Supplemental Information

Table S1. Primers used for ChIP assay to validate LANA binding sites by real-time PCR. Nearest associated gene is indicated to the right.

Table S2. Oligonucleotides used for probes or competitors in EMSA for binding to purified recombinant LANA. Nearest associated gene is indicated.

Table S3. Primers used for RT-PCR using real-time PCR analysis. Nearest associated gene is indicated.

Table S4. ChIP-Seq read count and mapping data for two independent ChIP-Seq experiments is provided.

Table S5. List of genes that were aligned to LANA ChIP-seq peaks are indicated with NCBI accession number, chromosome location, peak location, and peak score.

Table S6. Focus genes in the pathway analysis network 1.

Table S7. Focus genes in the pathway analysis network 2.

Table S8. LANA Binding motifs aligned to LBS1 and LBS2.

Table S1 Primers for ChIP assays.

CATACCAGTAGGGCCCAAAGC	KSHV_R1_5'
GCCCTGTGGATACCTAGTCAAAA	KSHV_R1_3'
TTCACGTGATACTAGAAAGGGCATT	KSHV_R2_5'
CAAAATTCCATGTGGCTTCCTAA	KSHV_R2_3'
GGGCGCCCTCTCTCTACTG	KSHV_R3_5'
CCCAAACAGGCTCACACACA	KSHV_R3_3'
CCTGCCGGGGACGCCGCCGGGGCCT	KSHV_LBS1/2_5'
CTGAGGCGGCGCGCGGCCCCAT	KSHV_LBS1/2_3'
TCCTAGCTCTCCTGACGTTTGTT	ACVR1C_5'
CTCACAGCGCAACCTGGTT	ACVR1C_3'
TGGAAATGATCCCGGAGAGA	FBXO4_5'
CCTCTGGCCCGCTGACT	FBXO4_3'
CCCAGAGAGGGCTGTTGGTA	IFI6_5'
GGACTCCATCAGCCCTCATC	IFI6_3'
TCATCTCCACCTAGTATTCCCATTAA	IQGAP3_5'
GCCGGACTCGGGAACAC	IQGAP3_3'
TCTCCCACTTTCTGCCTAACCT	METTL2B_5'
CCCGGAGGAGTCGTATCTCA	METTL2B_3'
GTCTGTGCTGTGCTCAGTCCTAGGT	MRVI1_5'
GCACAGACATGGGGTGAGCAC	MRVI1_3'
TGGAAGAGGAGGAGACACTGACT	NIPAL2_5'
ACTGGAATTGCCAGGTAGAGATG	NIPAL2_3'
ATGAGGAATGTGGTAGCCATAGG	NIPBL_5'
ATCTGAAGCAAACCCAATCCA	NIPBL_3'
TGCTCTCTGCTTTATTCCCACTT	MEI1_5'
GCTCCAGGGTCAGTCGTATGA	MEI1_3'
CATGGCCCGACCTTACCA	PARL_5'
ACTGCTCCTCGTGCTCTATGG	PARL_3'
GGGAAAGCGAAATCGAAAGC	TAP1_5’

GGCAGGCCACTTTTGGAA	TAP1_3’
GGTTGGTGGCCAGTAGTCTTG	TMBIM6_5'
AACAGCGGCTGCTTAGTTCAG	TMBIM6_3'

Table S2 Oligos for EMSA.

