Figure SI 1. Plasmid diagrams for production of TF domains. Five protein expression plasmids were used to produce TFs for Fab-phage selections: (A-C) Intracellular *E. coli* expression of soluble biotinylated TF domains from Rutgers, SGC, and the RAN, respectively. (D) Expression of soluble biotinylated TFs by IVTT in an *E. coli* cell free extract, courtesy of Sutro Biopharma. (E) Plasmid map for expression of TFs by Yeast antigen display system. His and GST tags were used for purification purposes while Avi tag was used for efficient biotinylation of the proteins at a single site and TEV protease site was included for "catch-and-release" of antigens during Fab-phage selections.

Figure SI 2. Examples of 8 protein antigens that entered the Fab selection pipeline. Four antigens were considered to be high quality and resulted in successful Fab selections where 4 were low quality antigens with no successfully validated Fabs.

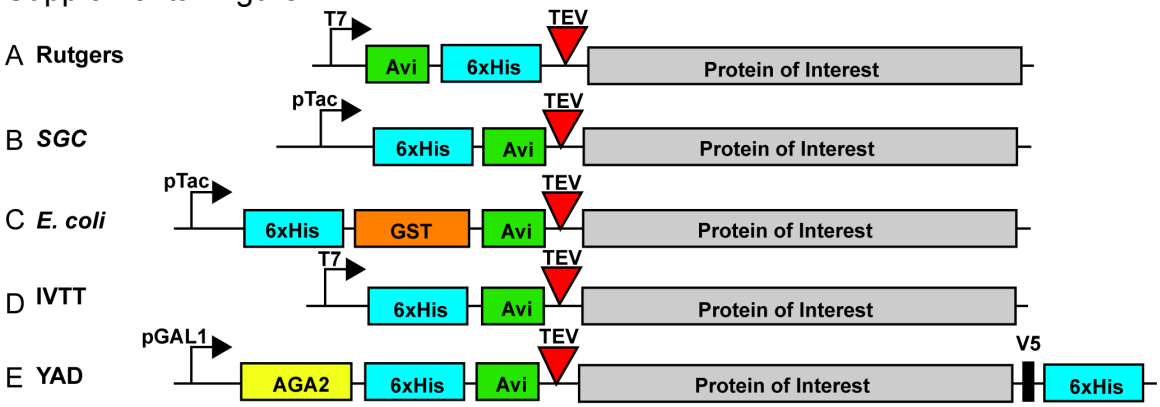
Figure SI 3. Graphical depiction of the competition ELISA test used for primary Fab validation. In all cases 20nM biotinylated antigen was adsorbed onto Streptavidin or Neutravidin coated plates then blocked with PBS buffer that contained 0.2% BSA and 10uM Biotin. (Left) Direct Fab-phage binding was monitored for 96 single colony isolates from selection rounds 3 or 4 where phage culture supernatant was diluted and plated on antigen coated wells. Binding was detected by incubation with anti-M13-HRP secondary antibody and signal was developed by the addition of TMB substrate. OD_{650} (kinetic mode) or OD450

(endpoint mode). (Right) Similar to the direct ELISA a competitive binding ELISA was preformed, where 20nM soluble biotinylated antigen was incubated with Fab-phage 15 minutes prior to addition to antigen coated ELISA plates.

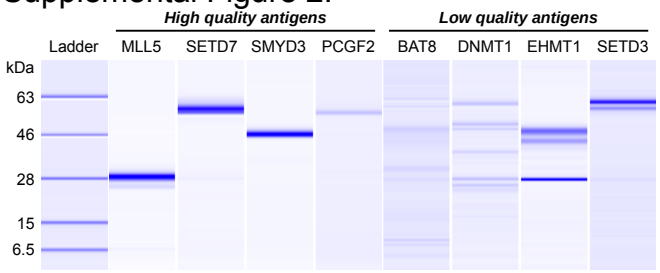
Figure SI 4. Representative photomicrographs showing expression of target antigens on the surface of yeast. DIC images from 3 different Yeast strains, (Top Row) control cells expressed ER localized BirA, (Middle Row) cells that expressed Sox7 and ER localized BirA, and (Bottom Row) cells that expressed only Sox7. Antigen expression was monitored by staining cells with the V5-FITC antibody and clearly showed staining only when target Sox7 antigen was expressed. To verify that the antigens were biotinylated, we monitored Avi tag biotinylation with Strep-Rho antibody and clearly showed that staining was detected in cells where the antigen and BirA were co-expressed. Merged images showed co-staining of both the antigen and biotinylation signal suggestive that the expressed antigen was biotinylated.

Figure SI 5. Representative photomicrographs of siRNA KD experiments showing a reduction in protein expression in cellculture. One BATF Fab showed binding to wild type A2780cis cells or lack of binding to siRNA knockdown of target TF. A2780cis cells were also stained with anti-Flag antibody and DAPI as a negative staining control. Graphs showed the relative staining intensities as determined by ImageJ of siRNA KD and siRNA control treated cells (** $p<0.001$). Scale bar =50uM.

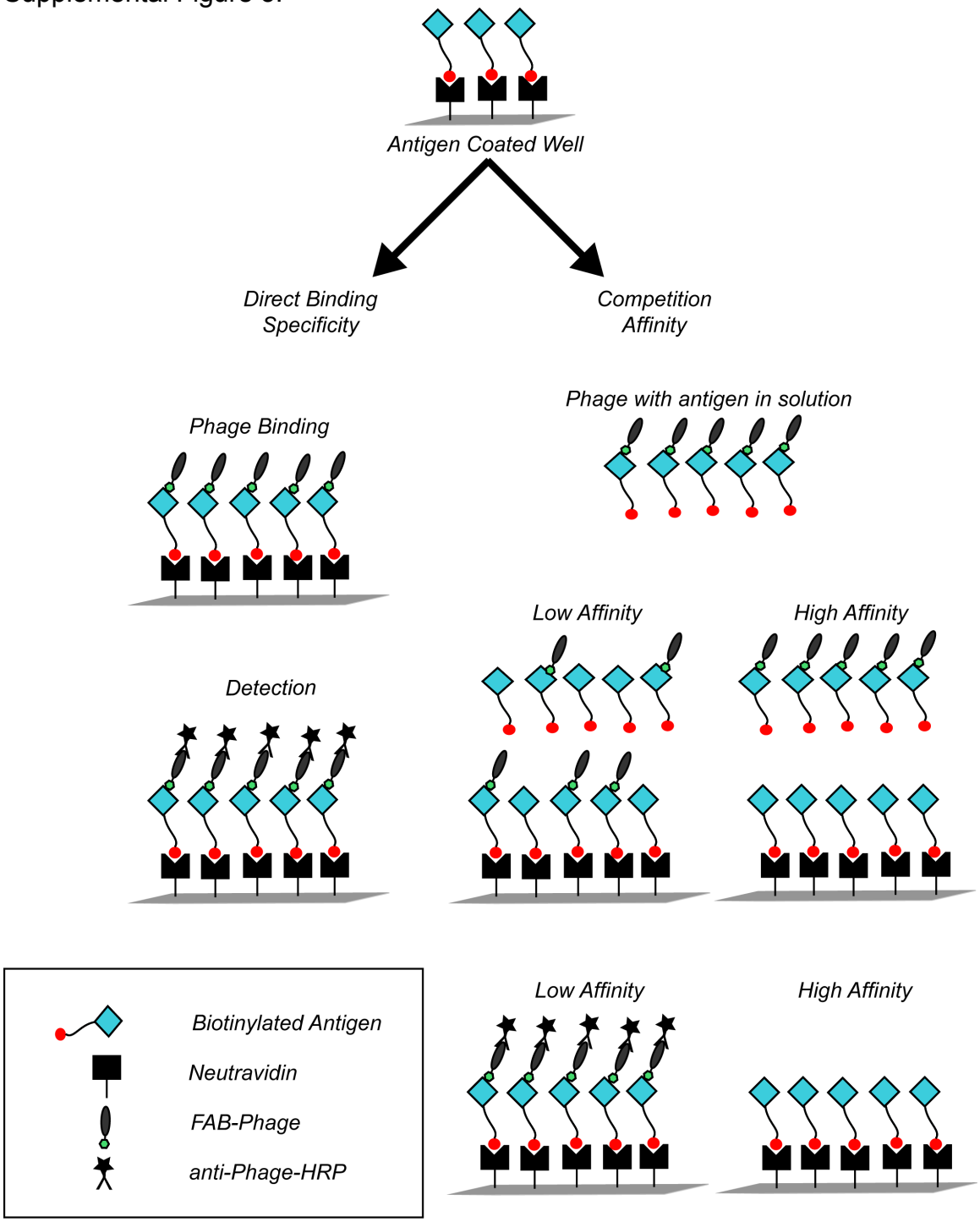
Supplemental Figure 1:



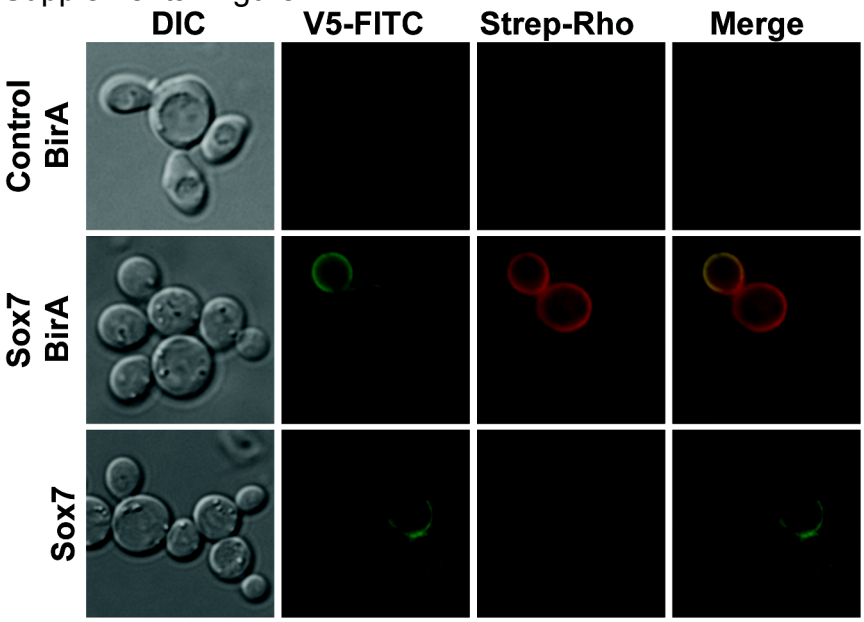
Supplemental Figure 2:



Supplemental Figure 3:



Supplemental Figure 4:



Supplemental Figure 5:

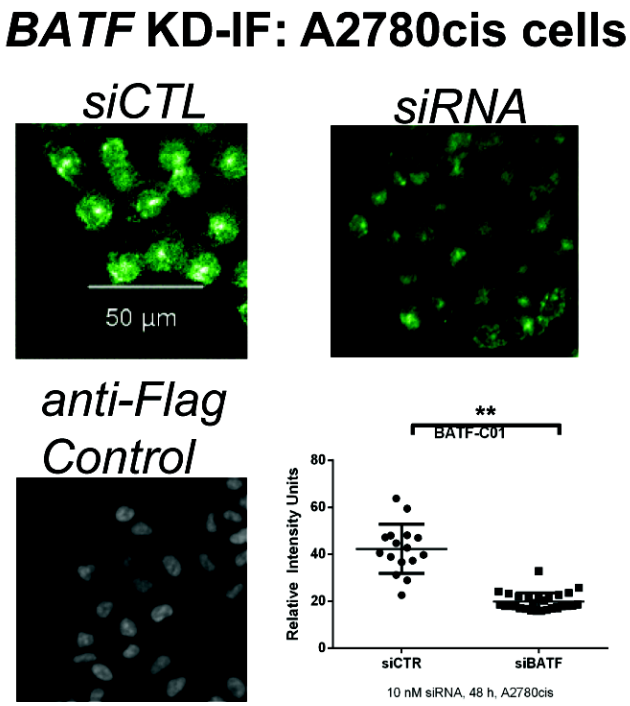


Table SI 1: Antigens (n=557) from RAN, Rutgers, or SGC that have entered the Fab selection pipeline. Antigen molecular weight, pI, domain type, and Amino acid sequence with tags are shown along with success through primary validation experiments.

HGCN	Uniprot ID	Antigen ID	Antigen Source	MW (Da)	pI	Common Domain Names	Primary Validation (pass/fail)	construct seq (with tag)
ALX3	O95076	HR7916A.001	Rutgers	13409.06	9.4315	Homeobox	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMTFSTFQLEELEKVFQKTHYPDVYARE QLALRTDLTEARVRVWFQNRRAKWRKRERYGKIQEGRNPFTAAYDISVLPR
ANAPC2	Q9UJX6	HR6941B.004	Rutgers	14427.21	4.9166	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMSDDESDSGMASQADQKEEELLLFWT YIQAMLTNLESLSLDRIYNMLRMFVVTGPALAEIDLQELQGYLQKKVRDQQLVYSAGVY RLPKNCS
ANKZF1	Q9H8Y5	HR8423A.001	Rutgers	15275.28	7.3485	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMAKAPGQPELWNALLAACRAGDVGVL KLQLAPSPADPRVLSLLSAPLGSGGFTLLHAAAAAGRGSVVRLLLEAGADPTVQDSRA RPPYTVAADKSTRNEFRRFMEKNPD
ARID3A	Q99856	HR4394C.020	Rutgers	17133.62	8.9416	Misc	pass	MGHHHHHHSHMPDHGDWTYEEQFKQLYELDGDPKRKEFLDDLFSFMQKRGTPVNRI PIMAKQVLDLFMLYVLVTEKGGLVEVINKKLWREITKGLNLPTSITSAAFTLRTQYMKYLY PYECEKRGLSNPNELQAAIDSNRREGRR
ARID3A	Q99856	HR4394C.025	Rutgers	61836.32	5.53	Misc	fail	
ARID3A	Q99856	Arid3a	RAN	10747.7	9.9104	Misc	pass	MKIEEHHHHHHHSSGKLGSTEDLYFQSAAQPALDGDPKRKEFLDDLFSFMQKRGTPVN RIPIMAKQVLDLFMLYVLVTEKGGLVEVINKKLWREITKGLNLPTSITSAAFTLRTQYMKYL YPYE
ARID4B	Q4LE39	ARID4B-A003	SGC	32199.01	4.8554	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGKQIDELLGKVVCVDYISLDKKKALWFPALVVCPDC SDEIAVKKDNILVRSFKDGKFTSVPRKDVHEITSDTAPKPDAVLKQAFEQALEFHKSRTIP ANWKTELKEDSSSSEAEEEEEEEDDEKEKEDNSSEEEEEIEPFPEERENFLQQLYKFM EDRGTPINKRPVLGYRNLNLFKLFRLVHKLGGFDNIESGAVWKQVYQDLGIPVLNSAAG YNVKCAYKKYLYGFEEYCRSANIEFQMALPEKVVNKGGSGHHHHHH
ARX	Q96QS3	Arx	RAN	7253.24	10.7376	Homeobox	pass	MKIEEHHHHHHHSSGKLGSTEDLYFQSAAQPARRYRTTFTSYQLEELERAFQKTHYPDV FTREELAMRLDLTEARVQVWFQNRRAKWRK
ASF1B	Q9NVP2	ASF1B-A001	SGC	25754.94	4.5613	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGAKVSVLNVAVLENPSPFHSPFRFEISFECSEALAD DLEWKIIYVGSAESEEFDQILDSVLVGPVPAGRHMFVFQADAPNPSLIPETDAVGVTVVL ITCTYHGQEFIRVGYYVNNEYLNPELRENPPMKPDFSQLQRNILASNPRVTRFHINWDN NMDRLEAIETQDPSLGCGLPLNCTPIKGLGLPGCIPGLLPENSMDCIGGSGHHHHHH
ASH1L	Q9NR48	ASH1LA-A001	SGC	20271.77	6.7762	Bromodomain	fail	MHHHHHHHHHHHDLGTENLYFQSMAEENIEVARAARLAQIFKEICDGIISYKDSSRQALA APLLNLPPKKKNADYYEKISDPLDLITIEKQILTGYYKTVEAFDADMLKVFRNAEKYYGRK SPVGRDVCRLRKAYYNARHEASAQIDEIVGETASESSKGGYGLNDIFEAQKIEWHE
ASH1L	Q9NR48	ASH1LA-A004	SGC	20271.77	6.7762	Bromodomain	pass	MHHHHHHHHHHHDLGTENLYFQSMAEENIEVARAARLAQIFKEICDGIISYKDSSRQALA APLLNLPPKKKNADYYEKISDPLDLITIEKQILTGYYKTVEAFDADMLKVFRNAEKYYGRK SPVGRDVCRLRKAYYNARHEASAQIDEIVGETASESSKGGYGLNDIFEAQKIEWHE
ASH1L	Q9NR48	HR7137C.007	Rutgers	18107.16	6.1719	SET	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMREEKGWGIRTKEPLKAGQFIIEYLG EVVSEQEFRNRMIEQYHNHSDHYCLNLDSGMVIDSYRMGNEARFINHSCDPNCEMQK WSVNGVYRIGLYALKDMPAGTELTYDYNFHSFNVEKQ
ATAD2	Q6PL18	ATAD2A-A001	SGC	20504.97	5.8323	Bromodomain	pass	MHHHHHHHHHHHDLGTENLYFQSMQEEDTFRELRIFLRNVTHRLAIDKRFRVFTKPVDP DEVPDYVTVIKQPMDLSSVISKIDLHKYLTVKDYLRDIDLICSNALEYNPDRDPGDRLIRH RACALRDTAYAIIKEELDEDFEQLCEEIQESRSSKGGYGLNDIFEAQKIEWHE
ATAD2B	Q9ULI0	KIAA1240A-A001	SGC	20882.54	6.1337	Bromodomain	pass	MHHHHHHHHHHHDLGTENLYFQSMEDQEENTLRELRLFLRDVTKRLATDKRFNIFSKPV DIEEVSDYLEVIKEPMDLSTVITKIDKHNYLTAKDFLKDIDLICSNALEYNPDKDPGDKIIRH RACTLKDTAHAIIAAELDPEFNKLCEEIKEARIKRGSSKGGYGLNDIFEAQKIEWHE
ATF2	P15336	Atf2	RAN	7648.77	10.6487	bZip	pass	MKIEEHHHHHHHSSGKLGSTEDLYFQSAAQPAEDPDEKRRKFLERNRAAASRCRQKRK VWVQSLEKKAEDLSSLNGQLQSEVTLLRNEVAQLKQLLL
ATF4	P18848	HR6914A.001	Rutgers	11325.83	7.8355	bZip	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKKLLKKMEQNKTAATRYRQKKRAEQE ALTGECKELEKKNEALKERADSLAKEIQYLKDLIEEV
ATF4	P18848	Atf4	RAN	7580.74	9.8267	bZip	pass	MKIEEHHHHHHHSSGKLGSTEDLYFQSAAQPAEKLDKKLKKMEQNKTAATRYRQKKRAE QEALTGECKELEKKNEALKERADSLAKEIQYLKDLIE
ATF7	P17544	Atf7	RAN	7605.71	10.8992	bZip	pass	MKIEEHHHHHHHSSGKLGSTEDLYFQSAAQPADPDERRQRFLERNRAAASRCRQKRKL WVSSLEKKAEELTSQNIQLSNEVTLLRNEVAQLKQLLL
ATMIN	O43313	HR8351A.005	Rutgers	21934.08	8.6341	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGELIQPSVSELSRAVRTNILCTVRGC GKILPNSPALNMHLVKSHRLQDGIVNPTIRKDLKTGPKFYCCPIEGCPRGPERPFSQFSL VKQHFMKMHAEKKHKCSKCSNSYGTEWDLKRHAEDCGKTFRCTCGCPYASRTALQS HIYRTGHEIPAEHRDPP
BARX2	Q9UMQ3	HR7561.004	Rutgers	24938.57	9.4001	Homeobox	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMHCHAELRLSSPGQLKAARRRYKTFMI DEILSKETCDYFEKLSLYSVCPSLVVRPKPLHSCTGSPSLRAYPLLSVITRQPTVISHLVP ATPGIAQALSCHQVTEAVSAEAPGGEALASSESETEQPTPRQKKPRRSRTIFTELQLMG LEKKFQKQKYLSTPDRLDLAQSLGLTQLQVKTWYQNRRMK
BARX2	Q9UMQ3	HR7561A.002	Rutgers	13414.34	10.4729	Homeobox	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMSSESETEQPTPRQKKPRRSRTIFTEL QLMGLEKKFQKQKYLSTPDRLDLAQSLGLTQLQVKTWYQNRRMKWKKMVLKGG
BAZ1A	Q9NRL2	ACF1-A002	SGC	22143.04	8.0631	Bromodomain	pass	MHHHHHHHHHHHDLGTENLYFQSMRKRQSPEPSPVTLGRRSSGRQGGVHELSAFEQL VVELVRHDDSWPFLKLVSKIQVPDYYDIIKKPIALNIIREKVNKCEYKLASEFIDDIELMFS NCFEYNPRNTSEAKAGTRLQAFFHIQAQKLGLHVTPSNVDQVSTPPAAKKSRISSKGG YGLNDIFEAQKIEWHE
BAZ1B	Q9UIG0	BAZ1BA-A001	SGC	19396.02	7.5991	Bromodomain	pass	MHHHHHHHHHHHDLGTENLYFQSMRQSLELQKCEEILHMIVKYRFSWPFREPVTRDEA EDYYDVITHPMDFQTVQNKCSCGSYRSVQEFLTDMKQVFTNAEVYNCRGSHVLSCMV KTEQCLVALLHKHLPGHPYVRRKRKKFSSKGGYGLNDIFEAQKIEWHE
BAZ2A	Q9UIF9	BAZ2AA-A002	SGC	17569.52	5.8142	Bromodomain	pass	MHHHHHHHHHHHDLGTENLYFQSMHSDLTFCEIILMEMESHDAAWPFLEPVNPRLVSGY RRIIKNPMDFSTMRERLLRGGYTSSEEFAADALLVFDNCQTFNEDDSEVGKAGHIMRR FFESRWEEFYQSSKGGYGLNDIFEAQKIEWHE
BAZ2B	Q9UIF8	BAZ2BA-A001	SGC	16063.28	6.9118	Bromodomain	pass	MHHHHHHSSGVDLGTENLYFQSMSVKKPKRDDSKDLALCSMILTEMETHEDAWPFLL PVNLKLVPGYKKVIKKPMDFSTIREKLSSGQYPNLETFALDVRLVFDNCETFNEDDSDIG RAGHNMRKYFEKKWTDTFKVS
BPTF	Q12830	FALZ/FALZA-A001	SGC	19511.89	6.3048	Bromodomain	pass	MHHHHHHHHHHHDLGTENLYFQSMSTEDAMTVLTPLTEKDYEGLKRVLRSLQAHKMAW PFLEPVDPNDAPDYYGVIKEPMDLATMEERVQRRYYEKLTEFVADMTKIFDNCRYYNPS DSPFYQCAEVLESFFVQKLKGFKASRSHSSKGGYGLNDIFEAQKIEWHE
BRD1	O95696	BRD1A-A002	SGC	17680.34	9.5346	PWWP	pass	MSGLNDIFEAQKIEWHEGSAGGSGSVLEPLKVVWAKCSGYPSYPALIIDPKMPRVPGH HNGVTIPAPPLDVLKIGEHMQTKSDEKLFLVLFFDNKRSWQWLPKSKMVPLGIDETIDKL KMMEGRNSSIRKAVRIAFDRAMNHLSRVHGEGGSGHHHHHH
BRD2	P25440	BRD2A-A001	SGC	18040.36	7.1082	Bromodomain	pass	MHHHHHHHHHHHDLGTENLYFQSMEQLKHCNGILKELLSKKHAAYAWPFYKPVDASAL GLHDYHDIIKHPMDLSTVKRKMENRDYRDAQEFAADVRLMFSNCYKYNPPDHDVVAM ARKLQDVFEFRYAKMPDSSKGGYGLNDIFEAQKIEWHE
BRD2	P25440	BRD2A-A002	SGC	20302.25	7.6688	Bromodomain	pass	MHHHHHHHHHHHSSGVDLGTENLYFQSMKPGRVTNQLQYLHKVVMKALWKHQFAWPF RQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYIYNK PTDDIVLMAQTLEKIFLQKVASMPQEEQELVVTIPKNSSKGGYGLNDIFEAQKIEWHE
BRD3	Q15059	BRD3A-A002	SGC	18358.81	6.9742	Bromodomain	pass	MHHHHHHHHHHHDLGTENLYFQSMGKLSEHLRYCDSILREMLSKKHAAYAWPFYKPVD AEALELHDYHDIIKHPMDLSTVKRKMDGREYPDAQGFAADVRLMFSNCYKYNPPDHEV VAMARKLQDVFEMRFAKMPSSKGGYGLNDIFEAQKIEWHE
BRD3	Q15059	BRD3A-A001	SGC	19645.34	7.1469	Bromodomain	pass	MHHHHHHHHHHHDLGTENLYFQSMPEVSNPSKPGRKTNQLQYMQMNVVVKTLWKHQFA WPFYQPVDAIKLNLPDYHKIIKNPMDMGTIKKRLENNYYWSASECMQDFNTMFTNCYIY NKPTDDIVLMAQALEKIFLQKVAQMPQEESSKGGYGLNDIFEAQKIEWHE
BRD4	O60885	BRD4A-A001	SGC	17720.16	6.8995	Bromodomain	pass	MHHHHHHHHHHHDLGTENLYFQSMKDVPDSQQHPAPEKSSKVSEQLKCCSGILKEMFA KKHAAYAWPFYKPVDVEALGLHDYCDIIKHPMDMSTIKSKLEAREYRDAQEFGADVRL MFSNCYKYNPPDHEVVAMARKLQDVFEMRFAKMPDE
BRD4	O60885	BRD4A-A005	SGC	20110.75	6.7046	Bromodomain	pass	MHHHHHHHHHHHDLGTENLYFQSMKDVPDSQQHPAPEKSSKVSEQLKCCSGILKEMFA KKHAAYAWPFYKPVDVEALGLHDYCDIIKHPMDMSTIKSKLEAREYRDAQEFGADVRL MFSNCYKYNPPDHEVVAMARKLQDVFEMRFAKMPDESSKGGYGLNDIFEAQKIEWHE
BRD7	Q9NPI1	BRD7A-A001	SGC	17991.46	6.9781	Bromodomain	pass	MHHHHHHHHHHHDLGTENLYFQSMEEVEQTPLQEALNQLMRQLQRKDPSAFFSFPVTD FIAPGYSMIIKHPMDFSTMKEKIKNNDYQSIEELKDNFKLMCTNAMIYNKPETIYYKAAKK LLHSGMKILSQERSSKGGYGLNDIFEAQKIEWHE
BRDT	Q58F21	BRDTA-A001	SGC	19222.9	7.623	Bromodomain	fail	MHHHHHHHHHHHDLGTENLYFQSMNTKKNGRLTNQLQYLQKVVLKDLWKHSFSWPFQ RPVDAVKLQLPDYYTIIKNPMDLNTIKKRLENKYYAKASECIEDFNTMFSNCYLYNKPGD DIVLMAQALEKLFMQKLSQMPQEESSKGGYGLNDIFEAQKIEWHE
BRDT	Q58F21	BRDTA-A007	SGC	18821.35	6.7068	Bromodomain	pass	MHHHHHHHHHHHDLGTENLYFQSMTVKVTEQLRHCSEILKEMLAKKHFSYAWPFYNPV DVNALGLHNYYDVVKNPMDLGTIKEKMDNQEYKDAYKFAADVRLMFMNCYKYNPPDH EVVTMARMLQDVFETHFSKIPIESSKGGYGLNDIFEAQKIEWHE
BRDT	Q58F21	BRDTA-A006	SGC	19222.9	7.623	Bromodomain	fail	MHHHHHHHHHHHDLGTENLYFQSMNTKKNGRLTNQLQYLQKVVLKDLWKHSFSWPFQ RPVDAVKLQLPDYYTIIKNPMDLNTIKKRLENKYYAKASECIEDFNTMFSNCYLYNKPGD DIVLMAQALEKLFMQKLSQMPQEESSKGGYGLNDIFEAQKIEWHE
BRPF1	P55201	BRPF1A-A002	SGC	19447.9	6.0627	Bromodomain	pass	
BRWD1	Q9NSI6	WDR9A-A002 monomer	SGC	19503.89	6.4208	Bromodomain	pass	

HGCN	Uniprot ID	Antigen ID	Antigen Source	MW (Da)	pI	Common Domain Names	Primary Validation (pass/fail)	construct seq (with tag)
BSX	Q3C1V8	HR8142A.001	Rutgers	12731.38	10.41	Homeobox	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPGKHCRRRKARTVFSDSQLSGLEKRFEIQRYLSTPERVELATALSLSETQVKTWFQNRRMKHKKQLRKSQDEP
C14orf169	Q9H6W3	FLJ21802A-A001	SGC	55638.89	5.7659	Cupin	pass	MSGLNDIFEAQKIEWHEGSAGGSGSPLRRVLAELNRIPSSRRRAARLFEWLIAPMPPDHFYRRLWEREAVLVRRQDHTYYQGLFSTADLDSMLRNEEVQFGQHLDAARYINGRRETLNPPGRALPAAAWSLYQAGCSLRLLCPQAFSTTVWQFLAVLQEQFGSMAGSNVYLTPPNSQGFAPHYDDIEAFVLQLEGRKLWRVYRPRAPTEELALTSSPNFSQDDLGEPVLQTVLEPGDLLYFPRGFIHQAECQDGVHSLHLTLSTYQRNTWGDFLEAILPLAVQAAMEENVEFRRGLPRDFMDYMGAQHSDSKDPRRTAFMEKVRVLVARLGHFAPVDAVADQRAKDFIHDSLPPVLTDRERALSVYGLPIRWEAGEPVNVGAQLTTETEVHMLQDGIARLVGEGGHLFLYYTVENSRVYHLEEPKCLEIYPQQADAMELLLGSYPEFVRVGDLPCDSVEDQLSLATTLYDKGLLLTKMPLALNGGSGHHHHHH
CAF1B	Q13112	CAF1B-A001	SGC	56395.64	7.1306	WD40	fail	MSGLNDIFEAQKIEWHEGSAGGSGMKVITCEIAWHNKEPVYSLDFQHGTAGRIHRLASAGVDTNVRIWKVEKGPDGKAIVEFLSNLARHTKAVNVVRFSPTGEILASGGDDAVILLWKVNDNKEPEQIAFQDEDEAQLNKENWTVVKTLRGHLEDVYDICWATDGNLMASASVDNTAIIWDVSKGQKISIFNEHKSYVQGVTWDPLGQYVATLSCDRVLRVYSIQKKRVAFNVSKMLSGIGAEGEARSYRMFHDDSMKSFFRRLSFTPDGSLLLTPAGCVESGENVMNTTYVFSRKNLKRPIAHLPCPGKATLAVRCCPVYFELRPVVETGVELMSLPYRLVFAVASEDSVLLYDTQQSFPFGYVSNIHYHTLSDISWSSDGAFLAISSTDGYCSFVTFEKDELGIPLKEKPVLNMRTPDTAKKTKSQTHRGSSPGPRPVEGTPASRTQDPSSPGTTPPQARQAPAPTVIRDPPSITPAVKSPLPGPSEEKTLQPSSQNTKAHPGGSGHHHHHH
CASP8AP2	Q9UKL3	HR8150A.003	Rutgers	11897.7	9.8998	Misc	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKNVIKKKGEIIILWTRNDDRVILLECQKRGPSSKTFAYLAAKLDKNPNQVSERFQQLMKLFEKSKCR
CBX1	P83916	CBX1A-A002	SGC	9333.38	6.1463	Misc	pass	MHHHHHHHHHHHDLGTENLYFQSMEYVVEKVLDRRVVKGKVEYLLKWKGFSDEDNTWEPEENLDCPDLIAEFLQSQKT
CBX1	P83916	CBX1-A003	SGC	13435.95	6.3569	Misc	pass	MHHHHHHHHHHHDLGTENLYFQSMKEESEKPRGFARGLEPERIIGATDSSGELMFLMKWKNSDEADLVPAKEANVKCPQVVISFYEERLTWHSYPSSKGGYGLNDIFEAQKIEWHE
CBX2	Q14781	CBX2-A003	SGC	13515.11	6.9786	Misc	pass	MHHHHHHHHHHHDLGTENLYFQSMEELSSVGEQVFAAECILSKRLRKGKLEYLVKWRGWSSKHNSWEPEENILDPRLLLAFQKKEHEKEVQNRSSKGGYGLNDIFEAQKIEWHE
CBX2	Q14781	HR6520A.001	Rutgers	10501.92	7.3481	Misc	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMEQVFAAECILSKRLRKGKLEYLVKWRGWSSKHNSWEPEENILDPRLLLAFQKKE
CBX2	Q14781	CBX2A-A002	SGC	9732.03	8.2041	Misc	pass	MHHHHHHHHHHHSSGVDLGTENLYFQSMEQVFAAECILSKRLRKGKLEYLVKWRGWSSKHNSWEPEENILDPRLLLAFQKKE
CBX3	Q13185	CBX3A-A001	SGC	9705.8	6.3256	Misc	pass	MHHHHHHHHHHHDLGTENLYFQSMEFVVEKVLDRRVVNGKVEYFLKWKGFTDADNTWEPEENLDCPELIEAFLNSQKAGKEK
CBX4	O00257	CBX4-A005	SGC	10649.78	7.2011	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGEHVFAVESIEKKRIRKGRVEYLVKWRGWSPKYNTWEPEENILDPRLLIAFQNRERQEQGGSGHHHHHH
CBX4	O00257	CBX4A-A002	SGC	10429.68	7.7134	Misc	fail	MHHHHHHHHHHHSSGVDLGTENLYFQSMEHVFAVESIEKKRIRKGRVEYLVKWRGWSPKYNTWEPEENILDPRLLIAFQNRERQEQ
CBX5	P45973	CBX5A-A001	SGC	10037.38	6.8869	Misc	pass	MHHHHHHHHHHHDLGTENLYFQSMEEYVVEKVLDRRVVKGQVEYLLKWKGFSEEHNTWEPEKNLDCPELISEFMKKYKKMKE
CBX5	P45973	CBX5-A001	SGC	11072.26	5.1487	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGREQSNDIARGFERGLEPEKIIGATDSCGDLMFLMKWKDTDEADLVLAKEANVKCPQIVIAFYEERLTGGSGHHHHHH
CBX8	Q9HC52	CBX8-A005	SGC	11712.08	6.8513	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGELSAVGERVFAAEALLKRRIRKGRMEYLVKWKGWSQKYSTWEPEENILDARLLAAFEEREREMELYGPKGGSGHHHHHH
CCDC101	Q96ES7	SGF29A-A001	SGC	20759.2	6.558	Misc	pass	MHHHHHHHHHHSSGVDLGTENLYFQSMGDKPPPLCGAIPASGDYVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDEEGKERHTLSRRRVIPLPQWKANPETDPEALFQKEQLVLALYPQTTCFYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVVACKEPKKK
CDC73	Q6P1J9	CDC5L-A001	SGC	24556.17	9.9676	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGNQKKGSRTPIIIIPAATTSLITMLNAKDLLQDLKFVPSDEKKKQGCQRENETLIQRRKDQMQPGGTAISVTVPYRVVDQPLKLMPQDWDRVVAVFVQGPAWQFKGWPWLLPDGSPVDIFAKIKAFHLKYDEVRLDPNVQKWDVTVLELSYHKRHLDRPVFLRFWETLDRYMVKHKSHLRFGGSGHHHHHH
CDX2	Q99626	HR7064A.001	Rutgers	12311.96	10.3336	Homeobox	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMTKDKYRVVYTDHQRLELEKEFHYSRYITIRRKAELAATLGLSERQVKIWFQNRRAKERKSNKKKLQQ
CDX2	Q99626	Cdx2	RAN	7125.18	10.7013	Homeobox	pass	MKIEEHHHHHHSSGKLGSTEDLYFQSAAQPADKYRVVYTDHQRLELEKEFHYSRYITIRRKAELAATLGLSERQVKIWFQNRRAKERK
CDYL	Q9Y232	CDYL-A002	SGC	32571.35	7.3625	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGAYRYRDIVVRKQDGFTHILLSTKSSENNSLNPEVMREVQSALSTAAADDSKLVLLSAVGSVFCCGLDFIYFIRRLTDDRKRESTKMAEAIRNFVNTFIQFKKPIIVAVNGPAIGLGASILPLCDVVWANEKAWFQTPYTTFGGQSPDGCSTVMFPKIMGGASANEMLLSGRKLTAQEACGKGLVSQVFWPGTFTQEVMVRIKELASCNPVVLEESKALVRCNMKMELEQANERECEVLKKIWGSAQGMDSMLKYLQRKIDEFGGSGHHHHHH
CEBPB	P17676	Cebpb	RAN	7804.97	11.0557	bZip	pass	MKIEEHHHHHHSSGKLGSTEDLYFQSAAQPAKHSDEYKIRRERNNIAVRKSRDKAKMRNLETQHKVLELTAENERLQKKVEQLSRELSTLRNLFK
CEBPG	P53567	Cebpg	RAN	7643.8	10.9578	bZip	pass	MKIEEHHHHHHSSGKLGSTEDLYFQSAAQPARNSDEYRQRRERNNMAVKKSRLKSKQKAQDTLQRVNQLKEENERLEAKIKLLTKELSVLKDLF
CEBPG	P53567	HR6439.004	Rutgers	14666.22	7.0976	bZip	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMDRNSDEYRQRRERNNMAVKKSRLKSKQKAQDTLQRVNQLKEENERLEAKIKLLTKELSVLKDLFLEHAHNLADNVQSISTENTTADGDNAGQ
CECR2	Q9BXF3	CECR2A-A004	SGC	18909.27	6.6138	Bromodomain	pass	MHHHHHHHHHHHDLGTENLYFQSMREEKKTKDLFELDDDFTAMYKVLDVVKAHKDSWPFLEPVDESYAPNYYQIIKAPMDISSMEKKLNGGLYCTKEEFVNDMKTMFRNCRKYNGESSEYTKMSDNLERCFHRAMMKHSSKGGYGLNDIFEAQKIEWHE
CECR2	Q9BXF3	CECR2A-A001	SGC	17921.17	6.5579	Bromodomain	fail	MHHHHHHHHHHHSSGVDLGTENLYFQSMPNSPMREEKKTKDLFELDDDFTAMYKVLDVVKAHKDSWPFLEPVDESYAPNYYQIIKAPMDISSMEKKLNGGLYCTKEEFVNDMKTMFRNCRKYNGESSEYTKMSDNLERCFHRAMMKHFPGED
CHAMP1 (ZNF828)	Q96JM3	HR7405B.004	Rutgers	19615.51	8.3493	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPEQSRNVLQFTEEKEAFISEEEIAKYMKRGKGKYYCKICCCRAMKKGAVLHHLVNKHNVHSPYKCTICGKAFLLESLLKNHVAAHGQSLLKCPRCNFESNFPRGFKKHLTHCQSRHNEEANKKLMEALEPPLEEQ
CHD1	O14646	CHD1-A001	SGC	25407.97	5.9469	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGQPEEEEFETIERFMDCRIGRKGATGATTTIYAVEADGDPNAGFEKNKEPGEIQYLIKWKGWSHIHNTWETEETLKQQNVRGMKKLDNYKKKDQETKRWLKNASPEDVEYYNCQQELTDDLHKQYQIVERIIAHSNQKSAAGYPDYYCKWQGLPYSECSWEDGALISKKFQACIDEYFSRNQSKTTPGGSGHHHHHH
CHD1	O14646	HR7210A.004	Rutgers	16458.23	6.1708	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMEEEFETIERFMDCRIGRKGATGATTTIYAVEADGDPNAGFEKNKEPGEIQYLIKWKGWSHIHNTWETEETLKQQNVRGMKKLDNYKKKDQETKRWLKNASPEDVEY
CHD2	O14647	CHD2-A001	SGC	26723.41	5.2222	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGGEGVDEQQDNSETIEKVLDSRLGKKGATGASTTVYAIEANGDPSGDFDTEKDEGEIQYLIKWKGWSYIHSTWESEESLQQQKVKGLKKLENFKKKEDEIKQWLGKVSPEDVEYFNCQQELASELNKQYQIVERVIAVKTSKSTLGQTDFPAHSRKPAPSNEPEYLCKWMGLPYSECSWEDEALIGKKFQNCIDSFHSRNNSKTGGSGHHHHHH
CHD3	Q12873-3	CHD3-A004	SGC	43160.85	4.7196	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGVAGEEEVDGYETDHQDYCEVCQQGGEIILCDTCPRAYHLVCLDPELDRAPEGKWSCPHCEKEGVQWEAKEEEEEYEEEGEEEGEKEEEDDHMEYCRVCKDGGELLCCDACISSYHIHCLNPPLPDIPNGEWLCPRCTCPVLKGRVQKILHWRWGEPPVAVPAPQQADGNPDVPPPRPLQGRSEREFFVKWVGLSYWHCSWAKELQLEIFHLVMYRNYQRKNDMDEPPPLDYGSGEDDGKSDKRKVKDPHYAEMEEKYYRFGIKPEWMTVHRIINHSVDKKGNYHYLVKWRDLPYDQSTWEEDEMNIPEYEEHKQSYWRHRELIMGEDPAQPRKYKKGGSGHHHHHH
CHD4	Q14839	CHD4-A001	SGC	32244.25	6.4051	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGEEDDHHMEFCRVCKDGGELLCCDTCPSSYHIHCLNPPLPEIPNGEWLCPRCTCPALKGKVQKILIWKWGQPPSPTPVPRPPDADPNTPSPKPLEGRPERQFFVKWQGMSYWHCSWVSELQLELHCQVMFRNYQRKNDMDEPPSGDFGGDEEKSRKRKNKDPKFAEMEERFYRYGIKPEWMMIHRILNHSVDKKGHVHYLIKWRDLPYDQASWESEDVEIQDYDLFKQSYWNHRELMRGEEGGGSGHHHHHH
CHD7	Q9P2D1	CHD7-A001	SGC	27488.21	4.8838	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGDPSNTSQSEQQESVDAEGPVVEKIMSSRSVKKQKESGEEVEIEEFYVKYKNFSYLHCQWASIEDLEKDKRIQQKIKRFKAKQGQNKFLSEIEDELFNPDYVEVDRIMDFARSTDDRGEPVTHYLVKWCSLPYEDSTWERRQDIDQAKIEEFEKLMSREPETERVERPPADDWKKSESSREYKNNNKLREYQLEGVNWLLGGSGHHHHHH
CIAO1	O76071	WDR39-A001	SGC			NA	pass	

HGCN	Uniprot ID	Antigen ID	Antigen Source	MW (Da)	pI	Common Domain Names	Primary Validation (pass/fail)	construct seq (with tag)
CREB3L4	Q8TEY5	HR7960.007	Rutgers	36628.35	5.1286	bZip	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMDLGIPDLLDAWLEPPEEIFSTGSVLELGLHCPPPEVPVTRLQEQGLQGWKSGGDRGCGLQESEPEDFLKLFIDPNEVYCSEASPGSDSGISEDPCHPDSPPAPRATSSPMLYEVVYEAGALERMQGETGPNVGLISIQLDQWSPAFMVPDSCMVSELPFDAHAHILPRAGTVAPVPCTTLLPCQTLFLTDEEKRLLGQEGVSLPSHLPLTKAEERVLKKVRRKIRNKQSAQDSRRRKKEYIDGLESRVAACSAQNQELQKKVQELERHNISLVAQLRQLQTLIAQTSNKAAQTSTCV
CREBBP	Q92793	CREBBPA-A001	SGC	19270.83	6.5704	Bromodomain	fail	MHHHHHHHHHHHDLGTENLYFQSMRKKIFKPEELRQALMPTLEALYRQDPESLPFRQPVDPQLLGIPDYFDIVKSPMDLSTIKRKLDTGQYQEPWQYVDDVWLMFNNAWLYNRKTSRVYKYCSKLAEVFEQEIDPVMQSLGSSKGGYGLNDIFEAQKIEWHE
CREBBP	Q92793	CREBBPA-A010	SGC	19295.88	6.5704	Bromodomain	pass	MHHHHHHHHHHHDLGTENLYFQSMRKKIFKPEELRQALMPTLEALYRQDPESLPFRQPVDPQLLGIPDYFDIVKNPMDLSTIKRKLDTGQYQEPWQYVDDIWLMFNNAWLYNRKTSRVYKFCSKLAEVFEQEIDPVMQSLGSSKGGYGLNDIFEAQKIEWHE
CSNK2B	P67870	CSNK2B-A001	SGC	28395.01	5.9558	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGmssseevswiswfcglrgneffcevdedyiqdkfnltglneqvphyrqaldmildlepdeeiednpnqsdlieqaaemlygliharyiltnrgiaqmlekyqqgdfgycprvycenqpmlpiglsdipgeamvklycpkcmdvytpkssrhhhtdgayfgtgfphmlfmvhpeyrpkrpanqfvprlygfkihpmayqlqlqaasnfkspvktirGGSGHHHHHH
CXXC1	Q9P0U4	HR7807A.004	Rutgers	13635.33	6.8362	PHD	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMEDSKSENGENAPIYCICRKPDINCFMIGCDNCNEWFHGDCIRITEKMAKAIREWYCRECREKDPKLEIRYRHKKSRERDG
DBX2	Q6ZNG2	HR7911A.006	Rutgers	12143.88	10.9474	Homeobox	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMDSNSKARRGILRRAVFSEDQRKALEKMFQKQKYISKTDRKKLAINLGLKESQVKIWFQNRRMKWRNS
DIDO1	Q9BTC0	DIDO1-A001	SGC	28903.27	4.7694	PHD	fail	MSGLNDIFEAQKIEWHEGSAGGSGTSCPATDAETASEGSVESASETRSGPQSASTAVKERpassEKVKGGDDHDDTSDSDSDGLTLKELQNRLRRKREQEPTERPLKGIQSRLRKKRREEGPAETVGSEASDTVEGVLPSKQEPENDQGVVSQAGKDDRESKLEGKAAQDIKDEEPGDLGRPKPECEGYDPNALYCICRQPHNNRFMICCDRCEEWFHGDCVGISEARGRLLERNGEDYICPNCTILQVQDETHSGGSGHHHHHH
DLX2	Q07687	Dlx2	RAN	6798.95	12.1777	Homeobox	pass	MKIEEHHHHHHSSGKLGSTEDLYFQSAAQPARKPRTIYSSFQLAALQRRFQKTQYLALPERAELAASLGLTQTQVKIWFQNRRSKFKK
DLX5	P56178	Dlx5	RAN	6736.92	11.9996	Homeobox	pass	MKIEEHHHHHHSSGKLGSTEDLYFQSAAQPARKPRTIYSSFQLAALQRRFQKTQYLALPERAELAASLGLTQTQVKIWFQNKRSKIKK
DNMT1	P26358	DNMT1-A004	SGC	36820.97	4.6025	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGPKCIQCGQYLDDPDLKYGQHPPDAVDEPQMLTNEKLSIFDANESGFESYEALPQHKLTCFSVYCKHGHLCPIDTGLIEKNIELFFSGSAKPIYDDDPSLEGGVNGKNLGPINEWWITGFDGGEKALIGFSTSFAEYILMDPSPEYAPIFGLMQEKIYISKIVVEFLQSNSDSTYEDLINKIETTVPPSGLNLNRFTEDSLLRHAQFVVEQVESYDEAGDSDEQPIFLTPCMRDLIKLAGVTLGQRRAQARRQTIRHSTREKDRGPTKATTTKLVYQIFDTFFAEQIEKDDREDKEGGSGHHHHHH
DNMT1	P26358	DNMT1-A003	SGC	52362.93	5.5852	Zinc Finger	pass	MHHHHHHHHHHHDLGTENLYFQSMPKCIQCGQYLDDPDLKYGQHPPDAVDEPQMLTNEKLSIFDANESGFESYEALPQHKLTCFSVYCKHGHLCPIDTGLIEKNIELFFSGSAKPIYDDDPSLEGGVNGKNLGPINEWWITGFDGGEKALIGFSTSFAEYILMDPSPEYAPIFGLMQEKIYISKIVVEFLQSNSDSTYEDLINKIETTVPPSGLNLNRFTEDSLLRHAQFVVEQVESYDEAGDSDEQPIFLTPCMRDLIKLAGVTLGQRRAQARRQTIRHSTREKDRGPTKATTTKLVYQIFDTFFAEQIEKDDREDKENAFKRRRCGVCEVCQQPECGKCKACKDMVKFGGSGRSKQACQERRCPNMAMKEADDDEEVDDNIPEMPSPKKMHQGKKKKQNKNRISWVGEAVKTDGKKSYYKKVCIDAETLEVGDCVSVIPSSKGGYGLNDIFEAQKIEWHE
DNMT3A	Q9Y6K1	DNMT3A_11-A002	SGC	22175.85	6.433	PWWP	pass	MHHHHHHHHHHHDLGTENLYFQSMGDDEPEYEDGRGFGIGELVWGKLRGFSWWPGRIVSWWMTGRSRAAEGTRWVMWFGDGKFSVVCVEKLMPLSSFCSAFHQATYNKQPMYRKAIYEVLQVASSRAGKLFPVCHDSDESDTAKAVEVQNKPMIEWALGGFQPSGPKGLEPPEESSKGGYGLNDIFEAQKIEWHE
DNMT3L	Q9UJW3	DNMT3L-A001	SGC	46805.13	5.9806	PHD	pass	MSGLNDIFEAQKIEWHEGSAGGSGAAIPALDPEAEPSMDVILVGSSELSSSVSPGTGRDLIAYEVKANQRNIEDICICCGSLQVHTQHPLFEGGICAPCKDKFLDALFLYDDDGYQSYCSICCSGETLLICGNPDCTRCYCFECVDSLVGPGTSGKVHAMSNWVCYLCLPSSRSGLLQRRRKWRSQLKAFYDRESENPLEMFETVPVWRRQPVRVLSLFEDIKKELTSLGFLESGSDPGQLKHVVDVTDTVRKDVEEWGPFDLVYGATPPLGHTCDRPPSWYLFQFHRLLQYARPKPGSPGPFFWMFVDNLVLNKEDLDVASRFLEMEPVTIPDVHGGSLQNAVRVWSNIPAIRSRHWALVSEEELSLLAQNKQSSKLAAKWPTKLVKNCFLPLREYFKYFSTELTSSLGGSGHHHHHH
DOT1L	Q8TEK3	DOT1L-A001	SGC	53007.12	9.1461	Misc	pass	MHHHHHHHHHHHDLGTENLYFQSMGEKLELRLKSPVGAEPAVYPWPLPVYDKHHDAAHEIIETIRWVCEEIPDLKLAMENYVLIDYDTKSFESMQRLCDKYNRAIDSIHQLWKGTTQPMKLNTRPSTGLLRHILQQVYNHSVTDPEKLNNYEPFSPEVYGETSFDLVAQMIDEIKMTDDDLFVDLGSGVGQVVLQVAAATNCKHHYGVEKADIPAKYAETMDREFRKWMKWYGKKHAEYTLERGDFLSEEWRERIANTSVIFVNNFAFGPEVDHQLKERFANMKEGGRIVSSKPFAPLNFRINSRNLSDIGTIMRVVELSPLKGSVSWTGKPVSYYLHTIDRTILENYFSSLKNPKLREEQEAARRRQQRESKSNAATPTKGPEGKVAGPADAPMDSGAEEEKAGAATVKKPSPSKARKKKLNKKGRKMAGRKRGRPKKMNTASSKGGYGLNDIFEAQKIEWHE
DPRX	A6NFQ7	HR8202A.004	Rutgers	12331.14	10.2493	Homeobox	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMHSHRKRTMFTKKQLEDLNILFNENPYPNPSLQKEMASKIDIHPTVLQVWFKNHRAKLKKAKCKHIHQKQ
DR1	Q01658	HR7601.001	Rutgers	23314.85	4.7974	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMASSSGNDDDLTIPRAAINKMIKETLPNVRVANDARELVVNCCTEFIHLISSEANEICNKSEKKTISPEHVIQALESLGFGSYISEVKEVLQECKTVALKRRKASSRLENLGIPEEELLRQQQELFAKARQQQAELAQQEWLQMQQAAQQAQLAAASASASNQAGSSQDEEDDDDI
EDF1	O60869	HR7307A.001	Rutgers	12562.33	10.1024	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMDRVTLEVGKVIQQGRQSKGLTQKDLATKINEKPQVIADYESGRAIPNNQVLGKIERAIGLKLRGKDIGKPIEKGPRAK
EED	O75530	EED-A001	SGC	49544.93	7.4055	WD40	pass	MSGLNDIFEAQKIEWHEGSAGGSGDAVSIESGTNTERPDTPTNTPNAPGRKSWGKGKWKSKKCKYSFKCVNSLKEDHNQPLFGVQFNWHSKEGDPLVFATVGSNRVTLYECHSQGEIRLLQSYVDADADENFYTCAWTYDSNTSHPLLAVAGSRGIIRIINPITMQCIKHYVGHGNAINELKFHPRDPNLLLSVSKDHALRLWNIQTDTLVAIFGGVEGHRDEVLSADYDLLGEKIMSCGMDHSLKLWRINSKRMMNAIKESYDYNPNKTNRPFISQKIHFPDFSTRDIHRNYVDCVRWLGDLILSKSCENAIVCWKPGKMEDDIDKIKPSESNVTILGRFDYSQCDIWYMRFSMDFWQKMLALGNQVGKLYVWDLEVEDPHKAKCTTLTHHKCGAAIRQTSFSRDSSILIAVCDDASIWRWDRLRGGSGHHHHHH
EGR1	P18146	HR4555D.006	Rutgers	10357.7	9.0455	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKPFQCRICMRNFSRSDHLTTHIRTHTGEKPFACDICGRKFARSDERKRHTKIH
EHMT1	Q9H9B1	EHMT1-A002	SGC	41896.05	6.2495	SET	pass	MHHHHHHHHHHHDLGTENLYFQSMDVTLKNKEGETPLQCASLNSQVWSALQMSKALQDSAPDRPSPVERIVSRDIARGYERIPIPCVNAVDSEPCPSNYKYVSQNCVTSPMNIDRNITHLQYCVCIDDCSSSNCMCGQLSMRCWYDKDGRLLPEFNMAEPPLIFECNHACSCWRNCRNRVVQNGLRARLQLYRTRDMGWGVRSLQDIPPGTFVCEYVGELISDSEADVREEDSYLFDLDNKDGEVYCIDARYFGNVSRFINHHCEPNLVPVRVFMAHQDLRFPRIAFFSTRLIEAGEQLGFDYGERFWDIKGKLFSCRCGSPKCRHSSAALAQRQASAAQEAQEDGSSKGGYGLNDIFEAQKIEWHE
EHMT2	Q96KQ7	BAT8-A002	SGC	43783.35	6.0446	Misc	pass	MHHHHHHHHHHHDLGTENLYFQSMNPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNTSSKGGYGLNDIFEAQKIEWHE
EP300	Q09472	EP300A-A002	SGC	19713.3	6.5704	Bromodomain	pass	MHHHHHHHHHHHDLGTENLYFQSMAPGQSKKKIFKPEELRQALMPTLEALYRQDPESLPFRQPVDPQLLGIPDYFDIVKSPMDLSTIKRKLDTGQYQEPWQYVDDIWLMFNNAWLYNRKTSRVYKYCSKLSEVFEQEIDPVMQSLGSSKGGYGLNDIFEAQKIEWHE
EPC1	Q9H2F5	EPC1-A003	SGC	25364.45	6.1785	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGQMPTGMEKEEESEHHLQRAISAQQVYGEKRDNMVIPVPEAESNIAYYESIYPGEFKMPKQLIHIQPFSLDAEQPDYDLDSEDEVFVNKLKKKMDICPLQFEEMIDRLEKGSGQQPVSLQEAKLLLKEDDELIREVYEYWIKKRKNCRGPSLIPSVKQEKRDGSSTNDPYVAFRRRTEKMQTRKNRKGGSGHHHHHH
ESR1	P03372	Esr1	RAN	8149.39	8.7488	Zinc Finger	pass	MKIEEHHHHHHSSGKLGSTEDLYFQSAAQPARYCAVCNDYASGYHYGVWSCEGCKAFFKRSIQGHNDYMCPATNQCTIDKNRRKSCQACRLRKCYEVGMMK
ESRRA	P11474	HR7097C.001	Rutgers	29158.56	5.1879	Hormone Receptor	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPVNALVSHLLVVEPEKLYAMPDPAGPDGHLPAVATLCDLFDREIVVTISWAKSIPGFSSLSLSDQMSVLQSVWMEVLVLGVAQRSLPLQDELAFAEDLVLDEEGARAAGLGELGAALLQLVRRLQALRLEREEYVLLKALALANSDSVHIEDAEAVEQLREALHEALLEYEAGRAGPGGGAERRRAGRLLLTLPLLRQTAGKVLAHFYGVKLEGKVPMHKLFLEKLEAMMD
ESRRA	P11474	Esrra	RAN	7817.21	8.9737	Zinc Finger	pass	MKIEEHHHHHHSSGKLGSTEDLYFQSAAQPARLCLVCGDVASGYHYGVASCEACKAFFKRTIQGSIEYSCPASNECEITKRRRKACQACRFTKCLRVGMLK

