

Supplementary File 1. Identity-by-descent allele-sharing analysis of 12q23 region in families with HELLP: microsatellite markers

Legends

Identity-by-descent (IBD) allele-sharing analysis in families with HELLP was performed with 26 microsatellite markers covering the 23.6 Mb region on 12q23 between D12S309 and D12S395. Non-parametric multipoint linkage (Allegro 2) complemented by pedigree analysis was performed in 7 HELLP families with affected sisters (families 1-7), 4 families with affected cousins (families 8-11) and 1 family with discordant monozygotic twin sisters (family 12). A total of 57 individuals with 36 affected females was analyzed.

Supplementary File 1A: Multipoint linkage analysis using $S_{mnallele}$ indicates the 4 marker region between PAH and D12S1647 with LOD and NPL scores >3 (box).

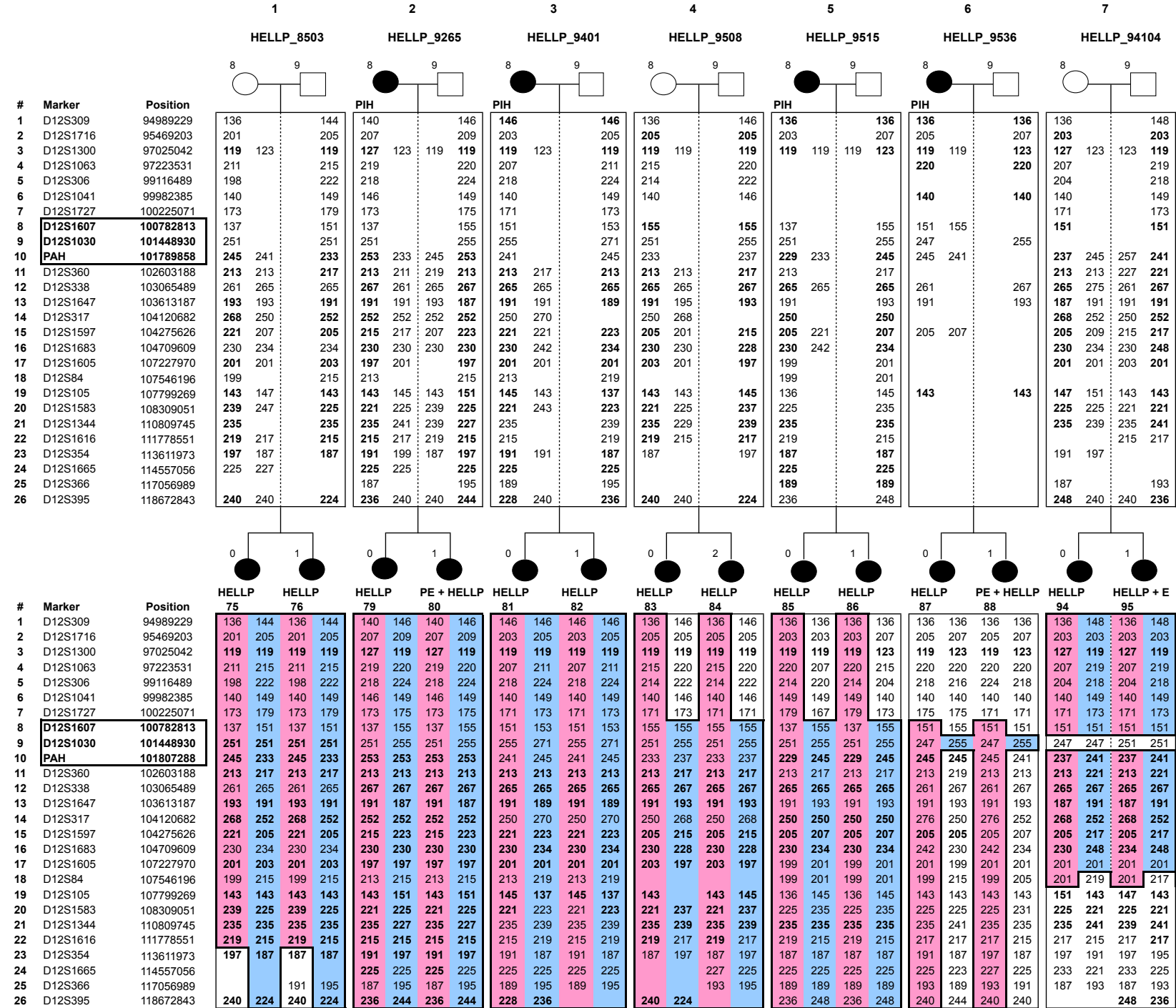
Supplementary files 1B-D: Pedigree analysis indicates the same region with the presence of two minimal critical regions (I: D12S1607-PAH, II: D12S338-D12S317) in affected sister-pairs (**1B**), affected cousin pairs (**1C**) and discordant monozygotic twin sisters (**1D**). Note the informative situation in family 11 (HELLP_93113) (**1C**) where two sisters from one family married two brothers from an unrelated family. In the affected cousins (93113/89, 93113/90) born from these couples, both alleles need to be shared in the region with linkage, as if these cousins were sisters. In the affected cousins (93113/89, 93113/90), both regions are supported. In their affected mothers (93113/12, 93113/8), maximal allele sharing is limited to the first region near D12S1030.

Supplementary File 1A: Multipoint linkage analysis of families with HELLP

Location ^a	LOD ^b	Dhat ^c	NPL ^d	Zlr ^e	Nplexactp ^f	Info ^g	Marker ^h
0.000	1.5181	1.0073	2.2686	2.6440	0.011835	0.7366	D12S1030
1.310	3.1605	1.9446	3.1727	3.8150	6.33e-04	0.6797	PAH
2.370	3.0472	1.7177	3.1866	3.7461	6.32e-04	0.7353	D12S360
3.510	3.1617	1.7433	3.2279	3.8158	5.99e-04	0.7518	D12S338
5.230	3.1711	2.1601	3.0243	3.8215	0.001445	0.6280	D12S1647
6.370	2.7642	1.9023	2.8938	3.5679	0.001939	0.6059	D12S317
8.090	2.5003	1.4707	2.8614	3.3933	0.002271	0.7158	D12S1597
8.100	2.4982	1.4677	2.8610	3.3919	0.002271	0.7170	D12S1683
8.650	2.6017	1.6258	2.8584	3.4614	0.002389	0.6648	D12S1605

Abbreviations: a. Relative location in cM, b. Allele sharing logarithm of the odds score, c. Maximum likelihood estimator of δ (difference), d. Non-parametric linkage score, e. Zlr: normalized likelihood ratio statistic for linkage, f. p value for NPL, g. Informativity (maximum 1.0), h. Microsatellite marker. For clarity, only the outcome for 9 of the 26 markers is shown.

Supplementary File 1B: Affected sister-pairs



HELLP_9147

#	Marker	Position
1	D12S309	94989229
2	D12S1716	95469203
3	D12S1300	97025042
4	D12S1063	97223531
5	D12S306	99116489
6	D12S1041	99982385
7	D12S1727	100225071
8	D12S1607	100782813
9	D12S1030	101448930
10	PAH	101789858
11	D12S360	102603188
12	D12S338	103065489
13	D12S1647	103613187
14	D12S317	104120682
15	D12S1597	104275626
16	D12S1683	104709609
17	D12S1605	107227970
18	D12S84	107546196
19	D12S105	107799269
20	D12S1583	108309051
21	D12S1344	110809745
22	D12S1616	111778551
23	D12S354	113611973
24	D12S1665	114557056
25	D12S366	117056989
26	D12S395	118672843

HELLP_93130

#	Marker	Position
1	D12S309	94989229
2	D12S1716	95469203
3	D12S1300	97025042
4	D12S1063	97223531
5	D12S306	99116489
6	D12S1041	99982385
7	D12S1727	100225071
8	D12S1607	100782813
9	D12S1030	101448930
10	PAH	101789858
11	D12S360	102603188
12	D12S338	103065489
13	D12S1647	103613187
14	D12S317	104120682
15	D12S1597	104275626
16	D12S1683	104709609
17	D12S1605	107227970
18	D12S84	107546196
19	D12S105	107799269
20	D12S1583	108309051
21	D12S1344	110809745
22	D12S1616	111778551
23	D12S354	113611973
24	D12S1665	114557056
25	D12S366	117056989
26	D12S395	118672843

HELLP_94126

#	Marker	Position
1	D12S309	94989229
2	D12S1716	95469203
3	D12S1300	97025042
4	D12S1063	97223531
5	D12S306	99116489
6	D12S1041	99982385
7	D12S1727	100225071
8	D12S1607	100782813
9	D12S1030	101448930
10	PAH	101789858
11	D12S360	102603188
12	D12S338	103065489
13	D12S1647	103613187
14	D12S317	104120682
15	D12S1597	104275626
16	D12S1683	104709609
17	D12S1605	107227970
18	D12S84	107546196
19	D12S105	107799269
20	D12S1583	108309051
21	D12S1344	110809745
22	D12S1616	111778551
23	D12S354	113611973
24	D12S1665	114557056
25	D12S366	117056989
26	D12S395	118672843

HELLP_93113

#	Marker	Position
1	D12S309	94989229
2	D12S1716	95469203
3	D12S1300	97025042
4	D12S1063	97223531
5	D12S306	99116489
6	D12S1041	99982385
7	D12S1727	100225071
8	D12S1607	100782813
9	D12S1030	101448930
10	PAH	101789858
11	D12S360	102603188
12	D12S338	103065489
13	D12S1647	103613187
14	D12S317	104120682
15	D12S1597	104275626
16	D12S1683	104709609
17	D12S1605	107227970

12

214	214	214	222	214	214	214	214
149	157	139	149	149	157	139	161
251	247	247	255	251	247	247	247
213	213	213	219	213	213	213	213
267	261	265	267	267	261	261	261
191	191	191	191	191	191	191	195
250	274	268	278	250	274	250	278
230	230	230	230	230	230	230	234
201	201	201	203	201	201	201	205
199	215	201	217	199	215	201	211
137	143	143	145	137	143	143	145
237	243	225	239	237	243	225	245
235	235	225	239	235	235	235	235
215	219	215	219	215	219	217	217
193	197	197	187	193	197	197	191
227	227	227	225	227	227	227	219
189	193	187	189	189	193	193	197

214	214	214	222	214	214	214	214
149	157	139	149	149	157	139	161
251	247	247	255	251	247	247	247
213	213	213	219	213	213	213	213
267	261	265	267	267	261	261	261
191	191	191	191	191	191	191	195
250	274	268	278	250	274	250	278
230	230	230	230	230	230	230	234
201	201	201	203	201	201	201	205
199	215	201	217	199	215	201	211
137	143	143	145	137	143	143	145
237	243	225	239	237	243	225	245
235	235	225	239	235	235	235	235
215	219	215	219	215	219	217	217
193	197	197	187	193	197	197	191
227	227	227	225	227	227	227	219
189	193	187	189	189	193	193	197

Supplementary File 2. Identity-by-descent allele-sharing analysis of 12q23 region in families with HELLP: SNP and IN/DEL markers

To discriminate between the two regions with linkage as found with microsatellite markers (**Supplementary File 1**), identity-by-descent analysis was complemented with 137 single nucleotide (SNP) or insertion/deletion (IN/DEL) markers located between D12S1607 and D12S318 out of a total of 181 identified by sequence analysis of coding sequences of 38 known and predicted genes in the 12q23 region.

The minimal critical region (MCR) as defined by the region with maximal allele sharing in families with HELLP is indicated in yellow. The minor alleles in the discordant monozygotic twin family (family 12) with heterozygous sharing between the affected twin sister and her partner, while completely absent in the partner of the non-affected twin sister are indicated in gray. The informative SNPs (rs12304817, rs7313075, rs35803805) used for parent-child transmission analysis in the twin family (**Figure 2**) are boxed.

For clarity, presentation is limited to 50 SNP/INDEL markers within and flanking the MCR. In addition, presentation in the families with cousins is limited to the haplotypes that, by descent, need to be identical.

Supplementary File 2: Minimal critical region as defined by maximal allele sharing in families with HELLP

#	SNP	chr12:hg18	1		2		3		4		5		6		7	8	9			10		11			12							
			75	76	79	80	81	82	83	84	85	86	87	88	94	95	77	78	93	91	92	96	97	98	89	90	3	4	5	6		
1	rs12230012	1008032046	C	C	C	C	C	C	C	T	C	T	C	C	C	C	C	C	C	C	C	C	C	C	T	C	C					
2	rs7960200	100803324	G	A	G	A	G	A	G	A	G	A	G	G	G	G	G	G	A	A	A	C	A	C	A	T	C	T				
3	rs6539017	100816074	T	C	T	C	T	C	T	C	T	T	T	T	T	T	T	T	C	C	C	C	C	C	T	C	T					
4	rs10745931	100816908	C	T	C	T	C	T	C	T	C	C	C	C	C	C	C	C	C	C	C	T	C	T	C	T	C					
5	rs7295569	100819349	T	C	T	C	T	C	T	C	T	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C						
6	rs11111078	100819350	C	T	C	T	C	T	C	T	C	C	C	C	C	C	C	C	C	C	T	C	C	C	C	C		T	C			
7	rs7302651	100835396	A	G	A	G	A	G	A	G	A	A	A	A	A	A	A	A	A	A	G	A	G	A	G	A						
8	rs10778159	100845443	G	A	G	A	G	A	G	A	G	A	G	A	A	A	A	A	A	A	G	G	A	G	A	A						
9		100845650	G	T	G	T	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	A						
10	rs4301835	100845714	C	T	C	T	C	T	C	T	C	C	C	C	C	C	C	C	C	C	C	C	C	T	T	T						
11	rs2271266	101030174	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T		T	T			
12		101036224	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G		G	G			
13	rs4764863	101038314	G	G	G	G	A	A	A	A	G	A	G	A	A	A	G	G	G	A	A	G	A	G	A	G		G	G			
14		101038352	G	G	G	G	G	G	G	G	G	A	G	A	G	G	G	G	G	G	G	G	G	G	G	G		G	G			
15	rs2036772	101041883	T	T	T	T	C	C	C	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T							
16	rs2036771	101041934	G	A	G	A	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G		G	G			
17	rs734597	101054932	C	T	C	T	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C							
18	rs12578176	101055184	C	A	A	A	G	G	G	G	A	A	A	A	A	A	A	A	A	A	A	C	G	C	A							
19	rs2102476	101072830	G	T	G	T	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G		G	G				
20	rs3794201	101083838	A	C	A	C	A	A	A	A	A	A	C	A	C	A	A	A	A	A	A	A	A	A	A		A	A				
21		101093570	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C		A	C				
22		101114674	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A							
23	rs12827335	101135247	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T		G	T				
24		101135328	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C		C	C				
25	rs10860846	101135501	T	G	T	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T		T	T				
26	rs34835268	101135671	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C		A	C				
27		101137449	G	5	G	5	G	G	G	G	G	5	G	5	G	G	G	G	G	G	G	G	G	G	G		G	G				
28		101137495	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G		G	G				
29	rs12304817	101137668	C	G	C	G	C	C	C	C	C	C	C	G	C	G	C	G	C	C	G	G	G	G	G		G	G				
30		101144273	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C		C	C				
31		101144418	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G		G	G				
32		101144745	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G		G	G				
33		101150784	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C		C	C				
34		101154808	G	C	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G		G	G				
35	rs7313075	101154809	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C		A	C				
36		101154867	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G		G	G				
37		101167483	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	ATG	ATG					A	A				
38	rs35803805	101186958	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A		G	G				
39		101188866	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C		C	C				
40	rs35909148	101268434	A	0	A	0	A	A	A	A	A	0	A	0	A	0	A	0	A	0	A	0	A	0	A		0	A				
41	rs855218	101430772	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G		G	G				
42	rs855216	101431432	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A		A	A				
43	rs7309412	101597223	A	A	A	A	C	A	C	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C		A	C				
44	rs11111392	101741876	T	T	T	T	C	C	C	C	A	T	T	T	T	T	T	T	T	T	T	T	T	T	T		C	T				
45	rs772897	101761598	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G		C	C				
46	rs1042503	101770830	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C		T	T				
47	rs1126758	101773054	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T		T	T				
48	rs2037639	101795480																									A	G				
49	rs3832799	101876338																									G	G				
50	rs7959408	102125895	G	G	G	G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A		G	A				

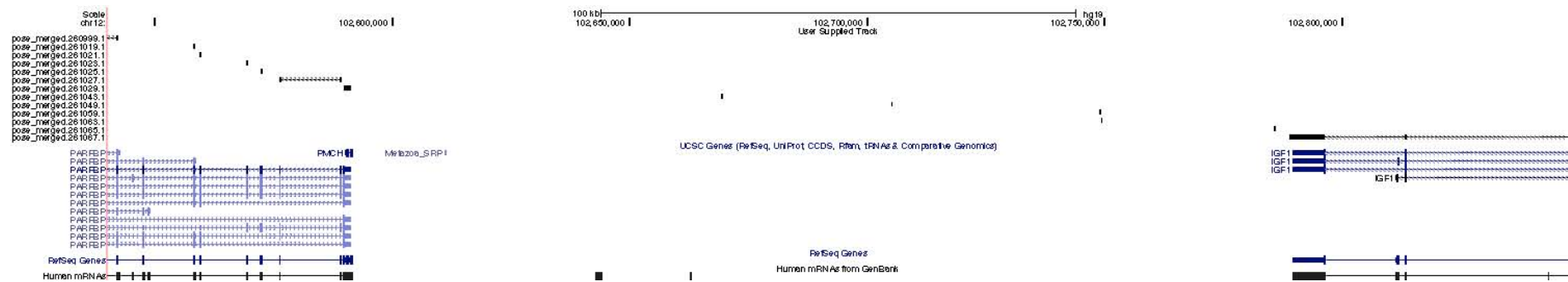
Supplementary File 3. Transcriptome assemblies in the 205 kb region of the LINC-HELLP gene

Legends

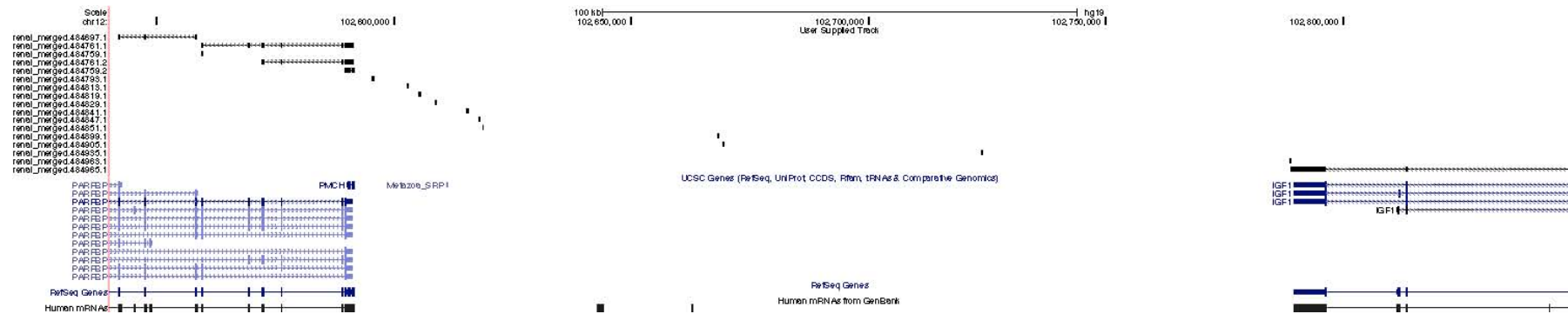
Transcriptome assemblies (Cufflinks) from 18 human tissues (adipose, adrenal, brain, breast, colon, foreskin, heart, kidney, liver, lung, lymph node, ovary, placenta, prostate, skeletal muscle, testes, thyroid, white blood cell) were downloaded from the human lincRNA catalog (Broad Institute), uploaded into the UCSC browser (hg19) and screened for the expression of novel transcripts in or near the 205 kb region between *PMCH* and *IGF1* containing the lincRNA transcript linked with the HELLP syndrome.

Expression of the linc-HELLP transcript as indicated by multiple alignments covering the 205 kb region is only seen in placenta and testes.

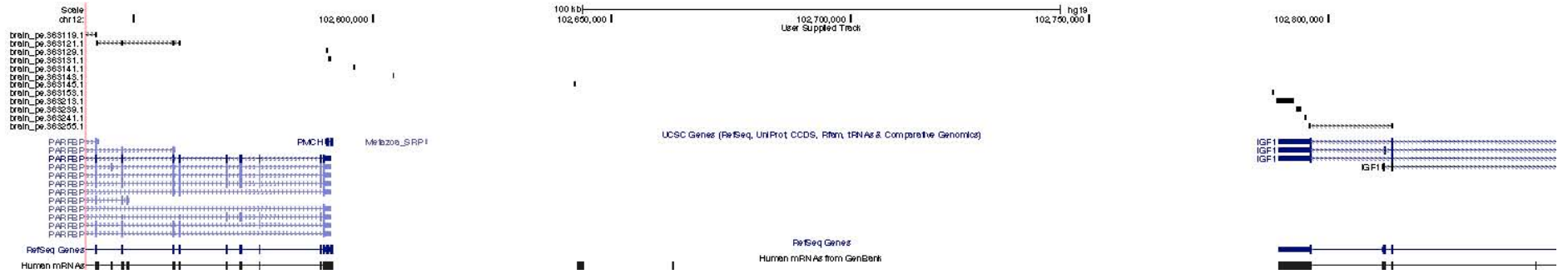
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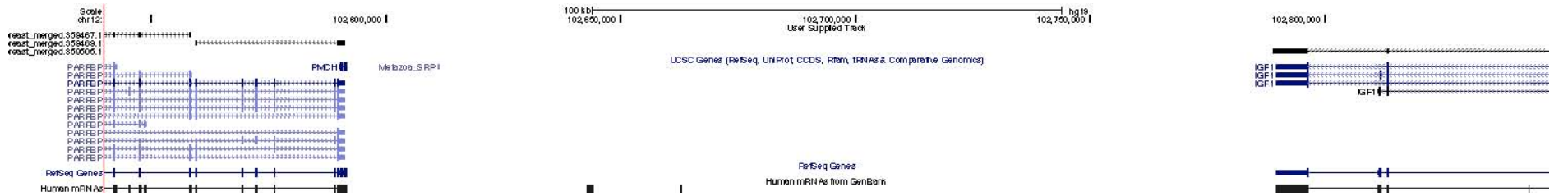
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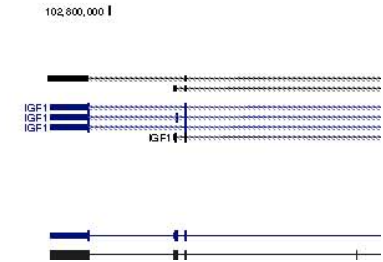
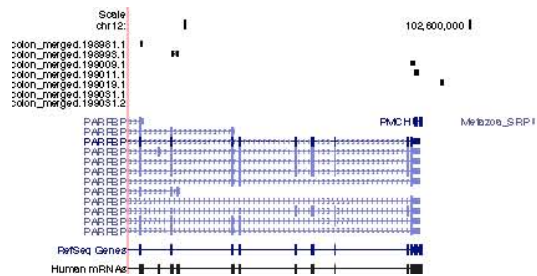
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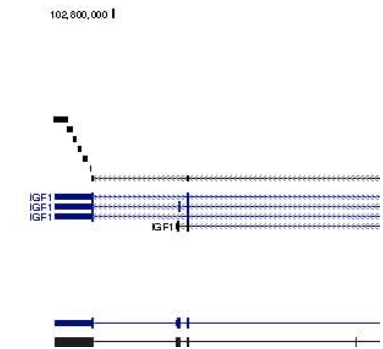
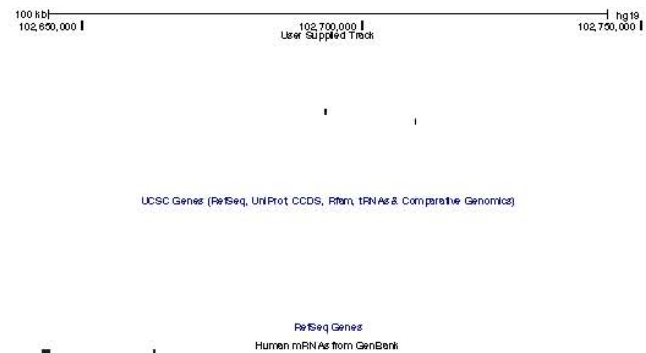
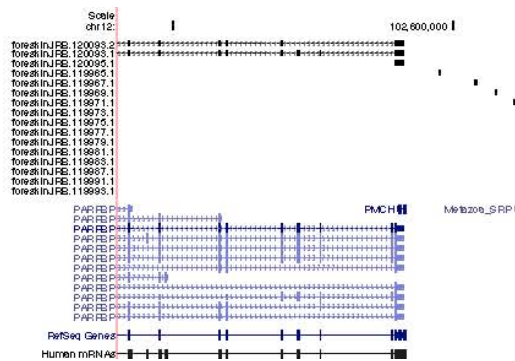
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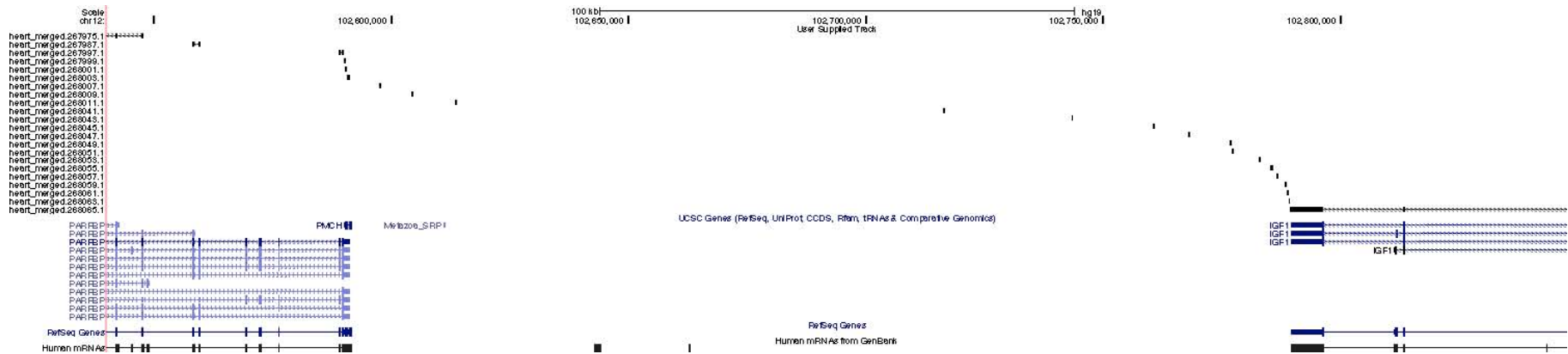
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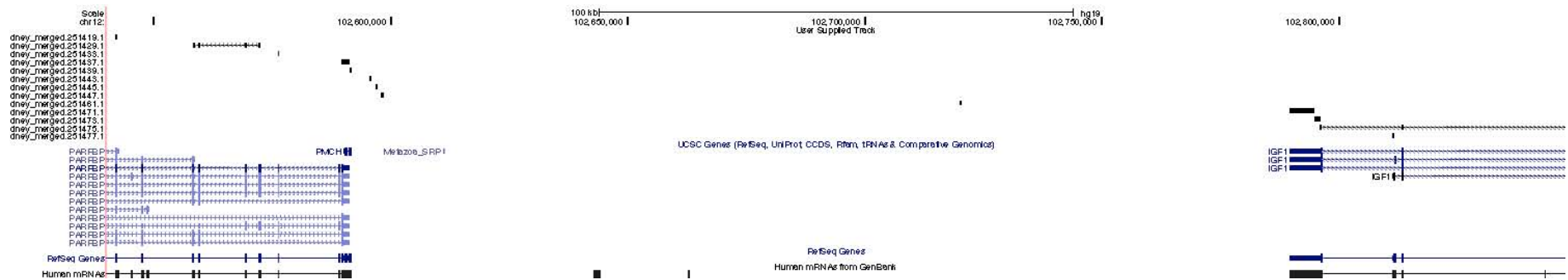
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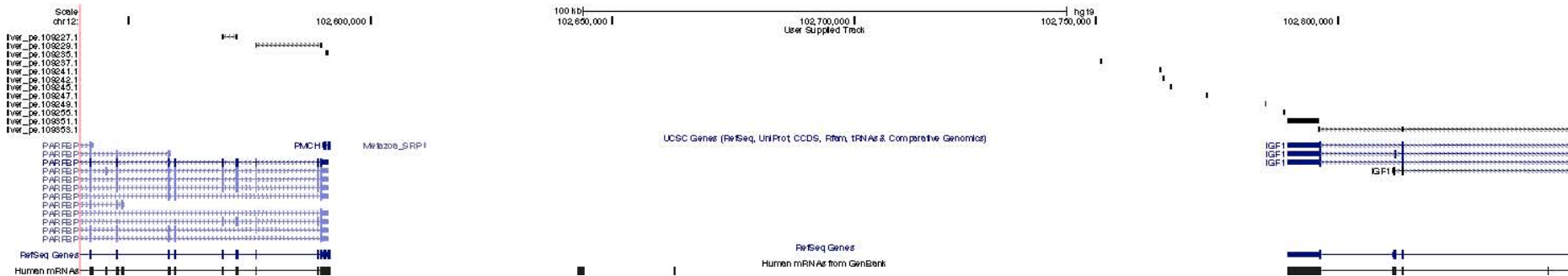
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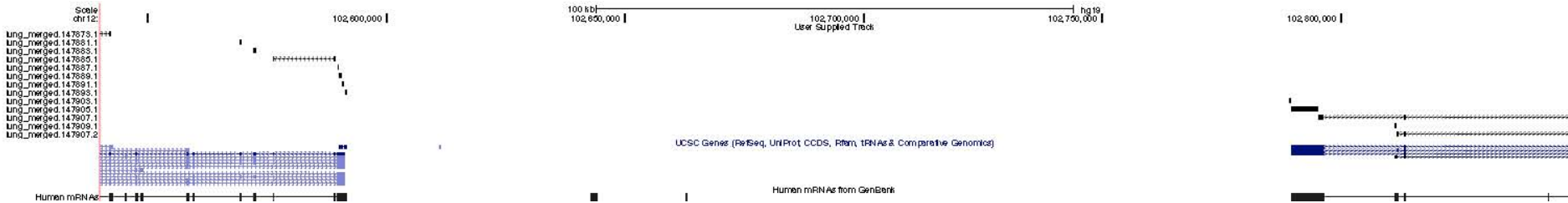
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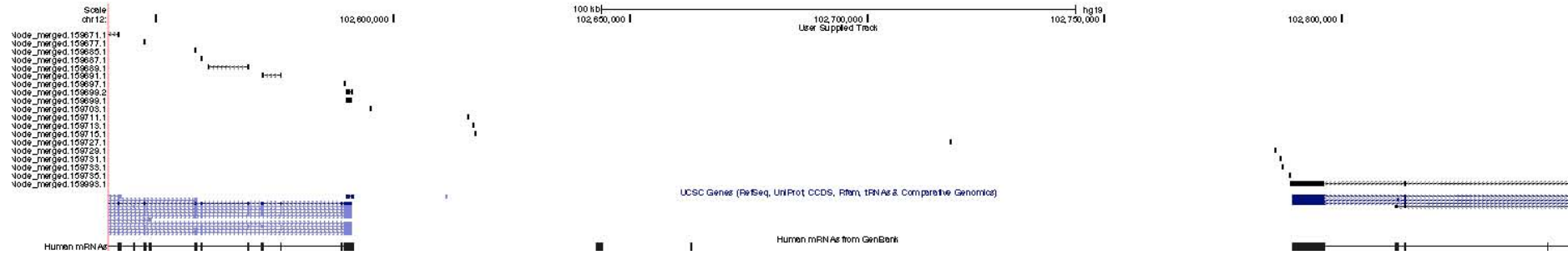
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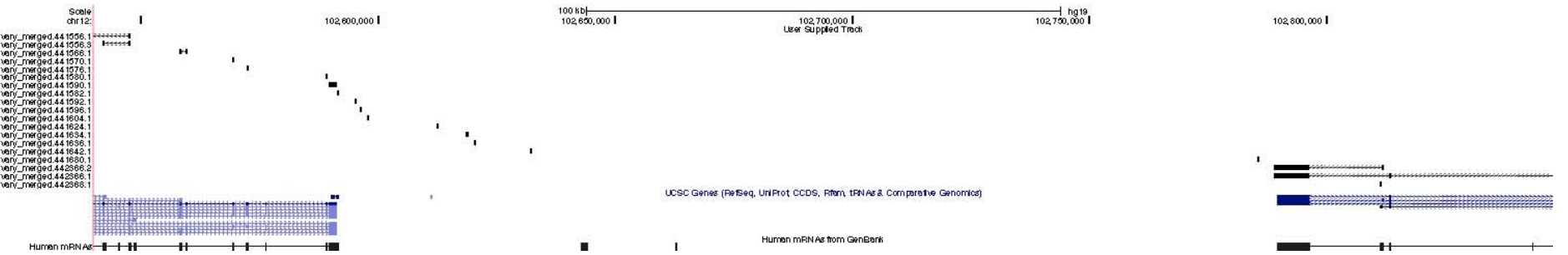
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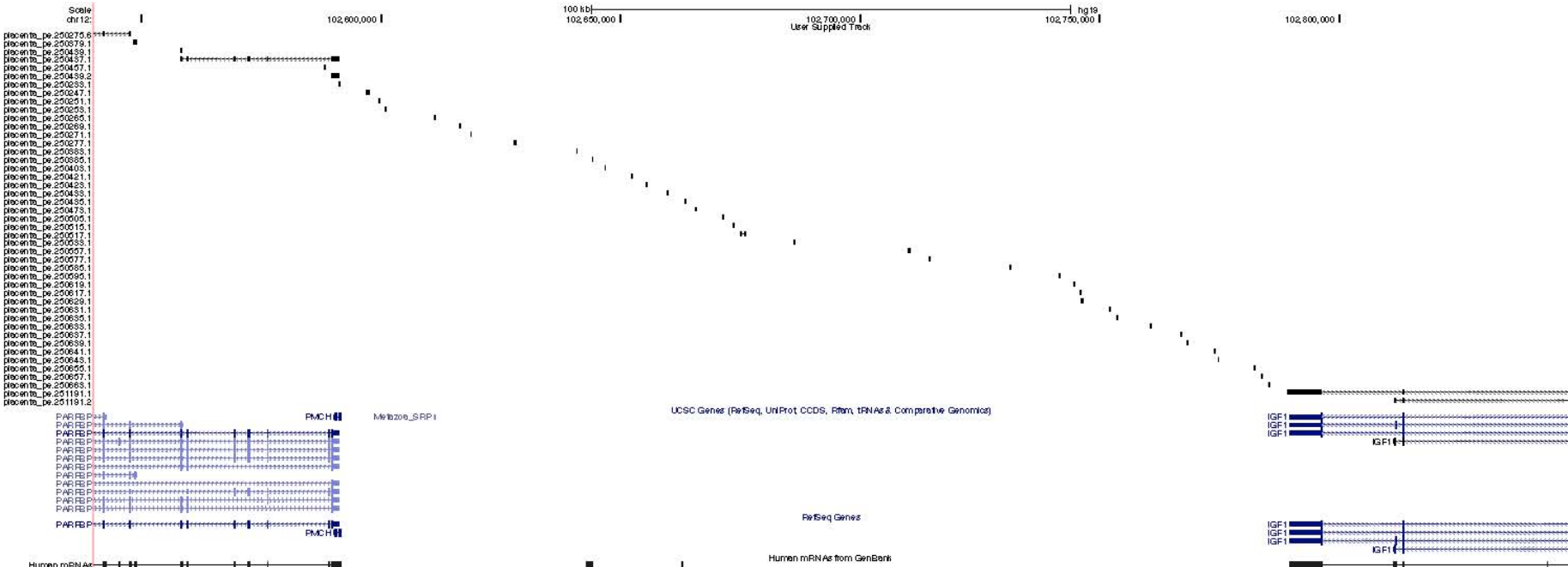
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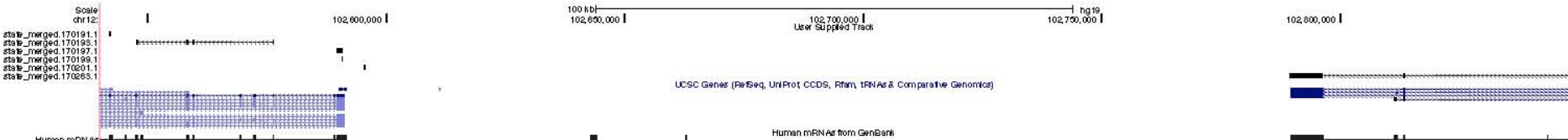
OVARY