CGCCGCCGGGGCCTGCGGCGCCTCCCGCCCGGGCATGGGGCCGCGC	LBS1/2_Fwd
GCGCGGCCCCATGCCCGGGCGGGAGGCGCCGCAGGCCCCGGCGGCG	LBS1/2_Rev
TTTAAATACGTTTTAGGATTCACGTGATACTAGAAAGGGCATTTAA	KSHV_R2_Fwd
TTAAATGCCCTTTCTAGTATCACGTGAATCCTAAAACGTATTTAAA	KSHV_R2_Rev
CTTGTGTGTGAGCCTGTTTGGGGGAGCCTCCTCAGTGCTTGCTACG	KSHV_R3_Fwd
CGTAGCAAGCACTGAGGAGGCTCCCCCAAACAGGCTCACACACAAG	KSHV_R3_Rev
AGGAATGGGGCTTCTCACGGGAGGAAAAGCCCCACTGAGACTTTAG	ACVR1C_Fwd
CTAAAGTCTCAGTGGGGCTTTTCCTCCCGTGAGAAGCCCCATTCCT	ACVR1C_Rev
GAAGAGGAGGTGGGCCCTGGAGGGATTCTCTGATGGACCACTCTTG	IFI6_Fwd
CAAGAGTGGTCCATCAGAGAATCCCTCCAGGGCCCACCTCCTCTTC	IFI6_Rev
CAGGCTCCTTTTCTGCTTAACAGTCTTATTCTAGCTGCTGCCCCTG	IQGAP3_Fwd
CAGGGGCAGCAGCTAGAATAAGACTGTTAAGCAGAAAAGGAGCCTG	IQGAP3_Rev
GTTACCCCATGTCTGTGCTGTGCTCACCCCATGTCTGTGCCGTGCT	MRVI1_Fwd
AGCACGGCACAGACATGGGGTGAGCACAGCACAGACATGGGGTAAC	MRVI1_Rev
ACGCCGTCCCGGTCCCGGCCGGGCCTGGGACTCTCCGCGCCCCGGT	TAP1_Fwd
ACCGGGGCGCGGAGAGTCCCAGGCCCGGCCGGGACCGGGACGGCGT	TAP1_Rev
CCCGCCCGGGCCTGGGGCCGCGGGCGCCCCCCGCCCGGGCCTGGGGCCGCGGGCGCCC	2 x Motif 1_Fwd
GGGCGCCCGCGGCCCCAGGCCCGGGCGGGGGGCGCCCGCGGCCCCAGGCCCGGGCGGG	2 x Motif 1_Rev
GAGCCCAGGGAGGGGAAGCGGGAGCCCAGGGAGGGGAAGCGG	2 x Motif 2_Fwd
CCGCTTCCCCTCCCTGGGCTCCCGCTTCCCCTCCCTGGGCTC	2 x Motif 2_Rev

Table S3 Primers for RTPCR.

CCTCTTTGGTGTTGAGCTTGATG	FBXO4_5'
CTGAGGCAAACCAGCTGTTG	FBXO4_3'
TGGGCTACACTGAGCACCAG	GAPDH_5'
GGGTGTCGCTGTTGAAGTCA	GAPDH_3'
AAGAGAGTTCTCATTTTCCCTATTCAA	IQGAP3_5'
GCCCCAACCTAAGGTGACTTT	IQGAP3_3'
CAAACTGGTGCCTTGGGTAGA	NIPBL_5'
ACAGGGATCGTAAAGTCTGAACAAC	NIPBL_3'
CCTTCCGATGTTCACGTTCA	PARL_5'
CATGGCGATAATGGCTTTCA	PARL_3'
GCTGCACGAGCGCATCTA	PSMB9_5'
CACGGCTTGGGCATCAG	PSMB9_3'
GGGTGACGGGATCTATAACAACA	TAP1_5'
CCAAACACCTCTCCCTGCAA	TAP1_3'

Table S4 Solexa sequencing and gene mapping summary

	Sample	Total sequence tags	Aligned to Human Genome	Aligned to KSHV Genome
ChIP-seq No. 1	LANA	14388640	13231288(91.96%)	116146(0.81%)
	IgG	15003308	13912136(92.73%)	13211(0.09%)
ChIP-seq No. 2	LANA	24557413	17488360(71.2%)	2052137(8.35%)
	IgG	26106367	15371726(58.9%)	105303(0.4%)

Table S5 LANA ChIP-seq peaks aligned to genes.