HGCN	Uniprot ID	Antigen ID	Antigen Source	MW (Da)	pI	Common Domain Names	Primary Validation (pass/fail)	construct seq (with tag)
ESRRG	P62508	HR7566D.001	Rutgers	15177.49	9.1765	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMSMPKRLCLVCGDIASGYHYGVASCEACKAFFKRTIQGNIEYSCPATNECEITKRRRKSCQACRFMKCLKVGMLKEGVRLDRVRGGRQKYKRRIDAENS
EZH2	Q15910	EZH2-A001	SGC	75538.31	6.1132	SET	fail	MSGLNDIFEAQKIEWHEGSAGGSGFMVEDETVLHNIPYMGDEVLDQDGTFIEELIKNYDGKVHGDRECGFINDEIFVELVNALGQYNDDDDDDDGDDPEEREEKQKDLEDHRDDKESRPPRKFPSDKIFEAISSMFPDKGTAEELKEKYKELTEQQLPGALPPECTPNIDGPNAKSVQREQSLHSFHTLFCRRCFKYDCFLHRKCNYSFHATPNTYKRKNTETALDNKPCGPQCYQHLEGAKEFAAALTAERIKTPPKRPGGRRRGRLPNNSSRPSTPTINVLESKDTDSDREAGTETGGENNDKEEEEKKDETSSSSEANSRCQTPIKMKPNIEPPENVEWSGAEASMFRVLIGTYYDNFCAIARLIGTKTCRQVYEFRVKESSIIAPAPAEDVDTPPRKKKRKHRLWAAHCRKIQLKKDGSSNHVYNYQPCDHPRQPCDSSCPCVIAQNFCEKFCQCSSECQNRFPGCRCKAQCNTKQCPCYLAVRECDPDLCLTCGAADHWDSKNVSCKNCSIQRGSKKHLLLAPSDVAGWGIFIKDPVQKNEFISEYCGEIISQDEADRRRGKVYDKYMCSFLFNLNNDFVVDATRKGNKIRFANHSVNPNCYAKVMMVNGDHRIGIFAKRAIQTGEELFFDYRYSQADALKYVGIEREMEIPGGSGHHHHHH
FEZF1	A0PJY2	HR6968B.004	Rutgers	25279.95	9.9952	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMGSPNAKPKVFTCEVCGKVFNAHYNLTRHMPVHTGARPFVCKVCGKGFRQASTLCRHKIIHTQEKPHKCNQCGKAFNRSSTLNTHTRIHAGYKPFVCEFCGKGFHQKGNYKNHKLTHSGEKQFKCNICNKAFHQVYNLTFHMHTHNDKKPFTCPTCGKGFCRNFDLKKHVRKLHDSSLGLARTPAGEPG
FIZ1	Q96SL8	HR8078B.003	Rutgers	22543.33	7.3244	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMPSEDTLYQCDCGTFFASAAALASHLEAHSGPATYGCGHCGALYAALAALEEHRRRVSHGEGGGEEAATAAREREPASGEPPSGSGRGKKIFGCSECEKLFRSPRDLERHVLVHTGEKPFPCLECGKFFRHECYLKRHRLLHGTERPFPCHICGKGFITLSNLSRHLKLHRG
FLI1	Q01543	HR4739B.004	Rutgers	14140.89	5.9556	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMPPNMTTNERRVIVPADPTLWTQEHVRQWLEWAIKEYSLMEIDTSFFQNMDGKELCKMNKEDFLRATTLYNTEVLLSHLSYLRESS
FOXD3	Q9UJU5	HR7150A.003	Rutgers	15400.49	9.0849	Fork Head	pass	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMVKPPYSYIALITMAILQSPQKKLTLSGICEFISNRFPYYREKFPAWQNSIRHNLSLNDCFVKIPREPGNPGKGNYWTLDPQSEDMFDNGSFLRRRKR
FOXF2	Q12947	HR7975A.002	Rutgers	14422.4	8.4882	Fork Head	pass	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMPPYSYIALIVMAIQSSPSKRLTLSEIYQFLQARFPFFRGAYQGWKNSVRHNLSLNECFIKLPKGLGRPGKGHYWTIDPASEFMFEEGSFR
FOXJ2	Q9P0K8	HR8000A.001	Rutgers	14565.48	9.738	Fork Head	fail	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMDGKPRYSYATLITYAINSSPAKKMTLSEIYRWICDNFPYYKNAGIGWKNSIRHNLSLNKCFRKVPRPRDDPGKGSYWTIDTCPDISRKRR
FOXP1	Q9H334	HR7590B.002	Rutgers	31282.46	7.7457	Fork Head	pass	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMPLYGHGVCKWPGCEAVCEDFQSFLKHLNSEHALDDRSTAQCRVQMQVVQQLELQLAKDKERLQAMMTHLHVKSTEPKAAPQPLNLVSSVTLSKSASEASPQSLPHTPTTPTAPLTPVTQGPSVITTTSMHTVGPIRRRYSDKYNVPISSADIAQNQEFYKNAEVRPPFTYASLIRQAILESPEKQLTLNEIYNWFTRMFAYFRRNAATWKNAVRHNLSLHKCFVRVENVKGAVWTVDEVEF
FOXP2	O15409	HR7934B.006	Rutgers	16138.96	6.7573	NA	pass	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMTSKASPPITHHSIVNGQSSVLSARRDSSSHEETGASHTLYGHGVCKWPGCESICEDFGQFLKHLNNEHALDDRSTAQCRVQMQVVQQLEIQLSKERERLQAMMTHLHM
FOXP4	Q8IVH2	HR6897B.001	Rutgers	30951.98	7.7256	Fork Head	pass	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMPLYGHGECKWPGCETLCEDLGQFIKHLNTEHALDDRSTAQCRVQMQVVQQLEIQLAKESERLQAMMAHLHMRPSEPKPFSQPLNPVPGSSSFSKVTVSAADSFPDGLVHPPTSAAAPVTPLRPPGLGSASLHGGGPARRRSSDKFCSPISSELAQNHEFYKNADVRPPFTYASLIRQAILETPDRQLTLNEIYNWFTRMFAYFRRNTATWKNAVRHNLSLHKCFVRVENVKGAVWTVDER
FXR2	P51116	FXR2-A001	SGC	17590.41	5.0307	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGLPVEVRGSNGAFYKGFVKDVHEDSVTIFFENNWQSERQIPFGDVRLPPPADYNKEITEGDEVEVYSRANEQEPCGWWLARVRMMKGDFYVIEYAACDATYNEIVTLERLRPVNPNPLATKGSFGGSGHHHHHH
GBX1	Q14549	HR8231A.006	Rutgers	13397.2	10.1766	Homeobox	fail	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMTGAEEGAPVTAGVTAPGGKSRRRRTAFTSEQLLELEKEFHCKKYLSLTERSQIAHALKLSEVQVKIWFQNRRAKWKRIKAGNV
GLI1	P08151	HR7937B.001	Rutgers	21226.62	7.7499	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMSNEKPYVCKLPGCTKRYTDPSSLRKHVKTVHGPDAHVTKRHRGDGPLPRAPSISTVEPKREREGGPIREESRLTVPEGAMKPQPSPGAQSSCSSDHSPAGSAANTDSGVEMTGNAGGSTEDLSSLDEGPCIAGTGLSTLRRLENLRLDQLHQLRPIGTRGLK
GLI3	P10071	HR7118B.006	Rutgers	22297	8.3013	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMETNCHWEGCAREFDTQEQLVHHINNDHIHGEKKEFVCRWLDCSREQKPFKAQYMLVVHMRRHTGEKPHKCTFEGCTKAYSRLENLKTHLRSHTGEKPYVCEHEGCNKAFSNASDRAKHQNRTHSNEKPYVCKIPGCTKRYTDPSSLRKHVKTVHGP
GLIS2	Q9BZE0	HR7416A.002	Rutgers	23880.16	9.0157	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMLTPPKDKCLSPDLPLPKQLVCRWAKCNQLFELLQDLVDHVNDYHVKPEKDAGYCCHWEGCARHGRGFNARYKMLIHIRTHTNEKPHRCPTCSKSFSRLENLKIHNRSHTGEKPYVCPYEGCNKRYSNSSDRFKHTRTHYVDKPYYCKMPGCHKRYTDPSSLRKHIKAHG
GMEB2	Q9UKD1	HR7418A.009	Rutgers	14420.5	7.3431	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMEAEIVYPITCGDSRANLIWRKFVCPGINVKCVQYDEHVISPKEFVHLAGKSTLKDWKRAIRMNGIMLRKIMDSGELDFYQHDKVCSNTCR
H1FX	Q92522	HR7057A.008	Rutgers	13031.74	10.0503	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMQPGKYSQLVVETIRRLGERNGSSLAKIYTEAKKVPWFDQQNGRTYLKYSIKALVQNDTLLQVKGTGANGSFKLNRKKLEG
HACE1	Q8IYU2	HACE1-A001	SGC	59069.01	5.1977	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGSTGTRESKPDALAGRQEASADCQDVISMTANRLSAVIQAFYMCCSCQMPPGMTSPRFIEFVCKHDEVLKCFVNRNPKIIFDHFHFLLECPELMSRFMHIIKAQPFKDRCEWFYEHLHSGQPDSDMVHRPVNENDILLVHRDSIFRSSCEVVSKANCAKLKQGIAVRFHGEEGMGQGVVREWFDILSNEIVNPDYALFTQSADGTTFQPNSNSYVNPDHLNYFRFAGQILGLALNHRQLVNIYFTRSFYKHILGIPVNYQDVASIDPEYAKNLQWILDNDISDLGLELTFSVETDVFGAMEEVPLKPGGGSILVTQNNKAEYVQLVTELRMTRAIQPQINAFLQGFHMFIPPSLIQLFDEYELELLLSGMPEIDVSDWIKNTEYTSGYEEDPVIQWFWEVVEDITQEERVLLLQFVTGSSRVPHGGFANIMGGSGLQNFTIAAVPYTPNLLPTSSTCINMLKLPEYPSKEILKDRLLVALHCGSYGYTMAGGSGHHHHHH
HDAC4	P56524	HDAC4-A003	SGC	50076.66	6.38	Hist Deacetyl	pass	MSGLNDIFEAQKIEWHEGSAGGSGTFPVSVQEPPTKPRFTTGLVYDTLMLKHQCTCGSSSSHPEHAGRIQSIWSRLQETGLRGKCECIRGRKATLEELQTVHSEAHTLLYGTNPLNRQKLDSKKLLGSLASVFVRLPCGGVGVDSDTIWNEVHSAGAARLAVGCVVELVFKVATGELKNGFAVVRPPGHHAEESTPMGFCYFNSVAVAAKLLQQRLSVSKILIVDWDVHHGNGTQQAFYSDPSVLYMSLHRYDDGNFFPGSGAPDEVGTGPGVGFNVNMAFTGGLDPPMGDAEYLAAFRTVVMPIASEFAPDVVLVSSGFDAVEGHPTPLGGYNLSARCFGYLTKQLMGLAGGRIVLALEGGHDLTAICDASEACVSALLGNELDPLPEKVLQQRPNANAVRSMEKVMEIHSKYWRCLQRTTSTAGRSLIEAQTCENEEAETVTAMASLSVGVKPAEGGSGHHHHHH
HDAC5	Q9UQL6	HDAC5-A003	SGC	47986.5	6.8035	Hist Deacetyl	fail	MSGLNDIFEAQKIEWHEGSAGGSGRTQSSPAAPGGMKSPPDQPVKHLFTTGVVYDTFMLKHQCMCGNTHVHPEHAGRIQSIWSRLQETGLLSKCERIRGRKATLDEIQTVHSEYHTLLYGTSPLNRQKLDSKKLLGPISQKMYAVLPCGGIGVDSDTVWNEMHSSSAVRMAVGCLLELAFKVAAGELKNGFAIIRPPGHHAEESTAMGFCFFNSVAITAKLLQQKLNVGKVLIVDWDIHHGNGTQQAFYNDPSVLYISLHRYDNGNFFPGSGAPEEVGGGPGVGYNVNVAWTGGVDPPIGDVEYLTAFRTVVMPIAHEFSPDVVLVSAGFDAVEGHLSPLGGYSVTARCFGHLTRQLMTLAGGRVVLALEGGHDLTAICDASEACVSALLSVELQPLDEAVLQQKPNINAVATLEKVIEIQSKHWSCVQKFAAGLGRGGSGHHHHHH
HDAC7	Q8WUI4	HDAC7-A003	SGC	48773.9	6.8535	Hist Deacetyl	pass	MSGLNDIFEAQKIEWHEGSAGGSGRAQSSPAAPASLSAPEPASQARVLSSSETPARTLPFTTGLIYDSVMLKHQCSCGDNSRHPEHAGRIQSIWSRLQERGLRSQCECLRGRKASLEELQSVHSERHVLLYGTNPLSRLKLDNGKLAGLLAQRMFVMLPCGGVGVDTDTIWNELHSSNAARWAAGSVTDLAFKVASRELKNGFAVVRPPGHHADHSTAMGFCFFNSVAIACRQLQQQSKASKILIVDWDVHHGNGTQQTFYQDPSVLYISLHRHDDGNFFPGSGAVDEVGAGSGEGFNVNVAWAGGLDPPMGDPEYLAAFRIVVMPIAREFSPDLVLVSAGFDAAEGHPAPLGGYHVSAKCFGYMTQQLMNLAGGAVVLALEGGHDLTAICDASEACVAALLGNRVDPLSEEGWKQKPNLNAIRSLEAVIRVHSKYWGCMQRLASGGSGHHHHHH
HDGF2	Q7Z4V5	HDGF2-A001	SGC	13960.57	8.1701	PWWP	pass	MSGLNDIFEAQKIEWHEGSAGGSGPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPNKYPIFFFGTHETAFLGPKDLFPYDKCKDKYGKPNKRKGFNEGLWEIQNNPHASYSGGSGHHHHHH
HES1	Q14469	HR7299A.007	Rutgers	9079.19	6.8579	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMKYRAGFSECMNEVTRFLSTCEGVNTEVRTRLLGHLANYMTQIHV
HES5	Q5TA89	Hes5	RAN	6815.96	10.7019	Misc	pass	MKIEEHHHHHHSSGKLGSTEDLYFQSAAQPANRLRKPVVEKMRRDRINSSIEQLKLLLEQEFARHQPNSKLEKADILEMAVSYLKHSK
HHEX	Q03014	HR7851A.001	Rutgers	11053.53	10.5849	Homeobox	fail	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMKGGQVRFSNDQTIELEKKFETQKYLSPPERKRLAKMLQLSERQVKTWFQNRRAKWRR

HGCN	Uniprot ID	Antigen ID	Antigen Source	MW (Da)	pI	Common Domain Names	Primary Validation (pass/fail)	construct seq (with tag)
HHEX	Q03014	HR7851A.006	Rutgers	11053.53	10.5849	Homeobox	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKGGQVRFSNDQTIELEKKFETQKYLS PPERKRLAKMLQLSERQVKTWFQNRRAKWRR
HIVEP3	Q5T1R4	HR7042B.004	Rutgers	16540.96	9.9306	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPKVFVPRPSQVSLKPTEEAHKKERKP QKPGKYICQYCSRPCAKPSVLQKHIRSHTGERPYPCGPCGFSFKTKSNLYKHRKSHAH RIKAGLASGMGGEMYPHGLEMERIPGE
HLX	Q14774	HR8006A.005	Rutgers	12110.86	10.99	Homeobox	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPQTYKRKRSWSRAVFSNLQRKGLEK RFEIQKYVTKPDRKQLAAMLGLTDAQVKVWFQNRRMKWRHS
HMGB1	P09429	HR7828A.004	Rutgers	12479.08	9.4382	HMG Box	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKPRGKMSSYAFFVQTCREEHKKKHP DASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTY
HMGB2	P26583	HR8015A.001	Rutgers	12929.49	9.4801	HMG Box	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGKGDPNKPRGKMSSYAFFVQTCREE HKKKHPDSSVNFAEFSKKCSERWKTMSAKEKSKFEDMAKSDKARYDREMKN
HMGXB4	Q9UGU5	HR7956.001	Rutgers	14295.28	9.5921	HMG Box	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMLHTDGHSEKKKKKEEKDKERERGEK PKKKNMSAYQVFCKEYRVTIVADHPGIDFGELSKKLAEVWKQLPEKDKLIWKQKAQYL QHK
HNF1B	P35680	Hnf1b	RAN	8980.04	10.0064	Homeobox	pass	MKIEEHHHHHHSSGKLGSTEDLYFQSAAQPARRNRFKWGPASQQILYQAYDRQKNPS KEEREALVEECNRAECLQRGVSPSKAHGLGSNLVTEVRVYNWFANRRKEE
HNF4A	P41235	HR7522C.007	Rutgers	29968.68	5.5327	Hormone Receptor	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMSLPSINALLQAEVLSRQITSPVSGING DIRAKKIASIADVCESMKEQLLVLVEWAKYIPAFCELPLDDQVALLRAHAGEHLLLGATKR SMVFKDVLLLGNDYIVPRHCPELAEMSRVSIRILDELVLPFQELQIDDNEYAYLKAIIFFDP DAKGLSDPGKIKRLRSQVQVSLEDYINDRQYDSRGRFGELLLLLPTLQSITWQMIEQIQF IKLFGMAKIDNLLQEMLLGG
HNF4A	P41235	Hnf4a	RAN	8092.51	10.4752	Zinc Finger	pass	MKIEEHHHHHHSSGKLGSTEDLYFQSAAQPAALCAICGDRATGKHYGASSCDGCKGFF RRSVRKNHMYSCRFSRQCVVDKDKRNQCRYCRLKKCFRAGMKK
HOXA10	P31260	HR8427A.001	Rutgers	11169.77	9.9256	Homeobox	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPYTKHQTLELEKEFLFNMYLTRERRL EISRSVHLTDRQVKIWFQNRRMKLKKMNRE
HOXA3	O43365	HR7187A.001	Rutgers	13100.88	10.3581	Homeobox	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMSSKRAHTAYTSAQLVELEKEFHFNRY LCRPRRVEMANLLNLTERQIKIWLQNRRMKYKKDQKGKGMLTSSGGQSPSR
Hoxa5	P20719	Hoxa5	RAN	7369.65	11.7522	Homeobox	pass	MKIEEHHHHHHSSGKLGSTEDLYFQSAAQPAKRARTAYTRYQTLELEKEFHFNRYLTRR RRIEIAHALCLSERQIKIWFQNRRMKWKK
HOXB3	P14651	HR8135A.002	Rutgers	11067.76	10.2983	Homeobox	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMTSAQLVELDKEFHFNRYLCRPRRVE MANLLNLIKRQIKIWFQNRRMKYKKDQKAKGL
HOXB5	P09067	HR8261.004	Rutgers	11373.99	10.2302	Homeobox	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMYTRYQTLELEKEFHFNRYLTRRRRIEI AHALCLSERQIKIWFQNRRMKWKKDNKLKS
HOXB5	P09067	Hoxb5	RAN	7369.65	11.7522	Homeobox	pass	MKIEEHHHHHHSSGKLGSTEDLYFQSAAQPAKRARTAYTRYQTLELEKEFHFNRYLTRR RRIEIAHALCLSERQIKIWFQNRRMKWKK
HOXB6	P17509	Hoxb6	RAN	7470.71	11.7034	Homeobox	pass	MKIEEHHHHHHSSGKLGSTEDLYFQSAAQPARRGRQTYTRYQTLELEKEFHYNRYLTR RRRIEIAHALCLTERQIKIWFQNRRMKWKK
Hoxb9	P17482	Hoxb9	RAN	7349.72	11.2138	Homeobox	pass	MKIEEHHHHHHSSGKLGSTEDLYFQSAAQPARKKRCPYTKYQTLELEKEFLFNMYLTR DRRHEVARLLNLSERQVKIWFQNRRMKMKK
HOXD11	P31277	HR8017A.001	Rutgers	12783.65	10.7289	Homeobox	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMSSSAVAPQRSRKKRCPYTKYQIRELE REFFFNVYINKEKRLQLSRMLNLTDRQVKIWFQNRRMKEKKLNR
HOXD11	P31277	Hoxd11	RAN	7426.79	11.2643	Homeobox	pass	MKIEEHHHHHHSSGKLGSTEDLYFQSAAQPARKKRCPYTKYQIRELEREFFFNVYINKE KRLQLSRMLNLTDRQVKIWFQNRRMKEKK
HOXD3	P31249	HR7220A.003	Rutgers	13174.96	9.7759	Homeobox	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGESCEDKSPPGPASKRVRTAYTSAQL VELEKEFHFNRYLCRPRRVEMANLLNLTERQIKIWFQNRRMKYKKDQKAKG
HSF1	Q00613	HR3023C.031	Rutgers	59080.07	5.58	Misc	fail	
INSM2	Q96T92	HR8043B.003	Rutgers	20485.23	8.4339	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPGSTSGGRGSEIFVCPYCHKKFRRQ AYLRKHLSTHEAGSARALAPGFGSERGAPLAFACPLCGAHFPTADIREKHRLWHAVRE ELLLPALAGAPPETSGPSGPSDGSAQQIFSCKHCPSTFFSSPGLTRHINKCHPSESRQV LLLQMPLRPGC
IRF2	P14316	HR7043A.001	Rutgers	17289.81	9.8384	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPVERMRMRPWLEEQINSNTIPGLKW LNKEKKIFQIPWMHAARHGWDVEKDAPLFRNWAIHTGKHQPGVDKPDPKTWKANFRC AMNSLPDIEEVKDKSIKKGNNAFRVYRMLP
IRF2	P14316	Irf2	RAN	13075.23	10.7405	Misc	pass	MKIEEHHHHHHSSGKLGSTEDLYFQSAAQPARMRMRPWLEEQINSNTIPGLKWLNKEK KIFQIPWMHAARHGWDVEKDAPLFRNWAIHTGKHQPGVDKPDPKTWKANFRCAMNS LPDIEEVKDKSIKKGNNAFRVYRMLPL
IRF6	O14896	HR7755.001	Rutgers	57714.7	5.1518	Misc	pass	MHHHHHHEFMSGLNDIFEAQKIEWHEGSAGGSGENLYFQGMALHPRRVRLKPWLVAQ VDSGLYPGLIWLHRDSKRFQIPWKHATRHSPQQEEENTIFKAWAVETGKYQEGVDDPD PAKWKAQLRCALNKSREFNLMYDGTKEVPMNPVKIYQVCDIPQPQGSIINPGSTGSAP WDEKDNDVDEEDEEDELDQSQHHVPIQDTFPFLNINGSPMAPASVGNCSVGNCSPEA VWPKTEPLEMEVPQAPIQPFYSSPELWISSLPMTDLDIKFQYRGKEYGQTMTVSNPQG CRLFYGDLGPMPDQEELFGPVSLEQVKFPGPEHITNEKQKLFTSKLLDVMDRGLILEVS GHAIYAIRLCQCKVYWSGPCAPSLVAPNLIERQKKVKLFCLETFLSDLIAHQKGQIEKQP PFEIYLCFGEEWPDGKPLERKLILVQIPVVARMIYEMFSGDFTRSFDSGSVRLQISTPDI KDNIVAQLKQLYRILQTQESWQPMQPTPSMQLPPALPPQ
IRF9	Q00978	HR7302A.002	Rutgers	25170.68	6.1113	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMQRSLEFLLPPEPDYSLLLTFIYNGRVV GEAQVQSLDCRLVAEPSGSESSMEQVLFPKPGPLEPTQRLLSQLERGILVASNPRGLF VQRLCPIPISWNAPQAPPGPGPHLLPSNECVELFRTAYFCRDLVRYFQGLGPPPKFQVT LNFWEESHGSSHTPQNLITVKMEQAFARYLLEQTPEQQAAILSLV
JMJD6	Q6NYC1	PTDSRB-A001	SGC	43056.56	9.335	JMJ	pass	MSGLNDIFEAQKIEWHEGSAGGSGNHKSKKRIREAKRSARPELKDSLDWTRHNYYES FSLSPAAVADNVERADALQLSVEEFVERYERPYKPVVLLNAQEGWSAQEKWTLERLKR KYRNQKFKCGEDNDGYSVKMKMKYYIEYMESTRDDSPLYIFDSSYGEHPKRRKLLEDY KVPKFFTDDLFQYAGEKRRPPYRWFVMGPPRSGTGIHIDPLGTSAWNALVQGHKRWC LFPTSTPRELIKVTRDEGGNQQDEAITWFNVIYPRTQLPTWPPEFKPLEILQKPGETVFV PGGWWHVVLNLDTTIAITQNFASSTNFPVVWHKTVRGRPKLSRKWYRILKQEHPELAV LADSVDLQESTGIGGSGHHHHHH
KAT2A	Q92830	GCN5L2-A007	SGC	18584.11	7.3162	Bromodomain	pass	MHHHHHHHHHHHDLGTENLYFQSMELKDPDQLYTTLKNLLAQIKSHPSAWPFMEPVKK SEAPDYYEVIRFPIDLKTMTERLRSRYYVTRKLFVADLQRVIANCREYNPPDSEYCRCA SALEKFFYFKLKEGGLIDKSSKGGYGLNDIFEAQKIEWHE
KAT2A	Q92830	GCN5L2A-A001	SGC	22465.99	9.3703	Misc	fail	MHHHHHHHHHHHSSGVDLGTENLYFQSMGIIEFHVIGNSLTPKANRRVLLWLVGLQNVF SHQLPRMPKEYIARLVFDPKHKTLALIKDGRVIGGICFRMFPTQGFTEIVFCAVTSNEQV KGYGTHLMNHLKEYHIKHNILYFLTYADEYAIGYFKKQGFSKDIKVPKSRYLGYIKDYEGA TLMECELNPRIPYT
KAT2B	Q92831	PCAFA-A003	SGC	19555.16	8.0104	Bromodomain	pass	MHHHHHHHHHHHSSGVDLGTENLYFQSMGKEKSKEPRDPDQLYSTLKSILQQVKSHQS AWPFMEPVKRTEAPGYYEVIRFPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCKEY NPPESEYYKCANILEKFFFSKIKEAGLIDSSKGGYGLNDIFEAQKIEWHE
KDM2A	Q9Y2K7	FBXL11A-A002	SGC	63297.31	5.782	JMJ	pass	MSGLNDIFEAQKIEWHEGSAGGSGAAQGAAAAVAAGTSGVAGEGEPGPGENAAAEGT APSPGRVSPPTPARGEPEVTVEIGETYLCRRPDSTWHSAEVIQSRVNDQEGREEFYVH YVGFNRRLDEWVDKNRLALTKTVKDAVQKNSEKYLSELAEQPERKITRNQKRKHDEIN HVQKTYAEMDPTTAALEKEHEAITKVKYVDKIHIGNYEIDAWYFSPFPEDYGKQPKLWL CEYCLKYMKYEKSYRFHLGQCQWRQPPGKEIYRKSNISVHEVDGKDHKIYCQNLCLLA KLFLDHKTLYFDVEPFVFYILTEVDRQGAHIVGYFSKEKESPDGNNVACILTLPPYQRRG YGKFLIAFSYELSKLESTVGSPEKPLSDLGKLSYRSYWSWVLLENLRDFRGTLSIKDLS QMTSITQNDIISTLQSLNMVKYWKGQHVICVTPKLVEEHLKSAQYKKPPITVDSVCLKWA PPKHKQVKLSKKGGSGHHHHHH

HGCN	Uniprot ID	Antigen ID	Antigen Source	MW (Da)	pI	Common Domain Names	Primary Validation (pass/fail)	construct seq (with tag)
KDM2A	Q9Y2K7	FBXL11A-A001	SGC	65137.46	5.9848	JMJ	pass	MHHHHHHHHHHDLGTENLYFQSMEPEEERIRYSQRLRGTMRRRYEDDGISDDEIEGK RTFDLEEKLHTNKYNANFVTFMEGKDFNVEYIQRGGLRDPLIFKNSDGLGIKMPDPDFT VNDVKMCVGSRRMVDVMDVNTQKGIEMTMAQWTRYYETPEEEREKLYNVISLEFSHT RLENMVQRPSTVDFIDWVDNMWPRHLKESQTESTNAILEMQYPKVQKYCLMSVRGCY TDFHVDFGGTSVWYHIHQGGKVFWLIPPTAHNLELYENWLLSGKQGDIFLGDRVSDCQ RIELKQGYTFVIPSGWIHAVYTPTDTLVFGGNFLHSFNIPMQLKIYNIEDRTRVPNKFRYP FYYEMCWYYLERYVYCITNRSHLTKEFQKESLSMDLELNGLESGNGDEEAVDREPRRL SSRRSVLTSPVANGVNLDYDGLGKTCRSLPSLKKTLAGDSSSDCSRGSHNGQVWDPQ CAPRKDRQVHLTHFELEGLRCLVDKLESLPLHKKCVPTGIEDEDALIADVKILLEELANS DPKLALTGVPIVQWPSSKGGYGLNDIFEAQKIEWHE
KDM3B	Q7LBC6	JMJD1BA-A001	SGC	40444.53	5.6602	JMJ	pass	MSGLNDIFEAQKIEWHEGSAGGSGLLCLHDPSNKNNWKIFRECWKQGQPVLVSGVHK KLKSELWKPEAFSQEFGDQDVDLVNCRNCAIISDVKVRDFWDGFEIICKRLRSEDGQP MVLKLKDWPPGEDFRDMMPTRFEDLMENLPLPEYTKRDGRLNLASRLPSYFVRPDLG PKMYNAYGLITAEDRRVGTTNLHLDVSDAVNVMVYVGIPIGEGAHDEEVLKTIDEGDAD EVTKQRIHDGKEKPGALWHIYAAKDAEKIRELLRKVGEEQGQENPPDHDPIHDQSWYL DQTLRKRLYEEYGVQGWAIVQFLGDAVFIPAGAPHQVHNLYSCIKVAEDFVSPEHVKGG SGHHHHHH
KDM4A	O75164	JMJD2AA-A017	SGC	44265.35	7.367	JMJ	pass	MHHHHHHSSGVDLGTENLYFQSMASESETLNPSARIMTFYPTMEEFRNFSRYIAYIESQ GAHRAGLAKVVPPKEWKPRASYDDIDDLVIPAPIQQLVTGQSGLFTQYNIQKKAMTVRE FRKIANSDKYCTPRYSEFEELERKYWKNLTFNPPIYGADVNGTLYEKHVDEWNIGRLRT ILDLVEKESGITIEGVNTPYLYFGMWKTSFAWHTEDMDLYSINYLHFGEPKSWYSVPPE HGKRLERLAKGFFPGSAQSCEAFLRHKMTLISPLMLKKYGIPFDKVTQEAGEFMITFPY GYHAGFNHGFNCAESTNFATRRWIEYGKQAVLCSCRKDMVKISMDVFVRKFQPERYKL WKAGKDNTVIDHTLPTPEAAEFLKESEL
KDM4A	O75164	JMJD2AA-A004	SGC	45034.02	7.2146	JMJ	pass	MSGLNDIFEAQKIEWHEGSAGGSGASESETLNPSARIMTFYPTMEEFRNFSRYIAYIES QGAHRAGLAKVVPPKEWKPRASYDDIDDLVIPAPIQQLVTGQSGLFTQYNIQKKAMTVR EFRKIANSDKYCTPRYSEFEELERKYWKNLTFNPPIYGADVNGTLYEKHVDEWNIGRLR TILDLVEKESGITIEGVNTPYLYFGMWKTSFAWHTEDMDLYSINYLHFGEPKSWYSVPP EHGKRLERLAKGFFPGSAQSCEAFLRHKMTLISPLMLKKYGIPFDKVTQEAGEFMITFP YGYHAGFNHGFNCAESTNFATRRWIEYGKQAVLCSCRKDMVKISMDVFVRKFQPERY KLWKAGKDNTVIDHTLPTPEAAEFLKESELGGSGHHHHHH
KDM4A	O75164	JMJD2AA-A001	SGC	44370.42	7.4492	JMJ	pass	MHHHHHHHHHHDLGTENLYFQSMASESETLNPSARIMTFYPTMEEFRNFSRYIAYIES QGAHRAGLAKVVPPKEWKPRASYDDIDDLVIPAPIQQLVTGQSGLFTQYNIQKKAMTVR EFRKIANSDKYCTPRYSEFEELERKYWKNLTFNPPIYGADVNGTLYEKHVDEWNIGRLR TILDLVEKESGITIEGVNTPYLYFGMWKTSFAWHTEDMDLYSINYLHFGEPKSWYSVPP EHGKRLERLAKGFFPGSAQSCEAFLRHKMTLISPLMLKKYGIPFDKVTQEAGEFMITFP YGYHAGFNHGFNCAESTNFATRRWIEYGKQAVLCSCRKDMVKISMDVFVRKFQPERY KLWKAGKDNTVIDHTLPTPEAAEFLKESE
KDM4A	O75164	JMJD2AA-A005	SGC	19663.69	5.2593	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGERAKGALQSITAGQKVISKHKNGRFYQCEVVRLT TETFYEVNFDDGSFSDNLYPEDIVSQDCLQFGPPAEGEVVQVRWTDGQVYGAKFVAS HPIQMYQVEFEDGSQLVVKRDDVYTLDEELPKRVKSRLSVASDMRFNEIFTGGSGHHH HHH
KDM4A	O75164	JMJD2AA-A006	SGC	16571.08	4.5926	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGQSITAGQKVISKHKNGRFYQCEVVRLTTETFYEV NFDDGSFSDNLYPEDIVSQDCLQFGPPAEGEVVQVRWTDGQVYGAKFVASHPIQMYQ VEFEDGSQLVVKRDDVYTLDEELPGGSGHHHHHH
KDM4A	O75164	JMJD2AA-A701	SGC	15802.41	4.5394	Misc	fail	MHHHHHHSSGVDLGTENLYFQSMQSITAGQKVISKHKNGRFYQCEVVRLTTETFYEVN FDDGSFSDNLYPEDIVSQDCLQFGPPAEGEVVQVRWTDGQVYGAKFVASHPIQMYQV EFEDGSQLVVKRDDVYTLDEELP
KDM4B	O94953	JMJD2BA-A002	SGC	45063.91	6.8465	JMJ	pass	MSGLNDIFEAQKIEWHEGSAGGSGGSEDHGAQNPSCKIMTFRPTMEEFKDFNKYVAYI ESQGAHRAGLAKIIPPKEWKPRQTYDDIDDVVIPAPIQQVVTGQSGLFTQYNIQKKAMT VGEYRRLANSEKYCTPRHQDFDDLERKYWKNLTFVSPIYGADISGSLYDDDVAQWNIG SLRTILDMVERECGTIIEGVNTPYLYFGMWKTTFAWHTEDMDLYSINYLHFGEPKSWYAI PPEHGKRLERLAIGFFPGSSQGCDAFLRHKMTLISPIILKKYGIPFSRITQEAGEFMITFP YGYHAGFNHGFNCAESTNFATLRWIDYGKVATQCTCRKDMVKISMDVFVRILQPERYEL WKQGKDLTVLDHTRPTALTSPELSSWSASRAGGSGHHHHHH
KDM4C	Q9H3R0	JMJD2CA-A705	SGC	16600.7	6.2866	Misc	fail	MHHHHHHSSGVDLGTENLYFQSMCEKVISVGQTVITKHRNTRYYSCRVMAVTSQTFYE VMFDDGSFSRDTFPEDIVSRDCLKLGPPAEGEVVQVKWPDGKLYGAKYFGSNIAHMY QVEFEDGSQIAMKREDIYTLDEELPKRVK
KDM4D	Q6B0I6	JMJD2DA-A003	SGC	43751.56	7.4226	JMJ	pass	MHHHHHHSSGVDLGTENLYFQSMETMKSKANCAQNPNCNIMIFHPTKEEFNDFDKYIA YMESQGAHRAGLAKIIPPKEWKARETYDNISEILIATPLQQVASGRAGVFTQYHKKKKA MTVGEYRHLANSKKYQTPPHQNFEDLERKYWKNRIYNSPIYGADISGSLFDENTKQWN LGHLGTIQDLLEKECGVVIEGVNTPYLYFGMWKTTFAWHTEDMDLYSINYLHLGEPKTW YVVPPEHGQRLERLARELFPGSSRGCGAFLRHKVALISPTVLKENGIPFNRITQEAGEF MVTFPYGYHAGFNHGFNCAEAINFATPRWIDYGKMASQCSCGEARVTFSMDAFVRILQ PERYDLWKRGQDRAVVDHMEPRVPASQEL
KDM5B	Q9UGL1	HR7375C.003	Rutgers	10479.68	5.3859	PHD	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMCPAVSCLQPEGDEVDWVQCDGSCN QWFHQVCVGVSPEMAEKEDYICVRCTVKDAPSRK
KDM5B	Q9UGL1	HR7375C.010	Rutgers	10479.68	5.3859	PHD	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMCPAVSCLQPEGDEVDWVQCDGSCN QWFHQVCVGVSPEMAEKEDYICVRCTVKDAPSRK
KDM5C	P41229	JARID1CA-A001	SGC	16541.63	7.6	Misc	pass	MHHHHHHHHHHHDLGTENLYFQSMNELEAQTRVKLNYLDQIAKFWEIQGSSLKIPNVER RILDLYSLSKIVVEEGGYEAICKDRRWARVAQRLNYPPGKNIGSLLRSHYERIVYPYEMY QSGANLVQCNTRPFDNEEKDK
KDM6B	O15054	JMJD3A-A005	SGC	40884.43	5.7602	JMJ	pass	MSGLNDIFEAQKIEWHEGSAGGSGLPREKLNPPTPSIYLESKRDAFSPVLLQFCTDPRN PITVIRGLAGSLRLNLGLFSTKTLVEASGEHTVEVRTQVQQPSDENWDLTGTRQIWPCE SSRSHTTIAKYAQYQASSFQESLQEEKESEDEESEEPDSTTGTPPSSAPDPKNHHIIKF GTNIDLSDAKRWKPQLQELLKLPAFMRVTSTGNMLSHVGHTILGMNTVQLYMKVPGSR TPGHQENNNFCSVNINIGPGDCEWFAVHEHYWETISAFCDRHGVDYLTGSWWPILDDL YASNIPVYRFVQRPGDLVWINAGTVHWVQATGWCNNIAWNVGPLTAYQYQLALERYE WNEVGGSGHHHHHH
KDM6B	O15054	JMJD3A-A025	SGC	40115.76	5.7763	JMJ	fail	MHHHHHHSSGVDLGTENLYFQSMLPREKLNPPTPSIYLESKRDAFSPVLLQFCTDPRN PITVIRGLAGSLRLNLGLFSTKTLVEASGEHTVEVRTQVQQPSDENWDLTGTRQIWPCE SSRSHTTIAKYAQYQASSFQESLQEEKESEDEESEEPDSTTGTPPSSAPDPKNHHIIKF GTNIDLSDAKRWKPQLQELLKLPAFMRVTSTGNMLSHVGHTILGMNTVQLYMKVPGSR TPGHQENNNFCSVNINIGPGDCEWFAVHEHYWETISAFCDRHGVDYLTGSWWPILDDL YASNIPVYRFVQRPGDLVWINAGTVHWVQATGWCNNIAWNVGPLTAYQYQLALERYE WNEV
KDM6B	O15054	JMJD3A-A037	SGC	65339.1	6.5809	JMJ	pass	MHHHHHHSSGMSDKIIHLTDDSFDTDVLKADGAILVDFWAEWCGPCKMIAPILDEIADE YQGKLTVAKLNIDQNPGTAPKYGIRGIPTLLLFKNGEVAATKVGALSKGQLKEFLDANLA GTENLYFQSMDVVRASRNAKVKGKFRESYLSPAQSVKPKINTEEKLPREKLNPPTPSIY LESKRDAFSPVLLQFCTDPRNPITVIRGLAGSLRLNLGLFSTKTLVEASGEHTVEVRTQV QQPSDENWDLTGTRQIWPCESSRSHTTIAKYAQYQASSFQESLQEEKESEDEESEEP DSTTGTPPSSAPDPKNHHIIKFGTNIDLSDAKRWKPQLQELLKLPAFMRVTSTGNMLSH VGHTILGMNTVQLYMKVPGSRTPGHQENNNFCSVNINIGPGDCEWFAVHEHYWETISA FCDRHGVDYLTGSWWPILDDLYASNIPVYRFVQRPGDLVWINAGTVHWVQATGWCNNI AWNVGPLTAYQYQLALERYEWNEVKNVKSIVPMIHVSWNVARTVKISDPDLFKMIKFCL LQSMKHCQVQRESLVRAGKKIAYQGRVKDEPAYYCNECDVEVFNILFVTS
KDM7A	Q6ZMT4	KIAA1718C-A001	SGC	54840.76	6.6631	PHD	pass	MSGLNDIFEAQKIEWHEGSAGGSGVYCVCRQPYDVNRFMIECDICKDWFHGSCVGVE EHHAVDIDLYHCPNCAVLHGSSLMKKRRNWHRHDYTEIDDGSKPVQAGTRTFIKELRS RVFPSADEIIIKMHGSQLTQRYLEKHGFDVPIMVPKLDDLGLRLPSPTFSVMDVERYVG GDKVIDVIDVARQADSKMTLHNYVKYFMNPNRPKVLNVISLEFSDTKMSELVEVPDIAKK LSWVENYWPDDSVFPKPFVQKYCLMGVQDSYTDFHIDFGGTSVWYHVLWGEKIFYLIK PTDENLARYESWSSSVTQSEVFFGDKVDKCYKCVVKQGHTLFVPTGWIHAVLTSQDC MAFGGNFLHNLNIGMQLRCYEMEKRLKTPDLFKFPFFEAICWFVAKNLLETLKELREDG FQPQTYLVQGVKALHTALKLWMKKELVSEHAFEIPDNVRPGHLIKELSKVIRAIEEENGG GSGHHHHHH
KDM8	Q8N371	FLJ13798A-A001	SGC	46585.05	6.1245	Cupin	pass	MSGLNDIFEAQKIEWHEGSAGGSGEKVERSVVTLLQRATELFYEGRRDECLQSSEVIL DYSWEKLNTGTWQDVDKDWRRVYAIGCLLKALCLCQAPEDANTVAAALRVCDMGLLM GAAILGDILLKVAAILQTHLPGKRPARGSLPEQPCTKKARADHGLIPDVKLEKTVPRLHR PSLQHFREQFLVPGRPVILKGVADHWPCMQKWSLEYIQEIAGCRTVPVEVGSRYTDEE WSQTLMTVNEFISKYIVNEPRDVGYLAQHQLFDQIPELKQDISIPDYCSLGDGEEEEITIN AWFGPQGTISPLHQDPQQNFLVQVMGRKYIRLYSPQESGALYPHDTHLLHNTSQVDVE NPDLEKFPKFAKAPFLSCILSPGEILFIPVKYWHYVRALDLSFSVSFWWSGGGSHHHHH H

HGCN	Uniprot ID	Antigen ID	Antigen Source	MW (Da)	pI	Common Domain Names	Primary Validation (pass/fail)	construct seq (with tag)
KDM8	Q8N371	FLJ13798A-A002	SGC	30969.9	5.9299	Cupin	pass	MSGLNDIFEAQKIEWHEGSAGGSGLEKTVPRLHRPSLQHFREQFLVPGRPVILKGVAD HWPCMQKWSLEYIQEIAGCRTVPVEVGSRYTDEEWSQTLMTVNEFISKYIVNEPRDVG YLAQHQLFDQIPELKQDISIPDYCSLGDGEEEEITINAWFGPQGTISPLHQDPQQNFLVQ VMGRKYIRLYSPQESGALYPHDTHLLHNTSQVDVENPDLEKFPKFAKAPFLSCILSPGEI LFIPVKYWHYVRALDLSFSVSFWWSGGSGHHHHHH
KIAA2018	Q68DE3	HR7682A.001	Rutgers	12305.04	10.2824	Misc	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPTKKQHRKKNRETHNAVERHRKKKI NAGINRIGELIPCSPALKQSKNMILDQAFKYITELKRQNDELLLNG
KLF1	Q13351	HR7553A.004	Rutgers	9199.2	8.3149	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKSSHLKAHLRTHTGEKPYACTWEGC GWRFARSDELTRHYRKHTG
KLF10	Q13118	HR6400B.005	Rutgers	20367.11	10.5189	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPNGTRLSPIAPAPGFSPSAAKVTPQID SSRIRSHICSHPGCGKTYFKSSHLKAHTRTHTGEKPFSCSWKGCERRFARSDELSRHR RTHTGEKKFACPMCDRRFMRSDHLTKHARRHLSAKKLPNWQMEVSKLNDIALPPTPAP TQ
KLF13	Q9Y2Y9	HR7797B.004	Rutgers	20943.37	10.4212	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPAGSGEPGLRQRVRRGRSRADLESP QRKHKCHYAGCEKVYGKSSHLKAHLRTHTGERPFACSWQDCNKKFARSDELARHYRT HTGEKKFSCPICEKRFMRSDHLTKHARRHANFHPGMLQRRGGGSRTGSLSDYSRSDA SSPTISpassP
KLF16	Q9BXK1	HR8436A.003	Rutgers	11988.43	8.3271	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHENLCFQSHMKSHRCPFPDCAKAYYKSSHLKSHLR THTGERPFACDWQGCDKKFARSDELARHHRTHTGEKRFSCPLCS
KLF5	Q13887	HR4433C.005	Rutgers	21083.71	9.5922	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMSPDRQAEMLQNLTPPPSYAATIASKL AIHNPNLPTTLPVNSQNIQPVRYNRRSNPDLEKRRIHYCDYPGCTKVYTKSSHLKAHLR THTGEKPYKCTWEGCDWRFARSDELTRHYRKHTGAKPFQCGVCNRSFSRSDHLALH MKRHQN
KLF6	Q99612	HR4668C.003	Rutgers	16844.87	10.2013	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGKVRSGTSGKPGDKGNGDASPDGR RRVHRCHFNGCRKVYTKSSHLKAHQRTHTGEKPYRCSWEGCEWRFARSDELTRHFR KHTGAKPFKCSHCDRCFSRSDHLALHMKRHL
KLF8	O95600	HR8376A.003	Rutgers	11547.03	9.9046	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMRRRIHQCDFAGCSKVYTKSSHLKAH RRIHTGEKPYKCTWDGCSWKFARSDELTRHFRKHTGIK
KMT2A	Q03164	MLL-A003	SGC	10042.44	9.2837	Zinc Finger	pass	MSGLNDIFEAQKIEWHEGSAGGSGKKGRRSRRCGQCPGCQVPEDCGVCTNCLDKPK FGGRNIKKQCCKMRKCQNLQWMPSKAGGGSHHHHHH
KMT2C	Q8NEZ4	MLL3-A003	SGC	24681.64	8.4805	SET	pass	MSGLNDIFEAQKIEWHEGSAGGSGTLNSTSTSKSFQSTVTGELNAPYSKQFVHSKSSQ YRKMKTEWKSNVYLARSRIQGLGLYAARDIEKHTMVIEYIGTIIRNEVANRKEKLYESQN RGVYMFRMDNDHVIDATLTGGPARYINHSCAPNCVAEVVTFERGHKIIISSSRRIQKGEE LCYDYKFDFEDDQHKIPCHCGAVNCRKWMNGGGSHHHHHH
KMT2E	Q8IZD2	MLL5-A004	SGC	19379.41	6.1197	PHD	pass	MHHHHHHHHHHHDLGTENLYFQSMARPPPTPPASPPPSVLISKNEVGIFTTPNFDETSSA TTISTSEDGSYGTDVTRCICGFTHDDGYMICCDKCSVWQHIDCMGIDRQHIPDTYLCER CQPRNLDKERAVLLQRRKRENMSDGDTSATESSSKGGYGLNDIFEAQKIEWHE
KMT2E	Q8IZD2	MLL5-A005	SGC	45378.97	9.2816	SET	pass	MHHHHHHHHHHHDLGTENLYFQSMQPRNLDKERAVLLQRRKRENMSDGDTSATESGD EVPVELYTAFQHTPTSITLTASRVSKVNDKRRKKSGEKEQHISKCKKAFREGSRKSSRV KGSAPEIDPSSDGSNFGWETKIKAWMDRYEEANNNQYSEGVQREAQRIALRLGNGND KKEMNKSDLNTNNLLFKPPVESHIQKNKKILKSAKDLPPDALIIEYRGKFMLREQFEANG YFFKRPYPPFVLFYSKFHGLEMCVDARTFGNEARFIRRSCTPNAEVRHEIQDGTIHLYIYS IHSIPKGTEITIAFDFDYGNCKYKVDCACLKENPECPVLKRSSESMENINSGYETRRKKG KKDKDISKEKDTQNQNITLSSKGGYGLNDIFEAQKIEWHE
L3MBTL1	Q9Y468	L3MBTL1-A003	SGC	42996.01	6.3191	Misc	pass	MHHHHHHHHHHHDLGTENLYFQSMGEKKECWSWESYLEEQKAITAPVSLFQDSQAVTH NKNGFKLGMKLEGIDPQHPSMYFILTVAEVCGYRLRLHFDGYSECHDFWVNANSPDIH PAGWFEKTGHKLQPPKGYKEEEFSWSQYLRSTRAQAAPKHLFVSQSHSPPPLGFQVG MKLEAVDRMNPSLVCVASVTDVVDSRFLVHFDNWDDTYDYWCDPSSPYIHPVGWCQK QGKPLTPPQDYPDPDNFCWEKYLEETGASAVPTWAFKVRPPHSFLVNMKLEAVDRRN PALIRVASVEDVEDHRIKIHFDGWSHGYDFWIDADHPDIHPAGWCSKTGHPLQPPLGPR EPSSASPGGSSKGGYGLNDIFEAQKIEWHE
L3MBTL2	Q969R5	L3MBTL2A-A002	SGC	54977.23	7.3346	Misc	pass	MHHHHHHHHHHHDLGTENLYFQSMTGQDALVLGFDWGKFLKDHSYKAAPVSCFKHVPL YDQWEDVMKGMKVEVLNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWC NLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRLVGSRTLPVDFHIKMVESM KYPFRQGMRLEVVDKSQVSRTRMAVVDTVIGGRLRLLYEDGDSDDDFWCHMWSPLIH PVGWSRRVGHGIKMSERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMK LEAIDPNLGNICVATVCKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKN DIELTPPKGYEAQTFNWENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLMEPR LICVATVKRVVHRLLSIHFDGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVAAEP ATPLKAKEATKKKKKQ
L3MBTL3	Q96JM7	L3MBTL3-A004	SGC	40790.11	6.8287	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGKKAWCWASYLEEEKAVAVPAKLFKEHQSFPYNK NGFKVGMKLEGVDPEHQSVYCVLTVAEVCGYRIKLHFDGYSDCYDFWVNADALDIHPV GWCEKTGHKLHPPKGYKEEEFNWQTYLKTCKAQAAPKSLFENQNITVIPSGFRVGMKL EAVDKKNPSFICVATVTDMVDNRFLVHFDNWDESYDYWCEASSPHIHPVGWCKEHRR TLITPPGYPNVKHFSWDKYLEETNSLPAPARAFKVKPPHGFQKKMKLEVVDKRNPMFIR VATVADTDDHRVKVHFDGWNNCYDYWIDADSPDIHPVGWCSKTGHPLQPPLSPLELM EGGGSHHHHHH
L3MBTL4	Q8NA19	HR6490A.007	Rutgers	51447.5	6.47	Misc	pass	
L3MBTL4	Q8NA19	L3MBTL4-A003	SGC			NA	pass	
LHX1	P48742	HR8129B.004	Rutgers	23027.92	9.882	Homeobox	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGPRTTIKAKQLETLKAAFAATPKPTRH IREQLAQETGLNMRVIQVWFQNRRSKERRMKQLSALGARRHAFFRSPRRMRPLVDRL EPGELIPNGPFSFYGDYQSEYYGPGGNYDFFPQGPPSSQAQTPVDLPFVPSSGPSGT PLGGLEHPLPGHHPSSEAQRFTDILAHPP
MAFB	Q9Y5Q3	HR6931A.007	Rutgers	15672.7	10.1053	bZip	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMDRFSDDQLVSMSVRELNRHLRGFTK DEVIRLKQKRRTLKNRGYAQSCRYKRVQQKHHLENEKTQLIQQVEQLKQEVSRLARER DAYKVKCEKLANSG
MAFF	Q9ULX9	HR8265A.002	Rutgers	9140.39	10.5507	bZip	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGLSVRELNRHLRGLSAEEVTRLKQR RRTLKNRGYAASCRVKRVC
MATR3	P43243	HR8183A.001	Rutgers	14404.49	9.3885	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMQKGRVETSRVVHIMDFQRGKNLRYQ LLQLVEPFGVISNHLILNKINEAFIEMATTEDAQAAVDYYTTTPALVFGKPVRVHLSQKYK RIKK
MBD4	O95243	HR4635D.004	Rutgers	16000.14	9.2422	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMIKRSSECNPLLQEPIASAQFGATAGTE CRKSVPCGWERVVKQRLFGKTAGRFDVYFISPQGLKFRSKSSLANYLHKNGETSLKPE DFDFTVLSKRGIKSRYKDCSMA
MBTD1	Q05BQ5	MBTD1-A003	SGC	54794.55	6.9677	Misc	pass	MHHHHHHHHHHHDLGTENLYFQSMAKTKAAVSMEGFSWGNYINSNSFIAAPVTCFKHA PMGTCWGDISENVRVEVPNTDCSLPTKVFWIAGIVKLAGYNALLRYEGFENDSGLDFW CNICGSDIHPVGWCAASGKPLVPPRTIQHKYTNWKAFLVKRLTGAKTLPPDFSQKVSES MQYPFKPCMRVEVVDKRHLCRTRVAVVESVIGGRLRLVYEESEDRTDDFWCHMHSPLI HHIGWSRSIGHRFKRSDITKKQDGHFDTPPHLFAKVKEVDQSGEWFKEGMKLEAIDPL NLSTICVATIRKVLADGFLMIGIDGSEAADGSDWFCYHATSPSIFPVGFCEINMIELTPPR GYTKLPFKWFDYLRETGSIAAPVKLFNKDVPNHGFRVGMKLEAVDLMEPRLICVATVTR IIHRLLRIHFDGWEEEYDQWVDCESPDLYPVGWCQLTGYQLQPPASQSSRSSKGGYG LNDIFEAQKIEWHE
MEN1	O00255	MEN1-A006	SGC	70919.35	6.5512	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGMGLKAAQKTLFPLRSIDDVVRLFAAELGREEPDL VLLSLVLGFVEHFLAVNRVIPTNVPELTFQPSPAPDPPGGLTYFPVADLSIIAALYARFTAQ IRGAVDLSLYPREGGVSSRELVKKVSDVIWNSLSRSYFKDRAHIQSLFSFITGTKLDSSG VAFAVVGACQALGLRDVHLALSEDHAWVVFGPNGEQTAEVTWHGKGNEDRRGQTVN AGVAERSWLYLKGSYMRCDRKMEVAFMVCAINPSIDLHTDSLELLQLQQKLLWLLYDLG HLERYPMALGNLADLEELEPTPGRPDPLTLYHKGIASAKTYYRDEHIYPYMYLAGYHCR NRNVREALQAWADTATVIQDYNYCREDEEIYKEFFEVANDVIPNLLKEAASLLEAGEER PGEQSQGTQSQGSALQDPECFAHLLRFYDGICKWEEGSPTPVLHVGWATFLVQSLGR FEGQVRQKVRIVSREAEAAEAEEPWGEEAREGRRRGPRRESKPEEPPPPKKPALDKG LGTGQGAVSGPPRKPPGTVAGTARGPEGGSTAQVPAPAASPPPEGPVLTFQSEKMKG MKELLVATKINSSAIKLQLTAQSQVQMKKQKVSTPSDYTLSFLKRQRKGLGGGSHHHHH H
MLL3	Q8NEZ4	MLL3-A002	SGC	23111.95	8.263	SET	pass	MSGLNDIFEAQKIEWHEGSAGGSGTGELNAPYSKQFVHSKSSQYRKMKTEWKSNVYL ARSRIQGLGLYAARDIEKHTMVIEYIGTIIRNEVANRKEKLYESQNRGVYMFRMDNDHVI DATLTGGPARYINHSCAPNCVAEVVTFERGHKIIISSSRRIQKGEELCYDYKFDFEDDQH KIPCHCGAVNCRKWMNGGGSHHHHHH
MPHOSPH8	Q99549	MPP8-A002	SGC	10652.88	6.2872	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGVFEVEKILDMKTEGGKVLYKVRWKGYTSDDDTW EPEIHLEDCKEVLLEFRKKIAENKAKAVGGSGHHHHHH

