.3	Endogenous
227	CXCL6	NM_002993.3	Endogenous
228	CXCL9	NM_002416.1	Endogenous
229	CXCR1	NM_000634.2	Endogenous
230	CXCR2	NM_001557.2	Endogenous
231	CXCR3	NM_001504.1	Endogenous
232	CXCR4	NM_003467.2	Endogenous
233	CXCR5	NM_001716.3	Endogenous
234	CXCR6	NM_006564.1	Endogenous
235	CYBB	NM_000397.3	Endogenous
236	CYFIP2	NM_001037332.2	Endogenous
237	CYLD	NM_015247.1	Endogenous
238	DDX43	NM_018665.2	Endogenous
239	DDX58	NM_014314.3	Endogenous
240	DEFB1	NM_005218.3	Endogenous
241	DMBT1	NM_007329.2	Endogenous
242	DOCK9	NM_001130048.1	Endogenous
243	DPP4	NM_001935.3	Endogenous
244	DUSP4	NM_057158.2	Endogenous

245	DUSP6	NM_001946.2	Endogenous
246	EBI3	NM_005755.2	Endogenous
247	ECSIT	NM_001142464.2	Endogenous
248	EGR1	NM_001964.2	Endogenous
249	EGR2	NM_000399.3	Endogenous
250	ELANE	NM_001972.2	Endogenous
251	ELK1	NM_005229.3	Endogenous
252	ENG	NM_001114753.1	Endogenous
253	ENTPD1	NM_001098175.1	Endogenous
254	EOMES	NM_005442.2	Endogenous
255	EP300	NM_001429.2	Endogenous
256	EPCAM	NM_002354.1	Endogenous
257	ETS1	NM_005238.3	Endogenous
258	EWSR1	NM_013986.3	Endogenous
259	F12	NM_000505.3	Endogenous
260	F13A1	NM_000129.3	Endogenous
261	F2RL1	NM_005242.3	Endogenous
262	FADD	NM_003824.2	Endogenous
263	FAS	NM_000043.3	Endogenous
264	FCER1A	NM_002001.2	Endogenous
265	FCER1G	NM_004106.1	Endogenous
266	FCER2	NM_002002.4	Endogenous
267	FCGR1A	NM_000566.3	Endogenous
268	FCGR2A	NM_021642.3	Endogenous
269	FCGR2B	NM_001002273.1	Endogenous
270	FCGR3A	NM_000569.6	Endogenous
271	FEZ1	NM_005103.4	Endogenous
272	FLT3	NM_004119.1	Endogenous
273	FLT3LG	NM_001459.3	Endogenous
274	FN1	NM_212482.1	Endogenous
275	FOS	NM_005252.2	Endogenous
276	FOXJ1	NM_001454.3	Endogenous
277	FOXP3	NM_014009.3	Endogenous
278	FPR2	NM_001462.3	Endogenous
279	FUT5	NM_002034.2	Endogenous
280	FUT7	NM_004479.3	Endogenous
281	FYN	NM_002037.3	Endogenous
282	GAGE1	NM_001040663.2	Endogenous
283	GATA3	NM_001002295.1	Endogenous
284	GNLY	NM_006433.2	Endogenous
285	GPI	NM_000175.2	Endogenous
286	GTF3C1	NM_001520.3	Endogenous
287	GZMA	NM_006144.2	Endogenous
288	GZMB	NM_004131.3	Endogenous
289	GZMH	NM_033423.3	Endogenous
290	GZMK	NM_002104.2	Endogenous
291	GZMM	NM_005317.2	Endogenous
292	HAMP	NM_021175.2	Endogenous
293	HAVCR2	NM_032782.3	Endogenous
294	HCK	NM_002110.2	Endogenous

295	HLA-A	NM_002116.5	Endogenous
296	HLA-B	NM_005514.6	Endogenous
297	HLA-C	NM_002117.4	Endogenous
298	HLA-DMA	NM_006120.3	Endogenous
299	HLA-DMB	NM_002118.3	Endogenous
300	HLA-DOB	NM_002120.3	Endogenous
301	HLA-DPA1	NM_033554.2	Endogenous
302	HLA-DPB1	NM_002121.4	Endogenous
303	HLA-DQA1	NM_002122.3	Endogenous
304	HLA-DQB1	NM_002123.3	Endogenous
305	HLA-DRA	NM_019111.3	Endogenous
306	HLA-DRB3	NM_022555.3	Endogenous
307	HLA-DRB4	NM_021983.4	Endogenous
308	HLA-E	NM_005516.4	Endogenous
309	HLA-G	NM_002127.4	Endogenous
310	HMGB1	NM_002128.4	Endogenous
311	HRAS	NM_005343.2	Endogenous
312	HSD11B1	NM_181755.1	Endogenous
313	ICAM1	NM_000201.2	Endogenous
314	ICAM2	NM_000873.3	Endogenous
315	ICAM3	NM_002162.3	Endogenous
316	ICAM4	NM_001039132.1	Endogenous
317	ICOS	NM_012092.2	Endogenous
318	ICOSLG	NM_015259.4	Endogenous
319	IDO1	NM_002164.3	Endogenous
320	IFI16	NM_005531.1	Endogenous
321	IFI27	NM_005532.3	Endogenous
322	IFI35	NM_005533.3	Endogenous
323	IFIH1	NM_022168.2	Endogenous
324	IFIT1	NM_001548.3	Endogenous
325	IFIT2	NM_001547.4	Endogenous
326	IFITM1	NM_003641.3	Endogenous
327	IFITM2	NM_006435.2	Endogenous
328	IFNA1	NM_024013.1	Endogenous
329	IFNA17	NM_021268.2	Endogenous
330	IFNA2	NM_000605.3	Endogenous
331	IFNA7	NM_021057.2	Endogenous
332	IFNA8	NM_002170.3	Endogenous
333	IFNAR1	NM_000629.2	Endogenous
334	IFNAR2*	NM_000874.3	Endogenous
335	IFNB1	NM_002176.2	Endogenous
336	IFNG	NM_000619.2	Endogenous
337	IFNGR1	NM_000416.1	Endogenous
338	IFNGR2	NM_005534.3	Endogenous
339	IFNL1	NM_172140.1	Endogenous
340	IFNL2	NM_172138.1	Endogenous
341	IGF1R	NM_000875.2	Endogenous
342	IGF2R	NM_000876.1	Endogenous
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344	IKBKB	NM_001556.1	Endogenous

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804	POS_F	ERCC_00034.1	Positive

Supplemental References

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