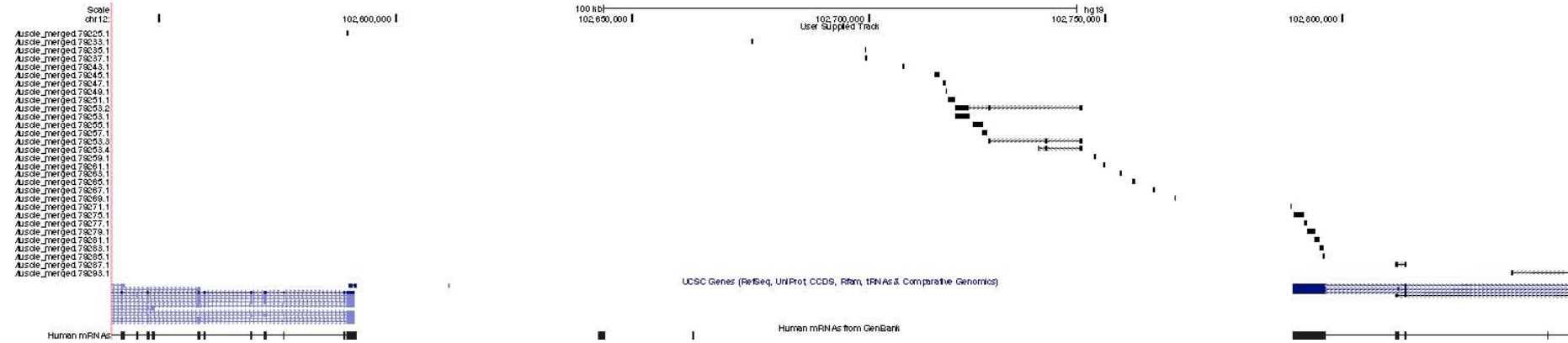
PLACENTA



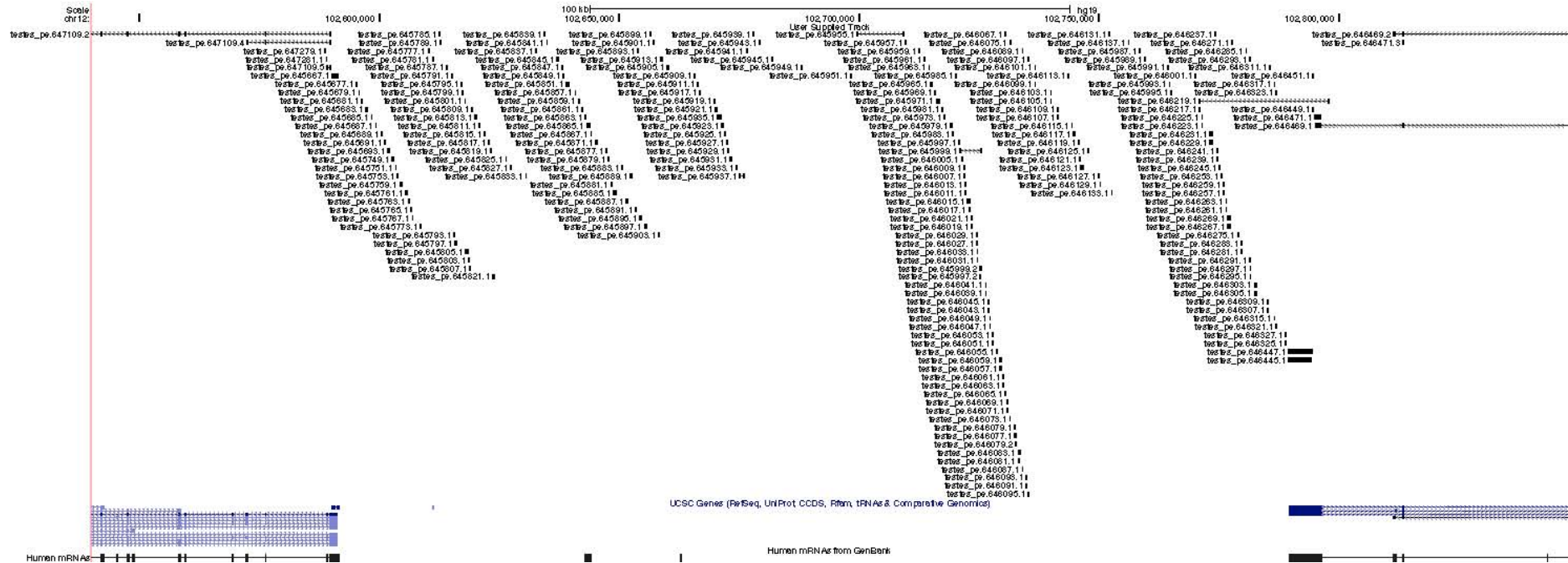
PROSTATE



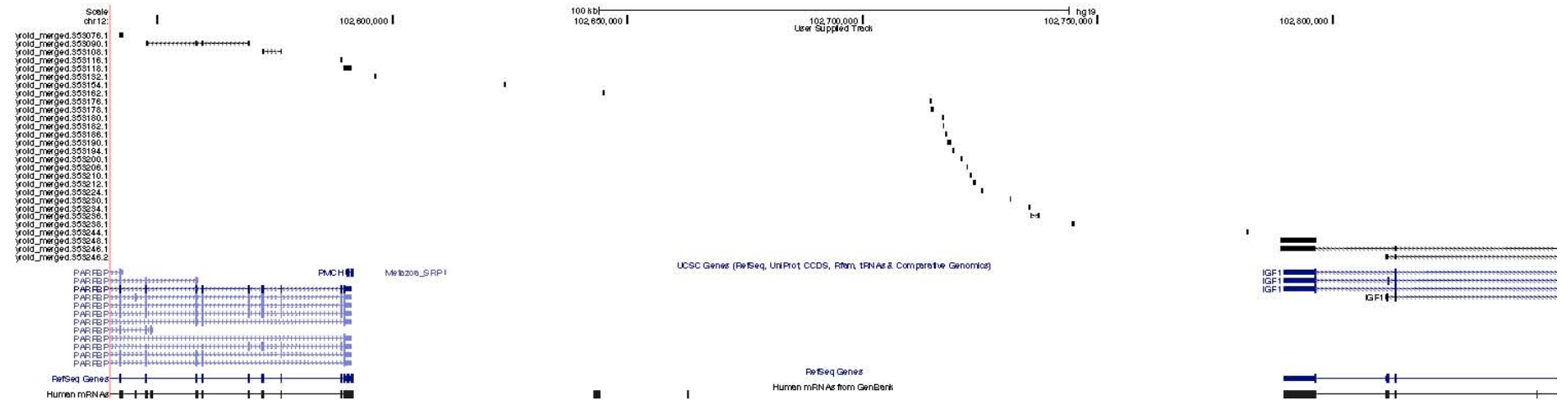
SKELETAL MUSCLE



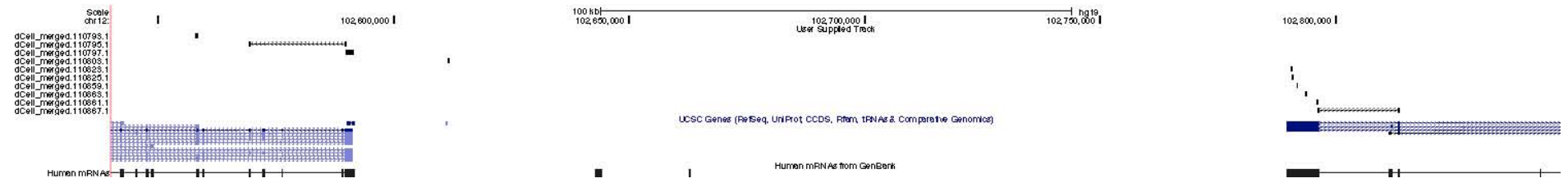
TESTES



THYROID

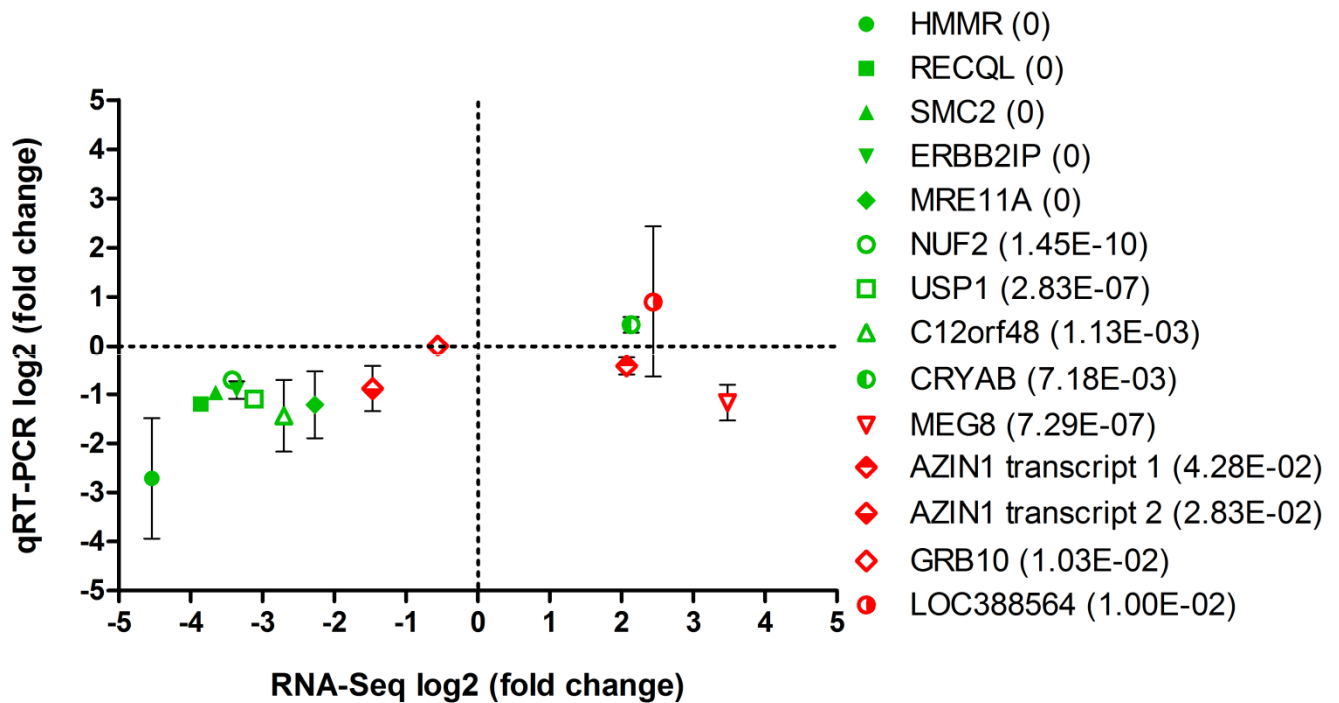


WHITE BLOOD CELL



Supplementary File 4: Validation of RNA-Sequencing results by quantitative RT-PCR

Validation of 14 differentially expressed genes as identified by RNA-Sequencing. qRT-PCR log₂ values (mean±SEM) are obtained from at least three independent siRNA-mediated knockdown experiments. Green symbols represent significant values ($p < 0.05$ in a one-sample t-test with theoretical mean of 0), red symbols indicate genes that could not be validated. The numbers in brackets behind the gene names indicate the q-values from the RNA-Sequencing analysis.



Supplementary File 5: Differentially expressed genes after siRNA-mediated knockdown of the HELLP transcript

gene_id	gene	locus	value_1	value_2	log2(fold_change)	test_stat	p_value	q_value
XLOC_010441	HMMR	chr5:162820094-162851530	27,6549	1,18794	-4,54101	8,82756	0	0
XLOC_006978	USP16	chr21:29318808-29348678	17,0301	1,06366	-4,00097	10,9503	0	0
XLOC_031032	BDP1	chr5:70787197-70899405	5,68732	0,380156	-3,90308	8,41524	0	0
XLOC_032726	SMC6	chr2:17707964-17830113	12,4622	0,844734	-3,88292	9,83896	0	0
XLOC_000966	CASP8AP2	chr6:90596261-90640876	7,76459	0,533335	-3,8638	10,55	0	0
XLOC_027374	RECQL	chr12:21481764-21545870	24,765	1,7066	-3,8591	15,8416	0	0
XLOC_020735	BRCA2	chr13:31787464-31872309	3,11785	0,223335	-3,80327	9,37025	0	0
XLOC_001023	ZNF644	chr1:91153444-91260400	9,78273	0,709275	-3,78582	10,6284	0	0
XLOC_005285	MTX3	chr5:79308294-79322844	2,97034	0,227036	-3,70964	9,75868	0	0
XLOC_020722	POSTN	chr13:37034718-37071068	388,911	30,9	-3,65376	10,3317	0	0
XLOC_024418	SMC2	chr9:105896361-105944997	25,756	2,04728	-3,65313	8,89497	0	0
XLOC_029048	MYSM1	chr1:58892998-58938335	4,2514	0,339439	-3,64672	8,77865	0	0
XLOC_027816	REV3L	chr6:111726923-112034167	6,48358	0,522064	-3,63449	10,5036	0	0
XLOC_023131	COPS2	chr15:47204762-47235146	16,9651	1,38899	-3,61046	8,44846	0	0
XLOC_029297	FAM171B	chr2:187266977-187337366	2,6766	0,22841	-3,5507	8,96919	0	0
XLOC_002313	SLC39A10	chr2:196185965-196310671	11,791	1,03266	-3,51324	8,41826	0	0
XLOC_013702	ZDBF2	chr2:206847608-206887393	1,8863	0,166681	-3,5004	12,818	0	0
XLOC_013786	C1orf9	chr1:170768714-170847596	10,7608	0,955539	-3,49332	10,4918	0	0
XLOC_022511	STAG2	chrX:122922155-123064186	22,2369	1,97803	-3,49082	12,421	0	0
XLOC_029307	KTN1	chr14:55116677-55221055	57,802	5,15605	-3,48678	11,8677	0	0
XLOC_027220	ZNF146	chr19:41364757-41421515	17,6897	1,62702	-3,4426	8,69611	0	0
XLOC_034960	ZNF37BP	chr10:42328966-42368287	2,27803	0,213778	-3,4136	9,95598	0	0
XLOC_026180	SENP7	chr3:102525807-102714848	2,94114	0,278427	-3,401	9,45913	0	0
XLOC_014703	PPIP5K2	chr5:102483862-102566808	7,47846	0,726098	-3,36451	10,6645	0	0
XLOC_017684	ANKRD36B	chr2:97474451-97572860	1,39844	0,136312	-3,35884	8,47225	0	0
XLOC_001690	ERBB2IP	chr5:65257290-65412606	23,0692	2,25361	-3,35566	8,88249	0	0
XLOC_001855	ARAP2	chr4:35744014-35922854	3,49154	0,345191	-3,3384	8,39814	0	0
XLOC_018023	CHD9	chr16:51646445-51918915	6,71713	0,664543	-3,33741	9,7892	0	0
XLOC_018391	ROCK2	chr2:11237358-11402249	16,1853	1,60622	-3,33294	8,39258	0	0
XLOC_007018	ZNF780A	chr19:45266824-45288694	2,78822	0,277212	-3,33029	9,4531	0	0

XLOC_027723	CCPG1	chr15:53390958-53587724	11,8771	1,18713	-3,32263	8,83976	0	0
XLOC_001409	TTC14	chr3:181802476-181879977	8,98279	0,910381	-3,30262	8,72975	0	0
XLOC_025421	AHI1	chr6:135646802-136558402	7,08937	0,753196	-3,23456	11,3763	0	0
XLOC_018371	TROVE2	chr1:191248118-191327714	7,84638	0,83392	-3,23405	9,58038	0	0
XLOC_000502	SACS	chr13:22800964-22905841	6,83507	0,732145	-3,22275	8,71338	0	0
XLOC_014786	JMJD1C	chr10:64596993-64896620	10,2414	1,09907	-3,22006	15,1135	0	0
XLOC_006810	ANKRD26	chr10:27300826-27429441	3,88663	0,418343	-3,21576	9,58058	0	0
XLOC_025373	TRPC1	chr3:143925532-144009419	5,3046	0,575067	-3,20544	8,96555	0	0
XLOC_009638	PRPF39	chr14:44623004-44673482	10,8071	1,17766	-3,19799	10,778	0	0
XLOC_025303	SKIL	chr3:171558166-171593674	14,2479	1,56921	-3,18264	10,7657	0	0
XLOC_018804	GXYLT1	chr12:40740155-40824966	7,57506	0,8358	-3,18003	11,0523	0	0
XLOC_018550	ZNF195	chr11:3335732-3357028	3,47758	0,391572	-3,15074	8,50717	0	0
XLOC_018187	NEK1	chr4:170550995-170770448	5,15372	0,5804	-3,15049	12,932	0	0
XLOC_027856	PCM1	chr8:17824609-17931737	21,1744	2,39968	-3,1414	9,70127	0	0
XLOC_004279	HLTF	chr3:150230593-150287031	13,3682	1,57098	-3,08907	9,6589	0	0
XLOC_029990	VPS13A	chr9:78981491-79222219	8,57414	1,01768	-3,07471	11,7386	0	0
XLOC_014913	GOLGB1	chr3:122864737-122952329	10,5777	1,26856	-3,05977	9,88542	0	0
XLOC_029315	CEP70	chr3:139695876-139795819	8,19269	1,00864	-3,02193	10,4108	0	0
XLOC_032701	CEP350	chr1:178190345-178350638	5,66751	0,707457	-3,002	11,6797	0	0
XLOC_020925	FANCB	chrX:14762242-14801151	3,48319	0,437207	-2,99402	9,00699	0	0
XLOC_026872	TOR1AIP2	chr1:178075724-178113913	18,8587	2,43961	-2,9505	8,60048	0	0
XLOC_031035	ITSN2	chr2:24279225-24437174	8,62794	1,12166	-2,94338	8,8938	0	0
XLOC_029097	CEP57L1	chr6:109523048-109592453	4,52867	0,59052	-2,93903	9,88987	0	0
XLOC_030954	SLTM	chr15:56958535-57013144	19,5134	2,62666	-2,89317	10,0406	0	0
XLOC_005983	DST	chr6:56430743-56816502	16,8818	2,34221	-2,84953	10,7716	0	0
XLOC_010817	ATP11C	chrX:138636170-138842866	9,15492	1,2972	-2,81915	8,73229	0	0
XLOC_020781	ZNF131	chr5:43156730-43211595	14,2252	2,09922	-2,76053	9,40407	0	0
XLOC_022549	ORC3	chr6:88356503-88433891	17,1036	2,54719	-2,74732	8,30071	0	0
XLOC_032724	CDC42BPA	chr1:225244188-225573949	11,4445	1,72199	-2,73251	9,07489	0	0
XLOC_025931	NAA16	chr13:40783340-40849166	5,13134	0,773679	-2,72953	8,61396	0	0
XLOC_032065	CSNK1G3	chr5:122874682-122980363	8,88955	1,34185	-2,72789	8,76694	0	0
XLOC_014724	ANLN	chr7:36330283-36459925	120,64	19,0794	-2,66062	9,41692	0	0
XLOC_034262	BIRC2	chr11:101723096-101754618	14,255	2,26092	-2,65649	9,09227	0	0
XLOC_030802	RASSF8	chr12:25996036-26124092	6,64715	1,07253	-2,63171	8,66814	0	0

XLOC_003576	CTNNB1	chr3:41215941-41256943	123,392	19,9257	-2,63055	8,41816	0	0
XLOC_030953	USP8	chr15:48503775-48626194	13,1525	2,13411	-2,62363	9,57382	0	0
XLOC_031408	ZNF83	chr19:57796169-57885698	12,6811	2,07077	-2,61444	8,50582	0	0
XLOC_001712	GPBP1	chr5:56505422-56596263	17,5118	3,00062	-2,545	8,47601	0	0
XLOC_018596	DMXL2	chr15:49527212-49702500	3,83656	0,659231	-2,54096	9,71727	0	0
XLOC_030944	ECT2	chr3:173950977-174021957	32,0368	5,53664	-2,53265	9,09135	0	0
XLOC_029072	WNT5A	chr3:55474782-55496371	18,5598	3,21361	-2,52992	8,72043	0	0
XLOC_017623	CLOCK	chr4:55988953-56108103	8,2359	1,43806	-2,5178	8,98331	0	0
XLOC_014935	BRCA1	chr17:38449831-38531026	15,2766	2,75722	-2,47004	9,39042	0	0
XLOC_022270	DICER1	chr14:94622317-94716096	8,91024	1,6718	-2,41407	11,8238	0	0
XLOC_022326	FNDCA3	chr13:48444845-48681916	16,3685	3,18084	-2,36344	9,16485	0	0
XLOC_024683	XIAP	chrX:122821342-122875510	5,89679	1,17339	-2,32924	8,64814	0	0
XLOC_022381	MRE11A	chr11:93788466-93874636	10,5078	2,18283	-2,26719	8,4275	0	0
XLOC_010455	SGOL1	chr3:20177088-20202728	11,7627	2,4554	-2,26018	10,3347	0	0
XLOC_017589	FMR1	chrX:146798640-146840339	14,2344	3,13457	-2,18304	8,85454	0	0
XLOC_024630	NFIB	chr9:14071841-14388982	9,43638	2,17132	-2,11966	8,69934	0	0
XLOC_027214	PLEKHA1	chr10:124124062-124181861	8,57388	1,98064	-2,11399	8,61721	0	0
XLOC_029669	ZNF180	chr19:49670672-49696584	3,49031	0,197583	-4,14282	8,19903	2,22E-16	6,12E-14
XLOC_022275	ATAD5	chr17:26182981-26257412	4,82551	0,323829	-3,89738	8,22269	2,22E-16	6,12E-14
XLOC_004879	USP53	chr4:120353186-120436621	7,56352	0,694676	-3,44465	8,27226	2,22E-16	6,12E-14
XLOC_025913	TRPM7	chr15:48636643-48766304	6,39494	0,648479	-3,3018	8,27048	2,22E-16	6,12E-14
XLOC_025917	ZFX	chrX:24077031-24145780	9,5079	1,33859	-2,82841	8,1995	2,22E-16	6,12E-14
XLOC_012086	GOLGA4	chr3:37257655-37383374	10,7463	0,873018	-3,62168	8,12969	4,44E-16	1,14E-13
XLOC_007261	C8orf83	chr8:93964933-94047639	2,73934	0,250274	-3,45225	8,13746	4,44E-16	1,14E-13
XLOC_024676	SAMD9L	chr7:92597273-92615638	1,57576	0,183269	-3,10401	8,11924	4,44E-16	1,14E-13
XLOC_007699	ANKRD12	chr18:9124643-9275983	1,99043	0,235191	-3,08117	8,15201	4,44E-16	1,14E-13
XLOC_029290	SSX2IP	chr1:84881977-84928828	5,07107	0,671098	-2,91769	8,12542	4,44E-16	1,14E-13
XLOC_008494	DMXL1	chr5:118434699-118612721	4,50993	0,607258	-2,89272	8,13504	4,44E-16	1,14E-13
XLOC_007668	PTPN13	chr4:87734467-87955352	6,81425	1,36084	-2,32406	8,14572	4,44E-16	1,14E-13
XLOC_025311	PRPF4B	chr6:3966036-4010218	22,8555	3,32839	-2,77965	8,09376	6,66E-16	1,66E-13
XLOC_017676	PDS5B	chr13:32058563-32250158	13,6767	2,19969	-2,63635	8,07464	6,66E-16	1,66E-13
XLOC_010796	DNM1L	chr12:32723224-32800301	21,4123	5,06418	-2,08004	8,09376	6,66E-16	1,66E-13
XLOC_029886	CUL2	chr10:35337484-35419576	16,1999	2,40454	-2,75215	8,00394	1,11E-15	2,75E-13
XLOC_015026	N4BP2	chr4:39720931-39836267	3,558	0,279204	-3,67168	7,98878	1,33E-15	3,27E-13

XLOC_008787	BBX	chr3:108724472-109012739	13,2998	2,01382	-2,7234	7,97331	1,55E-15	3,78E-13
XLOC_025369	CCDC88A	chr2:55366662-55500561	12,8448	0,976156	-3,71793	7,95174	1,78E-15	4,24E-13
XLOC_006048	EHBP1	chr2:62754489-63129160	15,7959	3,26611	-2,2739	7,95321	1,78E-15	4,24E-13
XLOC_014925	TTC3	chr21:37367406-37497278	27,0745	3,53768	-2,93606	7,93917	2,00E-15	4,68E-13
XLOC_025368	RWDD3	chr1:95330660-95485369	10,1469	1,94581	-2,3826	7,93546	2,00E-15	4,68E-13
XLOC_022331	SENP6	chr6:76368179-76485095	14,587	1,90989	-2,93313	7,89985	2,89E-15	6,54E-13
XLOC_018406	HAUS3	chr4:2043442-2213658	4,1787	0,570622	-2,87245	7,89419	2,89E-15	6,54E-13
XLOC_024619	ATP2B1	chr12:88505738-88629860	20,9105	3,61454	-2,53234	7,8952	2,89E-15	6,54E-13
XLOC_017627	SMARCD1	chr4:95347781-95431466	10,1763	1,10164	-3,20749	7,88199	3,33E-15	7,36E-13
XLOC_027249	NIPBL	chr5:36910249-37101678	12,4714	1,62109	-2,94359	7,8801	3,33E-15	7,36E-13
XLOC_002092	SLFN12	chr17:30757897-30784322	7,12638	1,46924	-2,2781	7,87676	3,33E-15	7,36E-13
XLOC_018145	CDK6	chr7:92072170-92303918	8,47399	0,954003	-3,15098	7,86291	3,77E-15	8,27E-13
XLOC_003521	DZIP3	chr3:109743528-109896383	6,01508	0,607412	-3,30784	7,8404	4,44E-15	9,57E-13
XLOC_026009	RIF1	chr2:151974642-152299247	12,119	0,87614	-3,78996	7,83673	4,66E-15	9,97E-13
XLOC_034123	SRSF10	chr1:24163837-24179741	39,7016	8,68597	-2,19244	7,82886	4,88E-15	1,04E-12
XLOC_010389	EDEM3	chr1:182926247-182990664	7,13043	0,577308	-3,62658	7,78491	6,88E-15	1,45E-12
XLOC_027399	CCP110	chr16:19442679-19472229	8,40413	1,06821	-2,97591	7,77846	7,33E-15	1,53E-12
XLOC_002225	PPP6R3	chr11:67983073-68139380	35,1929	5,81221	-2,59812	7,75889	8,66E-15	1,79E-12
XLOC_009527	MYEF2	chr15:46200460-46257851	5,58703	0,97049	-2,5253	7,72789	1,09E-14	2,22E-12
XLOC_031037	ELF2	chr4:140155739-140319848	16,4788	3,58736	-2,19962	7,71074	1,24E-14	2,50E-12
XLOC_008687	SLK	chr10:105716838-105779242	16,6322	1,2492	-3,7349	7,7084	1,27E-14	2,52E-12
XLOC_024681	IFT80	chr3:161457467-161650355	6,11947	0,650476	-3,23384	7,70005	1,35E-14	2,68E-12
XLOC_008640	TRIM23	chr5:64919949-65053697	4,87783	0,504024	-3,27468	7,69641	1,40E-14	2,75E-12
XLOC_032114	DIS3	chr13:72180495-72488592	8,52431	1,19393	-2,83586	7,67755	1,62E-14	3,16E-12
XLOC_008724	MIER1	chr1:67051159-67226890	10,2504	1,52995	-2,74411	7,67456	1,67E-14	3,22E-12
XLOC_030017	PPP1CB	chr2:28828117-28879310	39,7345	4,11357	-3,27193	7,64854	2,04E-14	3,90E-12
XLOC_024671	RAD17	chr5:68683308-68746387	9,30324	1,63972	-2,50429	7,64633	2,07E-14	3,91E-12
XLOC_024275	DOCK11	chrX:117513521-117717651	14,9185	1,79359	-3,05619	7,63796	2,20E-14	4,14E-12
XLOC_029294	KIAA1524	chr3:109743528-109896383	16,9152	1,50017	-3,49512	7,5696	3,75E-14	6,96E-12
XLOC_020712	ZNF302	chr19:39814689-39869923	5,27093	0,369146	-3,8358	7,55769	4,11E-14	7,57E-12
XLOC_027879	CREBZF	chr11:85046255-85054023	7,89919	1,61249	-2,29241	7,54349	4,57E-14	8,32E-12
XLOC_009192	ASPH	chr8:62363078-62789972	68,2713	9,09992	-2,90735	7,53467	4,88E-14	8,76E-12
XLOC_004180	PSIP1	chr9:15412781-15503029	110,019	19,5336	-2,49372	7,52908	5,11E-14	9,10E-12
XLOC_022209	KIAA1731	chr11:93034455-93114351	5,61954	0,755329	-2,89528	7,52435	5,31E-14	9,39E-12

XLOC_007094	MAP9	chr4:156483261-156517572	1,28402	0,0753756	-4,09043	7,5072	6,04E-14	1,05E-11
XLOC_022648	RAD50	chr5:131920410-132009236	9,67893	0,871716	-3,47292	7,50751	6,02E-14	1,05E-11
XLOC_023095	LOC100499177	chr4:84033628-84062733	8,54678	1,13772	-2,90923	7,49812	6,48E-14	1,13E-11
XLOC_002275	MPHOSPH9	chr12:122202713-122309150	12,4948	1,71563	-2,86451	7,47384	7,79E-14	1,34E-11
XLOC_005286	RASA2	chr3:142688543-142816370	4,46238	0,929778	-2,26286	7,42131	1,16E-13	1,99E-11
XLOC_025930	KRIT1	chr7:91661471-91868634	6,63548	0,881406	-2,91232	7,42014	1,17E-13	1,99E-11
XLOC_000476	TTC21B	chr2:166437547-166518594	4,72199	0,838086	-2,49422	7,4106	1,26E-13	2,13E-11
XLOC_023217	NBEAL1	chr2:203587776-203796549	2,54286	0,203358	-3,64436	7,40116	1,35E-13	2,27E-11
XLOC_022627	TBL1XR1	chr3:178221172-178398150	8,78533	1,47914	-2,57034	7,39182	1,45E-13	2,40E-11
XLOC_001791	THOC2	chrX:122562092-122696499	14,208	2,20073	-2,69065	7,37397	1,66E-13	2,72E-11
XLOC_007631	RAPGEF6	chr5:130787512-130998828	5,40305	0,813927	-2,7308	7,36633	1,75E-13	2,86E-11
XLOC_001086	VEZT	chr12:94135598-94221515	18,4257	4,14398	-2,15263	7,35914	1,85E-13	2,98E-11
XLOC_023079	KIAA1033	chr12:104025621-104087036	12,5865	1,44038	-3,12736	7,34893	2,00E-13	3,20E-11
XLOC_012824	SGOL2	chr2:201061928-201157063	9,55176	0,654318	-3,8677	7,34246	2,10E-13	3,33E-11
XLOC_008771	C9orf41	chr9:76785864-76833245	4,58025	0,339047	-3,75587	7,33459	2,22E-13	3,52E-11
XLOC_009471	GBP3	chr1:89244947-89261137	5,99874	0,619099	-3,27642	7,31337	2,60E-13	4,09E-11
XLOC_009165	ZBTB38	chr3:142525744-142651322	18,7028	4,1081	-2,18671	7,30547	2,76E-13	4,32E-11
XLOC_032226	SOCS4	chr14:54563593-54585959	5,26897	0,610778	-3,1088	7,29137	3,07E-13	4,74E-11
XLOC_031441	ZDHHC21	chr9:14601068-14683480	1,48783	0,171132	-3,12003	7,27337	3,51E-13	5,35E-11
XLOC_025990	ZNF138	chr7:63892205-63931460	2,21986	0,39782	-2,48028	7,26453	3,74E-13	5,68E-11
XLOC_018690	BROX	chr1:220858047-220973848	22,947	2,89091	-2,98871	7,26107	3,84E-13	5,78E-11
XLOC_025446	SLC25A36	chr3:142142911-142181475	8,36489	1,17697	-2,82927	7,26082	3,85E-13	5,78E-11
XLOC_025905	RBBP6	chr16:24458385-24491684	14,289	3,08302	-2,21249	7,25527	4,01E-13	5,98E-11
XLOC_017814	CEP97	chr3:102925364-102972081	5,89228	0,605287	-3,28314	7,24626	4,28E-13	6,36E-11
XLOC_022224	ARL15	chr5:53215636-53642200	11,1328	1,72427	-2,69076	7,23288	4,73E-13	6,98E-11
XLOC_003595	ESCO2	chr8:27687842-27751468	12,5487	0,986936	-3,66844	7,2215	5,14E-13	7,47E-11
XLOC_008512	RG9MTD2	chr4:100686886-100704212	2,07519	0,159352	-3,70295	7,22007	5,20E-13	7,48E-11
XLOC_034100	GABPA	chr21:26018661-26066642	3,96634	0,381151	-3,37937	7,21979	5,21E-13	7,48E-11
XLOC_031461	SPOPL	chr2:138975819-139047277	4,36128	0,870619	-2,32464	7,21154	5,53E-13	7,87E-11
XLOC_005879	SETX	chr9:134126647-134220243	11,6497	1,78494	-2,70635	7,20133	5,96E-13	8,34E-11
XLOC_007614	ZNF84	chr12:132123950-132149958	2,8598	0,364904	-2,97033	7,18702	6,62E-13	9,22E-11
XLOC_022983	NEDD1	chr12:95825131-95871600	14,522	1,9043	-2,9309	7,17526	7,22E-13	9,99E-11
XLOC_002212	ZNF638	chr2:71412396-71515697	15,6694	2,0826	-2,9115	7,16907	7,55E-13	1,03E-10
XLOC_001083	MAN1A2	chr1:117709247-117870461	13,5361	2,18654	-2,63009	7,14634	8,91E-13	1,22E-10

XLOC_027432	SERINC1	chr6:122806191-122834696	56,3898	7,76281	-2,86078	7,145	9,00E-13	1,22E-10
XLOC_017542	RSRC1	chr3:159310409-159746090	16,1611	2,26005	-2,8381	7,13069	9,99E-13	1,34E-10
XLOC_023172	ZSCAN12	chr6:28454576-28475523	4,68756	1,15348	-2,02285	7,13041	1,00E-12	1,34E-10
XLOC_013927	NUF2	chr1:161558346-161592177	21,8937	2,04702	-3,41892	7,11815	1,09E-12	1,45E-10
XLOC_001786	ZFYVE16	chr5:79739207-79874138	9,71123	0,760495	-3,67464	7,09244	1,32E-12	1,73E-10
XLOC_031484	PUM2	chr2:20311933-20413979	22,7359	4,58165	-2,31104	7,0889	1,35E-12	1,77E-10
XLOC_031423	POLQ	chr3:122632962-122747543	6,17168	0,80588	-2,93703	7,07742	1,47E-12	1,91E-10
XLOC_003701	C3orf64	chr3:69107057-69150555	7,37792	0,937229	-2,97674	7,06256	1,63E-12	2,12E-10
XLOC_003715	LIN9	chr1:224485485-224564493	6,60193	0,6799	-3,27949	7,06006	1,66E-12	2,15E-10
XLOC_025475	IKBIP	chr12:97531312-97562720	26,1999	3,78586	-2,79086	7,0457	1,85E-12	2,37E-10
XLOC_024749	CEP152	chr15:46817426-46890635	5,75015	0,730719	-2,97621	7,04426	1,86E-12	2,38E-10
XLOC_030845	GOLIM4	chr3:169209976-169296567	29,7404	3,30214	-3,17095	7,04327	1,88E-12	2,39E-10
XLOC_034315	MYNN	chr3:170972810-170993807	3,81769	0,630521	-2,59808	7,03887	1,94E-12	2,45E-10
XLOC_000878	PUS7L	chr12:42408678-42438863	2,33447	0,190192	-3,61756	7,02835	2,09E-12	2,62E-10
XLOC_007087	LIG4	chr13:107657792-107668717	4,08877	0,542647	-2,91358	7,02853	2,09E-12	2,62E-10
XLOC_032297	VGLL3	chr3:87069812-87123192	3,48329	0,377835	-3,20462	7,02473	2,14E-12	2,68E-10
XLOC_017961	LARP7	chr4:113679937-113798191	18,7149	1,80366	-3,37519	7,015	2,30E-12	2,83E-10
XLOC_006989	CENPE	chr4:104246411-104339015	5,85659	0,54691	-3,42068	7,00264	2,51E-12	3,08E-10
XLOC_003999	EEA1	chr12:91690415-91847238	5,55577	0,334544	-4,05372	6,97388	3,08E-12	3,75E-10
XLOC_034374	TTK	chr6:80771040-80809804	18,3359	1,44535	-3,66518	6,96743	3,23E-12	3,90E-10
XLOC_000192	ROD1	chr9:113798652-114152366	18,179	3,67251	-2,30744	6,9597	3,41E-12	4,09E-10
XLOC_001719	KIAA0020	chr9:2733533-2834136	19,6254	2,9848	-2,71702	6,94335	3,83E-12	4,55E-10
XLOC_032819	PHF20L1	chr8:133856769-133935582	11,9359	1,86895	-2,67501	6,92368	4,40E-12	5,18E-10
XLOC_018538	MTR	chr1:235025171-235133904	8,98444	1,55483	-2,53067	6,88452	5,80E-12	6,74E-10
XLOC_023151	RB1CC1	chr8:53697570-53789579	7,83959	0,503756	-3,95998	6,87487	6,20E-12	7,16E-10
XLOC_001678	ZNF148	chr3:126427202-126576888	9,0556	1,12145	-3,01344	6,87466	6,21E-12	7,16E-10
XLOC_029981	PNPLA8	chr7:107899306-107954006	11,2372	0,822832	-3,77155	6,87065	6,39E-12	7,33E-10
XLOC_024649	RAD54B	chr8:95453363-95556519	9,80752	1,1198	-3,13064	6,86718	6,55E-12	7,41E-10
XLOC_014817	CASC4	chr15:42368200-42495251	30,2544	3,5577	-3,08813	6,86724	6,55E-12	7,41E-10
XLOC_020776	PDIK1L	chr1:26310242-26324613	2,39142	0,292324	-3,03223	6,86829	6,50E-12	7,41E-10
XLOC_022708	OXR1	chr8:107351568-107834097	10,9392	2,42423	-2,1739	6,86046	6,86E-12	7,74E-10
XLOC_015014	FER	chr5:108111421-108552736	6,80639	0,88766	-2,93881	6,8572	7,02E-12	7,89E-10
XLOC_022870	CCDC144A	chr17:16534363-16648544	3,87418	0,377433	-3,3596	6,8476	7,51E-12	8,36E-10
XLOC_002268	GLS	chr2:191453121-191538021	26,7351	4,199	-2,67061	6,84291	7,76E-12	8,60E-10