HGCN	Uniprot ID	Antigen ID	Antigen Source	MW (Da)	pI	Common Domain Names	Primary Validation (pass/fail)	construct seq (with tag)
MSC	O60682	HR4485B.003	Rutgers	13966.83	9.8589	Misc	fail	MSGLNDIFEAQKIEWHEGSAGGSGDFSPGDLVWAKMEGYPWWPCLVYNHPFDGTFIREKGKSVRVHVQFFDDSPTRGWVSKRLLKPYTGSKSKEAQKGGHFYSAKPEILRAMQRADEALNKDKIKRLELAVCDEPSEPEGGSGHHHHHH
MSH6	P52701	MSH6-A001	SGC	16724.69	7.2625	PWWP	pass	MSGLNDIFEAQKIEWHEGSAGGSGGAPGQSPGAGRACESCYTTQSYQWYSWGPPNMQCRLCASCWTYWKKYGGLKMPTRLDGERPGPNRSNMSGGSGHHHHHH
MTA1	Q13330	MTA1-A002	SGC	11165.26	8.0661	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGCRDEMEEWSASEANLFEEALEKYGKDFTDIQQDFLPWKSLTSIIEYYYMWKTTDRYVQQKRLKAAEAESKGGSGHHHHHH
MTA1	Q13330	MTA1-A001	SGC	11936.04	5.1794	Misc	pass	MSGLNDIFEAQKIEWHHHHHHHHNLYFQSHMPETKRKEVKRYQCTFEGCPRTYSTAGNLRTHQKTHRGEYTFVCNQEGCGKAFLTSYSLRIHVRVHTKEKPFECDVQGCEKAFNTLYRLKAHQRLHTGKTFNCESEGCSKYFTTLSDLRKHIRTHTGEKPFRCDHDGCGKAFAASHHLKTHVRTHTGERPFFCPSNGCEKTFSTQYSLKSHMKGHDNKGHSYNALPQHNG
MTF1	Q14872	HR6907B.005	Rutgers	26873.09	9.0344	Zinc Finger	pass	
MTF2	Q9Y483	PCL2-A001	SGC	18508.79	6.5568	PHD	pass	MSGLNDIFEAQKIEWHEGSAGGSGKLSLQDGHKAKKPACKFEEGQDVLARWSDGLFYLGTIKKINILKQSCFIIFEDSSKSWVLWKDIQTGATGSGEMVCTICQEEYSEAPNEMVICDKCGQGYHQLCHTPHIDSSVIDSDEKWLCRQCVFATTTKRGGSGHHHHHH
MZF1	P28698	HR7215A.005	Rutgers	14382.2	6.0762	SCAN	pass	MSGLNDIFEAQKIEWHHHHHHHHNLYFQSHMDPGPEAARLRFRCFRYEEATGPQEALAQLRELCRQWLRPEVRSKEQMLELLVLEQFLGALPPEIQARVQGQRPGSPEEAAALVDGLRREPGG
NAP1L5	Q96NT1	NAP1L5-A001	SGC	19054.61	4.2431	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGPDSAAGQMAEEPQTPAENAPKPKNDFIESLPNSVKCRVLALKKLQKRCDKIEAKFDKEFQALEKKYNDIYKPLLAKIQELTGEMEGCAWTLEGEEEEEEEYEDDEEEGEDEEEEEAAAEAAAGAKHDDAHAEMPDDAKKGGSGHHHHHH
NCOA3	Q9Y6Q9	HR4453I.011	Rutgers	22241.04	5.9287	Misc	fail	MSGLNDIFEAQKIEWHHHHHHHHNLYFQSHMVSSTGQGVIDKDSLGPLLLQALDGFLFVVNRDGNIVFVSENVTQYLQYKQEDLVNTSVYNILHEEDRKDFLKNLPKSTVNGVSWTNETQRQKSHTFNCRMLMKTPHDILEDINASPEMRQRYETMQCFALSQPRAMMEEGEDLQSCMICVARRITTGER
NCOR1	O75376	NCOR1-A001	SGC	11286.45	7.6248	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGTEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAKMVGTKSEAQCKNFYFNYKRRHNLDNLLQQHQKGGSGHHHHHH
NEDD4L	Q96PU5-5	NEDD4L-A002	SGC	47792.36	5.6139	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGSREFKQKYDYFRKKLKKPADIPNRFEMKLHRNNIFEESYRRIMSVKRPDVLKARLWIEFESEKGLDYGGVAREWFFLLSKEMFNPYYGLFEYSATDNYTLQINPNSGLCNEDHLSYFTFIGRVAGLAVFHGKLLDGFFIRPFYKMMLGKQITLNDMESVDSEYYNSLKWILENDPTELDLMFCIDEENFGQTYQVDLKPNGSEIMVTNENKREYIDLVIQWRFVNRVQKQMNAFLEGFTELLPIDLIKIFDENELELLMCGLGDVDVNDWRQHSIYKNGYCPNHPVIQWFWKAVLLMDAEKRIRLLQFVTGTSRVPMNGFAELYGSNGPQLFTIEQWGSPEKLPRAHTCFNRLDLPPYETFDLREKLLMAVENGGSGHHHHHH
NFKB1	P19838	HR3633D.001	Rutgers	16427.51	6.2273	NA	pass	MSGLNDIFEAQKIEWHHHHHHHHNLYFQSHMSNLKIVRMDRTAGCVTGGEEIYLLCDKVQKDDIQIRFYEEEENGGVWEGFGDFSPTDVHRQFAIVFKTPKYKDINITKPASVFVQLRRKSDLETSEPKPFLYYPEIK
NKX2-5	P52952	Nkx2-5	RAN	7073.25	11.5762	Homeobox	pass	MKIEEHHHHHHHSSGKLGSTEDLYFQSAAQPARKPRVLFSQAQVYELERRFKQQRYLSAPERDQLASVLKLTSTQVKIWFQNRRYKCKR
NKX6-1	P78426	Nkx6-1	RAN	6832.85	11.3584	Homeobox	pass	MKIEEHHHHHHHSSGKLGSTEDLYFQSAAQPAKHTRPTFSGQQIFALEKTFEQTKYLAGPERARLAYSLGMTESQVKVWFQNRRTKWRK
NR1D1	P20393	HR8278A.001	Rutgers	14906.27	9.9178	Zinc Finger	pass	MSGLNDIFEAQKIEWHHHHHHHHNLYFQSHMTKLNGMVLLCKVCGDVASGFHYGVHACEGCKGFFRRSIQQNIQYKRCLKNENCSIVRINRNRCQQCRFKKCLSVGMSRDAVRFGRIPKREKQRM
NR1D2	Q14995	HR8341C.001	Rutgers	24561	5.9966	Hormone Receptor	pass	MSGLNDIFEAQKIEWHHHHHHHHNLYFQSHMGHEIWEEFSMSFTPAVKEVVEFAKRIPGFRDLSQHDQVNLLKAGTFEVLMVRFASLFDAKERTVTFLSGKKYSVDDLHSMGAGDLLNSMFEFSEKLNALQLSDEEMSLFTAVVLVSADRSGIENVNSVEALQETLIRALRTLIMKNHPNEASIFTKLLLKLPDLRSLNNMHSEELLAFKVHP
NR1I2	O75469	HR7870A.004	Rutgers	14952.42	10.1343	Zinc Finger	fail	MSGLNDIFEAQKIEWHHHHHHHHNLYFQSHMGPQICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFRKGACEITRKTRRQCQACRLRKCLESGMKKEMIMSDEAVEERRALIKRKKS
NR1I3	Q14994	HR7475A.002	Rutgers	15080.18	8.5116	Zinc Finger	pass	MSGLNDIFEAQKIEWHHHHHHHHNLYFQSHMDELRNCVVCGDQATGYHFNALTCEGCKGFFRRTVSKSIGPTCPFAGSCEVSKTQRRHCPACRLQKCLDAGMRKDMILSAEALALRRAKQAQRRAQQTPVQ
NR2C1	P13056	HR8155A.001	Rutgers	14280.39	8.8755	Zinc Finger	pass	MSGLNDIFEAQKIEWHHHHHHHHNLYFQSHMKVFDLCVVCGDKASGRHYGAVTCEGCKGFFKRSIRKNLVYSCRGSKDCIINKHHRNRCQYCRLQRCIAFGMKQDSVQCERKPIEVSREK
NR3C2	P08235	HR7785A.001	Rutgers	11997.8	8.1197	Zinc Finger	fail	MSGLNDIFEAQKIEWHHHHHHHHNLYFQSHMKICLVCGDEASGCHYGVVTCGSCKVFFKRAVEGQHNYLCAGRNDCIIDKIRRKNCPACRLQKCLQAGMNLGAR
NR4A2	P43354	HR8241A.001	Rutgers	13311.33	9.2367	Zinc Finger	pass	MSGLNDIFEAQKIEWHHHHHHHHNLYFQSHMGLCAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKRRRNRCQYCRFQKCLAVGMVKEVVRTDSLKGRR
NR4A2	P43354	Nr4a2	RAN	7911.35	9.7365	Zinc Finger	pass	MKIEEHHHHHHHSSGKLGSTEDLYFQSAAQPAGLCAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKRRRNRCQYCRFQKCLAVGMVK
NR4A3	Q92570	HR7224B.001	Rutgers	30025.44	5.9072	Hormone Receptor	fail	MSGLNDIFEAQKIEWHHHHHHHHNLYFQSHMICMMNALVRALTDSTPRDLDYSRYCPTDQAAAGTDAEHVQQFYNLLTASIDVSRSWAEKIPGFTDLPKEDQTLLIESAFLELFVLRLSIRSNTAEDKFVFCNGLVLHRLQCLRGFGEWLDSIKDFSLNLQSLNLDIQALACLSALSMITERHGLKEPKRVEELCNKITSSLKDHQSKGQALEPTESKVLGALVELRKICTLGLQRIFYLKLEDLVSPPSIIDKLFLDTLPF
NR4A3	Q92570	HR7224C.003	Rutgers	13584.62	9.4444	Zinc Finger	pass	MSGLNDIFEAQKIEWHHHHHHHHNLYFQSHMTCAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKRRRNRCQYCRFQKCLSVGMVKEVVRTDSLKGRGRL
NR5A1	Q13285	HR7993A.003	Rutgers	31706.75	6.1825	Hormone Receptor	pass	MSGLNDIFEAQKIEWHHHHHHHHNLYFQSHMGPNVPELILQLLQLEPDEDQVRARILGCLQEPTKSRPDQPAAFGLLCRMADQTFISIVDWARRCMVFKELEVADQMTLLQNCWSELLVFDHIYRQVQHGKEGSILLVTGQEVELTTVATQAGSLLHSLVLRAQELVLQLLALQLDRQEFVCLKFIILFSLDLKFLNNHILVKDAQEKANAALLDYTLCHYPHCGDKFQQLLLCLVEVRALSMQAKEYLYHKHLGNEMPRNNLLIEMLQAKQT
NR5A2	O00482	Nr5a2	RAN	8163.55	8.9535	Zinc Finger	pass	MKIEEHHHHHHHSSGKLGSTEDLYFQSAAQPAELCPVCGDKVSGYHYGLLTCESCKGFFKRTVQNNKRYTCIENQNCQIDKTQRKRCPYCRFQKCLSVGMKL
NR6A1	Q15406	HR7049C.002	Rutgers	16834.27	8.5732	Zinc Finger	pass	MSGLNDIFEAQKIEWHHHHHHHHNLYFQSHMDRAEQRTCLICGDRATGLHYGIISCEGCKGFFKRSICNKRVYRCSRDKNCVMSRKQRNRCQYCRLLKCLQMGMNRKAIREDGMPGGRNKSIGPVQISEEEIERIMSGQEFE
NRF1	Q16656	HR8346A.003	Rutgers	49745.08	6.2329	Misc	pass	MSGLNDIFEAQKIEWHHHHHHHHNLYFQSHMLNSTAAAEVTAHLTAAGPVGMAAAAAVATGKKRNRPHVFESNPSIRKRQQTRLLRKLRATLDEYTTRVGQQAIVLCISPSKPNPVFKVFGAAPLENVVRKYKSMILEDLESALAEHAPAPQEVNSELPPLTIDGIPVSVDKMTQAQLRAFIPEMLKYSTGRGKPGWGKESCKPIWWPEDIPWANVRSDVRTEEQKQRVSWTQALRTIVKNCYKQHGREDLLYAFEDQQTQTQATATHSIAHLVPSQTVVQTFSNPDGTVSLIQVGTGATVATLADASELPTTVTVAQVNYSAVADGEVEQNWATLQGGEMTIQTTQASEATQAVASLAEAAVAASQEMQQGATVTMALNSEAAAHAVATLAEATLQGGGQIVLSGETAAAVGALTGVQDANGLVQIPVSMYQTVVTSLAQGNGPVQVAMAPVTTRISDSAVT
NRL	P54845	HR7765A.002	Rutgers	8946.07	10.1105	bZip	pass	MSGLNDIFEAQKIEWHHHHHHHHNLYFQSHMERFSDAALVSMSVRELNRQLRGCGRDEALRLKQRRRTLKNRG
NSD1	Q96L73	NSD1-A004	SGC	39413.54	7.6962	PWWP	pass	MSGLNDIFEAQKIEWHEGSAGGSGHPRAVPSNIDKMRHDVGEFPVLFFGSNDYLWTHQARVFPYMEGDVSSKDKMGKGVDGTYKKALQEAAARFEELKAQKELRQLQEDRKNDKKPPPYKHIKVNRPIGRVQIFTADLSEIPRCNCKATDENPCGIDSECINRMLLYECHPTVCPAGGRCQNQCFSKRQYPEVEIFRTLQRGWGLRTKTDIKKGEFVNEYVGELIDEEECRARIRYAQEHDITNFYMLTLDKDRIIDAGPKGNYARFMNHCCQPNCETQKWSVNGDTRVGLFALSDIKAGTELTFNYNLECLGNGKTVCKCGAPNCSGFLGVRPKNQPIGGSGHHHHH
OSR2	Q8N2R0	HR6892B.004	Rutgers	22396.47	9.5712	Zinc Finger	fail	MSGLNDIFEAQKIEWHHHHHHHHNLYFQSHMPSRGRLPSKTKKEFICKFCGRHFTKSYNLLIHERTHTDERPYTCDICHKAFRRQDHLRDHRYIHSKEKPFKCQECGKGFCQSRTLAVHKTLHMQESPHKCPTCGRTFNQRSNLKTHLLTHTDIKPYSCEQCGKVFRRNCDLRRHSLTHTPRQDF
OVOL1	O14753	HR8136A.004	Rutgers	12819.56	9.0537	Zinc Finger	pass	MSGLNDIFEAQKIEWHHHHHHHHNLYFQSHMRDHGFLRTKMKVTLGDSPSGDLFTCRVCQKAFTYQRMLNRHMKCHNDVKRHLCTYCGKGFNDTFDLKRHVRTHTG
OVOL2	Q9BRP0	HR8149A.003	Rutgers	12149.85	9.1723	Zinc Finger	fail	MSGLNDIFEAQKIEWHHHHHHHHNLYFQSHMARSKIKFTTGTCSDSVVHSCDLCGKGFRLQRMLNRHLKCHNQVKRHLCTFCGKGFNDTFDLKRHVRTHTGI

HGCN	Uniprot ID	Antigen ID	Antigen Source	MW (Da)	pI	Common Domain Names	Primary Validation (pass/fail)	construct seq (with tag)
PARP14	Q460N5	PARP14A-A002	SGC	27283.94	6.444	Misc	pass	MHHHHHHHHHHDLGTENLYFQSMAAAGPGKTSWEKGSLVSPGGLQMLLVKEGVQNAKTDVVVNSVPLDLVLSRGPLSKSLLEKAGPELQEELDTVGQGVAVSMGTVLKTSSWNLDCRYVLHVVAPEWRNGSTSSLKIMEDIIRECMEITESLSLKSIAFPAIGTGNLGFPKNIFAELIISEVFKFSSKNQLKTLQEVHFLLHPSDHENIQAFSDEFARRANGNLVSSSKGGYGLNDIFEAQKIEWHE
PARP14	Q460N5	PARP14A-A003	SGC	25376.58	6.9608	Misc	pass	MHHHHHHHHHHDLGTENLYFQSMFYGTVSSPDSGVYEMKIGSIIFQVASGDITKEEADVIVNSTSNSFNLKAGVSKAILECAGQNVERECSQQAQQRKNDYIITGGGFLRCKNIIHVIGGNDVKSSVSSVLQECEKKNYSSICLPAIGTGNAKQHPDKVAEAIIDAIEDFVQKGSAQSVKKVKVVIFLPQVLDVFYANMKKREGTQLSSSSKGGYGLNDIFEAQKIEWHE
PBK	Q96KB5	TOPKA-A004	SGC	39537.63	5.0736	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFMQKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQKRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGEKSLNDLIEERYKASQDPFPAAIILKVALNMARGLKYLHQEKKLLHGDIKSSNVVIKGDFETIKICDVGVSLPLDENMTVTDPEACYIGTEPWKPKEAVEENGVITDKADIFAFGLTLWEMMTLSIPHINLSNDDDDEDKTFDESDFDDEAYYAALGTRPPINMEELDESYQKVIELFSVCTNEDPKDRPSAAHIVEALETDVGGGSHHHHHH
PBRM1	Q86U86	PB1A	SGC	15677.96	7.6373	Bromodomain	pass	MHHHHHHSSGVDLGTENLYFQSMSPAYLKEILEQLLEAIVVATNPSGRLISELFQKLPSKVQYPDYYAIIKEPIDLKTIAQRIQNGSYKSIHAMAKDIDLLAKNAKTYNEPGSQVFKDANSIKKIFYMKKAEIEHHE
PBRM1	Q86U86	PB1A-A010	SGC	20030.77	7.1558	Bromodomain	pass	MHHHHHHHHHHSSGVDLGTENLYFQSMSGISPKKSKYMTPMQQKLNEVYEAVKNYTDKRGRRLSAIFLRLPSRSELPDYYLTIKKPMDMEKIRSHMMANKYQDIDSMVEDFVMMFNNACTYNEPESLIYKDALVLHKVLLETRRDLEGDSSKGGYGLNDIFEAQKIEWHE
PBRM1	Q86U86	PB1A-A011	SGC	21217.89	7.3738	Bromodomain	pass	MHHHHHHHHHHDLGTENLYFQSMHHSVSTPGPSRKRRRLSNLPTVDPIAVCHELYNTIRDYKDEQGRLLCELFIRAPKRRNQPDYYEVVSQPIDLMKIQQKLKMEEYDDVNLLTADFQLLFNNAKSYYKPDSPEYKAACKLWDLYLRTRNEFVQKGESSKGGYGLNDIFEAQKIEWHE
PBRM1	Q86U86	PB1A-A012 monomer	SGC	18286.78	7.1987	Bromodomain	pass	MHHHHHHHHHHDLGTENLYFQSMSPAYLKEILEQLLEAIVVATNPSGRLISELFQKLPSKVQYPDYYAIIKEPIDLKTIAQRIQNGSYKSIHAMAKDIDLLAKNAKTYNEPGSQVFKDANSIKKIFYMKKAEIEHHESSKGGYGLNDIFEAQKIEWHE
PBX3	P40426	HR7892A.005	Rutgers	15547.59	7.3743	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMKNDVKNRSVYIKGFPTDATLDDIKEWLEDKGQVLNIQMRRTLHKAFKGSIFVVFDSIESAKKFVETPGQKYKETDLLILFKDDYFAKKNEERKQNKVE
PBX4	Q9BYU1	HR7406A.001	Rutgers	11525.86	9.7288	Homeobox	pass	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMARRKRRNFSKQATEVLNEYFYSHLNNPYPSEEAKEELARKGGLTISQVSNWFGNKRIRYKKNC
PGBD1	Q96JS3	HR2735A.005	Rutgers	20563.94	4.7512	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMPGPAPENEDGLVKVKEEDPTWEQVCNSQEGSSHTQEICRLRFRHFCYQEAHGPQEALAQLRELCHQWLRPEMHTKEQIMELLVLEQFLTILPKELQPCVKTYPLESGEEAVTVLENLETGSGDTGQQASVYIQGQDMHPMVAEYQ
PHF20L1	A8MW92	PHF20L1-A001	SGC	13431.96	6.9855	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGMSKKPPNRPGITFEIGARLEALDYLQKWYPSRIEKIDYEEGKMLVHFERWSHRYDEWIYWDSNRLRPLERPALRKEGLKDEGGSGHHHHHH
PHF8	Q9UPP1	PHF8A-A002	SGC	54854.47	6.6906	PHD	pass	MSGLNDIFEAQKIEWHEGSAGGSGASVPVYCLCRLPYDVTRFMIECDMCQDWFHGSCVGVEEEKAADIDLYHCPNCEVLHGPSIMKKRRGSSKGHDTHKGKPVKTGSPTFVRELRSRTFDSSDEVILKPTGNQLTVEFLEENSFSVPILVLKKDGLGMTLPSPSFTVRDVEHYVGSDKEIDVIDVTRQADCKMKLGDFVKYYYSGKREKVLNVISLEFSDTRLSNLVETPKIVRKLSWVENLWPEECVFERPNVQKYCLMSVRDSYTDFHIDFGGTSVWYHVLKGEKIFYLIRPTNANLTLFECWSSSSNQNEMFFGDQVDKCYKCSVKQGQTLFIPTGWIHAVLTPVDCLAFGGNFLHSLNIEMQLKAYEIEKRLSTADLFRFPNFETICWYVGKHILDIFRGLRENRRHPASYLVHGGKALNLAFRAWTRKEALPDHEDEIPETVRTVQLIKDLAREIRLVEDIFQQNGGSGHHHHHH
PHF8	Q9UPP1	PHF8A-A066	SGC	65547.03	6.4613	PHD	pass	MHHHHHHSSGMSDKIIHLTDDSFDTDVLKADGAILVDFWAEWCGPCKMIAPILDEIADEYQGKLTVAKLNIDQNPGTAPKYGIRGIPTLLLFKNGEVAATKVGALSKGQLKEFLDANLAGTENLYFQSMASVPVYCLCRLPYDVTRFMIECDMCQDWFHGSCVGVEEEKAADIDLYHCPNCEVLHGPSIMKKRRGSSKGHDTHKGKPVKTGSPTFVRELRSRTFDSSDEVILKPTGNQLTVEFLEENSFSVPILVLKKDGLGMTLPSPSFTVRDVEHYVGSDKEIDVIDVTRQADCKMKLGDFVKYYYSGKREKVLNVISLEFSDTRLSNLVETPKIVRKLSWVENLWPEECVFERPNVQKYCLMSVRDSYTDFHIDFGGTSVWYHVLKGEKIFYLIRPTNANLTLFECWSSSSNQNEMFFGDQVDKCYKCSVKQGQTLFIPTGWIHAVLTPVDCLAFGGNFLHSLNIEMQLKAYEIEKRLSTADLFRFPNFETICWYVGKHILDIFRGLRENRRHPASYLVHGGKALNLAFRAWTRKEALPDHEDEIPETVRTVQLIKDLAREIRLVEDIFQQN
PIKFYVE	Q9Y2I7	HR7108D.015	Rutgers	21042.17	5.2418	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMTEDERKILLDSVQLKDLWKKICHHSSGMEFQDHRYWLRTHPNCIVGKELVNWLIRNGHIATRAQAIAIGQAMVDGRWLDCVSHHDQLFRDEYALYRPLQSTEFSETPSPDSDSVNSVEGHSEPSWFKDIKFDDSDTEQIAEEGDDNL
PIKFYVE	Q9Y2I7	HR7108D.010	Rutgers	19741.74	5.5884	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMVQLKDLWKKICHHSSGMEFQDHRYWLRTHPNCIVGKELVNWLIRNGHIATRAQAIAIGQAMVDGRWLDCVSHHDQLFRDEYALYRPLQSTEFSETPSPDSDSVNSVEGHSEPSWFKDIKFDDSDTEQIAEEGDDNL
PITX2	Q99697	HR4722B.003	Rutgers	8744.65	7.3225	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMRDTCNSSLASLRLKAKQHSSFGYASVQNPASNLSACQYAVDRPV
PLAG1	Q6DJT9	HR7109C.007	Rutgers	10169.43	6.9541	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMETFKCEECGKNYNTKLGFKRHLALHAATSGDLTCKVCLQTFESTGVLLEHLKSHAG
PLAGL1	Q9UM63	HR7895A.004	Rutgers	9028.18	7.6707	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMDHCERCFYTRKDVRRHLVVHTGCKDFLCQFCAQRFGRKDHL
PLAGL2	Q9UPG8	HR7996A.003	Rutgers	10791.2	9.932	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMKKHPCDHCDRRFYTRKDVRRHLVVHTGRKDFLCQYCAQRFGRKDHLTRHVKKSHS
PLXNB1	O43157	HR7815A.001	Rutgers	18123.5	6.2756	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMDNRLLREDVEYRPLTLNALLAVGPGAGEAQGVPVKVLDCDTISQAKEKMLDQLYKGVPLTQRPDPRTLDVEWRSGVAGHLILSDEDVTSEVQGLWRRLNTLQHYKVPDGATVALVPCLTKHVLRENQ
PPARA	Q07869	HR7133A.001	Rutgers	12379.22	8.8186	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMALNIECRICGDKASGYHYGVHACEGCKGFFRRTIRLKLVYDKCDRSCKIQKKNRNKCQYCRFHKCLSVGMSH
PPARD	Q03181	HR8028A.005	Rutgers	12661.54	8.8263	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMECRVCGDKASGFHYGVHACEGCKGFFRRTIRMKLEYEKCERSCKIQKKNRNKCQYCRFQKCLALGMSHNAIRFG
PRDM1	O75626	PRDM1-A004	SGC	25150.99	5.6982	SET	pass	MSGLNDIFEAQKIEWHEGSAGGSGKMDMEDADMTLWTEAEFEEKCTYIVNDHPWDSGADGGTSVQAEASLPRNLLFKYATNSEEVIGVMSKEYIPKGTRFGPLIGEIYTNDTVPKNANRKYFWRIYSRGELHHFIDGFNEEKSNWMRYVNPAHSPREQNLAACQNGMNIYFYTIKPIPANQELLVWYCRDFAERLHYPYPGELTMMNLTQGGGSHHHHHH
PRDM1	O75626	PRDM1A-A001	SGC	24930.89	6.2146	SET	fail	MHHHHHHHHHHSSGVDLGTENLYFQSMKMDMEDADMTLWTEAEFEEKCTYIVNDHPWDSGADGGTSVQAEASLPRNLLFKYATNSEEVIGVMSKEYIPKGTRFGPLIGEIYTNDTVPKNANRKYFWRIYSRGELHHFIDGFNEEKSNWMRYVNPAHSPREQNLAACQNGMNIYFYTIKPIPANQELLVWYCRDFAERLHYPYPGELTMMNLTQ
PRDM10	Q9NQV6	PRDM10-A002	SGC			NA	pass	
PRDM10	Q9NQV6	PRDM10-A003	SGC	28134.67	6.6984	SET	pass	MHHHHHHHHHHDLGTENLYFQSMDDWEPDPPRPFDPHDLWCEECNNAHASVCPKHGPLHPIPNRPVLTRARASLPLVLYIDRFLGGVFSKRRIPKRTQFGPVEGPLVRGSELKDCYIHLKVSLDKGDRKERDLHEDLWFELSDETLCNWMMFVRPAQNHLEQNLVAYQYGHHVYYTTIKNVEPKQELKVWYAASYAEFVNQKIHDISEEERKVLREQSSKGGYGLNDIFEAQKIEWHE
PRDM11	Q9NQV5	PRDM11-A002	SGC	32670.66	6.6452	SET	pass	MHHHHHHHHHHDLGTENLYFQSMDSSAMEVEPKKLKGKRDLIVPKSFQQVDFWFCESCQEYFVDECPNHGPPVFVSDTPVPVGIPDRAALTIPQGMEVVKDTSGESDVRCVNEVIPKGHIFGPYEGQISTQDKSAGFFSWLIVDKNNRYKSIDGSDETKANWMRYVVISREEREQNLLAFQHSERIYFRACRDIRPGEWLRVWYSEDYMKRLHSMSQETIHRNLARGEKRLQREKSEQVLDNPEDLRGPIHLSVLRQGKSSKGGYGLNDIFEAQKIEWHE
PRDM12	Q9H4Q4	PRDM12A-A001	SGC	22308.04	5.8188	SET	fail	MHHHHHHHHHHSSGVDLGTENLYFQSMKTAFTAEVLAQSFSGEVQKLSSLVLPAEVIIAQSSIPGEGLGIFSKTWIKAGTEMGPFTGRVIAPEHVDICKNNNLMWEVFNEDGTVRYFIDASQEDHRSWMTYIKCARNEQENLEVVQIGTSIFYKAIEMIPPDQELLVWYGNSHNTFLGIPGVPGLEEDQKKNKHED
PRDM13	Q9H4Q3	HR8220A.003	Rutgers	17447.46	7.7656	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMPTTATPTHDEKGEERYICWYCWRTFRYPNSLKAHLRFHCVFSGGGGGAFLHHEHAARQGAVPAADGLGLSPKPPAPDFAAPSQAGTLRPHPLGPPPVQACGAREGIKREASSAPSATSPTPGKWGQP
PRDM14	Q9GZV8	HR7923A.003	Rutgers	18726.03	6.0144	SET	pass	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMDKDSLQLPEGLCLMQTVFGEVPHFGVFCSSFIAKGVRFGPFQGKVVNASEVKTYGDNSVMWEIFEDGHLSHFIDGKGGTGNWMSYVNCARFPKEQNLVAVQCQGHIFYESCKEIHQNQELLVWYGDCYEK

HGCN	Uniprot ID	Antigen ID	Antigen Source	MW (Da)	pI	Common Domain Names	Primary Validation (pass/fail)	construct seq (with tag)
PRDM16	Q9HAZ2	HR8160A.001	Rutgers	19794.34	4.6379	SET	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMVYIPEDIPIPADFELRESSIPGAGLGV WAKRKMEAGERLGPCVVVPRAAAEETDFGWEQILTDVEVSPQKGYITKISEDLGSEKF CVDANQAGAGSWLKYIRVACSCDDQNLTMCQISEQIYYKVIKDIEPGEELLVHVKEGV
PRDM2	Q13029	PRDM2A-A001	SGC	20116.77	6.7207	SET	fail	MHHHHHHHHHHSSGVDLGTENLYFQSMNQNTTEPVAATETLAEVPEHVLRGLPEEVR LFPSAVDKTRIGVWATKPILKGKKFGPFVGDKKKRSQVKNNVYMWEVYYPNLGWMCID ATDPEKGNWLRYVNWACSGEEQNLFPLEINRAIYYKTLKPIAPGEELLVWYNGEDNPEI
PRDM4	Q9UKN5	PRDM4-A003	SGC	22659.44	6.1739	SET	pass	MHHHHHHHHHHHDLGTENLYFQSMEHGPVTFVPDTPIESRARLSLPKQLVLRQSIVGAE VGVWTGETIPVRTCFGPLIGQQSHSMEVAEWTDKAVNHIWKIYHNGVLEFCIITTDENE CNWMMFVRKARNREEQNLVAYPHDGKIFFCTSQDIPPENELLFYYSRDYAQQIGVPES SKGGYGLNDIFEAQKIEWHE
PRDM4	Q9UKN5	PRDM4A-A001	SGC	20268.85	6.327	SET	fail	MHHHHHHHHHHHDLGTENLYFQSMEHGPVTFVPDTPIESRARLSLPKQLVLRQSIVGAE VGVWTGETIPVRTCFGPLIGQQSHSMEVAEWTDKAVNHIWKIYHNGVLEFCIITTDENE CNWMMFVRKARNREEQNLVAYPHDGKIFFCTSQDIPPENELLFYYSRDYAQQIGVPE
PRDM5	Q9NQX1	PRDM5-A002	SGC	31198.88	5.9525	SET	pass	MHHHHHHHHHHHDLGTENLYFQSMLGMYVPDRFSLKSSRVQDGMGLYTARRVRKGEK FGPFAGEKRMPEDLDENMDYRLMWEVRGSKGEVLYILDATNPRHSNWLRFVHEAPSQ EQKNLAAIQEGENIFYLAVEDIETDTELLIGYLDSDMEAEEEEQQIMTVIKEGEVENSRR QSTAGRKDRLGCKEDYACPQCESSFTSEDILAEHLQTLHQKPTEEKEFKCKNCGKKFP VKQALQRHVLQCTAKSSSSKGGYGLNDIFEAQKIEWHE
PRDM8	Q9NQV8	HR8098A.001	Rutgers	12184.78	8.6741	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMAQNWCAKCNASFRMTSDLVYHMRS HHKKEYAMEPLVKRRREEKLKCPICNESFRERHHLSRHMTSHN
PRDM9	Q9NQV7	PRDM9-A003	SGC	27070.11	6.0931	SET	pass	MHHHHHHHHHHHDLGTENLYFQSMSEPQDDDYLYCEMCQNFFIDSCAAHGPPTFVKDS AVDKGHPNRSALSLPPGLRIGPSGIPQAGLGVWNEASDLPLGLHFGPYEGRITEDEEA ANNGYSWLITKGRNCYEYVDGKDKSWANWMRYVNCARDDEEQNLVAFQYHRQIFYR TCRVIRPGCELLVWYGDEYGQELGIKWGSKWKKELMAGREPKPSSKGGYGLNDIFEA QKIEWHE
PRMT3	O60678	PRMT3A-001	SGC	39075.85	6.8397	Misc	pass	MHHHHHHHHHHHDLGTENLYFQSMDLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYR DFIYQNPHIFKDKVVLDVGCGTGILSMFAAKAGAKKVLGVDQSEILYQAMDIIRLNKLEDT ITLIKGKIEEVHLPVEKVDVIISEWMGYFLLFESMLDSVLYAKNKYLAKGGSVYPDICTISL VAVSDVNKHADRIAFWDDVYGFKMSCMKKAVIPEAVVEVLDPKTLISEPCGIKHIDCHTT SISDLEFSSDFTLKITRTSMCTAIAGYFDIYFEKNCHNRVVFSTGPQSTKTHWKQTVFLL EKPFSVKAGEALKGKVTVHKSKKDPRSLTVTLTLNNSTQTYGLQ
PRMT5	O14744	SKB1-A003	SGC	47729.67	5.748	Misc	pass	MHHHHHHHHHHHDLGTENLYFQSMTNHHSEKEFCSYLQYLEYLSQNRPPPNAYELFAK GYEDYLQSPLQPLMDNLESQTYEVFEKDPIKYSQYQQAIYKCLLDRVPEEEKDTNVQV LMVLGAGRGPLVNASLRAAKQADRRIKLYAVEKNPNAVVTLENWQFEEWGSQVTVVSS DMREWVAPEKADIIVSELLGSFADNELSPECLDGAQHFLKDDGVSIPGEYTSFLAPISSS KLYNEVRACREKDRDPEAQFEMPYVVRLHNFHQLSAPQPCFTFSHPNRDPMIDNNRY CTLEFPVEVNTVLHGFAGYFETVLYQDITLSIRPETHSPGMFSWFPILFPIKQPITVREGQ TICVRFWRCSNSKKVWYEWAVTAPVCSAIHNPTGRSYTIGLSSKGGYGLNDIFEAQKIE WHE
PRRX2	Q99811	HR7233A.003	Rutgers	12965.6	11.4411	Homeobox	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGSAAKRKKKQRRNRTTTFNSSQLQAL ERVFERTHYPDAFVREELARRVNLSEARVQVWFQNRRAKFRRNERAMLA
PSIP1	O75475	PSIP1-A001	SGC	14622.3	8.5438	PWWP	pass	MSGLNDIFEAQKIEWHEGSAGGSGDFKPGDLIFAKMKGYPHWPARVDEVPDGAVKPP TNKLPIFFFGTHETAFLGPKDIFPYSENKEKYGKPNKRKGFNEGLWEIDNNPKVKFSSQ QAATKQGGSGHHHHHH
RARA	P10276	Rara	RAN	8183.56	9.411	Zinc Finger	pass	MKIEEHHHHHHSSGKLGSTEDLYFQSAAQPAKPCFVCQDKSSGYHYGVSACEGCKGF FRRSIQKNMVYTCHRDKNCIINKVTRNRCQYCRLQKCFEVGMSK
RARG	P13631	HR7515B.002	Rutgers	31861.86	5.5634	Hormone Receptor	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMDSYELSPQLEELITKVSKAHQETFPSL CQLGKYTTNSSADHRVQLDLGLWDKFSELATKCIIKIVEFAKRLPGFTGLSIADQITLLKA ACLDILMLRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFAFAGQLLPLEMD DTETGLLSAICLICGDRMDLEEPEKVDKLQEPLLEALRLYARRRRPSQPYMFPRMLMKI TDLRGISTKGAERAITLKMEIPGPMPPLIREMLENPEMFE
RARG	P13631	HR7515A.007	Rutgers	13689.58	8.9784	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMRVYKPCFVCNDKSSGYHYGVSSCEG CKGFFRRSIQKNMVYTCHRDKNCIINKVTRNRCQYCRLQKCFEVGMSKEAVRNDRNK
RARG	P13631	Rarg	RAN	8185.54	9.411	Zinc Finger	pass	MKIEEHHHHHHSSGKLGSTEDLYFQSAAQPAKPCFVCNDKSSGYHYGVSSCEGCKGF FRRSIQKNMVYTCHRDKNCIINKVTRNRCQYCRLQKCFEVGMSK
RAX2	Q96IS3	HR8168A.004	Rutgers	11910.33	10.0991	Homeobox	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKKKHRRNRTTTFTTYQLHQLERAFEAS HYPDVYSREELAAKVHLPEVRVQVWFQNRRAKWRRQE
RBAK	Q9NYW8	HR7540C.003	Rutgers	9812.85	7.7488	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMCNECGKVFSQKSYLTVHYRTHSGEK PYECNECGKKFHHRSAFNSHQRIH
RBBP5	Q15291	RBBP5-A002	SGC	62474.02	4.891	WD40	pass	MSGLNDIFEAQKIEWHEGSAGGSGNLELLESFGQQNYPEEADGTLDCISMALTCTFNRW GTLLAVGCNDGRIVIWDFLTRGIAKIISAHIHPVCSLCWSRDGHKLVSASTDNIVSQWDV LSGDCDQRFRFPSPILKVQYHPRDQNKVLVCPMKSAPVMLTLSDSKHVVLPVDDDSDL NVVASFDRRGEYIYTGNAKGKILVLKTDSQDLVASFRVTTGTSNTTAIKSIEFARKGSCFL INTADRIIRVYDGREILTCGRDGEPEPMQKLQDLVNRTPWKKCCFSGDGEYIVAGSARQ HALYIWEKSIGNLVKILHGTRGELLLDVAWHPVRPIIASISSGVVSIWAQNQVENWSAFAP DFKELDENVEYEERESEFDIEDEDKSEPEQTGADAAEDEEVDVTSVDPIAAFCSSDEEL EDSKALLYLPIAPEVEDPEENPYGPPPDAVQTSLMDEGASSEKKRQSSADGSQPPKKK PKTTNIELQGVPNDEVHPLLGVKGDGKSKKKQAGRPKGSKGKEKDSPFKPKLYKGDR GLPLEGSAKGKVQAELSQPLTAGGAISELLGGSGHHHHHH
RLF	Q13129	HR7201C.001	Rutgers	11782.28	7.4327	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMLDMKNRREKCTYCRRHFMSAFHLRE HEQVHCGPQPYMCVSIDCYARFGSVNELLNHKQKHDDLR
RNMT	O43148	RNMT-A001	SGC	40118.74	7.3703	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGSQSRIFYLRNFNNWMKSVLIGEFLEKVRQKKKRD ITVLDLGCGKGGDLLKWKKGRINKLVCTDIADVSVKQCQQRYEDMKNRRDSEYIFSAEF ITADSSKELLIDKFRDPQMCFDICSCQFVCHYSFESYEQADMMLRNACERLSPGGYFIG TTPNSFELIRRLEASETESFGNEIYTVKFQKKGDYPLFGCKYDFNLEGVVDVPEFLVYFP LLNEMAKKYNMKLVYKKTFLEFYEEKIKNNENKMLLKRMQALEPYPANESSKLVSEKVD DYEHAAKYMKNSQVRLPLGTLSKSEWEATSIYLVFAFEKQQGGSGHHHHHH
RORA	P35398	Rora	RAN	7900.18	9.5608	Zinc Finger	pass	MKIEEHHHHHHSSGKLGSTEDLYFQSAAQPAIPCKICGDKSSGIHYGVITCEGCKGFFR RSQQSNATYSCPRQKNCLIDRTSRNRCQHCRLQKCLAVGMSR
RPRD1A	Q96P16	RPRD1A-A001	SGC	39041.07	7.0724	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGSAFSEAALEKKLSELSNSQQSVQTLSLWLIHHRK HSRPIVTVWERELRKAKPNRKLTFLYLANDVIQNSKRKGPEFTKDFAPVIVEAFKHVSSE TDESCKKHLGRVLSIWEERSVYENDVLEQLKQALYGDKKPRKRTYEQIKVDENENCSS LGSPSEPPQTLDLVRALQDLENAASGDAAVHQRIASLPVEVQEVSLLDKITDKESGERL SKMVEDACMLLADYNGRLAAEIDDRKQLTRMLADFLRCQKEALAEKEHKLEEYKRKLA RVSLVRKELRSRIQSLPDLSRLPNVTGSHMHLPFAGDIYSEDGGSGHHHHHH
RREB1	Q92766	HR7006B.006	Rutgers	21010.37	7.6823	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMTSSSPAGLEGSDLSSINTMMSAVMSV GKVTENGGSPQGIKSPSKPPGPNRIGRRNQETKEEKSSYNCPLCEKICTTQHQLTMHI RQHNTDTGGADHSCSICGKSLSSASSLDRHMLVHSGERPYKCTVCGQSFTTNGNMH RHMKIHEKDPNSATATAPP
SALL4	Q9UJQ4	HR6875A.001	Rutgers	10684.08	8.6743	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMEAALYKHKCKYCSKVFGTDSSLQIHL RSHTGERPFVCSVCGHRFTTKGNLKVHFHRHP
SCAND1	P57086	HR9601.006	Rutgers	22952.82	7.2992	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMAATEPILAATGSPAAVPPEKLEGAGSS SAPERNCVGSSLPEASPPAPEPSSPNAAVPEAIPTPRAAASAALELPLGPAPVSVAPQA EAEARSTPGPAGSRLGPETFRQRFRQFRYQDAAGPREAFRQLRELSRQWLRPDIRTK EQIVEMLVQEQLLAILPEAARARRIRRRTDVRITG
SCMH1	Q96GD3	SCMH1-A002	SGC	27350.97	7.4878	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGHFTWDKYLKETCSVPAPVHCFKQSYTPPSNEFKI SMKLEAQDPRNTTSTCIATVVGLTGARLRLRLDGSDNKNDFWRLVDSAEIQPIGNCEKN GGMLQPPLGFRLNASSWPMFLLKTLNGAEMAPIRIFHKEPPSPSHNFFKMGMKLEAVD RKNPHFICPATIGEVRGSEVLVTFDGWRGAFDYWCRFDSRDIFPVGWCSLTGDNLQPP GTKGGSGHHHHHH
SCML2	Q9UQR0	SCML2-A003	SGC	29946.67	6.3061	Misc	pass	MHHHHHHHHHHHDLGTENLYFQSMSSTSSVQRDDFHWEEYLKETGSISAPSECFRQS QIPPVNDFKVGMKLEARDPRNATSVCIATVIGITGARLRLRLDGSDNRNDFWRLVDSPDI QPVGTCEKEGDLLQPPLGYQMNTSSWPMFLLKTLNGSEMASATLFKKEPPKPPLNNF KVGMKLEAIDKKNPYLICPATIGDVKGDEVHITFDGWSGAFDYWCKYDSRDIFPAGWCR LTGDVLQPPGTSSSKGGYGLNDIFEAQKIEWHE

HGCN	Uniprot ID	Antigen ID	Antigen Source	MW (Da)	pI	Common Domain Names	Primary Validation (pass/fail)	construct seq (with tag)
SCML2	Q9UQR0	SCML2-A006	SGC	42497.12	8.8286	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGGQTVNEDSMDVKKENQEKTPQSSTSSVQRDDF HWEEYLKETGSISAPSECFRQSQIPPVNDFKVGMKLEARDPRNATSVCIATVIGITGARL RLRLDGSDNRNDFWRLVDSPDIQPVGTCEKEGDLLQPPLGYQMNTSSWPMFLLKTLN GSEMASATLFKKEPPKPPLNNFKVGMKLEAIDKKNPYLICPATIGDVKGDEVHITFDGWS GAFDYWCKYDSRDIFPAGWCRLTGDVLQPPGTSVPIVKNIAKTESSPSEASQHSMQSP QKTTLILPTQQVRRSSRIKPPGPTAVPKRSSSVKNITPRKKGPNSGKKEKPLPVICSTSA ASLKSLTRDRGMLYKDVASGPCKIVMSGGSGHHHHHH
SCML2	Q9UQR0	SCML2-A005	SGC	41769.94	7.2696	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGMSTVCVYVNKHGNFGPHLDPKRIQQLPDHFGPG PVNVVLRRIVQACVDCALETKTVFGYLKPDNRGGEVITASFDGETHSIQLPPVNSASFAL RFLENFCHSLQCDNLLSSQPFSSSRGHTHSSAEHDKNQSAKEDVTERQSTKRSPQQT VPYVVPLSPKLPKTKEYASEGEPLFAGGSAIPKEENLSEDSKSSSLNSGNYLNPACRNP MYIHTSVSQDFSRSVPGTTSSPLVGDISPKSSPHEVKFQMQRKSEAPSYIAVPDPSVLK QGFSKDPSTWSVDEVIQFMKHTDPQISGPLADLFRQHEIDGKALFLLKSDVMMKYMGL KLGPALKLCYYIEKLKEGKYSGGSGHHHHHH
SETD1A	O15047	SETD1A-A003	SGC	28711.41	9.4103	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGMDQEGGGDGQKAPSFQWRNYKLIVDPALDPALR RPSQKVYRYDGVHFSVNDSKYIPVEDLQDPRCHVRSKNRDFSLPVPKFKLDEFYIGQIP LKEVTFARLNDNVRETFLKDMCRKYGEVEEVEILLHPRTRKHLGLARVLFTSTRGAKET VKNLHLTSVMGNIIHAQLDIKGQQRMKYYELIVNGSYTPQTVPTGGKALSEKFQGSGAA TETAESRRRSGGGSHHHHHH
SETD1A	O15047	SETD1A-A005	SGC	16771.02	8.1746	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGKLDEFYIGQIPLKEVTFARLNDNVRETFLKDMCRK YGEVEEVEILLHPRTRKHLGLARVLFTSTRGAKETVKNLHLTSVMGNIIHAQLDIKGQQR MKYYELIVNGSYTPQTVPTGGGGSGHHHHHH
SETD2	Q9BYW2	SETD2-A001	SGC	47153.07	8.1584	SET	pass	MHHHHHHHHHHHDLGTENLYFQSMSHFSDQSDKFLLSLQKDKGSVQAPEISSNSIKDTL AVNEKKDFSKNLEKNDIKDRGPLKKRRQEIESDSESDGELQDRKKVRVEVEQGETSVP PGSALVGPSCVMDDFRDPQRWKECAKQGKMPCYFDLIEENVYLTERKKNKSHRDIKR MQCECTPLSKDERAQGEIACGEDCLNRLLMIECSSRCPNGDYCSNRRFQRKQHADVE VILTEKKGWGLRAAKDLPSNTFVLEYCGEVLDHKEFKARVKEYARNKNIHYYFMALKND EIIDATQKGNCSRFMNHSCEPNCETQKWTVNGQLRVGFFTTKLVPSGSELTFDYQFQR YGKEAQKCFCGSANCRGYLGGENRVSIRAAGGKMKKERSRKSSKGGYGLNDIFEAQK IEWHE
SETD3	Q86TU7	SETD3-A002	SGC	62223.61	6.7862	SET	pass	MHHHHHHHHHHHDLGTENLYFQSMGKKSRVKTQKSGTGATATVSPKEILNLTSELLQKC SSPAPGPGKEWEEYVQIRTLVEKIRKKQKGLSVTFDGKREDYFPDLMKWASENGASVE GFEMVNFKEEGFGLRATRDIKAEELFLWVPRKLLMTVESAKNSVLGPLYSQDRILQAMG NIALAFHLLCERASPNSFWQPYIQTLPSEYDTPLYFEEDEVRYLQSTQAIHDVFSQYKNT ARQYAYFYKVIQTHPHANKLPLKDSFTYEDYRWAVSSVMTRQNQIPTEDGSRVTLALIP LWDMCNHTNGLITTGYNLEDDRCECVALQDFRAGEQIYIFYGTRSNAEFVIHSGFFFDN NSHDRVKIKLGVSKSDRLYAMKAEVLARAGIPTSSVFALHFTEPPISAQLLAFLRVFCMT EEELKEHLLGDSAIDRIFTLGNSEFPVSWDNEVKLWTFLEDRASLLLKTYKTTIEEDKSV LKNHDLSVRAKMAIKLRLGEKEILEKAVKSAAVNREYYRQQMEEKAPSSKGGYGLNDIF EAQKIEWHE
SETD7	Q8WTS6	SETD7-A002	SGC	45882.37	4.5247	SET	pass	MHHHHHHHHHHHDLGTENLYFQSMDSDDEMVEEAVEGHLDDDGLPHGFCTVTYSSTD RFEGNFVHGEKNGRGKFFFFDGSTLEGYYVDDALQGQGVYTYEDGGVLQGTYVDGE LNGPAQEYDTDGRLIFKGQYKDNIRHGVCWIYYPDGGSLVGEVNEDGEMTGEKIAYVY PDERTALYGKFIDGEMIEGKLATLMSTEEGRPHFELMPGNSVYHFDKSTSSCISTNALLP DPYESERVYVAESLISSAGEGLFSKVAVGPNTVMSFYNGVRITHQEVDSRDWALNGNT LSLDEETVIDVPEPYNHVSKYCASLGHKANHSFTPNCIYDMFVHPRFGPIKCIRTLRAVE ADEELTVAYGYDHSPPGKSGPEAPEWYQVELKAFQATQQKSSKGGYGLNDIFEAQKIE WHE
SETD8	Q9NQR1-2	SETD8-A002	SGC	22681.37	7.1331	SET	pass	MSGLNDIFEAQKIEWHEGSAGGSGPVRRSSRKSKAELQSEERKRIDELIESGKEEGMKI DLIDGKGRGVIATKQFSRGDFVVEYHGDLIEITDAKKREALYAQDPSTGCYMYYFQYLS KTYCVDATRETNRLGRLINHSKCGNCQTKLHDIDGVRHLILIASRDIAAGEELLYDYGDR SKASIEAHPWLKHGGGSHHHHHH
SETDB1	Q15047	SETDB1-A001	SGC	17471.57	4.1727	SET	pass	MSGLNDIFEAQKIEWHEGSAGGSGTNRLVQHGLQVRLQLFKTQNKGWGIRCLDDIAKG SFVCIYAGKILTDDFADKEGLEMGDEYFANLDHIESVENFKEGYESDAPCSSDSSGVDL KDQEDGNSGTEDPEESNDDSSDDNFCKDEDFSTGGSGHHHHHH
SETDB1	Q15047	SETDB1-A003	SGC	27552.51	9.315	SET	pass	MSGLNDIFEAQKIEWHEGSAGGSGDLIVSMRILGKKRTKTWHKGTLIAIQTVGPGKKYK VKFDNKGKSLLSGNHIAYDYHPPADKLYVGSRVVAKYKDGNQVWLYAGIVAETPNVKNK LRFLIFFDDGYASYVTQSELYPICRPLKKTWEDIEDISCRDFIEEYVTAYPNRPMVLLKSG QLIKTEWEGTWWKSRVEEVDGSLVRILFLDDKRCEWIYRGSTRLEPMFSMKTGGSGH HHHHH
SETDB2	Q96T68	SETDB2-A001	SGC	29809.88	6.086	SET	fail	MSGLNDIFEAQKIEWHEGSAGGSGDENGRDENTMKNIFSKKRKLEVACSDCEVEVLPL GLETHPRTAKTEKCPPKFSNNPKELTMETKYDNISRIQYHSVIRDPESKTAIFQHNGKKM EFVSSESVTPEDNDGFKPPREHLNSKTKGAQKDSSSNHVDEFEDNLLIESDVIDITKYR EETPPRSRCNQATTLDNQNIKKAIEVQIQKPQEGRSTACQRQQVFCDEELLSETKNTSS DSLTKFNKGNVFLLDATKEGGSGHHHHHH
SETMAR	Q53H47	SETMAR-A003	SGC	37473.1	6.8676	Misc	pass	MHHHHHHHHHHHDLGTENLYFQSMSEVDNDQLRAIIEADPLTTTREVAEELNVNHSTVV RHLKQIGKVKKLDKWVPHELTENQKNRRFEVSSSLILRNHNEPFLDRIVTCDEKWILYD NRRRSAQWLDQEEAPKHFPKPILHPKKVMVTIWWSAAGLIHYSFLNPGETITSEKYAQE IDEMNQKLQRLQLALVNRKGPILLHDNARPHVAQPTLQKLNELGYEVLPHPPYSPDLLP TNYHVFKHLNNFLQGKRFHNQQDAENAFQEFVESQSTDFYATGINQLISRWQKCVDCN GSYFDSSKGGYGLNDIFEAQKIEWHE
SETMAR	Q53H47	SETMAR-A002	SGC	37473.1	6.8676	Misc	pass	MHHHHHHHHHHHDLGTENLYFQSMSEVDNDQLRAIIEADPLTTTREVAEELNVNHSTVV RHLKQIGKVKKLDKWVPHELTENQKNRRFEVSSSLILRNHNEPFLDRIVTCDEKWILYD NRRRSAQWLDQEEAPKHFPKPILHPKKVMVTIWWSAAGLIHYSFLNPGETITSEKYAQE IDEMNQKLQRLQLALVNRKGPILLHDNARPHVAQPTLQKLNELGYEVLPHPPYSPDLLP TNYHVFKHLNNFLQGKRFHNQQDAENAFQEFVESQSTDFYATGINQLISRWQKCVDCN GSYFDSSKGGYGLNDIFEAQKIEWHE
SETMAR	Q53H47	SETMAR-A005	SGC	35632.95	6.8482	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGSEVDNDQLRAIIEADPLTTTREVAEELNVNHSTVV RHLKQIGKVKKLDKWVPHELTENQKNRRFEVSSSLILRNHNEPFLDRIVTCDEKWILYD NRRRSAQWLDQEEAPKHFPKPILHPKKVMVTIWWSAAGLIHYSFLNPGETITSEKYAQE IDEMNQKLQRLQLALVNRKGPILLHDNARPHVAQPTLQKLNELGYEVLPHPPYSPDLLP TNYHVFKHLNNFLQGKRFHNQQDAENAFQEFVESQSTDFYATGINQLISRWQKCVDCN GSYFDGGSGHHHHHH
SFMBT1	Q9UHJ3	SFMBT1-A003	SGC			NA	pass	
SFMBT2	Q5VUG0	SFMBT2A-A001	SGC	57882.56	5.6317	Misc	pass	MHHHHHHHHHHHSSGVDLGTENLYFQSMMESTLSASNMQDPSSSPLEKCLGSANGNG DLDSEEGSSLEETGFNWGEYLEETGASAAPHTSFKHVEISIQSNFQPGMKLEVANKNN PDTYWVATIITTCGQLLLLRYCGYGEDRRADFWCDVVIADLHPVGWCTQNNKVLMPPD AIKEKYTDWTEFLIRDLTGSRTAPANLLEGPLRGKGPIDLITVGSLIELQDSQNPFQYWIV SVIENVGGRLRLRYVGLEDTESYDQWLFYLDYRLRPVGWCQENKYRMDPPSEIYPLK MASEWKCTLEKSLIDAAKFPLPMEVFKDHADLRSHFFTVGMKLETVNMCEPFYISPASV TKVFNNHFFQVTIDDLRPEPSKLSMLCHADSLGILPVQWCLKNGVSLTPPKGYSGQDF DWADYHKQHGAQEAPPFCFRNTSFSRGFTKNMKLEAVNPRNPGELCVASVVSVKGRL MWLHLEGLQTPVPEVIVDVESMDIFPVGWCEANSYPLTAPHKTVSQKK
SHARPIN	Q9H0F6	HT88B.001	Rutgers	37956.68	5.8238	Misc	pass	MHHHHHHEFMSGLNDIFEAQKIEWHEGSAGGSGENLYFQGMAPPAGGAAAAASDLG SAAVLLAVHAAVRPLGAGPDAEAQLRRLQLSADPERPGRFRLELLGAGPGAVNLEWPL ESVSYTIRGPTQHELQPPPGGPGTLSLHFLNPQEAQRWAVLVRGATVEGQNGSKSNS PPALGPEACPVSLPSPPEASTLKGPPPEADLPRSPGNLTEREELAGSLARAIAGGDEKG AAQVAAVLAQHRVALSVQLQEACFPPGPIRLQVTLEDAASAASAASSAHVALQVHPHCT VAALQEQVFSELGFPPAVQRWVIGRCLCVPERSLASYGVRQDGDPAFLYLLSAPREAP ATGPSPQHPQKMDGELG
SHPRH	Q149N8	HR6933A.001	Rutgers	12590.44	7.0749	PHD	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMTSDYRFECICGELDQIDRKPRVQCLK CHLWQHAKCVNYDEKNLKIKPFYCPHCLVAMEPVSTRATLIISPSSIC
SIRT1	Q96EB6	SIRT1-A003	SGC	60829.94	5.2982	SIR2	pass	MSGLNDIFEAQKIEWHEGSAGGSGGFHSCESDEEDRASHASSSDWTPRPRIGPYTFV QQHLMIGTDPRTILKDLLPETIPPPELDDMTLWQIVINILSEPPKRKKRKDINTIEDAVKLL QECKKIIVLTGAGVSVSCGIPDFRSRDGIYARLAVDFPDLPDPQAMFDIEYFRKDPRPFF KFAKEIYPGQFQPSLCHKFIALSDKEGKLLRNYTQNIDTLEQVAGIQRIIQCHGSFATASC LICKYKVDCEAVRGDIFNQVVPRCPRCPADEPLAIMKPEIVFFGENLPEQFHRAMKYDK DEVDLLIVIGSSLKVRPVALIPSSIPHEVPQILINREPLPHLHFDVELLGDCDVIINELCHRL GGEYAKLCCNPVKLSEITEKPPRTQKELAYLSELPPTPLHVSEDSSSPERTSPPDSSVIV TLLDQAAKSNDDLDVSESKGCMEEKPQEVQTSRNVESIAEQMENPDLKNVGSSTGEK NERTSVAGTVRKCWPNRVAKEQISRRLDGNQYLFLPPNRYIFHGAEVYSDSEDDGGS GHHHHHH