		ChIP-seq No. 1		ChIP-seq No.2	
Gene	**Chromosome**	**Peak Position**	**Peak Score**	**Peak Position**	**Peak Score**
AC002539.1	chr17	65564600	6.12	65564435	4.07
AC006038.4	chr2	42507495	7.5	42507290	4.03
AC012593.1	chr2	35032110	6.11	35032170	4.93
AC021593.2	chr17	73513535	6.94	73513325	2.42
AC023115.2	chr2	67359570	6.04	67359750	4.1
AC023115.3	chr2	67359570	6.04	67359750	4.1
AC037445.1	chr17	58624890	5.22	58624665	5
AC090044.1	chr3	592150	8.16	591955	5.62
AF508907	chr1	183843420	6.4	183843470	4.24
AF510427	chr1	183843420	6.4	183843470	4.24
AKAP13	chr15	83939965	5.01	83940020	4.74
AL110163 (TAOK1)	chr17	24900025	5.16	24899880	3.2
ANGPT1	chr8	108379485	7.74	108379450	7.17
ANKFN1	chr17	51776915	5.02	51776740	3.38
APPBP2	chr17	55902055	6.1	55901825	2.54
ATP6V1C1	chr8	104154705	10.08	104154485	5.78
AX748308	chr22	26603550	4.94	26603640	2.88
BC040863	chr2	67359570	6.04	67359750	4.1
BC044653	chr22	43912670	4.28	43912905	2.68
BCAP29	chr7	107033145	8.74	107033345	6.83
BCAS1	chr20	52043340	7.4	52043420	5.21
BCAS3	chr17	56566955	5.24	56631585	5.28
BCL2L13	chr22	16569275	4.53	16569085	2.53
BRIP1	chr17	57255670	6.09	57255550	3.5
BX647864	chr17	65564600	6.12	65564435	4.07
C16ORF87	chr16	45396355	5.06	45396365	3.24
C19ORF2	chr19	35130010	6.04	35152275	3.91
C19ORF24	chr19	1226625	5.19	1226580	39.23
CADM1	chr11	114785665	5.78	114785630	5.4
CASC4	chr15	42380125	7.64	42380215	8.25
CCDC123	chr19	38087900	4.1	38087955	1.97

CCDC46	chr17	61161915	5.68	61460060	4.85
CDR2	chr16	22289315	4.16	22289425	3.27
CIRBP	chr19	1226625	5.19	1226580	39.23
COX10	chr17	13936005	6.66	13936210	3.38
CSMD3	chr8	114151460	7.5	113386310	8.11
CTA-217C2.1	chr22	43912670	4.28	43912905	2.68
CTNNA2	chr2	80723000	6.75	80722770	4.01
DCAF6	chr1	166250145	7.88	166250010	4.76
DDHD2	chr8	38214710	8.63	38214725	10.2
DENND1B	chr1	195880345	8.27	195880360	5.66
DENND4A	chr15	63788485	5.16	63788620	5.14
DJ027059	chr1	197094850	6.86	197094725	5.8
DJ087819	chr17	55272090	7.08	55271690	3.16
DKFZP434I0850	chr16	69728525	7.46	69728520	6
DKFZP666C072	chr19	57334930	8.39	57335080	5.93
DNMT3A	chr2	25328250	7.3	25328305	39.82
DUSP11	chr2	73859170	6.22	73858925	5.85
DYM	chr18	44923775	7.47	44923740	4.95
EFR3A	chr8	133093485	8.75	133093380	6.11
EGLN1	chr1	229611905	7.24	229611830	4.62
EML4	chr2	42369685	9.86	42369920	4.56
ENSG00000064787	chr20	52043340	7.4	52043420	5.21
ENSG00000066032	chr2	80723000	6.75	80722770	4.01
ENSG00000081237	chr1	196890295	7.1	196890285	5.15
ENSG00000089335	chr19	39868780	4.02	39868750	2.1
ENSG00000100154	chr22	26965130	5.29	26965060	2.97
ENSG00000102290	chrX	91348795	4.23	91349015	4.09
ENSG00000104375	chr8	99564180	8.22	99563990	6.18
ENSG00000108506	chr17	57307515	5.1	57307445	2.12
ENSG00000119912	chr10	94271965	5.2	94272015	4.78
ENSG00000120071	chr17	41572695	5.02	41572625	4.75
ENSG00000122367	chr10	88460870	20.69	88460875	31.03
ENSG00000129292	chr8	133871875	7.72	133871685	7.74
ENSG00000131351	chr19	17037000	4.09	17036930	4.37
ENSG00000132294	chr8	133093485	8.75	133093380	6.11
ENSG00000132549	chr8	100784130	8.36	100783920	5.69