XLOC_005985	UCHL5	chr1:191248118-191327714	19,3022	3,82508	-2,3352	6,83721	8,07E-12	8,92E-10
XLOC_024416	ARL5A	chr2:152354222-152393255	8,52134	1,20078	-2,8271	6,83431	8,24E-12	9,06E-10
XLOC_004266	ELOVL6	chr4:111186449-111339788	21,3105	4,04167	-2,39854	6,83322	8,30E-12	9,09E-10
XLOC_010677	ZNF568	chr19:41980291-42180674	1,37865	0,15542	-3,14901	6,79463	1,09E-11	1,18E-09
XLOC_010352	CEP128	chr14:80013303-80478031	5,75219	1,19226	-2,27041	6,7924	1,10E-11	1,20E-09
XLOC_004869	MYBL1	chr8:67636963-67688116	7,99184	1,24284	-2,68488	6,79086	1,11E-11	1,21E-09
XLOC_017607	PHF6	chrX:133334816-133390488	20,9233	2,23889	-3,22426	6,78888	1,13E-11	1,22E-09
XLOC_022993	ZNF518A	chr10:97878958-97914378	2,26445	0,194704	-3,53981	6,78393	1,17E-11	1,25E-09
XLOC_012203	SRSF11	chr1:70443952-70491498	52,985	9,09416	-2,54257	6,78092	1,19E-11	1,27E-09
XLOC_032829	ABCA10	chr17:64655742-64835061	1,53208	0,184397	-3,0546	6,77567	1,24E-11	1,31E-09
XLOC_005672	METTL15	chr11:28086373-28311630	3,12406	0,480903	-2,6996	6,77164	1,27E-11	1,34E-09
XLOC_003664	HELLS	chr10:96294767-96363524	17,3259	2,77144	-2,64422	6,77212	1,27E-11	1,34E-09
XLOC_031331	SLC30A9	chr4:41687165-41795091	27,4501	4,28337	-2,68	6,76263	1,36E-11	1,42E-09
XLOC_025385	KRCC1	chr2:88107838-88136450	13,8289	1,40519	-3,29884	6,7558	1,42E-11	1,48E-09
XLOC_017704	PHC3	chr3:171285932-171382234	9,29112	2,00939	-2,20909	6,75547	1,42E-11	1,48E-09
XLOC_001710	KIAA1109	chr4:123292944-123503364	6,99094	0,834445	-3,0666	6,73058	1,69E-11	1,74E-09
XLOC_027869	BAZ2B	chr2:159883735-160181772	5,63528	0,955868	-2,55961	6,72366	1,77E-11	1,82E-09
XLOC_027860	RNF6	chr13:25684904-25694508	11,368	1,29974	-3,12868	6,71481	1,88E-11	1,93E-09
XLOC_013958	DBF4	chr7:87300909-87376792	8,1793	1,20654	-2,76111	6,71365	1,90E-11	1,94E-09
XLOC_033605	KIAA1009	chr6:84890678-84994100	2,08549	0,100997	-4,36801	6,71053	1,94E-11	1,97E-09
XLOC_030803	POLI	chr18:50049777-50078602	1,47916	0,18645	-2,98791	6,67349	2,50E-11	2,52E-09
XLOC_005311	MCM8	chr20:5879275-5927735	18,3804	3,5844	-2,35837	6,67365	2,50E-11	2,52E-09
XLOC_016758	MYO9A	chr15:69901538-70222846	5,71096	1,41018	-2,01785	6,67248	2,52E-11	2,53E-09
XLOC_022316	DENND1B	chr1:195740501-196011598	1,41676	0,230436	-2,62016	6,66612	2,63E-11	2,63E-09
XLOC_024076	VPS13C	chr15:59931881-60139972	5,72564	0,660376	-3,11608	6,65391	2,85E-11	2,85E-09
XLOC_022708	TOP2B	chr3:25614478-25681440	33,5631	5,66458	-2,56683	6,65325	2,87E-11	2,85E-09
XLOC_022558	BOD1L	chr4:13179463-13238566	8,93041	1,19475	-2,90201	6,63369	3,27E-11	3,23E-09
XLOC_025337	LRRFIP1	chr2:238200960-238355029	27,6988	4,88998	-2,50193	6,63154	3,32E-11	3,26E-09
XLOC_023081	BHLHB9	chrX:101862027-101895096	2,92538	0,673668	-2,11851	6,62774	3,41E-11	3,34E-09
XLOC_017995	FAM63B	chr15:56850612-56938634	4,26547	0,50003	-3,09262	6,62691	3,43E-11	3,34E-09
XLOC_032741	AKAP9	chr7:91407880-91577923	3,03675	0,264246	-3,52257	6,60684	3,93E-11	3,79E-09
XLOC_009612	TANK	chr2:161701711-161800929	17,1934	2,73423	-2,65265	6,60281	4,03E-11	3,88E-09
XLOC_018791	RC3H1	chr1:172166733-172258150	1,91782	0,377205	-2,34604	6,58697	4,49E-11	4,27E-09
XLOC_032869	ZC3H6	chr2:112749039-112814111	1,07448	0,166021	-2,6942	6,58003	4,70E-11	4,44E-09

XLOC_012107	RALGAPA1	chr14:35077308-35348305	3,28114	0,368243	-3,15547	6,57722	4,79E-11	4,49E-09
XLOC_023152	KIF18A	chr11:27998738-28086322	9,61723	0,657746	-3,87002	6,57183	4,97E-11	4,64E-09
XLOC_030022	RRM2B	chr8:103285904-103320714	9,19494	1,14795	-3,00178	6,56832	5,09E-11	4,74E-09
XLOC_014757	RBBP8	chr18:18767292-18860447	29,2127	3,82677	-2,9324	6,55306	5,64E-11	5,18E-09
XLOC_027997	ZNF280D	chr15:54709665-54813169	5,42055	0,950757	-2,51129	6,55111	5,71E-11	5,23E-09
XLOC_014775	FGD4	chr12:32443718-32690251	2,8856	0,356025	-3,01882	6,54226	6,06E-11	5,53E-09
XLOC_006992	PVRL3	chr3:112272867-112402873	6,4139	0,95613	-2,74592	6,54026	6,14E-11	5,58E-09
XLOC_029144	SEPT7	chr7:35807120-35979800	89,2819	8,35589	-3,4175	6,53703	6,28E-11	5,68E-09
XLOC_034411	PDP1	chr8:94998258-95007472	12,7865	2,63921	-2,27645	6,53463	6,38E-11	5,76E-09
XLOC_003993	MFN1	chr3:180548173-180594911	13,7012	2,28953	-2,58119	6,53374	6,41E-11	5,77E-09
XLOC_024579	FAM35A	chr10:88844918-88941202	12,7674	1,51224	-3,07771	6,52734	6,69E-11	6,00E-09
XLOC_017971	TAF1A	chr1:220794724-220830646	2,96106	0,515556	-2,52191	6,52102	6,98E-11	6,24E-09
XLOC_014914	ACAP2	chr3:196476753-196645121	9,88834	1,23413	-3,00224	6,49287	8,42E-11	7,48E-09
XLOC_009145	KIAA0528	chr12:22492784-22588938	11,4954	2,34851	-2,29124	6,48775	8,71E-11	7,71E-09
XLOC_025656	OPA1	chr3:194793626-194898294	15,0791	2,10218	-2,84259	6,48715	8,75E-11	7,71E-09
XLOC_017953	ZNF252	chr8:146169778-146202236	3,08402	0,337714	-3,19094	6,48437	8,91E-11	7,83E-09
XLOC_006052	PTBP2	chr1:96959540-97053193	4,0011	0,449603	-3,15367	6,47745	9,33E-11	8,17E-09
XLOC_033924	REST	chr4:57468798-57496767	8,05949	1,16771	-2,78701	6,47612	9,41E-11	8,22E-09
XLOC_004087	STK38L	chr12:27288344-27370157	4,33781	0,815264	-2,41163	6,47163	9,70E-11	8,44E-09
XLOC_023214	NARG2	chr15:58498821-58558636	8,43645	1,28412	-2,71585	6,47014	9,79E-11	8,49E-09
XLOC_027910	KIF21A	chr12:37973296-38123459	2,58118	0,204709	-3,65639	6,46548	1,01E-10	8,73E-09
XLOC_022472	CCDC14	chr3:125114963-125162970	18,7007	2,67082	-2,80774	6,46215	1,03E-10	8,90E-09
XLOC_024185	ZNF347	chr19:58333768-58354134	1,98899	0,207269	-3,26247	6,45549	1,08E-10	9,24E-09
XLOC_010895	ZNF224	chr19:49290321-49309176	4,17035	0,504798	-3,04639	6,43511	1,23E-10	1,04E-08
XLOC_005045	GTF2H2B	chr5:68891746-68926811	10,5188	2,54932	-2,04479	6,43422	1,24E-10	1,04E-08
XLOC_030839	C18orf54	chr18:50138065-50162402	3,91894	0,632514	-2,63129	6,4219	1,35E-10	1,12E-08
XLOC_024653	GCFC1	chr21:32922939-33066040	11,5123	2,44462	-2,2355	6,41989	1,36E-10	1,13E-08
XLOC_022320	ANKRD1	chr10:92661836-92671012	10,0148	0,769089	-3,70284	6,41919	1,37E-10	1,13E-08
XLOC_018745	PRKD3	chr2:37331149-37405496	19,0356	4,67276	-2,02636	6,41392	1,42E-10	1,16E-08
XLOC_025408	ZNF354B	chr5:178219543-178247537	2,05577	0,293577	-2,80787	6,4068	1,49E-10	1,21E-08
XLOC_034085	ARHGAP29	chr1:94407050-94485910	9,23209	1,45226	-2,66836	6,40103	1,54E-10	1,25E-08
XLOC_027953	C11orf82	chr11:82290384-82323347	9,24844	1,69955	-2,44406	6,39142	1,64E-10	1,33E-08
XLOC_018051	POLK	chr5:74701627-74937701	5,92261	0,362846	-4,0288	6,37968	1,77E-10	1,42E-08
XLOC_008506	USP47	chr11:11819440-11987493	11,9658	1,41977	-3,07519	6,37877	1,79E-10	1,42E-08

XLOC_002107	ZDHC20	chr13:20844709-20931508	18,8316	2,33072	-3,01431	6,3694	1,90E-10	1,51E-08
XLOC_027244	CEP170	chr1:241354324-242082077	19,3915	3,86051	-2,32856	6,34784	2,18E-10	1,73E-08
XLOC_020303	SLC35A3	chr1:100207285-100264787	6,20204	0,770787	-3,00834	6,34652	2,20E-10	1,74E-08
XLOC_009174	UACA	chr15:68724929-68844068	24,6973	1,97841	-3,64194	6,33214	2,42E-10	1,89E-08
XLOC_003505	ZNF790	chr19:41980291-42180674	1,20502	0,158126	-2,9299	6,33189	2,42E-10	1,89E-08
XLOC_006671	SHPRH	chr6:145988132-146327243	3,32653	0,431938	-2,94512	6,32644	2,51E-10	1,95E-08
XLOC_019949	LRRCC1	chr8:86206574-86245566	1,92012	0,110993	-4,11266	6,31677	2,67E-10	2,06E-08
XLOC_024020	DCAF17	chr2:171882158-172049808	3,44493	0,735158	-2,22835	6,30889	2,81E-10	2,16E-08
XLOC_018765	PPIG	chr2:170148577-170202500	24,0438	1,90497	-3,65783	6,30498	2,88E-10	2,21E-08
XLOC_022462	ZNF680	chr7:63597091-63660940	2,46284	0,229489	-3,42383	6,30234	2,93E-10	2,24E-08
XLOC_010830	PDE4D	chr5:58300622-59879241	2,5444	0,630305	-2,0132	6,29698	3,03E-10	2,31E-08
XLOC_009269	IFT81	chr12:109046522-109140983	6,46615	0,998817	-2,69461	6,2928	3,12E-10	2,37E-08
XLOC_009214	ALKBH8	chr11:106878662-106941671	3,69395	0,491919	-2,90867	6,29146	3,15E-10	2,38E-08
XLOC_030877	AEBP2	chr12:19483636-19566440	6,20485	1,15167	-2,42967	6,28911	3,19E-10	2,41E-08
XLOC_024718	PPP4R2	chr3:73128435-73198729	32,0335	3,17609	-3,33426	6,28183	3,35E-10	2,52E-08
XLOC_022280	OTUD3	chr1:20081407-20112024	2,98302	0,407892	-2,87051	6,28117	3,36E-10	2,52E-08
XLOC_031353	ATRX	chrX:76646438-76928375	7,55551	0,516984	-3,86934	6,26617	3,70E-10	2,75E-08
XLOC_017612	DEPDC1	chr1:68712422-68735387	15,1722	1,76137	-3,10666	6,26614	3,70E-10	2,75E-08
XLOC_018365	NCOA7	chr6:126143816-126294869	6,29152	1,34008	-2,23108	6,26577	3,71E-10	2,75E-08
XLOC_007807	SUV39H2	chr10:14960787-15054856	7,92726	1,63162	-2,28052	6,25536	3,97E-10	2,92E-08
XLOC_000910	ZCCHC6	chr9:88092434-88159261	6,03514	1,15367	-2,38715	6,2525	4,04E-10	2,97E-08
XLOC_027755	PIKFYVE	chr2:208839235-208931720	7,67624	1,46286	-2,39161	6,25165	4,06E-10	2,97E-08
XLOC_025981	DENND4A	chr15:63740010-63871685	5,82658	1,17769	-2,30669	6,25105	4,08E-10	2,98E-08
XLOC_004080	LZTFL1	chr3:45840433-45858631	7,60857	1,32926	-2,517	6,23486	4,52E-10	3,27E-08
XLOC_001310	NR1D2	chr3:23961754-23997113	10,0614	1,94678	-2,36967	6,23518	4,51E-10	3,27E-08
XLOC_026040	IRAK4	chr12:42438898-42469613	3,55317	0,721617	-2,2998	6,23272	4,58E-10	3,31E-08
XLOC_024460	DNAJB4	chr1:78182323-78256677	12,1831	0,949703	-3,68126	6,22537	4,80E-10	3,44E-08
XLOC_017825	ZNF711	chrX:84385497-84415025	1,26085	0,131448	-3,26183	6,2154	5,12E-10	3,65E-08
XLOC_008722	PLK4	chr4:129021465-129039827	18,4645	1,88565	-3,29162	6,20402	5,50E-10	3,90E-08
XLOC_032357	WDR67	chr8:124153994-124233573	7,62559	1,52211	-2,32478	6,19867	5,69E-10	4,03E-08
XLOC_027190	C12orf35	chr12:32002717-32037308	3,90015	0,393597	-3,30874	6,18974	6,03E-10	4,24E-08
XLOC_008493	ANKRD28	chr3:15683708-15876422	11,1217	2,29281	-2,27819	6,18541	6,19E-10	4,33E-08
XLOC_027505	ETAA1	chr2:67477945-67491037	7,10175	0,537891	-3,72279	6,18199	6,33E-10	4,40E-08
XLOC_023239	ACBD5	chr10:27524148-27571074	9,80984	1,89282	-2,37369	6,176	6,57E-10	4,55E-08

XLOC_007069	ADAM10	chr15:56668201-56829469	45,9743	5,56887	-3,04537	6,17144	6,77E-10	4,64E-08
XLOC_018680	TUBD1	chr17:55291621-55325088	4,37852	0,717257	-2,60988	6,17159	6,76E-10	4,64E-08
XLOC_025993	GEN1	chr2:17707964-17830113	6,22848	0,626451	-3,3136	6,16853	6,89E-10	4,71E-08
XLOC_002278	CTAGE5	chr14:38804215-38890148	3,54032	0,765234	-2,20991	6,15959	7,29E-10	4,97E-08
XLOC_018697	IBTK	chr6:82936674-83014174	9,70774	1,25949	-2,9463	6,15601	7,46E-10	5,07E-08
XLOC_003592	CEP44	chr4:175394384-175491106	4,92225	0,512742	-3,26301	6,15394	7,56E-10	5,11E-08
XLOC_018688	CHD1	chr5:98218227-98294613	9,30464	0,731666	-3,66869	6,1525	7,63E-10	5,15E-08
XLOC_001509	KIAA1715	chr2:176496915-176575272	5,87366	0,801282	-2,87388	6,1463	7,93E-10	5,34E-08
XLOC_025347	THUMPD2	chr2:39816703-39859920	3,44976	0,461977	-2,9006	6,14528	7,98E-10	5,36E-08
XLOC_023257	DCLRE1C	chr10:14960787-15054856	4,68004	1,13067	-2,04934	6,13143	8,71E-10	5,83E-08
XLOC_027191	ZNF451	chr6:57019214-57143057	11,6555	1,89857	-2,61802	6,12067	9,32E-10	6,21E-08
XLOC_005338	FKTN	chr9:107360231-107443220	5,35792	0,891452	-2,58745	6,10952	9,99E-10	6,63E-08
XLOC_018668	ZNF829	chr19:41980291-42180674	2,43769	0,195339	-3,64146	6,1028	1,04E-09	6,89E-08
XLOC_027375	NEK7	chr1:196392730-196558171	29,4994	2,26675	-3,70199	6,08933	1,13E-09	7,44E-08
XLOC_000531	SRFBP1	chr5:121325473-121395978	4,9916	0,629195	-2,98792	6,08837	1,14E-09	7,45E-08
XLOC_027299	STRN3	chr14:30432755-30632389	11,0291	1,88369	-2,54969	6,08273	1,18E-09	7,68E-08
XLOC_009286	MDM2	chr12:67488105-67643287	31,4662	3,92727	-3,00221	6,08137	1,19E-09	7,73E-08
XLOC_027364	LIN54	chr4:84064780-84153141	7,01536	1,32836	-2,40088	6,07769	1,22E-09	7,89E-08
XLOC_006791	ATP11B	chr3:183993959-184123726	23,155	3,70322	-2,64447	6,07526	1,24E-09	7,99E-08
XLOC_026024	BAZ1A	chr14:34291687-34415056	14,5438	1,68874	-3,10638	6,07357	1,25E-09	8,06E-08
XLOC_000453	FTSJD1	chr16:69873703-69881010	5,77006	0,883695	-2,70697	6,06834	1,29E-09	8,28E-08
XLOC_001145	FAM133B	chr7:92027331-92057642	4,72118	0,543034	-3,12003	6,06592	1,31E-09	8,37E-08
XLOC_033832	ZNF484	chr9:94648171-94680148	3,37435	0,363212	-3,21573	6,06479	1,32E-09	8,41E-08
XLOC_026862	SCFD1	chr14:30161193-30274769	29,2983	3,28947	-3,15489	6,04837	1,46E-09	9,24E-08
XLOC_027278	CSPP1	chr8:68139156-68271403	4,60768	0,80478	-2,51738	6,04777	1,47E-09	9,26E-08
XLOC_017729	SP3	chr2:174479432-174538676	17,1529	2,32178	-2,88515	6,0412	1,53E-09	9,62E-08
XLOC_027224	FBXO3	chr11:33719065-33752647	12,3176	2,82417	-2,12482	6,03831	1,56E-09	9,75E-08
XLOC_000468	OSBPL8	chr12:75269042-75478138	12,2258	1,04433	-3,54928	6,03707	1,57E-09	9,78E-08
XLOC_032206	ARHGAP12	chr10:32134714-32257799	6,27803	0,908689	-2,78845	6,03736	1,57E-09	9,78E-08
XLOC_009675	PDCD10	chr3:168884388-168935345	24,0517	3,04248	-2,98282	6,03537	1,59E-09	9,86E-08
XLOC_000558	CKAP2L	chr2:113210398-113238905	21,4498	2,73399	-2,97188	6,02564	1,68E-09	1,04E-07
XLOC_027912	CCNT2	chr2:135312655-135433385	5,50877	0,936067	-2,55705	6,01498	1,80E-09	1,11E-07
XLOC_024590	CXADR	chr21:17807049-17907139	6,82931	0,926234	-2,88229	6,01151	1,84E-09	1,13E-07
XLOC_000448	ZNF292	chr6:87920974-88030497	5,06184	0,387013	-3,70921	6,0109	1,84E-09	1,13E-07

XLOC_018352	NOL8	chr9:94099460-94472368	9,26657	1,1202	-3,04828	6,00153	1,95E-09	1,19E-07
XLOC_023216	NBN	chr8:91014739-91066289	14,7931	1,50675	-3,29542	5,99613	2,02E-09	1,23E-07
XLOC_022948	MBNL2	chr13:96672551-96844375	6,30582	0,736091	-3,09873	5,99545	2,03E-09	1,23E-07
XLOC_008474	SLC30A7	chr1:101134219-101219899	4,62767	0,78596	-2,55776	5,99219	2,07E-09	1,25E-07
XLOC_027169	DAAM1	chr14:58725104-58907589	5,48822	1,27133	-2,11	5,98246	2,20E-09	1,32E-07
XLOC_007667	ZNF33B	chr10:42404560-42454300	3,28524	0,279868	-3,55318	5,981	2,22E-09	1,33E-07
XLOC_024656	TERF1	chr8:74083455-74122541	6,89975	1,26827	-2,44368	5,98007	2,23E-09	1,34E-07
XLOC_006778	SEPT7P2	chr7:45729910-45775146	5,61831	1,05118	-2,41813	5,97498	2,30E-09	1,38E-07
XLOC_009191	SCP2	chr1:53165488-53289877	42,2352	7,59883	-2,4746	5,97376	2,32E-09	1,38E-07
XLOC_002254	UGCG	chr9:113697142-113737472	48,753	7,33763	-2,73211	5,97115	2,36E-09	1,40E-07
XLOC_000556	TMEM126B	chr11:85017269-85025231	23,2548	3,72348	-2,6428	5,96784	2,40E-09	1,43E-07
XLOC_033978	ZNF432	chr19:57226511-57248285	2,95041	0,56841	-2,37591	5,96725	2,41E-09	1,43E-07
XLOC_008711	FAM111B	chr11:58631233-58651464	18,7043	1,18955	-3,97489	5,94731	2,73E-09	1,60E-07
XLOC_012931	HECTD2	chr10:93056698-93361197	5,88659	0,825768	-2,83362	5,94281	2,80E-09	1,65E-07
XLOC_004054	AHCTF1	chr1:245069024-245162107	8,95125	1,49634	-2,58065	5,94165	2,82E-09	1,65E-07
XLOC_002067	ODF2L	chr1:86584525-86634739	5,33506	0,975548	-2,45122	5,93412	2,95E-09	1,72E-07
XLOC_027311	ATP7A	chrX:77052787-77192548	3,42716	0,749108	-2,19377	5,91072	3,41E-09	1,95E-07
XLOC_008625	ZNF25	chr10:38278800-38305567	1,73795	0,115986	-3,90537	5,90721	3,48E-09	1,99E-07
XLOC_006020	CLIP1	chr12:121321933-121473105	22,1375	3,15577	-2,81043	5,89788	3,68E-09	2,09E-07
XLOC_034115	UEVLD	chr11:18507763-18569958	7,12635	1,41192	-2,3355	5,89493	3,75E-09	2,13E-07
XLOC_000535	PIBF1	chr13:72180495-72488592	4,22882	0,163294	-4,69471	5,88332	4,02E-09	2,27E-07
XLOC_010981	C4orf21	chr4:113679937-113798191	3,86399	0,373109	-3,37242	5,87735	4,17E-09	2,35E-07
XLOC_017779	GCC2	chr2:108432008-108494638	4,63189	0,323953	-3,83774	5,87627	4,20E-09	2,35E-07
XLOC_023080	ZNF615	chr19:57186398-57203295	1,98403	0,145253	-3,7718	5,87598	4,20E-09	2,35E-07
XLOC_009188	PIK3CA	chr3:180348766-180435191	9,01376	0,989028	-3,18805	5,87468	4,24E-09	2,37E-07
XLOC_024745	STXBP3	chr1:109090754-109153671	10,3691	1,01267	-3,35604	5,86411	4,52E-09	2,51E-07
XLOC_026183	CCNE2	chr8:95904266-95977369	12,3524	1,16008	-3,41248	5,84942	4,93E-09	2,73E-07
XLOC_010426	ZBTB1	chr14:64041044-64070161	10,228	2,04493	-2,3224	5,84937	4,93E-09	2,73E-07
XLOC_005623	ZNF643	chr1:40688333-40705116	2,34132	0,227061	-3,36617	5,84899	4,95E-09	2,73E-07
XLOC_018341	SAMD8	chr10:76541064-76611887	8,3057	1,17172	-2,82547	5,84698	5,01E-09	2,76E-07
XLOC_008723	FAM126B	chr2:201546685-201644641	1,86753	0,241958	-2,94831	5,84458	5,08E-09	2,79E-07
XLOC_027809	XRN1	chr3:143508138-143649607	5,99704	0,919392	-2,7055	5,84383	5,10E-09	2,80E-07
XLOC_031443	CD46	chr1:205992005-206035484	51,3583	12,561	-2,03165	5,8432	5,12E-09	2,80E-07
XLOC_022298	USP1	chr1:62672763-62690732	37,1951	4,2738	-3,12152	5,84124	5,18E-09	2,83E-07

XLOC_025997	SNX16	chr8:82874372-82917076	2,83321	0,476214	-2,57276	5,84128	5,18E-09	2,83E-07
XLOC_012977	ULBP3	chr6:150425938-150432070	7,81137	1,04007	-2,90889	5,84012	5,22E-09	2,84E-07
XLOC_006017	HS2ST1	chr1:87152894-87348269	22,3172	3,87478	-2,52597	5,83932	5,24E-09	2,85E-07
XLOC_025958	PIK3C2A	chr11:17064699-17186092	10,8986	0,919315	-3,56743	5,8271	5,64E-09	3,05E-07
XLOC_022553	ZNF121	chr19:9532048-9556209	3,20819	0,276335	-3,53727	5,82386	5,75E-09	3,10E-07
XLOC_033973	PIGA	chrX:15247493-15263597	2,52161	0,39732	-2,66597	5,82373	5,75E-09	3,10E-07
XLOC_010541	SLMAP	chr3:57713950-57889934	13,782	2,60869	-2,40139	5,81906	5,92E-09	3,18E-07
XLOC_004281	C6orf120	chr6:169844143-169868113	13,9905	2,02243	-2,79028	5,81663	6,00E-09	3,22E-07
XLOC_006787	TTC37	chr5:94825354-94916465	22,0525	1,98405	-3,47443	5,81197	6,17E-09	3,30E-07
XLOC_009613	ZFP30	chr19:42815228-42838537	2,67291	0,631516	-2,08152	5,81021	6,24E-09	3,33E-07
XLOC_001694	RAB11FIP2	chr10:119754416-119959655	3,63212	0,670931	-2,43657	5,80816	6,32E-09	3,36E-07
XLOC_024302	CWC22	chr2:180517848-180580305	9,78324	0,90518	-3,43403	5,80631	6,39E-09	3,38E-07
XLOC_006856	MMS22L	chr6:97696757-97837879	10,5047	2,08653	-2,33185	5,80616	6,39E-09	3,38E-07
XLOC_025549	ESCO1	chr18:17363259-17434691	3,77155	0,199669	-4,23947	5,80372	6,49E-09	3,42E-07
XLOC_031390	ZNF24	chr18:31166175-31178834	10,8676	2,10734	-2,36654	5,7971	6,75E-09	3,55E-07
XLOC_018003	LACC1	chr13:43308423-43366068	2,49073	0,289304	-3,10591	5,78739	7,15E-09	3,75E-07
XLOC_014953	NADKD1	chr5:36228450-36278015	3,18559	0,620219	-2,36071	5,78192	7,39E-09	3,87E-07
XLOC_033580	ZNF642	chr1:40715087-40746936	1,24584	0,185983	-2,74387	5,77792	7,56E-09	3,96E-07
XLOC_000992	CENPC1	chr4:68013098-68093884	4,76807	0,51528	-3,20998	5,76753	8,04E-09	4,19E-07
XLOC_017661	KIAA1430	chr4:186317812-186362176	6,99874	1,08544	-2,68881	5,75911	8,46E-09	4,40E-07
XLOC_003415	LOC401397	chr7:112544008-112545873	15,3289	1,83147	-3,06518	5,75713	8,56E-09	4,44E-07
XLOC_007410	LARP1B	chr4:129201608-129363486	7,78209	1,77508	-2,13227	5,74835	9,01E-09	4,66E-07
XLOC_018278	SEMA3D	chr7:84462807-84654416	1,71002	0,151362	-3,49794	5,74792	9,03E-09	4,66E-07
XLOC_006045	MED13	chr17:57374747-57497453	14,294	2,89882	-2,30187	5,74713	9,08E-09	4,67E-07
XLOC_024391	C1GALT1	chr7:7188740-7265378	11,3067	1,14495	-3,30383	5,74386	9,25E-09	4,76E-07
XLOC_025918	THAP5	chr7:107989120-108002530	5,21004	0,593937	-3,13291	5,74009	9,46E-09	4,84E-07
XLOC_025389	KRR1	chr12:74160779-74191705	12,212	1,01673	-3,58628	5,73914	9,52E-09	4,86E-07
XLOC_003797	TMTC3	chr12:87060203-87117795	9,57059	0,527813	-4,18051	5,7331	9,86E-09	5,01E-07
XLOC_023218	NCAM2	chr21:21292494-21834728	3,81258	0,669011	-2,51067	5,73308	9,86E-09	5,01E-07
XLOC_004267	C5orf41	chr5:172415960-172498968	2,06061	0,321269	-2,68122	5,73095	9,99E-09	5,06E-07
XLOC_022258	RUNX2	chr6:44884882-45626797	2,13165	0,474112	-2,16867	5,73073	1,00E-08	5,06E-07
XLOC_027865	LARP4	chr12:49080858-49160056	18,8278	3,83055	-2,29724	5,72821	1,01E-08	5,12E-07
XLOC_003816	ZNF100	chr19:21698682-21742270	1,56323	0,130462	-3,58283	5,7267	1,02E-08	5,15E-07
XLOC_010324	SCG5	chr15:30682599-30776590	34,9526	6,58643	-2,40783	5,72521	1,03E-08	5,19E-07

XLOC_005153	NFYB	chr12:103034987-103056170	7,86674	1,29694	-2,60065	5,71508	1,10E-08	5,49E-07
XLOC_010421	ARHGAP42	chr11:100062335-100369876	3,60842	0,663787	-2,44257	5,7137	1,11E-08	5,52E-07
XLOC_018890	FAS	chr10:90684810-90766622	7,08904	1,26545	-2,48594	5,71308	1,11E-08	5,53E-07
XLOC_018440	WDFY1	chr2:224448308-224518296	20,889	4,68247	-2,1574	5,71287	1,11E-08	5,53E-07
XLOC_022487	GALNT1	chr18:31415808-31545796	17,5946	1,61548	-3,44509	5,71114	1,12E-08	5,57E-07
XLOC_005420	SUZ12	chr17:27288011-27352170	24,0491	2,86677	-3,06848	5,7011	1,19E-08	5,89E-07
XLOC_012989	BACH1	chr21:29593090-30234153	12,0063	2,16467	-2,47157	5,69194	1,26E-08	6,20E-07
XLOC_006054	MAN2A1	chr5:109049179-109232887	13,6632	2,14636	-2,67033	5,68856	1,28E-08	6,32E-07
XLOC_009681	ZNF529	chr19:41726356-41788018	2,57812	0,460226	-2,4859	5,68533	1,31E-08	6,41E-07
XLOC_025486	ARID4A	chr14:57834974-57910204	3,49203	0,248425	-3,81319	5,68427	1,31E-08	6,44E-07
XLOC_033579	NUCB2	chr11:17254825-17315655	27,9556	5,64116	-2,30907	5,68074	1,34E-08	6,56E-07
XLOC_020878	NEK2	chr1:209898221-209915612	29,6585	6,1726	-2,2645	5,6797	1,35E-08	6,58E-07
XLOC_029102	PRKRIR	chr11:75738621-75783708	26,2735	5,52979	-2,24831	5,67704	1,37E-08	6,67E-07
XLOC_023999	PRPF40A	chr2:153216352-153327119	23,2076	2,48257	-3,22469	5,67435	1,39E-08	6,76E-07
XLOC_026020	CEP55	chr10:95246358-95278839	60,4024	9,35431	-2,6909	5,6681	1,44E-08	6,99E-07
XLOC_018274	ZNF502	chr3:44729138-44740327	2,07083	0,358546	-2,52998	5,66732	1,45E-08	7,01E-07
XLOC_034278	DIAPH3	chr13:59137723-59636120	44,2224	7,44981	-2,5695	5,66595	1,46E-08	7,05E-07
XLOC_014757	PABPC4L	chr4:135282973-135342492	3,7079	0,566798	-2,7097	5,66483	1,47E-08	7,09E-07
XLOC_024289	DCUN1D4	chr4:52404032-52477760	6,91885	0,7375	-3,22982	5,66395	1,48E-08	7,11E-07
XLOC_027951	ALCAM	chr3:106568246-106778447	18,1395	2,50026	-2,85899	5,66359	1,48E-08	7,11E-07
XLOC_018388	CCDC122	chr13:43308423-43366068	2,87043	0,61995	-2,21104	5,65775	1,53E-08	7,32E-07
XLOC_026029	DBT	chr1:100371293-100487999	3,49549	0,308771	-3,50088	5,65732	1,54E-08	7,32E-07
XLOC_007378	C10orf118	chr10:115871138-115924354	2,86755	0,189956	-3,91608	5,64972	1,61E-08	7,63E-07
XLOC_022531	PLDN	chr15:43665437-43689201	15,343	1,68846	-3,18381	5,64174	1,68E-08	7,98E-07
XLOC_005319	APC	chr5:112071100-112209835	5,47889	0,925967	-2,56485	5,63854	1,71E-08	8,11E-07
XLOC_006064	DYNC2H1	chr11:102485369-102855801	3,78339	0,447694	-3,0791	5,63747	1,73E-08	8,15E-07
XLOC_024710	ZMYM1	chr1:35317558-35355130	7,33378	1,26186	-2,539	5,63339	1,77E-08	8,33E-07
XLOC_013205	NEMF	chr14:49320281-49389312	9,34586	0,829773	-3,49354	5,62546	1,85E-08	8,69E-07
XLOC_017992	LTN1	chr21:29222336-29287148	7,87374	0,720807	-3,44936	5,62333	1,87E-08	8,78E-07
XLOC_024474	ZNF23	chr16:70039003-70053638	3,07146	0,517264	-2,56995	5,62256	1,88E-08	8,81E-07
XLOC_007066	ARHGAP5	chr14:31615956-31698685	7,83635	0,845466	-3,21236	5,59831	2,16E-08	1,01E-06
XLOC_002142	EVI5	chr1:92746840-93030549	5,66957	0,602238	-3,23483	5,59309	2,23E-08	1,03E-06
XLOC_002314	ASPM	chr1:195319879-195382447	15,8212	0,967066	-4,0321	5,58783	2,30E-08	1,06E-06
XLOC_033569	ZNF182	chrX:47719193-47748361	2,12491	0,42474	-2,32275	5,58208	2,38E-08	1,09E-06