HGCN	Uniprot ID	Antigen ID	Antigen Source	MW (Da)	pI	Common Domain Names	Primary Validation (pass/fail)	construct seq (with tag)
SIRT5	Q9NXA8	SIRT5-A001	SGC	32694.96	7.7159	SIR2	pass	MSGLNDIFEAQKIEWHEGSAGGSGARPSSSMADFRKFFAKAKHIVIISGAGVSAESGVPTFRGAGGYWRKWQAQDLATPLAFAHNPSRVWEFYHYRREVMGSKEPNAGHRAIAECETRLGKQGRRVVVITQNIDELHRKAGTKNLLEIHGSLFKTRCTSCGVVAENYKSPICPALSGKGAPEPGTQDASIPVEKLPRCEEAGCGGLLRPHVVWFGENLDPAILEEVDRELAHCDLCLVVGTSSVVYPAAMFAPQVAARGVPVAEFNTETTPATNRFRFHFQGPCGTTLPEALAGGSGHHHHHH
SIRT6	Q8N6T7	SIRT6-A001	SGC	42440.26	8.9786	SIR2	pass	MSGLNDIFEAQKIEWHEGSAGGSGSVNYAAGLSPYADKGKCGLPEIFDPPEELERKVWELARLVWQSSSVVFHTGAGISTASGIPDFRGPHGVWTMEERGLAPKFDTTFESARPTQTHMALVQLERVGLLRFLVSQNVDGLHVRSGFPRDKLAELHGNMFVEECAKCKTQYVRDTVVGTMGLKATGRLCTVAKARGLRACRGELRDTILDWEDSLPDRDLALADEASRNADLSITLGTSLQIRPSGNLPLATKRRGGRLVIVNLQPTKHDRHADLRIHGYVDEVMTRLMKHLGLEIPAWDGPRVLERALPPLPRPPTPKLEPKEESPTRINGSIPAGPKQEPCAQHNGSEPASPKRERPTSPAPHRPPKRVKAKAVPSGGSGHHHHHH
SIRT7	Q9NRC8	SIRT7-A001	SGC	44741.7	9.415	SIR2	pass	MSGLNDIFEAQKIEWHEGSAGGSGAAGGLSRSERKAAERVRRLREEQQRERLRQVSRILRKAAAERSAEEGRLLAESADLVTELQGRSRRREGLKRRQEEVCDDPEELRGKVRELASAVRNAKYLVVYTGAGISTAASIPDYRGPNGVWTLLQKGRSVSAADLSEAEPTLTHMSITRLHEQKLVQHVVSQNCDGLHLRSGLPRTAISELHGNMYIEVCTSCVPNREYVRVFDVTERTALHRHQTGRTCHKCGTQLRDTIVHFGERGTLGQPLNWEAATEAASRADTILCLGSSLKVLKKYPRLWCMTKPPSRRPKLYIVNLQWTPKDDWAALKLHGKCDDVMRLLMAELGLEIPAYSRWQDPIFSLATPLRAGEEGSHSRKSLCRSREEAGGSGHHHHHH
SIX3	O95343	HR7143A.009	Rutgers	12994.52	10.1819	Homeobox	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMDGEQKTHCFKERTRSLLREWYLQDPYPNPSKKRELAQATGLTPTQVGNWFKNRRQRDRAAAAKNRLQHQAIGPSGMR
SIX3	O95343	HR7143A.010	Rutgers	12994.52	10.1819	Homeobox	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMDGEQKTHCFKERTRSLLREWYLQDPYPNPSKKRELAQATGLTPTQVGNWFKNRRQRDRAAAAKNRLQHQAIGPSGMR
SIX3	O95343	HR7143A.003	Rutgers	12994.52	10.1819	Homeobox	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMDGEQKTHCFKERTRSLLREWYLQDPYPNPSKKRELAQATGLTPTQVGNWFKNRRQRDRAAAAKNRLQHQAIGPSGMR
SIX3	O95343	Six3	RAN	6931.82	10.9776	Homeobox	pass	MKIEEHHHHHHSSGKLGSTEDLYFQSAAQPAEQKTHCFKERTRSLLREWYLQDPYPNPSKKRELAQATGLTPTQVGNWFKNRRQRDRA
SIX6	O95475	HR8072A.001	Rutgers	12565.02	9.9349	Homeobox	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMIWDGEQKTHCFKERTRHLLREWYLQDPYPNPSKKRELAQATGLTPTQVGNWFKNRRQRDRAAAAKNRLQQQ
SKOR2	Q2VWA4	HR8491C.001	Rutgers	16218.37	5.4132	Misc	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMDNFAFDVIITDSSDPMGPAESLFKESYYQLMKTALKEDGVLCCQGECQWLHLDLIKEMRQFCQSLFPVVAYAYCTIPTYPSGQIGFMLCSKNPSTNFQEPVQPQARTV
SMAD2	Q15796	HR4670B.006	Rutgers	21140.72	6.2895	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMTGRLDELEKAITTQNCNTKCVTIPSTCSEIWGLSTPNTIDQWDTTGLYSFSEQTRSLDGRLQVSHRKGLPHVIYCRLWRWPDLHSHHELKAIENCEYAFNLKKDEVCVNPYHYQRVETPVLPPVLVPRHTEILTELPPLDDYTHSIPE
SMARCA1	P28370	SNF2L-A001	SGC	39902.28	9.1407	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGKRERKANYAVDAYFREALRVSEPKIPKAPRPPKQPNVQDFQFFPPRLFELLEKEILYYRKTIGYKVPRNPDIPNPALAQREEQKKIDGAEPLTPEETEEKEKLLTQGFTNWTKRDFNQFIKANEKYGRDDIDNIAREVEGKSPEEVMEYSAVFWERCNELQDIEKIMAQIERGEARIQRRISIKKALDAKIARYKAPFHQLRIQYGTSKGKNYTEEEDRFLICMLHKMGFDRENVYEELRQCVRNAPQFRFDWFIKSRTAMEFQRRCNTLISLIEKENMEIEERERAEKKKRATKTPMVKFSAFSGGSGHHHHHH
SMARCA2	P51531	SMARCA2A-A001	SGC	22150.04	8.0338	Bromodomain	pass	MHHHHHHHHHHHDLGTENLYFQSMRRGRPPAEKLSPNPPKLTKQMNAIIDTVINYKDRCNVEKVPSNSQLEIEGNSSGRQLSEVFIQLPSRKELPEYYELIRKPVDFKKIKERIRNHKYRSLGDLEKDVMLLCHNAQTFNLEGSQIYEDSIVLQSVFKSARQKIAKEEESSKGGYGLNDIFEAQKIEWHE
SMARCA4	P51532	SMARCA4A-A001	SGC	20546.03	6.2242	Bromodomain	pass	MHHHHHHHHHHHDLGTENLYFQSMLSPNPPNLTKKMKKIVDAVIKYKDSSSGRQLSEVFIQLPSRKELPEYYELIRKPVDFKKIKERIRNHKYRSLNDLEKDVMLLCQNAQTFNLEGSLIYEDSIVLQSVFTSVRQKIEKEDDSEGEESEEEEESSKGGYGLNDIFEAQKIEWHE
SMARCA4	P51532	SMARCA4A-A005	SGC			NA	pass	
SMARCC1	Q92922	SMARCC1-A001	SGC	10164.97	5.093	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGSSSQDDEEWLRPVMRKEKQVLVHWGFYPDSYDTWVHSNDVDAEIEDPPIPEKPWKVGGSGHHHHHH
SMARCC2	Q8TAQ2	HR7400B.008	Rutgers	17884.1	6.7526	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMEQTHHIIIPSYAAWFDYNSVHAIERRALPEFFNGKNKSKTPEIYLAYRNFMIDTYRLNPQEYLTSTACRRNLAGDVCAIMRVHAFLEQWGLINYQVDAESRPTPMGPPPTSHFHVLADTP
SMARCC2	Q8TAQ2	SMARCC2-A001	SGC	15353.05	6.8823	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGEQTHHIIIPSYAAWFDYNSVHAIERRALPEFFNGKNKSKTPEIYLAYRNFMIDTYRLNPQEYLTSTACRRNLAGDVCAIMRVHAFLEQWGLINYQVDAESRGGSGHHHHHH
SMARCC2	Q8TAQ2	HR7400C.002	Rutgers	15087.05	7.1672	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMTHHIIIPSYAAWFDYNSVHAIERRALPEFFNGKNKSKTPEIYLAYRNFMIDTYRLNPQEYLTSTACRRNLAGDVCAIMRVHAFLEQWGLINYQV
SMARCE1	Q969G3	HR7811A.006	Rutgers	15698.68	6.8036	HMG Box	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGTNSRVTASSGITIPKPPKPPDKPLMPYMRYSRKVWDQVKASNPDLKLWEIGKIIGGMWRDLTDEEKQEYLNEYEAEKIEYNESMKAYHNSPAYLAYINAK
SMNDC1	O75940	SMNDC1-A001	SGC	26488.6	7.5097	Misc	fail	MSGLNDIFEAQKIEWHEGSAGGSGLKKDLQEVIELTKDLLSTQPSETLASSDSFASTQPTHSWKVGDKCMAVWSEDGQCYEAEIEEIDEENGTAAITFAGYGNAEVTPLLNLKPVEEGRKAKEDSGNKPMSKKEMIAQQREYKKKKALKKAQRIKELEQEREDQKVKWQQFNNRAYSKNKKGQVKRSIFASPESVTGKVGVGTCGIADKPMTQYQDTSKYNVRHLMPQGGSGHHHHHH
SMU1	Q2TAY7	SMU1-A001	SGC	60996.47	6.9777	WD40	pass	MSGLNDIFEAQKIEWHEGSAGGSGMSIEIESSDVIRLIMQYLKENSLHRALATLQEETTVSLNTVDSIESFVADINSGHWDTVLQAIQSLKLPDKTLIDLYEQVVLELIELRELGAARSLLRQTDPMIMLKQTQPERYIHLENLLARSYFDPREAYPDGSSKEKRRAAIAQALAGEVSVVPPSRLMALLGQALKWQQHQGLLPPGMTIDLFRGKAAVKDVEEEKFPTQLSRHIKFGQKSHVECARFSPDGQYLVTGSVDGFIEVWNFTTGKIRKDLKYQAQDNFMMMDDAVLCMCFSRDTEMLATGAQDGKIKVWKIQSGQCLRRFERAHSKGVTCLSFSKDSSQILSASFDQTIRIHGLKSGKTLKEFRGHSSFVNEATFTQDGHYIISASSDGTVKIWNMKTTECSNTFKSLGSTAGTDITVNSVILLPKNPEHFVVCNRSNTVVIMNMQGQIVRSFSSGKREGGDFVCCALSPRGEWIYCVGEDFVLYCFSTVTGKLERTLTVHEKDVIGIAHHPHQNLIATYSEDGLLKLWKPGGSGHHHHHH
SMURF1	Q9HCE7	SMURF1-A002	SGC	51692.83	6.6018	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGHHIMNHQCQLKEPSQPLPLPSEGSLEDEEELPAQRYERDLVQKLKVLRHELSLQQPQAGHCRIEVSREEIFEESYRQIMKMRPKDLKKRLMVKFRGEEGLDYGGVAREWLYLLCHEMLNPYYGLFQYSTDNIYMLQINPDSSINPDHLSYFHFVGRIMGLAVFHGHYINGGFTVPFYKQLLGKPIQLSDLESVDPELHKSLVWILENDITPVLDHTFCVEHNAFGRILQHELKPNGRNVPVTEENKKEYVRLYVNWRFMRGIEAQFLALQKGFNELIPQHLLKPFDQKELELIIGGLDKIDLNDWKSNTRLKHCVADSNIVRWFWQAVETFDEERRARLLQFVTGSTRVPLQGFKALQGSTGAAGPRLFTIHLIDANTDNLPKAHTCFNRIDIPPYESYEKLYEKLLTAVEETCGGGSGHHHHHH
SMYD2	Q9NRG4	SMYD2-A001	SGC	53081.52	6.6025	Zinc Finger	pass	MSGLNDIFEAQKIEWHEGSAGGSGRAEGLGGLERFCSPGKGRGLRALQPFQVGDLLFSCPAYAYVLTVNERGNHCEYCFTRKEGLSKCGRCKQAFYCNVECQKEDWPMHKLECSPMVVFGENWNPSETVRLTARILAKQKIHPERTPSEKLLAVKEFESHLDKLDNEKKDLIQSDIAALHHFYSKHLEFPDNDSLVVLFAQVNCNGFTIEDEELSHLGSAIFPDVALMNHSCCPNVIVTYKGTLAEVRAVQEIKPGEEVFTSYIDLLYPTEDRNDRLRDSYFFTCECQECTTKDKDKAKVEIRKLSDPPKAEAIRDMVRYARNVIEEFFRRAKHYKSPSELLEICELSQEKMSSVFEDSNVYMLHMMYQAMGVCLYMQDWEGALQYGQKIIKPYSKHYPLYSLNVASMWLKLGRLYMGLEHKAAGEKALKKAIAIMEVAHGKDHPYISEIKQEIESHGGSGHHHHHH
SMYD3	Q9H7B4	SMYD3-A003	SGC	54272.63	6.9005	Zinc Finger	pass	MHHHHHHHHHHHDLGTENLYFQSMEPLKVEKFATANRGNGLRAVTPLRPGELLFRSDPLAYTVCKGSRGVVCDRCLLGKEKLMRCSQCRVAKYCSAKCQKKAWPDHKRECKCLKSCKPRYPPDSVRLLGRVVFKLMDGAPSESEKLYSFYDLESNINKLTEDRKEGLRQLVMTFQHFMREEIQDASQLPPAFDLFEAFAKVICNSFTICNAEMQEVGVGLYPSISLLNHSCDPNCSIVFNGPHLLLRAVRDIEVGEELTICYLDMLMTSEERRKQLRDQYCFECDCFRCQTQDKDADMLTGDEQVWKEVQESLKKIEELKAHWKWEQVLAMCQAIISSNSERLPDINIYQLKVLDCAMDACINLGLLEEALFYGTRTMEPYRIFFPGSHPVRGVQVMKVGKLQLHQGMFPQAMKNLRLAFDIMRVTHGREHSLIEDLILLLEECDANIRASSSKGGYGLNDIFEAQKIEWHE
SMYD4	Q8IYR2	SMYD4-A001	SGC	25748.91	6.497	Misc	fail	MSGLNDIFEAQKIEWHEGSAGGSGLQPEDELFLKRLSKGYLVGKDSDAPLFYREEGNKKFQEKDYTGAAVLYSKGVSHSRPNTEDMSLCHANRSAALFHLGQYETCLKDINIAQTHGYPERLQPKIMLRKAECLVALGRLQEASQTISDLERNFTATPALADVLPQTLQRNLHRLKMKMQEKDSLTESFPAALAKTLEDAALREENEQLSNASSSIGLCVDPLGGSGHHHHHH

HGCN	Uniprot ID	Antigen ID	Antigen Source	MW (Da)	pI	Common Domain Names	Primary Validation (pass/fail)	construct seq (with tag)
SNAI2	O43623	HR7012B.004	Rutgers	23202.29	8.3477	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMSGSESPISDEEERLQSKLSDPHAIEAEKFQCNLCNKTYSTFSGLAKHKQLHCDAQSRKSFSCKYCDKEYVSLGALKMHIRTHTLPCVCKICGKAFSRPWLLQGHIRTHTGEKPFSCPHCNRAFADRSNLRAHLQTHSDVKKYQCKNCSKTFSRMSLLHKHEESGCCVAH
SOX12	O15370	HR7180A.002	Rutgers	13884.81	9.507	HMG Box	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGWCKTPSGHIKRPMNAFMVWSQHERRKIMDQWPDMHNAEISKRLGRRWQLLQDSEKIPFVREAERLRLKHMADYPDYKYR
SOX4	Q06945	HR8424A.001	Rutgers	14401.48	9.7249	HMG Box	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKADDPSWCKTPSGHIKRPMNAFMVWSQIERRKIMEQSPDMHNAEISKRLGKRWKLLKDSDKIPFIREAERLRLKHMADYPDYKYRP
SOX7	Q9BT81	Sox7	RAN	8312.65	10.5861	HMG Box	pass	MKIEEHHHHHHSSGKLGSTEDLYFQSAAQPAIRRPMNAFMVWAKDERKRLAVQNPDLHNAELSKMLGKSWKALTLSQKRPYVDEAERLRLQHMQDYPNYK
SOX8	P57073	HR7103A.002	Rutgers	12854.59	9.7731	HMG Box	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMVKRPMNAFMVWAQAARRKLADQYPHLHNAELSKTLGKLWRLLNESEKRPFVEEAERLRVQHKKDHPDYKYQPR
SOX8	P57073	Sox8	RAN	8280.58	10.6549	HMG Box	pass	MKIEEHHHHHHSSGKLGSTEDLYFQSAAQPAVKRPMNAFMVWAQAARRKLADQYPHLHNAELSKTLGKLWRLLSESEKRPFVEEAERLRVQHKKDHPDYK
SP1	P08047	HR4634D.004	Rutgers	25461.79	9.2097	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPDAQPQAGRRTRREACTCPYCKDSEGRGSGDPGKKKQHICHIQGCGKVYGKTSHLRAHLRWHTGERPFMCTWSYCGKRFTRSDELQRHKRTHTGEKKFACPECPKRFMRSDHLSKHIKTHQNKKGGPGVALSVGTLPLDSGAGSEGSGTATPSALITTNMVAMEAICPEGIARLANSGINVMQVADLQSINISGNGF
SP100	P23497	SP100-A001	SGC	25304.52	6.6693	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGVDPCPENSNICEVCNKWGRLFCCDTCPRSFHEHCHIPSVEANKNPWSCIFCRIKTIQERCPESQSGHQESEVLMRQMLPEEQLKCEFLLLKVYCDSKSCFFASEPYYNREGSQGPQKPMWLNKVKTSLNEQMYTRVEGFVQDMRLIFHNHKEFYREDKFTRLGIQVQDIFEKNFRNIFAIQETSGGSGHHHHHH
SP140	Q13342	SP140A-A002	SGC	26166.62	6.0945	PHD	pass	
SP2	Q02086	HR7855A.004	Rutgers	11007.48	9.4972	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKKHVCHIPDCGKTFRKTSLLRAHVRLHTGERPFVCNWFFCGKRFTRSDELQRHARTHTG
SP3	Q02447	HR4738B.004	Rutgers	23763.83	9.3665	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPNCKEGGGRGTNLGKKKQHICHIPGCGKVYGKTSHLRAHLRWHSGERPFVCNWMYCGKRFTRSDELQRHRRTHTGEKKFVCPECSKRFMRSDHLAKHIKTHQNKKGIHSSSTVLASVEAARDDTLITAGGTTLILANIQQGSVSGIGTVNTSATSNQDILTNTEIPLQLVTVSGNETME
SP4	Q02446	HR4504D.001	Rutgers	20285.89	9.1133	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPGKKKQHICHIEGCGKVYGKTSHLRAHLRWHTGERPFICNWMFCGKRFTRSDELQRHRRTHTGEKRFECPECSKRFMRSDHLSKHVKTHQNKKGGGTALAIVTSGELDSSVTEVLGSPRIVTVAAISQDSNPATPNVSTNMEEF
SP6	Q3SY56	HR7866A.003	Rutgers	12600.35	8.8733	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMCHIPGCGKAYAKTSHLKAHLRWHSGDRPFVCNWLFCGKRFTRSDELQRHLQTHTGTKKFPCAVCSRVFMRSDHL
SP7	Q8TDD2	HR7872A.003	Rutgers	11210.68	8.6875	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPIHSCHIPGCGKVYGKASHLKAHLRWHTGERPFVCNWLFCGKRFTRSDELERHVRTHTREK
SRRT	Q9BXP5	ARS2-A001	SGC	77706.14	5.3474	Misc	pass	MHHHHHHHHHHHDLGTENLYFQSMGSIAEIDLGVPPPVMKTFKEFLLSLDDSVDETEAVKRYNDYKLDFRRQQMQDFFLAHKDEEWFRSKYHPDEVGKRRQEARGALQNRLRVFLSLMETGWFDNLLLDIDKADAIVKMLDAAVIKMEGGTENDLRILEQEEEEEQAGKPGEPSKKEEGRAGAGLGDGERKTNDKDEKKEDGKQAENDSSNDDKTKKSEGDGDKEEKKEDSEKEAKKSSKKRNRKHSGDDSFDEGSVSESESESESGQAEEEKEEAEALKEKEKPKEEEWEKPKDAAGLECKPRPLHKTCSLFMRNIAPNISRAEIISLCKRYPGFMRVALSEPQPERRFFRRGWVTFDRSVNIKEICWNLQNIRLRECELSPGVNRDLTRRVRNINGITQHKQIVRNDIKLAAKLIHTLDDRTQLWASEPGTPPLPTSLPSQNPILKNITDYLIEEVSAEEEELLGSSGGAPPEEPPKEGNPAEINVERDEKLIKVLDKLLLYLRIVHSLDYYNTCEYPNEDEMPNRCGIIHVRGPMPPNRISHGEVLEWQKTFEEKLTPLLSVRESLSEEEAQKMGRKDPEQEVEKFVTSNTQELGKDKWLCPLSGKKFKGPEFVRKHIFNKHAEKIEEVKKEVAFFNNFLTDAKRPALPEIKSSKGGYGLNDIFEAQKIEWHE
SRY	Q05066	HR6924A.005	Rutgers	13492.37	10.1	HMG Box	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMVQDRVKRPMNAFIVWSRDQRRKMALENPRMRNSEISKQLGYQWKMLTEAEKWPFFQEAQKLQAMHREKYPNYKYRP
STAT1	P42224	HR8389A.002	Rutgers	70494.85	6.9276	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMLDKQKELDSKVRNVKDKVMCIEHEIKSLEDLQDEYDFKCKTLQNREHETNGVAKSDQKQEQLLLKKMYLMLDNKRKEVVHKIIELLNVTELTQNALINDELVEWKRRQQSACIGGPPNACLDQLQNWFTIVAESLQQVRQQLKKLEELEQKYTYEHDPITKNKQVLWDRTFSLFQQLIQSSFVVERQPCMPTHPQRPLVLKTGVQFTVKLRLLVKLQELNYNLKVKVLFDKDVNERNTVKGFRKFNILGTHTKVMNMEESTNGSLAAEFRHLQLKEQKNAGTRTNEGPLIVTEELHSLSFETQLCQPGLVIDLETTSLPVVVISNVSQLPSGWASILWYNMLVAEPRNLSFFLTPPCARWAQLSEVLSWQFSSVTKRGLNVDQLNMLGEKLLGPNASPDGLIPWTRFCKENINDKNFPFWLWIESILELIKKHLLPLWNDGCIMGFISKERERALLKDQQPGTFLLRFSESSREGAITFTWVERSQNGGEPDFHAVEPYTKKELSAVTFPDIIRNYKVMAAENIPENPLKYLYPNIDKDHAFGKYYSRPKEAPEPMELDGPKGTGYIKTELISVS
STAT2	P52630	HR3569E.008	Rutgers	16732.81	5.3961	Misc	pass	MGHHHHHHSHMAQWEMLQNLDSPFQDQLHQLYSHSLLPVDIRQYLAVWIEDQNWQEAALGSDDSKATMLFFHFLDQLNYECGRCSQDPESLLLQHNLRKFCRDIQPFSQDPTQLAEMIFNLLLEEKRILIQAQRAQLEQGE
SUPT6H	Q7KZ85	SUPT6H-A001	SGC	155713.59	5.4167	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGSRRSIFEMYEPSELESSHLTDQDNEIRATDLPERFQLRSIPVKGAEDDELEEEADWIYRNAFATPTISLQESCDYLDRGQpassFSRKGPSTIQKIKEALGFMRNQHFEVPFIAFYRKEYVEPELHINDLWRVWQWDEKWTQLRIRKENLTRLFEKMQAYQYEQISADPDKPLADGIRALDTTDMERLKDVQSMDELKDVYNHFLLYYGRDIPKMQNAAKASRKKLKRVREEGDEEGEGDEAEDEEQRGPELKQASRRDMYTICQSAGLDGLAKKFGLTPEQFGENLRDSYQRHETEQFPAEPLELAKDYVCSQFPTPEAVLEGARYMVALQIAREPLVRQVLRQTFQERAKLNITPTKKGRKDVDEAHYAYSFKYLKNKPVKELRDDQFLKICLAEDEGLLTTDISIDLKGVEGYGNDQTYFEEIKQFYYRDEFSHQVQEWNRQRTMAIERALQQFLYVQMAKELKNKLLAEAKEYVIKACSRKLYNWLRVAPYRPDQQVEEDDDFMDENQGKGIRVLGIAFSSARDHPVFCALVNGEGEVTDFLRLPHFTKRRTAWREEREKKAQDIETLKKFLLNKKPHVVTVAGENRDAQMLIEDVKRIVHELDQGQQLSSIGVELVDNELAILYMNSKKSEAEFRDYPPVLRQAVSLARRIQDPLIEFAQVCSSDEDILCLKFHPLQEHVVKEELLNALYCEFINRVNEVGVDVNRAIAHPYSQALIQYVCGLGPRKGTHLLKILKQNNTRLESRTQLVTMCHMGPKVFMNCAGFLKIDTASLGDSTDSYIEVLDGSRVHPETYEWARKMAVDALEYDESAEDANPAGALEEILENPERLKDLDLDAFAEELERQGYGDKHITLYDIRAELSCRYKDLRTAYRSPNTEEIFNMLTKETPETFYIGKLIICNVTGIAHRRPQGESYDQAIRNDETGLWQCPFCQQDNFPELSEVWNHFDSGSCPGQAIGVKTRLDNGVTGFIPTKFLSDKVVKRPEERVKVGMTVHCRIMKIDIEKFSADLTCRTSDLMDRNNEWKLPKDTYYDFDAEAADHKQEEDMKRKQQRTTYIKRVIAHPSFHNINFKQAEKMMETMDQGDVIIRPSSKGENHLTVTWKVSDGIYQHVDVREEGKENAFSLGATLWINSEEFEDLDEIVARYVQPMASFARDLLNHKYYQDCSGGDRKKLEELLIKTKKEKPTFIPYFICACKELPGKFLLGYQPRGKPRIEYVTVTPEGFRYRGQIFPTVNGLFRWFKDHYQDPVPGITPSSSSRTRTPASINATPANINLADLTRAVNALPQNMTSQMFSAIAAVTGQGQNPNATGGSGHHHHHH
SUV39H1	O43463	SUV39H1-A002	SGC			NA	pass	
SUV420H1	Q4FZB7-2	SUV420H1-A002	SGC	34404.63	7.0044	SET	pass	MSGLNDIFEAQKIEWHEGSAGGSGSSGMSAKELCENDDLATSLVLDPYLGFQTHKMNTSAFPSRSSRHFSKSDSFSHNNPVRFRPIKGRQEELKEVIERFKKDEHLEKAFKCLTSGEWARHYFLNKNKMQEKLFKEHVFIYLRMFATDSGFEILPCNRYSSEQNGAKIVATKEWKRNDKIELLVGCIAELSEIEENMLLRHGENDFSVMYSTRKNCAQLWLGPAAFINHDCRPNCKFVSTGRDTACVKALRDIEPGEEISCYYGDGFFGENNEFCECYTCERRGTGAFKSRGGGSHHHHHH
SUV420H2	Q86Y97	SUV420H2-A002	SGC	33372.68	7.5202	SET	pass	MHHHHHHHHHHHDLGTENLYFQSMGPDRVTARELCENDDLATSLVLDPYLGFRTHKMNVSPVPPLRRQQHLRSALETFLRQRDLEAAYRALTLGGWTARYFQSRGPRQEAALKTHVYRYLRAFLPESGFTILPCTRYSMETNGAKIVSTRAWKKNEKLELLVGCIAELREADEGLLRAGENDFSIMYSTRKRSAQLWLGPAAFINHDCKPNCKFVPADGNAACVKVLRDIEPGDEVTCFYGEGFFGEKNEHCECHTCERKGEGAFRTRPRESSKGGYGLNDIFEAQKIEWHE
SUV420H2	Q86Y97	SUV420H2-A003	SGC	33372.68	7.5202	SET	pass	MHHHHHHHHHHHDLGTENLYFQSMGPDRVTARELCENDDLATSLVLDPYLGFRTHKMNVSPVPPLRRQQHLRSALETFLRQRDLEAAYRALTLGGWTARYFQSRGPRQEAALKTHVYRYLRAFLPESGFTILPCTRYSMETNGAKIVSTRAWKKNEKLELLVGCIAELREADEGLLRAGENDFSIMYSTRKRSAQLWLGPAAFINHDCKPNCKFVPADGNAACVKVLRDIEPGDEVTCFYGEGFFGEKNEHCECHTCERKGEGAFRTRPRESSKGGYGLNDIFEAQKIEWHE
TAF1	P21675	TAF1A-A001	SGC	20221.83	6.7396	Bromodomain	pass	MHHHHHHHHHHHDLGTENLYFQSMRRTDPMVTLSSILESIINDMRDLPNTYPFHTPVNAKVVKDYYKIITRPMDLQTLRENVRKRLYPSREEFREHLELIVKNSATYNGPKHSLTQISQSMLDLCDEKLKEKEDKLARLEKAINPLLDDDDSSKGGYGLNDIFEAQKIEWHE

HGCN	Uniprot ID	Antigen ID	Antigen Source	MW (Da)	pI	Common Domain Names	Primary Validation (pass/fail)	construct seq (with tag)
TAF1L	Q8IZX4	TAF1LA-A001	SGC	19385.87	6.5525	Bromodomain	pass	MHHHHHHHHHHDLGTENLYFQSMVTLSSILESIINDMRDLPNTHPFHTPVNAKVVKDYY KIITRPMDLQTLRENVRKCLYPSREEFREHLELIVKNSATYNGPKHSLTQISQSMLDLCD EKLKEKEDKLARLEKAINPLLDDDDSSKGGYGLNDIFEAQKIEWHE
TBL1X	O60907	TBL1X-A001	SGC	21321.29	5.2067	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGSITSDEVNFLVYRYLQESGFSHSAFTFGIESHISQ SNINGTLVPPAALISILQKGLQYVEAEISINEDGTVFDGRPIESLSLIDAVMPDVVQTRQQ AFREKLAQQQASAAAAAAAATAAATAATTTSAGVSHQNPSKNREATVNGEENRAHSVN NHAKPMEIDGEVEIGGSGHHHHHH
TBX4	P57082	HR7232A.002	Rutgers	25620.39	9.4813	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMEQTIENIKVGLHEKELWKKFHEAGTE MIITKAGRRMFPSYKVKVTGMNPKTKYILLIDIVPADDHRYKFCDNKWMVAGKAEPAMP GRLYVHPDSPATGAHWMRQLVSFQKLKLTNNHLDPFGHIILNSMHKYQPRLHIVKADEN NAFGSKNTAFCTHVFPETSFISVTSYQNHKITQLKIENNPFAKG
TBX5	Q99593	HR8313A.001	Rutgers	24927.57	9.8109	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMEGIKVFLHERELWLKFHEVGTEMIITK AGRRMFPSYKVKVTGLNPKTKYILLMDIVPADDHRYKFADNKWSVTGKAEPAMPGRLY VHPDSPATGAHWMRQLVSFQKLKLTNNHLDPFGHIILNSMHKYQPRLHIVKADENNGF GSKNTAFRTHVFPETAFIAVTSYQNHKITQLKIENNPF
TBX5	Q99593	Tbx5	RAN	21276.62	10.3853	Misc	pass	MKIEEHHHHHHSSGKLGSTEDLYFQSAAQPAKVFLHERELWLKFHEVGTEMIITKAGRR MFPSYKVKVTGLNPKTKYILLMDIVPADDHRYKFADNKWSVTGKAEPAMPGRLYVHPD SPATGAHWMRQLVSFQKLKLTNNHLDPFGHIILNSMHKYQPRLHIVKADENNGFGSKNT AFCTHVFPETAFIAVTSYQNHKITQLKIENNPFAKGFRGS
TCF19	Q9Y242	TCF19-A004	SGC	17269.1	6.556	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGPCFQLLIRIGGGRGGDLYTFHPPAGAGCTYRLGH RADLCDVALRPQQEPGLISGIHAELHAEPRGDDWRVSLEDHSSQGTLVNNVRLPRGHR LELSDGDLLTFGPEGPPGTSPSEFYFMFQQVRVKPGGSGHHHHHH
TCF19	Q9Y242	HR6965A.004	Rutgers	19716.05	6.6254	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMLPCFQLLRIGGGRGGDLYTFHPPAGA GCTYRLGHRADLCDVALRPQQEPGLISGIHAELHAEPRGDDWRISLEDHSSQGTLVNN VRLPRGHRLELSDGDLLTFGPEGPPGTSPSEFYFMFQQVRVKPQDFAAITIPRSRGEA R
TCF21	O43680	HR8141A.004	Rutgers	14864.9	9.7729	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMSQEGKQVQRNAANARERARMRVLS KAFSRLKTTLPWVPPDTKLSKLDTLRLASSYIAHLRQILANDKYENGYIHPVNLTWPFMV AGKPESDLKEV
TDRD3	Q9H7E2	TDRD3-A001	SGC	10352.49	5.8957	Misc	pass	MHHHHHHHHHHHDLGTENLYFQSMKMWKPGDECFALYWEDNKFYRAEVEALHSSGMT AVVKFIDYGNYEEVLLSNIKPIQTEAWEEE
TDRKH	Q9Y2W6	TDRD2-A003	SGC	61946.64	4.7864	Misc	pass	MHHHHHHHHHHHDLGTENLYFQSMVGEDDIEIEMRVPQEAVKLIIGRQGANIKQLRKQT GARIDVDTEDVGDERVLLISGFPVQVCKAKAAIHQILTENTPVSEQLSVPQRSVGRIIGR GGETIRSICKASGAKITCDKESEGTLLLSRLIKISGTQKEVAAAKHLILEKVSEDEEILRKRI AHSAETRVPRKQPISVRREDMTEPGGAGEPALWKNTSSSMEPTAPLVTPPPKAGGDM AVVVSKEGSWEKPSDDSFQKSEAQAIPEMPMFEIPSPDFSFHADEYLEVYVSASEHPN HFWIQIVGSRSLQLDKLVNEMTQHYENSVPEDLTVHVGDIVAAPLPTNGSWYRARVLG TLENGNLDLYFVDFGDNGDCPLKDLRALRSDFLSLPFQAIECSLARIAPSGDQWEEEAL DEFDRLTHCADWKPLVAKISSYVQTGISTWPKIYLYDTSNGKKLDIGLELVHKGYAIELPE DIEENRAVPDMLKDMATETDASLSTLLTETKKSSGEITHTLSCLSLSEAASMSGDDNLED DYLLSSKGGYGLNDIFEAQKIEWHE
TERF2	Q15554	HR7931A.001	Rutgers	10548.97	9.8664	Misc	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKKQKWTVEESEWVKAGVQKYGEGN WAAISKNYPFVNRTAVMIKDRWRTMKRLGMN
TERF2IP	Q9NYB0	HR7939A.002	Rutgers	10651.88	7.4229	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGRIAFTDADDVAILTYVKENARSPSSV TGNALWKAMEKSSLTQHSWQSLKDRYLKHLRG
TGIF1	Q15583	HR4411B.045	Rutgers	8979.22	9.6916	Misc	pass	MGHHHHHHSHMNLPKESVQILRDWLYEHRYNAYPSEQEKALLSQQTHLSTLQVCNWF INARRRLLPDMLRKDGK
THAP9	Q9H5L6	HR7271B.004	Rutgers	15385.55	10.3777	Misc	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMTRSCSAVGCSTRDTVLSRERGLSFH QFPTDTIQRSKWIRAVNRVDPRSKKIWIPGPGAILCSKHFQESDFESYGIRRKLKKGAVP SVSLYKIPQGVHLKGK
TIF1	O15164	TIF1A-A002	SGC	19710.39	6.3587	Bromodomain	pass	MHHHHHHHHHHHSSGVDLGTENLYFQSMGLVKLTPIDKRKCERLLLFLYCHEMSLAFQD PVPLTVPDYYKIIKNPMDLSTIKKRLQEDYSMYSKPEDFVADFRLIFQNCAEFNEPDSEV ANAGIKLENYFEELLKNLYPEKRFPKPESSKGGYGLNDIFEAQKIEWHE
TNKS1	O95271	TNKS1A-A003	SGC	28479.84	7.47	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGTILLDLAPEDKEYQSVEEEMQSTIREHRDGGNAG GIFNRYNVIRIQKVVNKKLRERFCHRQKEVSEENHNHHNERMLFHGSPFINAIIHKGFDE RHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPTHKDRSCYICHRQMLFCRVTLG KSFLQFSTIKMAHAPPGHHSVIGRPSVNGLAYAEYVIYRGEQAYPEYLITYQIMKPEAPS QTATAAEQGGSGHHHHHH
TP53BP1	Q12888	53BP1-A001	SGC	17770.72	6.291	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGSSPGNSFVGLRVVAKWSSNGYFYSGKITRDVGA GKYKLLFDDGYECDVLGKDILLCDPIPLDTEVTALSEDEYFSAGVVKGHRKESGELYYSI EKEGQRKWYKRMAVILSLEQGNRLREQYGLGPYEGGSGHHHHHH
TRIM28	Q13263	TRIM28A-A001	SGC	26717.08	5.6118	PHD	pass	MHHHHHHHHHHHDLGTENLYFQSMGTLDDSATICRVCQKPGDLVMCNQCEFCFHLDCH LPALQDVPGEEWSCSLCHVLPDLKEEDGSLSLDGADSTGVVAKLSPANQRKCERVLLA LFCHEPCRPLHQLATDSTFSLDQPGGTLDLTLIRARLQEKLSPPYSSPQEFAQDVGRMF KQFNKLTEDKADVQSIIGLQRFFETRMNEAFGDTKFSAVLVESSKGGYGLNDIFEAQKIE WHE
TRPS1	Q9UHF7	HR8134A.005	Rutgers	17591.38	6.632	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMLLLHLSPGAAGSSRVKHQCHQCSFT TPDVDVLLFHYESVHESQASDVKQEANHLQGSDGQQSVKESKEHSCTKCDFITQVEE EISRHYRRAHSCYKCRQCSFTAADTQSLLEHFNTVHCQ
TSC2	P49815	TSC2-A004	SGC	28139.52	6.2473	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSE LAILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIMQ AVFHIATLMPTKDVDKHRCDKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTPL DYECNLVSLQCRKDMEGLVDTSVAKIVSDRNLPFVARQMALHANMASQVHHSRSNPT DIYPSKWIAGGGSHHHHHH
TSC22D4	Q9Y3Q8	HR7683A.005	Rutgers	9216.51	6.508	Misc	pass	MGHHHHHHSHMVGIDNKIEQAMDLVKSHLMFAVREEVEVLKEQIRELAERNAALEQEN GLLRALASPEQLAQLPSSGVPRLG
TSC22D4	Q9Y3Q8	HR7683A.014	Rutgers	12284.86	6.0067	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMNKIEQAMDLVKSHLMFAVREEVEVLK EQIRELAERNAALEQENGLLRALASPEQLAQLPSSGVPRLGPPAPNGPSV
TSC22D4	Q9Y3Q8	HR7683A.030	Rutgers	12285.86	5.7445	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMNKIEQAMDLVKSHLMFAVREEVEVLN EQIRELAERNAALEQENGLLRALASPEQLAQLPSSGVPRLGPPAPMGPPS
UHRF1	Q96T88-2	UHRF1A-A001	SGC	17077.29	7.4442	Misc	fail	MHHHHHHHHHHHSSGVDLGTENLYFQSMEPYSLTAQQSSLIREDKSNAKLWNEVLASLK DRPASGSPFQLFLSKVEETFQCICCQELVFRPITTVCQHNVCKDCLDRSFRAQVFSCPA CRYDLGRSYAMQVNQPLQTVLNQLFPGYGNGR
UHRF1	Q96T88-2	UHRF1-A005	SGC	81317.24	7.7084	PHD	pass	MHHHHHHHHHHHDLGTENLYFQSMPADEDMWDETELGLYKVNEYVDARDTNMGAWF EAQVVRVTRKAPSRDEPCSSTSRPALEEDVIYHVKYDDYPENGVVQMNSRDVRARAR TIIKWQDLEVGQVVMLNYNPDNPKERGFWYDAEISRKRETRTARELYANVVLGDDSLN DCRIIFVDEVFKIERPGEGSPMVDNPMRRKSGPSCKHCKDDVNRLCRVCACHLCGGR QDPDKQLMCDECDMAFHIYCLDPPLSSVPSEDEWYCPECRNDASEVVLAGERLRESK KKAKMASATSSSQRDWGKGMACVGRTKECTIVPSNHYGPIPGIPVGTMWRFRVQVSE SGVHRPHVAGIHGRSNDGAYSLVLAGGYEDDVDHGNFFTYTGSGGRDLSGNKRTAEQ SCDQKLTNTNRALALNCFAPINDQEGAEAKDWRSGKPVRVVRNVKGGKNSKYAPAEG NRYDGIYKVVKYWPEKGKSGFLVWRYLLRRDDDEPGPWTKEGKDRIKKLGLTMQYPE GYLEALANREREKENSKREEEEQQEGGFASPRTGKGKWKRKSAGGGPSRAGSPRRT SKKTKVEPYSLTAQQSSLIREDKSNAKLWNEVLASLKDRPASGSPFQLFLSKVEETFQCI CCQELVFRPITTVCQHNVCKDCLDRSFRAQVFSCPACRYDLGRSYAMQVNQPLQTVL NQLFPGYGNGRSSKGGYGLNDIFEAQKIEWHE
UHRF1	Q96T88-2	UHRF1-A006	SGC	16334.39	6.8408	PHD	pass	MHHHHHHHHHHHDLGTENLYFQSMMRRKSGPSCKHCKDDVNRLCRVCACHLCGGRQ DPDKQLMCDECDMAFHIYCLDPPLSSVPSEDEWYCPECRNDASEVVLAGERLRESKK KAKMASATSSSKGGYGLNDIFEAQKIEWHE
UHRF2	Q96PU4	UBH14-A003	SGC	27127.31	7.319	DUF	pass	MSGLNDIFEAQKIEWHEGSAGGSGSARARLIDPGFGIYKVNELVDARDVGLGAWFEAHI HSVTRASDGQSRGKTPLKNGSSCKRTNGNIKHKSKENTNKLDSVPSTSNSDCVAADE DVIYHIQYDEYPESGTLEMNVKDLRPRARTILKWNELNVGDVVMVNYNVESPGQRGF WFDAEITTLKTISRTKKELRVKIFMGGSEGTLNDCKIISVDEIFKIERPGAHPLSFADGKFL RGGSGHHHHHH
UHRF2	Q96PU4	UBH14-A004	SGC	30003.46	9.7433	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGMPSASTESRRDWGRGMACVGRTRECTIVPSNH YGPIPGIPVGSTWRFRVQVSEAGVHRPHVGGIHGRSNDGAYSLVLAGGFADEVDRGD EFTYTGSGGKNLAGNKRIGAPSADQTLTNMNRALALNCDAPLDDKIGAESRNWRAGK PVRVIRSFKGRKISKYAPEEGNRYDGIYKVVKYWPEISSSHGFLVWRYLLRRDDVEPAP WTSEGIERSSRRLCLRLQYPAGYPSDKEGKKPKGQGSGGSGHHHHHH
USP13	Q92995	USP13-A002	SGC	19212.3	6.1022	Zinc Finger	pass	MHHHHHHHHHHHDLGTENLYFQSMENELPVSKYANNLTQLDNGVRIPPSGWKCARCDL RENLWLNLTDGSVLCGKWFFDSSGGNGHALEHYRDMGYPLAVKLGTITPDGADVYSF QEEEPVLDPHLAKHLAHFGIDMLHMHGTENGLQDSSKGGYGLNDIFEAQKIEWHE

HGCN	Uniprot ID	Antigen ID	Antigen Source	MW (Da)	pI	Common Domain Names	Primary Validation (pass/fail)	construct seq (with tag)
USP7	Q93009	USP7-A007	SGC	29075.81	4.9365	Misc	pass	MHHHHHHHHHHDLGTENLYFQSMNHQQQQQQKAGEQQLSEPEDMEMEAGDTDD PPRITQNPVINGNVALSDGHNTAEEDMEDDTSWRSEATFQFTVERFSRLSESVLSPPC FVRNLPWKIMVMPRFYPDRPHQKSVGFFLQCNAESDSTSWSCHAQAVLKIINYRDDEK SFSRRISHLFFHKENDWGFSNFMAWSEVTDPEKGFIDDDKVTFEVFVQADAPHGVAW DSSSKGGYGLNDIFEAQKIEWHE
USP7	Q93009	USP7-A008	SGC	47822.88	6.2693	Misc	pass	MHHHHHHHHHHDLGTENLYFQSMSKKHTGYVGLKNQGATCYMNSLLQTLFFTNQLRK AVYMMPTEGDDSSKSVPLALQRVFYELQHSDKPVGTKKLTKSFGWETLDSFMQHDVQ ELCRVLLDNVENKMKGTCVEGTIPKLFRGKMVSYIQCKEVDYRSDRREDYYDIQLSIKG KKNIFESFVDYVAVEQLDGDNKYDAGEHGLQEAEKGVKFLTLPPVLHLQLMRFMYDPQ TDQNIKINDRFEFPEQLPLDEFLQKTDPKDPANYILHAVLVHSGDNHGGHYVVYLNPKG DGKWCKFDDDVVSRCTKEEAIEHNYGGHDDDLSVRHCTNAYMLVYIRESKLSEVLQAV TDHDIPQQLVERLQEEKRIEAQKRKERQEAHLYMQVQIVAEDSSKGGYGLNDIFEAQKI EWHE
USP7	Q93009	USP7-A001	SGC	67726.86	5.2744	Misc	pass	MSGLNDIFEAQKIEWHEGSAGGSGRESKLSEVLQAVTDHDIPQQLVERLQEEKRIEAQ KRKERQEAHLYMQVQIVAEDQFCGHQGNDMYDEEKVKYTVFKVLKNSSLAEFVQSLS QTMGFPQDQIRLWPMQARSNGTKRPAMLDNEADGNKTMIELSDNENPWTIFLETVDP ELAASGATLPKFDKDHDVMLFLKMYDPKTRSLNYCGHIYTPISCKIRDLLPVMCDRAGFI QDTSLILYEEVKPNLTERIQDYDVSLDKALDELMDGDIIVFQKDDPENDNSELPTAKEYF RDLYHRVDVIFCDKTIPNDPGFVVTLSNRMNYFQVAKTVAQRLNTDPMLLQFFKSQGY RDGPGNPLRHNYEGTLRDLLQFFKPRQPKKLYYQQLKMKITDFENRRSFKCIWLNSQF REEEITLYPDKHGCVRDLLEECKKAVELGEKASGKLRLLEIVSYKIIGVHQEDELLECLSP ATSRTFRIEEIPLDQVDIDKENEMLVTVAHFHKEVFGTFGIPFLLRIHQGEHFREVMKRIQ SLLDIQEKEFEKFKFAIVMMGRHQYINEDEYEVNLKDFEPQPGGSGHHHHHH
VAX2	Q9UIW0	HR8032A.001	Rutgers	14256.12	9.9004	Homeobox	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMVRDAKGTIREIVLPKGLDLDRPKRTRT SFTAEQLYRLEMEFQRCQYVVGRERTELARQLNLSETQVKVWFQNRRTKQKKDQSRD L
VENTX	O95231	HR7703A.001	Rutgers	11663.22	9.089	Homeobox	pass	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMAFTMEQVRTLEGVFQHHQYLSPLER KRLAREMQLSEVQIKTWFQNRRMKHKRQMQDPQLHSP
VSX1	Q9NZR4	HR7928A.002	Rutgers	12027.43	6.9258	Homeobox	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMEDRNDLKASPTLGKRKKRRHRTVFTA HQLEELEKAFSEAHYPDVYAREMLAVKTELPEDRIQVWFQN
VSX1	Q9NZR4	HR7928A.008	Rutgers	12027.43	6.9258	Homeobox	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMEDRNDLKASPTLGKRKKRRHRTVFTA HQLEELEKAFSEAHYPDVYAREMLAVKTELPEDRIQVWFQN
VSX2	P58304	HR8065A.001	Rutgers	11405.89	7.9168	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMSFICSECGKVFTMKSRLIEHQRTHTG EKPYICNECGKGFPGKRNLIVHQRNHTGEKSYICSECGK
WDR12	Q9GZL7	WDR12-A001	SGC	51160.54	6.051	WD40	pass	MSGLNDIFEAQKIEWHEGSAGGSGMAQLQTRFYTDNKKYAVDDVPFSIPAASEIADLSN IINKLLKDKNEFHKHVEFDFLIKGQFLRMPLDKHMEMENISSEEVVEIEYVEKYTAPQPE QCMFHDDWISSIKGAEEWILTGSYDKTSRIWSLEGKSIMTIVGHTDVVKDVAWVKKDSL SCLLLSASMDQTILLWEWNVERNKVKALHCCRGHAGSVDSIAVDGSGTKFCSGSWDK MLKIWSTVPTDEEDEMEESTNRPRKKQKTEQLGLTRTPIVTLSGHMEAVSSVLWSDAE EICSASWDHTIRVWDVESGSLKSTLTGNKVFNCISYSPLCKRLASGSTDRHIRLWDPRT KDGSLVSLSLTSHTGWVTSVKWSPTHEQQLISGSLDNIVKLWDTRSCKAPLYDLAAHED KVLSVDWTDTGLLLSGGADNKLYSYRYSPTTSHVGAGGSGHHHHHH
WDR45	Q9Y484-3	WDR45-A001	SGC	43320.16	6.9069	WD40	pass	MSGLNDIFEAQKIEWHEGSAGGSGMTQQPLRGVTSLRFNQDQSCFCCAMETGVRIYN VEPLMEKGHLDHEQVGSMGLVEMLHRSNLLALVGGGSSPKFSEISVLIWDDAREGKDS KEKLVLEFTFTKPVLSVRMRHDKIVIVLKNRIYVYSFPDNPRKLFEFDTRDNPKGLCDLC PSLEKQLLVFPGHKCGSLQLVDLASTKPGTSSAPFTINAHQSDIACVSLNQPGTVVASA SQKGTLIRLFDTQSKEKLVELRRGTDPATLYCINFSHDSSFLCASSDKGTVHIFALKDTRL NRRSALARVGKVGPMIGQYVDSQWSLASFTVPAESACICAFGRNTSKNVNSVIAICVD GTFHKYVFTPDGNCNREAFDVYLDICDDDDFGGSGHHHHHH
WDR48	Q8TAF3	HR2647C.001	Rutgers	17596.65	6.1136	DUF	pass	MHHHHHHEFMSGLNDIFEAQKIEWHEGSAGGSGENLYFQGNKIPFYLQPHASSGAKTL KKDRLSASDMLQVRKVMEHVYEKIINLDNESQTTSSSNNEKPGEQEKEEDIAVLAEEKI ELLCQDQVLDPNMDLRTVKHFIWKSGGDLTLHYRQK
WDR48	Q8TAF3	WDR48-A001	SGC	79663.06	6.9152	WD40	pass	MSGLNDIFEAQKIEWHEGSAGGSGMAAHHRQNTAGRRKVQVSYVIRDEVEKYNRNGV NALQLDPALNRLFTAGRDSIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISA SSDTTVKVWNAHKGFCMSTLRTHKDYVKALAYAKDKELVASAGLDRQIFLWDVNTLTAL TASNNTVTTSSLSGNKDSIYSLAMNQLGTIIVSGSTEKVLRVWDPRTCAKLMKLKGHTD NVKALLLNRDGTQCLSGSSDGTIRLWSLGQQRCIATYRVHDEGVWALQVNDAFTHVYS GGRDRKIYCTDLRNPDIRVLICEEKAPVLKMELDRSADPPPAIWVATTKSTVNKWTLKGI HNFRASGDYDNDCTNPITPLCTQPDQVIKGGASIIQCHILNDKRHILTKDTNNNVAYWDV LKACKVEDLGKVDFEDEIKKRFKMVYVPNWFSVDLKTGMLTITLDESDCFAAWVSAKD AGFSSPDGSDPKLNLGGLLLQALLEYWPRTHVNPMDEEENEVNHVNGEQENRVQKG NGYFQVPPHTPVIFGEAGGRTLFRLLCRDSGGETESMLLNETVPQWVIDITVDKNMPK FNKIPFYLQPHASSGAKTLKKDRLSASDMLQVRKVMEHVYEKIINLDNESQTTSSSNNE KPGEQEKEEDIAVLAEEKIELLCQDQVLDPNMDLRTVKHFIWKSGGDLTLHYRQKSTGG SGHHHHHH
WDR5	P61964	WDR5-A003	SGC	41750.04	7.7137	WD40	pass	MHHHHHHHHHHHDLGTENLYFQSMATEEKKPETEAARAQPTPSSSATQSKPTPVKPNY ALKFTLAGHTKAVSSVKFSPNGEWLASSSADKLIKIWGAYDGKFEKTISGHKLGISDVA WSSDSNLLVSASDDKTLKIWDVSSGKCLKTLKGHSNYVFCCNFNPQSNLIVSGSFDES VRIWDVKTGKCLKTLPAHSDPVSAVHFNRDGSLIVSSSYDGLCRIWDTASGQCLKTLID DDNPPVSFVKFSPNGKYILAATLDNTLKLWDYSKGKCLKTYTGHKNEKYCIFANFSVTG GKWIVSGSEDNLVYIWNLQTKEIVQKLQGHTDVVISTACHPTENIIASAALENDKTIKLWK SDCSSKGGYGLNDIFEAQKIEWHE
WDR5	P61964	WDR5-A002	SGC	41750.04	7.7137	WD40	pass	MHHHHHHHHHHHDLGTENLYFQSMATEEKKPETEAARAQPTPSSSATQSKPTPVKPNY ALKFTLAGHTKAVSSVKFSPNGEWLASSSADKLIKIWGAYDGKFEKTISGHKLGISDVA WSSDSNLLVSASDDKTLKIWDVSSGKCLKTLKGHSNYVFCCNFNPQSNLIVSGSFDES VRIWDVKTGKCLKTLPAHSDPVSAVHFNRDGSLIVSSSYDGLCRIWDTASGQCLKTLID DDNPPVSFVKFSPNGKYILAATLDNTLKLWDYSKGKCLKTYTGHKNEKYCIFANFSVTG GKWIVSGSEDNLVYIWNLQTKEIVQKLQGHTDVVISTACHPTENIIASAALENDKTIKLWK SDCSSKGGYGLNDIFEAQKIEWHE
WDR82	Q6UXN9	WDR82-A001	SGC	38531.62	7.1435	WD40	pass	MSGLNDIFEAQKIEWHEGSAGGSGMKLTDSVLRSFRVAKVFRENSDKINCFDFSPNGE TVISSSDDDSIVLYDCQEGKPKRTLYSKKYGVDLIRYTHAANTVVYSSNKIDDTIRYLSLH DNKYIRYFPGHSKRVVALSMSPVDDTFISGSLDKTIRLWDLRSPNCQGLMHLQGKPVC SFDPEGLIFAAGVNSEMVKLYDLRSFDKGPFATFKMQYDRTCEWTGLKFSNDGKLILIS TNGSFIRLIDAFKGVVMHTFGGYANSKAVTLEASFTPDSQFIMIGSEDGKIHVWNGESGI KVAVLDGKHTGPITCLQFNPKFMTFASACSNMAFWLPTIDDGGSGHHHHHH
WHSC1	O96028	HR7541B.001	Rutgers	17582.77	6.2199	SET	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPETKIIKTDGKGWGLVAKRDIRKGEFV NEYVGELIDEEECMARIKHAHENDITHFYMLTIDKDRIIDAGPKGNYSRFMNHSCQPNC ETLKWTVNGDTRVGLFAVCDIPAGTELTFNYNL
WHSC1	O96028	WHSC1-A002	SGC	27801.34	6.4821	SET	pass	MSGLNDIFEAQKIEWHEGSAGGSGKVNKPYGKVQIYTADISEIPKCNCKPTDENPCGFD SECLNRMLMFECHPQVCPAGEFCQNQCFTKRQYPETKIIKTDGKGWGLVAKRDIRKGE FVNEYVGELIDEEECMARIKHAHENDITHFYMLTIDKDRIIDAGPKGNYSRFMNHSCQPN CETLKWTVNGDTRVGLFAVCDIPAGTELTFNYNLDCLGNEKTVCRCGASNCSGFLGDR PKTGGGSHHHHHH
WHSC1L1	Q9BZ95	WHSC1L1-A002	SGC	23609.41	7.2776	PWWP	pass	MHHHHHHHHHHHDLGTENLYFQSMEAPVQPILSSVPTTEVSTGVKFQVGDLVWSKVGT YPWWPCMVSSDPQLEVHTKINTRGAREYHVQFFSNQPERAWVHEKRVREYKGHKQY EELLAEATKQASNHSEKQKIRKPRPQRERAQWDIGIAHAEKALKMTREERIEQYTFIYID KQPEEASSKGGYGLNDIFEAQKIEWHE
WHSC1L1	Q9BZ95	WHSC1L1-A003	SGC	28976.72	7.6808	SET	fail	MSGLNDIFEAQKIEWHEGSAGGSGNSRKPPPYKHIKANKVIGKVQIQVADLSEIPRCNC KPADENPCGLESECLNRMLQYECHPQVCPAGDRCQNQCFTKRLYPDAEIIKTERRGW GLRTKRSIKKGEFVNEYVGELIDEEECRLRIKRAHENSVTNFYMLTVTKDRIIDAGPKGN YSRFMNHSCNPNCETQKWTVNGDVRVGLFALCDIPAGMELTFNYNLDCLGNGRTECH CGADNCSGFLGVRPKSGGSGHHHHHH
YY1	P25490	HR8137B.005	Rutgers	22785.03	9.5165	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHENLYFQSHMPDYSEYMTGKKLPPGGIPGIDLSDPK QLAEFARMKPRKIKEDDAPRTIACPHKGCTKMFRDNSAMRKHLHTHGPRVHVCAECG KAFVESSKLKRHQLVHTGEKPFQCTFEGCGKRFSLDFNLRTHVRIHTGDRPYVCPFDG CNKKFAQSTNLKSHILTHAKAKNNQ
ZBED1	O96006	HR7328B.003	Rutgers	14401.16	6.9062	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMENKSLESSQTDLKLVAHPRAKSKVWK YFGFDTNAEGCILQWKKIYCRICMAQIAYSGNTSNLSYHLEKNHPEEFCEFVKSNTEQM REAF
ZBTB11	O95625	HR6940B.006	Rutgers	13712.52	8.4989	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMRGYHCTQCEKSFFEARDLRQHMNK HLGVKPFQCQFCDKCYSWKKDWYSHVKSHSVTEPYRCNICGKEFYEKALFRRHVK

HGCN	Uniprot ID	Antigen ID	Antigen Source	MW (Da)	pI	Common Domain Names	Primary Validation (pass/fail)	construct seq (with tag)
ZBTB16	Q05516	HR3471E.005	Rutgers	18304.79	5.1699	BTB	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMMGMIQLQNPSHPTGLLCKANQMRLAGTLCDVVIMVDSQEFHAHRTVLACTSKMFEILFHRNSQHYTLDFLSPKTFQQILEYAYTATLQAKAEDLDDLLYAAEILEIEYLEEQCLKMLETIQASDD
ZBTB16	Q05516	HR3471F.004	Rutgers	26919.5	7.3511	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMNHKADAVLSMPSSVTSGLHVQPALAVSMDFSTYGGLLPQGFIQRELFSKLGELAVGMKSESRTIGEQCSVCGVELPDNEAVEQHRKLHSGMKTYGCELCGKRFLDSLRLRMHLLAHSAGAKAFVCDQCGAQFSKEDALETHRQTHTGTDMAVFCLLCGKRFQAQSALQQHMEVHAGVRSYICSECNRTFPSHTALKRHLRSHTGDHPY
ZBTB21 (ZNF295)	Q9ULJ3	HR7401C.005	Rutgers	18721.07	6.1038	BTB	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMEGLLHYINPAHAISLLSALNEERLKGQLCDVLLIVGDQKFRAHKNVLAASSEYFQSLFTNKENESQTVFQLDFCEPDAFDNVLNYIYSSSLFVEKSSLAAVQELGYSLGISFLTNIVSKTPQAPFPTCPNRK
ZBTB24	O43167	HR7918A.001	Rutgers	18662.88	5.1825	BTB	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMAETSPEPSGQLVVHSDAHSDTVLASFEDQRKKGFLCDITLIVENVHFRAHKALLAASSEYFSMMFAEEGEIGQSIYMLEGMVADTFGILLEFIYTGYLHASEKSTEQILATAQFLKVYDLVKAYTDFQNNH
ZBTB32	Q9Y2Y4	HR7977A.001	Rutgers	15754.81	6.2189	BTB	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMSLPPIRLPSPYGSDRLVQLAARLRPALCDTLITVGSQEFPAHSLVLAGVSQQLGRRGQWALGEGISPSTFAQLLNFVYGESVELQPGELRPLQEAARALGVQSLEEACW
ZBTB39	O15060	HR7896A.006	Rutgers	17809.3	6.2699	BTB	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGMRIKLQSTNHPNNLLKELNKCRLSETMCDVTIVVGSRSFPAHKAVLACAAGYFQNLFLNTGLDAARTYVVDFITPANFEKVLSFVYTSELFTDLINVGVIYEVAERLGMEDLLQACHSTFPDL
ZBTB39	O15060	HR7896A.010	Rutgers	17809.3	6.2699	BTB	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGMRIKLQSTNHPNNLLKELNKCRLSETMCDVTIVVGSRSFPAHKAVLACAAGYFQNLFLNTGLDAARTYVVDFITPANFEKVLSFVYTSELFTDLINVGVIYEVAERLGMEDLLQACHSTFPDL
ZBTB41	Q5SVQ8	HR8293A.001	Rutgers	22157.01	6.177	BTB	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMEGNVAVECDQVTYTHSAGRPTPEALHCYQELPPSPDQRKLLSSLQYNKNLLKYLNDDRQKQPSFCDLLIIVEGKEFSAHKVVAVGSSYFHACLSKNPSTDVVTLDHVTHSVFQHLLEFLYTSEFFVYKYEIPLVLEAAKFLDIIDAVKLLNNENVAPFH
ZBTB7A	O95365	HR4695D.004	Rutgers	16405.42	4.9103	BTB	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPDHSSDILSGLNEQRTQGLLCDVVILVEGREFPTHRSVLAACSQYFKKLFTSGAVVDQQNVYEIDFVSAEALTALMDFAYTATLTVSTANVGDILSAARLLEIPAVSHVCADLLD
ZBTB7B	O15156	HR8347A.004	Rutgers	18657.08	5.3945	BTB	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGSPEDDLIGIPFPDHSSELLSCLNEQRQLGHLCDLTIRTQGLEYRTHRAVLAACSHYFKKLFTEGGGGAVMGAGGSGTATGGAGAGVCELDFVGPEALGALLEFAYTATLTTSSANMPAVLQAARLLEIPCVIAACMEILQG
ZBTB8B	Q8NAP8	HR7919A.001	Rutgers	18974.56	6.4267	BTB	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMEMQSYYAKLLGELNEQRKRDFFCDCSIIVEGRIFKAHRNILFANSGYFRALLIHYIQDSGRHSTASLDIVTSDAFSIILDFLYSGKLDLCGENVIEVMSAASYLQMNDVVNFCKTYIRSSLDICRKMEKE
ZEB2	O60315	HR4589D.004	Rutgers	11158.51	6.6013	Homeobox	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMSPINPYKDHMSVLKAYYAMNMEPNSDELLKISIAVGLPQEFVKEWFEQRKVYQYSNSRSPS
ZFP3	Q96NJ6	HR7037B.005	Rutgers	24119.08	7.3571	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMTGDKPYECNECGKTFGQNSEIIRHIRIHTGEKPYVCKECGKAFRGNSELLRHERIHTGEKPYECFECGKAFRRTSHLIVHQRIHTGEKPHQCNECARTFWDNSELLLHQKIHIGEKPYECSECEKTFSQHSQLIIHQRIHTGEKPYECQECQKTFSRSSHLLRHQSVHCME
ZFP64 (ZF64B)	Q9NTW7	HR9587A.004	Rutgers	14933.41	6.5044	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMHRDEAKTENRAPLGKEGLREGSSQHVAKIVTQRAFRCETCGASFVRDDSLRCHKKQHSDQSENKNSDLVTFPPESGASGQLSTLVSVGQLEAPLEPSQDL
ZFP69 (ZNF642)	Q49AA0	HR7858B.005	Rutgers	8594.77	6.4108	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMMPQQLLITLPTEASTWVKLQHPKKAVEGAPLWEDVTKMFE
ZFP69 (ZNF642)	Q49AA0	HR7858A.001	Rutgers	12605.23	8.374	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMRNTYKLDLINHPTSYIRTKTYECNICEKIFKQPIHLTEHMRIHTGEKPFRCKECGRAFSQSASLSTHQRIHTG
ZFP90	Q8TF47	HR7734B.004	Rutgers	15235.96	7.7663	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPQENFEQNKFGENSRLNTNLVTQLNIPARIRPSECETLGSNLGHNADLLNENNILAKKKPYKCDKCRKAFIHRSSLTKHEKTHKGEGAFPNGTDQGIYPG
ZFPM2	Q8WW38	HR6866A.004	Rutgers	23116.09	6.9205	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPARLLDSIQLLPQQAAMASILPTAIVNKDIFPCKSCGIWYRSERNLQAHLMYYCSGRQREAAPVSEENEDSAHQISSLCPFPQCTKSFSNARALEMHLNSHSGVKMEEFLPPGASLKCTVCSYTADSVINFHQHLFSHLTQAAFRCNHCHFGFQTQRELLQHQELHVPSG
ZFYVE20	Q9H1K0	HR8053A.011	Rutgers	10525.71	4.9375	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPEAEEPIEEELLLQQIDNIKAYIFDAKQCGRLDEVEVLTENLRELKHTLAKQKGGTD
ZGPAT	Q8N5A5	ZGPAT-A002	SGC	20011.98	4.8233	Zinc Finger	pass	MSGLNDIFEAQKIEWHEGSAGGSGEEEGEDEEELSGTKVSAPYYSSWGTLEYHNAMVVGTEEAEDGSAGVRVLYLYPTHKSLKPCPFFLEGKCRFKENCRFSHGQVVSLDELRPFQDPDLSSLQAGSACLAKHQDGLWHAARITDVDNGYYTVKFDSLLLREAVVEGDGILPPGGSGHHHHHH
ZHX1	Q9UKY1	HR7907E.003	Rutgers	11162.49	7.347	Homeobox	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMSGSTGKICKKTPEQLHMLKSAFVRTQWPSPEEYDKLAKESGLARTDIVSWFGDTRYAWKNGNL
ZHX1	Q9UKY1	HR7907F.007	Rutgers	12339.94	9.5295	Homeobox	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPDSFGIRAKKTKEQLAELKVSYLKNQFPHDSEIIRLMKITGLTKGEIKKWFSDTRYNQRNSKSNQCLHLNN
ZHX1	Q9UKY1	HR7907C.005	Rutgers	11531.89	6.8022	Homeobox	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMNNPLLLNTYNKFPYPTMSEITVLSAQAKYTEEQIKIWFSAQRLKHGVSWTPEEVEEARRKQFNG
ZIC1	Q15915	HR7728B.002	Rutgers	25526.2	9.0051	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMNVNMAAHHGAGAFFRYMRQPIKQELICKWIEPEQLANPKKSCNKTFSTMHELVTHVTVEHVGGPEQSNHICFWEECPREGKPFKAKYKLVNHIRVHTGEKPFPCPFPGCGKVFARSENLKIHKRTHTGEKPFKCEFEGCDRRFANSSDRKKHMHVHTSDKPYLCKMCDKSYTHPSSLRKHMKVHE
ZIC2	O95409	HR7748B.005	Rutgers	20300.03	8.1915	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGAFFRYMRQQCIKQELICKWIDPEQLSNPKKSCNKTFSTMHELVTHVSVEHVGGPEQSNHVCFWEECPREGKPFKAKYKLVNHIRVHTGEKPFPCPFPGCGKVFARSENLKIHKRTHTGEKPFQCEFEGCDRRFANSSDR
ZKSCAN1	P17029	HR8102A.005	Rutgers	14917.86	5.22	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPDPEIFRQRFRRFCYQNTFGPREALSRLKELCHQWLRPEINTKEQILELLVLEQFLSILPKELQVWLQEYRPDSGEEAVTLLEDLELDLSG
ZKSCAN2	Q63HK3	HR8296A.002	Rutgers	15260.32	6.1619	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMEGSDSSETFRKCFRQFCYEDVTGPHEAFSKLWELCCRWLKPEMRSKEQILELLVIEQFLTILPEKIQAWAQKQCPQSGEEAVALVVHLEKETGRLR
ZKSCAN4	Q969J2	HR7362A.006	Rutgers	14684.51	5.7343	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPERSRQRFRGFRYPEAAGPREALSRLRELCGQWLQPEMHSKEQILELLVLEQFLTILPGNLQSWVREQHPESGEEVVVLLEYLERQLDEP
ZKSCAN5	Q9Y2L8	HR7407A.005	Rutgers	14714.5	5.8432	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMNPPTFETFYQRFRHFQYHEASGPREALSQLRVLCCEWLRPELHTKEQILELLVLEQFLTILPEEFQPWVREHHPESGEEAVAVIENIQR
ZKSCAN7 (ZNF167)	Q9P0L1	HR7169A.005	Rutgers	14912.99	6.1694	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKNYPPVCEIFRLHFRQLCYHEMSGPQEALSRLRELCRWWLMPEVHTKEQILELLVLEQFLSILPGELRTWVQLHHPESGEEAVAVVEDFQR
ZKSCAN8 (ZNF192)	Q15776	HR8500A.002	Rutgers	14621.6	5.4737	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMLGQEVFRLRFRQLRYQETLGPREALIQLRALCHQWLRPDLNTKEQILELLVLEQFLTILPEELQTLVKEHRLENGEEEVTLLEDLERQ
ZMAT2	Q96NC0	HR7288B.006	Rutgers	20690.47	9.3068	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMASGSGTKNLDFRRKWDKDEYEKLAEKRLTEEREKKDGKPVQPVKRELLRHRDYKVDLESKLGKTIVITKTTPQSEMGGYYCNVCDCVVKDSINFLDHINGKKHQRNLGMSMRVERSTLDQVKKRFEVNKKKMEEKQKDYDF
ZNF100	Q8IYN0	HR8024A.003	Rutgers	12270.74	8.0727	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGFNWSSALTKHKRIHTGEKPYKCEECGKAFNESSNLTTHKMIHTGEKPYKCDECGKAFNRSSQLTAHKMIHTG
ZNF101	Q8IZC7	HR8250B.005	Rutgers	13411.2	10.4798	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPDCHLNKKSQTGVKPCKCSVCGKVFLRHSFLDRHMRAHAGHKRSECGGEWRETPRKQKQHGKASISPSSGARRTVTPTRKRPY
ZNF107	Q9UII5	HR7096B.005	Rutgers	16810.01	8.8078	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPHKCEECGKAYNRFSNLTIHKRIHTGEKPYQCAECGKAFNCSSTLNRHKIIHTGEKPYKCKECGKAFNLSSTLTAHKKIHTGEKPYKCEECGKAFNQSSNLTTHKKIHTSEKP
ZNF132	P52740	HR7834B.005	Rutgers	19034.4	7.2228	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPFLKDILHLAEHQGTQSEEKPYTCGACGRDFWLNANLHQHQKEHSGGKPFRWYKDRDALMKSSKVHLSENPFTCREGGKVILGSCDLLQLQAVDSGQKPYSNLGQLPEVCTTQKLFECSNCGKAFLKSSTLPNH
ZNF136	P52737	HR8079A.003	Rutgers	12152.63	8.7664	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMSYLNSFRTHEMIHTGEKPFECKRCGKAFRSSSSFRLHERTHTGQKPYHCKECGKAYSCRASFQRHMLTH

