Table SI. Statisticsof chromatin immunoprecipitation sequencing read alignment and peak enrichment.

Sample	SRR no.	Total reads	Filtered reads	uniqueMap reads	nodupMap reads	Nodup mapping rate (%)	Shift size x2	Peak no.
uniqueMap reads: reads that are uniquely mapped at the genome location. nodupMap reads: reads that have removed the duplicated reads.								
H2171								
BRD4	SRR617752	46,274,812	45,593,812	42,700,084	34,254,171	75.13	152	24,638
cMyc	SRR444473	47,430,412	45,155,090	43,383,424	34,650,346	76.74	172	39,686
H3K27Ac	SRR444438	37,703,344	29,935,748	28,414,775	26,602,557	88.87	179	34,131
H3K4me3	SRR444444	34,878,204	27,113,740	25,713,613	20,938,540	77.22	182	26,326
Max	SRR444474	41,944,382	39,792,115	38,761,443	24,291,754	61.05	162	56,629
Med1	SRR444452	31,905,501	29,601,448	28,281,755	24,910,159	84.15	163	9,817
PolII	SRR444475	51,191,292	48,367,011	45,542,840	28,464,760	58.85	170	22,308
WCE	SRR444476	35,526,743	28,488,105	27,684,495	26,553,721	93.21		
HUVEC								
BRD4	SRR1106515	26,656,632	24,338,550	22,378,751	17,840,590	73.30	179	9,958
H3K27Ac	SRR1106518	28,782,482	27,369,938	26,695,590	26,020,381	95.07	218	29,393
H3K4me3	SRR1106521	27,853,015	25,853,598	25,050,983	23,651,694	91.48	218	20,486
P65	SRR1106524	32,825,133	30,481,584	28,214,382	24,030,034	78.83	39	235
PolII	SRR1106527	30,294,197	22,858,324	20,778,939	19,054,074	83.36	205	17,117
WCE	SRR1106530	33,652,321	33,408,841	32,011,708	30,388,546	90.96		
BRD4	SRR1106516	32,027,136	29,348,226	27,688,070	22,428,484	76.42	180	10,190
H3K27Ac	SRR1106519	21,927,561	21,637,772	21,165,152	20,718,635	95.75	235	21,765

H3K4me3	SRR1106522	28,242,687	27,612,277	26,468,306	24,906,661	90.20	229	17,699
P65	SRR1106525	29,043,608	25,542,605	23,586,534	21,161,529	82.85	192	9,230
PolII	SRR1106528	26,895,353	23,893,090	21,894,042	17,107,631	71.60	179	17,021
WCE	SRR1106531	25,429,687	25,288,237	24,405,721	23,242,031	91.91		
KOPTK1								
BRD4	SRR1143134	27,728,442	23,959,296	23,007,703	21,464,756	89.59	174	17,984
H3K27Ac	SRR1143136	15,929,646	11,859,716	11,677,703	10,931,026	92.17	244	24,621
H3K4me3	SRR1143156	19,453,535	11,732,421	11,490,808	10,106,225	86.14	193	16,731
WCE	SRR1143161	25,109,739	19,784,261	19,074,062	18,433,098	93.17		
Ly1								
BCL6	SRR846913	21,975,536	20,986,618	16,467,117	11,585,842	55.21	157	3,634
BRD4	SRR846906	21,022,368	19,957,447	17,034,456	13,252,587	66.40	168	18,708
E2F1	SRR846912	28,320,755	24,485,655	20,434,088	10,013,557	40.90	165	9,944
H3K27Ac	SRR846902	28,525,297	28,176,365	26,875,138	23,053,100	81.82	179	27,211
H3K4me3	SRR846904	27,020,182	25,494,728	24,007,193	19,087,547	74.87	184	24,557
PolII	SRR846908	28,900,960	27,491,428	24,496,753	19,545,129	71.10	167	11,740
WCE	SRR846910	27,074,159	26,372,705	24,426,156	18,155,988	68.84		
MM.1S								
BRD4	SRR617757	46,935,006	32,000,043	30,250,078	24,755,449	77.36	201	2,079
cMyc	SRR444479	37,714,556	23,032,341	22,019,246	16,031,013	69.60	172	19,969
H3K27Ac	SRR444454	40,685,506	38,645,326	30,346,804	22,712,625	58.77	186	21,408
H3K4me3	SRR444455	33,787,303	27,122,264	24,924,465	24,100,830	88.86	175	27,007
IRF4	SRR942953	69781296	69486991	65749135	29702217	45.18	153	20,265
Med1	SRR617758	26,472,669	24,600,826	24,136,623	23,254,185	94.53	177	22,306
PolII	SRR444457	30,174,987	28,525,818	27,689,020	26,827,440	94.05	177	8,163
WCE	SRR444458	32,810,696	28,955,518	28,273,069	27,383,823	94.57		

U87								
BRD4	SRR747901	58,189,829	57,812,577	53,904,815	46,376,816	80.22	150	29,220
cMyc	SRR444432	53,593,219	46,824,035	37,018,672	27,143,480	57.97	155	11,155
H3K27Ac	SRR444436	48,963,070	38,800,957	37,775,139	22,217,895	57.26	181	34,704
H3K4me3	SRR444442	30,563,853	27,802,051	27,151,264	19,764,338	71.09	189	25,206
Max	SRR444448	51,775,588	47,040,250	39,095,568	31,805,354	67.61	163	57,793
Med1	SRR444453	52,598,199	41,701,281	39,219,826	32,367,887	77.62	165	27,174
PolII	SRR444478	60,181,947	55,008,501	46,204,440	15,892,513	28.89	146	16,324
WCE	SRR444467	39,915,674	37,933,099	36,176,909	32,346,671	85.27		

uniqueMap reads, reads that are uniquely mapped at the genome location; nodupMap reads, reads with duplicated reads removed.

Table SII. Overview of gene expression profile data.