XLOC_003788	TMEM41B	chr11:9258777-9292872	17,7615	2,91845	-2,60548	5,57958	2,41E-08	1,11E-06
XLOC_026262	ZNF92	chr7:64476202-64503433	2,33393	0,213457	-3,45075	5,57643	2,46E-08	1,12E-06
XLOC_027416	XRCC2	chr7:151970140-152004212	9,89675	1,62057	-2,61045	5,56961	2,55E-08	1,16E-06
XLOC_017818	SMURF2	chr17:59969091-60088927	12,6156	3,078	-2,03515	5,56803	2,58E-08	1,17E-06
XLOC_031360	ATM	chr11:107598738-107745036	7,10887	0,819681	-3,11649	5,56738	2,59E-08	1,17E-06
XLOC_027383	U2SURP	chr3:144202376-144262257	16,9922	2,96996	-2,51636	5,5674	2,59E-08	1,17E-06
XLOC_005256	SPG20	chr13:35773774-35842780	18,6061	4,07436	-2,19113	5,55775	2,73E-08	1,23E-06
XLOC_024512	ZNF286A	chr17:15543615-15564825	4,59255	0,903003	-2,34649	5,55638	2,75E-08	1,24E-06
XLOC_017847	ERGIC2	chr12:29193255-29425463	21,5949	1,88414	-3,51871	5,5438	2,96E-08	1,32E-06
XLOC_000646	NIN	chr14:50256230-50368757	19,094	2,91929	-2,70943	5,54408	2,95E-08	1,32E-06
XLOC_033798	ARID4B	chr1:233396832-233558155	8,5456	0,659134	-3,69654	5,54197	2,99E-08	1,33E-06
XLOC_029415	IFRD1	chr7:111850434-111918179	14,47	2,23322	-2,69586	5,53802	3,06E-08	1,36E-06
XLOC_007044	PHF14	chr7:10979964-11175775	10,3967	1,83178	-2,50481	5,53808	3,06E-08	1,36E-06
XLOC_011608	MRPL42	chr12:92385396-92421696	16,9402	4,21078	-2,00829	5,53567	3,10E-08	1,38E-06
XLOC_029999	N4BP2L2	chr13:31904929-32011293	15,1471	2,26248	-2,74306	5,52703	3,26E-08	1,44E-06
XLOC_024294	TRIM2	chr4:154293719-154479924	4,68746	0,774357	-2,59774	5,52331	3,33E-08	1,47E-06
XLOC_024059	PDE5A	chr4:120595348-120769429	1,83084	0,306461	-2,57873	5,52138	3,36E-08	1,48E-06
XLOC_025398	NMD3	chr3:162421761-162452772	11,2327	1,46572	-2,93802	5,51682	3,45E-08	1,52E-06
XLOC_024208	CCDC41	chr12:93226186-93377895	2,58358	0,348563	-2,88988	5,51372	3,51E-08	1,54E-06
XLOC_017945	PTAR1	chr9:71514257-71564740	5,20063	0,580985	-3,16211	5,51262	3,54E-08	1,55E-06
XLOC_030871	BRIP1	chr17:57111328-57295741	7,38207	1,16877	-2,65904	5,50659	3,66E-08	1,59E-06
XLOC_000942	DCUN1D1	chr3:184142016-184181890	7,17773	0,785315	-3,19218	5,49777	3,85E-08	1,67E-06
XLOC_007375	MAP3K2	chr2:127772714-127872711	5,5853	0,622246	-3,16608	5,4789	4,28E-08	1,85E-06
XLOC_017636	G2E3	chr14:30097208-30159736	6,58733	0,545984	-3,59276	5,47684	4,33E-08	1,87E-06
XLOC_009146	RNMT	chr18:13716703-13754554	10,8109	2,03261	-2,41108	5,47643	4,34E-08	1,87E-06
XLOC_017989	RMI1	chr9:85785456-85808807	6,32763	0,704599	-3,16679	5,47196	4,45E-08	1,91E-06
XLOC_005960	SAMD9	chr7:92566761-92585272	4,57454	0,332041	-3,78419	5,46063	4,74E-08	2,03E-06
XLOC_003973	ANUBL1	chr10:45431044-45488257	1,09062	0,217658	-2,32502	5,45188	4,98E-08	2,13E-06
XLOC_001081	CXorf23	chrX:19840900-19919092	1,73954	0,309038	-2,49285	5,44195	5,27E-08	2,25E-06
XLOC_031248	ZC3H12C	chr11:109468616-109547776	1,60722	0,313661	-2,35729	5,43353	5,53E-08	2,34E-06
XLOC_025476	NIPAL1	chr4:47713097-47736309	1,79927	0,337572	-2,41415	5,4294	5,65E-08	2,39E-06
XLOC_024659	DNA2	chr10:69843826-69903319	7,61918	1,55645	-2,29137	5,42633	5,75E-08	2,43E-06
XLOC_002252	FKBP14	chr7:30011585-30033409	28,4037	5,69421	-2,31851	5,41877	6,00E-08	2,53E-06
XLOC_001672	RGPD5	chr2:109907623-109972571	2,19889	0,363193	-2,59796	5,41697	6,06E-08	2,55E-06

XLOC_017649	GPATCH2	chr1:215667707-215871057	7,96764	1,77071	-2,16983	5,41653	6,08E-08	2,55E-06
XLOC_030099	GTPBP10	chr7:89813914-89858919	2,06397	0,222122	-3,216	5,41447	6,15E-08	2,57E-06
XLOC_032714	MIER3	chr5:56240843-56285800	6,00665	0,946436	-2,66598	5,41177	6,24E-08	2,61E-06
XLOC_023234	BCAT1	chr12:24854224-24993690	11,9016	1,91132	-2,63852	5,40906	6,34E-08	2,65E-06
XLOC_029872	CCT6P3	chr7:64136166-64179104	1,29746	0,226003	-2,52128	5,40847	6,36E-08	2,65E-06
XLOC_025403	IFT88	chr13:20039207-20163576	4,34069	0,882358	-2,29849	5,40828	6,36E-08	2,65E-06
XLOC_029079	ALG10B	chr12:36996781-37009795	1,00526	0,125897	-2,99725	5,40671	6,42E-08	2,66E-06
XLOC_029921	HIPK3	chr11:33234594-33335143	15,1174	2,65315	-2,51043	5,40691	6,41E-08	2,66E-06
XLOC_025665	RTKN2	chr10:63612802-63698639	3,78337	0,597478	-2,66271	5,40353	6,53E-08	2,70E-06
XLOC_006652	CLGN	chr4:141527901-141568560	2,78124	0,165895	-4,06738	5,38365	7,30E-08	3,01E-06
XLOC_018731	DMTF1	chr7:86619612-86687803	11,6507	2,32803	-2,32324	5,37805	7,53E-08	3,09E-06
XLOC_025876	CCDC66	chr3:56566223-56693633	3,77042	0,331909	-3,50586	5,3771	7,57E-08	3,10E-06
XLOC_010710	CACNA2D1	chr7:81415242-81911198	2,75513	0,394463	-2,80416	5,37307	7,74E-08	3,16E-06
XLOC_002133	ZNF26	chr12:132073005-132099226	3,01268	0,545164	-2,46628	5,36328	8,17E-08	3,33E-06
XLOC_017958	ELK3	chr12:95112260-95188254	20,6477	3,72556	-2,47045	5,35854	8,39E-08	3,40E-06
XLOC_000623	CENPJ	chr13:24354411-24395119	6,38357	1,18247	-2,43255	5,35857	8,39E-08	3,40E-06
XLOC_025636	KLHL24	chr3:184834935-184884998	2,62288	0,462202	-2,50455	5,35152	8,72E-08	3,52E-06
XLOC_008534	FANCM	chr14:44674879-44739994	2,37685	0,163511	-3,86159	5,33945	9,32E-08	3,73E-06
XLOC_005998	DISC1	chr1:229730784-230243641	16,5832	2,89886	-2,51616	5,33541	9,53E-08	3,80E-06
XLOC_022866	ZNF569	chr19:42593784-42650810	1,39083	0,116639	-3,57582	5,33368	9,62E-08	3,83E-06
XLOC_029125	FAM135A	chr6:71179817-71327598	1,99461	0,333516	-2,58027	5,33333	9,64E-08	3,83E-06
XLOC_005313	C6orf204	chr6:118888627-119137931	2,25412	0,443539	-2,34543	5,32954	9,85E-08	3,89E-06
XLOC_025521	TICAM2	chr5:114942237-114989775	21,6522	3,51901	-2,62127	5,32909	9,87E-08	3,89E-06
XLOC_006009	UGGT2	chr13:95251836-95503737	7,63682	0,819104	-3,22085	5,31889	1,04E-07	4,11E-06
XLOC_006779	KIF20B	chr10:91451346-91524680	10,515	0,714766	-3,87884	5,31835	1,05E-07	4,12E-06
XLOC_024664	LRIF1	chr1:111291334-111308661	8,92202	2,13633	-2,06223	5,31428	1,07E-07	4,20E-06
XLOC_032272	LMAN1	chr18:55146035-55177622	56,8658	10,1957	-2,47961	5,31017	1,10E-07	4,29E-06
XLOC_001847	LOC100294145	chr6:32969930-32979513	10,3274	2,1425	-2,26912	5,30686	1,12E-07	4,35E-06
XLOC_005651	ZNF260	chr19:41693428-41711088	3,53336	0,277801	-3,66892	5,30225	1,14E-07	4,45E-06
XLOC_018291	FAM91A1	chr8:124849606-124896871	12,2311	2,05731	-2,57172	5,30212	1,14E-07	4,45E-06
XLOC_003430	C5orf44	chr5:64919949-65053697	8,97026	1,43619	-2,6429	5,30007	1,16E-07	4,49E-06
XLOC_023948	POT1	chr7:124248478-124357344	6,38064	0,693068	-3,20263	5,29616	1,18E-07	4,57E-06
XLOC_018260	SREK1	chr5:65475840-65512470	18,0474	1,96555	-3,19879	5,29383	1,20E-07	4,62E-06
XLOC_007059	PPP1R2	chr3:196722509-196752811	14,6655	2,66005	-2,4629	5,28877	1,23E-07	4,74E-06

XLOC_018019	QSER1	chr11:32870937-32958390	10,4621	1,86331	-2,48924	5,28772	1,24E-07	4,76E-06
XLOC_018802	DNAJB14	chr4:101036625-101086902	8,6619	0,910757	-3,24955	5,27901	1,30E-07	4,98E-06
XLOC_009655	FAM161A	chr2:61905486-61935750	4,66549	0,787389	-2,56688	5,27897	1,30E-07	4,98E-06
XLOC_024222	TMF1	chr3:69151667-69184174	9,86397	0,684118	-3,84985	5,27664	1,32E-07	5,04E-06
XLOC_022305	SMCHD1	chr18:2645685-2795015	15,0781	1,69341	-3,15446	5,27336	1,34E-07	5,11E-06
XLOC_001740	TLR3	chr4:187227210-187246404	3,15177	0,3923	-3,00614	5,268	1,38E-07	5,26E-06
XLOC_010714	KIF14	chr1:198787247-198856485	9,33622	0,652904	-3,8379	5,26002	1,44E-07	5,47E-06
XLOC_018032	TGFBR1	chr9:100906283-100956294	12,2167	1,49188	-3,03366	5,26013	1,44E-07	5,47E-06
XLOC_029113	UPF3B	chrX:118848736-118871119	10,1835	0,871832	-3,54605	5,25568	1,47E-07	5,58E-06
XLOC_022525	PSD3	chr8:18429092-18915476	5,67783	1,12499	-2,33543	5,25442	1,48E-07	5,60E-06
XLOC_024424	SMC5	chr9:72063697-72159609	7,78751	0,553886	-3,8135	5,25343	1,49E-07	5,63E-06
XLOC_005150	PPP1R12A	chr12:78691473-78855369	22,4537	2,61813	-3,10035	5,24969	1,52E-07	5,73E-06
XLOC_027866	C4orf33	chr4:130234278-130253293	4,62036	0,601414	-2,94158	5,24986	1,52E-07	5,73E-06
XLOC_034272	C3orf63	chr3:56566223-56693633	9,63139	1,07373	-3,16511	5,24687	1,55E-07	5,80E-06
XLOC_017630	CCDC138	chr2:108769650-108859279	4,80492	0,67225	-2,83744	5,23023	1,69E-07	6,29E-06
XLOC_029679	GULP1	chr2:188864076-189168897	3,06385	0,539361	-2,50602	5,22916	1,70E-07	6,32E-06
XLOC_016426	ZNF91	chr19:23283170-23370276	1,64883	0,146677	-3,49073	5,22531	1,74E-07	6,43E-06
XLOC_024212	PLS3	chrX:114701432-114791435	82,3929	18,0718	-2,18878	5,22449	1,75E-07	6,45E-06
XLOC_024553	MIS18BP1	chr14:44741501-44792669	12,4042	0,892378	-3,79703	5,21248	1,86E-07	6,85E-06
XLOC_032068	LYRM7	chr5:130534539-130569018	2,53934	0,184669	-3,78144	5,21279	1,86E-07	6,85E-06
XLOC_023255	IFT74	chr9:26893367-27052931	5,55274	0,464432	-3,57966	5,21262	1,86E-07	6,85E-06
XLOC_032317	INTS2	chr17:57297509-57360199	3,59324	0,630575	-2,51054	5,20873	1,90E-07	6,98E-06
XLOC_024605	RIOK2	chr5:96522326-96544761	6,34046	1,33573	-2,24696	5,20254	1,97E-07	7,20E-06
XLOC_029482	CEBPZ	chr2:37277120-37312244	21,853	1,57297	-3,79627	5,20065	1,99E-07	7,24E-06
XLOC_012983	DOCK10	chr2:225338050-225615574	3,38223	0,763518	-2,14724	5,19775	2,02E-07	7,34E-06
XLOC_025321	CCDC90B	chr11:82649761-82675298	19,426	3,7552	-2,37102	5,19326	2,07E-07	7,50E-06
XLOC_024473	CWF19L2	chr11:106702281-106833782	5,92334	0,439107	-3,75377	5,19126	2,09E-07	7,57E-06
XLOC_033904	ZNF594	chr17:5022884-5035902	3,10687	0,353125	-3,13721	5,18288	2,18E-07	7,90E-06
XLOC_004069	LRRC40	chr1:70383072-70443949	9,76715	0,730962	-3,74007	5,17664	2,26E-07	8,16E-06
XLOC_018275	NRIP1	chr21:15255426-15359450	6,33561	0,826537	-2,93833	5,17529	2,28E-07	8,20E-06
XLOC_000402	DNAJC10	chr2:183289025-183352575	30,271	3,71892	-3,02498	5,16973	2,34E-07	8,43E-06
XLOC_022468	ZNF10	chr12:132200236-132246122	1,6545	0,227523	-2,86231	5,16931	2,35E-07	8,44E-06
XLOC_008446	ZNF267	chr16:31792579-31836880	3,03419	0,222496	-3,76946	5,16387	2,42E-07	8,67E-06
XLOC_034259	ZNF14	chr19:19682280-19704921	1,67331	0,0896621	-4,22207	5,16007	2,47E-07	8,83E-06

XLOC_017905	TRIM33	chr1:114736921-114855304	8,19031	1,77283	-2,20787	5,14566	2,67E-07	9,49E-06
XLOC_031469	SSFA2	chr2:182464692-182503709	26,6549	4,32869	-2,6224	5,14227	2,71E-07	9,65E-06
XLOC_006715	SNX13	chr7:17796909-17946656	6,14593	0,581317	-3,40223	5,1412	2,73E-07	9,69E-06
XLOC_005669	MOBK1A	chr4:71986927-72072755	4,46361	0,449149	-3,31295	5,14043	2,74E-07	9,71E-06
XLOC_025306	FAM76B	chr11:95141753-95162602	3,27841	0,424286	-2,94989	5,13766	2,78E-07	9,83E-06
XLOC_025432	ZRANB2	chr1:71090623-71319560	23,3611	3,73512	-2,64488	5,13633	2,80E-07	9,89E-06
XLOC_024463	AASDH	chr4:56899213-56950523	4,62312	1,04496	-2,14542	5,13169	2,87E-07	1,01E-05
XLOC_033622	BCLAF1	chr6:136619693-136653553	26,65	3,71622	-2,84223	5,13107	2,88E-07	1,01E-05
XLOC_029224	CPEB4	chr5:173247929-173319919	3,0027	0,579637	-2,37304	5,12586	2,96E-07	1,04E-05
XLOC_024005	ERAP2	chr5:96237399-96281162	21,08	3,69187	-2,51346	5,12485	2,98E-07	1,04E-05
XLOC_002287	CBR4	chr4:170145316-170168043	2,8723	0,586388	-2,29228	5,11637	3,11E-07	1,09E-05
XLOC_004907	SASS6	chr1:100321689-100371124	5,45891	0,54818	-3,31589	5,1151	3,14E-07	1,10E-05
XLOC_000564	TMEM106B	chr7:12217372-12243415	4,97434	0,687161	-2,85579	5,10807	3,25E-07	1,13E-05
XLOC_032331	ZNF268	chr12:132268067-132289534	5,34695	0,872532	-2,61544	5,1049	3,31E-07	1,15E-05
XLOC_024079	ZNF287	chr17:16394106-16413245	1,428	0,296625	-2,26729	5,10477	3,31E-07	1,15E-05
XLOC_025844	PMS1	chr2:190343237-190450600	5,53483	1,08712	-2,34803	5,10153	3,37E-07	1,17E-05
XLOC_024116	TRIM59	chr3:161457467-161650355	13,9916	1,64941	-3,08454	5,09741	3,44E-07	1,19E-05
XLOC_025384	OCLN	chr5:68823542-68891191	9,4278	1,51078	-2,64163	5,09497	3,49E-07	1,21E-05
XLOC_000898	BCCIP	chr10:127502093-127688151	44,8611	9,21432	-2,28351	5,09401	3,51E-07	1,21E-05
XLOC_008551	ZEB1	chr10:31648106-31858748	5,0333	0,70469	-2,83644	5,08027	3,77E-07	1,30E-05
XLOC_031510	UPF2	chr10:12002023-12125029	10,9729	1,56176	-2,8127	5,07718	3,83E-07	1,32E-05
XLOC_027890	SMC4	chr3:161457467-161650355	80,6347	7,07902	-3,50978	5,05571	4,29E-07	1,46E-05
XLOC_024750	PANK3	chr5:167908589-167940200	20,5312	4,03021	-2,34889	5,05359	4,34E-07	1,47E-05
XLOC_006999	ITGA4	chr2:182029863-182230079	5,70712	0,842749	-2,75959	5,05208	4,37E-07	1,48E-05
XLOC_020731	ZNF300	chr5:150253653-150264843	5,63887	0,756061	-2,89883	5,04756	4,47E-07	1,52E-05
XLOC_030018	ZNF441	chr19:11738814-11756673	1,85839	0,1666	-3,47959	5,04469	4,54E-07	1,53E-05
XLOC_002124	FRRS1	chr1:99945444-100004784	3,45768	0,328106	-3,39757	5,04432	4,55E-07	1,53E-05
XLOC_027988	RSF1	chr11:77048764-77261046	14,03	1,63046	-3,10517	5,04511	4,53E-07	1,53E-05
XLOC_027841	ANKIB1	chr7:91661471-91868634	15,9346	3,23603	-2,29987	5,04436	4,55E-07	1,53E-05
XLOC_022653	NAA15	chr4:140430520-140531385	17,8038	2,06413	-3,10858	5,03914	4,68E-07	1,56E-05
XLOC_024181	NXT2	chrX:108665665-108674583	3,53493	0,623397	-2,50346	5,03156	4,87E-07	1,62E-05
XLOC_020713	CCAR1	chr10:70150482-70222098	27,365	3,18872	-3,10128	5,02448	5,05E-07	1,67E-05
XLOC_017913	GMCL1	chr2:69910268-69961956	8,89726	1,83325	-2,27896	5,02038	5,16E-07	1,71E-05
XLOC_009196	EIF4E	chr4:100017595-100070809	4,0668	0,905953	-2,16638	5,01889	5,20E-07	1,72E-05

XLOC_026879	RAI14	chr5:34692189-34868474	51,3026	11,0031	-2,22112	5,01386	5,33E-07	1,76E-05
XLOC_027828	MAP4K5	chr14:49954960-50169534	12,9315	1,89353	-2,77174	5,00666	5,54E-07	1,82E-05
XLOC_017552	MNS1	chr15:54444889-54544636	5,88474	0,489629	-3,58722	4,98015	6,35E-07	2,08E-05
XLOC_018585	SMG1	chr16:18723675-18847035	11,2091	2,15475	-2,37907	4,98014	6,35E-07	2,08E-05
XLOC_033578	DNAJC2	chr7:102725108-102772556	12,4303	1,32551	-3,22925	4,97666	6,47E-07	2,11E-05
XLOC_009123	JAK2	chr9:4974805-5118183	1,57946	0,210883	-2,90492	4,96999	6,70E-07	2,18E-05
XLOC_007666	IMPA1	chr8:82731705-82761144	12,5793	2,73333	-2,20233	4,96847	6,75E-07	2,19E-05
XLOC_006820	ASNSD1	chr2:190234311-190243802	21,5803	2,72188	-2,98704	4,96751	6,78E-07	2,20E-05
XLOC_020726	JKAMP	chr14:59020913-59113302	13,5472	2,13249	-2,66738	4,96485	6,88E-07	2,22E-05
XLOC_006818	WRN	chr8:30972862-31150875	5,90176	1,09282	-2,43309	4,96322	6,93E-07	2,24E-05
XLOC_001668	DYNC2LI1	chr2:43854681-43890653	6,06946	1,46859	-2,04714	4,95986	7,05E-07	2,27E-05
XLOC_031447	PI4K2B	chr4:24844697-24890743	7,12103	1,22016	-2,54501	4,95774	7,13E-07	2,29E-05
XLOC_022536	SAMD12	chr8:119270875-119985229	2,06304	0,433623	-2,25026	4,95767	7,13E-07	2,29E-05
XLOC_027829	USP33	chr1:77934261-77998125	23,1481	5,30327	-2,12594	4,95396	7,27E-07	2,33E-05
XLOC_024714	ESF1	chr20:13641605-13747717	4,13815	0,363269	-3,50987	4,9413	7,76E-07	2,47E-05
XLOC_029423	CENPK	chr5:64849348-64894751	20,616	1,91118	-3,43123	4,94171	7,74E-07	2,47E-05
XLOC_007422	SWT1	chr1:183353840-183527536	2,28328	0,498504	-2,19543	4,93985	7,82E-07	2,48E-05
XLOC_020294	SLC39A6	chr18:31942491-32013416	20,665	2,94965	-2,80857	4,93901	7,85E-07	2,49E-05
XLOC_018622	NOC3L	chr10:95743590-96112723	10,1164	1,04177	-3,27959	4,92703	8,35E-07	2,63E-05
XLOC_018708	ZNF124	chr1:245382637-245402383	1,38138	0,119522	-3,53076	4,92521	8,43E-07	2,66E-05
XLOC_016526	ZNF404	chr19:49068354-49097799	1,29053	0,115472	-3,48234	4,92102	8,61E-07	2,70E-05
XLOC_022541	FOXN2	chr2:48395155-48459938	3,48414	0,616928	-2,49763	4,91729	8,78E-07	2,75E-05
XLOC_008626	MALAT1	chr11:65021808-65030515	26,1623	3,11694	-3,06929	4,91508	8,87E-07	2,77E-05
XLOC_006049	ANKRD32	chr5:93980146-94057329	6,48304	0,553706	-3,54948	4,91462	8,90E-07	2,78E-05
XLOC_033826	C12orf4	chr12:4467155-4518152	10,199	1,41196	-2,85266	4,9127	8,98E-07	2,80E-05
XLOC_027213	TBX18	chr6:85499797-85531445	1,57521	0,381947	-2,0441	4,91103	9,06E-07	2,82E-05
XLOC_032698	RDX	chr11:109557601-109672902	40,3417	7,08513	-2,50941	4,91054	9,08E-07	2,82E-05
XLOC_024150	ALG11	chr13:51484514-51505737	9,70925	1,90077	-2,35278	4,91076	9,07E-07	2,82E-05
XLOC_003707	DDX18	chr2:118288715-118308820	34,7496	7,57249	-2,19815	4,89769	9,70E-07	3,00E-05
XLOC_002241	KIF3A	chr5:132056221-132101164	3,253	0,333501	-3,286	4,89546	9,81E-07	3,03E-05
XLOC_029989	ROCK1	chr18:16783700-16945810	16,795	1,73433	-3,27559	4,89409	9,88E-07	3,04E-05
XLOC_031365	PKN2	chr1:88922509-89074526	15,9006	1,86608	-3,091	4,89337	9,91E-07	3,05E-05
XLOC_024283	JRKL	chr11:95762805-95766375	4,07148	0,715609	-2,50831	4,8928	9,94E-07	3,06E-05
XLOC_010388	CENPQ	chr6:49539027-49571458	16,7801	1,63945	-3,35546	4,89244	9,96E-07	3,06E-05

XLOC_030994	CD58	chr1:116858678-116915238	10,7575	1,95427	-2,46063	4,89079	1,00E-06	3,08E-05
XLOC_007430	SRP9	chr1:224032137-224044791	61,3214	11,6684	-2,39378	4,88804	1,02E-06	3,12E-05
XLOC_020274	GALNT3	chr2:166312558-166359535	2,06501	0,416924	-2,30829	4,88802	1,02E-06	3,12E-05
XLOC_025846	CCDC82	chr11:95725576-95762731	14,0718	1,55176	-3,18083	4,88526	1,03E-06	3,16E-05
XLOC_034072	ZFP112	chr19:49522545-49552696	2,27773	0,285051	-2,9983	4,8829	1,05E-06	3,19E-05
XLOC_007658	FSD1L	chr9:107250135-107351862	1,18194	0,0791248	-3,90089	4,88265	1,05E-06	3,19E-05
XLOC_010626	C14orf135	chr14:59628063-59671285	17,6779	4,36796	-2,01692	4,87554	1,09E-06	3,29E-05
XLOC_022357	RPAP3	chr12:46340765-46411072	10,9589	1,28404	-3,09335	4,86946	1,12E-06	3,38E-05
XLOC_014725	ZNF181	chr19:39916120-39926053	1,77282	0,268101	-2,7252	4,86091	1,17E-06	3,52E-05
XLOC_001085	SSPN	chr12:26239535-26278975	1,55732	0,353037	-2,14117	4,85848	1,18E-06	3,55E-05
XLOC_003630	SUCLA2	chr13:47414791-47473487	17,188	1,82759	-3,23339	4,85657	1,19E-06	3,58E-05
XLOC_007408	TMED5	chr1:93387886-93418834	11,9186	1,55104	-2,9419	4,85346	1,21E-06	3,63E-05
XLOC_024568	GAN	chr16:79904444-79977302	1,14101	0,225312	-2,34031	4,85262	1,22E-06	3,65E-05
XLOC_030795	CDC14A	chr1:100590610-100758421	1,59323	0,255963	-2,63795	4,85082	1,23E-06	3,67E-05
XLOC_033558	RAB18	chr10:27832856-27898768	34,6454	7,00365	-2,30649	4,85111	1,23E-06	3,67E-05
XLOC_009661	GPCPD1	chr20:5473009-5539688	5,30457	1,2175	-2,12331	4,84841	1,24E-06	3,71E-05
XLOC_008394	LPGAT1	chr1:209983421-210070819	10,1351	1,43945	-2,81577	4,84356	1,28E-06	3,78E-05
XLOC_032330	FAM82A1	chr2:38001430-38147789	1,93843	0,276159	-2,81131	4,84046	1,30E-06	3,84E-05
XLOC_017932	MARCH6	chr2:160276925-160469513	23,5371	3,64157	-2,69231	4,83138	1,36E-06	4,00E-05
XLOC_000899	C15orf29	chr15:32219929-32289589	3,2776	0,68437	-2,25979	4,83086	1,36E-06	4,01E-05
XLOC_017642	AGL	chr1:100088220-100162167	5,66924	0,875826	-2,69444	4,82882	1,37E-06	4,04E-05
XLOC_022346	BDNF	chr11:27484974-27700181	7,37858	1,56506	-2,23713	4,82883	1,37E-06	4,04E-05
XLOC_022537	THUMPDI	chr16:20652489-20661035	10,0628	1,33024	-2,91927	4,82795	1,38E-06	4,05E-05
XLOC_024496	ELMOD2	chr4:141664741-141694374	4,46951	0,578868	-2,94881	4,82693	1,39E-06	4,06E-05
XLOC_022713	TMEM188	chr16:48616613-48628500	8,20034	1,25316	-2,71011	4,82688	1,39E-06	4,06E-05
XLOC_023171	USP25	chr21:16024366-16174248	11,6686	2,52354	-2,20911	4,81517	1,47E-06	4,30E-05
XLOC_018000	ZNF708	chr19:21265802-21304052	1,65314	0,13403	-3,62459	4,81206	1,49E-06	4,35E-05
XLOC_009643	ZNF184	chr6:27525810-27549330	5,09163	0,882904	-2,5278	4,80739	1,53E-06	4,45E-05
XLOC_027239	RAB33B	chr4:140593735-140616519	4,22324	0,601369	-2,81203	4,80386	1,56E-06	4,52E-05
XLOC_004110	RAD51AP1	chr12:4518210-4539474	20,3879	2,1979	-3,21352	4,80273	1,57E-06	4,53E-05
XLOC_018044	PSMC6	chr14:52243630-52264466	24,2901	4,27967	-2,5048	4,78986	1,67E-06	4,82E-05
XLOC_023049	ZDHHC17	chr12:75681984-75771605	7,64502	0,975235	-2,9707	4,78484	1,71E-06	4,92E-05
XLOC_003922	MFSD8	chr4:129058409-129176541	3,35523	0,649089	-2,36992	4,78466	1,71E-06	4,92E-05
XLOC_027513	USP44	chr12:94434479-94469394	1,77273	0,378601	-2,22722	4,78263	1,73E-06	4,96E-05

XLOC_007685	KIAA1826	chr11:105372237-105398332	7,53203	1,75256	-2,10357	4,78162	1,74E-06	4,98E-05
XLOC_007080	C9orf102	chr9:97608190-97820443	4,73778	0,904837	-2,38848	4,78136	1,74E-06	4,98E-05
XLOC_027201	HAT1	chr2:172487180-172556846	56,0287	6,29445	-3,15401	4,77438	1,80E-06	5,12E-05
XLOC_014816	RPGR	chrX:38013366-38071732	1,34334	0,167264	-3,00563	4,76902	1,85E-06	5,24E-05
XLOC_020863	CCDC112	chr5:114630783-114660357	2,46632	0,252879	-3,28584	4,76396	1,90E-06	5,36E-05
XLOC_006817	LRRC58	chr3:121506560-121550934	10,9961	1,87135	-2,55483	4,75749	1,96E-06	5,51E-05
XLOC_034075	HSPA4L	chr4:128922798-128975096	5,38614	0,743186	-2,85746	4,75602	1,97E-06	5,54E-05
XLOC_001683	TTC3P1	chrX:74877097-74879639	2,84498	0,242713	-3,55109	4,75519	1,98E-06	5,56E-05
XLOC_022919	ZNF430	chr19:20995265-21034692	2,71981	0,250901	-3,43832	4,75408	1,99E-06	5,58E-05
XLOC_025384	NAA25	chr12:110948875-111032160	6,63787	1,38599	-2,2598	4,75091	2,03E-06	5,65E-05
XLOC_024108	SEMA3A	chr7:83423171-83662388	4,41676	0,626241	-2,8182	4,74952	2,04E-06	5,69E-05
XLOC_025367	EFHA2	chr8:16928459-17051517	1,61977	0,20847	-2,95788	4,74865	2,05E-06	5,71E-05
XLOC_006994	NUDT12	chr5:102912454-102926389	2,16726	0,234069	-3,21087	4,7371	2,17E-06	6,00E-05
XLOC_031268	RASA1	chr5:86599906-86745221	13,2641	2,63783	-2,33011	4,73015	2,24E-06	6,19E-05
XLOC_032551	MEGF10	chr5:126653784-126824815	1,17615	0,291776	-2,01114	4,72943	2,25E-06	6,21E-05
XLOC_027926	ARRDC3	chr5:90700296-90928679	12,1333	1,118	-3,43999	4,72921	2,25E-06	6,21E-05
XLOC_029048	RBAK	chr7:5051977-5079380	3,24632	0,560978	-2,53279	4,72759	2,27E-06	6,25E-05
XLOC_018029	CCDC132	chr7:92699588-92828074	5,97487	0,556694	-3,42395	4,72613	2,29E-06	6,29E-05
XLOC_025497	FAM172A	chr5:92979186-93473160	5,74541	1,07657	-2,41597	4,72115	2,35E-06	6,43E-05
XLOC_022987	RPS6KA3	chrX:20077949-20194671	31,3507	6,8968	-2,1845	4,71428	2,43E-06	6,62E-05
XLOC_006786	SLC2A13	chr12:38435089-38786160	1,14791	0,1763	-2,7029	4,71222	2,45E-06	6,67E-05
XLOC_031437	SIKE1	chr1:115113627-115124831	8,20718	1,3397	-2,61498	4,71232	2,45E-06	6,67E-05
XLOC_006808	FAP	chr2:162735445-162808291	7,10049	1,03743	-2,7749	4,71011	2,48E-06	6,74E-05
XLOC_005671	C12orf23	chr12:105870141-105905217	19,5388	2,27057	-3,10521	4,70879	2,49E-06	6,77E-05
XLOC_018710	TAB3	chrX:30755479-30817566	4,71729	1,14457	-2,04315	4,70589	2,53E-06	6,86E-05
XLOC_011861	KATNAL1	chr13:29674548-29779584	5,59238	1,28788	-2,11846	4,7046	2,54E-06	6,89E-05
XLOC_024674	TIA1	chr2:70290079-70329347	14,587	3,04796	-2,25877	4,70241	2,57E-06	6,95E-05
XLOC_008604	STXBP5	chr6:147204217-147753305	5,60922	1,296	-2,11374	4,70209	2,58E-06	6,96E-05
XLOC_022001	FPGT	chr1:74436483-74782704	2,03255	0,250301	-3,02155	4,70019	2,60E-06	7,00E-05
XLOC_031430	CDC37L1	chr9:4669565-4698194	6,56654	0,743382	-3,14296	4,69845	2,62E-06	7,05E-05
XLOC_017921	ATG5	chr6:106738828-106880388	13,9731	2,75346	-2,34333	4,68659	2,78E-06	7,43E-05
XLOC_003940	EMB	chr5:49727089-49773549	8,3754	1,00697	-3,05614	4,68581	2,79E-06	7,45E-05
XLOC_008536	NSUN6	chr10:18469611-19006946	3,91436	0,470383	-3,05687	4,68558	2,79E-06	7,45E-05
XLOC_012283	ITGB1	chr10:33229251-33289423	322,583	46,1513	-2,80523	4,67857	2,89E-06	7,69E-05

XLOC_029997	CD2AP	chr6:47553483-47702955	8,83118	0,837521	-3,39841	4,67386	2,96E-06	7,86E-05
XLOC_000963	UBR3	chr2:170392165-170648885	6,69851	1,48599	-2,17242	4,66658	3,06E-06	8,12E-05
XLOC_005346	EFCAB7	chr1:63679028-63810952	2,67219	0,235225	-3,50591	4,65466	3,25E-06	8,53E-05
XLOC_034354	ZNF284	chr19:49268136-49285679	1,83521	0,366462	-2,32421	4,65332	3,27E-06	8,57E-05
XLOC_022729	GMFB	chr14:54010958-54025494	14,1601	1,35289	-3,38772	4,65111	3,30E-06	8,65E-05
XLOC_012223	CAMSAP1L1	chr1:198974622-199096456	11,6048	2,60574	-2,15496	4,65074	3,31E-06	8,66E-05
XLOC_024428	RBM34	chr1:233361120-233391194	19,3713	4,36422	-2,15012	4,65045	3,31E-06	8,66E-05
XLOC_003669	C16orf87	chr16:45393459-45422805	9,64754	1,86716	-2,36931	4,65005	3,32E-06	8,67E-05
XLOC_017811	KCTD3	chr1:213806937-213861772	16,8655	2,8251	-2,5777	4,64861	3,34E-06	8,71E-05
XLOC_022692	ANXA1	chr9:74956600-74975127	206,247	18,7964	-3,45584	4,64311	3,43E-06	8,92E-05
XLOC_032903	ZNF684	chr1:40769819-40786428	1,58986	0,103844	-3,93641	4,63988	3,49E-06	9,04E-05
XLOC_031425	YOD1	chr1:205283816-205291045	2,05791	0,20161	-3,35154	4,62731	3,70E-06	9,56E-05
XLOC_022366	KPNA5	chr6:117109059-117169723	2,83195	0,251674	-3,49217	4,625	3,75E-06	9,63E-05
XLOC_007156	UBA6	chr4:68163082-68249490	14,8999	1,67832	-3,15022	4,62315	3,78E-06	9,70E-05
XLOC_007654	NET1	chr10:5444517-5490426	21,819	4,63768	-2,23411	4,62088	3,82E-06	9,79E-05
XLOC_029968	FAM76A	chr1:27925076-27962010	5,29612	1,20994	-2,13	4,62084	3,82E-06	9,79E-05
XLOC_029146	APPL1	chr3:57235361-57301750	12,4592	2,98037	-2,06365	4,61708	3,89E-06	9,95E-05
XLOC_007237	ZZZ3	chr1:77798330-77921680	12,6815	1,56677	-3,01685	4,61513	3,93E-06	0,0001003
XLOC_007070	TAF1B	chr2:9900444-9996153	10,454	1,87227	-2,48119	4,6109	4,01E-06	0,000102
XLOC_022900	CCDC18	chr1:93418868-93516875	2,99828	0,296363	-3,3387	4,6095	4,04E-06	0,0001024
XLOC_026019	RCBTB1	chr13:49004082-49057729	14,6117	3,01373	-2,27751	4,60691	4,09E-06	0,0001036
XLOC_007424	TMEM161B	chr5:87526778-87600421	3,96686	0,387264	-3,35661	4,60467	4,13E-06	0,0001046
XLOC_018674	SLC4A7	chr3:27389217-27500892	2,76819	0,333269	-3,05418	4,60272	4,17E-06	0,0001054
XLOC_029065	CASC5	chr15:38673527-38742173	15,7487	1,9631	-3,00403	4,60057	4,21E-06	0,0001063
XLOC_010336	TRMT11	chr6:126349268-126402113	9,37202	1,38655	-2,75687	4,59663	4,29E-06	0,0001081
XLOC_023119	FAM102B	chr1:108904273-108983472	5,68173	0,734774	-2,95096	4,59505	4,33E-06	0,0001089
XLOC_032218	DEK	chr6:18263597-18372932	96,3918	8,0792	-3,57663	4,59366	4,36E-06	0,0001094
XLOC_013950	TNPO1	chr5:72148173-72245971	37,5875	7,97205	-2,23723	4,58697	4,50E-06	0,0001126
XLOC_009148	EDEM1	chr3:5204266-5236650	16,4155	2,80459	-2,5492	4,58419	4,56E-06	0,0001139
XLOC_018405	ZNF606	chr19:63180252-63210386	2,14555	0,358406	-2,58168	4,58311	4,58E-06	0,0001143
XLOC_001722	GRAMD1C	chr3:115040321-115148711	1,27926	0,132577	-3,27041	4,57663	4,73E-06	0,0001172
XLOC_027158	STRN	chr2:36918344-37047246	5,58731	1,17486	-2,24967	4,57551	4,75E-06	0,0001178
XLOC_008449	DNAJC25	chr9:113433415-113472347	20,4604	3,10211	-2,72151	4,57345	4,80E-06	0,0001188
XLOC_030135	ZNF613	chr19:57122499-57141496	2,80555	0,516871	-2,44041	4,5695	4,89E-06	0,0001204