HGCN	Uniprot ID	Antigen ID	Antigen Source	MW (Da)	pI	Common Domain Names	Primary Validation (pass/fail)	construct seq (with tag)
ZNF148	Q9UQR1	HR3636D.005	Rutgers	21892.91	8.4338	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPAKILTINEDGSLGLKTPKSHVCEHCNAAFRTNYHLQRHVFIHTGEKPFQCSQCDMRFIQKYLLQRHEKIHTGEKPFRCDECGMRFIQKYHMERHKRTHSGEKPYQCEYCLQYFSRTDRVLKHKRMCHENHDKKLNRCAIKGGLLTSEED
ZNF165	P49910	HR8279A.005	Rutgers	18062.3	4.6581	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMNSPEDEGLLIVKIEEEEFIHGQDTCLQRSELLKQELCRQLFRQFCYQDSPGPREALSRLRELCCQWLKPEIHTKEQILELLVLEQFLTILPGDLQAWVHEHYPESGEEAVTILEDLERGT
ZNF174	Q15697	HR7831A.006	Rutgers	15418.68	7.3446	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKNCPDPELCRQSFRRFCYQEVSGPQEALSQLRQLCRQWLQPELHTKEQILELLVMEQFLTILPPEIQARVRHRCPMSSKEIVTLVEDFHRASKKPK
ZNF18	P17022	HR8047A.002	Rutgers	19808.52	5.487	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGQALGLLPSLAKAEDSQFSESDAALQEELSSPETARQLFRQFRYQVMSGPHETLKQLRKLCFQWLQPEVHTKEQILEILMLEQFLTILPGEIQMWVRKQCPGSGEEAVTLVESLKGDPQRLWQWISIQVLGQDILSEK
ZNF197	O14709	HR7496A.004	Rutgers	15066.92	6.4419	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMSSSSVWETSHLHFRQLRYHETSGPQEALSRLRELCRRWLRPEARTKAQILELLVLEQFLSILPGEIRTWVQLHHPGSGEEAVALVEELQKDLDGPA
ZNF20	P17024	HR7949A.002	Rutgers	13031.61	8.3499	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHER
ZNF202	O95125	HR7725A.006	Rutgers	15500.48	7.0885	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMRDDPVLETSHQNFRRFRYQEAASPREALIRLRELCHQWLRPERRTKEQILELLVLEQFLTVLPGELQSWVRGQRPESGEEAVTLVEGLQKQPRRPR
ZNF205	O95201	HR7127B.003	Rutgers	18792.51	6.366	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGACTGAVEVGQRVQTSSVAALGNVKPFRTRAGRVQWGVPQCAQEAACGRSSGPAKDSGQPAEPDRTPDAAPPDPSPTEPQEYRVPEKPNEEEKGAPESGEEGLAPDSEVGRKSYRCEQCGKGFSWHSHLVTHRRTHTGE
ZNF212	Q9UDV6	HR7117B.004	Rutgers	19083.59	8.9765	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPQTKKAKLHQCDVCLRSFSCKVSLVTHQRCHLQEGPSAGQHVQERFSPNSLVALPGHIPWRKSRSSLICGYCGKSFSHPSDLVRHQRIHTGERPYSCTECEKSFVQKQHLLQHQKIHQRERGGLALEPGRPNG
ZNF213	O14771	HR7052A.005	Rutgers	14534.37	5.9154	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMDSEACRQRFRQFCYGDVHGPHEAFSQLWELCCRWLRPELRTKEQILELLVLEQFLTVLPGEIQGWVREQHPGSGEEAVALVEDLQKQPVK
ZNF217	O75362	HR7041B.004	Rutgers	20002.59	8.1166	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPKEKNCKENEFSCEVCGQTFRVAFDVEIHMRTHKDSFTYGCNMCGRRFKEPWFLKNHMRTHNGKSGARSKLQQGLESSPATINEVVQVHAAESISSPYKICMVCGFLFPNKESLIEHRKVHTKKTAFGTSSAQTDSPQGGMP
ZNF22	P17026	HR7603A.005	Rutgers	11548.91	8.408	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKPYQCDECGRCFSQSSHLIQHQRTHTGEKPYQCSECGKCFSQSSHLRQHMKVHKEEKPRKTRGK
ZNF224	Q9NZL3	HR7317A.005	Rutgers	20165.78	8.2798	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMYNCEECGKAFIHDSQLQEHQRIHTGEKPFKCDICGKSFCGRSRLNRHSMVHTAEKPFRCDTCDKSFRQRSALNSHRMIHTGEKPYKCEECGKGFICRRDLYTHHMVHTGEKPYNCKECGKSFRWASCLLKHQRVHSGE
ZNF225	Q9UK10	HR7500B.004	Rutgers	23500.39	8.5019	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMYKCEECGKGFNSKFNLDMHQRVHTGERPYNCKECGKSFSRASSILNHKRLHGDEKPFKCEECGKRFTENSQLHSHQRVHTGEKPYKCEKCGKSFRWASTHLTHQRLHSREKLLQCEDCGKSIVHSSCLKDQQRDQSGEKTSKCEDCGKRYKRRLNLDTLLSLFLNDT
ZNF227	Q86WZ6	HR7039A.001	Rutgers	10995.44	6.0035	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMEAVTFKDVAVVFSREELRLLDLTQRKLYRDVMVENFKNLVAVGHLPFQPDMVSQLEAEEK
ZNF229	Q9UJW7	HR7249B.003	Rutgers	25764.75	7.1079	NA	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPIENSLDSLQGDGLIGLENQQFPAWRAIRPIPIQGSWAKAFVNQLGDVQERCKNLDTEDTVYKCNWDDDSFCWISCHVDHRFPEIDKPCGCNKCRKDCIKNSVLHRINPGENGLKSNEYRNGFRDDADLPPHPRVPLKEKLCQYDEFSEGLRHSAHLNRHQRVPTGEKSVKSLERGRGVRQNTHIRNHP
ZNF23	P17027	HR8056A.004	Rutgers	12272.56	6.8801	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMRCDSQLIQHQENNTEEKPYQCSECGKAFSINEKLIWHQRLHSGEKPFKCVECGKSFSYSSHYITHQTIHSG
ZNF230	Q9UIE0	HR7277B.004	Rutgers	22638.27	7.118	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGPHEDCPCQQIWEQTASDLTQSQDSIINNSHFFEQGDVPSQVEAGLSIIHTGQKPSQNGKCKQSFSDVAIFDPPQQFHSGEKSHTCNECGKSFCYISALRIHQRVHLREKLSKCDMRGKEFSQSSCLQTRERVHTGEKPFKCEQCGKGFRCRAILQVHCKLHTGE
ZNF232	Q9UNY5	HR7779A.001	Rutgers	13844.49	5.9192	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMEEEQSCEYETRLPGNHSTSQEIFRQRFRHLRYQETPGPREALSQLRVLCCEWLRPEKHTKEQILEFLVLEQFLTILPEELQ
ZNF234	Q14588	HR7425A.003	Rutgers	12339.82	8.96	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMSQASSLQLHQSVHTGEKPYKCDVCGKVFSRSSQLQYHRRVHTGEKPYKCEICGKRFSWRSNLVSHHKIHAAGT
ZNF248	Q8NDW4	HR7111A.004	Rutgers	10142.39	8.5144	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKPYKCNECGKTFCEKSALTKHQRTHTGEKPYECNACGKTFSQRSVLTKHQRIH
ZNF253	O75346	HR7737A.003	Rutgers	14153.87	8.4013	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMAFNQSANLTTHKRIHTGEKPYRCEECGKAFKQSSNLTTHKKIHTGEKPYKCEECGKAFNRSTDLTTHKIVHTGEKPYKCEECGKAFKHP
ZNF26	P17031	HR7634A.002	Rutgers	11982.47	9.0845	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPSKASLQIHQKTHSGEKPFKCSECGKAFTQKSSLSEHQRVHTGEKPWKCSECGKSFCWNSGLRIHRKTHK
ZNF260	Q3ZCT1	HR8255A.002	Rutgers	10314.56	7.7112	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKPYACKECGKAFNGKAYLTEHEKIHTGEKPFECNQCGRAFSQKQYLIKHQNIHTG
ZNF263	O14978	HR7211A.005	Rutgers	14833.68	5.7029	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMDPGPSPEASHLRFRRFRFQEAAGPREALSRLQELCHGWLRPEMRTKEQILELLVLEQFLTILPQEIQSRVQELHPESGEEAVTLVEDMQRELG
ZNF274	Q96GC6	HR7942A.004	Rutgers	13790.14	4.2401	Misc	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMVTAQQEEKQEDAAICPVTVLPEEPVTFQDVAVDFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELAPNSDIPEEEPA
ZNF280C	Q8ND82	HR8391A.004	Rutgers	10299.95	9.6054	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKNLLCPFCLKVSKMATPYMNHYMKHQKKGVHRCPKCRLQFLTSKEKAEHKAQH
ZNF287	Q9HBT7	HR7687A.003	Rutgers	14262.2	6.5998	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMTSRFLRDTETCRQNFRNFPYPDLAGPRKALSQLRELCLKWLRPEIHSKEQILELLVLEQFLTILPGEVRTWVKSQYPESSEEAVTLV
ZNF296	Q8WUU4	HR7438B.005	Rutgers	17240.54	6.7885	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPDRQPWTDKHPDLLTCGRCLQTFPLEAITAFMDHKKLGCQLFRGPSRGQGSEREELKALSCLRCGKQFTVAWKLLRHAQWDHGLSIYQTESEAPEAPLLGLAEVAAAVSAVVGPAAEAKSP
ZNF319	Q9P2F9	HR8348A.005	Rutgers	10653.04	8.5224	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKPLRCTLCERRFFSSSEFVQHRCDPAREKPLKCPDCEKRFKYASDLQRHRRVHTG
ZNF331	Q9NQX6	HR8085A.003	Rutgers	10275.33	7.7377	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKPYGCTECGKSFSHGHQLTQHQKTHSGAKSYECKECGKACNHLNHLREHQRIHNS
ZNF335	Q9H4Z2	HR8140B.005	Rutgers	16886.03	7.1172	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPMSSSTLAHSLAAIEALADGPTSTSTCLEAQGGPSSPVQLPPASGAEEPDLQSLEAMMEVVVVQQFKCKMCQYRSSTKATLLRHMRERHFRPVAAAAAAAGKKGRLRKWSTSTKSQEEEGP
ZNF337	Q9Y3M9	HR7962A.003	Rutgers	11470.89	8.7467	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKSYYSKHLKRHLREKRFCTG
ZNF343	Q6P1L6	HR7973A.002	Rutgers	9827.11	6.5078	Misc	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMEGKAQIVVPVTFRDVTVIFTEAEWKRLSPEQRNLYKEVMLENYRNLLSL
ZNF394	Q53GI3	HR7003A.006	Rutgers	15077.01	5.7374	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMAASPDPETSRLHFRQLRYQEVAGPEEALSRLRELCRRWLRPELLSKEQILELLVLEQFLTILPEELQAWVREHCPESGEEAVAVVRALQRALDGTS
ZNF397	Q8NF99	HR7436A.001	Rutgers	15453.27	4.5462	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMSTQSCQELFRQQFRKFCYQETPGPREALSRLQELCYQWLMPELHTKEQILELLVLEQFLSILPEELQIWVQQHNPESGEEAVTLLEDLEREFDDPG
ZNF41	P51814	HR6874B.004	Rutgers	23158.3	9.0487	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMALRMHQRIHTGEKPYVCADCGKAFIQKSHFNTHQRIHTGEKPYECSDCGKSFTKKSQLHVHQRIHTGEKPYICTECGKVFTHRTNLTTHQKTHTGEKPYMCAECGKAFTDQSNLIKHQKTHTGEKPYKCNGCGKAFIWKSRLKIHQKSHIGERHYECKDCGKAFIQ
ZNF423	Q2M1K9	HR7298C.003	Rutgers	9308.65	8.3622	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMLPYPCQFCDKSFIRLSYLKRHEQIHSDKLPFKCTYCSRLFKHK
ZNF425	Q6IV72	HR8124A.004	Rutgers	9713.99	7.6497	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMRPFQCPECGKGFLQKRSLKAHLCLHSGERPFSCDECGRSFTYVGALKTHIA
ZNF444	Q8N0Y2	HR7294A.006	Rutgers	13322.07	5.9532	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMFRRFHLGDAPGPREALGLLRALCRDWLRPEVHTKEQMLELLVLEQFLSALPADTQAWVCSRQPQSGEEAVALLEELWGPAASP

HGCN	Uniprot ID	Antigen ID	Antigen Source	MW (Da)	pI	Common Domain Names	Primary Validation (pass/fail)	construct seq (with tag)
ZNF446	Q9NWS9	HR8393A.006	Rutgers	15898.1	6.1064	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPETARLRFRGFCYQEVAGPREALARLRELCCQWLQPEAHSKEQMLEMLVLEQFLGTLPPEIQAWVRGQRPGSPEEAAALVEGLQHDPGQLLGWITAHVLKQEVLP
ZNF449	Q6P9G9	HR7503A.003	Rutgers	15288.37	5.7421	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMDCEVFRQRFRQFQYREAAGPHEAFNKLWELCCQWLKPKMRSKEQILELLVLEQFLTILPTEIETWVREHCPENRERVVSLIEDLQRELEIPE
ZNF462	Q96JM2	HR8320B.004	Rutgers	20308.31	6.1262	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMEVLQCDGCDFRAPSYEDLKAHIQDVHTAFLQPTDVAEDNVNELRCGSVNASNQTEVEFSSIKDEFAIAEDLSGQNATSLGTGGYYGHSPGYYGQHIAANPKPTNKFFQCKFCVRYFRSKNLLIEHTRKVHGAQAEGSSSGPPVPGSLNY
ZNF483	Q8TF39	HR7266B.002	Rutgers	14434.4	5.9572	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMAESFRQRFRWFCYSEVAGPRKALSQLWELCNQWLRPDIHTKEQILELLVFEQFLTILPGEIRIWVKSQHPESSEEVVTLIEDLTQML
ZNF485	Q8NCK3	HR8114A.002	Rutgers	11798.14	8.0727	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMEKGLDWEGRSSTEKNYKCKECGKVFKYNSSFISHQRNHTSEKPHKCKECGIAFMNSSSLLNHHKVHAG
ZNF490	Q9ULM2	HR7094B.006	Rutgers	19219.55	6.853	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPMVEALCENKEDCPCGKSTSQIPDLNTNLETPTGLKPCDCSVCGEVFMHQVSLNRHMRSHTEQKPNECHEYGEKPHKCKECGKTFTRSSSIRTHERIHTGEKPYECKECGKAFAFLFSFRNHIRIHTGETPYE
ZNF496	Q96IT1	HR7429A.005	Rutgers	14780.59	6.0199	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGELPSPESSRRLFRRFRYQEAAGPREALQRLWDLCGGWLRPERHTKEQILELLVLEQFLAILPREIQSWVRAQEPESGEQAVAAVEALEREPG
ZNF500	O60304	HR7635A.002	Rutgers	15057.22	6.7931	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPSPETFRQLFRLFCYQEVAGPREALSRLWELCCRWLRPELRTKEQILELLVLEQFLTVLPGEIQARVREQQPESGEEAVVLVEGLQRKPRKHR
ZNF512	Q96ME7	HR8068B.004	Rutgers	19584.32	8.2479	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMAKIAVYHLQELASAELAKEWPKRKVLQDLVPDDRKLKYTRPGLPTFSQEVLHKWKTDIKKYHRIQCPNQGCEAVYSSVSGLKAHLGSCTLGNFVAGKYKCLLCQKEFVSESGVKYHINSVHAEDWFVVNPTTTKSFE
ZNF512B	Q96KM6	HR8051B.003	Rutgers	19224.77	7.9314	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGRVRRTSAQVAVFHLQEIAEDELARDWTKRRMKDDLVPETARLNYTRPGLPTLNPQLLEAWKNEVKEKGHVNCPNDCCEAIYSSVSGLKAHLASCSKGAHLAGKYRCLLCPKEFSSESGVKYHILKTHAENWFR
ZNF516	Q92618	HR7203B.002	Rutgers	21207.72	7.851	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPSKAAQELRTLATCAAGSRGDAALQAQPGVAGAPPVLHSIKQEPVAEGHEKRLDILNIFKTYIPKDFATLYQGWGVSGPGLEHRGTLRTQARPGEFVCIECGKSFHQPGHLRAHMRAHSVVFESDGPRGSEVHTTSADAPKQGRDHSNTGTVQTVPLRKGT
ZNF519	Q8TB69	HR8275A.004	Rutgers	9423.66	8.984	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGHQKIHTGEKPYKCKKCDKAFNKSSHLAQHQRIHTGEKPFKCKECGK
ZNF521	Q96K83	HR8035F.010	Rutgers	10240.5	6.7326	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGEYICNQCGAKYTSLDSFQTHLKTHLDTVLPKLTCPQCNKEFPNQESLLKHVTIT
ZNF521	Q96K83	HR8035F.008	Rutgers	10276.54	6.7889	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGEYICNQCGAKYTSLDSFQTHLKTHLDTVLPKLTCPQCNKEFPNQESLLKHVTIH
ZNF521	Q96K83	HR8035H.004	Rutgers	19954.73	7.1069	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMEPMYGCDICGAAYTMETLLQNHQLRDHNIRPGESAIVKKKAELIKGNYKCNVCSRTFFSENGLREHMQTHLGPVKHYMCPICGERFPSLLTLTEHKVTHSKSLDTGNCRICKMPLQSEEEFLEHCQMHPDLRNSLTGFR
ZNF526	Q8TF50	HR7651B.005	Rutgers	16038.29	6.8503	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPRLPITGLYNKSPYYCGTCGRWFRAMAGLRLHQRVHARARTLTLQPPRSPSPAPPPPPEPQQTIMCTELGETIAIIETSQPLALEDTLQLCQAALGASEAGGLLQLDTAFV
ZNF536	O15090	HR6910B.003	Rutgers	20493.62	6.7996	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPLQRNHEDTLANAGVLFDKEKREYVLVGADGSKQKMPADLVHSTKVGSQRDLPSKLDPLESSRDFLSHGLNQTLEYNLQGPGNMKEKPTECPDCGRVFRTYHQVVVHSRVHKRDRKGEEDGLHVGLDERRGSGSDQESQSVSRSTTPG
ZNF540	Q8NDQ6	HR7987A.003	Rutgers	10705.15	8.7553	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGKAFSVCGQLTRHQKIHTGVKPYECKECGKTFRLSFYLTEHRRTHAGKKPYECKECGK
ZNF541	Q9H0D2	HR8055A.002	Rutgers	10702.84	5.3753	Misc	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMEPHINIGSRFQAEIPELQERSLAGTDEHVASLVWKPWGDMMISSETQDRVTELCNVACSS
ZNF552	Q9H707	HR7308B.005	Rutgers	18114.23	7.2081	NA	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPMAGVSPKKAHPCEMCGPILGDILHVADHQGTHHKQKLHRCEAWGNKLYDSGNFHQHQNEHIGEKPYRGSVEEALFAKRCKLHVSGESSVFSESGKDFLLRSGLLQQEATHTGKSNSKTECVSLFHGG
ZNF556	Q9HAH1	HR7560B.006	Rutgers	15096.02	10.0605	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPRPSTDVKSQTREKVYKCETCGKTYGWSSSLHKHERKHTGEKPVNAASVGKPSGGLCSSKNVRTQIGQKPSKCEKCGKAFSCPKAFQGHVRSHTGKKSCTSK
ZNF564	Q8TBZ8	HR7852B.004	Rutgers	16833.95	8.1142	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGRILRNHMEEGLSESKEYDQCGEAFSQILNLNLNKKIPTIVRPCECSLCGKVFMHHSSLSRHIRSHLGHKPYDYQEYGEKPYKCKQCGKAFSSCQSFRRHERTHTGEKPY
ZNF566	Q969W8	HR6953A.002	Rutgers	14378.2	8.5126	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMCKECGKSFRHPSRLTHHQKIHTGKKPFECKECGKTFICGSDLTRHHRIHTGEKPYECKECGKAFSSGSNFTRHQRIHTGEKPYECKECGK
ZNF569	Q5MCW4	HR8322A.003	Rutgers	10309.72	8.668	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMTPFKCNHCGKGFNQTLDLIRHLRIHTGEKPYECSNCRKAFSHKEKLIKHYKIH
ZNF57	Q68EA5	HR7036B.003	Rutgers	21505.96	7.8198	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPNFTGNNSCAYTLEKNCEGYGTEDHHKNLRNHMVDRFCTHNEGNQYGEAIHQMPDLTLHKKVSAGEKPYECTKCRTVFTHLSSLKRHVKSHCGRKAPPGEECKQACICPSHLHSHGRTDTEEKPYKCQACGQTFQHPRYLSHHVKTHTAEKTY
ZNF570	Q96NI8	HR8437A.002	Rutgers	10003.2	7.9963	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKPYECTVCGKAFSYCGSLAQHQRIHTGERPYECKECKKTFRQHAHLAHHQR
ZNF571	Q7Z3V5	HR7898A.001	Rutgers	10279.49	7.6694	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKPYECKECGRAFSRGSELTLHQRIHTGEKPYTCVQCGKDFRCPSQLTQHTRLHN
ZNF583	Q96ND8	HR8213A.007	Rutgers	10733.98	7.7492	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKPYECNVCGKAFSYSGSLTLHQRIHTGERPYECKDCRKSFRQRAHLAHHERIHTMES
ZNF620	Q6ZNG0	HR7004A.005	Rutgers	12710.42	8.7813	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGKRLSSNTALTQHQRIHTGEKPFECKECGKAFNQKITLIQHQRVHTGEKPYECKVCGKTFSWCGRFILHQKLHTQ
ZNF622	Q969S3	HR7076B.004	Rutgers	30693.99	8.467	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPLGAIPITDCLFCSHHSSSLMKNVAHMTKDHSFFIPDIEYLSDIKGLIKYLGEKVGVGKICLWCNEKGKSFYSTEAVQAHMNDKSHCKLFTDGDAALEFADFYDFRSSYPDHKEGEDPNKAEELPSEKNLEYDDETMELILPSGARVGHRSLMRYYKQRFGLSRAVAVAKNRKAVGRVLQQYRALGWTGSTGAALMRERDMQYVQRMKSKWMLKTGMKNNATKQMHFRVQVRF
ZNF624	Q9P2J8	HR8004A.003	Rutgers	10175.38	8.0584	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMRPYKCEECGKAFRTNSDFTVHLRMHTGEKPYKCNECGKAFRSSSSSLTVHQRIH
ZNF625	Q96I27	HR8159B.003	Rutgers	15159.93	8.1652	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGERLLESKKDHQHGEILTQVPDDMLKKKTPRVKSCGEVSVGHASLNRHHRADTGHKPYEYQEYGQKPYKCTYCKKAFSDLPYFRTHEWAHTGGKPY
ZNF626	Q68DY1	HR8312A.005	Rutgers	10369.69	7.3433	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKFYKCEECGKAFKCSSNLTTHKKIHTGERPYKCEECGKAFNQSSILTTHERIILE
ZNF629	Q9UEG4	HR7999A.001	Rutgers	8268.31	6.4995	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGQNPKTLVEEKPYLCPECGAGFTEVAALLLHRSCHPGVSL
ZNF639	Q9UID6	HR7646A.006	Rutgers	10585.89	6.6178	Zinc Finger	pass	MGHHHHHHSHMDDCGKGFSSMLEYCKHLNSHLSEGIYLCQYCEYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERELISHLPVHETT
ZNF663P (ZNF663)	pseudo gene	HR8538B.003	Rutgers	16305.46	9.5	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMYTGEKPDECKENEKALKKLYHTQNERTHAGEKVYDCKKCGKFFHEKACLTQHQRTHTTGKPSKCNDSERVLKESCLTPNQRIKTRLKQERKTVKVINVRNLSLRS
ZNF670	Q9BS34	HR6925B.005	Rutgers	17859.19	7.2411	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPGRNLSSHVVERLFEIKEGSQYGETFSQDSNLNLNKKVSTGVKPCECSVCGKVFICHSALHRHILSHIGNKLFECEECPEKLYHCKQCGKAFISLTSVDRHMVTHTSNGPYKGPVYEKPFDFP
ZNF671	Q8TAW3	HR7883A.002	Rutgers	12274.76	8.6597	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKPHKSTKLVSGFLMGQRYHRCGECGKAFTRKDTLARHQRIHTGERPYECNECGKFFSQSYDLFKHQTVHTG
ZNF687	Q8N1G0	HR7327B.004	Rutgers	17275.34	7.6331	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPLRYRSSSSTEQSLMMGLRVEDGAQQCLDCGLCFASPGSLSRHRFISHKKRRGVGKASALGLGDGEEEAPPSRSDPDGGDSPLPASGGPLTCKVCGKSCDSPLNLKTHFRTHGMAFIRARQGAVGD
ZNF699	Q32M78	HR8203A.004	Rutgers	10793.19	8.1742	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKPFECLECGKAFSCPSSFRRHVRSHTGEKPYECKECGKAFVCPAYFRRHVKTHTRENI
ZNF70	Q9UC06	HR7964A.003	Rutgers	9649.89	8.6619	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKPYTCECGKAFRHRSALIEHYKTHTREKPYVCNLCGKSFRGSSHLIRH

HGCN	Uniprot ID	Antigen ID	Antigen Source	MW (Da)	pI	Common Domain Names	Primary Validation (pass/fail)	construct seq (with tag)
ZNF75D	P51815	HR7456A.005	Rutgers	14455.43	6.7529	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPESACRHFWSFRYHEATGPLETISQLQKLCHQWLRPEIHSKEQILEMLVLEQFLSILPKETQNWVQKHHPQNVKQALVLVEFLQREP
ZNF76	P36508	HR6964B.003	Rutgers	14212.92	8.8178	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGDRAFRCGYKGCGRLYTTAHHLKVHERAHTGDRPYRCDFPSCGKAFATGYGLKSHVRTHTGEKPYKCPEELCSKAFKTSGDLQKHVRTHTG
ZNF787	Q6DD87	HR7915B.003	Rutgers	15759.35	6.6176	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPRSRRAPAPKPYVCLECGKGFGHGAGLLAHQRAQHGDGLGAAGGEEPAHICVECGEGFVQGAALRRHKKIHAVGAPSVCSSCGQSYYRAGGEEEDDDDDEAAGGRCPECRGGEGR
ZNF800	Q2TB10	HR8132B.003	Rutgers	18547.92	8.8539	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPVEIVTDEVAPTSDEQPQESQADLETSDNSDFGHQLICCLCRKEFNSRRGVRRHIRKVHKKKMEELKKYIETRKNPNQSSKGRSKNVLVPLSRSCPVCCKSFATKANVRRHFDEVHRGLRRDSITP
ZNF808	Q8N4W9	HR7014B.005	Rutgers	24318.55	9.4334	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMSGEKPYKCSECSKTFSQKATLLCHRRLHSGEKPYKCNDCGNTFRHWSSLVYHRRLHTGEKSYKCTVCDKAFVRNSYLARHIRIHTAEKPYKCNECGKAFNEQSHLSRHHRIHTGEKPYKCEACDKVFSRKSHLKRHRIIHTGEKPYKCNECGKAFSDRSTLIHHQAIHGIGKFD
ZNF83	P51522	HR7002C.004	Rutgers	19926.34	8.437	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMYKCDECDKAFSQNSHLVQHHRIHTGEKPYKCDECGKVFSQNSYLAYHWRIHTGEKAYKCNECGKVFGLNSSLAHHRKIHTGEKPFKCNECGKAFSMRSSLTNHHAIHTGEKHFKCNECGKLFRDNSYLVRHQRFHAG
ZNF84	P51523	HR8403A.002	Rutgers	10734.09	9.3151	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKPYGCSECRKAFSQKSQLVNHQRIHTGEKPYRCIECGKAFSQKSQLINHQRTHTVKKS
ZNF845	Q96IR2	HR8361A.004	Rutgers	12645.36	9.8445	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMNQQAHLACHHRIHTGEKPYKCNECGKTFRHNSVLVIHKTIHTGEKPYKCNECGKVFNRKAKLARHHRIHTGKKH
ZNF98	A6NK75	HR8498A.007	Rutgers	13883.63	8.1014	Zinc Finger	fail	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMGEKPYKCEECGKAFNQSSHLTTHKMIHTGEKPYKCEECGKAFNNSSILNRHKMIHTGEKLYKPESCNNACDNIAKISKYKRNCAGEK
ZSCAN1	Q8NBB4	HR7933A.001	Rutgers	14645.56	7.078	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMADPGPASPRDTEAQRLRFRQFQYHVASGPHLALGQLWTLCRQWLRPEARSKEQMLELLVLEQFLGALPSKMRTWVQSQGPRSCREAASLVEDL
ZSCAN12	O43309	HR8495A.005	Rutgers	15535.22	4.9048	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMNNTHSREVFRQYFRQFCYQETSGPREALSRLRELCHQWLRPETHTKEQILELLVLEQFLTILPEELQAWVQEQHPESGEEVVTVLEDLERELDEPG
ZSCAN16	Q9H4T2	HR7081B.004	Rutgers	14868.82	6.3091	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPHRRELYRQHFRKLCYQDAPGPREALTQLWELCRQWLRPECHTKEQILDLLVLEQFLSILPKDLQAWVRAHHPETGEEAVTVLEDLEREL
ZSCAN18	Q8TBC5	HR7698A.001	Rutgers	13775.43	6.4287	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMLDSHIFQCRFGKMLPLEKAFASPRSSPAPPDLPTPGSAAGVQQEEPETIPERTPADLEFSRLRFREFVYQEAAGPHQTLARLHELCR
ZSCAN2	Q7Z7L9	HR8010A.004	Rutgers	13905.51	6.1065	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPFPQSAGKGGPQEEVTRGPQGALGRLRELCRRWLRPEVHTKEQMLTMLPKEIQAWLQEHRPESSEEAAALVEDLTQTLQDSETASCVH
ZSCAN20	P17040	HR7843A.002	Rutgers	14699.54	6.4304	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPEASRQRFRQFQYRDAAGPHEAFSQLWALCCRWLRPEIRLKEQILELLVLEQFLTILPREVQTWVQARHPESGEEAVALVEDWHRETRT
ZSCAN21	Q9Y5A6	HR7530A.005	Rutgers	15349.34	4.8824	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMKYLPSLEMFRQRFRQFGYHDTPGPREALSQLRVLCCEWLRPEIHTKEQILELLVLEQFLTILPQELQAWVQEHCPESAEEAVTLLEDLERELDEP
ZSCAN22	P10073	HR7904A.001	Rutgers	14790.6	6.1266	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMDHIAHSEAARLRFRHFRYEEASGPHEALAHLRALCCQWLQPEAHSKEQILELLVLEQFLGALPPEIQAWVGAQSPKSGEEAAVLVEDLTQVLDKRG
ZSCAN23	Q3MJ62	HR7247A.004	Rutgers	15788.72	6.065	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMSRNNPHTREIFRRRFRQFCYQESPGPREALQRLQELCHQWLRPEMHTKEQILELLVLEQFLTILPEELQAWVRQHRPVSGEEAVTVLEDLERELDDP
ZSCAN25 (ZNF498)	Q6NSZ9	HR7643A.006	Rutgers	14310.21	6.1637	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMDPSPETFRLRFRQFRYQEAAGPQEALRELQELCRRWLRPELHTKEQILELLVLEQFLTILPREFYAWIREHGPESGKALAAMVEDL
ZSCAN26 (ZNF187)	Q16670	HR8379A.005	Rutgers	14473.37	5.4475	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMPLCKQFRQLRYEETTGPREALSRLRELCQQWLQPETHTKEQILELLVLEQFLIILPKELQARVQEHHPESREDVVVVLEDLQLDLGET
ZSCAN29	Q8IWY8	HR8429A.001	Rutgers	15474.25	5.2533	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMENGTNSETFRQRFRRFHYQEVAGPREAFSQLWELCCRWLRPEVRTKEQIVELLVLEQFLTVLPGEIQNWVQEQCPENGEEAVTLVEDLEREPGRPR
ZSCAN30	Q86W11	HR6932A.005	Rutgers	15613.49	4.9361	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMENPWSQEVFRQKFRQFSYSDSTGPREALSRLRELCCQWLRPEVHSKEQILELLMLEQFLAILPEELQAWLREHRPENGEEAVTMLEELEKELEEPR
ZSCAN31 (ZNF323)	Q96LW9	HR7473A.002	Rutgers	15265.96	4.8922	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMNNFSGQEASRQLFRQFCYQETPGPREALSRLRELCHQWLRPEIHTKEQILELLVLEQFLTILPEELQAWVREHHPESGEEAVAVVEDLEQELSEPG
ZSCAN5A	Q9BUG6	HR6950A.006	Rutgers	14441.59	6.1026	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMDVDPEISHVNFRMFSCPKESDPIQALRKLTELCHLWLRPDLHTKEQILDMLVMEQFMISMPQELQVLVMMNGVQSCKDLEDLLRNNRR
ZSCAN5B	A6NJL1	HR8432B.004	Rutgers	14325.46	6.4276	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMETWHMNFRMFSCPEESDPIQALRKLTELCHLWLRPDLHTKEQILDMLVMEQFMISMPQELQVLVKVNGVQSCKDLEDLLRNNRRPK
ZSCAN5C	A6NGD5	HR7759A.005	Rutgers	14433.54	6.1019	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMDSDPETCHVNFRMFSCPKESDPIQALRKLTELCHLWLRPDLHTKEQILDMLVMEQFMISMPQELQVLVMMNGVQSCKDLEDLLRNNRR
ZSCAN9 (ZNF193)	O15535	HR7141A.006	Rutgers	14870.83	5.92	SCAN	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMSNPLAREIFRRHFRQLCYQETPGPREALTRLQELCYQWLRPHVSTKEQILDLLVLEQFLSILPKELQGWVREHCPESGEEAVILLEDLERE
ZXDA	P98168	HR7812B.005	Rutgers	18095.38	8.1931	Zinc Finger	pass	MSGLNDIFEAQKIEWHEHHHHHHHENLYFQSHMFKCEVCEESFPTQAKLGAHQRSHFEPERPYQCAFSGCKKTFITVSALFSHNRAHFREQELFSCSFPGCSKQYDKACRLKIHLRSHTGERPFLCDFDGCGWNFTSMSKLLRHKRKHDDDRR

Table SI 2. 32 antigens were expressed in three expression systems (*E. coli,* IVTT, and YAD) shown with the number of Fabs that successfully passing the primary vaildation (Competition ELISA and Sequence Unique) pipeline. NA represents antigens that failed to produce enough purified protein to enter the Fab selection pipeline. Success rate was determined when ≥2 Fabs passed primary validation for a given antigen.

	# Primary Validation Passing Fabs		
Antigen	*E.coli*	IVTT	YAD
ARID3A	NA	1	1
ARX	2	6	1
ATF2	2	3	3
ATF4	26	NA	4
ATF7	40	7	0
CDX2	3	1	1
CEBPB	0	1	3
CEBPG	0	4	3
DLX2	0	7	6
DLX5	8	9	1
ESR1	NA	1	1
ESRRA	NA	5	1
HES5	3	5	0
HNF1B	0	7	1
HNF4A	NA	NA	1
HOXA5	2	1	9
HOXB5	5	0	5
HOXB6	0	5	0
HOXB9	2	2	0
HOXD11	0	1	0
IRF2	1	13	0
NKX2-5	2	2	3
NKX6-1	7	2	3
NR4A2	NA	4	1
NR5A2	NA	6	4
RARA	NA	5	5
RARG	NA	3	1
RORA	NA	4	5
SIX3	2	0	1
SOX7	NA	4	7
SOX8	NA	1	8
TBX5	1	7	2
Success Ra	**41%**	**66%**	**47%**

Table SI 3: Recombinant Fabs were screened against 6 human cell lines by immunofluroesence. Multiple microscopic fields were anlyzed by the Perkin Elmer Opera imager software Columbus in an unbiased assessment of nuclear to cytoplasmic staining intensities that was used to generate a Nuclear/Ctyoplasmic Ratio as shown for each human cell type.

		293T	A2780	A2780cis	JHOC9	HepG2	HPAF-II
Gene	**Fab ID**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**
ALX3	Fab-ALX3-1.0	1.20	1.45	1.24	1.06	1.13	0.92
ALX3	Fab-ALX3-1.1	1.16	1.29	1.31	1.05	1.05	0.86
ALX3	Fab-ALX3-1.2	1.16	1.10	1.07	0.87	0.95	0.91
ALX3	Fab-ALX3-1.3	1.10	1.23	1.18	1.05	0.98	0.77
ALX3	Fab-ALX3-1.4	1.15	1.06	1.07	0.90	0.92	0.83
ALX3	Fab-ALX3-1.5	1.40	1.09	1.07	0.94	0.89	0.82
ANKZF1	Fab-ANKZF1-2.0	1.22	1.16	1.09	0.92	1.13	0.88
ANKZF1	Fab-ANKZF1-2.1	0.98	1.07	0.98	0.82	0.96	0.83
ANKZF1	Fab-ANKZF1-2.2	1.15	1.03	1.04	0.74	0.97	0.85
ARID3a	Fab-ARID3a-3.0	1.44	1.39	1.36	1.25	1.39	0.90
ARID3a	Fab-ARID3a-3.1	1.28	1.27	1.35	1.14	1.29	0.83
ARID3a	Fab-ARID3a-3.2	1.16	1.35	1.38	1.18	1.55	0.71
ARID3a	Fab-ARID3a-3.3	1.24	1.31	1.44	1.12	1.29	0.94
ARNT1_Domain1	Fab-ARNT1_Domain1-4.0	1.34	1.27	1.31	1.17	1.27	0.65
ARNT2_Domain2	Fab-ARNT2_Domain2-5.0	1.29	0.99	0.97	0.81	0.97	0.71
ARX	Fab-ARX-6.0	1.07	1.10	1.05	1.01	0.99	0.94
ASH1L	Fab-ASH1L-7.0	0.97	1.08	0.93	0.69	1.02	0.93
ASH1L	Fab-ASH1L-7.1	1.06	1.07	0.94	0.83	0.96	0.88
ASH1L	Fab-ASH1L-7.2	1.20	1.19	1.14	0.99	1.14	0.99
ASH1L	Fab-ASH1L-7.3	1.07	1.07	1.07	0.87	1.10	1.08
ATF1	Fab-ATF1-8.0	1.71	2.07	1.71	1.35	1.63	1.47
Atf2	Fab-Atf2-9.0	1.35	1.27	1.29	0.89	1.41	0.86
ATF4	Fab-ATF4-10.0	1.14	0.98	1.03	0.97	1.02	0.96
ATF4	Fab-ATF4-10.1	1.10	1.37	1.06	0.91	1.09	0.91
ATF4	Fab-ATF4-10.2	1.34	1.44	1.21	1.04	1.24	0.73
ATF4	Fab-ATF4-10.3	1.13	1.31	1.04	0.94	1.02	0.91
ATF4	Fab-ATF4-10.4	1.25	1.34	1.05	0.91	1.13	0.67
Atf7	Fab-Atf7-11.0	1.02	0.95	0.96	0.53	0.99	0.54
Atf7	Fab-Atf7-11.1	1.27	1.05	1.05	0.69	1.10	0.50
Atf7	Fab-Atf7-11.2	1.23	0.80	1.03	0.53	1.06	0.66
Atf7	Fab-Atf7-11.3	1.10	0.97	1.02	0.72	1.10	0.64
BARX	Fab-BARX-12.0	1.11	1.09	0.94	0.81	0.85	0.77
BAZ1A/ACF2	Fab-BAZ1A/ACF2-13.0	1.12	1.22	1.12	1.02	1.11	0.95
BAZ2A	Fab-BAZ2A-14.0	0.99	1.12	0.95	0.79	0.96	0.80
BAZ2A	Fab-BAZ2A-14.1	0.97	0.92	0.76	0.78	0.84	0.68
BAZ2A	Fab-BAZ2A-14.2	1.06	1.24	0.97	0.93	1.00	1.00
BAZ2A	Fab-BAZ2A-14.3	1.05	1.21	1.01	0.92	1.12	0.93
BCL2A1	Fab-BCL2A1-15.0	1.13	1.14	1.06	0.91	1.09	0.94
BRD4	Fab-BRD4-16.0	0.96	1.21	0.93	0.91	1.18	0.79
BRD4	Fab-BRD4-16.1	1.02	0.97	0.83	0.63	0.93	0.76
BRD4	Fab-BRD4-16.2	1.08	1.09	0.96	0.80	1.04	0.77
BRD4	Fab-BRD4-16.3	0.99	1.11	0.96	0.82	1.30	0.88
BRD4	Fab-BRD4-16.4	1.04	1.35	1.04	0.95	1.23	1.16
BRDT	Fab-BRDT-17.0	1.08	1.07	0.97	0.69	1.02	0.91
BRDT	Fab-BRDT-17.1	1.00	1.10	0.92	0.77	0.92	0.85
BRDT	Fab-BRDT-17.2	0.92	1.04	0.98	0.77	0.94	0.86
BRDT	Fab-BRDT-17.3	1.12	1.09	1.00	0.91	1.09	1.00
BRDT	Fab-BRDT-17.4	0.90	0.97	0.85	0.65	0.88	0.88
BRPF1	Fab-BRPF1-18.0	1.08	1.12	1.01	0.82	0.99	1.02
BRPF1	Fab-BRPF1-18.1	0.99	1.12	1.01	0.89	0.97	0.94
BRPF1	Fab-BRPF1-18.2	1.14	1.24	1.13	0.95	1.14	1.00
BRWD1/WDR9	Fab-BRWD1/WDR9-19.0	0.98	1.23	0.95	1.01	1.18	0.96

		293T	A2780	A2780cis	JHOC9	HepG2	HPAF-II
Gene	**Fab ID**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**
BRWD1/WDR9	Fab-BRWD1/WDR9-19.1	1.08	1.23	1.02	0.97	1.07	0.86
BUB1	Fab-BUB1-20.0	0.94	1.09	0.93	0.77	1.00	0.84
BUB1	Fab-BUB1-20.1	1.07	1.15	0.99	0.90	1.04	0.71
CBX1	Fab-CBX1-21.0	1.04	1.39	1.01	1.04	1.24	0.89
CBX1	Fab-CBX1-21.1	1.14	1.01	0.78	0.48	1.15	0.85
CBX1	Fab-CBX1-21.2	1.10	1.18	0.92	1.00	1.10	0.89
CBX1	Fab-CBX1-21.3	1.10	1.11	1.00	0.70	1.17	0.85
CBX1	Fab-CBX1-21.4	1.12	0.93	0.80	0.48	1.06	0.81
CBX2	Fab-CBX2-22.0	1.03	1.04	0.87	0.69	1.01	0.86
CBX2	Fab-CBX2-22.1	1.14	0.98	0.81	0.70	1.00	0.73
CBX2	Fab-CBX2-22.2	1.10	1.61	0.99	0.87	1.15	0.70
CBX5	Fab-CBX5-23.0	0.99	1.10	1.00	0.83	1.01	0.67
CBX5	Fab-CBX5-23.1	1.21	1.02	0.90	0.80	1.24	0.79
CDC5L	Fab-CDC5L-24.0	1.26	1.98	1.02	0.82	1.14	0.98
CDC5L	Fab-CDC5L-24.1	0.91	2.22	1.22	1.27	1.55	1.13
CDC5L	Fab-CDC5L-24.2	0.97	1.77	1.14	1.07	1.37	1.09
CDC5L	Fab-CDC5L-24.3	0.99	1.60	0.96	0.78	1.20	0.84
CDX2	Fab-CDX2-25.0	1.05	1.10	1.01	0.99	1.06	0.93
CDX2	Fab-CDX2-25.1	1.07	1.14	1.07	0.98	1.05	0.79
CDX2	Fab-CDX2-25.2	1.13	0.86	0.90	0.60	0.99	0.59
CDX2	Fab-CDX2-25.3	1.12	1.18	1.06	1.00	1.13	0.98
CEBPG	Fab-CEBPG-26.0	1.09	1.30	1.21	0.85	1.08	0.64
CEBPG	Fab-CEBPG-26.1	1.19	1.18	1.11	0.80	1.35	0.69
CEBPG	Fab-CEBPG-26.2	1.65	1.51	1.22	0.95	1.39	0.75
CEBPG	Fab-CEBPG-26.3	1.34	1.19	1.19	0.91	1.16	0.87
CEBPG	Fab-CEBPG-26.4	1.08	1.07	1.00	0.65	1.06	0.86
CEBPG	Fab-CEBPG-26.5	1.11	1.08	1.08	0.84	1.07	1.05
CEBPG	Fab-CEBPG-26.6	1.02	1.05	1.17	1.02	1.12	0.94
CEBPG	Fab-CEBPG-26.7	1.43	1.07	1.14	1.00	0.88	0.77
CEBPG	Fab-CEBPG-26.8	1.11	1.06	1.05	0.92	0.90	0.75
CEBPG	Fab-CEBPG-26.9	1.09	1.09	1.12	0.93	0.94	0.83
CHD1	Fab-CHD1-27.0	1.05	1.29	1.12	1.07	1.33	0.96
CHD1	Fab-CHD1-27.1	1.94	2.05	2.41	1.66	2.59	2.31
CHD4	Fab-CHD4-28.0	1.22	1.95	1.15	1.08	1.66	1.56
CHD4	Fab-CHD4-28.1	1.12	2.14	1.25	1.05	1.17	1.38
CHD4	Fab-CHD4-28.2	1.01	1.75	1.06	1.06	1.55	1.38
CREB3L4	Fab-CREB3L4-29.0	1.31	1.60	1.52	1.40	1.43	1.15
CREB3L4	Fab-CREB3L4-29.1	0.99	1.03	0.91	0.78	0.90	0.84
CREBBP	Fab-CREBBP-30.0	1.09	1.15	1.03	0.92	1.04	0.86
CREBBP	Fab-CREBBP-30.1	0.86	1.03	0.77	0.70	1.00	0.85
CSNK2B	Fab-CSNK2B-31.0	2.15	2.01	2.15	1.43	1.72	1.24
CSNK2B	Fab-CSNK2B-31.1	1.45	1.72	1.67	1.23	1.44	0.83
CSNK2B	Fab-CSNK2B-31.2	1.28	1.27	1.20	1.09	1.08	0.94
CSNK2B	Fab-CSNK2B-31.3	1.00	1.18	0.91	0.86	1.11	0.88
CSNK2B	Fab-CSNK2B-31.4	1.12	1.24	0.88	1.00	1.25	0.90
DLX1	Fab-DLX1-32.0	2.11	2.82	1.68	1.27	2.13	1.94
Dlx2	Fab-Dlx2-33.0	1.43	1.04	1.09	0.90	1.03	0.83
DNMT3L	Fab-DNMT3L-34.0	1.12	1.11	1.05	0.98	1.06	0.96
DNMT3L	Fab-DNMT3L-34.1	1.06	1.09	1.02	0.97	1.03	1.03
DNMT3L	Fab-DNMT3L-34.2	1.11	1.06	1.02	0.89	1.04	0.74
ELF3	Fab-ELF3-35.0	1.18	1.05	1.04	0.94	1.01	0.82
ELF3	Fab-ELF3-35.1	1.32	1.23	1.19	1.10	1.18	1.00
ELF3	Fab-ELF3-35.2	1.39	1.34	1.41	1.21	1.25	0.96
ELF3	Fab-ELF3-35.3	1.17	1.12	1.37	0.95	1.18	0.74
ESRRA	Fab-ESRRA-36.0	1.00	1.04	0.87	0.69	0.90	0.81
ESRRA	Fab-ESRRA-36.1	0.95	1.03	0.86	0.81	0.93	0.66

		293T	A2780	A2780cis	JHOC9	HepG2	HPAF-II
Gene	**Fab ID**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**
ESRRA	Fab-ESRRA-36.2	0.99	1.07	0.99	0.82	0.93	0.71
EVX2	Fab-EVX2-37.0	1.09	1.12	0.94	0.80	0.93	0.78
EVX2	Fab-EVX2-37.1	1.06	1.14	1.17	1.04	1.12	0.84
FIZ1 (ZNF798)	Fab-FIZ1 (ZNF798)-38.0	1.21	1.16	1.15	1.08	1.15	0.76
FIZ1 (ZNF798)	Fab-FIZ1 (ZNF798)-38.1	1.46	1.49	1.37	1.31	1.45	0.82
FLI1	Fab-FLI1-39.0	1.34	1.14	1.00	0.83	0.95	0.64
FOXP1	Fab-FOXP1-40.0	1.17	1.03	1.12	0.75	1.02	0.68
FOXP1	Fab-FOXP1-40.1	1.08	0.98	1.06	0.83	0.97	0.60
FOXP1	Fab-FOXP1-40.2	1.43	1.00	0.96	0.83	0.98	0.40
FOXP1	Fab-FOXP1-40.3	1.11	1.07	0.97	0.75	0.95	0.64
FOXP1	Fab-FOXP1-40.4	1.24	1.12	1.33	1.00	0.96	0.90
FOXP4	Fab-FOXP4-41.0	1.10	1.25	1.18	0.90	1.08	0.69
FOXP4	Fab-FOXP4-41.1	1.39	1.23	1.11	0.89	1.20	0.42
FOXP4	Fab-FOXP4-41.2	1.34	1.31	1.34	1.10	0.99	0.84
FOXP4	Fab-FOXP4-41.3	1.20	1.08	1.04	0.86	0.97	0.52
FXR2	Fab-FXR2-42.0	1.02	0.82	0.84	0.79	1.11	0.86
FXR2	Fab-FXR2-42.1	1.13	0.86	0.80	0.63	1.25	0.77
GLI3	Fab-GLI3-43.0	1.32	1.63	1.06	1.05	0.97	0.82
GLI3	Fab-GLI3-43.1	1.53	1.15	1.08	1.02	1.02	0.91
GLI3	Fab-GLI3-43.2	1.25	1.19	1.22	1.06	1.14	1.26
GLI3	Fab-GLI3-43.3	1.67	1.23	1.12	1.01	1.32	0.93
GLI3	Fab-GLI3-43.4	2.16	1.25	1.15	1.18	1.21	0.84
GLI3	Fab-GLI3-43.5	1.13	1.06	1.06	1.06	1.09	0.92
GLIS2	Fab-GLIS2-44.0	0.97	1.07	1.04	0.89	1.04	0.82
GLIS2	Fab-GLIS2-44.1	1.12	1.10	1.09	0.86	1.00	0.64
GLIS2	Fab-GLIS2-44.2	1.08	1.04	1.04	1.01	1.24	0.94
GMEB2	Fab-GMEB2-45.0	1.15	1.19	1.13	0.80	1.05	0.82
GMEB2	Fab-GMEB2-45.1	1.49	1.03	1.12	0.62	1.00	0.75
H1FX	Fab-H1FX-46.0	1.27	1.38	1.26	1.02	1.09	0.80
H1FX	Fab-H1FX-46.1	0.97	1.18	0.94	0.85	1.05	0.91
H1FX	Fab-H1FX-46.2	0.99	1.27	1.08	1.04	1.14	1.01
H1FX	Fab-H1FX-46.3	0.89	1.09	0.94	0.74	0.90	0.88
HES1	Fab-HES1-47.0	1.71	1.95	1.59	1.11	1.73	1.41
HIC1	Fab-HIC1-48.0	1.17	1.21	1.18	1.04	1.14	0.82
hLRH	Fab-hLRH-49.0	1.25	1.02	1.05	0.64	1.06	0.84
hLRH	Fab-hLRH-49.1	1.14	1.08	1.19	0.73	1.04	0.83
HMBox1	Fab-HMBox1-50.0	1.36	1.22	1.15	1.12	1.20	0.73
HMBox1	Fab-HMBox1-50.1	1.36	1.23	1.26	0.99	1.08	0.53
HMBox1	Fab-HMBox1-50.2	1.17	1.05	1.53	0.50	1.02	0.68
HMBox1	Fab-HMBox1-50.3	1.40	1.24	1.28	0.92	1.12	0.70
HMG20B	Fab-HMG20B-51.0	1.13	1.44	1.31	1.14	1.13	0.95
HMG20B	Fab-HMG20B-51.1	1.15	1.14	0.98	0.81	0.97	0.76
HMGB1	Fab-HMGB1-52.0	1.42	1.24	1.26	0.97	1.04	0.75
HNF4A	Fab-HNF4A-53.0	1.05	1.03	0.99	0.97	1.02	0.70
HNF4A	Fab-HNF4A-53.1	1.11	0.85	0.86	0.50	0.93	0.81
HNF4A	Fab-HNF4A-53.2	0.99	0.93	0.94	0.71	0.92	0.68
HNF4A	Fab-HNF4A-53.3	1.30	1.10	1.15	0.77	1.07	0.87
HNF4A	Fab-HNF4A-53.4	1.02	0.95	0.99	0.50	1.00	0.65
HOXA10	Fab-HOXA10-54.0	1.07	1.09	1.04	0.78	0.96	0.91
HOXA10	Fab-HOXA10-54.1	1.12	0.99	1.01	0.84	0.98	0.75
HOXA10	Fab-HOXA10-54.2	1.13	1.09	1.02	0.91	1.02	0.84
HOXB3	Fab-HOXB3-55.0	1.12	1.17	1.08	0.89	1.07	0.80
HOXB3	Fab-HOXB3-55.1	1.22	1.28	1.17	0.99	1.09	0.87
HOXB5	Fab-HOXB5-56.0	1.55	1.78	1.66	1.09	1.10	0.97
HOXB5	Fab-HOXB5-56.1	1.50	1.36	1.14	1.19	1.31	1.12
HOXB5	Fab-HOXB5-56.2	1.16	1.16	1.19	0.91	1.32	0.84