ENSG00000137776	chr15	57007615	5.14	57007700	4.36
ENSG00000141376	chr17	56566955	5.24	56631585	5.28
ENSG00000141576	chr17	71742245	5.04	71742315	2.61
ENSG00000143164	chr1	166250145	7.88	166250010	4.76
ENSG00000143207	chr1	174267700	7.58	174267740	4.41
ENSG00000143341	chr1	184039545	6.6	184039335	4.2
ENSG00000144369	chr2	187324725	6.18	187324940	4.34
ENSG00000152061	chr1	172457070	6.4	172457030	6.33
ENSG00000152601	chr3	153510535	6.98	153510725	5.87
ENSG00000154188	chr8	108379485	7.74	108379450	7.17
ENSG00000155330	chr16	45396355	5.06	45396365	3.24
ENSG00000157423	chr16	69728525	7.46	69728520	6
ENSG00000162701	chr1	195880345	8.27	195880360	5.66
ENSG00000164796	chr8	114151460	7.5	113386310	8.11
ENSG00000164830	chr8	107749235	9.18	107749060	5.07
ENSG00000165816	chr10	115989135	9.12	115989290	82.44
ENSG00000166263	chr17	50418640	5.86	50418310	7.32
ENSG00000166734	chr15	42380125	7.64	42380215	8.25
ENSG00000166923	chr15	30812910	6.22	30813015	4.68
ENSG00000170776	chr15	83939965	5.01	83940020	4.74
ENSG00000170836	chr17	56034065	7.78	56034105	3.48
ENSG00000170921	chr17	58538905	5.42	58624665	5
ENSG00000170949	chr19	58263015	4.7	58262815	1.71
ENSG00000172148	chr19	14833490	5.58	14833720	1.97
ENSG00000174485	chr15	63788485	5.16	63788620	5.14
ENSG00000174837	chr19	6896480	4.71	6896485	1.5
ENSG00000176406	chr8	105162405	7	105162545	7.44
ENSG00000178104	chr1	143779530	10.06	143779735	5.82
ENSG00000178568	chr2	212654635	6.07	212654470	4.08
ENSG00000189042	chr19	41901335	4.59	41901570	1.72
ENSG00000196274	chr15	42380125	7.64	42380215	8.25
ENSG00000197857	chr19	12242875	5.28	12242650	2.5
ENSG00000202361	chr17	57307515	5.1	57307445	2.12
ENSG00000204866	chr19	51305750	5.01	51305800	1
ENSG00000219289	chr1	164917295	6.82	164917515	7.94
EPB41L5	chr2	120486780	10.14	120486970	9.82

ERBB4	chr2	212654635	6.07	212654470	4.08
ERN1	chr17	59558260	5.4	59558230	3.46
FAM171B	chr2	187324725	6.18	187324940	4.34
FBXO4	chr5	41960965	12.24	41961095	8.87
FBXO43	chr8	101224180	8.01	101224395	5.26
FOXP2	chr7	113645685	7.34	113645700	5.05
GDE1	chr16	19434325	5	19434215	4.35
GREM1	chr15	30812910	6.22	30813015	4.68
GS1-204I12.1	chr1	183843420	6.4	183843470	4.24
HAUS6	chr9	19087810	5.36	19087900	5.38
HAUS8	chr19	17037000	4.09	17036930	4.37
HELZ	chr17	62639555	6.21	62639530	3.84
HMCN1	chr1	184039545	6.6	184039335	4.2
HSSH-2	chr17	25151495	6.98	25151570	2.85
HYDIN	chr16	69728525	7.46	69728520	6
HYDIN2	chr16	69728525	7.46	69728520	6
ICAM2	chr17	59449615	6.19	59448800	4.36
IDE	chr10	94271965	5.2	94272015	4.78
IKZF3	chr17	35203075	5.32	35203140	2.68
INTS2	chr17	57307515	5.1	57307445	2.12
IQGAP3	chr1	154809185	39.47	154809175	28.61
ITCH	chr20	32463360	5.62	32463235	4.14
KIAA1245	chr1	143779530	10.06	143779735	5.82
KIAA1267	chr17	41645180	5.42	41572625	4.75
KIAA1343	chr1	209551265	6.14	209551415	4.15
KIAA1609	chr16	83096050	7.94	83096035	10.48
KLHL1	chr13	69429255	5.11	69429395	6.21
LARGE	chr22	31973525	4.86	31973565	3.38
LDB3	chr10	88460870	20.69	88460875	31.03
MARCH5	chr10	94103560	7.04	94103470	4.62
MBNL1	chr3	153510535	6.98	153510725	5.87
MET	chr7	116186015	8.42	116185855	5.07
MIR181A1	chr1	197094850	6.86	197094725	5.8
MIR181B1	chr1	197094850	6.86	197094725	5.8
MIR21	chr17	55272090	7.08	55271690	3.16
MIR548A3	chr15	45026280	6.79	45026095	4.08