XLOC_001674	ZNF311	chr6:29070184-29081384	1,71472	0,286475	-2,58149	4,56605	4,97E-06	0,0001222
XLOC_022112	EDIL3	chr5:83272017-83718005	36,6164	6,74467	-2,44067	4,56197	5,07E-06	0,0001241
XLOC_020214	TOPBP1	chr3:134802059-134863895	27,0391	4,64705	-2,54066	4,55848	5,15E-06	0,0001261
XLOC_025394	C12orf29	chr12:86953398-87060124	5,81751	0,722383	-3,00957	4,55211	5,31E-06	0,0001296
XLOC_018793	TFAM	chr10:59814889-59830870	20,3967	2,83321	-2,84782	4,55048	5,35E-06	0,0001305
XLOC_008424	RALGPS2	chr1:176959565-177157613	6,05909	1,19862	-2,33773	4,54841	5,41E-06	0,0001316
XLOC_003723	COPB1	chr11:14435624-14478017	56,7139	13,32	-2,0901	4,54696	5,44E-06	0,0001323
XLOC_018586	SNAPC1	chr14:61298827-61332927	6,49894	0,728903	-3,15641	4,54546	5,48E-06	0,0001332
XLOC_032552	SLC16A7	chr12:58276045-58468464	1,88983	0,329318	-2,5207	4,54155	5,58E-06	0,0001354
XLOC_001493	ZUFSP	chr6:117063473-117096666	4,9896	0,571181	-3,12691	4,53978	5,63E-06	0,0001363
XLOC_006807	IL6ST	chr5:55266681-55326578	31,1753	2,85037	-3,45118	4,53672	5,71E-06	0,0001379
XLOC_022429	FAM73A	chr1:78017829-78117108	4,82551	1,12956	-2,09492	4,53659	5,72E-06	0,0001379
XLOC_007369	SMAD9	chr13:36316604-36392409	1,27375	0,248577	-2,35732	4,53366	5,80E-06	0,0001397
XLOC_022557	BCAP29	chr7:107007245-107051066	13,5039	3,04263	-2,14999	4,53058	5,88E-06	0,0001416
XLOC_015015	ZBTB41	chr1:195389436-195437083	1,17856	0,120093	-3,29479	4,5302	5,89E-06	0,0001417
XLOC_002062	TLK1	chr2:171555532-171796070	10,8584	1,4969	-2,85876	4,5183	6,23E-06	0,0001494
XLOC_024577	SMEK2	chr2:55628006-55705558	18,1499	4,13574	-2,13374	4,51679	6,28E-06	0,0001502
XLOC_022321	MYO6	chr6:76515628-76839055	8,99876	2,24523	-2,00286	4,51402	6,36E-06	0,0001519
XLOC_027998	ZNF658	chr9:40760355-40782112	1,16181	0,210433	-2,46495	4,51255	6,41E-06	0,0001527
XLOC_025508	TPR	chr1:184532027-184611410	35,538	3,32406	-3,41834	4,50979	6,49E-06	0,0001544
XLOC_033625	ERO1L	chr14:52176587-52232468	17,1588	3,50846	-2,29004	4,50884	6,52E-06	0,000155
XLOC_026022	WDHD1	chr14:54475405-54563577	12,8935	1,86425	-2,78998	4,50642	6,59E-06	0,0001566
XLOC_029864	TBC1D23	chr3:101462375-101526784	8,53416	0,947587	-3,17092	4,50558	6,62E-06	0,000157
XLOC_004118	AGTPBP1	chr9:87351273-87546764	8,2644	1,84036	-2,16692	4,50182	6,74E-06	0,0001595
XLOC_025976	COMMD8	chr4:47147567-47160519	8,8395	1,29332	-2,77289	4,49426	6,98E-06	0,0001647
XLOC_019846	NUDCD1	chr8:110322323-110415526	8,48015	0,887653	-3,25602	4,49322	7,02E-06	0,0001653
XLOC_024024	SMC3	chr10:112316137-112354382	32,9867	3,14389	-3,39126	4,49132	7,08E-06	0,0001667
XLOC_013925	C2orf67	chr2:210575596-210744296	2,65544	0,61889	-2,10119	4,49096	7,09E-06	0,0001667
XLOC_001718	FAR1	chr11:13646781-13710469	11,3339	1,17379	-3,27139	4,49059	7,10E-06	0,0001668
XLOC_018024	DNTTIP2	chr1:94107601-94117350	19,8547	2,06512	-3,26519	4,48691	7,23E-06	0,0001691
XLOC_007679	ZNF280C	chrX:129164353-129230603	1,93073	0,365371	-2,40172	4,48689	7,23E-06	0,0001691
XLOC_000494	PRKACB	chr1:84316264-84476769	8,66986	1,40103	-2,62952	4,48623	7,25E-06	0,0001695
XLOC_020206	GORAB	chr1:168767886-168789598	2,8693	0,617109	-2,2171	4,48344	7,34E-06	0,0001714
XLOC_024178	DCLRE1A	chr10:115584473-115666338	4,27084	0,63432	-2,75124	4,48113	7,43E-06	0,0001729

XLOC_009315	DPY19L1	chr7:34935017-35044178	12,5047	2,47499	-2,33698	4,47979	7,47E-06	0,0001736
XLOC_027234	CCNL1	chr3:158348279-158363019	20,9987	5,21844	-2,00861	4,47291	7,72E-06	0,0001787
XLOC_018717	IFIH1	chr2:162831834-162927394	3,15695	0,662348	-2,25287	4,47034	7,81E-06	0,0001805
XLOC_031067	HSPA13	chr21:14665307-14677380	16,2726	1,70416	-3,25531	4,46603	7,97E-06	0,0001836
XLOC_009202	PCMTD1	chr8:52892692-52974288	4,28821	0,458687	-3,22479	4,46628	7,96E-06	0,0001836
XLOC_010836	TMEM65	chr8:125387670-125454388	12,3285	2,9453	-2,06551	4,46568	7,98E-06	0,0001837
XLOC_030744	AIMP1	chr4:107186681-107489830	12,4682	1,62278	-2,94171	4,46474	8,02E-06	0,0001842
XLOC_030969	HAUS6	chr9:19043140-19093815	7,90775	0,974635	-3,02033	4,4637	8,06E-06	0,0001847
XLOC_024165	ARHGAP18	chr6:129902075-130073132	14,5923	2,85473	-2,35378	4,46064	8,17E-06	0,0001866
XLOC_029896	TFRC	chr3:197237887-197293429	40,8506	10,1086	-2,01477	4,4604	8,18E-06	0,0001867
XLOC_010824	CPE	chr4:166519394-166639121	55,3011	10,1245	-2,44946	4,44773	8,68E-06	0,0001972
XLOC_027949	LIFR	chr5:38510821-38631264	4,81502	0,512338	-3,23237	4,44305	8,87E-06	0,0002009
XLOC_027369	ZNF44	chr19:12243624-12266714	2,76107	0,617839	-2,15992	4,44265	8,89E-06	0,0002009
XLOC_031229	SCLT1	chr4:130024601-130234214	8,25388	1,60352	-2,36383	4,44234	8,90E-06	0,000201
XLOC_022719	DNAJC13	chr3:133619059-133740566	17,0794	3,17605	-2,42695	4,43833	9,07E-06	0,0002046
XLOC_017933	UHRF1BP1L	chr12:98954993-99060773	7,02882	1,33272	-2,39891	4,43605	9,16E-06	0,0002064
XLOC_014828	NHLRC2	chr10:115584473-115666338	3,80566	0,799286	-2,25136	4,4348	9,22E-06	0,0002075
XLOC_010420	ZNF354A	chr5:178071127-178090309	3,1038	0,325379	-3,25384	4,42989	9,43E-06	0,0002117
XLOC_018061	ZNF770	chr15:33057833-33067789	8,12965	1,01176	-3,00633	4,42603	9,60E-06	0,0002154
XLOC_009636	NOP58	chr2:202838759-202876629	32,8107	3,51764	-3,22149	4,42205	9,78E-06	0,0002188
XLOC_007051	ZNF420	chr19:42260985-42313015	1,96067	0,386693	-2,34208	4,41788	9,97E-06	0,0002221
XLOC_033905	TTLL7	chr1:84104624-84237706	5,53281	0,872862	-2,66419	4,41261	1,02E-05	0,0002273
XLOC_034321	PWWP2A	chr5:159435469-159480359	9,12687	2,27653	-2,00328	4,40915	1,04E-05	0,0002303
XLOC_022333	RFC1	chr4:38965463-39044396	30,278	5,29608	-2,51527	4,40534	1,06E-05	0,0002336
XLOC_025527	NFE2L2	chr2:177803278-177838105	40,7908	8,39273	-2,28103	4,4044	1,06E-05	0,0002341
XLOC_002316	BMPR1A	chr10:88506331-88674925	9,67792	2,17358	-2,15463	4,40396	1,06E-05	0,0002344
XLOC_022989	KIF15	chr3:44765014-44869752	13,1811	1,55597	-3,08258	4,40311	1,07E-05	0,0002351
XLOC_031493	ZC3H15	chr2:187059129-187082332	28,6876	3,11575	-3,20278	4,39799	1,09E-05	0,0002401
XLOC_018270	TNFAIP8	chr5:118632292-118760973	10,6156	2,61501	-2,0213	4,39408	1,11E-05	0,0002441
XLOC_010705	MSH2	chr2:47483735-47563864	32,6561	4,76402	-2,7771	4,39231	1,12E-05	0,0002459
XLOC_022042	CENPF	chr1:212843154-212904537	30,9467	3,17029	-3,2871	4,39192	1,12E-05	0,0002461
XLOC_030008	HMG5	chrX:80255855-80440702	1,80233	0,181821	-3,30927	4,3915	1,13E-05	0,0002464
XLOC_018721	WDR43	chr2:28971036-29024584	17,9551	2,44267	-2,87786	4,39099	1,13E-05	0,0002467
XLOC_029888	SULT1E1	chr4:70741518-70760459	3,02786	0,302735	-3,32217	4,38964	1,14E-05	0,0002479

XLOC_018593	ZNF736	chr7:63410620-63451859	1,91579	0,396042	-2,27422	4,38708	1,15E-05	0,0002503
XLOC_024146	UTP15	chr5:72883780-72915020	5,58	0,827913	-2,75271	4,38612	1,15E-05	0,0002509
XLOC_031440	COG6	chr13:39127763-39263802	8,14502	0,885135	-3,20195	4,38261	1,17E-05	0,0002542
XLOC_032965	ZNF141	chr4:321579-359112	1,63592	0,259787	-2,6547	4,3805	1,18E-05	0,000256
XLOC_018340	CWC27	chr5:64100510-64350346	16,4826	1,82684	-3,17352	4,37889	1,19E-05	0,0002577
XLOC_017571	HSP90B1	chr12:102848318-102865833	566,488	65,5035	-3,1124	4,37039	1,24E-05	0,0002675
XLOC_005967	STAG1	chr3:137451856-137954613	16,0277	3,32909	-2,26737	4,36874	1,25E-05	0,0002693
XLOC_014801	CAPZA2	chr7:116289798-116346549	35,8466	3,93228	-3,1884	4,3655	1,27E-05	0,0002731
XLOC_025850	MORC3	chr21:36614356-36670814	6,95388	0,777841	-3,16027	4,36461	1,27E-05	0,000274
XLOC_018288	LYRM2	chr6:90199615-90405195	9,94204	2,14647	-2,21158	4,36119	1,29E-05	0,0002781
XLOC_017812	MOSPD2	chrX:14801275-14850363	7,00643	1,302	-2,42795	4,35769	1,31E-05	0,0002819
XLOC_001689	C11orf54	chr11:93114440-93135895	4,86655	1,12119	-2,11787	4,35289	1,34E-05	0,0002877
XLOC_018008	ATR	chr3:143650766-143780380	5,35912	1,17058	-2,19478	4,34818	1,37E-05	0,0002934
XLOC_009124	SYT1	chr12:77781903-78369919	1,47721	0,248579	-2,5711	4,34451	1,40E-05	0,0002972
XLOC_027922	FNIP1	chr5:131005305-131160655	9,18228	1,41114	-2,70199	4,34365	1,40E-05	0,0002982
XLOC_017557	C13orf27	chr13:102216463-102224150	14,649	2,83103	-2,3714	4,33622	1,45E-05	0,0003079
XLOC_018786	TWISTNB	chr7:19701609-19715185	7,40769	0,841578	-3,13785	4,33424	1,46E-05	0,0003102
XLOC_000916	CBFB	chr16:65620550-65692459	27,0226	6,05837	-2,15717	4,33424	1,46E-05	0,0003102
XLOC_009194	MAP3K7	chr6:91280068-91354422	26,0616	4,87305	-2,41903	4,33099	1,48E-05	0,0003141
XLOC_024195	TRAPPC8	chr18:27663133-27777238	9,72847	1,90165	-2,35496	4,33104	1,48E-05	0,0003141
XLOC_009153	SCAF11	chr12:44599180-44670668	18,7229	2,21563	-3,07901	4,32576	1,52E-05	0,0003209
XLOC_032851	SREK1IP1	chr5:64021890-64100252	3,0271	0,347144	-3,12433	4,32497	1,53E-05	0,0003215
XLOC_007085	LOC283624	chr14:20738077-20744899	2,72598	0,329218	-3,04966	4,32398	1,53E-05	0,0003224
XLOC_030894	LOC100506710	chr9:37069863-37080398	7,50478	1,3823	-2,44073	4,32343	1,54E-05	0,0003227
XLOC_027067	BNIP2	chr15:57738640-57769264	19,1368	3,08004	-2,63533	4,32101	1,55E-05	0,0003255
XLOC_008532	KLHL11	chr17:37258297-37275199	3,82258	0,915714	-2,06158	4,32019	1,56E-05	0,0003264
XLOC_027273	DDX3X	chrX:41077594-41094468	79,6182	17,1893	-2,21158	4,3087	1,64E-05	0,0003423
XLOC_024608	GK5	chr3:143358939-143427139	3,07542	0,524779	-2,551	4,30754	1,65E-05	0,0003436
XLOC_025441	ZNF614	chr19:57208388-57223793	3,15706	0,534559	-2,56216	4,30249	1,69E-05	0,0003501
XLOC_005284	C6orf211	chr6:151815114-151832925	13,5876	1,5632	-3,11971	4,30227	1,69E-05	0,0003502
XLOC_000536	CHM	chrX:85002840-85189222	6,84221	0,950303	-2,848	4,29778	1,73E-05	0,000356
XLOC_025830	ZNF93	chr19:19872713-19908300	9,23337	0,690923	-3,74026	4,29558	1,74E-05	0,0003593
XLOC_022051	SGMS2	chr4:108965169-109055652	7,47487	1,67217	-2,16032	4,29535	1,74E-05	0,0003594
XLOC_025354	KIF5B	chr10:32337244-32385740	66,7475	6,67792	-3,32124	4,29489	1,75E-05	0,0003596

XLOC_025999	DHX29	chr5:54587829-54639278	11,9991	1,37472	-3,12571	4,29503	1,75E-05	0,0003596
XLOC_009800	FAM126A	chr7:22947402-23020295	14,0993	3,15722	-2,1589	4,29326	1,76E-05	0,0003614
XLOC_023066	DDX60	chr4:169374016-169476533	3,60009	0,420568	-3,09762	4,28655	1,81E-05	0,0003699
XLOC_008611	PIGK	chr1:77327254-77457720	13,6394	1,56609	-3,12254	4,28535	1,82E-05	0,0003713
XLOC_007416	ZNF160	chr19:58260021-58298602	4,40332	1,03477	-2,08928	4,2776	1,89E-05	0,0003822
XLOC_027918	TDRD3	chr13:59868591-60046014	4,74466	1,17333	-2,0157	4,27465	1,91E-05	0,0003864
XLOC_032203	CDK1	chr10:62208094-62224733	69,3668	7,83448	-3,14634	4,27086	1,95E-05	0,0003919
XLOC_025346	KLHL2	chr4:166348182-166463758	7,29945	1,62067	-2,1712	4,26335	2,01E-05	0,0004037
XLOC_018001	LTV1	chr6:144206200-144226636	17,1911	2,02229	-3,0876	4,26316	2,02E-05	0,0004038
XLOC_010840	C18orf25	chr18:42007431-42100953	8,1546	1,91178	-2,0927	4,26182	2,03E-05	0,0004059
XLOC_032622	SEC62	chr3:171167273-171198855	15,6098	1,79502	-3,12038	4,2613	2,03E-05	0,0004065
XLOC_009633	SOS2	chr14:49645099-49768439	11,1563	2,3042	-2,27552	4,26079	2,04E-05	0,0004072
XLOC_005633	DNAJC3	chr13:95127393-95245244	12,1644	1,41305	-3,10578	4,25948	2,05E-05	0,0004089
XLOC_031117	WDR35	chr2:19973509-20053375	4,47279	0,835382	-2,42067	4,25802	2,06E-05	0,0004113
XLOC_023088	RND3	chr2:151032954-151052426	21,6014	2,67735	-3,01225	4,25683	2,07E-05	0,0004129
XLOC_018010	RNF219	chr13:78086421-78131315	9,0331	1,06873	-3,07933	4,24869	2,15E-05	0,0004253
XLOC_023142	BLZF1	chr1:167603817-167663294	7,11631	0,864919	-3,04049	4,24524	2,18E-05	0,0004303
XLOC_011713	DHX36	chr3:155472371-155524982	16,2502	2,73036	-2,5733	4,2443	2,19E-05	0,0004317
XLOC_001687	UBXN2B	chr8:59486376-59526614	6,70103	1,2942	-2,37232	4,24422	2,19E-05	0,0004317
XLOC_013923	ARL13B	chr3:95181672-95257212	8,47117	1,07027	-2,98458	4,23989	2,24E-05	0,0004391
XLOC_003705	GPR180	chr13:94052104-94084900	2,85491	0,394817	-2,85419	4,2395	2,24E-05	0,0004392
XLOC_034031	C21orf91	chr21:18071591-18114717	3,48386	0,863825	-2,01188	4,23768	2,26E-05	0,0004418
XLOC_004151	B3GALNT1	chr3:162284364-162305854	3,61277	0,815944	-2,14656	4,23289	2,31E-05	0,00045
XLOC_031492	STYX	chr14:52266632-52328165	4,97427	0,687115	-2,85586	4,228	2,36E-05	0,0004579
XLOC_032091	EXOC5	chr14:56737025-56826550	6,54647	0,915158	-2,83862	4,22727	2,37E-05	0,0004584
XLOC_030134	PAPD5	chr16:48744310-48826720	1,99563	0,454404	-2,1348	4,22757	2,36E-05	0,0004584
XLOC_005612	YES1	chr18:711591-803466	22,8724	3,28423	-2,79998	4,22708	2,37E-05	0,0004585
XLOC_024213	SFR1	chr10:105871677-105876133	3,72493	0,730224	-2,3508	4,22477	2,39E-05	0,0004625
XLOC_032538	MANEA	chr6:96132093-96164049	3,22259	0,389026	-3,05028	4,2241	2,40E-05	0,0004634
XLOC_024140	FAM204A	chr10:120055427-120091829	9,16807	1,65706	-2,46799	4,2232	2,41E-05	0,0004644
XLOC_032280	CDC40	chr6:110608035-110660115	9,60881	1,74563	-2,46061	4,22247	2,42E-05	0,0004656
XLOC_029883	MLH3	chr14:74549820-74587988	1,29676	0,271707	-2,25479	4,22155	2,43E-05	0,000467
XLOC_026012	TWF1	chr12:42473792-42486689	12,9075	1,55932	-3,04923	4,21949	2,45E-05	0,0004707
XLOC_029866	CDKN2AIP	chr4:184602744-184606043	8,7299	2,12861	-2,03605	4,21805	2,46E-05	0,0004727

XLOC_011707	RAP2A	chr13:96884475-96918253	6,28439	0,757075	-3,05327	4,21775	2,47E-05	0,000473
XLOC_009221	ITGB3BP	chr1:63679028-63810952	26,0235	6,14372	-2,08263	4,20432	2,62E-05	0,0004995
XLOC_017952	TTC33	chr5:40747434-40791829	2,52321	0,307781	-3,03529	4,20219	2,64E-05	0,0005035
XLOC_007795	DNAAF2	chr14:49161641-49171698	3,3435	0,668912	-2,32147	4,20107	2,66E-05	0,0005053
XLOC_008751	ZNF277	chr7:111633878-111771225	4,29	0,586729	-2,87021	4,1996	2,67E-05	0,0005082
XLOC_003496	SETDB2	chr13:48916392-48967140	1,96104	0,338431	-2,53468	4,19796	2,69E-05	0,0005115
XLOC_029071	REL	chr2:60962126-61008997	2,53442	0,488808	-2,37432	4,19772	2,70E-05	0,0005117
XLOC_030862	NFXL1	chr4:47544013-47611478	2,58337	0,536833	-2,26671	4,19619	2,71E-05	0,0005144
XLOC_005331	ARSK	chr5:94916539-94967564	5,04428	0,737397	-2,77414	4,1947	2,73E-05	0,0005175
XLOC_017911	ADAM9	chr8:38973661-39081936	109,891	12,1032	-3,18261	4,19309	2,75E-05	0,0005204
XLOC_022463	SLC25A46	chr5:110102652-110126489	16,3137	2,26696	-2,84725	4,19295	2,75E-05	0,0005204
XLOC_027219	THAP6	chr4:76623270-76675522	2,99284	0,444892	-2,74999	4,19046	2,78E-05	0,0005246
XLOC_018603	TMEM154	chr4:153763256-153820796	8,79992	1,71418	-2,35997	4,18548	2,85E-05	0,0005351
XLOC_001645	LUM	chr12:90021362-90029673	47,3397	5,67516	-3,06032	4,18398	2,86E-05	0,0005376
XLOC_022221	CIR1	chr2:174921123-175060057	16,7943	2,0573	-3,02915	4,18272	2,88E-05	0,0005402
XLOC_033845	HINT3	chr6:126319553-126343082	4,52073	0,558164	-3,01779	4,1791	2,93E-05	0,0005481
XLOC_024167	MNAT1	chr14:60246008-60505488	22,0409	3,9468	-2,48142	4,17812	2,94E-05	0,0005497
XLOC_003688	IFI44	chr1:78888064-78902351	2,86708	0,428969	-2,74063	4,17558	2,97E-05	0,000555
XLOC_024716	CEP290	chr12:86953398-87060124	1,37443	0,176707	-2,9594	4,17224	3,02E-05	0,0005617
XLOC_025454	AP1AR	chr4:113372343-113410660	3,77505	0,476737	-2,98523	4,16163	3,16E-05	0,0005844
XLOC_022946	LOC728323	chr2:242679430-242751142	1,46734	0,315263	-2,21857	4,16067	3,17E-05	0,0005859
XLOC_013974	ABCB10	chr1:227718951-227761381	5,73702	1,14859	-2,32045	4,15987	3,18E-05	0,0005869
XLOC_020192	KITLG	chr12:87410700-87498381	3,16742	0,539891	-2,55257	4,15953	3,19E-05	0,0005873
XLOC_027514	CCT6P1	chr7:64749358-64873243	1,68674	0,139554	-3,59534	4,15718	3,22E-05	0,0005918
XLOC_025902	OSTM1	chr6:108469305-108502634	12,5438	1,54872	-3,01782	4,14603	3,38E-05	0,0006173
XLOC_033921	PHIP	chr6:79700854-79844730	9,04651	1,56159	-2,53435	4,14253	3,43E-05	0,0006257
XLOC_009734	PAPD4	chr5:78943998-79019441	8,82243	1,74778	-2,33566	4,14084	3,46E-05	0,0006295
XLOC_031373	ARL5B	chr10:18469611-19006946	5,54513	0,658457	-3,07406	4,13284	3,58E-05	0,0006496
XLOC_029422	NUS1	chr6:118103309-118138579	9,14042	1,58576	-2,52708	4,12975	3,63E-05	0,0006575
XLOC_000493	HOMER1	chr5:78704749-78846219	3,47517	0,729275	-2,25255	4,12857	3,65E-05	0,0006604
XLOC_003789	TFPI	chr2:188037202-188127464	50,0964	11,919	-2,07144	4,12611	3,69E-05	0,0006671
XLOC_018736	BARD1	chr2:215298295-215382723	11,4877	2,34619	-2,29169	4,12441	3,72E-05	0,0006707
XLOC_000664	TAF9B	chrX:77246321-77281922	12,8867	2,60732	-2,30525	4,1197	3,79E-05	0,0006813
XLOC_003412	ZWILCH	chr15:64584484-64644889	22,8512	3,09652	-2,88355	4,11575	3,86E-05	0,000692

XLOC_027191	MBTD1	chr17:46609784-46692472	3,55944	0,703557	-2,33891	4,11077	3,94E-05	0,0007044
XLOC_018819	MTBP	chr8:121474657-121605993	7,31279	1,26194	-2,53478	4,1058	4,03E-05	0,0007178
XLOC_014949	TMEM181	chr6:158877211-158976654	19,4087	4,59408	-2,07886	4,09808	4,17E-05	0,0007402
XLOC_009626	FAM200A	chr7:98981858-98987693	2,81571	0,350929	-3,00425	4,09745	4,18E-05	0,0007417
XLOC_007626	BRWD3	chrX:79811642-79951889	2,5599	0,405493	-2,65833	4,09041	4,31E-05	0,0007621
XLOC_027324	LMBRD2	chr5:36139170-36187772	3,92705	0,506359	-2,95522	4,08977	4,32E-05	0,0007637
XLOC_014873	WAPAL	chr10:88184971-88271592	16,0492	3,30735	-2,27875	4,08514	4,41E-05	0,000778
XLOC_027238	TMEM123	chr11:101772265-101828985	68,2292	8,33686	-3,03281	4,08252	4,45E-05	0,0007853
XLOC_002226	NAPG	chr18:10515872-10542766	7,98967	1,59588	-2,32379	4,07597	4,58E-05	0,000803
XLOC_008602	FUT8	chr14:64947062-65280592	12,2301	2,20104	-2,47418	4,07207	4,66E-05	0,000816
XLOC_004931	SESTD1	chr2:179674663-179837752	2,62805	0,55155	-2,25243	4,06919	4,72E-05	0,0008235
XLOC_002290	ABCD3	chr1:94656520-94756807	20,526	4,12978	-2,31331	4,06307	4,84E-05	0,0008437
XLOC_000578	GRPEL2	chr5:148705169-148714339	5,56201	0,726051	-2,93747	4,06175	4,87E-05	0,0008479
XLOC_025511	ECHDC1	chr6:127651549-127706447	13,0581	3,02008	-2,11228	4,05475	5,02E-05	0,0008692
XLOC_029870	TBC1D8B	chrX:105932574-106006033	1,33613	0,275854	-2,27608	4,05213	5,08E-05	0,0008779
XLOC_029868	TBK1	chr12:63132106-63182166	8,8282	1,15911	-2,9291	4,04486	5,24E-05	0,000902
XLOC_011705	XRCC4	chr5:82409072-82685335	7,43369	1,1037	-2,75173	4,04451	5,24E-05	0,000902
XLOC_026184	TMEM67	chr8:94836247-94900636	3,57294	0,711522	-2,32813	4,04444	5,24E-05	0,000902
XLOC_017856	SEMA3C	chr7:80209789-80386603	39,5386	4,97018	-2,99189	4,04183	5,30E-05	0,0009099
XLOC_034250	ZNF595	chr4:43226-188445	3,36343	0,588172	-2,51562	4,04044	5,34E-05	0,0009122
XLOC_004078	STK17B	chr2:196706551-196744581	7,42428	0,973705	-2,93069	4,03519	5,46E-05	0,0009298
XLOC_027786	FGF2	chr4:123967312-124460054	10,093	1,21989	-3,04853	4,03299	5,51E-05	0,0009374
XLOC_023159	REEP3	chr10:64951128-65054889	15,4191	2,00423	-2,94359	4,03214	5,53E-05	0,0009402
XLOC_030859	ZNF570	chr19:42651821-42671370	1,43699	0,287563	-2,32111	4,02127	5,79E-05	0,0009766
XLOC_032201	TMX3	chr18:64491904-64533333	16,7675	2,19447	-2,93372	4,01918	5,84E-05	0,0009822
XLOC_018353	WBP5	chrX:102498035-102500053	65,8757	13,1238	-2,32756	4,01539	5,93E-05	0,0009972
XLOC_001731	SUMO1	chr2:202779147-202812943	42,5143	10,1346	-2,06866	4,0149	5,95E-05	0,0009972
XLOC_018389	CLPX	chr15:63227613-63265027	15,8522	3,52837	-2,16761	4,01409	5,97E-05	0,0009996
XLOC_034255	SNX4	chr3:126648183-126721750	15,0545	2,00436	-2,90898	4,01369	5,98E-05	0,0010003
XLOC_001746	UFM1	chr13:37821941-37835143	14,1668	1,88442	-2,91032	4,0097	6,08E-05	0,001016
XLOC_010364	PYROXD1	chr12:21481764-21545870	1,31757	0,148694	-3,14746	4,00791	6,13E-05	0,0010212
XLOC_017993	TTC35	chr8:109525028-109568312	11,4594	1,54112	-2,89448	4,00656	6,16E-05	0,001024
XLOC_006770	AGGF1	chr5:76361962-76396814	8,72789	1,6317	-2,41926	4,00328	6,25E-05	0,0010366
XLOC_032648	SP4	chr7:21434085-21520676	2,66331	0,538261	-2,30684	4,00321	6,25E-05	0,0010366

XLOC_006805	C8orf37	chr8:96325594-96891547	1,54228	0,353418	-2,12562	4,00254	6,27E-05	0,0010386
XLOC_006858	BAG4	chr8:38140014-38189976	7,21244	1,3452	-2,42267	3,99584	6,45E-05	0,0010627
XLOC_018578	SEPT10	chr2:109657664-109733853	32,9162	7,128	-2,20723	3,99592	6,44E-05	0,0010627
XLOC_020373	FBXO30	chr6:145988132-146327243	4,71988	0,89572	-2,39763	3,99464	6,48E-05	0,0010674
XLOC_013760	MINA	chr3:99023520-99173985	3,04277	0,385099	-2,98208	3,99206	6,55E-05	0,0010752
XLOC_032319	YEATS4	chr12:68039779-68070843	15,44	3,07814	-2,32654	3,99206	6,55E-05	0,0010752
XLOC_029885	HACE1	chr6:105282660-105414487	4,91885	0,952188	-2,369	3,99149	6,57E-05	0,0010771
XLOC_017898	COQ10B	chr2:198026475-198048096	13,0079	1,76048	-2,88536	3,98674	6,70E-05	0,0010962
XLOC_002274	ACSL4	chrX:108771219-108867416	25,3779	4,18771	-2,59934	3,9846	6,76E-05	0,0011041
XLOC_017567	CKAP2	chr13:51927495-51948764	51,4803	10,1713	-2,33951	3,9828	6,81E-05	0,0011112
XLOC_029321	CEP135	chr4:56509226-56594284	4,34132	0,875008	-2,31077	3,97962	6,90E-05	0,001122
XLOC_017950	RSBN1L	chr7:77151103-77250242	8,04264	1,53443	-2,38997	3,97881	6,93E-05	0,0011251
XLOC_005336	C12orf48	chr12:101037361-101115744	8,62367	1,32882	-2,69815	3,97795	6,95E-05	0,0011286
XLOC_027983	THOC1	chr18:148335-258059	10,8404	1,33432	-3,02224	3,97486	7,04E-05	0,0011412
XLOC_007645	DCP2	chr5:112340305-112852595	7,52303	1,82857	-2,0406	3,97296	7,10E-05	0,0011476
XLOC_032085	DNAJC24	chr11:31347952-31487761	3,12406	0,387655	-3,01058	3,97187	7,13E-05	0,0011507
XLOC_002129	ZEB2	chr2:144858411-144994428	6,20541	1,4731	-2,07468	3,9701	7,18E-05	0,0011579
XLOC_022502	PCF11	chr11:82545784-82574483	7,6357	1,60079	-2,25397	3,96859	7,23E-05	0,0011646
XLOC_009140	C2orf74	chr2:61225746-61245468	10,3511	1,40436	-2,8818	3,95456	7,67E-05	0,0012277
XLOC_003840	RLIM	chrX:73718908-73751300	8,65925	2,08508	-2,05414	3,95472	7,66E-05	0,0012277
XLOC_002335	AFTPH	chr2:64604828-64673642	7,09621	1,67138	-2,08601	3,95205	7,75E-05	0,0012377
XLOC_000420	TAF13	chr1:109406645-109441079	21,797	4,22758	-2,36622	3,95074	7,79E-05	0,001243
XLOC_025710	CCDC76	chr1:100371293-100487999	2,67713	0,366473	-2,86891	3,9491	7,84E-05	0,0012508
XLOC_034107	MIR221	chrX:45489711-45491474	1,41442	0,142537	-3,31079	3,9485	7,86E-05	0,0012517
XLOC_024225	ABHD3	chr18:17484855-17538764	9,59218	1,86683	-2,36127	3,94862	7,86E-05	0,0012517
XLOC_010808	FAM18B1	chr17:18625306-18650751	8,87764	1,23511	-2,84553	3,94044	8,13E-05	0,0012906
XLOC_016526	MTF2	chr1:93317379-93377810	8,77901	1,60893	-2,44796	3,93973	8,16E-05	0,001293
XLOC_010433	UTP23	chr8:117847922-117856102	5,35027	0,74364	-2,84693	3,93895	8,18E-05	0,0012949
XLOC_003699	LIN7C	chr11:27471737-27484902	4,59059	0,615745	-2,89828	3,93132	8,45E-05	0,0013319
XLOC_027323	PPIL4	chr6:149867323-149908931	17,1074	2,78962	-2,61647	3,93136	8,45E-05	0,0013319
XLOC_010403	RLF	chr1:40399627-40479180	7,10144	1,00625	-2,81912	3,92896	8,53E-05	0,0013428
XLOC_003695	METTL18	chr1:168028295-168129700	3,13351	0,402328	-2,96134	3,92874	8,54E-05	0,0013431
XLOC_001659	EXOC6	chr10:94584449-94809241	7,69102	1,31086	-2,55266	3,92845	8,55E-05	0,0013431
XLOC_025268	MAP4K3	chr2:39329925-39681988	13,5565	2,62592	-2,36809	3,9275	8,58E-05	0,0013461