		293T	A2780	A2780cis	JHOC9	HepG2	HPAF-II
Gene	**Fab ID**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**
HOXB5	Fab-HOXB5-56.3	1.07	1.07	0.96	0.77	0.92	0.68
HOXB9	Fab-HOXB9-57.0	1.37	1.39	1.18	1.07	1.17	0.89
HOXB9	Fab-HOXB9-57.1	1.12	1.21	1.11	0.93	1.01	0.96
HOXD3	Fab-HOXD3-58.0	1.27	1.30	1.06	0.93	0.95	0.75
HOXD8	Fab-HOXD8-59.0	1.03	1.08	1.15	0.97	0.94	0.77
HOXD8	Fab-HOXD8-59.1	1.12	1.12	1.19	0.98	1.15	0.85
Irf2	Fab-Irf2-60.0	1.24	1.15	1.16	0.88	1.06	0.83
Irf2	Fab-Irf2-60.1	1.27	1.16	1.08	0.78	1.11	0.86
IRF3	Fab-IRF3-61.0	1.13	1.05	0.94	0.84	0.77	0.69
IRF5	Fab-IRF5-62.0	1.25	1.33	1.09	0.95	1.15	0.81
IRF5	Fab-IRF5-62.1	1.14	1.40	0.95	0.84	1.06	0.77
IRF5	Fab-IRF5-62.2	1.19	1.14	0.93	0.85	1.07	0.76
IRF5	Fab-IRF5-62.3	1.16	1.31	0.90	0.84	1.04	0.82
IRF5	Fab-IRF5-62.4	1.22	1.25	0.98	0.85	0.99	0.73
IRF5	Fab-IRF5-62.5	1.07	1.27	1.06	0.93	1.01	0.93
IRF5	Fab-IRF5-62.6	1.14	1.31	1.09	0.95	1.01	0.91
IRF5	Fab-IRF5-62.7	1.15	1.35	1.09	0.95	1.13	0.94
IRF5	Fab-IRF5-62.8	1.08	1.16	1.09	0.96	1.03	0.93
IRF5	Fab-IRF5-62.9	1.02	1.15	1.06	0.98	0.94	0.97
IRF5	Fab-IRF5-62.10	1.31	1.25	0.97	0.80	0.96	0.63
IRF5	Fab-IRF5-62.11	1.11	1.18	1.12	0.93	1.03	0.88
IRF5	Fab-IRF5-62.12	1.23	1.23	0.94	0.81	1.03	0.72
IRF5	Fab-IRF5-62.13	1.14	1.13	1.08	0.97	0.96	0.92
IRF5	Fab-IRF5-62.14	1.13	1.29	1.08	0.84	1.01	0.77
IRF5	Fab-IRF5-62.15	1.16	1.21	0.99	0.87	1.01	0.60
IRF5	Fab-IRF5-62.16	1.15	1.26	1.03	0.93	1.03	0.90
IRF5	Fab-IRF5-62.17	1.07	1.17	1.06	1.00	0.96	0.90
IRF5	Fab-IRF5-62.18	1.17	1.22	1.04	0.90	0.97	0.88
IRF5	Fab-IRF5-62.19	1.19	1.21	1.06	0.95	0.97	0.80
IRF5	Fab-IRF5-62.20	1.13	1.25	1.13	1.00	1.01	0.80
IRF5	Fab-IRF5-62.21	1.17	1.25	0.99	0.86	1.00	0.75
IRF5	Fab-IRF5-62.22	1.03	1.04	1.11	0.99	1.57	0.96
IRF5	Fab-IRF5-62.23	1.05	1.04	1.13	0.94	0.90	0.73
IRF5	Fab-IRF5-62.24	1.06	1.14	1.21	0.99	1.01	0.80
IRF5	Fab-IRF5-62.25	1.10	1.19	1.24	1.05	1.15	0.78
IRF6	Fab-IRF6-63.0	1.03	1.18	1.19	0.99	1.14	0.85
IRF6	Fab-IRF6-63.1	1.29	1.33	1.39	1.21	1.06	0.75
IRF6	Fab-IRF6-63.2	1.21	1.26	1.17	1.09	1.00	0.82
IRF6	Fab-IRF6-63.3	1.09	1.15	1.18	0.98	1.02	0.92
IRF9	Fab-IRF9-64.0	1.15	1.20	1.02	0.85	0.87	0.65
JDP2	Fab-JDP2-65.0	1.17	1.14	1.12	1.01	1.03	0.79
JDP2	Fab-JDP2-65.1	1.30	1.48	1.49	1.19	1.00	0.70
JDP2	Fab-JDP2-65.2	1.14	1.12	1.19	1.01	0.99	0.71
JDP2	Fab-JDP2-65.3	1.16	1.11	1.14	0.91	0.94	0.72
JDP2	Fab-JDP2-65.4	1.23	1.63	1.60	1.23	1.03	0.76
JDP2	Fab-JDP2-65.5	1.03	1.04	1.15	0.97	1.09	0.93
JDP2	Fab-JDP2-65.6	1.15	1.16	1.19	0.97	0.96	0.75
JDP2	Fab-JDP2-65.7	1.24	1.14	1.17	0.89	0.93	0.80
JDP2	Fab-JDP2-65.8	1.05	1.08	1.09	0.88	0.97	0.74
JDP2	Fab-JDP2-65.9	1.03	1.02	1.01	0.80	0.82	
JDP2	Fab-JDP2-65.10	1.49	1.78	1.88	1.29	1.12	0.67
JMJD6	Fab-JMJD6-66.0	1.13	1.12	1.07	0.87	1.15	0.73
JMJD6	Fab-JMJD6-66.1	1.05	1.07	1.01	0.82	1.32	0.83
JMJD6	Fab-JMJD6-66.2	1.09	1.03	0.95	0.73	1.19	0.83
JMJD6/ PTDSRB	Fab-JMJD6/ PTDSRB-67.0	1.09	1.08	1.08	0.98	1.07	0.91
JMJD6/ PTDSRB	Fab-JMJD6/ PTDSRB-67.1	1.17	1.13	1.08	0.98	1.10	0.87

		293T	A2780	A2780cis	JHOC9	HepG2	HPAF-II
Gene	**Fab ID**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**
JMJD6/ PTDSRB	Fab-JMJD6/ PTDSRB-67.2	1.04	1.10	1.06	0.95	0.81	0.79
KAT2A/GCN5L2	Fab-KAT2A/GCN5L2-68.0	1.14	1.19	1.14	0.97	1.19	1.00
KAT2A/GCN5L2	Fab-KAT2A/GCN5L2-68.1	0.90	1.05	0.90	0.76	0.88	0.80
KAT2A/GCN5L2	Fab-KAT2A/GCN5L2-68.2	1.09	1.17	1.01	0.95	1.02	0.93
KAT2A/GCN5L2	Fab-KAT2A/GCN5L2-68.3	1.03	1.18	1.08	0.91	1.09	0.99
KAT2B/PCAF	Fab-KAT2B/PCAF-69.0	1.09	1.17	1.17	0.96	1.10	1.00
KDM2A/FBXL11A	Fab-KDM2A/FBXL11A-70.0	1.10	0.96	1.05	0.96	1.05	0.65
KDM2A/FBXL11A	Fab-KDM2A/FBXL11A-70.1	1.12	1.05	1.09	1.00	0.91	0.99
KDM2A/FBXL11A	Fab-KDM2A/FBXL11A-70.2	1.23	1.18	1.14	1.06	1.19	0.99
KDM2A/FBXL11A	Fab-KDM2A/FBXL11A-70.3	1.36	1.32	1.32	1.01	1.10	1.06
KDM2A/FBXL11A	Fab-KDM2A/FBXL11A-70.4	1.24	1.30	1.32	1.09	1.16	0.89
KDM3B/JMJD1B	Fab-KDM3B/JMJD1B-71.0	0.98	1.09	0.84	1.01	1.10	1.00
KDM3B/JMJD1B	Fab-KDM3B/JMJD1B-71.1	1.00	1.20	0.93	1.08	1.05	0.88
KDM3B/JMJD1B	Fab-KDM3B/JMJD1B-71.2	1.14	1.18	1.06	1.07	1.13	1.07
KDM3B/JMJD1B	Fab-KDM3B/JMJD1B-71.3	0.86	1.11	0.88	0.73	0.85	0.70
KDM4A	Fab-KDM4A-72.0	1.03	1.22	1.05	0.80	1.07	0.83
KDM4A/JMJD2A	Fab-KDM4A/JMJD2A-73.0	1.05	1.00	0.95	0.67	1.45	0.74
KDM4A/JMJD2A	Fab-KDM4A/JMJD2A-73.1	1.77	0.99	1.08	0.75	1.24	0.82
KDM4A/JMJD2A	Fab-KDM4A/JMJD2A-73.2	1.18	1.02	0.91	0.46	1.09	0.76
KDM4A/JMJD2A	Fab-KDM4A/JMJD2A-73.3	1.06	1.32	0.98	0.81	1.28	0.85
KDM4A/JMJD2A	Fab-KDM4A/JMJD2A-73.4	1.11	1.14	1.01	0.98	1.09	0.77
KDM4A/JMJD2A	Fab-KDM4A/JMJD2A-73.5	0.99	1.19	1.05	1.03	1.16	0.87
KDM4A/JMJD2A	Fab-KDM4A/JMJD2A-73.6	1.10	1.13	1.03	0.81	1.26	0.81
KDM7A/ JHDM1D/ KIAA1718C	Fab-KDM7A/ JHDM1D/ KIAA17	1.00	1.06	1.00	0.97	0.98	0.88
KDM7A/ JHDM1D/ KIAA1718C	Fab-KDM7A/ JHDM1D/ KIAA17	1.22	1.07	1.01	0.88	0.93	0.76
KLF8	Fab-KLF8-75.0	1.27	1.10	1.05	0.98	1.25	0.99
KLF8	Fab-KLF8-75.1	1.64	1.14	1.06	0.85	0.97	0.96
KLF8	Fab-KLF8-75.2	1.19	1.08	1.03	0.87	1.05	0.74
L3MBTL1	Fab-L3MBTL1-76.0	1.36	1.16	1.43	0.92	0.99	1.10
L3MBTL1	Fab-L3MBTL1-76.1	1.22	1.10	1.47	0.78	0.97	0.81
L3MBTL1	Fab-L3MBTL1-76.2	1.26	1.17	1.16	0.95	0.96	1.17
MAFB	Fab-MAFB-77.0	1.28	1.10	1.05	0.81	0.93	0.63
MAFB	Fab-MAFB-77.1	1.34	1.40	1.19	0.90	1.01	0.79
MAFB	Fab-MAFB-77.2	1.24	1.23	1.33	0.84	0.99	0.72
MAFB	Fab-MAFB-77.3	1.28	1.21	1.26	0.92	1.01	0.93
MAFB	Fab-MAFB-77.4	1.29	1.32	1.34	0.88	1.02	0.87
MAFB	Fab-MAFB-77.5	1.40	1.62	1.38	0.95	1.10	0.84
MBD4	Fab-MBD4-78.0	1.23	1.23	1.22	1.00	1.08	0.82
MBD4	Fab-MBD4-78.1	1.34	1.33	1.20	1.01	1.10	0.79
MBD4	Fab-MBD4-78.2	1.12	1.43	1.34	1.01	1.20	1.00
MLL3	Fab-MLL3-79.0	1.35	1.09	1.04	0.96	1.07	0.93
MLL3	Fab-MLL3-79.1	1.06	0.96	0.95	0.65	0.86	0.77
MLL3	Fab-MLL3-79.2	1.07	1.02	0.92	0.60	0.85	0.72
MSH6	Fab-MSH6-80.0	1.36	1.07	1.29	1.04	1.03	0.97
MSH6	Fab-MSH6-80.1	1.30	1.18	1.17	1.05	1.00	1.02
MSH6	Fab-MSH6-80.2	1.78	1.61	1.50	1.22	1.07	1.08
MSH6	Fab-MSH6-80.3	2.10	1.74	1.64	1.53	1.27	0.86
MSH6	Fab-MSH6-80.4	2.15	1.82	1.70	1.34	1.25	1.08
MTA1	Fab-MTA1-81.0	1.03	1.09	1.05	0.79	1.05	0.99
MTA1	Fab-MTA1-81.1	1.05	1.09	0.90	0.85	0.97	0.79
MTA1	Fab-MTA1-81.2	1.05	1.13	1.04	0.71	1.04	0.92
MTA1	Fab-MTA1-81.3	1.17	1.24	1.22	1.14	1.21	1.04
MTF1	Fab-MTF1-82.0	1.31	1.09	1.06	0.89	0.81	0.89
MZF1	Fab-MZF1-83.0	2.75	3.00	2.66	1.64	1.50	1.60
MZF1	Fab-MZF1-83.1	2.35	1.75	1.62	1.31	1.00	0.97
MZF1	Fab-MZF1-83.2	1.19	1.47	1.57	1.16	0.99	1.04

		293T	A2780	A2780cis	JHOC9	HepG2	HPAF-II
Gene	**Fab ID**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**
MZF1	Fab-MZF1-83.3	1.29	1.76	1.18	1.08	1.13	0.85
MZF1	Fab-MZF1-83.4	1.13	1.34	1.36	0.84	1.25	0.64
NEDD4L	Fab-NEDD4L-84.0	1.26	1.23	1.29	0.82	0.90	0.74
NEDD4L	Fab-NEDD4L-84.1	1.07	1.06	1.18	0.75	0.81	0.82
NEDD4L	Fab-NEDD4L-84.2	1.43	1.31	1.30	0.84	1.00	0.87
NEDD4L	Fab-NEDD4L-84.3	1.15	1.67	1.31	1.24	1.39	1.09
NFIL3	Fab-NFIL3-85.0	1.33	1.28	1.28	1.02	1.15	0.63
NFU1	Fab-NFU1-86.0	1.07	1.23	1.07	0.88	1.10	0.93
NKX2-5	Fab-NKX2-5-87.0	1.11	1.07	1.01	0.88	0.84	0.70
NR1D1	Fab-NR1D1-88.0	1.69	1.40	1.15	1.19	1.04	0.85
NR1D1	Fab-NR1D1-88.1	1.41	1.64	1.06	1.09	1.00	0.80
NR1D1	Fab-NR1D1-88.2	1.29	1.22	1.06	0.83	1.08	0.64
NR1D2	Fab-NR1D2-89.0	1.29	1.65	1.43	1.08	1.24	0.92
NR1D2	Fab-NR1D2-89.1	1.20	1.20	1.15	1.07	1.22	0.92
NR1D2	Fab-NR1D2-89.2	1.36	1.22	1.05	0.93	0.93	0.90
NR1D2	Fab-NR1D2-89.3	1.52	1.12	1.08	0.93	1.19	1.06
NR1D2	Fab-NR1D2-89.4	1.29	1.16	1.12	1.05	1.29	1.01
NR1D2	Fab-NR1D2-89.5	1.21	1.36	1.15	0.93	0.91	0.79
NR1D2	Fab-NR1D2-89.6	1.20	1.16	1.21	0.85	1.06	0.68
NR2F6	Fab-NR2F6-90.0	1.43	1.19	1.20	1.15	1.32	0.81
NR4A2	Fab-NR4A2-91.0	1.30	1.05	1.06	0.95	1.11	0.74
NR4A3	Fab-NR4A3-92.0	1.07	1.00	1.08	0.90	1.10	0.95
NR4A3	Fab-NR4A3-92.1	1.34	1.46	1.35	0.75	1.16	0.80
NR4A3	Fab-NR4A3-92.2	1.36	1.23	1.14	0.86	0.95	0.69
NR4A3	Fab-NR4A3-92.3	1.54	1.25	1.10	0.67	1.12	0.79
NR4A3	Fab-NR4A3-92.4	1.35	1.50	1.29	0.86	1.05	0.75
NR4A3	Fab-NR4A3-92.5	1.06	1.21	1.10	0.84	0.87	0.68
NR5A1	Fab-NR5A1-93.0	1.11	1.06	1.04	0.89	0.97	0.71
NR5A1	Fab-NR5A1-93.1	1.21	1.08	1.09	0.93	1.07	0.83
NR5A1	Fab-NR5A1-93.2	1.10	1.35	1.10	1.03	1.16	0.99
NR5A1	Fab-NR5A1-93.3	1.31	1.09	0.95	0.92	0.80	0.83
NR5A2	Fab-NR5A2-94.0	1.62	1.42	1.38	1.34	1.52	0.68
NR5A2	Fab-NR5A2-94.1	1.21	1.09	1.11	0.99	1.13	0.77
NR6A1	Fab-NR6A1-95.0	1.23	1.24	1.29	1.09	1.20	1.02
NR6A1	Fab-NR6A1-95.1	0.99	1.28	1.11	0.71	0.79	0.67
NR6A1	Fab-NR6A1-95.2	1.20	1.47	1.29	0.69	1.01	0.68
NR6A1	Fab-NR6A1-95.3	1.45	1.30	1.16	0.88	1.07	0.73
NR6A1	Fab-NR6A1-95.4	1.18	1.31	1.28	0.83	1.26	0.82
NR6A1	Fab-NR6A1-95.5	1.08	0.96	0.90	0.53	0.94	0.63
NR6A1	Fab-NR6A1-95.6	0.87	1.06	1.00	0.93	1.03	0.93
NR6A1	Fab-NR6A1-95.7	0.96	1.04	1.02	0.91	0.93	0.95
NRF1	Fab-NRF1-96.0	1.47	1.41	1.32	1.08	1.11	0.79
NRF1	Fab-NRF1-96.1	1.18	1.35	1.23	1.02	1.16	1.02
NRF1	Fab-NRF1-96.2	1.23	1.47	1.10	0.85	1.12	0.96
NRL	Fab-NRL-97.0	2.85	2.87	2.50	1.77	1.51	1.67
NRL	Fab-NRL-97.1	1.82	1.70	1.09	0.90	0.98	0.96
NRL	Fab-NRL-97.2	1.20	1.27	1.26	0.99	1.02	0.99
NRL	Fab-NRL-97.3	1.07	1.03	1.00	0.98	1.14	0.97
NSD1	Fab-NSD1-98.0	0.98	0.96	0.85	0.78	0.80	0.76
OR138.004	Fab-OR138.004-99.0	1.24	1.34	1.14	0.90	1.14	0.91
OTX2	Fab-OTX2-100.0	1.28	1.23	1.70	1.31	1.13	0.70
OTX2	Fab-OTX2-100.1	1.25	1.24	1.53	1.19	1.01	0.71
PAX6	Fab-PAX6-101.0	1.15	1.19	1.02	0.82	0.90	0.73
PAX7	Fab-PAX7-102.0	2.07	1.97	3.00	1.75	1.83	1.07
PAX7	Fab-PAX7-102.1	1.33	1.37	1.24	1.09	1.28	0.91
PBRM1/PB1A	Fab-PBRM1/PB1A-103.0	1.10	1.21	1.06	1.03	1.09	0.85

		293T	A2780	A2780cis	JHOC9	HepG2	HPAF-II
Gene	**Fab ID**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**
PBRM1/PB1A	Fab-PBRM1/PB1A-103.1	1.19	1.37	1.28	1.12	1.26	1.07
PBRM1/PB1A	Fab-PBRM1/PB1A-103.2	1.21	1.27	1.19	1.01	1.17	0.97
PBRM1/PB1A	Fab-PBRM1/PB1A-103.3	1.06	1.57	1.30	1.27	1.39	1.40
PBRM1/PB1A	Fab-PBRM1/PB1A-103.4	1.17	1.54	1.25	1.10	1.30	1.37
PBRM1/PB1A	Fab-PBRM1/PB1A-103.5	1.54	1.45	1.45	1.06	1.42	1.34
PBRM1/PB1A	Fab-PBRM1/PB1A-103.6	0.97	1.15	0.91	0.75	0.97	0.95
PBX1	Fab-PBX1-104.0	1.19	1.25	1.26	1.13	1.01	0.76
PBX1	Fab-PBX1-104.1	1.33	1.26	1.44	1.14	1.09	0.87
PBX3	Fab-PBX3-105.0	3.13	3.08	2.66	1.90	2.79	1.68
PBX4	Fab-PBX4-106.0	1.44	1.28	1.12	0.91	1.26	0.86
PBX4	Fab-PBX4-106.1	1.45	1.20	1.20	0.93	1.49	0.85
PBX4	Fab-PBX4-106.2	1.26	1.32	1.14	0.90	1.04	0.74
PBX4	Fab-PBX4-106.3	1.00	1.18	1.08	0.79	0.83	0.67
PDCD2	Fab-PDCD2-107.0	1.08	0.96	0.81	0.71	0.81	0.73
PDCD2	Fab-PDCD2-107.1	1.03	1.01	0.89	0.82	0.98	1.10
PGBD1	Fab-PGBD1-108.0	1.20	1.30	1.29	0.93	1.28	0.60
PGBD1	Fab-PGBD1-108.1	1.42	1.01	1.05	0.73	0.90	0.47
PGBD1	Fab-PGBD1-108.2	1.46	1.21	1.19	0.87	1.07	0.46
PGBD1	Fab-PGBD1-108.3	1.02	2.41	3.11	1.36	1.63	0.96
PGBD1	Fab-PGBD1-108.4	1.08	2.85	2.31	1.63	1.60	1.00
PIKFYVE	Fab-PIKFYVE-109.0	1.46	1.08	1.18	0.97	1.15	0.89
PIKFYVE	Fab-PIKFYVE-109.1	1.22	1.10	1.09	0.86	1.20	0.66
PIKFYVE	Fab-PIKFYVE-109.2	0.94	0.83	0.93	0.70	0.98	0.53
PIKFYVE	Fab-PIKFYVE-109.3	1.31	0.90	0.99	0.67	1.08	0.52
PITX2	Fab-PITX2-110.0	1.09	1.06	1.03	0.89	1.05	0.92
PITX2	Fab-PITX2-110.1	1.37	0.94	0.78	0.67	0.84	0.76
POU2F2	Fab-POU2F2-111.0	1.08	1.04	1.09	0.84	0.88	0.83
POU2F3	Fab-POU2F3-112.0	1.13	1.02	0.90	0.76	0.85	0.75
POU6F1	Fab-POU6F1-113.0	1.23	1.23	1.16	0.95	1.08	0.84
POU6F1	Fab-POU6F1-113.1	1.07	1.17	0.91	0.83	1.02	0.83
POU6F1	Fab-POU6F1-113.2	1.23	1.27	1.14	0.96	1.08	0.76
POU6F1	Fab-POU6F1-113.3	1.10	1.17	1.12	0.97	1.14	0.80
POU6F1	Fab-POU6F1-113.4	1.24	1.32	1.12	0.94	1.12	0.76
POU6F1	Fab-POU6F1-113.5	1.11	1.20	1.07	0.94	0.80	0.72
POU6F1	Fab-POU6F1-113.6	1.11	1.26	1.05	0.94	1.03	0.89
POU6F1	Fab-POU6F1-113.7	1.05	1.17	1.24	1.00	1.14	0.95
POU6F1	Fab-POU6F1-113.8	1.22	1.27	1.25	0.99	1.19	0.86
POU6F1	Fab-POU6F1-113.9	0.99	1.04	0.85	0.91	0.96	0.81
POU6F1	Fab-POU6F1-113.10	1.08	1.17	1.22	0.97	1.11	0.85
POU6F1	Fab-POU6F1-113.11	1.24	1.39	1.39	1.12	1.25	0.80
POU6F1	Fab-POU6F1-113.12	1.05	1.18	1.29	0.99	1.12	0.90
POU6F1	Fab-POU6F1-113.13	1.12	1.18	1.18	0.89	1.05	0.83
PRDM11	Fab-PRDM11-114.0	1.40	1.44	1.12	1.18	0.97	1.05
PRDM11	Fab-PRDM11-114.1	1.29	1.17	1.29	1.04	0.99	1.08
PRDM11	Fab-PRDM11-114.2	1.27	1.26	1.37	1.10	0.96	0.93
PRDM11	Fab-PRDM11-114.3	1.33	1.22	1.25	1.14	0.95	0.92
PRDM11	Fab-PRDM11-114.4	1.56	1.29	1.41	1.04	1.02	1.11
PRDM14	Fab-PRDM14-115.0	2.12	1.11	1.10	0.76	1.05	0.68
PRDM14	Fab-PRDM14-115.1	1.27	1.13	1.11	0.72	1.12	0.83
PRDM14	Fab-PRDM14-115.2	0.99	0.84	0.87	0.44	1.03	0.71
PRDM14	Fab-PRDM14-115.3	1.09	1.09	1.12	0.88	1.05	0.70
PRDM14	Fab-PRDM14-115.4	0.82	1.12	1.04	0.82	1.10	0.70
PRDM4	Fab-PRDM4-116.0	1.22	1.39	1.48	1.16	0.98	1.20
PRDM9	Fab-PRDM9-117.0	1.33	1.14	1.36	1.04	1.00	1.12
PRDM9	Fab-PRDM9-117.1	1.45	1.07	1.33	0.90	1.05	0.99
PRDM9	Fab-PRDM9-117.2	1.22	1.15	1.29	0.63	1.01	1.05

		293T	A2780	A2780cis	JHOC9	HepG2	HPAF-II
Gene	**Fab ID**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**
PRDM9	Fab-PRDM9-117.3	1.50	1.34	1.58	0.69	1.01	0.72
PRDM9	Fab-PRDM9-117.4	1.28	1.29	1.48	0.66	0.97	0.90
PRDM9	Fab-PRDM9-117.5	1.27	1.84	1.42	0.84	0.93	0.81
PRMT5/SKB1	Fab-PRMT5/SKB1-118.0	1.21	1.28	1.45	0.89	0.95	0.82
PRMT5/SKB1	Fab-PRMT5/SKB1-118.1	1.33	1.31	1.40	1.04	1.04	1.17
PRMT5/SKB1	Fab-PRMT5/SKB1-118.2	1.41	1.23	1.30	0.86	0.95	0.92
PRMT5/SKB1	Fab-PRMT5/SKB1-118.3	1.35	1.25	1.24	1.01	0.94	0.80
PRMT5/SKB1	Fab-PRMT5/SKB1-118.4	1.30	1.12	1.23	1.04	0.99	0.96
PRMT5/SKB1	Fab-PRMT5/SKB1-118.5	1.42	1.24	1.34	0.77	1.08	1.04
PRMT5/SKB1	Fab-PRMT5/SKB1-118.6	1.30	1.19	1.27	1.12	1.15	1.06
PRMT5/SKB1	Fab-PRMT5/SKB1-118.7	1.33	1.21	1.25	1.11	1.08	1.11
PRMT5/SKB1	Fab-PRMT5/SKB1-118.8	1.21	1.15	1.22	0.96	1.02	0.82
PROP1	Fab-PROP1-119.0	1.10	1.17	0.92	0.78	0.88	0.82
PROP1	Fab-PROP1-119.1	1.09	1.19	1.06	0.99	1.00	0.91
PROP1	Fab-PROP1-119.2	1.20	1.39	1.02	0.88	1.10	0.76
PROP1	Fab-PROP1-119.3	1.11	1.20	1.08	0.95	1.01	0.89
PROP1	Fab-PROP1-119.4	1.21	1.17	1.04	0.89	1.06	0.76
PRRX2	Fab-PRRX2-120.0	1.95	1.27	1.08	0.82	1.33	0.89
RARA	Fab-RARA-121.0	1.23	1.13	1.16	0.99	1.15	0.82
RARA	Fab-RARA-121.1	1.06	1.32	1.27	1.01	1.13	0.94
RARG	Fab-RARG-122.0	1.26	1.16	1.03	0.96	0.69	0.88
RARG	Fab-RARG-122.1	1.25	1.29	1.22	1.02	1.22	0.99
RARG	Fab-RARG-122.2	1.27	1.29	1.31	1.12	1.34	1.25
RARG	Fab-RARG-122.3	1.44	1.10	1.07	0.97	1.15	0.93
RARG	Fab-RARG-122.4	1.32	1.05	1.02	0.99	0.88	0.56
RARG	Fab-RARG-122.5	1.15	1.06	1.06	1.00	1.06	0.91
RBAK	Fab-RBAK-123.0	1.55	1.55	1.69	1.17	1.24	0.96
RBAK	Fab-RBAK-123.1	2.49	1.37	1.60	1.21	1.21	0.88
RBAK	Fab-RBAK-123.2	1.39	1.26	1.31	1.01	1.23	0.84
RBAK	Fab-RBAK-123.3	1.09	1.26	1.27	0.92	1.34	0.81
RBAK	Fab-RBAK-123.4	1.35	1.43	1.62	1.09	1.20	0.89
RHOXF2	Fab-RHOXF2-124.0	1.03	1.12	0.98	0.81	0.99	0.89
RLF	Fab-RLF-125.0	1.45	1.00	0.76	0.65	0.77	0.69
RNMT	Fab-RNMT-126.0	1.12	1.18	1.03	0.87	1.09	0.91
RNMT	Fab-RNMT-126.1	1.19	1.55	1.34	1.21	1.41	1.51
RPRD1A	Fab-RPRD1A-127.0	2.39	2.49	2.47	1.44	1.34	1.58
RPRD1A	Fab-RPRD1A-127.1	1.56	1.39	1.11	1.03	1.15	1.02
RPRD1A	Fab-RPRD1A-127.2	1.56	1.44	1.29	0.76	1.09	0.80
RPRD1A	Fab-RPRD1A-127.3	2.36	2.14	2.08	1.49	1.35	0.98
RPRD1A	Fab-RPRD1A-127.4	1.37	1.25	1.21	0.58	1.03	1.05
RREB1	Fab-RREB1-128.0	1.42	1.46	1.29	1.08	1.23	0.86
RREB1	Fab-RREB1-128.1	1.27	1.13	0.81	0.69	0.92	0.73
SALL4	Fab-SALL4-129.0	1.26	2.04	1.27	1.11	1.00	0.81
SCML2	Fab-SCML2-130.0	1.41	1.31	1.29	1.06	1.02	1.05
SCML2	Fab-SCML2-130.1	1.46	1.30	1.51	1.18	1.33	1.00
SCML2	Fab-SCML2-130.2	1.24	1.09	1.23	0.98	0.98	0.85
SCML2	Fab-SCML2-130.3	1.50	1.40	1.45	0.96	1.04	1.09
SCML2	Fab-SCML2-130.4	1.44	1.21	1.15	0.91	0.96	1.27
SCML2	Fab-SCML2-130.5	1.42	1.32	1.30	1.01	1.04	0.99
SCML2	Fab-SCML2-130.6	1.70	1.43	1.52	1.08	1.08	1.19
SCML2	Fab-SCML2-130.7	1.77	1.30	1.52	0.84	0.99	1.16
SCML2	Fab-SCML2-130.8	1.36	1.12	1.28	1.02	1.08	1.02
SCML2	Fab-SCML2-130.9	1.12	1.21	1.16	0.76	1.02	0.94
SCML2	Fab-SCML2-130.10	1.40	1.63	1.47	1.03	1.08	0.97
SCML2	Fab-SCML2-130.11	1.40	1.15	1.16	0.89	0.98	0.70
SCML2	Fab-SCML2-130.12	1.37	1.18	1.17	0.83	1.04	0.73

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Gene	**Fab ID**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**
SETD7	Fab-SETD7-131.0	1.16	1.02	1.40	0.80	1.11	1.08
SETD7	Fab-SETD7-131.1	1.20	1.04	1.13	0.83	1.00	0.87
SETD7	Fab-SETD7-131.2	1.41	1.17	1.27	0.75	1.02	0.73
SETD7	Fab-SETD7-131.3	1.32	1.24	1.46	1.03	1.06	0.91
SETD7	Fab-SETD7-131.4	1.32	1.16	1.33	0.85	1.00	1.08
SETDB1	Fab-SETDB1-132.0	1.21	1.12	1.12	0.72	1.00	0.66
SETDB1	Fab-SETDB1-132.1	1.30	1.22	1.20	0.80	0.99	0.67
SETDB1	Fab-SETDB1-132.2	1.31	1.21	1.05	0.84	0.98	0.75
SETDB1	Fab-SETDB1-132.3	1.74	1.63	1.51	0.79	1.26	0.87
SETDB1	Fab-SETDB1-132.4	1.15	1.15	1.12	0.88	0.90	0.69
SHOX2	Fab-SHOX2-133.0	1.04	1.14	1.10	0.94	1.08	0.92
SHOX2	Fab-SHOX2-133.1	1.19	1.09	1.17	0.97	0.95	0.77
SHOX2	Fab-SHOX2-133.2	1.17	1.07	1.15	0.94	0.90	0.70
SIRT1	Fab-SIRT1-134.0	1.20	1.08	1.07	0.94	0.99	0.89
SIRT1	Fab-SIRT1-134.1	1.11	1.05	1.07	0.92	1.03	1.00
SIRT1	Fab-SIRT1-134.2	1.04	1.01	1.00	0.62	0.85	0.78
SIRT1	Fab-SIRT1-134.3	1.22	1.08	0.90	0.94	1.02	0.95
SIRT5	Fab-SIRT5-135.0	1.19	1.16	1.18	1.06	1.11	0.72
SIRT5	Fab-SIRT5-135.1	1.11	1.04	1.07	0.95	1.07	0.82
SIRT5	Fab-SIRT5-135.2	1.10	1.06	1.07	0.93	1.02	0.91
SIRT5	Fab-SIRT5-135.3	1.08	1.01	1.02	0.76	0.82	0.52
SIRT5	Fab-SIRT5-135.4	1.20	1.13	1.15	1.06	1.07	1.18
SIRT5	Fab-SIRT5-135.5	1.24	1.16	1.65	1.17	0.98	0.90
SIRT5	Fab-SIRT5-135.6	1.32	1.29	1.33	0.91	1.19	0.73
SIRT5	Fab-SIRT5-135.7	1.20	1.31	1.29	0.96	1.08	1.07
SIRT5	Fab-SIRT5-135.8	1.22	1.15	1.31	0.81	1.04	0.78
SIRT7	Fab-SIRT7-136.0	1.21	1.23	1.23	1.14	0.99	0.73
SIX1	Fab-SIX1-137.0	1.20	1.28	1.13	0.98	1.24	0.83
SIX2	Fab-SIX2-138.0	1.21	1.36	1.34	1.08	1.10	0.85
SMAD2	Fab-SMAD2-139.0	1.06	0.92	0.96	0.72	1.03	0.79
SMAD2	Fab-SMAD2-139.1	1.12	0.99	1.07	0.74	1.01	0.76
SMAD3	Fab-SMAD3-140.0	1.03	1.56	1.07	1.07	1.03	0.87
SMAD3	Fab-SMAD3-140.1	1.05	1.27	1.26	0.92	1.14	0.90
SMAD3	Fab-SMAD3-140.2	1.20	1.29	1.23	1.02	1.19	0.81
SMAD3	Fab-SMAD3-140.3	0.99	1.21	1.19	0.98	1.11	0.89
SMAD3	Fab-SMAD3-140.4	1.03	1.92	3.18	1.48	1.83	1.12
SMAD3	Fab-SMAD3-140.5	1.03	1.28	1.50	0.94	1.11	0.59
SMARCA1/ SNF2L	Fab-SMARCA1/ SNF2L-141.0	1.09	1.22	0.83	1.00	1.04	0.93
SMARCA1/SNF2L	Fab-SMARCA1/SNF2L-142.0	1.13	1.15	1.07	0.99	1.08	0.86
SMARCA4	Fab-SMARCA4-143.0	1.32	1.13	1.22	0.82	0.98	0.94
SMARCA4	Fab-SMARCA4-143.1	1.23	1.15	1.60	1.02	1.23	1.08
SMARCA4	Fab-SMARCA4-143.2	1.40	1.12	1.17	0.74	0.94	0.52
SMARCA4	Fab-SMARCA4-143.3	1.20	1.17	1.39	0.97	1.22	0.96
SMARCA4	Fab-SMARCA4-143.4	1.14	1.16	1.17	0.88	1.13	1.04
SMARCC2	Fab-SMARCC2-144.0	1.55	1.00	1.03	0.54	1.02	0.72
SMARCC2	Fab-SMARCC2-144.1	1.55	0.80	0.85	0.46	0.99	0.86
SMARCE1	Fab-SMARCE1-145.0	1.02	1.32	1.45	0.84	1.08	0.91
SMU1	Fab-SMU1-146.0	1.10	1.06	1.05	1.03	0.98	1.10
SMU1	Fab-SMU1-146.1	0.99	1.33	1.31	0.99	1.14	0.93
SMU1	Fab-SMU1-146.2	1.44	2.73	2.97	1.75	3.19	2.00
SMURF1	Fab-SMURF1-147.0	1.25	1.46	1.49	0.86	1.28	0.91
SMURF1	Fab-SMURF1-147.1	1.91	1.48	1.32	0.82	1.17	0.81
SMURF1	Fab-SMURF1-147.2	1.24	1.28	1.21	0.79	0.93	0.75
SMURF1	Fab-SMURF1-147.3	1.57	1.19	1.10	0.81	0.84	0.78
SMURF1	Fab-SMURF1-147.4	1.21	1.27	1.06	0.87	0.89	0.85
SMYD2	Fab-SMYD2-148.0	1.26	1.14	1.22	0.95	1.10	0.67

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Gene	**Fab ID**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**
SMYD2	Fab-SMYD2-148.1	1.50	1.13	1.20	0.76	1.23	1.03
SOX12	Fab-SOX12-149.0	1.05	1.05	0.89	0.73	0.80	0.63
SOX12	Fab-SOX12-149.1	1.08	1.13	1.19	0.92	0.92	0.83
SOX12	Fab-SOX12-149.2	1.37	1.51	1.46	1.25	1.09	0.65
SOX12	Fab-SOX12-149.3	1.05	0.89	1.00	0.62	0.81	0.71
SOX12	Fab-SOX12-149.4	1.57	1.78	1.77	1.43	1.25	1.00
SOX12	Fab-SOX12-149.5	1.01	1.07	1.05	0.83	0.78	0.77
SOX13	Fab-SOX13-150.0	1.25	1.21	1.00	0.84	1.01	0.81
SOX13	Fab-SOX13-150.1	1.33	1.32	1.07	1.00	1.13	0.95
SOX13	Fab-SOX13-150.2	1.02	0.98	1.05	0.86	0.75	0.76
SOX18	Fab-SOX18-151.0	1.20	1.01	0.91	0.73	0.83	0.68
SOX21	Fab-SOX21-152.0	1.00	0.90	0.87	0.74	0.75	0.71
SOX30	Fab-SOX30-153.0	1.19	1.21	1.16	1.02	1.09	0.91
SOX30	Fab-SOX30-153.1	1.17	1.18	0.97	0.81	1.07	0.82
SOX30	Fab-SOX30-153.2	1.10	1.23	1.22	0.96	1.08	0.76
SOX30	Fab-SOX30-153.3	1.12	1.16	1.14	0.94	1.01	0.94
SOX30	Fab-SOX30-153.4	1.13	1.22	1.28	1.07	1.09	0.94
SOX30	Fab-SOX30-153.5	1.12	1.15	1.20	0.86	1.07	0.91
SOX30	Fab-SOX30-153.6	1.18	1.12	1.05	0.72	0.97	0.98
SOX30	Fab-SOX30-153.7	1.29	1.25	1.09	1.01	1.12	0.99
SOX30	Fab-SOX30-153.8	1.21	1.32	1.26	1.13	1.06	0.80
SOX30	Fab-SOX30-153.9	1.07	1.20	1.00	0.81	1.14	
SOX30	Fab-SOX30-153.10	1.09	1.13	1.14	0.92	0.93	0.68
SOX30	Fab-SOX30-153.11	1.15	1.17	1.19	0.96	0.94	0.73
SOX30	Fab-SOX30-153.12	1.11	1.23	1.23	0.95	1.13	0.90
SOX30	Fab-SOX30-153.13	1.27	1.21	1.14	1.05	1.05	0.89
SOX4	Fab-SOX4-154.0	1.45	1.42	1.26	0.91	1.14	0.74
SOX4	Fab-SOX4-154.1	1.24	1.37	1.31	0.90	1.18	0.82
SOX4	Fab-SOX4-154.2	1.28	1.20	1.10	0.84	1.00	0.66
SOX4	Fab-SOX4-154.3	1.15	1.22	1.23	0.85	0.90	0.62
SOX4	Fab-SOX4-154.4	1.26	1.16	1.10	0.72	0.86	0.82
SOX4	Fab-SOX4-154.5	1.23	1.40	1.20	0.85	1.25	0.76
SOX4	Fab-SOX4-154.6	1.33	1.17	1.09	0.82	1.03	0.71
SOX4	Fab-SOX4-154.7	1.33	1.19	1.09	0.88	0.88	0.77
SOX4	Fab-SOX4-154.8	1.05	1.16	1.30	0.98	1.02	0.86
SOX4	Fab-SOX4-154.9	1.33	1.18	1.30	0.99	1.10	0.95
Sox7	Fab-Sox7-155.0	1.17	1.09	1.21	0.92	1.22	0.95
Sox7	Fab-Sox7-155.1	1.22	0.99	1.01	0.63	1.07	0.68
Sox7	Fab-Sox7-155.2	1.17	1.20	1.26	0.99	1.64	0.58
Sox7	Fab-Sox7-155.3	1.05	0.97	1.06	0.83	1.07	0.76
SP2	Fab-SP2-156.0	1.44	1.30	1.16	1.19	1.00	0.89
SP2	Fab-SP2-156.1	1.16	1.32	1.00	0.96	0.94	0.78
SP2	Fab-SP2-156.2	1.29	1.35	1.11	1.03	1.18	0.97
SP2	Fab-SP2-156.3	1.21	1.24	1.15	1.01	1.18	0.92
SP2	Fab-SP2-156.4	1.33	1.26	1.12	0.88	1.02	0.73
SP2	Fab-SP2-156.5	1.29	1.42	1.21	0.91	1.24	0.61
SP4	Fab-SP4-157.0	1.24	1.08	1.09	0.99	1.06	0.92
SP4	Fab-SP4-157.1	1.14	0.97	1.08	0.84	1.04	0.93
SP4	Fab-SP4-157.2	1.11	0.98	0.71	0.49	0.73	0.80
SP7	Fab-SP7-158.0	1.35	0.97	1.01	0.68	0.96	0.77
SP7	Fab-SP7-158.1	1.24	1.08	1.11	0.82	0.97	0.79
SP7	Fab-SP7-158.2	1.35	1.07	1.20	0.79	1.06	0.73
SPDEF	Fab-SPDEF-159.0	1.08	1.43	1.45	1.16	1.28	0.97
STAT1	Fab-STAT1-160.0	1.10	1.35	1.20	0.95	1.16	1.15
SUPT6H	Fab-SUPT6H-161.0	1.13	2.91	2.67	1.86	2.78	2.53
SUPT6H	Fab-SUPT6H-161.1	1.15	2.08	1.47	1.33	1.67	1.26

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Gene	**Fab ID**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**
SUPT6H	Fab-SUPT6H-161.2	3.60	2.88	2.24	1.79	2.46	2.04
SUPT6H	Fab-SUPT6H-161.3	1.25	2.51	2.03	1.74	2.40	1.70
TBL1X	Fab-TBL1X-162.0	1.28	1.22	1.23	0.95	1.05	1.08
TBL1X	Fab-TBL1X-162.1	1.41	1.53	1.45	1.16	1.16	1.09
TBL1X	Fab-TBL1X-162.2	1.44	1.51	1.55	1.38	1.17	1.23
TBL1X	Fab-TBL1X-162.3	1.45	1.61	1.32	1.34	1.34	1.22
TBX4	Fab-TBX4-163.0	1.08	1.21	0.91	0.94	1.09	0.75
TBX4	Fab-TBX4-163.1	1.10	1.13	1.07	1.02	1.08	0.96
TBX4	Fab-TBX4-163.2	1.02	1.07	1.01	0.91	1.00	0.86
TBX5	Fab-TBX5-164.0	1.47	1.17	1.26	0.82	1.02	0.96
TBX5	Fab-TBX5-164.1	1.22	1.32	1.11	1.02	1.05	0.65
TBX5	Fab-TBX5-164.2	1.04	1.19	0.91	0.88	0.98	0.71
TBX5	Fab-TBX5-164.3	1.04	1.45	1.31	1.13	1.22	0.89
TBX5	Fab-TBX5-164.4	1.14	1.12	1.08	0.92	1.09	0.89
Tbx5	Fab-Tbx5-164.5	0.97	1.00	1.13	0.76	1.02	0.73
TDRD3	Fab-TDRD3-165.0	1.32	1.29	1.38	1.17	1.32	0.95
TDRD3	Fab-TDRD3-165.1	1.58	1.22	1.36	1.15	1.27	1.02
TDRKH/TDRD2	Fab-TDRKH/TDRD2-166.0	0.76	1.08	1.18	0.72	1.00	0.82
TDRKH/TDRD2	Fab-TDRKH/TDRD2-166.1	1.25	1.02	1.28	0.76	0.97	0.84
TDRKH/TDRD2	Fab-TDRKH/TDRD2-166.2	0.94	0.94	0.96	0.59	0.97	0.90
TDRKH/TDRD2	Fab-TDRKH/TDRD2-166.3	1.24	1.24	0.86	0.57	1.09	0.95
TDRKH/TDRD2	Fab-TDRKH/TDRD2-166.4	1.23	1.44	1.27	0.82	0.98	0.94
TRIM24/TIF1A	Fab-TRIM24/TIF1A-167.0	1.15	1.44	1.09	1.06	1.17	1.04
TRIM24/TIF1A	Fab-TRIM24/TIF1A-167.1	1.12	2.37	2.21	1.47	2.28	1.59
TRPS1	Fab-TRPS1-168.0	1.06	1.00	0.78	0.64	0.87	0.99
TRPS1	Fab-TRPS1-168.1	1.14	1.12	1.01	0.93	1.08	0.95
TRPS1	Fab-TRPS1-168.2	1.11	1.24	1.08	0.84	1.11	1.06
TSC22D4	Fab-TSC22D4-169.0	1.42	1.20	1.32	0.95	1.35	0.77
TSC22D4	Fab-TSC22D4-169.1	1.08	1.14	1.18	0.85	1.07	0.76
TSC22D4	Fab-TSC22D4-169.2	2.11	0.99	1.03	0.55	0.96	0.64
TSC22D4	Fab-TSC22D4-169.3	1.16	1.01	1.07	0.70	1.05	0.67
TSC22D4	Fab-TSC22D4-169.4	1.12	1.06	1.08	0.80	1.13	0.72
TSC22D4	Fab-TSC22D4-169.5	1.16	1.11	1.21	0.77	1.04	0.81
TSC22D4	Fab-TSC22D4-169.6	1.15	1.05	1.04	0.68	1.16	0.77
TSC22D4	Fab-TSC22D4-169.7	1.01	1.11	0.91	0.80	1.20	0.82
TSC22D4	Fab-TSC22D4-169.8	1.05	1.00	0.93	0.74	1.00	0.75
UBH14	Fab-UBH14-170.0	1.27	1.22	1.34	0.93	1.20	0.77
UHRF1	Fab-UHRF1-171.0	1.45	1.64	1.61	1.34	1.40	1.46
UHRF1	Fab-UHRF1-171.1	1.27	1.33	1.29	1.04	1.18	1.04
UHRF1	Fab-UHRF1-171.2	1.15	1.05	1.49	0.99	0.99	0.93
UHRF2	Fab-UHRF2-172.0	1.64	1.83	1.94	1.38	1.56	1.19
UHRF2	Fab-UHRF2-172.1	1.29	1.23	1.28	1.09	1.06	0.83
UNCX	Fab-UNCX-173.0	1.06	0.85	1.07	0.80	0.78	0.71
UNCX	Fab-UNCX-173.1	1.27	1.27	0.93	0.64	1.01	0.76
UNCX	Fab-UNCX-173.2	1.55	1.19	1.35	1.16	1.10	0.64
UNCX	Fab-UNCX-173.3	1.21	0.82	0.82	0.57	0.51	0.55
UNCX	Fab-UNCX-173.4	0.80	1.13	1.11	0.99	0.86	0.69
USP13	Fab-USP13-174.0	1.38	1.14	1.08	0.88	1.06	0.79
USP13	Fab-USP13-174.1	1.72	1.50	1.40	0.97	1.05	0.92
USP13	Fab-USP13-174.2	1.53	1.14	1.08	0.83	0.99	0.79
USP7	Fab-USP7-175.0	1.52	1.34	1.31	1.01	1.26	0.97
USP7	Fab-USP7-175.1	1.26	1.51	1.44	1.12	1.22	1.10
USP7	Fab-USP7-175.2	1.57	1.44	1.52	1.08	1.19	1.00
USP7	Fab-USP7-175.3	1.07	1.47	1.15	0.89	0.92	0.72
USP7	Fab-USP7-175.4	1.31	1.30	1.50	1.09	1.37	0.85
USP7	Fab-USP7-175.5	1.47	1.26	1.41	1.10	1.39	1.07

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Gene	**Fab ID**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**
USP7	Fab-USP7-175.6	1.11	1.44	1.43	0.91	1.23	0.84
USP7	Fab-USP7-175.7	1.24	1.46	1.18	0.93	1.19	0.80
VAX1	Fab-VAX1-176.0	1.15	1.13	0.99	0.62	0.84	0.79
VAX2	Fab-VAX2-177.0	1.19	1.11	1.07	0.83	1.04	0.69
VENTX	Fab-VENTX-178.0	0.99	1.02	1.05	0.90	0.97	0.89
VENTX	Fab-VENTX-178.1	1.02	1.03	0.94	0.61	0.83	0.91
VSX1	Fab-VSX1-179.0	1.08	1.16	1.30	0.97	1.10	0.83
VSX1	Fab-VSX1-179.1	1.06	1.13	1.23	0.94	1.00	0.93
VSX1	Fab-VSX1-179.2	1.08	1.19	1.20	0.94	0.97	0.77
VSX1	Fab-VSX1-179.3	1.31	1.33	1.26	1.12	1.02	0.81
VSX1	Fab-VSX1-179.4	1.26	1.28	1.27	0.99	1.05	0.92
WDR12	Fab-WDR12-180.0	1.27	1.22	1.09	1.05	1.16	0.66
WDR12	Fab-WDR12-180.1	2.37	2.34	3.34	1.53	1.80	0.98
WDR12	Fab-WDR12-180.2	1.30	3.31	2.96	1.67	2.60	1.19
WDR45	Fab-WDR45-181.0	1.31	2.04	1.89	1.25	1.53	1.04
WDR45	Fab-WDR45-181.1	1.09	1.56	1.17	1.07	1.34	0.98
WDR45	Fab-WDR45-181.2	0.96	0.99	0.92	0.69	0.93	0.80
WDR48	Fab-WDR48-182.0	1.18	1.02	0.99	0.84	0.98	0.82
WDR48	Fab-WDR48-182.1	1.09	1.04	1.07	1.04	1.06	0.96
WDR48	Fab-WDR48-182.2	0.98	1.02	0.99	0.75	0.93	0.81
WDR5	Fab-WDR5-183.0	1.20	1.17	1.02	0.67	0.99	0.82
WDR5	Fab-WDR5-183.1	1.31	1.13	1.43	1.06	1.07	1.18
WDR5	Fab-WDR5-183.2	1.15	0.94	1.44	1.01	1.01	1.04
WDR5	Fab-WDR5-183.3	1.85	1.33	1.25	0.87	1.03	1.03
WDR5	Fab-WDR5-183.4	1.13	1.26	1.14	0.69	1.18	0.98
WDR5	Fab-WDR5-183.5	1.17	1.13	1.06	0.85	1.08	0.71
WDR82	Fab-WDR82-184.0	1.06	0.99	0.98	0.77	0.91	0.80
ZBTB16	Fab-ZBTB16-185.0	1.15	1.05	0.95	0.74	0.93	0.90
ZBTB16	Fab-ZBTB16-185.1	2.46	1.35	0.99	0.98	1.04	0.82
ZBTB16	Fab-ZBTB16-185.2	1.36	1.25	1.07	0.87	0.94	0.89
ZBTB16	Fab-ZBTB16-185.3	1.37	1.46	1.02	0.99	1.00	0.84
ZBTB16	Fab-ZBTB16-185.4	0.98	0.98	0.96	0.74	0.78	0.72
ZBTB16	Fab-ZBTB16-185.5	0.97	0.96	0.83	0.63	0.68	0.95
ZBTB16	Fab-ZBTB16-185.6	1.28	1.15	1.10	0.92	0.76	0.88
ZBTB21 (ZNF295)	Fab-ZBTB21 (ZNF295)-186.0	1.11	1.06	1.10	0.81	1.03	0.94
ZBTB24	Fab-ZBTB24-187.0	2.47	1.20	1.01	1.01	1.00	0.67
ZBTB24	Fab-ZBTB24-187.1	1.11	1.34	1.42	1.16	1.23	0.98
ZBTB24	Fab-ZBTB24-187.2	1.63	1.20	1.22	0.95	1.29	0.82
ZBTB24	Fab-ZBTB24-187.3	1.38	1.18	1.31	0.95	1.30	0.71
ZBTB24	Fab-ZBTB24-187.4	1.38	1.34	1.45	0.96	1.24	0.81
ZBTB24	Fab-ZBTB24-187.5	1.35	1.49	1.38	0.92	1.18	0.73
ZBTB32	Fab-ZBTB32-188.0	1.68	1.09	1.09	1.03	1.15	0.70
ZBTB32	Fab-ZBTB32-188.1	1.14	1.21	1.13	1.04	1.18	0.74
ZBTB39	Fab-ZBTB39-189.0	1.04	1.00	1.06	0.86	0.93	0.54
ZBTB39	Fab-ZBTB39-189.1	0.99	0.99	0.98	0.79	0.86	0.57
ZBTB39	Fab-ZBTB39-189.2	1.07	1.03	1.02	0.64	0.96	0.62
ZBTB39	Fab-ZBTB39-189.3	1.05	1.04	1.03	0.94	0.99	0.85
ZBTB39	Fab-ZBTB39-189.4	0.91	1.09	0.98	0.61	0.89	0.77
ZBTB39	Fab-ZBTB39-189.5	1.17	1.22	1.21	1.04	1.25	0.53
ZBTB39	Fab-ZBTB39-189.6	1.04	1.04	1.22	0.79	1.05	0.60
ZBTB39	Fab-ZBTB39-189.7	1.06	1.29	1.36	0.95	1.25	0.63
ZBTB39	Fab-ZBTB39-189.8	1.22	1.12	1.31	0.72	1.19	0.77
ZBTB39	Fab-ZBTB39-189.9	1.08	1.20	1.28	0.98	1.12	0.52
ZBTB39	Fab-ZBTB39-189.10	1.44	1.47	1.40	1.15	1.29	0.55
ZBTB39	Fab-ZBTB39-189.11	1.33	1.25	1.17	1.05	1.06	0.96
ZBTB39	Fab-ZBTB39-189.12	1.18	1.12	1.46	0.89	1.01	0.56

		293T	A2780	A2780cis	JHOC9	HepG2	HPAF-II
Gene	**Fab ID**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**
ZBTB39	Fab-ZBTB39-189.13	1.18	1.12	1.34	0.81	0.90	0.57
ZBTB39	Fab-ZBTB39-189.14	1.48	1.56	1.65	1.26	1.40	0.52
ZBTB39	Fab-ZBTB39-189.15	1.36	1.14	1.48	0.99	0.92	0.54
ZBTB39	Fab-ZBTB39-189.16	1.29	1.27	1.51	0.87	0.88	0.55
ZBTB39	Fab-ZBTB39-189.17	1.24	1.00	1.03	0.95	0.90	0.59
ZBTB39	Fab-ZBTB39-189.18	1.36	1.18	1.08	0.79	1.09	0.67
ZBTB39	Fab-ZBTB39-189.19	0.87	1.18	1.11	0.96	1.08	0.86
ZBTB39	Fab-ZBTB39-189.20	1.39	1.34	1.33	1.12	1.09	1.15
ZBTB41	Fab-ZBTB41-190.0	1.19	1.00	1.08	0.91	0.98	0.84
ZBTB41	Fab-ZBTB41-190.1	1.33	1.46	1.12	1.01	1.06	0.92
ZBTB41	Fab-ZBTB41-190.2	1.24	1.12	1.17	1.03	1.03	0.93
ZBTB41	Fab-ZBTB41-190.3	1.16	1.07	1.03	0.93	0.89	0.81
ZBTB41	Fab-ZBTB41-190.4	1.17	1.14	1.02	0.91	1.06	0.73
ZBTB7B	Fab-ZBTB7B-191.0	1.22	1.18	1.11	0.96	0.96	0.81
ZBTB7B	Fab-ZBTB7B-191.1	1.12	1.12	1.04	0.87	0.98	0.62
ZBTB7B	Fab-ZBTB7B-191.2	1.24	1.14	1.09	0.96	1.12	0.85
ZBTB7B	Fab-ZBTB7B-191.3	1.11	1.22	1.16	0.82	0.93	0.80
ZBTB7B	Fab-ZBTB7B-191.4	1.34	1.30	1.47	0.85	1.31	1.13
ZBTB7B	Fab-ZBTB7B-191.5	1.19	1.36	1.12	0.89	0.86	0.86
ZBTB7B	Fab-ZBTB7B-191.6	1.04	1.22	1.07	0.87	0.83	0.63
ZBTB7b	Fab-ZBTB7b-191.7	1.02	1.38	1.41	1.01	1.21	0.85
ZEB2	Fab-ZEB2-192.0	1.03	1.00	0.98	0.93	0.94	0.86
ZFP3	Fab-ZFP3-193.0	1.12	1.03	1.01	0.69	0.98	0.85
ZFP64	Fab-ZFP64-194.0	1.01	1.01	0.93	0.76	0.88	0.81
ZFP64	Fab-ZFP64-194.1	1.03	1.05	1.07	1.00	1.04	0.95
ZFP69	Fab-ZFP69-195.0	1.16	1.11	1.08	0.91	0.96	0.77
ZFP69	Fab-ZFP69-195.1	0.98	1.08	1.21	1.00	1.19	0.95
ZFP69	Fab-ZFP69-195.2	1.26	1.11	1.18	0.90	1.07	0.96
ZFP69 (ZNF642)	Fab-ZFP69 (ZNF642)-196.0	1.21	1.34	1.32	1.24	1.26	0.70
ZFP90	Fab-ZFP90-197.0	0.99	1.06	1.05	1.01	0.98	0.96
ZFP90	Fab-ZFP90-197.1	1.02	1.02	1.01	0.98	1.01	0.94
ZGPAT	Fab-ZGPAT-198.0	1.13	1.34	1.57	1.05	0.98	1.00
ZGPAT	Fab-ZGPAT-198.1	1.17	1.19	1.23	1.05	1.08	1.22
ZGPAT	Fab-ZGPAT-198.2	1.35	1.05	1.20	0.63	1.04	1.11
ZGPAT	Fab-ZGPAT-198.3	1.42	1.09	1.37	0.80	1.18	0.72
ZGPAT	Fab-ZGPAT-198.4	1.12	1.11	1.33	0.81	1.20	0.75
ZGPAT	Fab-ZGPAT-198.5	1.64	1.08	1.33	0.93	1.18	1.38
ZHX1	Fab-ZHX1-199.0	1.09	1.19	1.15	0.89	0.95	0.86
ZHX1	Fab-ZHX1-199.1	1.29	1.38	1.48	1.10	1.07	0.81
ZHX1	Fab-ZHX1-199.2	1.03	1.01	1.01	1.00	0.95	0.96
ZHX1	Fab-ZHX1-199.3	1.05	0.87	0.79	0.62	0.84	0.80
ZIC2	Fab-ZIC2-200.0	1.15	1.38	1.46	0.96	1.09	1.00
ZKSCAN1	Fab-ZKSCAN1-201.0	0.81	0.96	0.91	0.79	0.76	0.65
ZKSCAN1	Fab-ZKSCAN1-201.1	1.24	1.09	0.88	0.80	0.77	1.14
ZKSCAN1	Fab-ZKSCAN1-201.2	1.03	1.07	1.04	0.83	1.00	0.91
ZKSCAN2	Fab-ZKSCAN2-202.0	1.61	1.04	0.97	0.87	0.92	1.00
ZKSCAN2	Fab-ZKSCAN2-202.1	1.13	1.41	1.06	0.97	1.08	0.76
ZKSCAN2	Fab-ZKSCAN2-202.2	1.32	1.61	1.08	1.04	0.99	0.86
ZKSCAN2	Fab-ZKSCAN2-202.3	1.19	1.09	1.06	0.99	1.11	0.94
ZKSCAN2	Fab-ZKSCAN2-202.4	1.15	1.19	1.19	0.85	1.06	0.64
ZKSCAN2	Fab-ZKSCAN2-202.5	1.24	1.16	1.08	0.82	0.94	0.63
ZKSCAN2	Fab-ZKSCAN2-202.6	1.14	1.15	1.01	0.88	0.95	0.65
ZKSCAN4	Fab-ZKSCAN4-203.0	1.37	1.20	1.14	0.97	1.15	0.97
ZKSCAN5	Fab-ZKSCAN5-204.0	1.09	1.45	1.42	1.01	1.41	0.89
ZKSCAN5	Fab-ZKSCAN5-204.1	1.16	0.89	1.05	0.75	1.02	0.77
ZKSCAN5	Fab-ZKSCAN5-204.2	0.94	1.07	1.04	0.48	0.72	0.46