MIR548W	chr17	58538905	5.42	58624665	5
MTBP	chr8	121535860	10.14	121535975	7.4
MTMR3	chr22	28684990	4.59	28685090	3.16
NBPF10	chr1	143779530	10.06	143779735	5.82
NBPF14	chr1	143779530	10.06	143779735	5.82
NBPF20	chr1	143779530	10.06	143779735	5.82
NBPF8	chr1	143779530	10.06	143779735	5.82
NCAM2	chr21	21355195	5.08	21355365	4.22
NSMCE2	chr8	126314595	9.08	126314475	6.46
NUCKS1	chr1	203947410	7.19	203947590	4.87
OXR1	chr8	107713155	11.71	107593185	6.66
PARL	chr3	185085365	7.19	185085250	43.84
PBX1	chr1	162970820	7.71	162970900	4.15
PCDH11X	chrX	91348795	4.23	91349015	4.09
PDE4DIP	chr1	143779530	10.06	143779735	5.82
PHF20L1	chr8	133871875	7.72	133871685	7.74
PITPNB	chr22	26603550	4.94	26603640	2.88
PPM1D	chr17	56034065	7.78	56034105	3.48
PPM1E	chr17	54349765	6.23	54349775	2.9
PPP2R5E	chr14	62956135	5.67	62956330	4.58
PRRG4	chr11	32807780	9.24	32807910	13.74
PSMB9	chr6	32929395	11.8	32929410	34.82
PTEN	chr10	89722855	6.16	89722610	4.18
PTPRC	chr1	196890295	7.1	196890285	5.15
PTPRD	chr9	9900060	5.46	9899880	4.88
RABGAP1L	chr1	172457070	6.4	172457030	6.33
RAD51C	chr17	54129175	5.89	54129105	4.34
RALYL	chr8	85379770	7.45	85379660	6.62
RBFOX1	chr16	7082035	4.38	7081790	3.39
RBFOX2	chr22	34683670	5.75	34583940	4.74
RBX1	chr22	39690020	4.59	39690270	3.68
RCOR3	chr1	209551265	6.14	209551415	4.15
RFWD2	chr1	174267700	7.58	174267740	4.41
RIMS2	chr8	105162405	7	105162545	7.44
RNF157	chr17	71742245	5.04	71742315	2.61
RP11-31E23.1	chr1	197094850	6.86	197094725	5.8

RP11-382E9.1	chr1	197469380	6.7	197469195	4.1
RP11-492E3.1	chr9	131285620	14.36	131285455	20.87
RP11-541F9.2	chr1	190150750	8.35	190150745	4.35
RP3-477H23.3	chr22	26667760	4.3	26667845	3.01
RSPRY1	chr16	55782705	4.72	55782855	4.07
SBF2	chr11	10272520	10.62	10272460	49.74
SEMA3A	chr7	83634755	7.17	83634670	5.1
SGMS1	chr10	52054925	7.02	52054770	31.19
SLC25A17	chr22	39523150	4.14	39523120	2.6
SLC36A1	chr17	55902055	6.1	55901825	2.54
SLTM	chr15	57007615	5.14	57007700	4.36
SPRYD3	chr12	51759790	9.65	51759645	16.36
SSH2	chr17	25151495	6.98	25151570	2.85
STK3	chr8	99564180	8.22	99563990	6.18
STXBP4	chr17	50418640	5.86	50418310	7.32
SYNPO	chr5	149961010	6.29	149960945	16.21
TANC2	chr17	58538905	5.42	58624665	5
TAP1	chr6	32929395	11.8	32929410	34.82
TMEM49	chr17	55272090	7.08	55271690	3.16
TNRC6C	chr17	73513535	6.94	73513325	2.42
TRIM2	chr4	154363670	8.72	154363645	38.16
TRPM4	chr19	54404165	5.92	54404185	1.37
TTC28	chr22	26965130	5.29	27092045	3.96
TTC28-AS1	chr22	26667760	4.3	26667845	3.01
UBA2	chr19	39651140	6.55	39651300	1.67
UBE2G1	chr17	4163635	5	4163695	2.54
UHRF2	chr9	6402590	7.31	6402700	22.14
UNQ2573	chr15	42380125	7.64	42380215	8.25
VPS13B	chr8	100784130	8.36	100783920	5.69
VWA2	chr10	115989135	9.12	115989290	82.44
WHSC1L1	chr8	38336050	7.09	38336105	5.23
XPNPEP3	chr22	39690020	4.59	39690270	3.68
ZBTB41	chr1	195394310	7.54	195394310	4.51
ZNF160	chr19	58263015	4.7	58262815	1.71
ZNF221	chr19	49159365	4.26	49159385	2.81
ZNF302	chr19	39868780	4.02	39868750	2.1