XLOC_034121	FNBP1L	chr1:93686275-93792806	13,7623	2,90819	-2,24252	3,92682	8,61E-05	0,0013488
XLOC_025428	RANBP6	chr9:6001018-6005640	8,91742	1,49031	-2,58101	3,9264	8,62E-05	0,0013499
XLOC_018818	LRCH2	chrX:114251438-114374900	2,15848	0,412062	-2,38908	3,92232	8,77E-05	0,0013705
XLOC_013884	TRAPPC6B	chr14:38685363-38709737	7,522	1,27389	-2,56188	3,92058	8,83E-05	0,0013789
XLOC_025424	SYDE2	chr1:85395943-85439316	2,21773	0,320205	-2,79202	3,91872	8,90E-05	0,0013888
XLOC_001661	ANP32E	chr1:148457340-148475128	38,3442	4,94628	-2,95459	3,91419	9,07E-05	0,0014118
XLOC_030062	SECISBP2L	chr15:47068127-47126052	11,7008	1,72582	-2,76125	3,91335	9,10E-05	0,001415
XLOC_014877	ZNF624	chr17:16464772-16497892	1,18458	0,184559	-2,68222	3,90837	9,29E-05	0,0014403
XLOC_003596	ERI2	chr16:20682812-20768491	11,5864	2,11392	-2,45444	3,90456	9,44E-05	0,0014615
XLOC_022133	METTL14	chr4:119825421-119856000	10,205	1,75719	-2,53793	3,90359	9,48E-05	0,0014657
XLOC_001053	CRYZ	chr1:74943759-75004948	6,97219	1,25315	-2,47606	3,90072	9,59E-05	0,0014797
XLOC_034341	NCAPG	chr4:17421622-17632589	29,2313	3,66102	-2,9972	3,89961	9,63E-05	0,0014857
XLOC_017849	LRP6	chr12:12160175-12311276	9,25622	2,10797	-2,13457	3,89071	1,00E-04	0,0015351
XLOC_018048	C17orf104	chr17:40089287-40108691	1,84664	0,261234	-2,82148	3,88926	0,000101	0,0015425
XLOC_017565	DTWD1	chr15:47235267-47726142	3,14109	0,732492	-2,10038	3,88757	0,000101	0,0015506
XLOC_024612	CCDC34	chr11:27316636-27341371	19,5365	3,72154	-2,3922	3,88679	0,000102	0,0015538
XLOC_006997	ZNF616	chr19:57308491-57335058	2,74147	0,641355	-2,09575	3,88574	0,000102	0,0015587
XLOC_025713	DOCK4	chr7:111153399-111633725	1,5416	0,36474	-2,07949	3,88009	0,000104	0,0015889
XLOC_008613	SPPL2A	chr15:48785876-48845890	24,3397	4,65345	-2,38694	3,87756	0,000106	0,001602
XLOC_009152	HECA	chr6:139497941-139543639	3,39896	0,487595	-2,80134	3,87566	0,000106	0,0016118
XLOC_033851	USP12	chr13:26538286-26644033	7,01899	1,24211	-2,49847	3,87064	0,000109	0,0016407
XLOC_029476	PAN3	chr13:27607654-27767475	5,55616	1,08429	-2,35733	3,8692	0,000109	0,0016495
XLOC_000583	KLHL15	chrX:23911753-24006851	2,88507	0,536974	-2,42569	3,86442	0,000111	0,0016746
XLOC_024757	MATR3	chr5:138637339-138695265	76,0833	14,6427	-2,3774	3,86326	0,000112	0,0016816
XLOC_010435	USP34	chr2:61258058-61551546	14,7008	2,73071	-2,42854	3,86103	0,000113	0,0016942
XLOC_034238	GNPDA2	chr4:44374704-44423438	7,59684	1,02417	-2,89095	3,8585	0,000114	0,0017089
XLOC_025928	LAMTOR3	chr4:101018517-101034726	5,59728	0,948264	-2,56137	3,85748	0,000115	0,0017151
XLOC_024351	LCLAT1	chr2:30523626-30720595	5,78872	0,951238	-2,60537	3,85719	0,000115	0,0017162
XLOC_018343	EIF3E	chr8:109283147-109330191	103,236	14,0352	-2,87883	3,85198	0,000117	0,0017443
XLOC_022431	ZNF227	chr19:49408530-49433261	3,74272	0,49337	-2,92334	3,85161	0,000117	0,001746
XLOC_010989	KIF11	chr10:94342779-94408797	44,2094	5,66243	-2,96486	3,85001	0,000118	0,0017538
XLOC_018758	EFHA1	chr13:20964827-21076355	18,3684	2,65223	-2,79194	3,84765	0,000119	0,0017656
XLOC_034117	FAM164A	chr8:79740836-79794552	1,78883	0,322267	-2,47269	3,84499	0,000121	0,0017799
XLOC_008615	ZNF295	chr21:42280008-42303565	3,78322	0,929603	-2,02493	3,84125	0,000122	0,0018033

XLOC_032316	ITGAV	chr2:187163034-187253873	15,7572	2,26798	-2,79653	3,83232	0,000127	0,0018563
XLOC_018388	MTIF2	chr2:55253187-55359602	12,876	2,53812	-2,34285	3,831	0,000128	0,0018626
XLOC_007646	MIB1	chr18:17575542-17704910	9,38419	1,34968	-2,79762	3,82924	0,000129	0,0018739
XLOC_025757	DNAJC21	chr5:34965395-34994826	28,3011	5,4448	-2,37791	3,82508	0,000131	0,0018997
XLOC_025413	RPGRIP1L	chr16:52189858-52295335	3,63023	0,756835	-2,26201	3,82192	0,000132	0,00192
XLOC_033847	PTN	chr7:136562634-136679086	21,4448	3,14925	-2,76755	3,81613	0,000136	0,0019539
XLOC_002149	METAP2	chr12:94391952-94434149	31,0054	4,76777	-2,70114	3,81625	0,000135	0,0019539
XLOC_030996	RBM27	chr5:145563320-145649576	9,69735	1,71811	-2,49676	3,81574	0,000136	0,001956
XLOC_031503	B3GNT5	chr3:184378524-184629234	4,06595	0,937718	-2,11636	3,80749	0,00014	0,0020105
XLOC_000538	IPMK	chr10:59621283-59697700	1,57394	0,233403	-2,75349	3,80555	0,000141	0,0020252
XLOC_013241	SSB	chr2:170363634-170389706	60,342	8,14151	-2,8898	3,80001	0,000145	0,0020677
XLOC_020043	DYNLT3	chrX:37583032-37591833	8,45018	1,25951	-2,74612	3,79978	0,000145	0,0020685
XLOC_009596	BRMS1L	chr14:35363518-35414511	6,27884	1,3231	-2,24658	3,79702	0,000146	0,0020872
XLOC_005329	MAK16	chr8:33462226-33490245	10,9913	1,53024	-2,84453	3,7966	0,000147	0,0020896
XLOC_034032	ZNF391	chr6:27464496-27482905	1,42724	0,308943	-2,20782	3,79355	0,000149	0,0021132
XLOC_025498	ZBTB6	chr9:124710155-124715430	3,12585	0,467993	-2,73969	3,79324	0,000149	0,0021147
XLOC_033899	MMD	chr17:50824972-50854340	2,00368	0,289298	-2,79202	3,79033	0,00015	0,002134
XLOC_009197	LYSMD3	chr5:89806436-89861758	4,19212	0,61374	-2,77198	3,78306	0,000155	0,002188
XLOC_010551	SCRN3	chr2:174921123-175060057	5,71259	1,26262	-2,17773	3,78195	0,000156	0,0021948
XLOC_031409	TPP2	chr13:102047286-102129524	15,2533	3,7648	-2,01848	3,78207	0,000156	0,0021948
XLOC_025986	HCFC2	chr12:102982365-103024433	3,59821	0,608385	-2,56422	3,7805	0,000157	0,0022048
XLOC_007035	ZBTB33	chrX:119268634-119276279	5,03634	1,01865	-2,30571	3,77616	0,000159	0,0022377
XLOC_009653	ZNF501	chr3:44746111-44755510	1,183	0,250378	-2,24027	3,77353	0,000161	0,002259
XLOC_032301	TXNDC9	chr2:99301918-99319292	16,7033	2,5158	-2,73105	3,77207	0,000162	0,0022711
XLOC_003740	C5orf51	chr5:41940226-41957495	9,82575	1,66687	-2,55943	3,77127	0,000162	0,0022772
XLOC_027959	LOC647979	chr20:34096953-34102373	62,7047	12,3537	-2,34363	3,76728	0,000165	0,0023089
XLOC_027228	EIF2S2	chr20:32139718-32163746	26,117	5,26242	-2,31119	3,7655	0,000166	0,0023219
XLOC_009602	NSRP1	chr17:25467959-25537612	12,5011	1,88609	-2,72858	3,76231	0,000168	0,0023492
XLOC_031089	RELL1	chr4:37131946-37364394	6,4058	1,11443	-2,52307	3,7579	0,000171	0,0023836
XLOC_005348	BBS10	chr12:75262396-75266353	4,35465	0,66435	-2,71254	3,75517	0,000173	0,0024085
XLOC_008462	MLLT3	chr9:20334282-20612516	1,65112	0,275887	-2,5813	3,75489	0,000173	0,0024099
XLOC_027982	IFT57	chr3:109362348-109424107	6,97243	1,43867	-2,27692	3,75325	0,000175	0,0024232
XLOC_031088	FZD6	chr8:104379836-104414270	30,2006	5,29127	-2,51289	3,75197	0,000175	0,0024318
XLOC_010805	TRIM61	chr4:166095047-166118268	1,76318	0,309895	-2,50833	3,7517	0,000176	0,0024332

XLOC_025576	CCDC91	chr12:28301399-28594366	5,74035	0,878434	-2,70813	3,74963	0,000177	0,0024496
XLOC_024652	TMEM30A	chr6:76019357-76051352	45,3754	6,25673	-2,85843	3,74823	0,000178	0,0024582
XLOC_022520	TMX1	chr14:50776436-50794877	15,4242	2,32582	-2,72939	3,74835	0,000178	0,0024582
XLOC_025957	LOC100506233	chr11:82460755-82462402	5,50992	1,33091	-2,04962	3,74712	0,000179	0,0024678
XLOC_024120	RGPD6	chr2:111012127-111052778	2,98439	0,456089	-2,71005	3,74629	0,000179	0,002472
XLOC_007020	UBXN4	chr2:136215658-136259103	38,0804	6,66045	-2,51536	3,74304	0,000182	0,0024966
XLOC_029707	INSIG2	chr2:118562519-118584067	5,47122	0,840292	-2,7029	3,74245	0,000182	0,0025006
XLOC_018022	TMEM167A	chr5:82354524-82409028	13,7337	2,43804	-2,49393	3,74199	0,000183	0,0025006
XLOC_024189	MAPK6	chr15:50098702-50145754	22,283	4,12775	-2,43251	3,74157	0,000183	0,0025036
XLOC_013889	PBK	chr8:27687842-27751468	38,0808	7,13802	-2,41547	3,73965	0,000184	0,0025189
XLOC_023001	CETN3	chr5:89725284-89741359	15,7135	3,14247	-2,32203	3,73415	0,000188	0,0025667
XLOC_006790	TWSG1	chr18:9324764-9392418	38,3237	5,72621	-2,74258	3,73099	0,000191	0,0025925
XLOC_010316	HSP90AA1	chr14:101616827-101675839	288,277	36,8445	-2,96794	3,72889	0,000192	0,0026088
XLOC_022614	RAB21	chr12:70434875-70470695	20,0393	3,63484	-2,46287	3,72777	0,000193	0,0026166
XLOC_025550	CCDC59	chr12:81270213-81397147	11,2494	2,4153	-2,21958	3,72778	0,000193	0,0026166
XLOC_006780	C8orf39	chr8:94427870-94822949	1,49355	0,0460626	-5,01901	3,72437	0,000196	0,0026453
XLOC_012000	WDR36	chr5:110455768-110494099	6,76696	1,04074	-2,70089	3,71702	0,000202	0,0027112
XLOC_009173	SCYL2	chr12:99166802-99259435	16,075	2,84693	-2,49734	3,7156	0,000203	0,0027223
XLOC_008735	SPP1	chr4:89115825-89123587	8,45416	1,72563	-2,29253	3,7133	0,000205	0,0027416
XLOC_020296	NAE1	chr16:65394281-65422380	29,6927	6,35733	-2,22361	3,70843	0,000209	0,0027865
XLOC_009215	ZNF654	chr3:88183789-88289805	1,85427	0,263651	-2,81415	3,70817	0,000209	0,0027879
XLOC_027306	PYGO1	chr15:53620023-53669577	3,6105	0,847599	-2,09074	3,7011	0,000215	0,002854
XLOC_034363	CASD1	chr7:93977016-94024264	2,31408	0,489822	-2,24011	3,69677	0,000218	0,0028958
XLOC_018539	AP4E1	chr15:48988237-49085389	5,05828	0,789519	-2,6796	3,6923	0,000222	0,0029385
XLOC_022323	BTBD1	chr15:81476184-81527171	28,2085	4,13201	-2,77121	3,68969	0,000225	0,0029644
XLOC_018886	ZNF486	chr19:20138996-20172201	3,35728	0,709599	-2,24222	3,68733	0,000227	0,0029847
XLOC_008633	PLS1	chr3:143797918-143915195	7,88676	1,24041	-2,66862	3,68652	0,000227	0,0029927
XLOC_012911	CHAC2	chr2:53750620-53942174	5,84438	1,00633	-2,53795	3,68312	0,00023	0,0030255
XLOC_024444	DNAJC27	chr2:25020008-25048467	1,78789	0,374352	-2,25579	3,68116	0,000232	0,0030414
XLOC_008451	ZNF449	chrX:134306361-134325309	1,59515	0,333153	-2,25944	3,68009	0,000233	0,0030526
XLOC_026081	HAUS2	chr15:40574795-40652259	15,814	3,77742	-2,06573	3,67944	0,000234	0,0030575
XLOC_029101	PGGT1B	chr5:114569504-114627115	4,72051	0,938196	-2,33098	3,67586	0,000237	0,0030962
XLOC_014879	OGFRL1	chr6:72054649-72075369	21,7323	4,38952	-2,3077	3,67521	0,000238	0,0030985
XLOC_023059	TTF1	chr9:134240757-134272059	8,57447	2,0686	-2,05139	3,67399	0,000239	0,0031113

XLOC_008664	CEP57	chr11:95163289-95302998	16,3575	2,41148	-2,76196	3,67136	0,000241	0,0031388
XLOC_010417	FIGNL1	chr7:50471049-50485582	15,3939	3,64275	-2,07926	3,66988	0,000243	0,0031525
XLOC_000525	CTDSPL2	chr15:42506655-42608792	16,0842	3,13891	-2,35731	3,66753	0,000245	0,0031704
XLOC_000979	DENND4C	chr9:19280698-19365508	7,22609	1,69436	-2,09248	3,6672	0,000245	0,0031708
XLOC_020719	EIF1AX	chrX:20052556-20070009	12,3412	1,95603	-2,65748	3,66577	0,000247	0,0031866
XLOC_007650	BCL10	chr1:85504047-85515175	7,3686	1,41447	-2,38113	3,66118	0,000251	0,0032348
XLOC_008645	RPS6KB1	chr17:55325224-55382568	10,2229	1,61451	-2,66264	3,66054	0,000252	0,0032413
XLOC_030797	FXR1	chr3:182112894-182183233	61,7451	10,4536	-2,56232	3,65733	0,000255	0,0032789
XLOC_010834	ADSS	chr1:242634078-242682403	19,199	4,56489	-2,07238	3,65721	0,000255	0,0032789
XLOC_000481	ZNF215	chr11:6904229-6935854	1,03591	0,154442	-2,74576	3,65374	0,000258	0,0033157
XLOC_013885	NTN4	chr12:94575713-94708719	10,6494	2,05212	-2,37558	3,64718	0,000265	0,0033867
XLOC_004213	C14orf142	chr14:92738989-92765314	9,42151	1,39448	-2,75623	3,6439	0,000269	0,0034253
XLOC_009128	ASF1A	chr6:119241314-119300303	8,40878	1,35882	-2,62954	3,63839	0,000274	0,0034895
XLOC_034136	OTUD4	chr4:146274145-146322690	10,2134	2,41575	-2,07992	3,63649	0,000276	0,0035103
XLOC_025305	C2orf69	chr2:200484223-200501241	3,17112	0,51409	-2,6249	3,63386	0,000279	0,003543
XLOC_003703	MET	chr7:116099231-116225676	14,07	3,45879	-2,02428	3,62543	0,000288	0,0036381
XLOC_029412	FAM3C	chr7:120776140-120823743	10,7099	2,07836	-2,36543	3,61974	0,000295	0,0036998
XLOC_013212	TYW5	chr2:200501878-200537092	2,29947	0,466529	-2,30126	3,61904	0,000296	0,0037063
XLOC_007805	PEX13	chr2:61021051-61133468	6,25512	1,1924	-2,39117	3,61687	0,000298	0,0037323
XLOC_024491	UBE2Q2	chr15:73921094-73980443	12,4941	2,95222	-2,08138	3,61639	0,000299	0,0037375
XLOC_026190	RANBP2	chr2:108701920-108768699	16,328	2,45627	-2,73281	3,61355	0,000302	0,0037733
XLOC_034102	SS18	chr18:21850214-21925144	30,5777	6,51915	-2,22972	3,60933	0,000307	0,003821
XLOC_009318	KIAA2026	chr9:5909007-5998003	3,19466	0,52239	-2,61246	3,60698	0,00031	0,0038467
XLOC_029291	RFK	chr9:78190252-78199264	5,53625	0,912825	-2,6005	3,59954	0,000319	0,0039347
XLOC_000561	CSGALNACT2	chr10:42952790-43000755	7,53424	1,66782	-2,1755	3,59817	0,00032	0,0039519
XLOC_026232	MUT	chr6:49506031-49539000	9,784	2,27892	-2,10207	3,5972	0,000322	0,0039649
XLOC_014937	ZFP62	chr5:180203249-180220973	5,92248	1,36903	-2,11305	3,59576	0,000323	0,0039849
XLOC_004088	FAM199X	chrX:103230553-103327238	8,12339	1,36791	-2,57011	3,5933	0,000327	0,0040099
XLOC_029995	FBXL3	chr13:76477389-76499332	11,0028	1,70341	-2,69137	3,59293	0,000327	0,0040125
XLOC_025967	MRPL1	chr4:79002269-79092968	14,8258	2,40319	-2,62509	3,59222	0,000328	0,004021
XLOC_011814	PRKCI	chr3:171422913-171506464	14,2201	2,31865	-2,61657	3,59115	0,000329	0,0040357
XLOC_030958	KIAA0232	chr4:6835336-6936800	9,01668	1,91267	-2,23701	3,58973	0,000331	0,0040541
XLOC_000844	UBE2W	chr8:74863028-74953675	4,58418	1,03903	-2,14142	3,58711	0,000334	0,0040875
XLOC_029894	C12orf39	chr12:21570522-21575497	1,56113	0,145073	-3,42774	3,58662	0,000335	0,0040933

XLOC_026039	SLC25A24	chr1:108472965-108545666	23,338	3,75097	-2,63734	3,586	0,000336	0,0040993
XLOC_023984	PLOD2	chr3:147269917-147361972	68,6307	11,3947	-2,59049	3,58476	0,000337	0,0041132
XLOC_017919	SNRNP48	chr6:7535430-7557199	5,77383	0,954783	-2,59628	3,5838	0,000339	0,0041227
XLOC_001632	PLEKHA5	chr12:19173797-19420600	10,3954	1,93203	-2,42775	3,57716	0,000347	0,0042167
XLOC_008608	CYB5R4	chr6:84626088-84728253	6,07551	1,16798	-2,37899	3,57278	0,000353	0,0042748
XLOC_003578	ATAD1	chr10:89497626-89567970	14,4605	2,65559	-2,44501	3,5705	0,000356	0,0043027
XLOC_018814	UBE2V2	chr8:49083201-49138616	26,6344	5,5147	-2,27194	3,57049	0,000356	0,0043027
XLOC_010376	LCA5	chr6:80251426-80308824	1,59571	0,271006	-2,5578	3,56906	0,000358	0,0043204
XLOC_007627	RAB8B	chr15:61268780-61347026	13,4156	2,21918	-2,59581	3,56453	0,000365	0,0043898
XLOC_013134	CAPZA1	chr1:112963597-113015764	79,3489	12,2165	-2,69938	3,56314	0,000366	0,004405
XLOC_004888	PTPN4	chr2:120233656-120455678	3,76698	0,866173	-2,12068	3,56055	0,00037	0,0044348
XLOC_010983	LIMS1	chr2:108517242-108670134	18,172	4,41122	-2,04246	3,56017	0,000371	0,0044392
XLOC_004022	ARFGEF1	chr8:68272450-68419799	10,4516	2,30138	-2,18315	3,55924	0,000372	0,0044451
XLOC_025926	MRPL19	chr2:75727240-75793867	6,63675	1,54215	-2,10553	3,55662	0,000376	0,0044796
XLOC_000324	SNX2	chr5:122138648-122193701	27,9221	4,65187	-2,58552	3,55508	0,000378	0,0044997
XLOC_009583	TXNDC16	chr14:51967057-52089051	8,40546	1,49976	-2,4866	3,55516	0,000378	0,0044997
XLOC_014835	MBIP	chr14:35837514-35859633	9,29931	2,11416	-2,13704	3,55114	0,000384	0,0045556
XLOC_018678	ATF2	chr2:175645270-175741521	21,9704	4,76157	-2,20605	3,54895	0,000387	0,0045814
XLOC_006796	CMTM6	chr3:32497807-32519407	44,625	7,32086	-2,60777	3,54598	0,000391	0,004621
XLOC_025401	ZC3H8	chr2:112689910-112729146	3,46214	0,658276	-2,3949	3,54007	0,0004	0,0046987
XLOC_018739	MBTPS2	chrX:21767576-21813462	8,61782	1,86982	-2,20442	3,53477	0,000408	0,004771
XLOC_007362	GNAI1	chr7:79602075-79686661	15,9193	2,68563	-2,56745	3,53139	0,000413	0,0048239
XLOC_024631	RWDD4	chr4:184797782-184817325	3,64605	0,649001	-2,49004	3,53029	0,000415	0,0048398
XLOC_017471	UGDH	chr4:39176769-39205613	17,5797	2,97259	-2,56412	3,52888	0,000417	0,0048615
XLOC_034267	UHMK1	chr1:160733587-160766043	18,1472	2,89695	-2,64713	3,52626	0,000421	0,0049054
XLOC_023008	TPRKB	chr2:73810143-73820640	24,9975	5,62364	-2,15221	3,52413	0,000425	0,004943
XLOC_000232	HRSP12	chr8:99183742-99198594	7,34155	1,24316	-2,56207	3,52074	0,00043	0,0049957
XLOC_023247	VAMP7	chrX:154764136-154826627	8,34416	1,66903	-2,32175	3,51835	0,000434	0,0050322
XLOC_029489	DLGAP5	chr14:54684586-54728149	47,8514	8,07188	-2,56759	3,51549	0,000439	0,0050779
XLOC_000873	ZNF280B	chr22:21168771-21193505	2,07882	0,479681	-2,11562	3,5141	0,000441	0,0050935
XLOC_031482	GALNT7	chr4:174325499-174493599	17,4213	4,3014	-2,01797	3,51316	0,000443	0,0051071
XLOC_030922	ZNF253	chr19:19837713-19865293	1,64655	0,266578	-2,62681	3,51238	0,000444	0,0051178
XLOC_000555	AHR	chr7:17304800-17352300	7,50617	1,28133	-2,55043	3,50982	0,000448	0,0051561
XLOC_027443	CCNJ	chr10:97461525-97839982	2,65023	0,551053	-2,26586	3,50799	0,000452	0,0051828

XLOC_022925	EXTL2	chr1:101110528-101133006	14,2663	2,82408	-2,33676	3,50772	0,000452	0,0051859
XLOC_025692	CNOT6	chr5:179826741-179938241	14,757	3,2844	-2,16769	3,50481	0,000457	0,0052339
XLOC_008435	C1orf96	chr1:227523374-227545311	4,94773	0,850721	-2,54001	3,50435	0,000458	0,0052389
XLOC_008778	MOSPD1	chrX:133849325-133877162	8,93504	2,03615	-2,13363	3,50432	0,000458	0,0052389
XLOC_025984	ATP1B1	chr1:167342570-167603810	20,7322	3,37011	-2,62101	3,4946	0,000475	0,0053966
XLOC_007797	STAM2	chr2:152681560-152740752	5,98144	1,03591	-2,5296	3,48594	0,00049	0,0055413
XLOC_022800	ATAD2	chr8:124400295-124478526	43,2807	6,63109	-2,70641	3,48479	0,000493	0,0055604
XLOC_003811	PRPF38B	chr1:109036454-109045945	17,3761	3,13823	-2,46908	3,48441	0,000493	0,005566
XLOC_017823	ZBED5	chr11:10830826-10836196	11,752	2,71718	-2,11272	3,48259	0,000497	0,0055923
XLOC_008531	KIN	chr10:7837372-7869950	6,44392	1,13062	-2,51083	3,47589	0,000509	0,0057097
XLOC_005046	GTF2F2	chr13:44591977-44758241	26,6168	5,12178	-2,37762	3,47599	0,000509	0,0057097
XLOC_016532	ZNF844	chr19:12036521-12053319	1,85106	0,410715	-2,17214	3,47014	0,00052	0,0058114
XLOC_029311	ALMS1	chr2:73466393-73766202	4,83606	1,07572	-2,16853	3,46968	0,000521	0,0058189
XLOC_025480	ZNF507	chr19:37528353-37570413	5,62863	1,2138	-2,21325	3,4648	0,000531	0,0059108
XLOC_010873	EXOC1	chr4:56414572-56466001	11,0535	2,33834	-2,24095	3,46385	0,000532	0,0059267
XLOC_022057	PTEN	chr10:89608897-89718512	11,8926	2,36552	-2,32983	3,45713	0,000546	0,0060487
XLOC_003541	HMGB2	chr4:174325499-174493599	246,951	57,294	-2,10777	3,45678	0,000547	0,0060517
XLOC_004276	RBM43	chr2:151812973-151826635	2,17654	0,384856	-2,49965	3,45438	0,000552	0,0060956
XLOC_010795	TATDN1	chr8:125556188-125810024	5,61396	1,107	-2,34237	3,45212	0,000556	0,0061344
XLOC_011619	SLC35A1	chr6:88239361-88278776	6,77566	1,46491	-2,20955	3,45183	0,000557	0,0061384
XLOC_022347	KLHL23	chr2:170210180-170317824	7,89003	1,89165	-2,06039	3,44784	0,000565	0,0062195
XLOC_031433	SLC35F5	chr2:114180963-114230870	9,10286	2,20865	-2,04316	3,44541	0,00057	0,0062626
XLOC_022932	ELK4	chr1:203843693-203868623	5,29182	1,13882	-2,21623	3,4451	0,000571	0,0062666
XLOC_010826	SEPSECS	chr4:24730724-24809225	1,61192	0,267212	-2,59272	3,43925	0,000583	0,0063938
XLOC_007342	NCKAP1	chr2:183497849-183611474	64,4747	10,8666	-2,56883	3,43878	0,000584	0,0063996
XLOC_012981	PTPN11	chr12:111340918-111432100	39,5939	6,72998	-2,5566	3,43775	0,000587	0,0064188
XLOC_025929	PNN	chr14:38714137-38722173	43,1582	7,48873	-2,52684	3,43382	0,000595	0,0065021
XLOC_025382	SGTB	chr5:64919949-65053697	3,43994	0,614903	-2,48395	3,43249	0,000598	0,0065286
XLOC_003861	C10orf18	chr10:5766597-5898061	10,6924	2,22514	-2,26462	3,43139	0,0006	0,0065525
XLOC_004191	WDR89	chr14:63133509-63178344	3,66287	0,6728	-2,44472	3,43117	0,000601	0,0065525
XLOC_002136	BMPR2	chr2:202948551-203140719	13,675	3,22752	-2,08305	3,4312	0,000601	0,0065525
XLOC_025916	CYP1B1	chr2:38148249-38156827	9,25576	1,64525	-2,49204	3,42961	0,000604	0,0065848
XLOC_013283	C1orf124	chr1:229531344-229557360	5,98749	1,38096	-2,11627	3,42741	0,000609	0,0066251
XLOC_017647	ACVR2A	chr2:148319039-148987514	1,98662	0,338998	-2,55097	3,42596	0,000613	0,0066498

XLOC_007637	CHORDC1	chr11:89573245-89596180	5,27674	0,948223	-2,47635	3,42355	0,000618	0,0066924
XLOC_018671	RAB3GAP2	chr1:218113241-218512672	9,53974	2,20305	-2,11445	3,41499	0,000638	0,0068703
XLOC_026006	PUS10	chr2:61021051-61133468	2,21377	0,523715	-2,07965	3,41413	0,00064	0,0068864
XLOC_005640	RGPD8	chr2:112842416-112907693	3,30313	0,594619	-2,4738	3,41321	0,000642	0,0069043
XLOC_025361	METTL4	chr18:2527523-2561489	4,28644	0,775843	-2,46594	3,41096	0,000647	0,0069503
XLOC_017512	GNB4	chr3:180595100-180652463	19,7512	3,61077	-2,45156	3,40909	0,000652	0,0069896
XLOC_025974	FRS2	chr12:68150395-68259829	6,49831	1,50969	-2,10581	3,4061	0,000659	0,007058
XLOC_031328	RB1	chr13:47775883-47954027	28,1505	5,50657	-2,35393	3,40134	0,000671	0,0071622
XLOC_003849	ACBD3	chr1:224399002-224441046	14,4695	2,60873	-2,4716	3,40048	0,000673	0,0071759
XLOC_027165	CRYAB	chr11:111284556-111302805	1,81323	7,96837	2,13572	-3,40051	0,000673	0,0071759
XLOC_027325	ZMYM6	chr1:35224353-35270236	3,29881	0,761899	-2,11427	3,39797	0,000679	0,0072279
XLOC_010324	ARL6IP6	chr2:153216352-153327119	14,7396	3,0953	-2,25155	3,3938	0,000689	0,0073153
XLOC_001734	GPX8	chr5:54444555-54504762	25,9093	5,19682	-2,31777	3,39181	0,000694	0,00736
XLOC_031031	BLM	chr15:89061582-89159690	10,9652	2,00447	-2,45164	3,37363	0,000742	0,0077894
XLOC_002298	GPSM2	chr1:109221120-109307659	14,2529	2,96399	-2,26564	3,3719	0,000747	0,0078324
XLOC_005981	CMPK1	chr1:47488397-47618081	24,9126	4,28906	-2,53814	3,37002	0,000752	0,0078766
XLOC_017663	PJA2	chr5:108698308-108773574	28,5265	5,12957	-2,47539	3,36976	0,000752	0,0078812
XLOC_030990	NEDD4	chr15:53906413-54073127	12,4555	2,19678	-2,50333	3,36847	0,000756	0,0079057
XLOC_025881	GLMN	chr1:92484542-92640314	4,78048	1,16268	-2,0397	3,36428	0,000767	0,0080045
XLOC_026047	MFAP3	chr5:153398711-153418641	14,5924	3,22748	-2,17673	3,36061	0,000778	0,0080777
XLOC_029415	CD164	chr6:109794409-109811424	68,1337	12,9698	-2,39322	3,35131	0,000804	0,0083023
XLOC_001144	CASP3	chr4:185785843-185807623	23,7692	5,849	-2,02283	3,35119	0,000805	0,0083023
XLOC_023252	SPCS3	chr4:177475781-177501078	35,2239	6,2753	-2,4888	3,3457	0,000821	0,0084274
XLOC_024464	RRP15	chr1:216525251-216577948	3,25344	0,607211	-2,4217	3,34025	0,000837	0,0085733
XLOC_031495	FCHO2	chr5:72287563-72422105	4,48605	0,845818	-2,40703	3,33999	0,000838	0,008578
XLOC_017768	MTMR6	chr13:24718340-24759704	8,10018	1,8141	-2,1587	3,33729	0,000846	0,0086386
XLOC_018336	TXLNG	chrX:16714463-16798455	10,3215	2,08802	-2,30544	3,33299	0,000859	0,0087533
XLOC_024699	HIATL1	chr9:96176581-96263023	41,4033	7,4607	-2,47236	3,33115	0,000865	0,0088012
XLOC_027864	ATP6V1C1	chr8:104102423-104154461	12,5611	2,34255	-2,42281	3,32536	0,000883	0,0089419
XLOC_024426	ZNF273	chr7:64001054-64035222	3,39386	0,54485	-2,639	3,3237	0,000888	0,0089782
XLOC_025535	SHOC2	chr10:112669290-112763415	12,9378	2,42544	-2,41527	3,32339	0,000889	0,0089814
XLOC_000495	FAM35B2	chr10:46799725-46841244	1,11668	0,203145	-2,45863	3,32123	0,000896	0,0090343
XLOC_009644	GOLGA5	chr14:92330402-92376057	18,8141	4,14468	-2,18248	3,31964	0,000901	0,0090788
XLOC_018002	HBS1L	chr6:135323213-135417729	14,4185	2,92697	-2,30044	3,31951	0,000902	0,0090799

XLOC_010790	PLA2G12A	chr4:110850593-110870700	5,14453	1,22802	-2,06671	3,31634	0,000912	0,0091764
XLOC_004864	LRRRC49	chr15:68971981-69129490	4,33275	0,788924	-2,45733	3,31543	0,000915	0,0091989
XLOC_014704	TNFRSF10D	chr8:23049045-23077485	19,6748	4,8233	-2,02826	3,31491	0,000917	0,0092095
XLOC_023956	RG9MTD1	chr3:102763401-102767779	10,2014	1,94035	-2,39438	3,31127	0,000929	0,0093025
XLOC_018284	B4GALT6	chr18:27456206-27518684	3,16071	0,601882	-2,39269	3,30905	0,000936	0,0093518
XLOC_024446	PROS1	chr3:95074570-95175624	18,6925	3,82027	-2,29071	3,30736	0,000942	0,0094017
XLOC_024151	TGDS	chr13:94024308-94046512	4,61664	0,880588	-2,3903	3,30459	0,000951	0,0094455
XLOC_010842	POGLUT1	chr3:120670474-120696244	6,14288	1,2687	-2,27557	3,29693	0,000977	0,0096565
XLOC_032308	TMOD3	chr15:49909116-49991623	31,1023	5,81241	-2,41981	3,2919	0,000995	0,0097983
XLOC_033786	BET1	chr7:93458935-93471626	4,5527	0,874966	-2,37942	3,29199	0,000995	0,0097983
XLOC_003583	SMARCA5	chr4:144654065-144698092	27,4021	5,06256	-2,43635	3,28609	0,001016	0,0099696
XLOC_034329	ACTR6	chr12:99118704-99142332	7,56342	1,4586	-2,37446	3,28589	0,001017	0,0099732
XLOC_005288	WWC2	chr4:184255167-184478923	13,1753	3,22485	-2,03054	3,285	0,00102	0,0099895

Supplementary File 6: Top 10 functions from Ingenuity Pathway Analysis

Function annotation	z-score ^a	Genes ^b	Function annotation	z-score ^a	Genes ^b
cell death of lung cancer cell lines	2.357	17	infection of cells	-7,833	75
G1/S phase transition of tumor cell lines	2.219	8	cell survival	-6,814	76
segregation of chromosomes	1.732	12	proliferation of endothelial cell lines	-2,753	9
delay in mitosis	1.671	6	repair of DNA	-2,709	29
reactivation of virus	1.432	5	ubiquitination	-2,606	20
nucleation of cells	1.276	7	G2 phase	-2,599	18
G1 phase of tumor cell lines	1.211	21	migration of lung cancer cell lines	-2,567	7
mitosis of cervical cancer cell lines	1.091	7	activation of enzyme	-2,449	6
DNA damage	1.002	11	hydrolysis of nucleotide	-2,449	6
apoptosis of ovarian cancer cell lines	0.86	9	G2/M phase	-2,401	13

^aRegulation z-score: z-scores >2 or <-2 are significant. Positive scores mean increase in function, negative scores a decrease.

^bNumber of genes from the submitted gene list that are present in the annotated function.