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Gene	**Fab ID**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**
ZKSCAN5	Fab-ZKSCAN5-204.3	1.35	1.43	1.71	0.90	1.17	0.73
ZKSCAN5	Fab-ZKSCAN5-204.4	1.28	1.45	1.49	1.05	1.09	0.64
ZNF132	Fab-ZNF132-205.0	0.97	0.95	0.86	0.67	0.76	0.91
ZNF132	Fab-ZNF132-205.1	1.03	0.98	0.90	0.76	0.81	0.86
ZNF132	Fab-ZNF132-205.2	0.99	0.90	0.86	0.64	0.69	0.84
ZNF165	Fab-ZNF165-206.0	1.15	1.04	1.05	1.00	0.94	0.77
ZNF165	Fab-ZNF165-206.1	1.08	0.72	0.78	0.34	0.86	0.80
ZNF165	Fab-ZNF165-206.2	1.14	0.96	1.04	0.94	1.00	0.84
ZNF167	Fab-ZNF167-207.0	1.23	1.22	1.14	0.96	1.09	0.83
ZNF167	Fab-ZNF167-207.1	1.07	1.16	1.07	0.86	1.01	0.84
ZNF167	Fab-ZNF167-207.2	1.31	1.14	1.10	0.91	1.09	0.86
ZNF167	Fab-ZNF167-207.3	3.38	1.05	1.06	0.94	1.12	0.85
ZNF167	Fab-ZNF167-207.4	1.13	1.10	1.12	0.97	0.82	1.02
ZNF174	Fab-ZNF174-208.0	1.12	1.21	1.12	0.99	0.95	0.93
ZNF174	Fab-ZNF174-208.1	1.08	1.11	1.00	0.80	1.01	0.78
ZNF174	Fab-ZNF174-208.2	1.12	1.13	1.05	0.95	1.09	0.95
ZNF174	Fab-ZNF174-208.3	1.19	0.98	1.06	0.90	1.79	0.74
ZNF174	Fab-ZNF174-208.4	1.26	1.12	1.03	0.81	1.01	0.66
ZNF174	Fab-ZNF174-208.5	1.06	1.10	1.05	0.75	1.29	0.68
ZNF18	Fab-ZNF18-209.0	1.13	0.86	0.91	0.40	0.98	0.61
ZNF192	Fab-ZNF192-210.0	1.20	1.19	1.12	0.95	0.91	0.81
ZNF192	Fab-ZNF192-210.1	1.14	1.09	1.07	0.83	0.74	0.92
ZNF197	Fab-ZNF197-211.0	1.20	1.21	1.13	1.00	1.08	0.99
ZNF197	Fab-ZNF197-211.1	1.20	1.12	1.06	0.92	0.93	0.78
ZNF197	Fab-ZNF197-211.2	1.23	1.13	1.05	0.79	1.19	0.81
ZNF197	Fab-ZNF197-211.3	1.12	1.19	1.33	0.83	1.08	0.76
ZNF197	Fab-ZNF197-211.4	1.29	1.25	1.20	0.98	1.17	0.73
ZNF213	Fab-ZNF213-212.0	1.45	0.97	1.05	0.82	1.01	0.86
ZNF213	Fab-ZNF213-212.1	1.28	0.95	0.97	0.85	0.91	0.91
ZNF213	Fab-ZNF213-212.2	1.20	1.04	0.96	0.89	0.95	0.71
ZNF213	Fab-ZNF213-212.3	1.24	1.17	1.13	1.05	1.09	0.62
ZNF213	Fab-ZNF213-212.4	1.03	1.23	1.13	0.73	0.94	0.73
ZNF213	Fab-ZNF213-212.5	1.51	1.22	1.20	0.79	1.34	0.68
ZNF213	Fab-ZNF213-212.6	1.19	1.19	0.99	0.76	0.95	0.59
ZNF217	Fab-ZNF217-213.0	1.16	1.43	1.24	1.05	1.13	0.94
ZNF217	Fab-ZNF217-213.1	1.04	1.10	1.08	1.03	1.05	0.99
ZNF217	Fab-ZNF217-213.2	0.99	0.99	0.93	0.69	0.89	0.82
ZNF22	Fab-ZNF22-214.0	1.01	0.99	1.00	0.82	0.81	0.75
ZNF22	Fab-ZNF22-214.1	1.26	1.21	1.08	0.90	0.96	0.78
ZNF22	Fab-ZNF22-214.2	1.14	0.91	0.98	0.63	0.85	0.82
ZNF22	Fab-ZNF22-214.3	1.06	1.44	1.18	1.03	0.96	0.88
ZNF224	Fab-ZNF224-215.0	1.27	1.43	1.15	1.03	1.07	0.86
ZNF224	Fab-ZNF224-215.1	1.30	1.13	1.17	1.05	1.17	0.89
ZNF224	Fab-ZNF224-215.2	1.51	1.56	1.51	1.28	1.52	0.97
ZNF224	Fab-ZNF224-215.3	1.15	1.10	1.08	0.88	1.02	0.91
ZNF224	Fab-ZNF224-215.4	1.13	1.25	1.15	0.91	1.04	0.73
ZNF227	Fab-ZNF227-216.0	1.12	1.06	1.06	0.84	0.97	0.91
ZNF227	Fab-ZNF227-216.1	0.87	0.92	0.82	0.59	0.78	0.84
ZNF227	Fab-ZNF227-216.2	1.11	1.10	1.09	0.88	0.97	0.63
ZNF229	Fab-ZNF229-217.0	0.99	1.10	1.10	0.87	1.08	0.75
ZNF23	Fab-ZNF23-218.0	1.23	1.03	1.22	0.79	1.04	0.93
ZNF232	Fab-ZNF232-219.0	1.35	2.05	1.21	1.20	1.16	0.89
ZNF232	Fab-ZNF232-219.1	1.51	1.38	1.06	1.04	1.11	1.04
ZNF232	Fab-ZNF232-219.2	1.24	1.13	1.06	0.90	1.50	0.85
ZNF232	Fab-ZNF232-219.3	1.50	1.24	1.27	0.83	1.29	0.66
ZNF232	Fab-ZNF232-219.4	1.55	1.22	1.46	0.91	1.14	0.74

		293T	A2780	A2780cis	JHOC9	HepG2	HPAF-II
Gene	**Fab ID**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**
ZNF287	Fab-ZNF287-220.0	1.06	1.03	0.88	0.76	0.90	0.79
ZNF295	Fab-ZNF295-221.0	1.46	1.29	1.30	1.12	1.09	0.88
ZNF295	Fab-ZNF295-221.1	1.22	1.13	1.17	0.93	1.05	0.95
ZNF295	Fab-ZNF295-221.2	1.02	0.91	0.95	0.73	0.82	0.66
ZNF296	Fab-ZNF296-222.0	1.23	1.58	1.49	1.08	1.12	0.72
ZNF343	Fab-ZNF343-223.0	1.14	1.00	1.06	0.91	0.93	0.70
ZNF343	Fab-ZNF343-223.1	1.17	1.06	1.12	1.00	0.94	0.69
ZNF343	Fab-ZNF343 (HOXD11?)-224.0	1.21	1.14	1.23	1.06	1.09	0.73
ZNF343	Fab-ZNF343 (ZNF319?)-225.0	1.12	0.93	0.96	0.83	0.79	0.62
ZNF394	Fab-ZNF394 (ZKSCAN14)-226.0	1.20	1.04	1.34	0.92	1.11	0.61
ZNF394	Fab-ZNF394 (ZKSCAN14)-226.1	1.22	0.97	1.14	0.81	0.96	0.72
ZNF394	Fab-ZNF394 (ZKSCAN14)-226.2	1.06	0.98	0.97	0.68	0.94	0.67
ZNF394	Fab-ZNF394 (ZKSCAN14)-226.3	1.26	1.09	1.11	0.91	1.01	0.56
ZNF394	Fab-ZNF394 (ZKSCAN14)-226.4	1.15	1.04	0.96	0.87	1.01	0.72
ZNF394	Fab-ZNF394 (ZKSCAN14)-226.5	1.15	1.27	1.19	0.86	1.12	0.65
ZNF394	Fab-ZNF394 (ZKSCAN14)-226.6	1.04	1.05	1.10	0.67	0.98	0.68
ZNF394	Fab-ZNF394 (ZKSCAN14)-226.7	1.24	1.02	0.94	0.68	0.93	0.66
ZNF394	Fab-ZNF394 (ZKSCAN14)-226.8	1.28	1.01	1.11	0.82	1.00	0.71
ZNF394	Fab-ZNF394 (ZKSCAN14)-226.9	1.28	0.98	1.05	0.69	1.01	0.58
ZNF394	Fab-ZNF394 (ZKSCAN14)-226.1	0.98	1.12	1.41	0.78	1.13	0.48
ZNF394	Fab-ZNF394 (ZKSCAN14)-226.1	1.06	1.05	1.16	0.77	0.90	0.32
ZNF394	Fab-ZNF394 (ZKSCAN14)-226.1	0.97	0.99	1.06	0.70	0.93	0.49
ZNF394	Fab-ZNF394 (ZKSCAN14)-226.1	1.08	1.06	1.22	0.88	0.99	0.71
ZNF394	Fab-ZNF394 (ZKSCAN14)-226.1	1.14	1.24	1.33	1.20	1.15	1.13
ZNF394	Fab-ZNF394 (ZKSCAN14)-226.1	1.21	1.09	1.05	0.84	1.09	0.59
ZNF397	Fab-ZNF397-227.0	1.13	1.11	1.08	0.92	1.07	0.85
ZNF397	Fab-ZNF397-227.1	1.59	1.06	1.22	0.74	0.96	0.55
ZNF397	Fab-ZNF397-227.2	1.80	1.04	2.23	0.89	1.11	0.63
ZNF397	Fab-ZNF397-227.3	2.71	1.11	1.50	1.02	1.39	0.82
ZNF397	Fab-ZNF397-227.4	1.15	1.20	1.32	1.11	0.98	0.82
ZNF397	Fab-ZNF397-227.5	1.03	0.93	0.88	0.66	0.85	0.54
ZNF397	Fab-ZNF397-227.6	1.23	2.03	1.71	1.13	1.16	0.74
ZNF397	Fab-ZNF397-227.7	1.14	1.28	1.17	1.02	0.86	0.55
ZNF397	Fab-ZNF397-227.8	1.23	1.20	1.31	1.07	0.88	0.59
ZNF397	Fab-ZNF397-227.9	1.09	1.27	1.45	0.98	0.91	0.46
ZNF397	Fab-ZNF397-227.10	1.17	1.79	1.83	1.30	0.95	0.67
ZNF41	Fab-ZNF41-228.0	1.09	1.18	1.11	0.94	0.87	0.88
ZNF41	Fab-ZNF41-228.1	1.06	0.97	0.97	0.79	0.91	0.95
ZNF41	Fab-ZNF41-228.2	1.08	1.03	1.00	0.87	0.92	0.99
ZNF423	Fab-ZNF423-229.0	1.57	1.05	1.09	0.76	1.25	0.68
ZNF423	Fab-ZNF423-229.1	1.27	1.23	1.12	0.87	1.10	0.83
ZNF446	Fab-ZNF446-230.0	1.37	1.13	1.15	0.88	0.78	0.88
ZNF446	Fab-ZNF446-230.1	1.19	1.75	1.54	1.46	1.25	1.00
ZNF449	Fab-ZNF449-231.0	1.03	1.09	1.00	0.85	0.91	0.51
ZNF449	Fab-ZNF449-231.1	1.27	1.07	1.01	0.91	0.79	0.69
ZNF449	Fab-ZNF449-231.2	1.37	1.15	1.11	0.90	1.10	0.73
ZNF449	Fab-ZNF449-231.3	1.15	1.37	1.34	1.07	1.19	0.87
ZNF449	Fab-ZNF449-231.4	1.16	1.12	1.16	1.03	1.13	0.98
ZNF483	Fab-ZNF483-232.0	1.54	1.32	1.16	0.95	0.94	0.87
ZNF483	Fab-ZNF483-232.1	1.22	1.21	1.09	0.86	0.95	0.71
ZNF483	Fab-ZNF483-232.2	1.16	1.40	1.24	1.05	1.22	0.96
ZNF483	Fab-ZNF483-232.3	1.18	1.01	0.92	0.73	0.82	0.79
ZNF483	Fab-ZNF483-232.4	1.14	1.13	1.00	0.95	1.25	0.84
ZNF483	Fab-ZNF483-232.5	1.25	1.24	1.08	0.96	1.30	0.65
ZNF483	Fab-ZNF483-232.6	1.34	1.15	1.24	1.10	1.20	0.91
ZNF483	Fab-ZNF483-232.7	1.04	1.36	1.13	1.04	1.02	0.53

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Gene	Fab ID	Nuc/Cyto	Nuc/Cyto	Nuc/Cyto	Nuc/Cyto	Nuc/Cyto	Nuc/Cyto
ZNF483	Fab-ZNF483-232.8	1.08	1.10	1.03	1.02	1.14	0.97
ZNF485	Fab-ZNF485-233.0	1.28	1.11	1.11	0.89	1.64	0.94
ZNF485	Fab-ZNF485-233.1	1.14	1.11	1.19	0.92	0.94	0.97
ZNF485	Fab-ZNF485-233.2	1.21	1.11	1.12	0.79	1.01	0.94
ZNF485	Fab-ZNF485-233.3	1.68	1.07	1.20	0.99	1.09	1.17
ZNF485	Fab-ZNF485-233.4	1.33	1.20	1.16	0.89	1.12	0.57
ZNF496	Fab-ZNF496-234.0	1.36	1.05	1.30	1.08	1.00	0.82
ZNF496	Fab-ZNF496-234.1	1.22	1.13	1.28	1.03	1.12	0.66
ZNF496	Fab-ZNF496-234.2	1.24	1.13	1.05	1.08	1.05	0.66
ZNF496	Fab-ZNF496-234.3	1.14	1.07	1.09	0.97	0.95	0.65
ZNF496	Fab-ZNF496-234.4	1.29	1.18	1.25	0.99	1.04	0.67
ZNF500	Fab-ZNF500-235.0	1.47	1.39	1.14	0.92	0.94	0.81
ZNF500	Fab-ZNF500-235.1	1.47	1.28	1.02	1.00	0.91	0.78
ZNF500	Fab-ZNF500-235.2	1.18	1.22	1.29	0.97	1.29	0.92
ZNF500	Fab-ZNF500-235.3	1.11	1.07	1.15	1.02	1.06	0.81
ZNF500	Fab-ZNF500-235.4	1.14	1.39	1.11	0.80	1.05	0.72
ZNF500	Fab-ZNF500-235.5	1.42	1.47	1.25	0.90	1.20	0.76
ZNF500	Fab-ZNF500-235.6	1.08	1.24	1.11	0.84	0.93	0.81
ZNF512	Fab-ZNF512-236.0	0.93	1.07	1.10	0.79	1.12	0.86
ZNF512	Fab-ZNF512-236.1	0.98	0.98	0.94	0.65	0.92	0.87
ZNF512B	Fab-ZNF512B-237.0	1.14	1.05	1.14	0.96	1.07	0.67
ZNF516	Fab-ZNF516-238.0	1.06	1.20	1.03	1.16	1.13	0.77
ZNF521	Fab-ZNF521-239.0	0.84	0.89	0.84	0.61	0.85	0.89
ZNF536	Fab-ZNF536-240.0	0.92	0.96	0.89	0.66	0.81	0.79
ZNF564	Fab-ZNF564-241.0	0.92	1.00	0.87	0.70	0.79	0.54
ZNF566	Fab-ZNF566-242.0	1.26	1.12	1.16	1.10	1.18	1.01
ZNF57	Fab-ZNF57-243.0	1.07	1.43	1.15	0.99	0.99	0.95
ZNF583	Fab-ZNF583-244.0	1.20	1.16	1.15	1.06	1.01	0.93
ZNF583	Fab-ZNF583-244.1	1.01	1.00	0.82	0.79	0.81	0.96
ZNF625	Fab-ZNF625-245.0	1.01	0.90	0.78	0.66	0.65	0.89
ZNF642	Fab-ZNF642-246.0	1.36	1.39	1.79	1.03	1.64	1.06
ZNF642	Fab-ZNF642-246.1	1.19	1.27	1.29	0.96	1.27	0.73
ZNF642	Fab-ZNF642-246.2	1.44	1.33	1.21	0.89	1.16	0.80
ZNF642	Fab-ZNF642-246.3	1.55	1.43	1.29	0.88	1.18	0.68
ZNF687	Fab-ZNF687-247.0	0.99	1.03	0.93	0.73	0.92	0.85
ZNF687	Fab-ZNF687-247.1	0.99	1.03	0.98	0.78	0.95	0.90
ZNF687	Fab-ZNF687-247.2	0.95	0.95	0.91	0.66	0.88	0.85
ZNF699	Fab-ZNF699-248.0	1.31	1.33	1.38	1.02	1.21	0.82
ZNF699	Fab-ZNF699-248.1	1.41	1.11	0.96	0.79	1.09	0.72
ZNF70	Fab-ZNF70-249.0	1.37	1.02	1.03	0.65	1.02	0.71
ZNF76	Fab-ZNF76-250.0	0.91	1.04	1.02	0.77	1.03	0.81
ZNF76	Fab-ZNF76-250.1	0.93	0.97	0.89	0.68	0.89	0.86
ZNF800	Fab-ZNF800-251.0	0.99	1.04	0.97	0.82	1.01	0.97
ZNF83	Fab-ZNF83-252.0	1.01	1.06	1.02	0.90	1.00	0.94
ZSCAN12	Fab-ZSCAN12-253.0	1.17	1.16	1.23	0.93	1.12	0.62
ZSCAN12	Fab-ZSCAN12-253.1	1.17	1.08	1.07	0.91	1.05	0.73
ZSCAN12	Fab-ZSCAN12-253.2	1.09	1.02	1.01	0.87	0.99	0.54
ZSCAN12	Fab-ZSCAN12-253.3	1.01	0.82	0.96	0.68	0.84	0.72
ZSCAN12	Fab-ZSCAN12-253.4	1.23	1.03	1.05	0.92	1.08	0.82
ZSCAN12	Fab-ZSCAN12-253.5	1.20	1.16	1.25	0.79	1.09	0.50
ZSCAN12	Fab-ZSCAN12-253.6	1.05	0.98	0.95	0.70	0.89	0.42
ZSCAN12	Fab-ZSCAN12-253.7	1.64	1.38	1.67	1.21	1.42	0.90
ZSCAN12	Fab-ZSCAN12-253.8	1.16	1.16	1.21	0.91	1.01	0.66
ZSCAN12	Fab-ZSCAN12-253.9	1.07	1.06	0.91	0.76	0.96	0.68
ZSCAN12	Fab-ZSCAN12-253.10	1.23	1.20	1.13	0.87	1.03	0.74
ZSCAN12	Fab-ZSCAN12-253.11	1.48	1.33	1.09	0.89	1.06	0.67

		293T	A2780	A2780cis	JHOC9	HepG2	HPAF-II
Gene	**Fab ID**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**
ZSCAN12	Fab-ZSCAN12-253.12	1.55	1.14	1.40	0.84	0.95	0.90
ZSCAN12	Fab-ZSCAN12-253.13	1.23	1.45	1.78	0.95	1.19	0.81
ZSCAN18	Fab-ZSCAN18-254.0	1.39	1.40	1.37	0.94	1.12	0.76
ZSCAN20	Fab-ZSCAN20-255.0	1.10	0.97	1.04	0.89	0.95	0.52
ZSCAN20	Fab-ZSCAN20-255.1	1.08	0.95	1.04	0.79	0.99	0.42
ZSCAN20	Fab-ZSCAN20-255.2	1.15	1.07	1.20	0.86	1.00	0.61
ZSCAN20	Fab-ZSCAN20-255.3	1.20	1.17	1.21	1.04	1.24	0.64
ZSCAN20	Fab-ZSCAN20-255.4	0.90	0.93	1.04	0.81	0.91	0.54
ZSCAN20	Fab-ZSCAN20-255.5	1.11	1.00	1.22	0.75	0.97	0.43
ZSCAN20	Fab-ZSCAN20-255.6	1.01	1.05	0.94	0.64	0.96	0.54
ZSCAN20	Fab-ZSCAN20-255.7	1.12	1.20	1.16	1.02	1.08	0.55
ZSCAN20	Fab-ZSCAN20-255.8	1.59	1.55	2.42	1.40	1.70	1.15
ZSCAN20	Fab-ZSCAN20-255.9	1.17	0.99	1.09	0.95	0.83	0.65
ZSCAN22	Fab-ZSCAN22-256.0	1.86	1.27	1.08	0.94	0.89	0.74
ZSCAN22	Fab-ZSCAN22-256.1	1.12	1.64	0.93	0.80	1.29	0.88
ZSCAN22	Fab-ZSCAN22-256.2	1.39	1.06	0.87	0.77	1.12	0.84
ZSCAN22	Fab-ZSCAN22-256.3	0.99	1.07	0.97	0.68	1.60	0.76
ZSCAN22	Fab-ZSCAN22-256.4	0.97	1.09	0.91	0.49	1.47	0.75
ZSCAN23	Fab-ZSCAN23-257.0	1.38	1.44	1.15	0.97	1.10	0.77
ZSCAN23	Fab-ZSCAN23-257.1	1.21	1.17	1.13	0.97	1.07	0.77
ZSCAN23	Fab-ZSCAN23-257.2	1.21	1.07	1.01	0.79	0.84	0.91
ZSCAN23	Fab-ZSCAN23-257.3	1.17	1.01	0.94	0.79	0.88	0.79
ZSCAN23	Fab-ZSCAN23-257.4	1.14	1.30	1.33	1.11	1.29	0.94
ZSCAN25	Fab-ZSCAN25-258.0	1.07	1.12	1.21	0.87	0.95	0.72
ZSCAN25	Fab-ZSCAN25-258.1	1.85	1.23	1.03	0.92	0.95	0.76
ZSCAN25	Fab-ZSCAN25-258.2	1.22	1.25	1.19	1.00	0.96	0.90
ZSCAN26 (ZNF187)	Fab-ZSCAN26 (ZNF187)-259.0	0.96	0.98	0.98	0.80	0.92	0.53
ZSCAN26 (ZNF187)	Fab-ZSCAN26 (ZNF187)-259.1	1.17	0.88	1.09	0.63	1.09	0.54
ZSCAN26 (ZNF187)	Fab-ZSCAN26 (ZNF187)-259.2	1.03	1.07	1.22	0.83	1.11	0.63
ZSCAN26 (ZNF187)	Fab-ZSCAN26 (ZNF187)-259.3	1.14	1.17	1.64	0.87	1.17	0.46
ZSCAN26 (ZNF187)	Fab-ZSCAN26 (ZNF187)-259.4	1.16	1.10	1.65	0.79	1.02	0.62
ZSCAN26 (ZNF187)	Fab-ZSCAN26 (ZNF187)-259.5	1.05	0.93	1.17	0.73	0.88	0.50
ZSCAN26 (ZNF187)	Fab-ZSCAN26 (ZNF187)-259.6	0.98	0.97	0.88	0.74	0.90	0.54
ZSCAN26 (ZNF187)	Fab-ZSCAN26 (ZNF187)-259.7	1.38	1.12	1.28	0.82	1.11	0.72
ZSCAN26 (ZNF187)	Fab-ZSCAN26 (ZNF187)-259.8	1.42	1.09	1.33	0.68	1.13	0.63
ZSCAN26 (ZNF187)	Fab-ZSCAN26 (ZNF187)-259.9	1.27	0.92	0.91	0.71	0.78	0.45
ZSCAN26 (ZNF187)	Fab-ZSCAN26 (ZNF187)-259.10	1.28	0.93	1.50	0.51	0.91	0.60
ZSCAN26 (ZNF187)	Fab-ZSCAN26 (ZNF187)-259.11	1.30	1.04	1.04	0.83	0.94	0.67
ZSCAN26 (ZNF187)	Fab-ZSCAN26 (ZNF187)-259.12	1.21	1.11	1.13	0.98	0.95	0.56
ZSCAN26 (ZNF187)	Fab-ZSCAN26 (ZNF187)-259.13	1.20	1.02	1.01	0.84	0.89	0.54
ZSCAN26 (ZNF187)	Fab-ZSCAN26 (ZNF187)-259.14	1.51	1.31	1.18	1.03	1.06	0.92
ZSCAN26 (ZNF187)	Fab-ZSCAN26 (ZNF187)-259.15	1.13	0.86	1.35	0.91	1.01	0.90
ZSCAN26 (ZNF187)	Fab-ZSCAN26 (ZNF187)-259.16	1.21	1.56	1.50	0.98	1.17	0.83
ZSCAN29	Fab-ZSCAN29-260.0	1.86	1.34	1.34	1.01	1.24	0.94
ZSCAN29	Fab-ZSCAN29-260.1	2.88	1.46	0.84	0.77	0.89	0.61
ZSCAN29	Fab-ZSCAN29-260.2	1.12	1.34	1.13	0.91	1.00	0.92
ZSCAN30	Fab-ZSCAN30-261.0	1.01	1.05	1.00	0.74	0.97	0.62
ZSCAN30	Fab-ZSCAN30-261.1	1.99	1.04	1.26	0.67	0.89	0.51
ZSCAN30	Fab-ZSCAN30-261.2	1.24	1.22	1.10	0.82	0.87	0.65
ZSCAN31 (ZNF323)	Fab-ZSCAN31 (ZNF323)-262.0	1.20	1.06	1.86	0.68	1.08	0.74
ZSCAN31 (ZNF323)	Fab-ZSCAN31 (ZNF323)-262.1	1.32	1.11	1.39	0.88	1.05	0.70
ZSCAN31 (ZNF323)	Fab-ZSCAN31 (ZNF323)-262.2	1.41	1.40	1.39	0.88	1.18	0.60
ZSCAN31 (ZNF323)	Fab-ZSCAN31 (ZNF323)-262.3	1.48	1.38	1.54	0.85	1.24	0.54
ZSCAN31 (ZNF323)	Fab-ZSCAN31 (ZNF323)-262.4	1.46	1.16	1.61	0.66	1.26	0.67
ZSCAN31 (ZNF323)	Fab-ZSCAN31 (ZNF323)-262.5	1.27	1.33	1.22	1.06	1.02	0.67
ZSCAN31 (ZNF323)	Fab-ZSCAN31 (ZNF323)-262.6	1.36	1.69	1.77	1.09	1.20	0.92

		293T	A2780	A2780cis	JHOC9	HepG2	HPAF-II
Gene	**Fab ID**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**
ZSCAN31 (ZNF323)	Fab-ZSCAN31 (ZNF323)-262.7	1.23	1.02	1.26	0.69	0.88	0.70
ZSCAN5A (ZNF495)	Fab-ZSCAN5A (ZNF495)-263.0	1.09	0.98	1.29	0.95	1.30	0.67
ZSCAN5A (ZNF495)	Fab-ZSCAN5A (ZNF495)-263.1	1.03	0.91	1.12	0.68	0.83	0.53
ZSCAN5A (ZNF495)	Fab-ZSCAN5A (ZNF495)-263.2	1.32	1.02	1.05	0.75	1.02	0.61
ZSCAN5A (ZNF495)	Fab-ZSCAN5A (ZNF495)-263.3	1.07	1.00	1.00	0.70	1.09	0.65
ZSCAN5A (ZNF495)	Fab-ZSCAN5A (ZNF495)-263.4	1.10	0.96	0.96	0.79	0.96	0.66
ZSCAN5A (ZNF495)	Fab-ZSCAN5A (ZNF495)-263.5	0.94	0.99	1.09	0.37	1.05	0.48
ZSCAN5A (ZNF495)	Fab-ZSCAN5A (ZNF495)-263.6	1.14	0.91	1.00	0.76	0.99	0.49
ZSCAN5A (ZNF495)	Fab-ZSCAN5A (ZNF495)-263.7	1.42	1.14	1.59	0.78	1.03	0.44
ZSCAN5A (ZNF495)	Fab-ZSCAN5A (ZNF495)-263.8	0.92	1.06	1.24	0.76	1.05	0.75
ZSCAN5A (ZNF495)	Fab-ZSCAN5A (ZNF495)-263.9	1.79	1.14	1.10	0.77	1.00	0.48
ZSCAN5A (ZNF495)	Fab-ZSCAN5A (ZNF495)-263.10	1.49	0.99	1.22	0.76	0.99	0.31
ZSCAN5A (ZNF495)	Fab-ZSCAN5A (ZNF495)-263.11	1.11	1.35	1.69	0.94	1.21	0.63
ZSCAN5A (ZNF495)	Fab-ZSCAN5A (ZNF495)-263.12	1.19	1.19	1.38	0.77	1.19	0.70
ZSCAN5A (ZNF495)	Fab-ZSCAN5A (ZNF495)-263.13	1.07	1.12	1.66	0.84	1.17	0.56
ZSCAN5A (ZNF495)	Fab-ZSCAN5A (ZNF495)-263.14	3.37	0.97	1.06	0.68	0.83	0.43
ZSCAN5A (ZNF495)	Fab-ZSCAN5A (ZNF495)-263.15	1.36	1.07	1.52	0.66	1.01	0.32
ZSCAN5A (ZNF495)	Fab-ZSCAN5A (ZNF495)-263.16	3.21	1.12	1.20	0.69	0.92	0.54
ZSCAN5A (ZNF495)	Fab-ZSCAN5A (ZNF495)-263.17	0.86	1.03	1.42	0.72	0.91	0.25
ZSCAN5A (ZNF495)	Fab-ZSCAN5A (ZNF495)-263.18	1.30	1.14	1.26	0.71	0.95	0.38
ZSCAN5A (ZNF495)	Fab-ZSCAN5A (ZNF495)-263.19	2.24	0.97	0.99	0.63	0.92	0.31
ZSCAN5A (ZNF495)	Fab-ZSCAN5A (ZNF495)-263.20	1.93	1.12	1.29	0.81	1.01	0.46
ZSCAN5A (ZNF495)	Fab-ZSCAN5A (ZNF495)-263.21	1.20	1.05	1.09	0.94	0.92	0.46
ZSCAN5A (ZNF495)	Fab-ZSCAN5A (ZNF495)-263.22	1.12	1.02	1.07	0.91	0.87	0.54
ZSCAN5A (ZNF495)	Fab-ZSCAN5A (ZNF495)-263.23	0.98	0.90	1.01	0.93	1.02	0.79
ZSCAN5A (ZNF495)	Fab-ZSCAN5A (ZNF495)-263.24	1.01	1.41	1.26	0.93	0.94	0.48
ZSCAN5B	Fab-ZSCAN5B-264.0	1.27	1.05	1.13	0.70	1.00	0.60
ZSCAN5B	Fab-ZSCAN5B-264.1	0.99	1.02	1.07	0.80	0.94	0.56
ZSCAN5B	Fab-ZSCAN5B-264.2	1.11	0.92	1.25	0.64	0.90	0.39
ZSCAN5B	Fab-ZSCAN5B-264.3	1.67	1.08	1.00	0.66	0.95	0.58
ZSCAN5B	Fab-ZSCAN5B-264.4	2.32	0.97	1.05	0.65	0.87	0.40
ZSCAN5B	Fab-ZSCAN5B-264.5	1.13	1.08	1.13	1.06	1.08	0.78
ZSCAN5B	Fab-ZSCAN5B-264.6	1.14	0.95	0.92	0.85	0.80	0.83
ZSCAN5B	Fab-ZSCAN5B-264.7	1.36	1.18	1.15	1.02	1.04	0.84
ZSCAN5B	Fab-ZSCAN5B-264.8	1.13	1.03	1.06	1.02	1.03	0.75
ZSCAN5B	Fab-ZSCAN5B-264.9	1.09	1.02	0.97	0.90	0.93	0.72
ZSCAN5B	Fab-ZSCAN5B-264.10	1.10	1.00	0.98	0.85	0.98	0.55
ZSCAN5B	Fab-ZSCAN5B-264.11	1.22	1.07	1.15	0.90	0.95	0.49
ZSCAN5B	Fab-ZSCAN5B-264.12	1.25	1.07	1.20	0.90	1.00	0.72
ZSCAN5B	Fab-ZSCAN5B-264.13	1.25	1.17	1.11	0.98	1.00	0.55
ZSCAN5B	Fab-ZSCAN5B-264.14	1.24	1.12	1.23	0.83	1.04	0.69
ZSCAN5B	Fab-ZSCAN5B-264.15	1.25	1.16	1.24	1.05	1.04	0.62
ZSCAN5B	Fab-ZSCAN5B-264.16	1.21	0.97	1.21	0.96	0.97	0.73
ZSCAN5B	Fab-ZSCAN5B-264.17	1.21	1.03	1.24	0.90	0.96	0.66
ZSCAN5B	Fab-ZSCAN5B-264.18	1.11	1.05	1.03	0.95	1.06	0.99
ZSCAN5B	Fab-ZSCAN5B-264.19	1.44	1.15	1.16	0.90	1.02	0.46
ZSCAN5C	Fab-ZSCAN5C-265.0	0.99	1.04	1.03	0.75	0.97	0.45
ZSCAN5C	Fab-ZSCAN5C-265.1	1.07	1.05	1.12	0.76	0.97	0.66
ZSCAN5C	Fab-ZSCAN5C-265.2	1.02	0.95	1.09	0.74	0.92	0.52
ZSCAN5C	Fab-ZSCAN5C-265.3	0.76	0.82	1.12	0.61	1.01	0.51
ZSCAN5C	Fab-ZSCAN5C-265.4	1.09	0.95	1.11	0.83	1.01	0.71
ZSCAN5C	Fab-ZSCAN5C-265.5	1.22	1.10	1.07	1.02	0.94	0.80
ZSCAN5C	Fab-ZSCAN5C-265.6	1.43	1.05	0.86	0.96	1.03	0.74
ZSCAN5C	Fab-ZSCAN5C-265.7	1.27	1.14	1.15	1.07	1.06	0.76
ZSCAN5C	Fab-ZSCAN5C-265.8	1.25	1.21	0.60	1.00	1.05	0.75
ZSCAN5C	Fab-ZSCAN5C-265.9	1.24	1.16	1.10	1.05	1.09	0.78

		293T	A2780	A2780cis	JHOC9	HepG2	HPAF-II
Gene	**Fab ID**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**	**Nuc/Cyto**
ZSCAN5C	Fab-ZSCAN5C-265.10	1.10	0.95	1.00	0.94	0.89	0.69
ZSCAN5C	Fab-ZSCAN5C-265.11	1.20	1.10	0.68	0.87	0.96	0.60
ZSCAN5C	Fab-ZSCAN5C-265.12	1.25	1.06	1.04	0.95	0.95	0.54
ZSCAN5C	Fab-ZSCAN5C-265.13	1.34	1.38	1.47	1.02	0.95	0.66
ZSCAN5C	Fab-ZSCAN5C-265.14	1.19	0.98	1.02	0.89	0.77	0.53
ZSCAN5C	Fab-ZSCAN5C-265.15	1.31	1.04	1.12	0.87	0.80	0.57
ZSCAN5C	Fab-ZSCAN5C-265.16	1.19	1.13	1.35	1.00	0.96	0.47
ZSCAN5C	Fab-ZSCAN5C-265.17	1.08	0.95	0.99	0.83	0.82	0.57
ZSCAN9	Fab-ZSCAN9-266.0	2.41	2.72	2.58	1.99	1.54	1.20
ZSCAN9	Fab-ZSCAN9-266.1	2.86	2.81	2.88	2.08	1.62	1.05
ZSCAN9 (ZNF193)	Fab-ZSCAN9 (ZNF193)-267.0	0.93	1.11	1.07	0.81	0.98	0.85
ZXDA	Fab-ZXDA-268.0	1.04	1.28	1.00	1.03	1.06	0.98
ZXDA	Fab-ZXDA-268.1	1.01	0.99	0.90	0.66	0.96	0.91

Table SI 4: Fabs (n=670)that passed primary (Competition ELISA and Sequence Unique) and secondary validation (Spiked-IP) that have been prepared for distribution. Were IF was conducted staining location was shown for each of the 6 human cell lines screened (NT= Not currently tested by IF).

HGCN	Fab name	Primary validation	Secondary validation	JHOC9_IF	A293T_IF	a2780_IF	a2780cis_IF	HPAFII_IF	HEPG2_IF
ANAPC2	anti-ANAPC2-RAB-C75	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ANAPC2	anti-ANAPC2-RAB-C76	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ANAPC2	anti-ANAPC2-RAB-C77	PASS	PASS	cyto	nuc	cyto	cyto	cyto	cyto
ANKZF1	anti-ANKZF1-RAB-C54	PASS	PASS	cyto	NT	cyto	cyto	cyto	cyto
ANKZF1	anti-ANKZF1-RAB-C55	PASS	PASS	cyto	NT	cyto	nuc	cyto	cyto
ANKZF1	anti-ANKZF1-RAB-C56	PASS	PASS	cyto	NT	cyto	cyto	cyto	cyto
ANKZF1	anti-ANKZF1-RAB-C57	PASS	PASS	cyto	cyto	cyto	cyto	nuc	cyto
ANKZF1	anti-ANKZF1-RAB-C58	PASS	PASS	cyto	NT	cyto	cyto	cyto	cyto
ARID3A	anti-ARID3A-RAB-T4	PASS	PASS	nuc	cyto	cyto	cyto	cyto	cyto
ARID3A	anti-ARID3A-RAB-T5	PASS	PASS	nuc	cyto	cyto	cyto	cyto	cyto
ARID3A	anti-ARID3A-RAB-T6	PASS	PASS	nuc	cyto	misc	misc	cyto	cyto
ARID4B	anti-ARID4B-RAB-C258	PASS	PASS	NT	NT	NT	NT	NT	NT
ASF1B	anti-ASF1B-RAB-C64	PASS	PASS	NT	NT	NT	NT	NT	NT
ASF1B	anti-ASF1B-RAB-C65	PASS	PASS	NT	NT	NT	NT	NT	NT
ASF1B	anti-ASF1B-RAB-C66	PASS	PASS	NT	NT	NT	NT	NT	NT
ASF1B	anti-ASF1B-RAB-C67	PASS	PASS	NT	NT	NT	NT	NT	NT
ASF1B	anti-ASF1B-RAB-C68	PASS	PASS	NT	NT	NT	NT	NT	NT
ASF1B	anti-ASF1B-RAB-C69	PASS	PASS	NT	NT	NT	NT	NT	NT
ASF1B	anti-ASF1B-RAB-C259	PASS	PASS	NT	NT	NT	NT	NT	NT
ASF1B	anti-ASF1B-RAB-C260	PASS	PASS	NT	NT	NT	NT	NT	NT
ATAD2	anti-ATAD2-RAB-C261	PASS	PASS	NT	NT	NT	NT	NT	NT
ATAD2B	anti-ATAD2B-RAB-C262	PASS	PASS	NT	NT	NT	NT	NT	NT
BAZ1B	anti-BAZ1B-RAB-C263	PASS	PASS	NT	NT	NT	NT	NT	NT
BAZ1B	anti-BAZ1B-RAB-C264	PASS	PASS	NT	NT	NT	NT	NT	NT
BAZ1B	anti-BAZ1B-RAB-C265	PASS	PASS	NT	NT	NT	NT	NT	NT
BAZ2B	anti-BAZ2B-RAB-C266	PASS	PASS	NT	NT	NT	NT	NT	NT
BPTF	anti-BPTF-RAB-C267	PASS	PASS	NT	NT	NT	NT	NT	NT
BPTF	anti-BPTF-RAB-C268	PASS	PASS	NT	NT	NT	NT	NT	NT
BPTF	anti-BPTF-RAB-C269	PASS	PASS	NT	NT	NT	NT	NT	NT
BRD1	anti-BRD1-RAB-C234	PASS	PASS	NT	NT	NT	NT	NT	NT
BRD1	anti-BRD1-RAB-C235	PASS	PASS	NT	NT	NT	NT	NT	NT
BRD1	anti-BRD1-RAB-C236	PASS	PASS	NT	NT	NT	NT	NT	NT
BRD1	anti-BRD1-RAB-C237	PASS	PASS	NT	NT	NT	NT	NT	NT
BRD2	anti-BRD2-RAB-C270	PASS	PASS	NT	NT	NT	NT	NT	NT
BRD2	anti-BRD2-RAB-C271	PASS	PASS	NT	NT	NT	NT	NT	NT
BRD2	anti-BRD2-RAB-C272	PASS	PASS	NT	NT	NT	NT	NT	NT
BRD2	anti-BRD2-RAB-C273	PASS	PASS	NT	NT	NT	NT	NT	NT
BRD3	anti-BRD3-RAB-C278	PASS	PASS	NT	NT	NT	NT	NT	NT
BRD3	anti-BRD3-RAB-C279	PASS	PASS	NT	NT	NT	NT	NT	NT
BRD3	anti-BRD3-RAB-C280	PASS	PASS	NT	NT	NT	NT	NT	NT
BRD3	anti-BRD3-RAB-C274	PASS	PASS	NT	NT	NT	NT	NT	NT
BRD3	anti-BRD3-RAB-C275	PASS	PASS	NT	NT	NT	NT	NT	NT
BRD3	anti-BRD3-RAB-C276	PASS	PASS	NT	NT	NT	NT	NT	NT
BRD3	anti-BRD3-RAB-C277	PASS	PASS	NT	NT	NT	NT	NT	NT
BRD4	anti-BRD4-RAB-C281	PASS	PASS	cyto	cyto	cyto	cyto	cyto	nuc
BRD4	anti-BRD4-RAB-C131	PASS	PASS	nuc	cyto	nuc	cyto	cyto	cyto
BRD7	anti-BRD7-RAB-C282	PASS	PASS	NT	NT	NT	NT	NT	NT
BRD7	anti-BRD7-RAB-C283	PASS	PASS	NT	NT	NT	NT	NT	NT
C14orf169	anti-C14ORF169-RAB-C351	PASS	PASS	NT	NT	NT	NT	NT	NT
C14orf169	anti-C14ORF169-RAB-C349	PASS	PASS	NT	NT	NT	NT	NT	NT
C14orf169	anti-C14ORF169-RAB-C350	PASS	PASS	NT	NT	NT	NT	NT	NT
CBX1	anti-CBX1-RAB-C100	PASS	PASS	misc	cyto	cyto/nuc	cyto	cyto	cyto
CBX1	anti-CBX1-RAB-C101	PASS	PASS	nuc	cyto	nuc	cyto	cyto	cyto
CBX1	anti-CBX1-RAB-C102	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
CBX1	anti-CBX1-RAB-C103	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
CBX1	anti-CBX1-RAB-C145	PASS	PASS	nuc	nuc	nuc	cyto	nuc	nuc
CBX2	anti-CBX2-RAB-C238	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
CBX2	anti-CBX2-RAB-C239	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
CBX3	anti-CBX3-RAB-C132	PASS	PASS	NT	NT	NT	NT	NT	NT
CBX4	anti-CBX4-RAB-C284	PASS	PASS	NT	NT	NT	NT	NT	NT
CBX4	anti-CBX4-RAB-C285	PASS	PASS	NT	NT	NT	NT	NT	NT
CBX4	anti-CBX4-RAB-C286	PASS	PASS	NT	NT	NT	NT	NT	NT
CBX4	anti-CBX4-RAB-C287	PASS	PASS	NT	NT	NT	NT	NT	NT
CBX5	anti-CBX5-RAB-C288	PASS	PASS	NT	NT	NT	NT	NT	NT
CBX5	anti-CBX5-RAB-C289	PASS	PASS	NT	NT	NT	NT	NT	NT
CBX5	anti-CBX5-RAB-C290	PASS	PASS	NT	NT	NT	NT	NT	NT
CBX5	anti-CBX5-RAB-C133	PASS	PASS	NT	NT	NT	NT	NT	NT
CBX8	anti-CBX8-RAB-C291	PASS	PASS	NT	NT	NT	NT	NT	NT
CDC73	anti-CDC5L-RAB-C146	PASS	PASS	nuc	nuc	nuc	nuc	nuc	cyto
CDC73	anti-CDC5L-RAB-C147	PASS	PASS	nuc	nuc	nuc	nuc	nuc	nuc
CDC73	anti-CDC5L-RAB-C148	PASS	PASS	nuc	nuc	nuc	nuc	nuc	nuc
CDC73	anti-CDC5L-RAB-C149	PASS	PASS	nuc	nuc	nuc	cyto	nuc	cyto
CDYL	anti-CDYL-RAB-C292	PASS	PASS	NT	NT	NT	NT	NT	NT
CECR2	anti-CECR2-RAB-C293	PASS	PASS	NT	NT	NT	NT	NT	NT
CECR2	anti-CECR2-RAB-C294	PASS	PASS	NT	NT	NT	NT	NT	NT
CHD1	anti-CHD1-RAB-C295	PASS	PASS	NT	NT	NT	NT	NT	NT

HGCN	Fab name	Primary validation	Secondary validation	JHOC9_IF	A293T_IF	a2780_IF	a2780cis_IF	HPAFII_IF	HEPG2_IF
CHD1	anti-CHD1-RAB-C296	PASS	PASS	NT	NT	NT	NT	NT	NT
CHD1	anti-CHD1-RAB-C297	PASS	PASS	NT	NT	NT	NT	NT	NT
CHD1	anti-CHD1-RAB-C298	PASS	PASS	NT	NT	NT	NT	NT	NT
CHD1	anti-CHD1-RAB-C299	PASS	PASS	NT	NT	NT	NT	NT	NT
CHD1	anti-CHD1-RAB-C300	PASS	PASS	NT	NT	NT	NT	NT	NT
CHD2	anti-CHD2-RAB-C301	PASS	PASS	NT	NT	NT	NT	NT	NT
CHD2	anti-CHD2-RAB-C302	PASS	PASS	NT	NT	NT	NT	NT	NT
CHD3	anti-CHD3-RAB-C303	PASS	PASS	NT	NT	NT	NT	NT	NT
CHD3	anti-CHD3-RAB-C304	PASS	PASS	NT	NT	NT	NT	NT	NT
CHD4	anti-CHD4-RAB-C305	PASS	PASS	nuc	nuc	nuc	nuc	nuc	nuc
CHD4	anti-CHD4-RAB-C306	PASS	PASS	NT	NT	NT	NT	NT	NT
CHD4	anti-CHD4-RAB-C307	PASS	PASS	NT	NT	NT	NT	NT	NT
CHD4	anti-CHD4-RAB-C308	PASS	PASS	nuc	nuc	nuc	nuc	nuc	cyto/nuc
CHD4	anti-CHD4-RAB-C211	PASS	PASS	NT	NT	NT	NT	NT	NT
CHD4	anti-CHD4-RAB-C212	PASS	PASS	nuc	nuc	nuc	nuc	nuc	cyto/nuc
CHD7	anti-CHD7-RAB-C309	PASS	PASS	NT	NT	NT	NT	NT	NT
CIAO1	anti-CIAO1-RAB-C491	PASS	PASS	NT	NT	NT	NT	NT	NT
CIAO1	anti-CIAO1-RAB-C492	PASS	PASS	NT	NT	NT	NT	NT	NT
DNMT1	anti-DNMT1-RAB-C310	PASS	PASS	NT	NT	NT	NT	NT	NT
DNMT3A	anti-DNMT3A-RAB-C311	PASS	PASS	NT	NT	NT	NT	NT	NT
DOT1L	anti-DOT1L-RAB-C312	PASS	PASS	NT	NT	NT	NT	NT	NT
EED	anti-EED-RAB-C313	PASS	PASS	NT	NT	NT	NT	NT	NT
EED	anti-EED-RAB-C314	PASS	PASS	NT	NT	NT	NT	NT	NT
EED	anti-EED-RAB-C315	PASS	PASS	NT	NT	NT	NT	NT	NT
EED	anti-EED-RAB-C316	PASS	PASS	NT	NT	NT	NT	NT	NT
EHMT1	anti-EHMT1-RAB-C317	PASS	PASS	NT	NT	NT	NT	NT	NT
EP300	anti-EP300-RAB-C318	PASS	PASS	NT	NT	NT	NT	NT	NT
ESRRA	anti-ESRRA-RAB-C31	PASS	PASS	cyto	cyto	cyto	cyto	nuc	cyto
ESRRA	anti-ESRRA-RAB-C32	PASS	PASS	cyto	misc	cyto	nuc	cyto	cyto
ESRRA	anti-ESRRA-RAB-C33	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ESRRA	anti-ESRRA-RAB-C34	PASS	PASS	misc	cyto	cyto	misc	cyto	cyto
ESRRA	anti-ESRRA-RAB-C35	PASS	PASS	cyto	cyto	cyto	misc	cyto	cyto
ESRRA	anti-ESRRA-RAB-C36	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
FOXD3	anti-FOXD3-RAB-C99	PASS	PASS	NT	NT	NT	NT	NT	NT
FOXP1	anti-FOXP1-RAB-S36	PASS	PASS	cyto	cyto	NT	cyto	cyto	cyto
FOXP1	anti-FOXP1-RAB-S37	PASS	PASS	misc	cyto	misc	misc	cyto	misc
FOXP1	anti-FOXP1-RAB-S38	PASS	PASS	misc	nuc	misc	misc	cyto	misc
FOXP4	anti-FOXP4-RAB-S39	PASS	PASS	misc	nuc	NT	misc	cyto	nuc
FOXP4	anti-FOXP4-RAB-S40	PASS	PASS	NT	cyto	NT	cyto	cyto	cyto
FOXP4	anti-FOXP4-RAB-S41	PASS	PASS	NT	NT	NT	NT	NT	NT
FOXP4	anti-FOXP4-RAB-S42	PASS	PASS	NT	NT	NT	NT	NT	NT
FXR2	anti-FXR2-RAB-C150	PASS	PASS	NT	NT	NT	NT	NT	NT
FXR2	anti-FXR2-RAB-C151	PASS	PASS	NT	NT	NT	NT	NT	NT
FXR2	anti-FXR2-RAB-C152	PASS	PASS	NT	NT	NT	NT	NT	NT
FXR2	anti-FXR2-RAB-C153	PASS	PASS	NT	NT	NT	NT	NT	NT
FXR2	anti-FXR2-RAB-C154	PASS	PASS	NT	NT	NT	NT	NT	NT
GMEB2	anti-GMEB2-RAB-S200	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
GMEB2	anti-GMEB2-RAB-S201	PASS	PASS	cyto/nuc	cyto	cyto	nuc	cyto	cyto
H1FX	anti-H1FX-RAB-C497	PASS	PASS	nuc	nuc	nuc	nuc	nuc	cyto
H1FX	anti-H1FX-RAB-C498	PASS	PASS	cyto	nuc	nuc	nuc	nuc	cyto
H1FX	anti-H1FX-RAB-C499	PASS	PASS	cyto	misc	cyto	nuc	cyto	cyto
HACE1	anti-HACE1-RAB-C319	PASS	PASS	NT	NT	NT	NT	NT	NT
HDAC4	anti-HDAC4-RAB-C320	PASS	PASS	NT	NT	NT	NT	NT	NT
HDAC7	anti-HDAC7-RAB-C321	PASS	PASS	NT	NT	NT	NT	NT	NT
HDGFRP2	anti-HDGFRP2-RAB-C322	PASS	PASS	NT	NT	NT	NT	NT	NT
HOXB5	anti-HOXB5-RAB-C240	PASS	PASS	cyto	cyto	nuc	nuc	cyto	cyto
HOXB5	anti-HOXB5-RAB-C241	PASS	PASS	cyto/nuc	cyto	cyto	cyto/nuc	cyto/nuc	cyto/nuc
HOXB5	anti-HOXB5-RAB-C242	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
JMJD6	anti-JMJD6-RAB-C166	PASS	PASS	cyto	cyto	nuc	cyto	cyto	cyto
JMJD6	anti-JMJD6-RAB-C167	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
JMJD6	anti-JMJD6-RAB-C168	PASS	PASS	cyto	NT	cyto	cyto	cyto	cyto
JMJD6	anti-JMJD6-RAB-C169	PASS	PASS	NT	cyto/nuc	NT	NT	NT	NT
KDM2A	anti-KDM2A-RAB-C323	PASS	PASS	NT	NT	NT	NT	NT	NT
KDM2A	anti-KDM2A-RAB-C324	PASS	PASS	NT	nuc	NT	NT	NT	NT
KDM4A	anti-KDM4A-RAB-C325	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
KDM4A	anti-KDM4A-RAB-C155	PASS	PASS	cyto/nuc	cyto	cyto	cyto	cyto	cyto
KDM4A	anti-KDM4A-RAB-C156	PASS	PASS	NT	NT	NT	NT	NT	NT
KDM4A	anti-KDM4A-RAB-C157	PASS	PASS	misc	misc	cyto	cyto	cyto	cyto
KDM4A	anti-KDM4A-RAB-C158	PASS	PASS	misc	cyto	NT	cyto	cyto	cyto
KDM4A	anti-KDM4A-RAB-C159	PASS	PASS	NT	NT	NT	NT	NT	NT
KDM4A	anti-KDM4A-RAB-C160	PASS	PASS	nuc	NT	nuc	NT	nuc	nuc
KDM4A	anti-KDM4A-RAB-C161	PASS	PASS	nuc	NT	cyto	NT	cyto	nuc
KDM4A	anti-KDM4A-RAB-C162	PASS	PASS	cyto/nuc	NT	nuc	NT	cyto	nuc
KDM4A	anti-KDM4A-RAB-C163	PASS	PASS	NT	NT	NT	NT	NT	NT
KDM4B	anti-KDM4B-RAB-C326	PASS	PASS	NT	NT	NT	NT	NT	NT
KDM4D	anti-KDM4D-RAB-C327	PASS	PASS	NT	NT	NT	NT	NT	NT
KDM5C	anti-KDM5C-RAB-C328	PASS	PASS	NT	NT	NT	NT	NT	NT
KDM6B	anti-KDM6B-RAB-C329	PASS	PASS	NT	NT	NT	NT	NT	NT

HGCN	Fab name	Primary validation	Secondary validation	JHOC9_IF	A293T_IF	a2780_IF	a2780cis_IF	HPAFII_IF	HEPG2_IF
KDM6B	anti-KDM6B-RAB-C330	PASS	PASS	NT	NT	NT	NT	NT	NT
KDM8	anti-KDM8-RAB-C331	PASS	PASS	NT	NT	NT	NT	NT	NT
L3MBTL1	anti-L3MBTL1-RAB-C213	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
L3MBTL1	anti-L3MBTL1-RAB-C214	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
L3MBTL1	anti-L3MBTL1-RAB-C215	PASS	PASS	NT	NT	NT	NT	NT	cyto
L3MBTL2	anti-L3MBTL2-RAB-C225	PASS	PASS	NT	NT	NT	NT	NT	NT
L3MBTL2	anti-L3MBTL2-RAB-C226	PASS	PASS	NT	NT	NT	NT	NT	NT
L3MBTL2	anti-L3MBTL2-RAB-C227	PASS	PASS	NT	NT	NT	NT	NT	NT
L3MBTL3	anti-L3MBTL3-RAB-C335	PASS	PASS	NT	NT	NT	NT	NT	NT
L3MBTL3	anti-L3MBTL3-RAB-C336	PASS	PASS	NT	NT	NT	NT	NT	NT
L3MBTL3	anti-L3MBTL3-RAB-C333	PASS	PASS	NT	NT	NT	NT	NT	NT
L3MBTL3	anti-L3MBTL3-RAB-C334	PASS	PASS	NT	NT	NT	NT	NT	NT
L3MBTL3	anti-L3MBTL3-RAB-C332	PASS	PASS	NT	NT	NT	NT	NT	NT
L3MBTL3	anti-L3MBTL3-RAB-C337	PASS	PASS	NT	NT	NT	NT	NT	NT
L3MBTL3	anti-L3MBTL3-RAB-C338	PASS	PASS	NT	NT	NT	NT	NT	NT
L3MBTL4	anti-L3MBTL4-RAB-C74	PASS	PASS	NT	NT	NT	NT	NT	NT
L3MBTL4	anti-L3MBTL4-RAB-C339	PASS	PASS	NT	NT	NT	NT	NT	NT
MBD4	anti-MBD4-RAB-C139	PASS	PASS	NT	NT	NT	NT	NT	NT
MBD4	anti-MBD4-RAB-C73	PASS	PASS	cyto/nuc	nuc	cyto	cyto	cyto	nuc
MBTD1	anti-MBTD1-RAB-C343	PASS	PASS	NT	NT	NT	NT	NT	NT
MBTD1	anti-MBTD1-RAB-C340	PASS	PASS	NT	NT	NT	NT	NT	NT
MBTD1	anti-MBTD1-RAB-C341	PASS	PASS	NT	NT	NT	NT	NT	NT
MBTD1	anti-MBTD1-RAB-C342	PASS	PASS	NT	NT	NT	NT	NT	NT
MEN1	anti-MEN1-RAB-C345	PASS	PASS	NT	NT	NT	NT	NT	NT
MEN1	anti-MEN1-RAB-C344	PASS	PASS	NT	NT	NT	NT	NT	NT
MPHOSPH8	anti-MPHOSPH8-RAB-C346	PASS	PASS	NT	NT	NT	NT	NT	NT
MSH6	anti-MSH6-RAB-C104	PASS	PASS	nuc	nuc	cyto	nuc	cyto	cyto
MSH6	anti-MSH6-RAB-C105	PASS	PASS	nuc	cyto	NT	nuc	cyto	cyto
MSH6	anti-MSH6-RAB-C106	PASS	PASS	nuc	nuc	nuc	nuc	nuc	nuc
MSH6	anti-MSH6-RAB-C141	PASS	PASS	nuc	nuc	nuc	nuc	nuc	nuc
MSH6	anti-MSH6-RAB-C164	PASS	PASS	nuc	nuc	nuc	nuc	nuc	cyto/nuc
MTF2	anti-MTF2-RAB-C347	PASS	PASS	NT	NT	NT	NT	NT	NT
MTF2	anti-MTF2-RAB-C348	PASS	PASS	NT	NT	NT	NT	NT	NT
MZF1	anti-MZF1-RAB-C196	PASS	PASS	nuc	cyto	nuc	nuc	nuc	cyto
MZF1	anti-MZF1-RAB-C197	PASS	PASS	nuc	cyto	nuc	nuc	cyto	cyto
MZF1	anti-MZF1-RAB-C445	PASS	PASS	misc	misc	misc	misc	cyto	cyto
NEDD4L	anti-NEDD4L-RAB-C500	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto/nuc
NR1D2	anti-NR1D2-RAB-C446	PASS	PASS	cyto/nuc	cyto	nuc	cyto	cyto	cyto
NR1D2	anti-NR1D2-RAB-C447	PASS	PASS	cyto	nuc	cyto/nuc	cyto	cyto	cyto/nuc
NR6A1	anti-NR6A1-RAB-C494	PASS	PASS	NT	NT	NT	NT	cyto	NT
NSD1	anti-NSD1-RAB-C485	PASS	PASS	NT	NT	NT	NT	NT	NT
NSD1	anti-NSD1-RAB-C486	PASS	PASS	misc	misc	misc	cyto	misc	misc
PARP14	anti-PARP14-RAB-C352	PASS	PASS	NT	NT	NT	NT	NT	NT
PARP14	anti-PARP14-RAB-C353	PASS	PASS	NT	NT	NT	NT	NT	NT
PARP14	anti-PARP14-RAB-C354	PASS	PASS	NT	NT	NT	NT	NT	NT
PBK	anti-PBK-RAB-C423	PASS	PASS	NT	NT	NT	NT	NT	NT
PBK	anti-PBK-RAB-C421	PASS	PASS	NT	NT	NT	NT	NT	NT
PBK	anti-PBK-RAB-C422	PASS	PASS	NT	NT	NT	NT	NT	NT
PBRM1	anti-PBRM1-RAB-C355	PASS	PASS	NT	NT	NT	NT	NT	NT
PBRM1	anti-PBRM1-RAB-C356	PASS	PASS	NT	NT	NT	NT	NT	NT
PBRM1	anti-PBRM1-RAB-C357	PASS	PASS	NT	NT	NT	NT	NT	NT
PGBD1	anti-PGBD1-RAB-S43	PASS	PASS	cyto	cyto	cyto/nuc	cyto	cyto	cyto/nuc
PGBD1	anti-PGBD1-RAB-S44	PASS	PASS	cyto/nuc	NT	cyto/nuc	cyto	cyto	nuc
PGBD1	anti-PGBD1-RAB-S45	PASS	PASS	misc	NT	cyto	misc	cyto	cyto
PGBD1	anti-PGBD1-RAB-S46	PASS	PASS	NT	NT	NT	NT	NT	NT
PGBD1	anti-PGBD1-RAB-S47	PASS	PASS	NT	NT	NT	NT	NT	NT
PGBD1	anti-PGBD1-RAB-S48	PASS	PASS	NT	NT	NT	NT	NT	NT
PHF20L1	anti-PHF20L1-RAB-C358	PASS	PASS	NT	NT	NT	NT	NT	NT
PHF20L1	anti-PHF20L1-RAB-C359	PASS	PASS	NT	NT	NT	NT	NT	NT
PHF20L1	anti-PHF20L1-RAB-C360	PASS	PASS	NT	NT	NT	NT	NT	NT
PIKFYVE	anti-PIKFYVE-RAB-S1	PASS	PASS	NT	NT	NT	NT	NT	NT
PIKFYVE	anti-PIKFYVE-RAB-S2	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
PIKFYVE	anti-PIKFYVE-RAB-S3	PASS	PASS	NT	NT	cyto	cyto	NT	NT
PIKFYVE	anti-PIKFYVE-RAB-S4	PASS	PASS	cyto	cyto	cyto	cyto	cyto	NT
PIKFYVE	anti-PIKFYVE-RAB-S5	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
PLXNB1	anti-PLXNB1-RAB-C45	PASS	PASS	nuc	nuc	nuc	nuc	nuc	cyto
PRDM1	anti-PRDM1-RAB-C501	PASS	PASS	NT	NT	NT	NT	NT	NT
PRDM1	anti-PRDM1-RAB-C502	PASS	PASS	NT	NT	NT	NT	NT	NT
PRDM10	anti-PRDM10-RAB-C363	PASS	PASS	NT	NT	NT	NT	NT	NT
PRDM10	anti-PRDM10-RAB-C364	PASS	PASS	NT	NT	NT	NT	NT	NT
PRDM10	anti-PRDM10-RAB-C365	PASS	PASS	NT	NT	NT	NT	NT	NT
PRDM10	anti-PRDM10-RAB-C366	PASS	PASS	NT	NT	NT	NT	NT	NT
PRDM10	anti-PRDM10-RAB-C362	PASS	PASS	NT	NT	NT	NT	NT	NT
PRDM10	anti-PRDM10-RAB-C361	PASS	PASS	NT	NT	NT	NT	NT	NT
PRDM11	anti-PRDM11-RAB-C107	PASS	PASS	nuc	nuc	nuc	nuc	nuc	cyto
PRDM11	anti-PRDM11-RAB-C108	PASS	PASS	NT	NT	NT	NT	NT	NT
PRDM11	anti-PRDM11-RAB-C109	PASS	PASS	cyto	cyto	cyto	nuc	cyto	cyto
PRDM11	anti-PRDM11-RAB-C110	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto

HGCN	Fab name	Primary validation	Secondary validation	JHOC9_IF	A293T_IF	a2780_IF	a2780cis_IF	HPAFII_IF	HEPG2_IF
PRDM11	anti-PRDM11-RAB-C111	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
PRDM11	anti-PRDM11-RAB-C165	PASS	PASS	nuc	cyto	NT	nuc	cyto	cyto
PRDM14	anti-PRDM14-RAB-S192	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
PRDM4	anti-PRDM4-RAB-C367	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
PRDM4	anti-PRDM4-RAB-C368	PASS	PASS	NT	NT	NT	NT	NT	NT
PRDM5	anti-PRDM5-RAB-C503	PASS	PASS	NT	NT	NT	NT	NT	NT
PRDM5	anti-PRDM5-RAB-C504	PASS	PASS	NT	NT	NT	NT	NT	NT
PRDM5	anti-PRDM5-RAB-C505	PASS	PASS	NT	NT	NT	NT	NT	NT
PRDM9	anti-PRDM9-RAB-C371	PASS	PASS	cyto	cyto	nuc	cyto	cyto	cyto
PRDM9	anti-PRDM9-RAB-C370	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
PRDM9	anti-PRDM9-RAB-C369	PASS	PASS	nuc	cyto	cyto	NT	cyto	cyto
PRMT3	anti-PRMT3-RAB-C372	PASS	PASS	NT	NT	NT	NT	NT	NT
PRMT5	anti-PRMT5-RAB-C134	PASS	PASS	nuc	cyto	cyto	nuc	cyto	cyto
PRMT5	anti-PRMT5-RAB-C135	PASS	PASS	nuc	cyto	cyto	cyto	cyto	cyto
PRMT5	anti-PRMT5-RAB-C136	PASS	PASS	nuc	cyto	cyto	cyto	cyto	cyto
PRMT5	anti-PRMT5-RAB-C137	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
PRMT5	anti-PRMT5-RAB-C138	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
PSIP1	anti-PSIP1-RAB-C373	PASS	PASS	NT	NT	NT	NT	NT	NT
PSIP1	anti-PSIP1-RAB-C374	PASS	PASS	NT	NT	NT	NT	NT	NT
PSIP1	anti-PSIP1-RAB-C375	PASS	PASS	NT	NT	NT	NT	NT	NT
RARG	anti-RARG-RAB-C448	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
RBAK	anti-RBAK-RAB-S190	PASS	PASS	nuc	cyto/nuc	nuc	nuc	nuc	nuc
RBAK	anti-RBAK-RAB-S191	PASS	PASS	nuc	nuc	nuc	nuc	nuc	nuc
RBBP5	anti-RBBP5-RAB-C376	PASS	PASS	NT	NT	NT	NT	NT	NT
RBBP5	anti-RBBP5-RAB-C377	PASS	PASS	NT	NT	NT	NT	NT	NT
RBBP5	anti-RBBP5-RAB-C378	PASS	PASS	NT	NT	NT	NT	NT	NT
RBBP5	anti-RBBP5-RAB-C379	PASS	PASS	NT	NT	NT	NT	NT	NT
RPRD1A	anti-RPRD1A-RAB-C380	PASS	PASS	NT	NT	NT	NT	NT	NT
RPRD1A	anti-RPRD1A-RAB-C112	PASS	PASS	nuc	nuc	nuc	nuc	cyto	nuc
RPRD1A	anti-RPRD1A-RAB-C113	PASS	PASS	cyto	nuc	nuc	cyto	cyto	nuc
RPRD1A	anti-RPRD1A-RAB-C114	PASS	PASS	cyto/nuc	cyto	cyto	cyto	cyto	cyto
RPRD1A	anti-RPRD1A-RAB-C170	PASS	PASS	nuc	nuc	nuc	nuc	nuc	nuc
RPRD1A	anti-RPRD1A-RAB-C171	PASS	PASS	nuc	nuc	nuc	nuc	nuc	nuc
SALL4	anti-SALL4-RAB-C191	PASS	PASS	cyto/nuc	cyto	nuc	cyto	cyto	cyto
SCMH1	anti-SCMH1-RAB-C382	PASS	PASS	NT	NT	NT	NT	NT	NT
SCMH1	anti-SCMH1-RAB-C381	PASS	PASS	NT	NT	NT	NT	NT	NT
SCML2	anti-SCML2-RAB-C115	PASS	PASS	cyto	nuc	cyto	cyto	cyto	cyto
SCML2	anti-SCML2-RAB-C116	PASS	PASS	nuc	nuc	cyto	cyto	cyto	cyto
SCML2	anti-SCML2-RAB-C117	PASS	PASS	nuc	nuc	cyto	cyto	cyto	cyto
SCML2	anti-SCML2-RAB-C118	PASS	PASS	nuc	nuc	cyto	nuc	cyto	cyto
SCML2	anti-SCML2-RAB-C119	PASS	PASS	nuc	nuc	nuc	nuc	cyto	cyto
SCML2	anti-SCML2-RAB-C120	PASS	PASS	nuc	nuc	nuc	nuc	cyto	cyto
SCML2	anti-SCML2-RAB-C121	PASS	PASS	nuc	cyto	cyto	cyto	cyto	cyto
SCML2	anti-SCML2-RAB-C142	PASS	PASS	nuc	nuc	nuc	nuc	nuc	nuc
SCML2	anti-SCML2-RAB-C216	PASS	PASS	nuc	cyto	cyto	cyto	cyto	cyto
SCML2	anti-SCML2-RAB-C217	PASS	PASS	nuc	nuc	nuc	nuc	cyto	cyto
SCML2	anti-SCML2-RAB-C218	PASS	PASS	nuc	nuc	nuc	cyto	cyto	cyto
SETD2	anti-SETD2-RAB-C383	PASS	PASS	NT	NT	NT	NT	NT	NT
SETD3	anti-SETD3-RAB-C384	PASS	PASS	NT	NT	NT	NT	NT	NT
SETD3	anti-SETD3-RAB-C385	PASS	PASS	NT	NT	NT	NT	NT	NT
SETD3	anti-SETD3-RAB-C386	PASS	PASS	NT	NT	NT	NT	NT	NT
SETD3	anti-SETD3-RAB-C388	PASS	PASS	NT	NT	NT	NT	NT	NT
SETD3	anti-SETD3-RAB-C387	PASS	PASS	NT	NT	NT	NT	NT	NT
SETD7	anti-SETD7-RAB-C172	PASS	PASS	NT	NT	NT	NT	NT	NT
SETD7	anti-SETD7-RAB-C173	PASS	PASS	NT	NT	NT	NT	NT	NT
SETD7	anti-SETD7-RAB-C174	PASS	PASS	NT	NT	NT	NT	NT	NT
SETD7	anti-SETD7-RAB-C219	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
SETD7	anti-SETD7-RAB-C220	PASS	PASS	cyto	NT	cyto	cyto	cyto	cyto
SETD7	anti-SETD7-RAB-C221	PASS	PASS	NT	NT	NT	NT	NT	NT
SETD7	anti-SETD7-RAB-C70	PASS	PASS	NT	NT	NT	NT	NT	NT
SETMAR	anti-SETMAR-RAB-C391	PASS	PASS	NT	NT	NT	NT	NT	NT
SETMAR	anti-SETMAR-RAB-C389	PASS	PASS	NT	NT	NT	NT	NT	NT
SETMAR	anti-SETMAR-RAB-C392	PASS	PASS	NT	NT	NT	NT	NT	NT
SETMAR	anti-SETMAR-RAB-C393	PASS	PASS	NT	NT	NT	NT	NT	NT
SETMAR	anti-SETMAR-RAB-C390	PASS	PASS	NT	NT	NT	NT	NT	NT
SETMAR	anti-SETMAR-RAB-C394	PASS	PASS	NT	NT	NT	NT	NT	NT
SFMBT1	anti-SFMBT1-RAB-C395	PASS	PASS	NT	NT	NT	NT	NT	NT
SFMBT1	anti-SFMBT1-RAB-C396	PASS	PASS	NT	NT	NT	NT	NT	NT
SFMBT1	anti-SFMBT1-RAB-C397	PASS	PASS	NT	NT	NT	NT	NT	NT
SFMBT2	anti-SFMBT2-RAB-C399	PASS	PASS	NT	NT	NT	NT	NT	NT
SFMBT2	anti-SFMBT2-RAB-C398	PASS	PASS	NT	NT	NT	NT	NT	NT
SIRT5	anti-SIRT5-RAB-C175	PASS	PASS	nuc	nuc	nuc	nuc	NT	cyto
SIRT5	anti-SIRT5-RAB-C176	PASS	PASS	nuc	cyto	nuc	nuc	cyto/nuc	cyto
SIRT5	anti-SIRT5-RAB-C177	PASS	PASS	nuc	nuc	nuc	cyto	cyto	nuc
SIRT5	anti-SIRT5-RAB-C178	PASS	PASS	nuc	nuc	nuc	nuc	cyto/nuc	nuc
SIRT5	anti-SIRT5-RAB-C179	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
SIRT7	anti-SIRT7-RAB-C400	PASS	PASS	cyto/nuc	cyto/nuc	cyto/nuc	cyto/nuc	cyto/nuc	cyto
SMARCA2	anti-SMARCA2-RAB-C401	PASS	PASS	NT	NT	NT	NT	NT	NT

HGCN	Fab name	Primary validation	Secondary validation	JHOC9_IF	A293T_IF	a2780_IF	a2780cis_IF	HPAFII_IF	HEPG2_IF
SMARCA4	anti-SMARCA4-RAB-C402	PASS	PASS	nuc	NT	cyto	nuc	cyto	nuc
SMARCA4	anti-SMARCA4-RAB-C180	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
SMARCA4	anti-SMARCA4-RAB-C181	PASS	PASS	cyto	nuc	nuc	nuc	cyto/nuc	nuc
SMARCA4	anti-SMARCA4-RAB-C182	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
SMARCC2	anti-SMARCC2-RAB-S22	PASS	PASS	misc	cyto	cyto/nuc	cyto/nuc	cyto	cyto
SMARCC2	anti-SMARCC2-RAB-C403	PASS	PASS	NT	NT	NT	NT	NT	NT
SMARCC2	anti-SMARCC2-RAB-C404	PASS	PASS	NT	NT	NT	NT	NT	NT
SMARCC2	anti-SMARCC2-RAB-C405	PASS	PASS	NT	NT	NT	NT	NT	NT
SMARCC2	anti-SMARCC2-RAB-C406	PASS	PASS	NT	NT	NT	NT	NT	NT
SMARCE1	anti-SMARCE1-RAB-S17	PASS	PASS	NT	NT	NT	NT	NT	NT
SMARCE1	anti-SMARCE1-RAB-S18	PASS	PASS	NT	NT	NT	NT	NT	NT
SMARCE1	anti-SMARCE1-RAB-S19	PASS	PASS	NT	NT	NT	NT	NT	NT
SMARCE1	anti-SMARCE1-RAB-S20	PASS	PASS	nuc	nuc	nuc	nuc	nuc	cyto
SMURF1	anti-SMURF1-RAB-C449	PASS	PASS	misc	cyto	misc	misc	cyto	misc
SMURF1	anti-SMURF1-RAB-C450	PASS	PASS	cyto	NT	cyto	cyto	cyto	cyto
SMURF1	anti-SMURF1-RAB-C451	PASS	PASS	cyto	cyto	cyto/nuc	cyto	cyto	misc
SMYD2	anti-SMYD2-RAB-C183	PASS	PASS	NT	NT	NT	NT	NT	NT
SMYD2	anti-SMYD2-RAB-C184	PASS	PASS	NT	NT	NT	NT	NT	NT
SMYD2	anti-SMYD2-RAB-C224	PASS	PASS	NT	NT	NT	NT	NT	NT
SMYD3	anti-SMYD3-RAB-C228	PASS	PASS	NT	NT	NT	NT	NT	NT
SMYD3	anti-SMYD3-RAB-C229	PASS	PASS	NT	NT	NT	NT	NT	NT
SMYD3	anti-SMYD3-RAB-C230	PASS	PASS	NT	NT	NT	NT	NT	NT
SMYD3	anti-SMYD3-RAB-C231	PASS	PASS	NT	NT	NT	NT	NT	NT
SMYD3	anti-SMYD3-RAB-C232	PASS	PASS	NT	NT	NT	NT	NT	NT
SMYD3	anti-SMYD3-RAB-C233	PASS	PASS	NT	NT	NT	NT	NT	NT
SMYD3	anti-SMYD3-RAB-C71	PASS	PASS	NT	NT	NT	NT	NT	NT
SMYD3	anti-SMYD3-RAB-C72	PASS	PASS	NT	NT	NT	NT	NT	NT
SP7	anti-SP7-RAB-S202	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
SP7	anti-SP7-RAB-S203	PASS	PASS	cyto	cyto	cyto	cyto	cyto/nuc	cyto
SRRT	anti-SRRT-RAB-C407	PASS	PASS	NT	NT	NT	NT	NT	NT
SRRT	anti-SRRT-RAB-C408	PASS	PASS	NT	NT	NT	NT	NT	NT
SRY	anti-SRY-RAB-C97	PASS	PASS	NT	NT	NT	NT	NT	NT
SRY	anti-SRY-RAB-C98	PASS	PASS	NT	NT	NT	NT	NT	NT
STAT2	anti-STAT2-RAB-T12	PASS	PASS	nuc	cyto	cyto	misc	cyto	cyto
SUV39H1	anti-SUV39H1-RAB-C487	PASS	PASS	NT	NT	NT	NT	NT	NT
SUV39H1	anti-SUV39H1-RAB-C488	PASS	PASS	NT	NT	NT	NT	NT	NT
SUV39H1	anti-SUV39H1-RAB-C489	PASS	PASS	NT	NT	NT	NT	NT	NT
SUV39H1	anti-SUV39H1-RAB-C490	PASS	PASS	NT	NT	NT	NT	NT	NT
SUV420H2	anti-SUV420H2-RAB-C409	PASS	PASS	NT	NT	NT	NT	NT	NT
TAF1	anti-TAF1-RAB-C410	PASS	PASS	NT	NT	NT	NT	NT	NT
TAF1	anti-TAF1-RAB-C411	PASS	PASS	NT	NT	NT	NT	NT	NT
TAF1	anti-TAF1-RAB-C412	PASS	PASS	NT	NT	NT	NT	NT	NT
TAF1	anti-TAF1-RAB-C413	PASS	PASS	NT	NT	NT	NT	NT	NT
TAF1L	anti-TAF1L-RAB-C414	PASS	PASS	NT	NT	NT	NT	NT	NT
TAF1L	anti-TAF1L-RAB-C415	PASS	PASS	NT	NT	NT	NT	NT	NT
TAF1L	anti-TAF1L-RAB-C416	PASS	PASS	NT	NT	NT	NT	NT	NT
TBL1X	anti-TBL1X-RAB-C122	PASS	PASS	NT	NT	NT	NT	NT	NT
TBL1X	anti-TBL1X-RAB-C123	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
TBL1X	anti-TBL1X-RAB-C124	PASS	PASS	nuc	nuc	nuc	cyto	nuc	nuc
TBL1X	anti-TBL1X-RAB-C125	PASS	PASS	nuc	nuc	nuc	cyto	cyto/nuc	nuc
TBL1X	anti-TBL1X-RAB-C126	PASS	PASS	nuc	nuc	nuc	nuc	nuc	nuc
TBX4	anti-TBX4-RAB-C78	PASS	PASS	cyto	cyto	misc	misc	NT	cyto
TBX4	anti-TBX4-RAB-C79	PASS	PASS	cyto	nuc	nuc	nuc	cyto	cyto
TBX4	anti-TBX4-RAB-C80	PASS	PASS	cyto	cyto	NT	NT	NT	NT
TBX4	anti-TBX4-RAB-C81	PASS	PASS	NT	NT	NT	NT	NT	NT
TBX4	anti-TBX4-RAB-C82	PASS	PASS	NT	NT	NT	NT	NT	NT
TBX5	anti-TBX5-RAB-C46	PASS	PASS	cyto	nuc	cyto	nuc	cyto	cyto
TBX5	anti-TBX5-RAB-C47	PASS	PASS	nuc	cyto	nuc	nuc	cyto	cyto/nuc
TBX5	anti-TBX5-RAB-C48	PASS	PASS	cyto	cyto	cyto	nuc	cyto	cyto
TCF19	anti-TCF19-RAB-C417	PASS	PASS	NT	NT	NT	NT	NT	NT
TDRD3	anti-TDRD3-RAB-C419	PASS	PASS	nuc	nuc	nuc	nuc	NT	nuc
TDRD3	anti-TDRD3-RAB-C418	PASS	PASS	nuc	nuc	nuc	nuc	nuc	nuc
TDRKH	anti-TDRKH-RAB-C127	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
TDRKH	anti-TDRKH-RAB-C128	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
TDRKH	anti-TDRKH-RAB-C129	PASS	PASS	cyto	NT	cyto	cyto	NT	cyto
TDRKH	anti-TDRKH-RAB-C130	PASS	PASS	nuc	nuc	nuc	cyto	cyto	cyto
TDRKH	anti-TDRKH-RAB-C143	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
TGIF1	anti-TGIF-RAB-T13	PASS	PASS	cyto	cyto	cyto	cyto	cyto	.
TNKS1	anti-TNKS1-RAB-C420	PASS	PASS	NT	NT	NT	NT	NT	NT
TP53BP1	anti-TP53BP1-RAB-C424	PASS	PASS	NT	NT	NT	NT	NT	NT
TP53BP1	anti-TP53BP1-RAB-C425	PASS	PASS	NT	NT	NT	NT	NT	NT
TP53BP1	anti-TP53BP1-RAB-C426	PASS	PASS	NT	NT	NT	NT	NT	NT
TP53BP1	anti-TP53BP1-RAB-C427	PASS	PASS	NT	NT	NT	NT	NT	NT
TP53BP1	anti-TP53BP1-RAB-C428	PASS	PASS	NT	NT	NT	NT	NT	NT
TRIM28	anti-TRIM28-RAB-C429	PASS	PASS	NT	NT	NT	NT	NT	NT
TRIM28	anti-TRIM28-RAB-C430	PASS	PASS	NT	NT	NT	NT	NT	NT
TSC2	anti-TSC2-RAB-C433	PASS	PASS	NT	NT	NT	NT	NT	NT
TSC2	anti-TSC2-RAB-C431	PASS	PASS	NT	NT	NT	NT	NT	NT

HGCN	Fab name	Primary validation	Secondary validation	JHOC9_IF	A293T_IF	a2780_IF	a2780cis_IF	HPAFII_IF	HEPG2_IF
TSC2	anti-TSC2-RAB-C432	PASS	PASS	NT	NT	NT	NT	NT	NT
TSC22D4	anti-TSC22D4-RAB-C20	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
TSC22D4	anti-TSC22D4-RAB-C21	PASS	PASS	cyto	cyto	cyto	nuc	cyto	cyto
TSC22D4	anti-TSC22D4-RAB-C22	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
TSC22D4	anti-TSC22D4-RAB-C23	PASS	PASS	nuc	cyto	nuc	cyto	cyto	nuc
TSC22D4	anti-TSC22D4-RAB-C24	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
TSC22D4	anti-TSC22D4-RAB-S6	PASS	PASS	cyto	cyto	cyto	nuc	cyto	cyto
TSC22D4	anti-TSC22D4-RAB-S7	PASS	PASS	nuc	cyto	cyto	cyto	cyto	cyto
TSC22D4	anti-TSC22D4-RAB-S8	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
TSC22D4	anti-TSC22D4-RAB-T11	PASS	PASS	nuc	cyto	nuc	nuc	cyto	nuc
USP7	anti-USP7-RAB-C434	PASS	PASS	NT	NT	NT	NT	NT	NT
USP7	anti-USP7-RAB-C435	PASS	PASS	NT	NT	NT	NT	NT	NT
USP7	anti-USP7-RAB-C452	PASS	PASS	cyto	cyto	cyto/nuc	cyto/nuc	cyto/nuc	cyto/nuc
USP7	anti-USP7-RAB-C453	PASS	PASS	cyto	cyto	cyto	cyto	cyto/nuc	cyto
VAX2	anti-VAX2-RAB-S34	PASS	PASS	cyto	cyto	nuc	cyto	cyto	cyto
VENTX	anti-VENTX-RAB-C42	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
VENTX	anti-VENTX-RAB-C43	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
VENTX	anti-VENTX-RAB-C44	PASS	PASS	cyto	NT	NT	NT	cyto	cyto
WDR45	anti-WDR45-RAB-C454	PASS	PASS	nuc	nuc	nuc	nuc	nuc	nuc
WDR45	anti-WDR45-RAB-C455	PASS	PASS	nuc	nuc	nuc	nuc	nuc	nuc
WDR5	anti-WDR5-RAB-C222	PASS	PASS	nuc	nuc	nuc	nuc	cyto	cyto
WDR5	anti-WDR5-RAB-C223	PASS	PASS	NT	NT	nuc	nuc	nuc	nuc
WDR5	anti-WDR5-RAB-C440	PASS	PASS	nuc	nuc	cyto/nuc	cyto/nuc	cyto	nuc
WDR5	anti-WDR5-RAB-C436	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
WDR5	anti-WDR5-RAB-C437	PASS	PASS	NT	NT	NT	NT	NT	NT
WDR5	anti-WDR5-RAB-C438	PASS	PASS	nuc	nuc	nuc	nuc	nuc	cyto
WDR5	anti-WDR5-RAB-C439	PASS	PASS	cyto	cyto	cyto/nuc	cyto	cyto	cyto
WHSC1L1	anti-WHSC1L1-RAB-C441	PASS	PASS	NT	NT	NT	NT	NT	NT
WHSC1L1	anti-WHSC1L1-RAB-C442	PASS	PASS	NT	NT	NT	NT	NT	NT
WHSC1L1	anti-WHSC1L1-RAB-C443	PASS	PASS	NT	NT	NT	NT	NT	NT
WHSC1L1	anti-WHSC1L1-RAB-C444	PASS	PASS	NT	NT	NT	NT	NT	NT
ZBTB16	anti-ZBTB16-RAB-C208	PASS	PASS	misc	cyto	misc	misc	cyto	cyto
ZBTB16	anti-ZBTB16-RAB-C243	PASS	PASS	misc	misc	misc	misc	cyto	cyto
ZBTB16	anti-ZBTB16-RAB-C244	PASS	PASS	misc	misc	misc	misc	cyto	cyto
ZBTB16	anti-ZBTB16-RAB-C456	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZBTB21	anti-ZBTB21-RAB-C144	PASS	PASS	NT	NT	NT	NT	NT	NT
ZBTB21	anti-ZBTB21-RAB-C83	PASS	PASS	cyto/nuc	nuc	nuc	cyto	cyto	cyto
ZBTB21	anti-ZBTB21-RAB-C84	PASS	PASS	cyto	nuc	cyto	cyto	nuc	cyto
ZBTB21	anti-ZBTB21-RAB-C85	PASS	PASS	cyto	nuc	nuc	cyto	cyto	cyto
ZBTB24	anti-ZBTB24-RAB-C245	PASS	PASS	cyto	cyto	misc	cyto	cyto	cyto
ZBTB24	anti-ZBTB24-RAB-C246	PASS	PASS	cyto	cyto	cyto	cyto	cyto/nuc	cyto
ZBTB24	anti-ZBTB24-RAB-C247	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZBTB24	anti-ZBTB24-RAB-C457	PASS	PASS	nuc	nuc	nuc	nuc	nuc	nuc
ZBTB24	anti-ZBTB24-RAB-C458	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZBTB39	anti-ZBTB39-RAB-C459	PASS	PASS	NT	NT	NT	NT	NT	NT
ZBTB39	anti-ZBTB39-RAB-C86	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZBTB39	anti-ZBTB39-RAB-C87	PASS	PASS	nuc	nuc	nuc	nuc	nuc	nuc
ZBTB39	anti-ZBTB39-RAB-C88	PASS	PASS	NT	NT	NT	NT	NT	NT
ZBTB39	anti-ZBTB39-RAB-S194	PASS	PASS	cyto	cyto/nuc	cyto	cyto	cyto	cyto/nuc
ZBTB39	anti-ZBTB39-RAB-S195	PASS	PASS	NT	NT	NT	nuc	NT	cyto
ZBTB39	anti-ZBTB39-RAB-S196	PASS	PASS	cyto	cyto	cyto	misc	cyto	cyto
ZBTB39	anti-ZBTB39-RAB-S197	PASS	PASS	cyto/nuc	cyto	nuc	nuc	cyto	nuc
ZBTB39	anti-ZBTB39-RAB-S198	PASS	PASS	misc	cyto	NT	cyto/nuc	cyto	nuc
ZBTB41	anti-ZBTB41-RAB-C201	PASS	PASS	cyto	cyto	nuc	cyto	cyto	cyto
ZBTB41	anti-ZBTB41-RAB-C202	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZBTB7B	anti-ZBTB7B-RAB-C206	PASS	PASS	misc	misc	cyto/nuc	cyto/nuc	cyto	cyto
ZBTB7B	anti-ZBTB7B-RAB-C207	PASS	PASS	cyto	cyto	cyto	cyto/nuc	cyto	cyto
ZBTB7B	anti-ZBTB7B-RAB-C248	PASS	PASS	misc	misc	misc	misc	cyto	misc
ZBTB7B	anti-ZBTB7B-RAB-C249	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZBTB7B	anti-ZBTB7B-RAB-C460	PASS	PASS	cyto	misc	cyto	misc	nuc	cyto
ZBTB7B	anti-ZBTB7B-RAB-C461	PASS	PASS	misc	misc	cyto	cyto	cyto	cyto
ZFP69	anti-ZFP69-RAB-C495	PASS	PASS	cyto	cyto	cyto	cyto	nuc	cyto/nuc
ZFP83	anti-ZNF83-RAB-C484	PASS	PASS	NT	NT	NT	NT	NT	NT
ZFP90	anti-ZFP90-RAB-C483	PASS	PASS	NT	NT	NT	NT	NT	NT
ZFYVE20	anti-ZFYVE20-RAB-C11	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZFYVE20	anti-ZFYVE20-RAB-C12	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZFYVE20	anti-ZFYVE20-RAB-C13	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZFYVE20	anti-ZFYVE20-RAB-C14	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZFYVE20	anti-ZFYVE20-RAB-C15	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZFYVE20	anti-ZFYVE20-RAB-C16	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZFYVE20	anti-ZFYVE20-RAB-C17	PASS	PASS	nuc	nuc	cyto	nuc	nuc	nuc
ZFYVE20	anti-ZFYVE20-RAB-C18	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZFYVE20	anti-ZFYVE20-RAB-C19	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZGPAT	anti-ZGPAT-RAB-C185	PASS	PASS	nuc	nuc	nuc	nuc	nuc	cyto
ZGPAT	anti-ZGPAT-RAB-C186	PASS	PASS	NT	cyto	nuc	nuc	nuc	cyto
ZGPAT	anti-ZGPAT-RAB-C187	PASS	PASS	cyto	NT	NT	NT	NT	cyto
ZGPAT	anti-ZGPAT-RAB-C188	PASS	PASS	cyto	cyto	nuc	cyto	cyto/nuc	cyto
ZGPAT	anti-ZGPAT-RAB-C189	PASS	PASS	cyto	NT	nuc	cyto	cyto	cyto

HGCN	Fab name	Primary validation	Secondary validation	JHOC9_IF	A293T_IF	a2780_IF	a2780cis_IF	HPAFII_IF	HEPG2_IF
ZGPAT	anti-ZGPAT-RAB-C190	PASS	PASS	NT	NT	nuc	NT	cyto	cyto
ZHX1	anti-ZHX1-RAB-C59	PASS	PASS	cyto	NT	nuc	nuc	cyto	nuc
ZHX1	anti-ZHX1-RAB-C60	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZHX1	anti-ZHX1-RAB-C61	PASS	PASS	cyto	NT	cyto	cyto	nuc	cyto
ZHX1	anti-ZHX1-RAB-C62	PASS	PASS	cyto	NT	cyto	cyto	cyto	cyto
ZHX1	anti-ZHX1-RAB-C63	PASS	PASS	cyto	misc	cyto	nuc	cyto	cyto
ZKSCAN1	anti-ZKSCAN1-RAB-C462	PASS	PASS	misc	cyto	misc	misc	cyto	cyto
ZKSCAN1	anti-ZKSCAN1-RAB-C463	PASS	PASS	misc	cyto/nuc	misc	misc	nuc	cyto
ZKSCAN2	anti-ZKSCAN2-RAB-C203	PASS	PASS	cyto	cyto	nuc	cyto	cyto/nuc	cyto/nuc
ZKSCAN2	anti-ZKSCAN2-RAB-C204	PASS	PASS	cyto	cyto	cyto	cyto/nuc	cyto	cyto
ZKSCAN2	anti-ZKSCAN2-RAB-C205	PASS	PASS	cyto	cyto	nuc	cyto	cyto/nuc	cyto
ZKSCAN2	anti-ZKSCAN2-RAB-C250	PASS	PASS	cyto	cyto	cyto	cyto	cyto	misc
ZKSCAN2	anti-ZKSCAN2-RAB-C464	PASS	PASS	cyto	misc	misc	cyto	cyto	cyto
ZKSCAN2	anti-ZKSCAN2-RAB-C465	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZKSCAN4	anti-ZKSCAN4-RAB-C198	PASS	PASS	cyto/nuc	cyto	cyto/nuc	cyto/nuc	cyto	cyto
ZKSCAN5	anti-ZKSCAN5-RAB-S75	PASS	PASS	NT	NT	NT	NT	NT	NT
ZKSCAN5	anti-ZKSCAN5-RAB-S76	PASS	PASS	NT	NT	NT	NT	NT	NT
ZKSCAN5	anti-ZKSCAN5-RAB-S77	PASS	PASS	cyto/nuc	cyto/nuc	nuc	cyto/nuc	nuc	cyto/nuc
ZKSCAN5	anti-ZKSCAN5-RAB-S78	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZKSCAN7	anti-ZKSCAN7-RAB-C496	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZKSCAN8	anti-ZKSCAN8-RAB-C49	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZKSCAN8	anti-ZKSCAN8-RAB-C50	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZKSCAN8	anti-ZKSCAN8-RAB-C51	PASS	PASS	cyto	cyto	cyto	cyto	nuc	cyto
ZKSCAN8	anti-ZKSCAN8-RAB-C52	PASS	PASS	NT	NT	NT	NT	NT	NT
ZKSCAN8	anti-ZKSCAN8-RAB-C53	PASS	PASS	cyto	NT	cyto	cyto	cyto	cyto
ZNF165	anti-ZNF165-RAB-C140	PASS	PASS	NT	NT	NT	NT	NT	NT
ZNF165	anti-ZNF165-RAB-C466	PASS	PASS	NT	NT	NT	NT	NT	NT
ZNF165	anti-ZNF165-RAB-C89	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZNF165	anti-ZNF165-RAB-C90	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZNF165	anti-ZNF165-RAB-C91	PASS	PASS	NT	NT	NT	NT	NT	NT
ZNF165	anti-ZNF165-RAB-C92	PASS	PASS	cyto	nuc	cyto	cyto	NT	cyto
ZNF165	anti-ZNF165-RAB-C93	PASS	PASS	cyto	nuc	NT	cyto	cyto	NT
ZNF165	anti-ZNF165-RAB-C94	PASS	PASS	cyto	cyto	NT	cyto	cyto	cyto
ZNF165	anti-ZNF165-RAB-C95	PASS	PASS	cyto	cyto	nuc	cyto	cyto	cyto
ZNF165	anti-ZNF165-RAB-C96	PASS	PASS	cyto	cyto	misc	misc	cyto	cyto
ZNF174	anti-ZNF174-RAB-C467	PASS	PASS	nuc	NT	nuc	NT	NT	NT
ZNF174	anti-ZNF174-RAB-C468	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZNF18	anti-ZNF18-RAB-S12	PASS	PASS	nuc	cyto	cyto	cyto	cyto	cyto
ZNF18	anti-ZNF18-RAB-S13	PASS	PASS	misc	cyto	cyto/nuc	cyto	cyto	cyto
ZNF18	anti-ZNF18-RAB-S14	PASS	PASS	NT	NT	NT	NT	NT	NT
ZNF18	anti-ZNF18-RAB-S15	PASS	PASS	NT	NT	NT	NT	NT	NT
ZNF18	anti-ZNF18-RAB-S16	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZNF18	anti-ZNF18-RAB-S199	PASS	PASS	NT	NT	NT	NT	NT	NT
ZNF197	anti-ZNF197-RAB-C209	PASS	PASS	cyto	cyto	cyto	cyto	cyto/nuc	cyto
ZNF197	anti-ZNF197-RAB-C210	PASS	PASS	cyto	cyto	cyto	misc	cyto	cyto
ZNF197	anti-ZNF197-RAB-C251	PASS	PASS	cyto	cyto	cyto	nuc	cyto	cyto
ZNF197	anti-ZNF197-RAB-C469	PASS	PASS	cyto/nuc	nuc	nuc	cyto	cyto	cyto
ZNF213	anti-ZNF213-RAB-C192	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZNF213	anti-ZNF213-RAB-C193	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZNF213	anti-ZNF213-RAB-C194	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZNF213	anti-ZNF213-RAB-C195	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZNF213	anti-ZNF213-RAB-C470	PASS	PASS	misc	misc	misc	cyto	cyto	misc
ZNF213	anti-ZNF213-RAB-C471	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZNF213	anti-ZNF213-RAB-C472	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZNF232	anti-ZNF232-RAB-C473	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZNF263	anti-ZNF263-RAB-S49	PASS	PASS	NT	NT	NT	NT	NT	NT
ZNF263	anti-ZNF263-RAB-S50	PASS	PASS	NT	NT	NT	NT	NT	NT
ZNF263	anti-ZNF263-RAB-S51	PASS	PASS	NT	NT	NT	NT	NT	NT
ZNF263	anti-ZNF263-RAB-S52	PASS	PASS	NT	NT	NT	NT	NT	NT
ZNF343	anti-ZNF343-RAB-S21	PASS	PASS	NT	NT	NT	NT	NT	NT
ZNF394	anti-ZNF394-RAB-S53	PASS	PASS	NT	NT	NT	NT	NT	NT
ZNF394	anti-ZNF394-RAB-S54	PASS	PASS	NT	NT	NT	NT	NT	NT
ZNF394	anti-ZNF394-RAB-S55	PASS	PASS	NT	NT	NT	NT	NT	NT
ZNF394	anti-ZNF394-RAB-S56	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZNF394	anti-ZNF394-RAB-S57	PASS	PASS	NT	NT	NT	NT	NT	NT
ZNF394	anti-ZNF394-RAB-S58	PASS	PASS	NT	NT	NT	NT	NT	NT
ZNF394	anti-ZNF394-RAB-S59	PASS	PASS	NT	NT	NT	NT	NT	NT
ZNF394	anti-ZNF394-RAB-S60	PASS	PASS	NT	NT	NT	NT	NT	NT
ZNF394	anti-ZNF394-RAB-S61	PASS	PASS	NT	NT	NT	NT	NT	NT
ZNF394	anti-ZNF394-RAB-S62	PASS	PASS	NT	NT	NT	NT	NT	NT
ZNF394	anti-ZNF394-RAB-S63	PASS	PASS	cyto	cyto	NT	cyto	cyto	cyto/nuc
ZNF394	anti-ZNF394-RAB-S64	PASS	PASS	cyto	cyto	cyto	cyto	NT	cyto
ZNF394	anti-ZNF394-RAB-S65	PASS	PASS	cyto	cyto	NT	cyto	cyto	cyto/nuc
ZNF394	anti-ZNF394-RAB-S66	PASS	PASS	misc	misc	misc	misc	cyto	misc
ZNF394	anti-ZNF394-RAB-S67	PASS	PASS	cyto	cyto	NT	misc	cyto/nuc	cyto
ZNF394	anti-ZNF394-RAB-S68	PASS	PASS	misc	cyto	cyto/nuc	misc	cyto	misc
ZNF394	anti-ZNF394-RAB-S69	PASS	PASS	misc	cyto	misc	misc	cyto	misc
ZNF394	anti-ZNF394-RAB-S70	PASS	PASS	misc	misc	misc	misc	cyto	misc

HGCN	Fab name	Primary validation	Secondary validation	JHOC9_IF	A293T_IF	a2780_IF	a2780cis_IF	HPAFII_IF	HEPG2_IF
ZNF394	anti-ZNF394-RAB-S71	PASS	PASS	cyto/nuc	NT	cyto/nuc	cyto/nuc	cyto/nuc	cyto/nuc
ZNF394	anti-ZNF394-RAB-S72	PASS	PASS	misc	cyto	cyto	NT	cyto	misc
ZNF394	anti-ZNF394-RAB-S73	PASS	PASS	cyto/nuc	cyto	cyto	cyto	cyto	cyto
ZNF394	anti-ZNF394-RAB-S74	PASS	PASS	misc	cyto	cyto	NT	cyto	misc
ZNF397	anti-ZNF397-RAB-S79	PASS	PASS	cyto/nuc	cyto	nuc	cyto/nuc	cyto	misc
ZNF397	anti-ZNF397-RAB-S80	PASS	PASS	cyto	NT	cyto	NT	cyto/nuc	cyto
ZNF397	anti-ZNF397-RAB-S81	PASS	PASS	misc	cyto/nuc	cyto	misc	cyto	NT
ZNF397	anti-ZNF397-RAB-S82	PASS	PASS	cyto/nuc	NT	nuc	nuc	cyto/nuc	nuc
ZNF41	anti-ZNF41-RAB-C252	PASS	PASS	misc	cyto/nuc	cyto	cyto	cyto	cyto
ZNF446	anti-ZNF446-RAB-C25	PASS	PASS	nuc	nuc	nuc	nuc	nuc	nuc
ZNF446	anti-ZNF446-RAB-C26	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZNF446	anti-ZNF446-RAB-C27	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZNF446	anti-ZNF446-RAB-C28	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZNF446	anti-ZNF446-RAB-C29	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZNF446	anti-ZNF446-RAB-C30	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZNF449	anti-ZNF449-RAB-C253	PASS	PASS	misc	misc	misc	misc	cyto	cyto
ZNF449	anti-ZNF449-RAB-C254	PASS	PASS	misc	nuc	misc	misc	cyto	cyto
ZNF449	anti-ZNF449-RAB-C474	PASS	PASS	nuc	NT	nuc	NT	NT	NT
ZNF483	anti-ZNF483-RAB-C255	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZNF483	anti-ZNF483-RAB-C256	PASS	PASS	nuc	nuc	nuc	nuc	NT	NT
ZNF483	anti-ZNF483-RAB-C475	PASS	PASS	misc	cyto	misc	misc	cyto	cyto
ZNF500	anti-ZNF500-RAB-C257	PASS	PASS	cyto/nuc	nuc	cyto/nuc	nuc	cyto	cyto/nuc
ZNF500	anti-ZNF500-RAB-C476	PASS	PASS	NT	NT	NT	NT	NT	NT
ZNF500	anti-ZNF500-RAB-C477	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZNF500	anti-ZNF500-RAB-C478	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZNF500	anti-ZNF500-RAB-C479	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZNF639	anti-ZNF639-RAB-T10	PASS	PASS	cyto	misc	nuc	misc	cyto	cyto
ZNF639	anti-ZNF639-RAB-T8	PASS	PASS	nuc	cyto	cyto	cyto	cyto	cyto
ZNF639	anti-ZNF639-RAB-T9	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZNF699	anti-ZNF699-RAB-S204	PASS	PASS	nuc	nuc	nuc	nuc	cyto	cyto
ZNF699	anti-ZNF699-RAB-S205	PASS	PASS	misc	cyto	misc	misc	cyto	misc
ZNF70	anti-ZNF70-RAB-S193	PASS	PASS	NT	NT	NT	NT	NT	NT
ZSCAN1	anti-ZSCAN1-RAB-S83	PASS	PASS	NT	NT	NT	NT	NT	NT
ZSCAN1	anti-ZSCAN1-RAB-S84	PASS	PASS	NT	NT	NT	NT	NT	NT
ZSCAN1	anti-ZSCAN1-RAB-S85	PASS	PASS	NT	NT	NT	NT	NT	NT
ZSCAN1	anti-ZSCAN1-RAB-S86	PASS	PASS	NT	NT	NT	NT	NT	NT
ZSCAN1	anti-ZSCAN1-RAB-S87	PASS	PASS	NT	NT	NT	NT	NT	NT
ZSCAN1	anti-ZSCAN1-RAB-S88	PASS	PASS	NT	NT	NT	NT	NT	NT
ZSCAN1	anti-ZSCAN1-RAB-S89	PASS	PASS	NT	NT	NT	NT	NT	NT
ZSCAN1	anti-ZSCAN1-RAB-S90	PASS	PASS	NT	NT	NT	NT	NT	NT
ZSCAN1	anti-ZSCAN1-RAB-S91	PASS	PASS	NT	NT	NT	NT	NT	NT
ZSCAN1	anti-ZSCAN1-RAB-S92	PASS	PASS	NT	NT	NT	NT	NT	NT
ZSCAN1	anti-ZSCAN1-RAB-S93	PASS	PASS	NT	NT	NT	NT	NT	NT
ZSCAN1	anti-ZSCAN1-RAB-S94	PASS	PASS	NT	NT	NT	NT	NT	NT
ZSCAN12	anti-ZSCAN12-RAB-S100	PASS	PASS	misc	cyto	cyto/nuc	misc	cyto	misc
ZSCAN12	anti-ZSCAN12-RAB-S101	PASS	PASS	misc	misc	misc	misc	misc	misc
ZSCAN12	anti-ZSCAN12-RAB-S102	PASS	PASS	misc	cyto	cyto	misc	cyto	cyto
ZSCAN12	anti-ZSCAN12-RAB-S103	PASS	PASS	misc	cyto	misc	misc	cyto	misc
ZSCAN12	anti-ZSCAN12-RAB-S104	PASS	PASS	misc	cyto	misc	misc	misc	misc
ZSCAN12	anti-ZSCAN12-RAB-S105	PASS	PASS	misc	cyto	misc	misc	cyto	misc
ZSCAN12	anti-ZSCAN12-RAB-S95	PASS	PASS	NT	NT	NT	NT	NT	NT
ZSCAN12	anti-ZSCAN12-RAB-S96	PASS	PASS	NT	NT	NT	NT	NT	NT
ZSCAN12	anti-ZSCAN12-RAB-S97	PASS	PASS	NT	NT	NT	NT	NT	NT
ZSCAN12	anti-ZSCAN12-RAB-S98	PASS	PASS	NT	NT	NT	NT	NT	NT
ZSCAN12	anti-ZSCAN12-RAB-S99	PASS	PASS	misc	cyto/nuc	nuc	nuc	cyto	nuc
ZSCAN20	anti-ZSCAN20-RAB-S106	PASS	PASS	NT	NT	NT	NT	NT	NT
ZSCAN20	anti-ZSCAN20-RAB-S107	PASS	PASS	misc	cyto	cyto	misc	cyto	cyto
ZSCAN20	anti-ZSCAN20-RAB-S108	PASS	PASS	cyto	cyto	cyto	misc	cyto	cyto
ZSCAN20	anti-ZSCAN20-RAB-S109	PASS	PASS	misc	misc	misc	misc	cyto	misc
ZSCAN20	anti-ZSCAN20-RAB-S110	PASS	PASS	misc	cyto	cyto/nuc	cyto/nuc	cyto	nuc
ZSCAN20	anti-ZSCAN20-RAB-S111	PASS	PASS	NT	cyto	NT	NT	cyto	NT
ZSCAN20	anti-ZSCAN20-RAB-S112	PASS	PASS	misc	cyto	cyto	cyto/nuc	cyto	cyto
ZSCAN20	anti-ZSCAN20-RAB-S113	PASS	PASS	cyto	cyto	nuc	cyto	cyto	cyto
ZSCAN20	anti-ZSCAN20-RAB-S114	PASS	PASS	misc	cyto	cyto	misc	cyto	cyto
ZSCAN21	anti-ZSCAN21-RAB-S115	PASS	PASS	NT	NT	NT	NT	NT	NT
ZSCAN21	anti-ZSCAN21-RAB-S116	PASS	PASS	NT	NT	NT	NT	NT	NT
ZSCAN21	anti-ZSCAN21-RAB-S117	PASS	PASS	NT	NT	NT	NT	NT	NT
ZSCAN21	anti-ZSCAN21-RAB-S118	PASS	PASS	NT	NT	NT	NT	NT	NT
ZSCAN22	anti-ZSCAN22-RAB-C37	PASS	PASS	cyto	cyto	nuc	cyto	cyto	nuc
ZSCAN22	anti-ZSCAN22-RAB-C38	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZSCAN22	anti-ZSCAN22-RAB-C39	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZSCAN22	anti-ZSCAN22-RAB-C40	PASS	PASS	cyto	cyto	cyto	cyto	nuc	cyto
ZSCAN22	anti-ZSCAN22-RAB-C41	PASS	PASS	cyto	cyto	cyto	nuc	cyto	cyto
ZSCAN23	anti-ZSCAN23-RAB-C480	PASS	PASS	cyto	cyto	cyto	cyto/nuc	cyto	cyto
ZSCAN23	anti-ZSCAN23-RAB-C481	PASS	PASS	misc	cyto	misc	misc	cyto	cyto
ZSCAN23	anti-ZSCAN23-RAB-C482	PASS	PASS	cyto/nuc	cyto/nuc	cyto/nuc	nuc	cyto	nuc
ZSCAN25	anti-ZSCAN25-RAB-C199	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZSCAN25	anti-ZSCAN25-RAB-C200	PASS	PASS	cyto	cyto	nuc	cyto	cyto	cyto

HGCN	Fab name	Primary validation	Secondary validation	JHOC9_IF	A293T_IF	a2780_IF	a2780cis_IF	HPAFII_IF	HEPG2_IF
ZSCAN26	anti-ZSCAN26-RAB-S119	PASS	PASS	cyto	cyto	cyto/nuc	nuc	cyto/nuc	NT
ZSCAN26	anti-ZSCAN26-RAB-S120	PASS	PASS	cyto/nuc	cyto	cyto	NT	cyto	cyto
ZSCAN26	anti-ZSCAN26-RAB-S121	PASS	PASS	cyto	cyto	cyto	cyto	misc	cyto
ZSCAN26	anti-ZSCAN26-RAB-S122	PASS	PASS	cyto	cyto	cyto	cyto	misc	cyto
ZSCAN26	anti-ZSCAN26-RAB-S123	PASS	PASS	misc	cyto	cyto	misc	cyto	misc
ZSCAN26	anti-ZSCAN26-RAB-S124	PASS	PASS	misc	cyto	cyto	misc	cyto	cyto
ZSCAN26	anti-ZSCAN26-RAB-S125	PASS	PASS	cyto	cyto	nuc	NT	cyto	nuc
ZSCAN26	anti-ZSCAN26-RAB-S126	PASS	PASS	misc	NT	misc	misc	cyto	cyto
ZSCAN26	anti-ZSCAN26-RAB-S127	PASS	PASS	NT	NT	NT	nuc	cyto/nuc	nuc
ZSCAN26	anti-ZSCAN26-RAB-S128	PASS	PASS	cyto	cyto	NT	NT	NT	NT
ZSCAN26	anti-ZSCAN26-RAB-S129	PASS	PASS	cyto	cyto	cyto/nuc	cyto/nuc	cyto	nuc
ZSCAN29	anti-ZSCAN29-RAB-C1	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZSCAN29	anti-ZSCAN29-RAB-C10	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZSCAN29	anti-ZSCAN29-RAB-C2	PASS	PASS	cyto	NT	cyto	cyto	cyto	cyto
ZSCAN5A	anti-ZSCAN5A-RAB-S145	PASS	PASS	cyto	NT	cyto	cyto	cyto	cyto
ZSCAN5A	anti-ZSCAN5A-RAB-S146	PASS	PASS	cyto	cyto	nuc	cyto	cyto	cyto/nuc
ZSCAN5A	anti-ZSCAN5A-RAB-S147	PASS	PASS	NT	NT	NT	nuc	NT	NT
ZSCAN5A	anti-ZSCAN5A-RAB-S148	PASS	PASS	cyto	cyto	nuc	cyto	misc	cyto/nuc
ZSCAN5A	anti-ZSCAN5A-RAB-S149	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZSCAN5A	anti-ZSCAN5A-RAB-S150	PASS	PASS	cyto	NT	cyto/nuc	cyto	cyto	cyto/nuc
ZSCAN5A	anti-ZSCAN5A-RAB-S151	PASS	PASS	cyto	cyto	NT	cyto	misc	cyto/nuc
ZSCAN5A	anti-ZSCAN5A-RAB-S152	PASS	PASS	misc	NT	misc	cyto	misc	misc
ZSCAN5A	anti-ZSCAN5A-RAB-S153	PASS	PASS	cyto	NT	nuc	cyto	cyto	nuc
ZSCAN5A	anti-ZSCAN5A-RAB-S154	PASS	PASS	NT	NT	nuc	nuc	cyto	nuc
ZSCAN5B	anti-ZSCAN5B-RAB-S167	PASS	PASS	misc	cyto	misc	misc	cyto	misc
ZSCAN5B	anti-ZSCAN5B-RAB-S168	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZSCAN5B	anti-ZSCAN5B-RAB-S169	PASS	PASS	nuc	cyto	cyto	nuc	cyto	nuc
ZSCAN5B	anti-ZSCAN5B-RAB-S170	PASS	PASS	cyto	NT	cyto	cyto	cyto	cyto
ZSCAN5B	anti-ZSCAN5B-RAB-S171	PASS	PASS	nuc	nuc	cyto/nuc	nuc	cyto	nuc
ZSCAN5B	anti-ZSCAN5B-RAB-S172	PASS	PASS	cyto	NT	nuc	cyto	cyto	cyto
ZSCAN5B	anti-ZSCAN5B-RAB-S173	PASS	PASS	misc	cyto	cyto	misc	cyto	cyto
ZSCAN5B	anti-ZSCAN5B-RAB-S174	PASS	PASS	cyto	cyto	cyto	misc	cyto	misc
ZSCAN5B	anti-ZSCAN5B-RAB-S175	PASS	PASS	nuc	cyto	nuc	nuc	cyto	nuc
ZSCAN5B	anti-ZSCAN5B-RAB-S176	PASS	PASS	cyto	cyto	nuc	nuc	cyto	cyto
ZSCAN5C	anti-ZSCAN5C-RAB-S177	PASS	PASS	NT	NT	NT	NT	NT	NT
ZSCAN5C	anti-ZSCAN5C-RAB-S178	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZSCAN5C	anti-ZSCAN5C-RAB-S179	PASS	PASS	misc	cyto	cyto	misc	cyto	misc
ZSCAN5C	anti-ZSCAN5C-RAB-S180	PASS	PASS	misc	misc	misc	misc	cyto	misc
ZSCAN5C	anti-ZSCAN5C-RAB-S181	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZSCAN5C	anti-ZSCAN5C-RAB-S182	PASS	PASS	NT	NT	NT	NT	NT	NT
ZSCAN5C	anti-ZSCAN5C-RAB-S183	PASS	PASS	nuc	nuc	NT	NT	NT	nuc
ZSCAN5C	anti-ZSCAN5C-RAB-S184	PASS	PASS	cyto	cyto	cyto	cyto	cyto	cyto
ZSCAN5C	anti-ZSCAN5C-RAB-S185	PASS	PASS	nuc	cyto	cyto	NT	cyto	cyto
ZSCAN5C	anti-ZSCAN5C-RAB-S186	PASS	PASS	misc	cyto	cyto	cyto	cyto	cyto
ZSCAN5C	anti-ZSCAN5C-RAB-S187	PASS	PASS	nuc	cyto	nuc	nuc	cyto	cyto
ZSCAN5C	anti-ZSCAN5C-RAB-S188	PASS	PASS	nuc	cyto	nuc	nuc	cyto	cyto/nuc
ZSCAN5C	anti-ZSCAN5C-RAB-S189	PASS	PASS	nuc	cyto	cyto	NT	cyto	cyto
ZSCAN9	anti-ZSCAN9-RAB-C493	PASS	PASS	nuc	nuc	nuc	nuc	nuc	nuc

Table SI 5: Comparison of IF staining with overlapping antibodies that were developed at the RAN and the Protein Atlas showing staining location and cell types.

HGCN	PA IF	PA Cell Line	RAN IF	RAN Cell Line	Match
ANAPC2	nuc	U2-OS	nuc	293T	Y
ANKZF1	cyto/nuc	A-431	cyto	HPAF-II	partial
ARID3a	cyto/nuc	U2-OS	nuc	JHOC-9	partial
BRD4	nuc	U2-OS	nuc	JHOC-9	Y
CBX1	nuc	U2-OS	nuc	JHOC-9	Y
CBX2	cyto/nuc	U-251 MG	cyto	ALL	partial
CDC73	nuc	U2-OS	nuc	ALL	Y
CHD4	nuc	U-251 MG	nuc	ALL	Y
ESRRA	cyto/nuc/misc	MCF-7	cyto	ALL	partial
FOXP1	nuc	A-431	misc	ALL	N
FOXP4	cyto	A-431	cyto	ALL	Y
H1FX	nuc	U2-OS	nuc	ALL	Y
KDM4A	cyto/nucleoli	A-431	cyto	293T	Y
MBD4	nuc	U2-OS	cyto/nuc	HepG2	Y
MSH6	nuc	U2-OS	nuc	ALL	Y
NR1D2	nuc	U2-OS	nuc	A2780	Y
PGBD1	cyto/nuc	U2-OS	cyto/nuc	A2780	Y
PIKFYVE	nuc	U2-OS	cyto	ALL	N
RPRD1A	nuc/golgi	U2-OS	nuc	ALL	Y
SCML2	nucleoli	A-431	nuc	ALL	Y
SETD7	nucleoli	US-OS	cyto	ALL	N
SIRT5	misc	A-431	cyto/nuc	HPAF-II	partial
SMARCA4	nuc	U2-OS	nuc	A2780	Y
SMARCE1	nuc	U2-OS	nuc	ALL	Y
STAT2	cyto	U2-OS	cyto	A2780	Y
TDRD3	nuc	U2-OS	nuc	ALL	Y
TDRKH	cyto	U2-OS	cyto	ALL	Y
TGIF1	nuc	A549	cyto	ALL	N
TSC22D4	cyto	U2-OS	cyto	ALL	Y
USP7	misc	HepG2	cyto/nuc	A2780	partial
WDR45	nucleoli	U2-OS	nuc	ALL	Y
WDR5	nuc	U2-OS	nuc	ALL	Y
ZBTB16	nuc/nucleoli	A-431	misc	ALL	N
ZBTB21	cyto/nuc	U2-OS	cyto/nuc	293T	Y
ZBTB41	cyto/nuc rim	U2-OS	cyto	ALL	partial
ZBTB7B	nuc	U2-OS	nuc	HPAF-II	Y
ZFYVE20	cyto/misc	U2-OS	cyto	ALL	Y
ZHX1	nuc	U2-OS	nuc	A2780	Y
ZKSCAN1	nuc	A-431	nuc	HPAF-II	Y
ZKSCAN8	cyto/nuc	U2-OS	cyto	ALL	partial
ZNF18	cyto/nuc	U2-OS	cyto/nuc	A2780	Y
ZNF174	cyto/nuc	U2-OS	nuc	JHOC9	Y
ZNF197	nuc	U2-OS	nuc	A2780	Y
ZNF213	cyto	U2-OS	cyto	ALL	Y
ZNF394	cyto/nuc	U2-OS	cyto	ALL	partial
ZNF397	cyto/nuc	U2-OS	cyto/nuc	HPAF-II	Y
ZNF446	nuc	U2-OS	nuc	ALL	Y
ZNF449	misc	U2-OS	misc	ALL	Y
ZNF500	cyto/nuc	U2-OS	cyto/nuc	HepG2	Y
ZNF639	nuc	U2-OS	nuc	JHOC9	Y
ZSCAN12	cyto	U2-OS	cyto	ALL	Y
ZSCAN20	nuc	U2-OS	nuc	A2780	Y
ZSCAN22	cyto	U2-OS	cyto	ALL	Y
ZSCAN25	nuc	U2-OS	nuc	A2780	Y
ZSCAN9	nuc	U2-OS	nuc	ALL	Y
				Total	55
				Total Matches	50
				Total Mismatches	5
				Percent Match	**90.91%**