ZNF44	chr19	12242875	5.28	12242650	2.5
ZNF507	chr19	37566560	5.78	37540440	2.48
ZNF564	chr19	12499915	4.28	12499845	3.2
ZNF567	chr19	41901335	4.59	41901570	1.72
ZNF616	chr19	57334930	8.39	57335080	5.93
ZNF833P	chr19	11657940	4.83	11657810	4.71
ZSCAN5A	chr19	61560500	4.35	61560535	1.41

Table S6 Focus genes in the pathway analysis network 1

Symbol	Entrez Gene Name	Peak position	Peak Score
AKAP13	A kinase (PRKA) anchor protein 13	Chr15:83939965	5.01
ANGPT1	angiopoietin 1	Chr8:108379485	7.74
BRIP1	BRCA1 interacting protein C-terminal helicase 1	Chr17:57255670	6.09
CTNNA2	catenin (cadherin-associated protein), alpha 2	Chr2:80723000	6.75
DNMT3A	DNA (cytosine-5-)-methyltransferase 3 alpha	Chr2:25328305	39.82
DUSP11	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	Chr2:73859170	6.22
IDE	insulin-degrading enzyme	Chr10:94271965	5.2
ITCH	itchy E3 ubiquitin protein ligase homolog (mouse)	Chr20:32463360	5.62
MET	met proto-oncogene (hepatocyte growth factor receptor)	Chr7:116186015	8.42
PPM1D	protein phosphatase, Mg2+/Mn2+ dependent, 1D	chr17:56034065	7.78
PTEN	phosphatase and tensin homolog	Chr10:89722855	6.16
RFWD2	ring finger and WD repeat domain 2	Chr1:174267700	7.58
SSH2	slingshot homolog 2 (Drosophila)	Chr1:25151495	6.98
STXBP4	syntaxin binding protein 4	Chr17:50418310	7.32
TAOK1	TAO kinase 1	Chr17:24900025	5.16

Table S7 Focus genes in the pathway analysis network 2

Symbol	Entrez Gene Name	Peak position	Peak Score
EGLN1	egl nine homolog 1 (C. elegans)	Chr1:229611905	7.24
ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	Chr2:212654635	6.07
mir-21	microRNA 21	Chr17:55272090	7.08
PTPRC	protein tyrosine phosphatase, receptor type, C	Chr1:196890295	7.1
PSMB9	proteasome subunit, beta type, 9 (large multifunctional peptidase 2)	Chr6:32929410	34.82
SEMA3A	sema domain, immunoglobulin domain, short basic domain, secreted, 3A	Chr7:83634755	7.17
SYNPO	synaptopodin	chr5:149960945	16.21
TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	Chr6:32929410	34.82
ZNF616	zinc finger protein 616	Chr19:57334930	8.39

Table S8 LANA binding motifs aligned to LBS1 and LBS2.

Motif 1

Name	*E value*	*Alignment*
LBS1	1.1102e-16	SGGNNNSNNSNGNNSCNGGNSNNGSCGNG ----------GCCCCATGCCCGGGCG--
LBS2	6.3625e-12	SGGNNNSNNSNGNNSCNGGNSNNGSCGNG- ----------CCGCAGGCCCCGGCGGCG

Motif 2

Name	*E value*	*Alignment*
LBS1	1.7621e-05	GNRNMCNGGSNNGGGNNGNNG -CGCCCGGGCATGGGGC----
LBS2	9.3032e-04	GNRNMCNGGSNNGGGNNGNNG --CCGCAGGCCCCGGCGGCG-