Sets	GSM	GSE	Name	Source name	Platform
Train set	GSM1094084	GSE44929	MM1S_CONTROL_1	Multiple myeloma	PrimeView2
	GSM1094085	GSE44929	MM1S_CONTROL_2	Multiple myeloma	PrimeView2
	GSM1094090	GSE44929	MM1S_JQ1(500nm)_3h_1	Multiple myeloma	PrimeView2
	GSM1094091	GSE44929	MM1S_JQ1(500nm)_3h_2	Multiple myeloma	PrimeView2
	GSM1094092	GSE44929	MM1S_JQ1(500nm)_6h_1	Multiple myeloma	PrimeView2
	GSM1094093	GSE44929	MM1S_JQ1(500nm)_6h_2	Multiple myeloma	PrimeView2
	GSM1094096	GSE44929	MM1S_JQ1(50nm)_6h_1	Multiple myeloma	PrimeView2
	GSM1094097	GSE44929	MM1S_JQ1(50nm)_6h_2	Multiple myeloma	PrimeView2
	GSM1094098	GSE44929	MM1S_JQ1(5000nm)_6h_1	Multiple myeloma	PrimeView2
	GSM1094099	GSE44929	MM1S_JQ1(5000nm)_6h_2	Multiple myeloma	PrimeView2
	GSM1094100	GSE44929	MM1S_DMSO_6h_1	Multiple myeloma	PrimeView2
	GSM1094101	GSE44929	MM1S_DMSO_6h_2	Multiple myeloma	PrimeView2
	GSM1305222	GSE53999	HUVEC_CONTROL_1	Endothelium	PrimeView2
	GSM1305223	GSE53999	HUVEC_CONTROL_2	Endothelium	PrimeView2
	GSM1305224	GSE53999	HUVEC_CONTROL_3	Endothelium	PrimeView2
	GSM1305225	GSE53999	HUVEC_JQ1_1	Endothelium	PrimeView2
	GSM1305226	GSE53999	HUVEC_JQ1_2	Endothelium	PrimeView2
	GSM1305227	GSE53999	HUVEC_JQ1_3	Endothelium	PrimeView2
	GSM1305228	GSE53999	HUVEC_TNFa_1	Endothelium	PrimeView2
	GSM1305229	GSE53999	HUVEC_TNFa_2	Endothelium	PrimeView2
	GSM1305230	GSE53999	HUVEC_TNFa_3	Endothelium	PrimeView2
	GSM1305231	GSE53999	HUVEC_TNFa_JQ1_1	Endothelium	PrimeView2
	GSM1305232	GSE53999	HUVEC_TNFa_JQ1_2	Endothelium	PrimeView2
	GSM1305233	GSE53999	HUVEC_TNFa_JQ1_3	Endothelium	PrimeView2
	GSM1110909	GSE45630	Ly1_6h_DMSO_A	DLBCL	HuGene-1_0-st
	GSM1110910	GSE45630	Ly1_6h_DMSO_B	DLBCL	HuGene-1_0-st
	GSM1110911	GSE45630	Ly1_6h_DMSO_C	DLBCL	HuGene-1_0-st
	GSM1110912	GSE45630	Ly1_6h_JQ1_A	DLBCL	HuGene-1_0-st
	GSM1110913	GSE45630	Ly1_6h_JQ1_B	DLBCL	HuGene-1_0-st

	GSM1110914	GSE45630	Ly1_6h_JQ1_C	DLBCL	HuGene-1_0-st
	GSM1110915	GSE45630	Ly1_12h_DMSO_A	DLBCL	HuGene-1_0-st
	GSM1110916	GSE45630	Ly1_12h_DMSO_B	DLBCL	HuGene-1_0-st
	GSM1110917	GSE45630	Ly1_12h_DMSO_C	DLBCL	HuGene-1_0-st
	GSM1110918	GSE45630	Ly1_12h_JQ1_A	DLBCL	HuGene-1_0-st
	GSM1110919	GSE45630	Ly1_12h_JQ1_B	DLBCL	HuGene-1_0-st
	GSM1110920	GSE45630	Ly1_12h_JQ1_C	DLBCL	HuGene-1_0-st
	GSM1110921	GSE45630	Ly1_24h_DMSO_A	DLBCL	HuGene-1_0-st
	GSM1110922	GSE45630	Ly1_24h_DMSO_B	DLBCL	HuGene-1_0-st
	GSM1110923	GSE45630	Ly1_24h_DMSO_C	DLBCL	HuGene-1_0-st
	GSM1110924	GSE45630	Ly1_24h_JQ1_A	DLBCL	HuGene-1_0-st
	GSM1110925	GSE45630	Ly1_24h_JQ1_B	DLBCL	HuGene-1_0-st
	GSM1110926	GSE45630	Ly1_24h_JQ1_C	DLBCL	HuGene-1_0-st
Test set	GSM777654	GSE31365	KMS11_DMSO_24h_1	Multiple myeloma	HuGene-1_0-st
	GSM777655	GSE31365	KMS11_DMSO_24h_2	Multiple myeloma	HuGene-1_0-st
	GSM777656	GSE31365	KMS11_JQ1_24h_1	Multiple myeloma	HuGene-1_0-st
	GSM777657	GSE31365	KMS11_JQ1_24h_2	Multiple myeloma	HuGene-1_0-st
	GSM777658	GSE31365	OPM1_DMSO_24h_1	Multiple myeloma	HuGene-1_0-st
	GSM777659	GSE31365	OPM1_DMSO_24h_2	Multiple myeloma	HuGene-1_0-st
	GSM777660	GSE31365	OPM1_JQ1_24h_1	Multiple myeloma	HuGene-1_0-st
	GSM777661	GSE31365	OPM1_JQ1_24h_2	Multiple myeloma	HuGene-1_0-st
	GSM1061875	GSE43392	Kelly_DMSO_24h_1	Neuroblastoma	PrimeView
	GSM1061876	GSE43392	Kelly_JQ1_24h_1	Neuroblastoma	PrimeView
	GSM1061877	GSE43392	Kelly_DMSO_24h_2	Neuroblastoma	PrimeView
	GSM1061878	GSE43392	Kelly_JQ1_24h_2	Neuroblastoma	PrimeView
	GSM1061879	GSE43392	Kelly_DMSO_24h_3	Neuroblastoma	PrimeView
	GSM1061880	GSE43392	Kelly_JQ1_24h_3	Neuroblastoma	PrimeView
	GSM1061881	GSE43392	Be2C_DMSO_24h_1	Neuroblastoma	PrimeView
	GSM1061882	GSE43392	Be2C_JQ1_24h_1	Neuroblastoma	PrimeView
	GSM1061883	GSE43392	Be2C_DMSO_24h_2	Neuroblastoma	PrimeView
	GSM1061884	GSE43392	Be2C_JQ1_24h_2	Neuroblastoma	PrimeView
	GSM1061885	GSE43392	Be2C_DMSO_24h_3	Neuroblastoma	PrimeView
	GSM1061886	GSE43392	Be2C_JQ1_24h_3	Neuroblastoma	PrimeView
	GSM728964	GSE29449	Raji_Ctrl_0hr_rep2	Burkitt lymphoma	HuEx-1_0-st