Supplementary File 7: Oligonucleotide sequences

Haplotype block analysis

#	Name	SNP	Hg18	Forward	Reverse
1	DRAM	rs12230012	100803246	5'-TTTTGGGTTATGACAAGTGTGTG-3'	5'-TGAGACAGGTAATAAAACAAGATCAAT-3'
2	DRAM	rs7960200	100803324	5'-TTTTGGGTTATGACAAGTGTGTG-3'	5'-TGAGACAGGTAATAAAACAAGATCAAT-3'
3	DRAM	rs6539017	100816074	5'-CAGGGTCTCTGTCATCCAGG-3'	5'-TGCAGTGGCTCACACCTAT-3'
4	DRAM	rs10745931	100816908	5'-GCAACCTTGTCTATAAGCCAATTA-3'	5'-TCAGCATCACTGTCCCTTCTC-3'
5	DRAM	rs7295569	100819349	5'-TGATACAAAGCTGCTCCTGTT-3'	5'-TCTCTTCAGACACATACACTCCA-3'
6	DRAM	rs11111078	100819350	5'-TGATACAAAGCTGCTCCTGTT-3'	5'-TCTCTTCAGACACATACACTCCA-3'
7	DRAM	rs7302651	100835396	5'-TGGTGAGGAAGAGAATGATCC-3'	5'-TCCAACTCCTGGGTACAAGC-3'
8	AW452512	rs10778159	100845443	5'-TTTTGCAAATGTTATCTTGCCCTT-3'	5'-TCCCACACCATCTACTGCAA-3'
9	AW452512		100845650	5'-TTTTGCAAATGTTATCTTGCCCTT-3'	5'-TCCCACACCATCTACTGCAA-3'
10	AW452512	rs4301835	100845714	5'-TTTTGCAAATGTTATCTTGCCCTT-3'	5'-TCCCACACCATCTACTGCAA-3'
11	NUP37	rs2271266	101030174	5'-AAGCTATGCCATCAACCCTG-3'	5'-TGTGAGGCTTAGACAACTTTGG-3'
12	NUP37		101036224	5'-TTATAATCTGTAGTTAATAGCTTTG-3'	5'-TCATTGATCTTCCTCCTCTA-3'
13	C12orf48-EX1	rs4764863	101038314	5'-TGATGTTTTATTGACATGGA-3'	5'-AACTGGTGATACTATAATTCAAAAT-3'
14	C12orf48-EX1		101038352	5'-TGATGTTTTATTGACATGGA-3'	5'-AACTGGTGATACTATAATTCAAAAT-3'
15	C12orf48-EX2	rs2036772	101041883	5'-CACTGAGTAGAGCTTTATGTGAA-3'	5'-ATTCAGTGATTTGAAAGGGA-3'
16	C12orf48-EX2	rs2036771	101041934	5'-CACTGAGTAGAGCTTTATGTGAA-3'	5'-ATTCAGTGATTTGAAAGGGA-3'
17	C12orf48	rs7314597	101054932	5'-TTTTATCCTGTGTTTGAGCTCTATT-3'	5'-GGTGGATCACGAAGTCAGG-3'
18	C12orf48	rs12578176	101055184	5'-GCACAATCTCCGCTCACTGT-3'	5'-TCTTTTCTTTTCTCCCACCTTAACA-3'
20	R2232	rs55772007	101069693	5'-ATGAGAAGGCCACCCTTGA-3'	5'-CATTTCTCTGAGATGCCTGG-3'
21	C12orf48-EX4	rs2102476	101072830	5'-ACTTAGCTTTATGAAGTAAATTACAG-3'	5'-TGGTCATTTCAATATCCCTT-3'
22	C12orf48	rs3794201	101083838	5'-ACCACCACCATCAGATCCTT-3'	5'-TTGGCCAAAACCTCAGAATCA-3'
23	C12orf48		101093570	5'-TTGAAAAGTGTTAACTCTGAAAA-3'	5'-AGCAATAATAAACCATTTCTACA-3'
24	PMCH		101114674	5'-TCATTTTGGTTTACTCAGAATTAGTTA-3'	5'-GTAGCAGTATGGGCTTCTCC-3'
25	LINC1941		101117158	5'-TTTTAGAAATCCTTCTCAATCCTTAGA-3'	5'-GGATACCTAACTAGAACCTTAATATCCTG-3'
26	LINC1940B		101123716	5'-AGGCTGAAGAGGATGGATCA-3'	5'-CTTTGTTGGTAACCCAATGTTGA-3'
27	LINC1939D	rs11111210	101131418	5'-TTGTGTACTTCAAATGCTATTAGTTTTC-3'	5'-GCCTGGTATATATTATTAGAGGCAA-3'
28	SRP-EA	rs12827335	101135247	5'-GGAAATATGCTTTGATGCAGG-3'	5'-TGACCTCGTGATCTGCCC-3'
29	SRP-EA	rs10860846	101135501	5'-GGAAATATGCTTTGATGCAGG-3'	5'-TGACCTCGTGATCTGCCC-3'
30	SRP-EA	rs34835268	101135671	5'-GGAAATATGCTTTGATGCAGG-3'	5'-TGACCTCGTGATCTGCCC-3'
31	HAPLO1	rs73386932	101137495	5'-CAAACCTCAAACATTCACT-3'	5'-GCCAGATATAATGAAGCCAC-3'
32	HAPLO1	rs12304817	101137668	5'-CAAACCTCAAACATTCACT-3'	5'-GCCAGATATAATGAAGCCAC-3'
33	HAPLO3		101138696	5'-AGAGGATTTCCGGACTATTT-3'	5'-ACAGTATGTATTGGTTGCCC-3'
34	HAPLO5	rs73185996	101139298	5'-ATGAGAAGACCTCTTTGCTG-3'	5'-TTACCTCTCCAACCTTTGGTT-3'
35	HAPLO5	rs10860847	101139626	5'-ATGAGAAGACCTCTTTGCTG-3'	5'-TTACCTCTCCAACCTTTGGTT-3'
36	HAPLO5	rs11614122	101139646	5'-ATGAGAAGACCTCTTTGCTG-3'	5'-TTACCTCTCCAACCTTTGGTT-3'
37	HAPLO6	rs34260252	101140020	5'-ATTGCTCTTGAGATAGTGGC-3'	5'-GGGCCTGGTACTCATCTT-3'
38	piRNA2		101144273	5'-GCACTCTAAAATTGGGATGTTTT-3'	5'-ATTGTGTGGAATCCTGGCTC-3'
39	HAPLO15		101144418	5'-ACATTGGCTCTCTTAATGCT-3'	5'-GGATGGTGGCTAATATCAT-3'
40	piRNA2		101144745	5'-GCACTCTAAAATTGGGATGTTTT-3'	5'-ATTGTGTGGAATCCTGGCTC-3'
41	HAPLO17	rs34522212	101145062	5'-AAAGTTACAGGAATGTAGGGA-3'	5'-AGAAACATGCAGAACACATC-3'

42	HAPLO24	rs4764867	101148424	5'-AGAGCCATGGTGAAATAAGA-3'	5'-TGAAGTCAAAATATTACTGGTAGC-3'
43	HAPLO29		101149414	5'-TATTTATTTTCCCCTCCTCC-3'	5'-GAGCCTCAGACGTCTTACAT-3'
44	HAPLO29	rs12811642	101150784	5'-TATTTATTTTCCCCTCCTCC-3'	5'-GAGCCTCAGACGTCTTACAT-3'
45	HAPLO29	rs10745937	101150811	5'-TATTTATTTTCCCCTCCTCC-3'	5'-GAGCCTCAGACGTCTTACAT-3'
46	HAPLO31	rs1858173	101150849	5'-TGTGTGACTGGTAACCTTCCT-3'	5'-TGGTCTTAAGTGGGGTGAC-3'
47	HAPLO33	rs4764868	101151741	5'-CCAGTTTGCGAATGATTT-3'	5'-GAACTCTTTGGCCCTAGC-3'
48	HAPLO33	rs4764692	101152912	5'-CCAGTTTGCGAATGATTT-3'	5'-GAACTCTTTGGCCCTAGC-3'
49	HAPLO34		101152934	5'-AGTTTGTGGCCTTCAAAAG-3'	5'-AGGGTATGGTCTCAATCATCT-3'
50	HAPLO36		101153314	5'-TGGGTGGCCTAAACACTA-3'	5'-ATTGGCTTAGGAGCCTGTA-3'
51	HAPLO36	rs7312533	101154426	5'-TGGGTGGCCTAAACACTA-3'	5'-ATTGGCTTAGGAGCCTGTA-3'
52	HAPLO36	rs17032362	101154433	5'-TGGGTGGCCTAAACACTA-3'	5'-ATTGGCTTAGGAGCCTGTA-3'
53	HAPLO37		101154809	5'-AAGTTACCTCAAGCAAAAGTT-3'	5'-CTTGACATTCTGCACATAC-3'
54	HAPLO38		101154867	5'-TAGAAAAGAGAAGTGGCAGC-3'	5'-AAAAGAACCAGAGAAGCAA-3'
55	HAPLO40		101155228	5'-GCTATAATTTTACACACTGCTTTA-3'	5'-CCTGATTTAGTCTTCGGATG-3'
56	HAPLO40	rs11111221	101156216	5'-GCTATAATTTTACACACTGCTTTA-3'	5'-CCTGATTTAGTCTTCGGATG-3'
57	HAPLO41		101156263	5'-CCGTTTATTTTGAGTTAGCA-3'	5'-GAACCAGCTTTGCATCC-3'
58	HAPLO42		101156723	5'-GTATCATCCTGACAAAAGCC-3'	5'-CCCAAGAGCATGGAATTT-3'
59	HAPLO44	rs10860849	101157240	5'-GAAAATTCATGCTCTTG-3'	5'-TTTATGTTCCCAACAACAA-3'
60	HAPLO49		101159651	5'-TGACACATCTCACAGCTAAG-3'	5'-AATGGCTAAACAGAAGTAAA-3'
61	HAPLO50		101160771	5'-AATCCAAGAGATGTTTTGTC-3'	5'-ACAACACAATTCATTCACAA-3'
62	HAPLO54	rs12820880	101161074	5'-TTGTAAAAGGGATTGAGTTC-3'	5'-AAATCTTAAACAACCAAAGA-3'
63	HAPLO57	rs6539029	101162705	5'-GATAATAGTTGTAACAGGAAAA-3'	5'-AGCTTTTACAAACCAGTGAC-3'
64	HAPLO57		101164186	5'-GATAATAGTTGTAACAGGAAAA-3'	5'-AGCTTTTACAAACCAGTGAC-3'
65	HAPLO57	rs7954204	101164195	5'-GATAATAGTTGTAACAGGAAAA-3'	5'-AGCTTTTACAAACCAGTGAC-3'
66	HAPLO59	rs11111224	101164381	5'-AATAGTGCCTATTGGCTAAG-3'	5'-CAAGGTTTTAAGATGACCAC-3'
67	HAPLO64		101165214	5'-GAGGTTAATTCCTCCAGTTA-3'	5'-CTAACAACGGTGAAATCCT-3'
68	HAPLO65		101168137	5'-ACCTGGTTTAGTTGAGACTT-3'	5'-CAAATAGGCAAAGTTCTCTC-3'
69	HAPLO66	rs7955830	101168164	5'-ATTTCAAGAATCCAATCTG-3'	5'-GGGGAAAAGAAAGAGAGA-3'
70	HAPLO67		101168698	5'-TTTTAATTATTAGGGGACAAA-3'	5'-CATCTTAAATAAGTGGGGAA-3'
71	HAPLO69		101169321	5'-GTTTCCAGAAATAATCCTC-3'	5'-TGTGGTCTACACAAGCACT-3'
72	HAPLO74	rs11111228	101170063	5'-CAGGTTTCGAATGAGTTTCT-3'	5'-GGTGTAAAGGAAGGGGTC-3'
73	HAPLO77		101172864	5'-GTGGTGGGAGGGTTAAT-3'	5'-TTAATTTCAATTCTTTGGTCC-3'
74	HAPLO79	rs12300530	101175237	5'-TCTGATTTGATATGCTAATTT-3'	5'-TATATCCTAATTGCCAGCAT-3'
75	HAPLO81		101175405	5'-CTATAGTGATGTGCCTTCCT-3'	5'-ATCCTTCAAGTATTCATGGT-3'
76	HAPLO84		101176213	5'-TGAGAGTCATTTATATTTACCCTT-3'	5'-AATGATTGCTGTCTTCTCATC-3'
77	HAPLO84	rs35512374	101177543	5'-TGAGAGTCATTTATATTTACCCTT-3'	5'-AATGATTGCTGTCTTCTCATC-3'
78	HAPLO84	rs11111229	101177694	5'-TGAGAGTCATTTATATTTACCCTT-3'	5'-AATGATTGCTGTCTTCTCATC-3'
79	HAPLO84	rs11111230	101177816	5'-TGAGAGTCATTTATATTTACCCTT-3'	5'-AATGATTGCTGTCTTCTCATC-3'
80	HAPLO86	rs4503597	101177857	5'-AGCTAATCTTCTCTGGCAA-3'	5'-TCTTACAATGCCGAAGATGT-3'
81	HAPLO87	rs34787414	101178702	5'-CTTTCTGGGATCCAAACTA-3'	5'-ACACCTCACTATCTGTTTATCTAAT-3'
82	HAPLO91		101179134	5'-TGAAGAATGTGAGTGATTTAGG-3'	5'-ATCAGTTTCAGCATCCACAC-3'
83	HAPLO91	rs11111231	101180825	5'-TGAAGAATGTGAGTGATTTAGG-3'	5'-ATCAGTTTCAGCATCCACAC-3'
84	HAPLO93		101181057	5'-GGCGACATTACCACAATAGTA-3'	5'-AAATGAATATAACCGGACCC-3'
85	HAPLO93	rs12316898	101181915	5'-GGCGACATTACCACAATAGTA-3'	5'-AAATGAATATAACCGGACCC-3'
86	HAPLO94		101182103	5'-ACTGGGATCCCTCATCTTAT-3'	5'-TGGAGGAAAGGAATCCA-3'

87	HAPLO102	rs34494977	101185135	5'-CAGATGTTGACTTTGGCATA-3'	5'-GCCTTAGCCTTCCAAACT-3'
88	HAPLO104		101186958	5'-GGTTGAGCTGGTAAGTGGTA-3'	5'-ATTGATCTGCCTCAAATACA-3'
89	HAPLO104		101187009	5'-GGTTGAGCTGGTAAGTGGTA-3'	5'-ATTGATCTGCCTCAAATACA-3'
90	HAPLO104		101187247	5'-GGTTGAGCTGGTAAGTGGTA-3'	5'-ATTGATCTGCCTCAAATACA-3'
91	HAPLO112	rs35460681	101188866	5'-AAATAACATTGAAACATATTGCT-3'	5'-CTGGTAGACAGTTATAAGCATTG-3'
92	HAPLO114		101190932	5'-TCTTGTAGGCCTGTACGAGT-3'	5'-TGGAAGCTGGTATAATTAGCTTCA-3'
93	HAPLO117	rs73186002	101192963	5'-CCATTGACACAAAGATATTCC-3'	5'-AAATTGGCTCTTCTTGGC-3'
94	HAPLO122		101193278	5'-CTCATCCTCACAATCTTTCG-3'	5'-GGGAAAACCTCATGAAATCAG-3'
95	HAPLO122		101195683	5'-CTCATCCTCACAATCTTTCG-3'	5'-GGGAAAACCTCATGAAATCAG-3'
96	HAPLO127	rs10467018	101197958	5'-AAACCCAGATGGTGTAGTGT-3'	5'-CTAATACAAGGCCTAAACTAATG-3'
97	HAPLO127		101198278	5'-AAACCCAGATGGTGTAGTGT-3'	5'-CTAATACAAGGCCTAAACTAATG-3'
98	HAPLO128		101198354	5'-TGGAACCTGCAGGACTCA-3'	5'-ACGTTACCTTCATGACCAAC-3'
99	HAPLO128		101201630	5'-TGGAACCTGCAGGACTCA-3'	5'-ACGTTACCTTCATGACCAAC-3'
100	HAPLO140	rsr5912895	101201965	5'-CAGTGGTGGTATCCCTCTTA-3'	5'-ACTCAGCTCTGGATCAAATG-3'
101	HAPLO145		101206668	5'-TGCGATGTTCCCTTAC-3'	5'-TCTTCTCCTCCAAATGATTG-3'
102	HAPLO145	rs61935375	101206749	5'-TGCGATGTTCCCTTAC-3'	5'-TCTTCTCCTCCAAATGATTG-3'
103	HAPLO145	rs36012093	101206860	5'-TGCGATGTTCCCTTAC-3'	5'-TCTTCTCCTCCAAATGATTG-3'
104	HAPLO147	rs2946829	101206934	5'-TTGGGAACACACTCCTGTAT-3'	5'-TCTACTGGTCCCAATTTACTG-3'
105	HAPLO149	rs61935376	101207687	5'-GGACAATGAGATCTAGGCTG-3'	5'-CAATCCATACGTTTTCTTC-3'
106	HAPLO149		101208411	5'-GGACAATGAGATCTAGGCTG-3'	5'-CAATCCATACGTTTTCTTC-3'
107	HAPLO157	rs10860850	101208621	5'-CAAGCCATCCTCCTACCT-3'	5'-TCACCCTAACAGCCTCATT-3'
108	HAPLO158	rs11111235	101212584	5'-TGGTTATGACCTGAATTATCTT-3'	5'-CATATGTCTGCTAAGGGCATA-3'
109	HAPLO158	rs11111236	101212949	5'-TGGTTATGACCTGAATTATCTT-3'	5'-CATATGTCTGCTAAGGGCATA-3'
110	HAPLO158	rs10860851	101212980	5'-TGGTTATGACCTGAATTATCTT-3'	5'-CATATGTCTGCTAAGGGCATA-3'
111	HAPLO158	rs11111237	101213064	5'-TGGTTATGACCTGAATTATCTT-3'	5'-CATATGTCTGCTAAGGGCATA-3'
112	HAPLO159	rs10745938	101213111	5'-TCTGTGGATAAATGTTTTCTGA-3'	5'-CCGATGTAACAAACAAGC-3'
113	HAPLO159		101213386	5'-TCTGTGGATAAATGTTTTCTGA-3'	5'-CCGATGTAACAAACAAGC-3'
114	HAPLO160	rs10778172	101213463	5'-TTGAATTGTCTTGACACCTTT-3'	5'-AGAACTACCACTGGACCC-3'
115	HAPLO162	rs2971584	101213725	5'-AGTCCTTTGTGAGAGGCATA-3'	5'-TCATATTCACAGAATTAGAAAA-3'
116	HAPLO163	rs7302155	101214607	5'-GCTGTTTTAGTCAATGTAGCC-3'	5'-CAGAGCAATCAGGTAAAAGA-3'
117	HAPLO165		101215308	5'-GTGTGATGAATCACCCCTTTT-3'	5'-AGATTGCTAGCTAGATTAACCA-3'
118	HAPLO165	rs2971583	101216004	5'-GTGTGATGAATCACCCCTTTT-3'	5'-AGATTGCTAGCTAGATTAACCA-3'
119	HAPLO168	rs7294768	101216214	5'-TCTTCCTGTTGTATTGACTTCTT-3'	5'-CACTAGACTGGTCCTCCAAG-3'
120	HAPLO169		101217529	5'-ACTTTGGGAAGCTAAGTGG-3'	5'-AAAGCCTTTGTGAAATATAAAAGT-3'
121	HAPLO169	rs55694252	101217949	5'-ACTTTGGGAAGCTAAGTGG-3'	5'-AAAGCCTTTGTGAAATATAAAAGT-3'
122	HAPLO169	rs56335245	101218047	5'-ACTTTGGGAAGCTAAGTGG-3'	5'-AAAGCCTTTGTGAAATATAAAAGT-3'
123	HAPLO169		101218157	5'-ACTTTGGGAAGCTAAGTGG-3'	5'-AAAGCCTTTGTGAAATATAAAAGT-3'
124	HAPLO170	rs11559894	101218208	5'-CAGGGAAGTTTTCTTGAAGT-3'	5'-ATAATCCTGTCCAAAGGGAA-3'
125	HAPLO173		101218716	5'-TTGTTCTCTGTTTCTGCTT-3'	5'-TCAAGGCATTTCTTTCTCT-3'
126	HAPLO173	rs1949557	101219299	5'-TTGTTCTCTGTTTCTGCTT-3'	5'-TCAAGGCATTTCTTTCTCT-3'
127	HAPLO175	rs7308233	101219901	5'-AATCTTCCTGGAGTTTCAGTC-3'	5'-TCTATATTCCAGGGCATTGT-3'
128	HAPLO175		101220782	5'-AATCTTCCTGGAGTTTCAGTC-3'	5'-TCTATATTCCAGGGCATTGT-3'
129	HAPLO177	rs7959169	101221052	5'-GAACAGGGACAATGACAGA-3'	5'-AGGTTTTCAATTTTGTCTGG-3'
130	HAPLO178	rs10860852	101222042	5'-TACAGGCATCTGTAAAGCA-3'	5'-GAGCTCCAAAATCCAAGAG-3'
131	HAPLO179	rs1949556	101222657	5'-CCCAGGAGTGCTGAGTAAA-3'	5'-CAGTGCATTGTTGTTTCATT-3'

132	HAPLO180	rs1949555	101222932	5'-GCTTATACTTTAGGCCTGGG-3'	5'-GCTTAGCACCCAATATCAAA-3'
133	HAPLO180	rs1949554	101223078	5'-GCTTATACTTTAGGCCTGGG-3'	5'-GCTTAGCACCCAATATCAAA-3'
134	HAPLO180	rs1949553	101223080	5'-GCTTATACTTTAGGCCTGGG-3'	5'-GCTTAGCACCCAATATCAAA-3'
135	HAPLO180		101223100	5'-GCTTATACTTTAGGCCTGGG-3'	5'-GCTTAGCACCCAATATCAAA-3'
136	HAPLO181	rs11519708	101223514	5'-GGCAAACCTTTTCTCTCTCT-3'	5'-CTCTTGTTGCCCAGGCT-3'
137	HAPLO181	rs12426137	101223830	5'-GGCAAACCTTTTCTCTCTCT-3'	5'-CTCTTGTTGCCCAGGCT-3'
138	HAPLO182	rs12426121	101224064	5'-GCAAAACCCCATCTTTACT-3'	5'-TTTGAGCTTGTAGAGGCTTT-3'
139	HAPLO182	rs35304190	101224093	5'-GCAAAACCCCATCTTTACT-3'	5'-TTTGAGCTTGTAGAGGCTTT-3'
140	HAPLO183	rs12371296	101224358	5'-CCATCTTGTTTCATGTCCTT-3'	5'-ACCGGCATAATTTAGACAAA-3'
141	HAPLO183	rs7957647	101224821	5'-CCATCTTGTTTCATGTCCTT-3'	5'-ACCGGCATAATTTAGACAAA-3'
142	HAPLO184	rs61935381	101225095	5'-CTCTAAGAGCCTGGATTCCCT-3'	5'-CCAGTCATTTTACTTTAGGACA-3'
143	HAPLO186		101225472	5'-TTTGATCCTCAGTGGTTTGT-3'	5'-TGGGATGCAAGGCTAGT-3'
144	HAPLO186	rs4764872	101227750	5'-TTTGATCCTCAGTGGTTTGT-3'	5'-TGGGATGCAAGGCTAGT-3'
145	HAPLO186	rs9706539	101227839	5'-TTTGATCCTCAGTGGTTTGT-3'	5'-TGGGATGCAAGGCTAGT-3'
146	HAPLO186	rs4579975	101227882	5'-TTTGATCCTCAGTGGTTTGT-3'	5'-TGGGATGCAAGGCTAGT-3'
147	HAPLO186		101227980	5'-TTTGATCCTCAGTGGTTTGT-3'	5'-TGGGATGCAAGGCTAGT-3'
148	HAPLO198		101233976	5'-CAGAAATGAAAAGTGGGTCT-3'	5'-TCAGTTGCCCTTTCCCT-3'
149	HAPLO199		101233984	5'-GTGAATCTGCTGTGATTCTG-3'	5'-AAGTGATGGGAAGCTGG-3'
150	HAPLO200		101234302	5'-GGTCATTGCTTATATCCCAA-3'	5'-AAAGGCAAATTTTCAATAGC-3'
151	HAPLO200	rs1113483	101234622	5'-GGTCATTGCTTATATCCCAA-3'	5'-AAAGGCAAATTTTCAATAGC-3'
152	HAPLO201	rs17032405	101234814	5'-TGTTTACAGGTTTTCTGCCT-3'	5'-TTTTGATGAAACCTGATGGT-3'
153	HAPLO202	rs10860854	101235164	5'-GTGAGCCGCAGTAAACTATT-3'	5'-TAATTTCTCTCTTTTCCCC-3'
154	HAPLO203	rs6539033	101235572	5'-AAAGATTGCATGGAAATGAC-3'	5'-GGAACTTTTAATTATTATGCAGG-3'
155	HAPLO203	rs66834777	101236133	5'-AAAGATTGCATGGAAATGAC-3'	5'-GGAACTTTTAATTATTATGCAGG-3'
156	HAPLO203		101236326	5'-AAAGATTGCATGGAAATGAC-3'	5'-GGAACTTTTAATTATTATGCAGG-3'
157	HAPLO203	rs7316642	101236328	5'-AAAGATTGCATGGAAATGAC-3'	5'-GGAACTTTTAATTATTATGCAGG-3'
158	HAPLO205		101236389	5'-GTTACAGTGTGGGCAGTACC-3'	5'-ATCAAGGCTGGATATGACAA-3'
159	HAPLO205	rs7969401	101236926	5'-GTTACAGTGTGGGCAGTACC-3'	5'-ATCAAGGCTGGATATGACAA-3'
160	HAPLO207	rs2971581	101237203	5'-TGAGTTTCTTACTGGTGGAGA-3'	5'-AATTCTATACTTACTGGAATTGTTAG-3'
161	HAPLO208		101238028	5'-CTCTCTCTTCTATGAGCAAA-3'	5'-TTTCTACCAATGACCAGAAAA-3'
162	HAPLO209	rs4764874	101238450	5'-ACCATGTCCTGCTTTTGA-3'	5'-GTTACACCACACCCAGAAAG-3'
163	HAPLO208	rs2946836	101238635	5'-CTCTCTCTTCTATGAGCAAA-3'	5'-TTTCTACCAATGACCAGAAAA-3'
164	HAPLO210	rs7978057	101238645	5'-TTTGAGCATTATGACACCTCT-3'	5'-CTATGGCAAGGAGAGGATTA-3'
165	HAPLO210		101239365	5'-TTTGAGCATTATGACACCTCT-3'	5'-CTATGGCAAGGAGAGGATTA-3'
166	HAPLO212		101239778	5'-TTTTCGTAAAAGAGGCTTTG-3'	5'-CCAACCACAAGCCATAGA-3'
167	HAPLO213		101240704	5'-CCTGGGTTTTCTTTAAGTTT-3'	5'-GCACCCAGTATAATACCAACA-3'
168	HAPLO213	rs61201343	101240867	5'-CCTGGGTTTTCTTTAAGTTT-3'	5'-GCACCCAGTATAATACCAACA-3'
169	HAPLO214		101241107	5'-TGTTTTCTTCAGTAGACGTGTT-3'	5'-TGTGTTTCCCATCATTTCTTT-3'
170	HAPLO215	rs2946832	101241930	5'-CCTCCCGCAAGTTGTACT-3'	5'-GACTCAAAAGGGCAAGTAAG-3'
171	HAPLO217	rs57521049	101242139	5'-ATATGCAAAGGAGACCAATG-3'	5'-CCATTAGCAAGAAAATGTGG-3'
172	HAPLO218		101243024	5'-GCAGCTGCATCTGGTAAG-3'	5'-AGATGTGCAGAGAGAAGTGG-3'
173	HAPLO220	rs7971863	101243440	5'-TTAGAGACTTGGAGGGCTAA-3'	5'-GGAAAGCCCCTTATAAAATC-3'
174	HAPLO221		101244377	5'-CAGGTATCCTATAATCCCCA-3'	5'-TGAAACATAATGCAGTGCTC-3'
175	HAPLO221		101244619	5'-CAGGTATCCTATAATCCCCA-3'	5'-TGAAACATAATGCAGTGCTC-3'
176	HAPLO222	rs17032431	101244779	5'-GGAATGCAATTAACCTAAC-3'	5'-ACAGAAACACACATTTACAGAG-3'

177	HAPLO223	rs61935387	101245092	5'-GTTGGAGAAGCTGGAGAAA-3'	5'-CTCTGACTTTTCCCTCCAC-3'
178	HAPLO223	rs1520224	101245561	5'-GTTGGAGAAGCTGGAGAAA-3'	5'-CTCTGACTTTTCCCTCCAC-3'
179	HAPLO224	rs61935388	101245829	5'-AACAGTCACAGAACAATGTGATA-3'	5'-GTTGGTTTTCTTATCATGGC-3'
180	HAPLO224	rs61935389	101245980	5'-AACAGTCACAGAACAATGTGATA-3'	5'-GTTGGTTTTCTTATCATGGC-3'
181	HAPLO224		101246147	5'-AACAGTCACAGAACAATGTGATA-3'	5'-GTTGGTTTTCTTATCATGGC-3'
182	HAPLO226		101246173	5'-ATTACTGGACACTGGCTCTG-3'	5'-ACAGGTATGAAGGAAAAGCA-3'
183	HAPLO227	rs1581307	101247354	5'-ATGGATCTTGGAGAATAGCA-3'	5'-TCCACTTAAAATTAGCAGCTT-3'
184	HAPLO227	rs1581306	101247733	5'-ATGGATCTTGGAGAATAGCA-3'	5'-TCCACTTAAAATTAGCAGCTT-3'
185	HAPLO228		101247794	5'-AATGGACCTCTTTGGATTTT-3'	5'-AGGCAGTGTAACAGGAGTTG-3'
186	HAPLO230	rs61935390	101248229	5'-TTTAAGGACCCAATGATGTC-3'	5'-TGTGAATGTGAATGGAATGT-3'
187	HAPLO231		101249046	5'-AGGAGAAAAGATTACTCAGACC-3'	5'-TCTCTGAGTCCAGTGGGTAA-3'
188	HAPLO232	rs2090724	101249434	5'-GCTTTGCCCTAGAACTTGT-3'	5'-GAAGCAAGCCACTTCTTAAA-3'
189	HAPLO232	rs2090723	101250034	5'-GCTTTGCCCTAGAACTTGT-3'	5'-GAAGCAAGCCACTTCTTAAA-3'
190	HAPLO235		101250040	5'-GCTTCAGGATGAATTGTACC-3'	5'-TGATGAGTGATAGAAGATCTGA-3'
191	HAPLO235	rs1115322	101251271	5'-GCTTCAGGATGAATTGTACC-3'	5'-TGATGAGTGATAGAAGATCTGA-3'
192	HAPLO235	rs71303539	101251308	5'-GCTTCAGGATGAATTGTACC-3'	5'-TGATGAGTGATAGAAGATCTGA-3'
193	HAPLO238	rs2139568	101252558	5'-TGCTCTTCATTCTTTCACAC-3'	5'-AGGGAATAAAACCAACAGTC-3'
194	HAPLO241	rs1607693	101252904	5'-TCCTGGATTACTTGTGTGATT-3'	5'-CCTACTGCTGGGCATAAATA-3'
195	HAPLO241	rs11111243	101254198	5'-TCCTGGATTACTTGTGTGATT-3'	5'-CCTACTGCTGGGCATAAATA-3'
196	HAPLO243	rs61935391	101254494	5'-CTTTCACCTCTCCTGTTCCA-3'	5'-GATCTCCTGACCTCGTGA-3'
197	HAPLO244		101255354	5'-TTCCATAGACACTCCTGTGG-3'	5'-TTGGAGTCAGTAAGATGAAAAT-3'
198	HAPLO244		101255614	5'-TTCCATAGACACTCCTGTGG-3'	5'-TTGGAGTCAGTAAGATGAAAAT-3'
199	HAPLO244		101255711	5'-TTCCATAGACACTCCTGTGG-3'	5'-TTGGAGTCAGTAAGATGAAAAT-3'
200	HAPLO246	rs61935392	101255734	5'-TAATGGAACTTTTGGTTTGC-3'	5'-AAGTGCCTCTCTTTCTCAA-3'
201	HAPLO246	rs12814254	101256595	5'-TAATGGAACTTTTGGTTTGC-3'	5'-AAGTGCCTCTCTTTCTCAA-3'
202	HAPLO247	rs7138782	101256927	5'-AACTCCTCACCATGACCTG-3'	5'-CCGGGTAACAGAGCAAG-3'
203	HAPLO248	rs12370366	101257279	5'-CCAGTGCATCTCATTGAA-3'	5'-GGGAGGCGTTTAACAAAT-3'
204	HAPLO250		101257457	5'-CAAATAAAGTTCCAGCACCT-3'	5'-AAAGTTGAGGCTGCAGTG-3'
205	HAPLO250	rs11111244	101256442	5'-CAAATAAAGTTCCAGCACCT-3'	5'-AAAGTTGAGGCTGCAGTG-3'
206	HAPLO251	rs61935393	101258567	5'-TAGGACATTCTAGCCTTTT-3'	5'-GATTTCTCCTAACCTGAGGC-3'
207	HAPLO252		101258988	5'-CACAGGTAAGATATGCCAAAG-3'	5'-ATTGATGGACAGAAATCAGC-3'
208	HAPLO259	rs10860856	101259506	5'-TTCCCTTTCCCTTTTCTTAC-3'	5'-ACCATATCAGCCAATAAGCA-3'
209	HAPLO260	rs11111247	101262811	5'-TGGAACAATTTTACTTTCCC-3'	5'-TTTGCAAATTATGTATCTAACAAC-3'
210	HAPLO260		101263123	5'-TGGAACAATTTTACTTTCCC-3'	5'-TTTGCAAATTATGTATCTAACAAC-3'
211	HAPLO260	rs55816203	101263537	5'-TGGAACAATTTTACTTTCCC-3'	5'-TTTGCAAATTATGTATCTAACAAC-3'
212	HAPLO263		101264952	5'-TATGAATTTCCAGAGGACA-3'	5'-GTGGGGATTTTAGTTCCATT-3'
213	HAPLO264		101265034	5'-AAGTACAAACTCCAGAACAGTCT-3'	5'-CCAGGGATTAGGAAAGATTCT-3'
214	HAPLO264	rs7970321	101265193	5'-AAGTACAAACTCCAGAACAGTCT-3'	5'-CCAGGGATTAGGAAAGATTCT-3'
215	HAPLO265	rs1520218	101265472	5'-GAGGCCAAGTGTTCTTCAC-3'	5'-AAAACCACCCTAAGCAACTA-3'
216	HAPLO268	rs1533686	101266373	5'-ATTTAAGTGAATCAAAGAACTC-3'	5'-GGAATCATCTTGTGGCATT-3'
217	HAPLO268		101267346	5'-ATTTAAGTGAATCAAAGAACTC-3'	5'-GGAATCATCTTGTGGCATT-3'
218	HAPLO269		101267507	5'-AATGCAAAATGCTACTGGTTT-3'	5'-GATAAGCCTTTTCATCACAAGA-3'
219	HAPLO270	rs35909148	101267539	5'-ATAGGTCTGTAGTCCAGCC-3'	5'-CAGGTGGAAGATGACTGAAA-3'
220	HAPLO271	rs2971579	101268619	5'-CTGCACCTTGTGAGGACTGA-3'	5'-GCAGAGGAATGTGGAAGGAC-3'
221	HAPLO272		101268621	5'-ACTTGGGAGTCCGATGTTTG-3'	5'-TTAAATTCACCTTGCCCCAC-3'