	GSM728966	GSE29449	Raji_JQ1_8hr_rep1	Burkitt lymphoma	HuEx-1_0-st
	GSM728968	GSE29449	Raji_Ctrl_0hr_rep1	Burkitt lymphoma	HuEx-1_0-st
	GSM728970	GSE29449	Raji_JQ1R_4hr_rep1	Burkitt lymphoma	HuEx-1_0-st
	GSM728972	GSE29449	Raji_JQ1_4hr_rep2	Burkitt lymphoma	HuEx-1_0-st
	GSM728973	GSE29449	Raji_JQ1_4hr_rep1	Burkitt lymphoma	HuEx-1_0-st
	GSM728974	GSE29449	Raji_JQ1R_8hr_rep1	Burkitt lymphoma	HuEx-1_0-st
	GSM728975	GSE29449	Raji_JQ1R_4hr_rep2	Burkitt lymphoma	HuEx-1_0-st
	GSM728980	GSE29449	Raji_JQ1_8hr_rep2	Burkitt lymphoma	HuEx-1_0-st
	GSM728983	GSE29449	Raji_JQ1R_8hr_rep2	Burkitt lymphoma	HuEx-1_0-st
	GSM1234970	GSE51020	MB002_JQ1	Medulloblastoma	HuGene-1_0-st
	GSM1234971	GSE51020	MB002_JQ1R	Medulloblastoma	HuGene-1_0-st
	GSM1234972	GSE51020	MB004_JQ1	Medulloblastoma	HuGene-1_0-st
	GSM1234973	GSE51020	MB004_JQ1R	Medulloblastoma	HuGene-1_0-st
	GSM1234974	GSE51020	D283_JQ1	Medulloblastoma	HuGene-1_0-st
	GSM1234975	GSE51020	D283_JQ1R	Medulloblastoma	HuGene-1_0-st
	GSM1234976	GSE51020	D458_JQ1	Medulloblastoma	HuGene-1_0-st
	GSM1234977	GSE51020	D458_JQ1R	Medulloblastoma	HuGene-1_0-st
	GSM1234978	GSE51020	D556_JQ1	Medulloblastoma	HuGene-1_0-st
	GSM1234979	GSE51020	D556_JQ1R	Medulloblastoma	HuGene-1_0-st
Expression set	GSM229912	GSE9055	HUVEC.TNFa	Endothelium	Hgu133plus2
	GSM862922	GSE35169	U-87.Ctrl	Glioblastoma	Hgu133plus2
	GSM862923	GSE35169	U-87.Ctrl	Glioblastoma	Hgu133plus2
	GSM862924	GSE35169	U-87.Ctrl	Glioblastoma	Hgu133plus2
	GSM1314113	GSE54380	KOPT-K1.Ctrl	T-ALL	Hgu133plus2
	GSM1314114	GSE54380	KOPT-K1.Ctrl	T-ALL	Hgu133plus2
	GSM1374685	GSE57083	MM1.S.Ctrl	Multiple myeloma	Hgu133plus2
	GSM1374783	GSE57083	OCI-Ly1.Ctrl	DLBCL	Hgu133plus2

DLBCL, diffuse large B-cell lymphoma; T-ALL, T-cell acute lymphoblastic leukemia.

Table SIII. Super-enriched regions in the H2171 cell line.

chr	St	Ed	Genes	EnhancerType
chr1	1356299	1369226	TMEM88B;ANKRD65;VWA1	Super
chr1	2362467	2402521	PLCH2;PEX10	Super
chr1	10597077	10617239	PEX14	Super
chr1	10808787	10864962	CASZ1	Super
chr1	16552759	16575817	RSG1	Super
chr1	16982966	16996094	FAM231A;MST1P2	Super
chr1	17064377	17077521	FAM231A;MST1L	Super
chr1	17221670	17241328	CROCC	Super
chr1	18006798	18052422	nrg_ACTL8;ACTL8	Super
chr1	18155827	18174818	nrg_ACTL8;ACTL8	Super
chr1	18551489	18583342	IGSF21	Super
chr1	21894645	21919501	RAP1GAP;ALPL	Super
chr1	22938582	22953499	C1QA	Super
chr1	23871069	23886581	E2F2;ID3	Super
chr1	23917639	23946794	MDS2;ID3	Super
chr1	26058108	26093154	SEPN1;nrg_SEPN1	Super
chr1	27181265	27192655	SFN	Super
chr1	27844530	27855902	WASF2	Super
chr1	31207767	31224172	MATN1;LAPTM5	Super
chr1	31848568	31868200	FABP3;SERINC2	Super
chr1	31944207	31958651	LINC01225	Super
chr1	41826579	41883253	FOXO6;nrg_FOXO6	Super
chr1	41930311	41982378	nrg_EDN2;EDN2	Super
chr1	53573549	53621989	SLC1A7	Super

chr1	54001355	54020459	nrg_DMRTB1	Super
chr1	54037503	54058895	nrg_DMRTB1	Super
chr1	54083086	54107557	GLIS1	Super
chr1	54752622	54823099	SSBP3;nrg_SSBP3-AS1	Super
chr1	60688166	60701482	nrg_C1orf87	Super
chr1	61323396	61334106	LOC101926964	Super
chr1	61352205	61401449	nrg_LOC101926964;nrg_LOC100996570;LOC100996570	Super
chr1	62641104	62651321	L1TD1	Super
chr1	62821900	62850913	nrg_KANK4;KANK4;nrg_USP1	Super
chr1	68110942	68119213	GADD45A	Super
chr1	1.08E+08	1.08E+08	nrg_VAV3	Super
chr1	1.12E+08	1.12E+08	KCND3-IT1;nrg_KCND3-IT1	Super
chr1	1.12E+08	1.13E+08	KCND3	Super
chr1	1.17E+08	1.17E+08	nrg_ATP1A1	Super
chr1	1.17E+08	1.17E+08	IGSF3	Super
chr1	1.44E+08	1.44E+08	nrg_FAM72C	Super
chr1	1.6E+08	1.6E+08	NHLH1	Super
chr1	1.63E+08	1.63E+08	C1orf110	Super
chr1	1.83E+08	1.83E+08	RGS16	Super
chr1	1.83E+08	1.83E+08	LAMC2	Super
chr1	2.02E+08	2.02E+08	NAV1	Super
chr1	2.02E+08	2.02E+08	nrg_ELF3;GPR37L1;ELF3;nrg_GPR37L1	Super
chr1	2.02E+08	2.02E+08	GPR37L1	Super
chr1	2.02E+08	2.02E+08	LGR6	Super
chr1	2.02E+08	2.02E+08	LGR6;nrg_UBE2T	Super
chr1	2.06E+08	2.06E+08	SLC45A3;ELK4	Super

chr1	2.31E+08	2.31E+08	CAPN9	Super
chr1	2.33E+08	2.33E+08	SIPA1L2	Super
chr1	2.35E+08	2.35E+08	TARBP1	Super
chr1	2.35E+08	2.35E+08	IRF2BP2;LINC00184	Super
chr1	2.35E+08	2.35E+08	LINC01132	Super
chr1	2.37E+08	2.37E+08	RYR2	Super
chr1	2.44E+08	2.44E+08	SDCCAG8	Super
chr1	2.44E+08	2.44E+08	AKT3	Super
chr10	1493702	1512414	nrg_ADARB2-AS1	Super
chr10	80988577	81046606	nrg_PPIF	Super
chr10	97054734	97087625	PDLIM1	Super
chr10	1.13E+08	1.13E+08	PDCD4-AS1;nrg_PDCD4-AS1	Super
chr11	22355490	22371649	SLC17A6	Super
chr11	31893410	31898420	nrg_PAUPAR	Super
chr11	32008584	32028908	nrg_RCN1	Super
chr11	33912602	33935030	LMO2	Super
chr11	44947442	45020052	TP53I11;LOC221122;nrg_LOC221122	Super
chr11	45043027	45078718	PRDM11;nrg_PRDM11;nrg_LOC221122	Super
chr11	45104890	45132683	PRDM11	Super
chr11	45353838	45399442	SYT13;nrg_SYT13	Super
chr11	45532659	45560960	nrg_CHST1	Super
chr11	46360344	46385676	DGKZ	Super
chr11	48019801	48046921	PTPRJ	Super
chr11	60834964	60859661	CD5	Super
chr11	61370238	61403787	RPLP0P2	Super
chr11	65244529	65266999	MALAT1	Super

chr11	78644354	78671060	nrg_NARS2	Super
chr11	86195082	86200298	nrg_CCDC81	Super
chr11	1.11E+08	1.11E+08	COLCA1	Super
chr11	1.11E+08	1.11E+08	LOC100132078	Super
chr11	1.16E+08	1.16E+08	nrg_LINC00900	Super
chr11	1.16E+08	1.16E+08	nrg_LINC00900	Super
chr11	1.26E+08	1.26E+08	CDON;nrg_CDON;nrg_RPUSD4	Super
chr12	271615	298834	SLC6A12;LOC574538	Super
chr12	1930751	1958596	LRTM2;nrg_LRTM2	Super
chr12	2025356	2046780	LINC00940;CACNA2D4	Super
chr12	2683386	2696245	nrg_CACNA1C-AS1	Super
chr12	3311957	3357727	nrg_PRMT8;TSPAN9	Super
chr12	3807592	3837836	EFCAB4B	Super
chr12	6479993	6485132	LTBR;SCNN1A	Super
chr12	6641617	6644688	GAPDH	Super
chr12	6739729	6747490	LPAR5	Super
chr12	6872977	6888641	PTMS;LAG3	Super
chr12	7052278	7054359	C12orf57	Super
chr12	7070155	7080492	SCARNA12;EMG1	Super
chr12	8122885	8129939	SLC2A3	Super
chr12	27899739	27906774	MANSC4;nrg_MANSC4	Super
chr12	50257888	50267168	BCDIN3D	Super
chr12	50432873	50451510	RACGAP1;ASIC1	Super
chr12	53264035	53274232	nrg_KRT8;KRT78	Super
chr12	54550098	54569472	SMUG1;nrg_SMUG1	Super
chr12	55381910	55419007	TESPA1;NEUROD4	Super

chr12	55444888	55466388	nrg_NEUROD4	Super
chr12	57607896	57634785	NDUFA4L2;SHMT2;NXPH4	Super
chr12	75973069	75996533	nrg_KRR1	Super
chr12	1.25E+08	1.25E+08	nrg_NCOR2;nrg_SCARB1	Super
chr12	1.25E+08	1.25E+08	SCARB1;nrg_SCARB1	Super
chr12	1.25E+08	1.25E+08	UBC	Super
chr13	48729126	48743515	nrg_ITM2B;nrg_MED4	Super
chr13	52356118	52409556	LINC00282;DHRS12	Super
chr13	53741274	53757565	nrg_OLFM4	Super
chr13	60023419	60027415	nrg_DIAPH3-AS1	Super
chr13	72086834	72100550	DACH1	Super
chr13	72176065	72196766	DACH1	Super
chr13	72371318	72389708	DACH1	Super
chr13	72427671	72453926	DACH1	Super
chr13	1E+08	1E+08	CLYBL-AS2;nrg_CLYBL-AS2	Super
chr13	1E+08	1.01E+08	nrg_ZIC5;nrg_CLYBL-AS1	Super
chr13	1.01E+08	1.01E+08	ZIC5;ZIC2	Super
chr14	19636475	19643192	DUXAP10	Super
chr14	19932183	19938859	DUXAP10	Super
chr14	21562428	21578639	ZNF219	Super
chr14	23445833	23479896	AJUBA;C14orf93	Super
chr14	24834618	24878571	NYNRIN;NFATC4	Super
chr14	29681583	29693825	nrg_C14orf23	Super
chr14	55556098	55589942	LGALS3;nrg_MAPK1IP1L	Super
chr14	74855282	74870188	SYNDIG1L;nrg_SYNDIG1L	Super
chr14	75099827	75116006	LTBP2	Super

chr14	77372941	77423541	nrg_LRRC74;nrg_IRF2BPL	Super
chr14	77493848	77537609	LOC102724190;LOC283575;IRF2BPL	Super
chr14	81420922	81454299	TSHR	Super
chr14	90976238	90989791	nrg_LINC00642	Super
chr14	94429140	94454634	ASB2;LINC00521	Super
chr14	1.01E+08	1.01E+08	WDR25	Super
chr14	1.01E+08	1.01E+08	WDR25	Super
chr14	1.01E+08	1.01E+08	WDR25;nrg_BEGAIN	Super
chr14	1.01E+08	1.01E+08	BEGAIN;LINC00523	Super
chr14	1.01E+08	1.01E+08	DLK1	Super
chr14	1.06E+08	1.06E+08	nrg_TMEM121	Super
chr14	1.06E+08	1.06E+08	ELK2AP	Super
chr14	1.06E+08	1.06E+08	nrg_KIAA0125;KIAA0125	Super
chr15	31498919	31573537	KLF13;nrg_LOC283710;LOC283710	Super
chr15	31587689	31599091	KLF13	Super
chr15	31617498	31695670	KLF13;nrg_KLF13	Super
chr15	31756214	31781299	nrg_KLF13	Super
chr15	39844276	39851392	THBS1	Super
chr15	40384351	40406977	BMF	Super
chr15	46591192	46608806	nrg_SQRDL	Super
chr15	47798112	47815327	nrg_SEMA6D	Super
chr15	66437747	66465514	MEGF11	Super
chr15	69261341	69309354	NOX5	Super
chr15	69336246	69367376	NOX5;LINC00277	Super
chr15	69425545	69453151	GLCE	Super
chr15	70540637	70557092	nrg_TLE3	Super