222	HAPLO272	rs1850965	101269119	5'-ACTTGGGAGTCCGATGTTTG-3'	5'-TTAAATTCACCTTGCCCCAC-3'
223	HAPLO272	rs34052481	101269190	5'-ACTTGGGAGTCCGATGTTTG-3'	5'-TTAAATTCACCTTGCCCCAC-3'
224	HAPLO273		101269348	5'-TGCCTGTGAGAGTATTTCTGGA-3'	5'-CACACTTGGCACATAGCAGG-3'
225	HAPLO273		101269585	5'-TGCCTGTGAGAGTATTTCTGGA-3'	5'-CACACTTGGCACATAGCAGG-3'
226	HAPLO274		101270380	5'-CATCCATCTTCTGTTGGTGC-3'	5'-CAACCAGGCAATCTAAACCC-3'
227	HAPLO277		101270386	5'-TTTGGTCATGCCACAAGAAA-3'	5'-CCAACATCTGTAGCCCCATT-3'
228	HAPLO279		101271458	5'-CATTGAGTGCCTTTGGCTTT-3'	5'-TGGCTTAGGGTATCAGGTGG-3'
229	HAPLO279	rs1829517	101272792	5'-CATTGAGTGCCTTTGGCTTT-3'	5'-TGGCTTAGGGTATCAGGTGG-3'
230	HAPLO281	rs10860857	101272832	5'-TGACCCTTCTCAATGATTCCA-3'	5'-GCCTAGAATACCACCAGGCA-3'
231	HAPLO283	rs10860858	101273695	5'-TGCTGTAACATCTCCTTCAAACA-3'	5'-TGCTGAAAGAACTGGGAACA-3'
232	HAPLO284	rs10707673	101274701	5'-CTCCACACTGTACTGGGGC-3'	5'-AAAGCAAAACCACAATTGG-3'
233	HAPLO286	rs1996656	101275335	5'-AGACTTCAACAATCTTTGGCAG-3'	5'-CCCCTTGGTATTGTCCTCAC-3'
234	HAPLO288	rs73187920	101276092	5'-CAATTCCCCAAATCCTTGAA-3'	5'-AACTTACAACTGACATGTGCTTTC-3'
235	HAPLO289		101277008	5'-CCTGCTGCTTTCTACCTGTG-3'	5'-GGCAAGTCCATTAAAAGGAAAA-3'
236	HAPLO289	rs10860859	101277190	5'-CCTGCTGCTTTCTACCTGTG-3'	5'-GGCAAGTCCATTAAAAGGAAAA-3'
237	HAPLO290		101277457	5'-TGTGCATTGTGAAGCTGTGA-3'	5'-TCAGGGCTTCTCTGTCACTCT-3'
238	HAPLO291	rs11111250	101278039	5'-TGTGCATTGTGAAGCTGTGA-3'	5'-TCAGGGCTTCTCTGTCACTCT-3'
239	HAPLO294	rs58016032	101278461	5'-CAGAATAGCACAGACTAGATCCCT-3'	5'-GATGAAGAACTGAAATTTAGGTGA-3'
240	IGF1		101393530	5'-GAGGCCTAGGATGGCTGC-3'	5'-TCACCTTCACCAGCTCTGC-3'
241		rs855218	101430772	5'-GTGGACACCCCTTTCTCCTT-3'	5'-TCTCAGTCTCTGTGCTTGGG-3'
242		rs855216	101431432	5'-TGTGATTTCTCAGGTCCTATGTAGA-3'	5'-AAACAGAAGGGGCAAGGC-3'
243		rs7309412	101597223	5'-GCTACCATTAGCAGGGCTTG-3'	5'-GGCTCCAACTTTCCAAGAG-3'
244	BC037211	rs11111392	101741876	5'-CTCCCTGCACTTAAACAGA-3'	5'-ATCGCGCTTCCCCTTTC-3'
245	PAH	rs772897	101761598	5'-GCAGCAGGGAATCCTGATCC-3'	5'-CCAACCACCCACAGATGAG-3'
246	PAH	rs1042503	101770830	5'-GGTCTCCTAGTGCCCTGACTC-3'	5'-TCTTGCAGCAGGAAAAGATG-3'
247	PAH	rs1126758	101773054	5'-CCTAACCTGCGTTCTGCTGT-3'	5'-TCTCCTCTGCCTCAATCCTC-3'
248	PAH	rs2037639	101795480	5'-ACTCACAGGGTGGTCAGCAT-3'	5'-GGGTTATCTGGAAGCCAGC-3'
249		rs7959408	102125895	5'-TCACCAGTGCTTACAGGCAA-3'	5'-ATCCTGGAGGATTTGTGGGT-3'
250	C12orf42		102220312	5'-CTGAGGCCTCCTGTCCC-3'	5'-CCTCTGCAGGAGGAGCC-3'
251	C12orf42	rs12317808	102286768	5'-TTCATGAGCCAATGAATTTCC-3'	5'-CAGTACCCTGCTCCAGATTCA-3'
252	C12orf42	rs10778257	102396302	5'-TTAGTGGCTGAAATGGAGCA-3'	5'-TTCATGGATAGGATGATTCTGG-3'
253	BC041342	rs4086099	102465749	5'-GGAAGTGAAGGTTTCCAGA-3'	5'-GCAATGCAGTGGATTATCTT-3'
254	BC041342	rs4405407	102466587	5'-TTGATAGAATGAAGACATCACAT-3'	5'-TTCAGCAAGAGTTGGAAAAT-3'
255	BC041342	rs4531575	102466684	5'-TTGATAGAATGAAGACATCACAT-3'	5'-TTCAGCAAGAGTTGGAAAAT-3'
256	BC041342	rs4405408	102466686	5'-TTGATAGAATGAAGACATCACAT-3'	5'-TTCAGCAAGAGTTGGAAAAT-3'
257	BC041342	rs4540923	102466844	5'-TTGATAGAATGAAGACATCACAT-3'	5'-TTCAGCAAGAGTTGGAAAAT-3'
258	BC041342	rs11111644	102467468	5'-GCTTTACATGCACCTGTTTG-3'	5'-GAAAATCCACTTAAGCATTACC-3'
259	BC041342		102467495	5'-GCTTTACATGCACCTGTTTG-3'	5'-GAAAATCCACTTAAGCATTACC-3'
260	BC041342		102475511	5'-AGCCATGGTACATTCTGTTT-3'	5'-AAGCAAGGCCAATTTAACA-3'
261	BC041342		102475559	5'-AGCCATGGTACATTCTGTTT-3'	5'-AAGCAAGGCCAATTTAACA-3'
262	BC041342	rs10861037	102475671	5'-AGCCATGGTACATTCTGTTT-3'	5'-AAGCAAGGCCAATTTAACA-3'
263	BC041342	rs10861038	102477187	5'-AGGGAGAGAAATTTAGTGAGAGA-3'	5'-CAAGTTTCCAGGTGTCCTC-3'
264	BC041342		102477295	5'-GTTGGTAGCACTTTACTCAGG-3'	5'-TCAATAACAATTACACTTGCTG-3'
265	BC041342	rs10861039	102477379	5'-GTTGGTAGCACTTTACTCAGG-3'	5'-TCAATAACAATTACACTTGCTG-3'
266	BC041342	rs118336672	102477522	5'-GTTGGTAGCACTTTACTCAGG-3'	5'-TCAATAACAATTACACTTGCTG-3'

267	BC041342	rs1183830	102477531	5'-GTTGGTAGCACTTTACTCAGG-3'	5'-TCAATAACAATTACACTTGCTG-3'
268	BC041342		102477576	5'-GTTGGTAGCACTTTACTCAGG-3'	5'-TCAATAACAATTACACTTGCTG-3'
269	STAB2		102558178	5'-AAAGAAGAATGCCAGCTGAAG-3'	5'-CAGCAATGACTGGACACCAT-3'
270	STAB2		102568460	5'-TGTTGCCTGATTTTACTCCTCC-3'	5'-AAGGTA CTCCCTACTAAGGCTTTT-3'
271	STAB2	rs831427	102578564	5'-CAAGAGTGAAGTGTTGCATTT-3'	5'-AGGCAGGATAACCTGATGAA-3'
272	STAB2	rs11614418	102591942	5'-CTCAGTGCTTGGCTTGTCC-3'	5'-AGCGTCATTAAGTGCCATCC-3'
273	STAB2	rs703644	102592027	5'-CTCAGTGCTTGGCTTGTCC-3'	5'-AGCGTCATTAAGTGCCATCC-3'
274	STAB2	rs703651	102610761	5'-AGCAGAAACCCAGAGATCA-3'	5'-GGACGATAAACAACAAAGGGA-3'
275	STAB2	rs697210	102617126	5'-AAGCTGGGTAAGTGTCAAGG-3'	5'-AGCCAAGACACTATTCTCTCA-3'
276	STAB2		102621239	5'-GGCAATTGTCTATTGCTAACC-3'	5'-AATAGAAAAGCCTTATGCCCC-3'
277	STAB2	rs697212	102624747	5'-TTTCTACACCGAGGCTGGAC-3'	5'-CCTGCATATTCTGTTGGT-3'
278	STAB2	rs10778281	102648041	5'-GAAGCAATTTGTGTCTATTTCACTT-3'	5'-TGACTTCGAATCAGAATAGAGATGAT-3'
279	STAB2	rs4981042	102648191	5'-GAAGCAATTTGTGTCTATTTCACTT-3'	5'-TGACTTCGAATCAGAATAGAGATGAT-3'
280	STAB2	rs35102665	102660419	5'-TCAGATGCCACAGCACATTT-3'	5'-CAGGGAGCACACAGTCAAAA-3'
281	STAB2	rs2292688	102660446	5'-TCAGATGCCACAGCACATTT-3'	5'-CAGGGAGCACACAGTCAAAA-3'
282	STAB2	rs2056128	102664647	5'-TTGGAAAGTCTCCTTAGATGGG-3'	5'-AAGTCCTGCTCCTCTCCAC-3'
283	STAB2	rs3751200	102671301	5'-CATTGTTGGAACACTGCCA-3'	5'-AAAGGGCTGCACTTCCG-3'
284	STAB2	rs7296626	102673381	5'-GGGGAATCAGACATTAACCA-3'	5'-ATACCTGCTTTGAGGCAACC-3'
285	STAB2	rs7313163	102673650	5'-GGGGAATCAGACATTAACCA-3'	5'-ATACCTGCTTTGAGGCAACC-3'
286	STAB2	rs2271637	102677134	5'-TTTTCTTCGTCATCCCCATC-3'	5'-CAGGAACCTTGCATGCATTATC-3'
287	NT5DC3	rs11616136	102690225	5'-TTATGAGGAGTTTCCCCTG-3'	5'-ATCAGAATTTAACGTGGCAG-3'
288	NT5DC3	rs11612164	102690226	5'-TTATGAGGAGTTTCCCCTG-3'	5'-ATCAGAATTTAACGTGGCAG-3'
289	NT5DC3	rs9132	102690373	5'-TTATGAGGAGTTTCCCCTG-3'	5'-ATCAGAATTTAACGTGGCAG-3'
290	NT5DC3	rs3087891	102690659	5'-TTATGAGGAGTTTCCCCTG-3'	5'-ATCAGAATTTAACGTGGCAG-3'
291	NT5DC3	rs15918	102691154	5'-GTAAAAGGCCAGATAGGAAG-3'	5'-AGCCCTTTGTACCCATA-3'
292	NT5DC3	rs9084	102691512	5'-AGTTAATTTAGCTTTGGGCA-3'	5'-CAGCTTGTCTTGGTAAATCA-3'
293	NT5DC3	rs9142	102691534	5'-AGTTAATTTAGCTTTGGGCA-3'	5'-CAGCTTGTCTTGGTAAATCA-3'
294	NT5DC3		102693120	5'-TATAATGGTGAAGGTGACCC-3'	5'-TACACAGTCAGTGAGCCTTG-3'
295	NT5DC3	rs10861096	102693486	5'-TATAATGGTGAAGGTGACCC-3'	5'-TACACAGTCAGTGAGCCTTG-3'
296	NT5DC3	rs11111761	102693958	5'-TATTCTTTTGTGGAGGG-3'	5'-CCTAGAAGCAAGCAAACAAT-3'
297	NT5DC3	rs10861097	102694604	5'-AACTCCTGGACCCCTTTTG-3'	5'-TTAGCTTCAATGTCCTTCG-3'
298	NT5DC3	rs3751205	102695401	5'-TCTCCCAATGGTTAAGACAG-3'	5'-CTAGCTGGCAGGTTTTGA-3'
299	NT5DC3	rs3751204	102695585	5'-AAAAGAAGTGATTTTGATTTCA-3'	5'-TCAAGTGGTCTCACCTATCC-3'
300	NT5DC3	rs1866295	102711076	5'-TTGCAGATTGACAAATATCAT-3'	5'-GGATTTTACCAAGACACACC-3'
301	NT5DC3	rs10861107	102732998	5'-TTTCTTTAGGAATCATACTAACC-3'	5'-CAAGGCTGTTCTAAGAGGAA-3'
302	NT5DC3	rs11111797	102733102	5'-TTTCTTTAGGAATCATACTAACC-3'	5'-CAAGGCTGTTCTAAGAGGAA-3'
303	LOC253724	rs11111817	102779062	5'-TTGCACAATGAATGTAACCA-3'	5'-CCACTGGTAGGGGCACTTT-3'
304	LOC253724	rs11612613	102784338	5'-TTGGGTAGGTATCTGGTATCTG-3'	5'-CCAGGAGGAGATTGACTCTG-3'
305	LOC253724	rs10778292	102784417	5'-TTGGGTAGGTATCTGGTATCTG-3'	5'-CCAGGAGGAGATTGACTCTG-3'
306	LOC253724	rs2583237	102801702	5'-TTTTGCTGCAGTATTTCAAG-3'	5'-AACATAGCACTGGTAAAGGGA-3'
307	LOC253724	rs10745988	102807336	5'-CCTGGCTCATGTTAGCTCTG-3'	5'-CTTGTATGTGGCTCCTGCTT-3'
308	LOC253724	rs10778298	102807525	5'-CCTGGCTCATGTTAGCTCTG-3'	5'-CTTGTATGTGGCTCCTGCTT-3'
309	LOC253724	rs2583235	102811245	5'-ACTCCCATATTGTACCTACTCT-3'	5'-CTTCCCTGTGCAGGAATCTA-3'
310	LOC253724	rs2583234	102824209	5'-CCTTCTTCCCTTCCCTGGTA-3'	5'-AGAGAGAGCCACCCATTTCT-3'
311	LOC253724	rs10861141	102824221	5'-CCTTCTTCCCTTCCCTGGTA-3'	5'-AGAGAGAGCCACCCATTTCT-3'

312	LOC253724	rs9788136	102829287	5'-AACATGTAGAATCGAAATGTGAA-3'	5'-GGATTGCGTTTACCAAAGTC-3'
313	LOC253724	rs10861143	102832607	5'-TGGAGACTTCCTCCCTGACT-3'	5'-TCCTTTCACAAGGAAGACCT-3'
314	LOC253724	rs9788014	102833513	5'-GTGGCTGTGCTAGGATGAAA-3'	5'-TTTTGGCAGCAACATAGAGA-3'
315	LOC253724	rs7295489	102833558	5'-GTGGCTGTGCTAGGATGAAA-3'	5'-TTTTGGCAGCAACATAGAGA-3'
316	LOC253724		102833689	5'-GTGGCTGTGCTAGGATGAAA-3'	5'-TTTTGGCAGCAACATAGAGA-3'
317	LOC253724	rs2583273	102833842	5'-GTGGCTGTGCTAGGATGAAA-3'	5'-TTTTGGCAGCAACATAGAGA-3'
318	HSP90B1	rs2722187	102848278	5'-GATTGGTGGGTTCATGTTT-3'	5'-ATGGTGACGTCCCTTGG-3'
319	HSP90B1	rs2070908	102848312	5'-GATTGGTGGGTTCATGTTT-3'	5'-ATGGTGACGTCCCTTGG-3'
320	HSP90B1	rs17797090	102848396	5'-GATTGGTGGGTTCATGTTT-3'	5'-ATGGTGACGTCCCTTGG-3'
321	HSP90B1		102849403	5'-GATTGGTGGGTTCATGTTT-3'	5'-ATGGTGACGTCCCTTGG-3'
322	HSP90B1	rs6615	102852109	5'-CCTCAATATTTGTTTGGCAT-3'	5'-GAGAGTCAAGATCCTCACCA-3'
323	GLT8D2	rs2930855	102949008	5'-TGCAAAGGAGCAATCAAT-3'	5'-AGGTGGTGGGACATCATAG-3'
324	GLT8D2		102948128	5'-TGCAAAGGAGCAATCAAT-3'	5'-AGGTGGTGGGACATCATAG-3'
325	GLT8D2	rs35155010	102949615	5'-CAGTTTCTGGGGGATGAG-3'	5'-AACCTAGAGCCAGATCCTCT-3'
326	GLT8D2	rs2723869	102949799	5'-CAGTTTCTGGGGGATGAG-3'	5'-AACCTAGAGCCAGATCCTCT-3'
327	GLT8D2		102950147	5'-GTCTGTCTCTGCTCTTCTG-3'	5'-TCCCTTTTCTCTGCATCA-3'
328	GLT8D2		102907198	5'-GCCAATAAACATTGTTCTTTA-3'	5'-CTGAGGTCAGTTTACCTTCTATT-3'
329	GLT8D2	rs35844634	102968083	5'-ACAGCATCTTCCTTTACGTC-3'	5'-GCAATGAAACAGAAACCTAGA-3'
330	HCFC2	rs2272477	103013250	5'-TTTtaggtgttttctatTTTgAT-3'	5'-CTATTAAATTCCTCCACCGAT-3'
331	NFYB		103039238	5'-GGTTGTTAGGAAGGTGATGGTT-3'	5'-CAACAGAGCGATACTCCACC-3'
332	TXNRD1	rs7960443	103169493	5'-GCATCATCATGTTTTCTTT-3'	5'-TGAGCTCAAAAGTCTGTCAA-3'
333	TXNRD1	rs7975161	103169535	5'-GCATCATCATGTTTTCTTT-3'	5'-TGAGCTCAAAAGTCTGTCAA-3'
334	TXNRD1		103176207	5'-CAGGGTACTCTCCTGGAGCTAA-3'	5'-CCCTGCCAAAATTTCTGAAT-3'
335	TXNRD1	rs7310505	103178678	5'-TTCTGGGTCCAAAAGTAGCC-3'	5'-CATTATCCTGCCCATCTCT-3'
336	TXNRD1	rs9668964	103194579	5'-CTGCTGAAGTGCCAGTTGAA-3'	5'-AAGAGCCGACAGCTAGTCCA-3'
337	TXNRD1	rs11111979	103204912	5'-CGAGGAGTGGATTTCTGCTT-3'	5'-TCAGGACTCGACCACCTTTC-3'
338	TXNRD1	rs1128446	103204972	5'-AGGAAACAGCAACCCTTTCA-3'	5'-ATATCTTCCCTTCCCCGAGA-3'
339	TXNRD1	rs11111981	103208903	5'-CCTGGTTTTAATGGCAATGG-3'	5'-GCAGTCCCAGCACTTTAGGA-3'
340	TXNRD1	rs61937909	103221691	5'-TTAGTCGCGTGTGAGGTCAG-3'	5'-GCCACGGGTATCTCTGAGG-3'
341	EID3	rs11111987	103222712	5'-GCAGAAGTTGGACCTGAGTAGTT-3'	5'-TGCTTCAGTTTACATTTTACTCTCCA-3'
342	TXNRD1		103241387	5'-ATGATCTTTGCCAGCAGTT-3'	5'-TACTTTAACATTTTCTAACCAAAG-3'
343	CHST11		103375242	5'-TCTCAGCACTTCAGACCAA-3'	5'-GAGCGCGAGAGAGAAGAAAA-3'
344	CHST11	rs1704894	103506559	5'-CACAGACTGGCTCATTCCAA-3'	5'-GTGCTGTAAGGATGGCAGGT-3'
345	CHST11	rs1650130	103506598	5'-CACAGACTGGCTCATTCCAA-3'	5'-GTGCTGTAAGGATGGCAGGT-3'
346	CHST11	rs1650129	103506845	5'-ACCTGCCATCCTTACAGCAC-3'	5'-TGTCCTTTTGTGCTGGCTTT-3'
347	BC030271	rs2468110	103676521	5'-GCCCTGAAGATAGAGCGTTG-3'	5'-TAGGGGTCATGGACCTTCTG-3'
348	BC030271	rs2463018	103677127	5'-GCAATGGTTTTTACCCCTCA-3'	5'-GAAATGGGGCATGGATTATG-3'
349	BC030271	rs2453154	103677338	5'-CATAATCCATGCCCCATTTTC-3'	5'-TCCCACCCTCCCCTATTATT-3'
350	BC030271		103677535	5'-AGCCACATCCCTCTTACAGC-3'	5'-GTATAGTTGCTGCGCCCTTC-3'
351	BC030271	rs7847	103679735	5'-CCTCCAACCTTTTTCCATCA-3'	5'-TTGAATGGCTTTTCTGGAG-3'
352	SLC41A2	rs11112201	103723168	5'-AATTGAATCAGGGCCAACGTG-3'	5'-GTTTAGGCTTGTGGCCATGT-3'
353	SLC41A2		103827499	5'-GTAGATGCCAAGTTGGGAAA-3'	5'-TGCAGAAGCATATCAGAGAA-3'
354	SLC41A2	rs1745056	103846392	5'-TGATTCATCTGCTGTGGTT-3'	5'-AGTCATCATACTTTTGGCTG-3'
355	C12orf45	rs1129593	103904282	5'-CCCCTTACCCGAGCCTT-3'	5'-GGCTCCCAAACCTGCACC-3'
356	C12orf45		103904315	5'-CCCCTTACCCGAGCCTT-3'	5'-GGCTCCCAAACCTGCACC-3'

357	C12orf45		103912363	5'-AAATCCTGGGTTTCAGAATTTAC-3'	5'-TTCTTAGGTGACAGGCAGACC-3'
358	APPL2	rs8015	104091261	5'-GCCCTAGTTTTTGGGAAATTG-3'	5'-GGGTGCAGCTCTACCAGTTC-3'
359	APPL2	rs703683	104091265	5'-GCCCTAGTTTTTGGGAAATTG-3'	5'-GGGTGCAGCTCTACCAGTTC-3'
360	APPL2		104093899	5'-CCAAATCACATTTGTCTAAA-3'	5'-TGAAAAGACTCTTGGTATGTGT-3'
361	APPL2	rs1196852	104106375	5'-ACCTCAGCCTTCAACAAGTA-3'	5'-TTCACATCTTATTTCAATGGC-3'
362	APPL2		104107877	5'-ACCTCAGCCTTCAACAAGTA-3'	5'-TTCACATCTTATTTCAATGGC-3'
363	APPL2	rs2272495	104108007	5'-ACCTCAGCCTTCAACAAGTA-3'	5'-TTCACATCTTATTTCAATGGC-3'
364	APPL2		104121802	5'-ATGCTGCCATATTGTTATCC-3'	5'-ATGTTTCTTTCTACGACGATG-3'
365	APPL2		104121810	5'-ATGCTGCCATATTGTTATCC-3'	5'-ATGTTTCTTTCTACGACGATG-3'
366	APPL2		104125065	5'-ATGCTGCCATATTGTTATCC-3'	5'-ATGTTTCTTTCTACGACGATG-3'
367	APPL2		104125827	5'-CTTGACGCATATTCTCTTATT-3'	5'-ATCTTACAGTGGCTCTAAGCTG-3'
368	APPL2		104125949	5'-CTTGACGCATATTCTCTTATT-3'	5'-ATCTTACAGTGGCTCTAAGCTG-3'
369	APPL2		104153915	5'-AGGTACCTGGGGGCTGTC-3'	5'-CTCACCACACTTCCGGTTTC-3'
370	APPL2	rs1196785	104153995	5'-AGGTACCTGGGGGCTGTC-3'	5'-CTCACCACACTTCCGGTTTC-3'
371	OCC1	rs11538192	104288828	5'-GGCTTAAGGCTAATACATTTT-3'	5'-CCATTTACCAATTTTACAGC-3'
372	OCC1	rs6797	104289114	5'-AACTTAAGATGATAAGGCACTA-3'	5'-AATGCCATGTGTGACTTTA-3'
373	OCC1	rs1061749	104289227	5'-AACTTAAGATGATAAGGCACTA-3'	5'-AATGCCATGTGTGACTTTA-3'
374	RFX4		105519268	5'-GCCATGTTGATCACTAGCTGCTCA-3'	5'-ATTGCAGCTCCAGAAACGCTACAT-3'
375	RFX4		105607189	5'-GGTAGGATGGCCCCAGCTTTCCCTT-3'	5'-ACCTCAGCCTCCCAAGTGCTGAAA-3'
376	RFX4		105614331	5'-TGGCCTTGGTGGAGTCCCAAGCTT-3'	5'-CTTTACAAGGGAGGCCTCTGGACA-3'
377	RFX4		105650195	5'-TGCAACCTATGACCATGAGGAGAT-3'	5'-GATACCACTTAACCTGTTCACCAT-3'
378	ACACB	rs2878960	108062118	5'-CAAGAAGCAGGCAAACATCA-3'	5'-TCAGCTTCACCTGTGGTCAG-3'
379	ACACB		108089137	5'-GCACGTCTGTCCCTCATTTCT-3'	5'-AGTGCCGAGACCCATCTGTA-3'
380	FOXN4	rs10774641	108202080	5'-CCCTTTTTCTACAACACATGACTT-3'	5'-GGGAACACCCTGTTCTAGTCAGTT-3'
381	FOXN4	rs17177336	108207616	5'-TCCAACCTTGAGGCTGAGTGTC-3'	5'-TTCTGTGTGCGTGTGCGTGTA-3'
382	FOXN4	rs7959782	108210071	5'-GCCCCATAACTGGCCACAGAGACA-3'	5'-CCATGTGCTGGGTGAGTAACTGA-3'
383	FOXN4	rs11609341	108210090	5'-GCCCCATAACTGGCCACAGAGACA-3'	5'-CCATGTGCTGGGTGAGTAACTGA-3'
384	UBE3B		108421917	5'-GAGCCACAGGCAGGGAG-3'	5'-GGAAGAAGAAGATGGTGGGA-3'
385	UBE3B		108432615	5'-CTGTCCTCCCCTTGCTCTCT-3'	5'-CATGAGAGCTGAGTGCTCG-3'
386	UBE3B		108433517	5'-CTGTCCTCCCCTTGCTCTCT-3'	5'-CATGAGAGCTGAGTGCTCG-3'
387	UBE3B		108446231	5'-CCAATCCAAACACTGCATCA-3'	5'-GCCATCTCCTTCTGGGACTT-3'
388	ANAPC7		109308495	5'-CTTGTCATGTGGAAGAGAGAT-3'	5'-AGACTTCCAGACAAGCAAAG-3'
389	CCDC63		109815399	5'-TTGATCACGTTACTGTCTGC-3'	5'-GAAAGGCTGCTGTGGAC-3'
390	RPH3A	rs2240194	111803983	5'-ATGACAGCTGAGCACTGG-3'	5'-AACCCTGGGTATCTGCC-3'
391	RPH3A	rs4141253	111810012	5'-GGCACACAGTGGTGCTCTTA-3'	5'-AATTTCAGACCCAGAGGAAG-3'
392	OAS1	rs3741981	111833253	5'-GTGACTGAAGGAAATTCAGAG-3'	5'-TCCCTTCTTTCTCTCCTCC-3'
393	OAS1	rs1051042	111841620	5'-CGTAAATGCTCACTGAATCC-3'	5'-TGAAAATGAAGGAACTGGTC-3'
394	OAS2		111842229	5'-GGAAAACGAAACCAGAAATC-3'	5'-ACCGTAAGCCTATGTGAGG-3'
395	P/OKc1.4	rs1859330	111860771	5'-GGAAAACGAAACCAGAAATC-3'	5'-ACCGTAAGCCTATGTGAGG-3'
396	P/OKc1.4	rs1859329	111860835	5'-GGAAAACGAAACCAGAAATC-3'	5'-ACCGTAAGCCTATGTGAGG-3'
397	P/OKc1.4	rs12819767	111863773	5'-AGGTTGCAAGGCCACTAGAA-3'	5'-CCCTCTGGTCCACATAGCTC-3'
398	OAS2		111909276	5'-CAAGAGTCGTGTGCTATCAA-3'	5'-TGCGTTGAGCTGTATACCTA-3'
399	OAS2	rs1293756	111919676	5'-CAAGAGTCGTGTGCTATCAA-3'	5'-TGCGTTGAGCTGTATACCTA-3'
400	OAS2	rs1293755	111919833	5'-TGTAGGCATTCTAGCAAAGG-3'	5'-CAGCACTGGCTTGATAGG-3'
401	DDX54	rs2072137	111925304	5'-TTGGGAGAGGCAGGGTA-3'	5'-CTTCCCTTCTCAAGTTTCT-3'

402	LHX5		112092191	5'-CACCCCTTGCCTGGCTGT-3'	5'-CAGGATGGCGTTGGAGG-3'
403	LHX5	rs11609339	112393998	5'-CTGCTGAGACAAGAGGCGAA-3'	5'-GGGTATCCCCTTCCCCAG-3'
404	LHX5		112394044	5'-CTGCTGAGACAAGAGGCGAA-3'	5'-GGGTATCCCCTTCCCCAG-3'
405	LHX5		112394095	5'-CTGCTGAGACAAGAGGCGAA-3'	5'-GGGTATCCCCTTCCCCAG-3'

Transcript analysis

Name	Hg18	sequence (5'-3')
Race_Walk1 F	101233655	AAAAGATGAAGGCCCAAGGTGGGTGAG
Race_Walk1 R	101237219	GAGGCTCTCTTCCCGTTCCCCAAAGTA
Race_Walk2 F	101237189	TGCTTACTTTGGGGAACGGGAAGAGAG
Race_Walk2 R	101242034	TCCTTCCCACTGCCGTCTCTGCTAATC
Race_Walk3 F	101241978	AATGGAATTGGAGCTGGGATCTGAGG
Race_Walk3 R	101247020	CATCGGGCCCACTGTGAGATAAACTG
Race_Walk4 F	101246722	AAGGGAAGGCTGGATCCCCTTGAGGAA
Race_Walk4 R	101251829	ACAGTTGGAGACTTCGGACACACCTCT
Race_Walk5 F	101251665	GACCTGTAGCCTATGGCTGGCATTTTG
Race_Walk5 R	101256730	TGCTGGGTGGATGATGTAGTCTACGAGGA
Race_Walk6 F	101256702	TCCTCGTAGACTACATCATCCACCCAGCA
Race_Walk6 R	101261885	GCCAAAAGCACCCCTGCAGAAATTACC
Race_Walk7 F	101261742	TCCCACCTTGTCCTGCCTCCTGTTTAG
Race_Walk7 R	101266762	GGCCATTTCCCAGGTTCCCCAACTTA
Race_Walk8 F	101266580	CTGTGTGCTCCCAGGTGTATGGCAATG
Race_Walk8 R	101271724	GGGGAGGTTTCCCCTGTGCTATTCTCA
Race_Walk9 F	101271222	AGGGCTAGCCAATCAGCCCAACAAT
Race_Walk9 R	101276748	CATCACTCAGGACTCAGGCTTGCAGA
Race_Walk10 F	101276645	GAAGCCTTTAGGTTTCAGCGGAGGAGACA
Race_Walk10 R	101281465	GCCACTGCTGGAAGCCTCATTTAAAGC
Race_Walk11 F	101281208	TTGCAGTATTCGTGCTGAAGCCTGCTC
Race_Walk11 R	101286183	TGGGAACAATCTCCCAGACTGCCCTAA
Race_Walk12 F	101285758	CCCCAACATCCAAGAAAGCAGGAGT
Race_Walk12 R	101290792	AAACTCCCCAACATGGCATGGAAAA
Race_Walk13 F	101290701	GAAGGCAAAGCAGGCACTTGGAGACCT
Race_Walk13 R	101295749	CAGCTAACATGGCCCTCCCCTAAATGG
Race_Walk14 F	101295672	ACCATGGGGAGGAGAGCCTGCAAGTAT
Race_Walk14 R	101300704	GAGCTTTCACATGGCAAAGGAACAGTC
Race_Walk15 F	101300675	CTGACTGTTCCCTTTTGCCATGTGAAAGCTC
Race_Walk15 R	101305936	CACCCTACTTGGAAGCTTCCCCTTGCT
Race_Walk16 F	101305786	TGCTAAGGTTGGGTCCAGGAGTTCAACA
Race_Walk16 R	101310861	AATGACAGATGGATGGCAGAGCCTTCG
Race_Walk17 F	101310661	CATCTCATTCCATCACAGGGCGAAGAA
Race_Walk17 R	101313513	CCCCTCACTGTCACCCAACAGTGACTT
Race_Walk18 F	101118209	TTCATACACACTGGCCAAAGCCTCCAG
Race_Walk18 R	101123574	AGCCACCACGCCTGGCCTTACATAACT
Race_Walk19 F	101115733	TGTCAGCCTGCTTGGTAAACGATTCTG
Race_Walk19 R	101118743	TCCTACCAAGAAAACACCAAACCCAAAG

Race_Walk20 F	101123350	GGACTAGCTGCTTCCCTGGATCTCGTT
Race_Walk20 R	101129130	TGTCTTACCGCAGTCTTGACCTCCTGA
Race_Walk21 F	101128830	CTTAACCGCTCCAGATGTGGCCTTTC
Race_Walk21 R	101135455	AGCCTGGGAGTTCTGGGCTGTAATGT
Race_Walk22 F	101134694	GTTCCAGGACACCAAACAAAATCCAG
Race_Walk22 R	101140647	CTTTCTAGCGTGAGCAAGTGGGGAGAG
Race_Walk23 F	101140478	TGCCACTTCAACTTCAACATCCGAAAC
Race_Walk23 R	101146459	GATTCCGGTCCATGCCAACACTAATTC
Race_Walk24 F	101146231	GCTTCTGTGGGTTCTGTGTCTCCGTAA
Race_Walk24 R	101151965	TGTGGGGTACCAGAGACCCCTGTTCTA
Race_Walk25 F	101151542	AAATCCCTAGGAGTGGATGGCCAGAAA
Race_Walk25 R	101154646	TTGGTGTCTCCAGAACCACAAATTGGA
Race_Walk26 F	101154180	CTCTTGACCGGTGGATGAATCTCCCTA
Race_Walk26 R	101159606	TTGCATGTCAGAGGAGGATGACAATGA
Race_Walk27a F	101159533	CTCTGCTCTGCTTGGCCTGAAAAATGT
Race_Walk27a R	101163296	TGTGGTGGCTCACACACATAGCAAGA
Race_Walk27b F	101163213	TGCTCAGTTTGCTCCTGGATTTGACA
Race_Walk27b R	101167582	CCTTGAGGAAGGGTGAAGGAAATGGA
Race_Walk28 F	101167421	CCAGGCAAGCAGTAACCTCCTCCACAG
Race_Walk28 R	101174489	TCATGTGGCTCCAAATTTTGCTCTGC
Race_Walk29 F	101174472	AAATTTGGAGCCACATGATGTTTTGGA
Race_Walk29 R	101178523	GTGGAAGCCCAGAGATGGCACTAATGT
Race_Walk30 F	101178202	ACAGGCCACTGAGGCTGTGTTCACTTT
Race_Walk30 R	101185100	CAAGTCCTGAGGAAAAACAGGGGGAGT
Race_Walk31a F	101184752	TTCTCCCTCCCATGACCATGAATC
Race_Walk31a R	101188776	GCCCGACCGCCTTTTGAATTTTT
Race_Walk31b F	101188283	AATGGAGATCCTGAAATGCCATTCTG
Race_Walk31b R	101191826	GGGGATTCAAACCCAAGTCATTTGCT
Race_Walk32 F	101191617	TGGGCTGCTTTTCAATTTCTTGTAGGC
Race_Walk32 R	101197606	AAGTTTGTGCTTACCTGCCCCCAACTT
Race_Walk33 F	101197535	AGAAACTTGGGAGGCAAAGCTTCTACG
Race_Walk33 R	101203267	AAGAAAAAGCGCAAGGGAGAGGATGAC
Race_Walk34 F	101203015	GGGTTGGTCACAGCAACTAAGCTGACA
Race_Walk34 R	101208933	GCTCCAATCCATACGTTTTCTTCCAC
Race_Walk35 F	101208645	GAGACTGGTTGCCCTGTGTTCCAGAT
Race_Walk35 R	101215625	CAAGACAAGCATATCCAATCTCAGCATTCC
Race_Walk36 F	101215200	AGTGTGGGATGTTTCCCCATTTGTGTT
Race_Walk36 R	101221633	GGCTCAGAGATTTTGCCCAAACGTAGA
Race_Walk37 F	101221381	AGGGTTCCTCCCAGATGTCTTGCTTTC
Race_Walk37 R	101225487	ACCTTCTTTGCATAGCTAGGGGACATGG
Race_Walk38 F	101224534	TCCACCTTCCAGGGAACACGAATTTTA
Race_Walk38 R	101231685	TTGTAAAACGGGGGAAGAGCCAAGATG
Race_Walk39 F	101231662	CTTGGCTCTTCCCCCGTTTTACAATTT
Race_Walk39 R	101234973	ACAATTTGCAGAGGCATGTGGACAAAA
Race_Walk40 F	101313495	GTTGGGTGACAGTGAGGGGATTTTACG

Race_Walk40 R	101320366	TGCTCTGCACGAGTTACCTG
Race_Walk19a R (5' RACE)	101116025	GAGCCTGATGTCCTGTGGTCTTCCT
Race_Walk56 F (3' RACE)	101320285	GGGAAACGCCCATCTTTTAA

Fluorescent in situ hybridization

Name	Hg18	sequence (5'-3')
HELLP antisense probe	101181968	DIG-AAGGGCAAAGTATTAGAATCAACATCCAGCCAAAATCAAATGTCACTATC-DIG
HELLP sense probe	101181919	DIG-GATAGTGACATTTGATTTTGGCTGGATGTTGATTCTAATACTTTGCCCTT-DIG

siRNA-mediated knockdown

Name	Hg18	sequence (5'-3')
HELLP siRNA target 1	101151748	GAATATAAGTCTTGGGAA
HELLP siRNA target 2	101184144	GGAAAGAAGTCCATATAT
HELLP siRNA target 3	101270916	GGTCAGAGGTGGAGATAT
HELLP siRNA target 4	101304213	GCATAGAATTTAAGAGCAA

quantitative RT-PCR

Name	Hg18	sequence (5'-3')
HELLP qRT-PCR F1	101121296	GAAGCAGATGTCACGTACGG
HELLP qRT-PCR R1	101121494	CTGACCTCAATGGTATGGAT
HELLP qRT-PCR probe1	101121327	FAM-TGTCGCTTATCTGCTGGCTCA-TAMRA
HELLP qRT-PCR F2	101175253	ACACCATTTTGAGTATCATAA
HELLP qRT-PCR R2	101175397	CAGTCAATCTGATAAGAGAG
HELLP qRT-PCR probe2	101175280	FAM-CTGTTGCCATCCTGCTGTGTC-TAMRA

Morpholino-mediated block

Name	mutation (Hg18)	sequence (5'-3'), mutation in red
RW18-5	101120459	GGAAAATG GT GGTACATGTAAACTC
HAPLO378	101319702	CTTTGAGGCCAATCATTTT T AGGCA
HAPLO215Rev	101241930	AGAGAATATACC C TTGCTGAACTTC