chr15	70636103	70679526	nrg_TLE3	Super
chr15	74510357	74552312	STRA6;CCDC33	Super
chr15	75113389	75126336	CPLX3	Super
chr15	79461078	79486093	nrg_ANKRD34C;nrg_RASGRF1	Super
chr15	93351736	93383630	nrg_ASB9P1;LOC100507217	Super
chr16	2514285	2521907	C16orf59;NTN3	Super
chr16	11135754	11152357	CLEC16A	Super
chr16	11167076	11207333	CLEC16A;nrg_SOCS1	Super
chr16	11230272	11263078	nrg_SOCS1	Super
chr16	11874534	11891563	ZC3H7A	Super
chr16	27905447	27940517	GSG1L	Super
chr16	48989399	49006507	nrg_CBLN1	Super
chr16	49525364	49627363	nrg_C16orf78	Super
chr16	70719610	70749765	MTSS1L	Super
chr16	85253474	85348864	LINC00311;nrg_LINC00311	Super
chr16	85382192	85399556	nrg_LINC00311	Super
chr16	85418336	85437099	nrg_LINC00311	Super
chr16	85452273	85519671	nrg_GSE1;nrg_LINC00311	Super
chr16	85619841	85683767	GSE1;MIR7851	Super
chr17	1693002	1701221	SMYD4;nrg_SERPINF1	Super
chr17	3782291	3809079	P2RX1;CAMKK1	Super
chr17	7784804	7792962	CHD3	Super
chr17	17394761	17427296	RASD1	Super
chr17	17571129	17598400	RAI1	Super
chr17	17726693	17753856	SREBF1	Super
chr17	18870349	18897563	SLC5A10;FAM83G	Super

chr17	18964474	18974210	GRAP;LOC388436	Super
chr17	19078610	19106289	LOC388436	Super
chr17	32939889	32948115	TMEM132E	Super
chr17	34959298	34986274	MRM1;nrg_MRM1	Super
chr17	37763737	37778727	NEUROD2;PPP1R1B	Super
chr17	38210345	38232284	MED24;THRA	Super
chr17	41471140	41517098	nrg_ARL4D;ARL4D	Super
chr17	41530404	41561618	DHX8	Super
chr17	46079759	46104401	COPZ2;nrg_COPZ2;nrg_CDK5RAP3	Super
chr17	55311356	55338221	MSI2	Super
chr17	55518409	55562640	nrg_LOC101927557	Super
chr17	55579802	55685685	nrg_LOC101927539;LOC101927557;nrg_LOC101927557;LOC101927539	Super
chr17	55738990	55750235	nrg_LOC101927539	Super
chr17	55976180	56018925	CUEDC1	Super
chr17	60765097	60805675	MIR548W	Super
chr17	70403346	70436840	LINC00673	Super
chr17	72327901	72340232	KIF19	Super
chr17	74519032	74543850	CYGB;PRCD	Super
chr17	75759517	75800389	nrg_FLJ45079	Super
chr17	75861304	75884666	FLJ45079;nrg_FLJ45079	Super
chr17	77770587	77787807	CBX8	Super
chr18	53071853	53091659	TCF4	Super
chr19	3036069	3076516	TLE2;AES	Super
chr19	13063749	13094920	GADD45GIP1;NFIX;DAND5	Super
chr19	13133226	13172705	NFIX	Super
chr19	13720546	13752058	nrg_CCDC130;nrg_CACNA1A	Super

chr19	29796691	29829182	nrg_UQCRFS1	Super
chr19	31117331	31155266	nrg_ZNF536	Super
chr19	38527405	38569959	SIPA1L3;nrg_DPF1	Super
chr19	48833190	48854654	TMEM143;EMP3;nrg_EMP3	Super
chr19	48867217	48876867	SYNGR4	Super
chr19	49137446	49158492	DBP;CA11	Super
chr2	2010633	2021327	nrg_PXDN	Super
chr2	2321792	2333330	MYT1L;MYT1L-AS1	Super
chr2	2844430	2854944	nrg_LINC01250	Super
chr2	8817851	8826506	ID2;LOC100506299	Super
chr2	10466569	10501855	HPCAL1	Super
chr2	19951109	19960298	nrg_LINC00954	Super
chr2	20737712	20751209	nrg_HS1BP3-IT1	Super
chr2	20797824	20836045	HS1BP3-IT1;HS1BP3	Super
chr2	23752786	23769240	KLHL29	Super
chr2	23806657	23823034	KLHL29	Super
chr2	28600793	28636929	FLJ31356;FOSL2	Super
chr2	50756572	50774460	nrg_NRXN1	Super
chr2	50978236	51020532	NRXN1	Super
chr2	51047075	51103375	NRXN1	Super
chr2	51239809	51260019	NRXN1	Super
chr2	55324225	55348371	RTN4;nrg_RTN4	Super
chr2	56236114	56246095	nrg_EFEMP1	Super
chr2	70311984	70317267	PCBP1-AS1;PCBP1	Super
chr2	70350813	70370530	nrg_PCBP1;C2orf42	Super
chr2	85647634	85685537	CAPG;nrg_SH2D6;SH2D6	Super

chr2	85955933	86028467	LOC284950;ATOH8	Super
chr2	1.32E+08	1.32E+08	nrg_ARHGEF4;nrg_AMER3	Super
chr2	1.35E+08	1.35E+08	TMEM163	Super
chr2	1.35E+08	1.35E+08	TMEM163	Super
chr2	1.37E+08	1.37E+08	CXCR4	Super
chr2	1.56E+08	1.56E+08	KCNJ3	Super
chr2	1.74E+08	1.74E+08	nrg_CDCA7	Super
chr2	1.75E+08	1.75E+08	nrg_SP3;SP3	Super
chr2	1.78E+08	1.78E+08	TTC30A;TTC30B;nrg_TTC30A	Super
chr2	1.82E+08	1.82E+08	CERKL	Super
chr2	1.82E+08	1.83E+08	CERKL	Super
chr2	1.83E+08	1.83E+08	NEUROD1	Super
chr2	2.17E+08	2.17E+08	LINC01280;IGFBP2	Super
chr2	2.19E+08	2.19E+08	CTDSP1;SLC11A1	Super
chr2	2.33E+08	2.33E+08	PTMA	Super
chr20	5815713	5830583	nrg_CHGB	Super
chr20	5844577	5868067	CHGB	Super
chr20	12508461	12517033	nrg_LOC101929486	Super
chr20	19730679	19747202	nrg_RIN2	Super
chr20	20054140	20076698	C20orf26	Super
chr20	20179752	20235393	nrg_INSM1;nrg_C20orf26	Super
chr20	20342995	20357292	INSM1	Super
chr20	20376630	20391965	nrg_INSM1	Super
chr20	20420703	20549906	nrg_INSM1;RALGAPA2	Super
chr20	20570948	20592530	RALGAPA2	Super
chr20	23950511	23976896	GGTLC1;nrg_GGTLC1	Super

chr20	24442426	24456555	SYNDIG1	Super
chr20	24698778	24704026	nrg_CST7	Super
chr20	30191536	30201227	ID1	Super
chr20	30217859	30228519	COX4I2	Super
chr20	30295860	30312093	BCL2L1	Super
chr20	31098726	31127096	nrg_LOC101929698;LOC101929698	Super
chr20	45427324	45444329	nrg_SLC2A10;nrg_EYA2	Super
chr20	45587975	45608516	EYA2	Super
chr20	45984807	45990911	ZMYND8	Super
chr20	46464683	46505754	nrg_SULF2;SULF2	Super
chr20	48883780	48925824	LINC01271;LINC01270;LINC01272	Super
chr20	52352353	52368051	nrg_SUMO1P1	Super
chr20	61405232	61428193	MRGBP;LINC00659	Super
chr21	34505974	34525408	LOC101928107;nrg_C21orf54	Super
chr21	39218147	39251764	KCNJ6	Super
chr21	43484130	43518507	UMODL1;C21orf128	Super
chr21	46518644	46549113	ADARB1	Super
chr22	16184026	16206202	BMS1P17;nrg_BMS1P17	Super
chr22	18792616	18815207	GGT3P	Super
chr22	20704681	20721199	ZNF74	Super
chr22	21596318	21616467	POM121L8P	Super
chr22	23846606	23865687	LOC388882	Super
chr22	30089554	30141545	CABP7;ZMAT5	Super
chr22	37726918	37751191	nrg_CYTH4	Super
chr22	37802296	37831512	ELFN2	Super
chr22	37844276	37894886	MFNG;ELFN2	Super

chr22	40393786	40419693	FAM83F;TNRC6B	Super
chr22	42691055	42807253	nrg_TCF20;nrg_NFAM1;NFAM1	Super
chr22	43185128	43210872	ARFGAP3	Super
chr22	44981998	44996471	LINC00229;nrg_LINC00207	Super
chr22	49314756	49327775	nrg_WI2-81516E3.1	Super
chr3	10494837	10513639	ATP2B2	Super
chr3	11324046	11349050	ATG7	Super
chr3	16842528	16866271	nrg_PLCL2	Super
chr3	1.26E+08	1.26E+08	CHST13;C3orf22	Super
chr3	1.27E+08	1.27E+08	ABTB1;nrg_ABTB1	Super
chr3	1.28E+08	1.28E+08	nrg_DNAJB8-AS1	Super
chr3	1.29E+08	1.29E+08	nrg_H1FOO;PLXND1	Super
chr3	1.4E+08	1.4E+08	CLSTN2	Super
chr3	1.4E+08	1.4E+08	nrg_CLSTN2-AS1	Super
chr3	1.7E+08	1.7E+08	nrg_CLDN11	Super
chr3	1.7E+08	1.7E+08	SLC7A14	Super
chr4	8031248	8056374	ABLIM2	Super
chr4	79963014	79972983	LINC01088	Super
chr4	80106626	80133967	nrg_NAA11	Super
chr4	80236645	80259983	NAA11	Super
chr4	80300799	80320295	GK2;nrg_GK2	Super
chr4	1.41E+08	1.41E+08	SCOC	Super
chr5	14138764	14165416	TRIO	Super
chr5	14732044	14757136	nrg_OTULIN	Super
chr5	22185791	22195442	nrg_PMCHL1	Super
chr5	35353249	35371134	nrg_PRLR	Super

chr5	38420612	38427232	EGFLAM	Super
chr5	43007411	43020648	LOC648987	Super
chr5	1.35E+08	1.35E+08	nrg_NEUROG1;TIFAB	Super
chr5	1.42E+08	1.42E+08	nrg_ARHGAP26-AS1	Super
chr5	1.5E+08	1.5E+08	SYNPO	Super
chr6	6657274	6663577	LY86-AS1	Super
chr6	6676854	6705186	nrg_LY86-AS1	Super
chr6	14384389	14409302	nrg_LINC01108	Super
chr6	14428644	14455116	nrg_LINC01108	Super
chr6	15131474	15153543	nrg_JARID2	Super
chr6	17415492	17432415	CAP2	Super
chr6	17473537	17492636	nrg_LOC101928491	Super
chr6	20686226	20709220	CDKAL1	Super
chr6	21586852	21597592	SOX4	Super
chr6	25620656	25638782	SCGN	Super
chr6	32935182	32940619	BRD2	Super
chr6	33711682	33739845	IP6K3;LEMD2	Super
chr6	33918028	33956700	nrg_LINC01016	Super
chr6	35005232	35018728	nrg_TCP11	Super
chr6	41638497	41650405	nrg_MDFI	Super
chr6	43766223	43825394	nrg_VEGFA	Super
chr6	1.08E+08	1.08E+08	OSTM1	Super
chr6	1.12E+08	1.12E+08	TRAF3IP2	Super
chr6	1.12E+08	1.12E+08	TRAF3IP2;FYN;nrg_TRAF3IP2	Super
chr6	1.15E+08	1.15E+08	nrg_HS3ST5	Super
chr7	1021528	1041173	nrg_CYP2W1;CYP2W1	Super

chr7	1309305	1342136	nrg_UNCX	Super
chr7	1444338	1469212	nrg_MICALL2;MICALL2	Super
chr7	3214366	3232811	nrg_SDK1	Super
chr7	5463111	5468933	TNRC18	Super
chr7	31024257	31068835	nrg_GHRHR;GHRHR;ADCYAP1R1	Super
chr7	31718032	31732696	PPP1R17	Super
chr7	47802500	47822059	C7orf69;LINC00525	Super
chr7	1.06E+08	1.06E+08	CDHR3;nrg_SYPL1	Super
chr7	1.27E+08	1.27E+08	nrg_SND1-IT1	Super
chr8	53134572	53168108	ST18	Super
chr8	62045387	62063609	nrg_CLVS1	Super
chr8	62256522	62260241	CLVS1	Super
chr8	62286048	62297413	CLVS1	Super
chr8	62324852	62327960	CLVS1	Super
chr8	62456605	62476857	ASPH	Super
chr8	62503659	62509088	ASPH	Super
chr8	62698290	62718620	nrg_ASPH	Super
chr8	63074282	63112138	NKAIN3;nrg_NKAIN3	Super
chr8	93107248	93121114	RUNX1T1	Super
chr8	93616870	93625048	nrg_FLJ46284	Super
chr8	1.24E+08	1.24E+08	nrg_ZHX2	Super
chr8	1.26E+08	1.26E+08	MTSS1;nrg_MTSS1	Super
chr8	1.29E+08	1.29E+08	MYC	Super
chr8	1.34E+08	1.34E+08	nrg_NDRG1	Super
chr9	85919396	85933100	FRMD3	Super
chr9	1.02E+08	1.02E+08	TGFBR1;nrg_ALG2	Super

chr9	1.12E+08	1.12E+08	EPB41L4B	Super
chr9	1.2E+08	1.2E+08	ASTN2	Super
chr9	1.26E+08	1.26E+08	nrg_CRB2	Super
chr9	1.26E+08	1.26E+08	nrg_CRB2	Super
chr9	1.3E+08	1.3E+08	ANGPTL2	Super
chr9	1.3E+08	1.3E+08	STXBP1;FAM129B	Super
chr9	1.32E+08	1.32E+08	LINC00963;nrg_LINC00963	Super
chr9	1.32E+08	1.32E+08	LINC00963	Super
chr9	1.33E+08	1.33E+08	NCS1	Super
chr9	1.33E+08	1.33E+08	ASS1	Super
chr9	1.35E+08	1.35E+08	RAPGEF1	Super
chr9	1.35E+08	1.35E+08	nrg_RAPGEF1	Super
chr9	1.35E+08	1.35E+08	nrg_RAPGEF1	Super
chr9	1.35E+08	1.35E+08	MED27	Super
chr9	1.35E+08	1.35E+08	MED27	Super
chr9	1.35E+08	1.35E+08	nrg_NTNG2;SETX;NTNG2	Super
chr9	1.37E+08	1.37E+08	nrg_SARDH	Super
chr9	1.37E+08	1.37E+08	RXRA	Super
chr9	1.37E+08	1.37E+08	COL5A1;nrg_COL5A1	Super
chr9	1.38E+08	1.38E+08	COL5A1;nrg_FCN2	Super
chr9	1.38E+08	1.38E+08	OLFM1	Super
chr9	1.38E+08	1.38E+08	OLFM1;LOC401557	Super
chr9	1.38E+08	1.38E+08	C9orf62;nrg_C9orf62	Super
chr9	1.39E+08	1.4E+08	EGFL7;nrg_NOTCH1;NOTCH1;nrg_EGFL7	Super
chrX	39670493	39715603	nrg_BCOR	Super

Table SIV. Super-enriched regions in the HUVEC line.

chr	St	Ed	Genes
chr1	21587620	21608029	ECE1
chr1	21647457	21661513	ECE1
chr1	22250701	22301961	HSPG2;CELA3B
chr1	39643982	39658556	MACF1
chr1	56913781	56968986	PPAP2B;nrg_PPAP2B
chr1	66797507	66841169	PDE4B
chr1	85763188	85811292	BCL10;nrg_BCL10
chr1	86041692	86051162	CYR61
chr1	94129654	94147903	BCAR3
chr1	95248764	95268053	LINC01057
chr1	1.01E+08	1.01E+08	LOC100128787;nrg_LOC100128787
chr1	1.01E+08	1.01E+08	VCAM1
chr1	1.01E+08	1.01E+08	nrg_EXTL2;EXTL2
chr1	1.02E+08	1.02E+08	S1PR1;nrg_S1PR1
chr1	1.02E+08	1.02E+08	nrg_RNU6-31P;nrg_S1PR1
chr1	1.5E+08	1.5E+08	HIST2H2AA3;HIST2H3A
chr1	1.55E+08	1.55E+08	SLC50A1;EFNA1
chr1	1.7E+08	1.7E+08	SELE
chr1	1.72E+08	1.72E+08	nrg_C1orf105
chr1	1.73E+08	1.73E+08	nrg_TNFSF18
chr1	1.83E+08	1.83E+08	NMNAT2
chr1	1.86E+08	1.86E+08	MIR548F1
chr1	1.87E+08	1.87E+08	PTGS2
chr1	1.87E+08	1.87E+08	PLA2G4A
chr1	1.87E+08	1.87E+08	PLA2G4A
chr1	2.05E+08	2.05E+08	nrg_NUAK2;NUAK2;TMCC2
chr1	2.08E+08	2.08E+08	PLXNA2
chr1	2.35E+08	2.35E+08	nrg_SNORA14B
chr10	3816315	3830091	KLF6
chr10	3919243	3938896	nrg_KLF6
chr10	3961547	3978753	nrg_KLF6
chr10	4806050	4823579	nrg_AKR1E2;AKR1E2
chr10	8089671	8108119	GATA3-AS1;GATA3
chr10	13923467	13937237	nrg_PRPF18
chr10	21651747	21659511	nrg_CASC10
chr10	21807215	21824724	SKIDA1;MLLT10
chr10	25326825	25370448	nrg_THNSL1;ENKUR
chr10	33537067	33575670	NRP1
chr10	62174116	62190327	ANK3
chr10	74055593	74081545	nrg_DDIT4;nrg_DNAJB12
chr10	94449124	94459955	HHEX
chr10	94574975	94594036	EXOC6

chr10	95218287	95242816	MYOF
chr10	1.02E+08	1.02E+08	DNMBP
chr11	33710408	33724018	C11orf91
chr11	61730082	61746797	FTH1
chr11	65258314	65267436	MALAT1
chr11	65657796	65687406	FOSL1;CCDC85B;C11orf68
chr11	69064219	69090091	MYEOV;nrg_MYEOV
chr11	71639629	71660358	RNF121
chr11	86166855	86197319	nrg_CCDC81
chr11	86225955	86236756	nrg_CCDC81;ME3
chr11	86303038	86319978	ME3
chr11	86510957	86530033	PRSS23
chr11	1.02E+08	1.02E+08	BIRC2
chr11	1.03E+08	1.04E+08	nrg_DDI1
chr11	1.22E+08	1.22E+08	MIR100HG
chr11	1.28E+08	1.28E+08	nrg_ETS1
chr11	1.29E+08	1.29E+08	SENCR
chr11	1.32E+08	1.32E+08	NTM
chr12	6249979	6292093	VWF;CD9
chr12	11948219	11975954	RNU6-19P
chr12	12030293	12039667	RNU6-19P
chr12	14986479	15003071	ART4
chr12	46761204	46808412	SLC38A2
chr12	46823067	46853844	nrg_SLC38A2
chr12	46866408	46887389	nrg_SLC38A2
chr12	47040262	47061896	nrg_SLC38A4
chr12	54811587	54827233	ITGA5
chr12	59310578	59320540	LRIG3
chr12	59462908	59479664	nrg_LRIG3
chr12	65995825	66007039	nrg_HMGA2
chr12	66024243	66061235	nrg_HMGA2
chr12	89548728	89560800	nrg_LOC728084
chr12	89605148	89632973	nrg_DUSP6
chr12	89738590	89748624	DUSP6
chr12	93395657	93427142	nrg_EEA1
chr12	96587563	96614023	ELK3
chr12	96813722	96840795	CDK17
chr12	1.06E+08	1.06E+08	nrg_C12orf75
chr12	1.21E+08	1.21E+08	PXN
chr13	28903291	28932097	FLT1
chr13	40347691	40361691	COG6
chr13	40436681	40469873	nrg_COG6
chr13	41069661	41083012	LINC00598
chr13	97875783	97927775	MBNL2

chr13	97947647	97988308	MBNL2;nrg_RAP2A
chr14	34032747	34040537	nrg_EGLN3
chr14	35868053	35874969	NFKBIA
chr14	59787895	59804564	DAAM1
chr14	69238111	69262929	nrg_ZFP36L1;ZFP36L1
chr14	75078103	75088106	LTBP2
chr14	85932595	85942693	nrg_FLRT2
chr14	85993278	85999991	FLRT2
chr15	39109630	39138775	nrg_C15orf53
chr15	39175695	39189233	nrg_C15orf53
chr15	39283053	39289949	nrg_C15orf54
chr15	39402439	39434445	nrg_C15orf54
chr15	39538496	39563955	nrg_C15orf54;C15orf54
chr15	39650239	39658643	nrg_C15orf54
chr15	39870564	39890989	THBS1
chr15	42222342	42250850	EHD4;nrg_LOC101928363;LOC101928363
chr15	62399703	62434499	nrg_C2CD4B;nrg_C2CD4A
chr15	62454078	62469387	C2CD4B
chr15	66905920	66954587	LINC01169;SMAD6;nrg_SMAD6
chr15	67357200	67443865	SMAD3
chr15	74934831	74957644	EDC3;nrg_CLK3
chr15	95382598	95389549	nrg_MCTP2;nrg_LINC01197
chr15	95830219	95848680	LINC01197
chr15	96864808	96901160	NR2F2-AS1;nrg_NR2F2;NR2F2
chr16	20911240	20923476	LYRM1
chr16	29272633	29284058	SNX29P2
chr16	56639617	56644871	MT2A
chr16	66392527	66417402	CDH5
chr16	77321478	77342940	nrg_SYCE1L
chr16	77488646	77492797	ADAMTS18
chr16	77598510	77630927	nrg_NUDT7;nrg_ADAMTS18
chr16	81719600	81745769	nrg_PLCG2
chr16	86598573	86620577	FOXC2;FOXL1
chr16	86694976	86716072	nrg_FOXL1
chr16	86933324	86966562	nrg_LOC101928708
chr16	88267554	88279877	nrg_LOC101928880
chr17	32547889	32585964	CCL2
chr17	41653921	41673583	ETV4
chr17	57502558	57519018	LOC101927728;nrg_YPEL2
chr17	57830641	57870219	VMP1
chr17	57902808	57933564	TUBD1;nrg_TUBD1
chr17	62719771	62729435	nrg_LOC146880
chr17	78762323	78768241	LOC101928855;nrg_LOC101928855
chr18	20045847	20052459	nrg_CTAGE1

chr18	20130975	20143721	nrg_CTAGE1
chr18	20247471	20255559	nrg_CTAGE1
chr18	26298952	26317566	nrg_CDH2
chr18	26372202	26383905	nrg_CDH2
chr18	46454861	46479060	SMAD7
chr18	47185802	47228185	nrg_LIPG;nrg_ACAA2
chr18	53167245	53179182	TCF4
chr19	10375694	10399082	ICAM4;ICAM1
chr19	12893382	12905557	HOOK2;JUNB
chr19	13947454	13977217	NANOS3
chr2	20644977	20653553	RHOB
chr2	20761095	20784774	nrg_HS1BP3-IT1;HS1BP3-IT1
chr2	20798735	20818444	HS1BP3-IT1
chr2	28609737	28633709	FLJ31356;FOSL2
chr2	36677465	36720859	CRIM1;nrg_FEZ2
chr2	36768539	36798291	FEZ2;nrg_FEZ2
chr2	56212279	56220822	nrg_EFEMP1
chr2	85961737	86000390	ATOH8
chr2	1E+08	1E+08	AFF3
chr2	1.14E+08	1.14E+08	IL1A;nrg_IL1B
chr2	1.44E+08	1.44E+08	KYNU
chr2	1.6E+08	1.6E+08	TANC1;nrg_WDSUB1
chr2	1.61E+08	1.61E+08	ITGB6
chr2	1.7E+08	1.7E+08	ABCB11
chr2	1.87E+08	1.87E+08	nrg_ZC3H15;ITGAV
chr2	1.95E+08	1.95E+08	nrg_LOC101927406
chr2	2.02E+08	2.02E+08	CFLAR
chr2	2.08E+08	2.08E+08	KLF7
chr2	2.08E+08	2.08E+08	nrg_LOC101927865
chr2	2.32E+08	2.32E+08	ARMC9
chr2	2.37E+08	2.37E+08	ACKR3
chr2	2.38E+08	2.38E+08	nrg_COPS8;nrg_ACKR3
chr2	2.38E+08	2.38E+08	nrg_COPS8
chr2	2.38E+08	2.38E+08	nrg_COPS8
chr2	2.38E+08	2.38E+08	nrg_COPS8;COPS8
chr20	1353967	1381087	FKBP1A-SDCBP2
chr20	10646971	10656136	JAG1
chr20	11159026	11227470	nrg_LOC101929413
chr20	19782154	19798795	nrg_RIN2
chr20	19887209	19896311	RIN2
chr20	19909868	19918519	RIN2
chr20	31053068	31073425	NOL4L
chr21	33888601	33897494	nrg_TCP10L
chr21	43035959	43069650	nrg_LINC00111;LINC00111

chr21	45579443	45605932	nrg_C21orf33
chr22	30587978	30609266	nrg_LIF
chr22	41680982	41699156	RANGAP1;ZC3H7B
chr3	10206175	10248071	IRAK2
chr3	11225745	11250446	HRH1
chr3	15671779	15690125	BTD
chr3	30196913	30206400	nrg_RBMS3-AS1
chr3	30323411	30336448	nrg_TGFBR2
chr3	30382483	30392841	nrg_TGFBR2
chr3	30552928	30591639	nrg_TGFBR2
chr3	30647350	30653079	TGFBR2
chr3	64884438	64908709	MIR548A2
chr3	1.29E+08	1.29E+08	PLXND1
chr3	1.49E+08	1.49E+08	WWTR1
chr3	1.52E+08	1.52E+08	nrg_TMEM14E;MBNL1;TMEM14E
chr3	1.7E+08	1.7E+08	nrg_SLC7A14;nrg_RPL22L1
chr3	1.71E+08	1.71E+08	nrg_RPL22L1
chr3	1.72E+08	1.72E+08	PLD1
chr3	1.72E+08	1.72E+08	FNDC3B
chr3	1.73E+08	1.73E+08	NLGN1
chr3	1.94E+08	1.94E+08	TMEM44-AS1
chr3	1.95E+08	1.95E+08	nrg_XXYLT1-AS1
chr3	1.95E+08	1.95E+08	nrg_XXYLT1-AS1;XXYLT1-AS2;nrg_XXYLT1-AS2
chr4	38052131	38108367	TBC1D1;nrg_TBC1D1
chr4	55934467	55950590	KDR
chr4	74568217	74610587	IL8
chr4	74733833	74739075	CXCL1
chr4	74959683	74983527	CXCL2
chr4	1.2E+08	1.2E+08	LOC645513;nrg_LOC645513
chr4	1.38E+08	1.38E+08	nrg_LINC00613
chr4	1.39E+08	1.39E+08	SLC7A11
chr4	1.39E+08	1.39E+08	nrg_LINC00499
chr4	1.45E+08	1.46E+08	nrg_HHIP
chr4	1.46E+08	1.46E+08	HHIP-AS1;HHIP
chr4	1.59E+08	1.59E+08	nrg_FAM198B
chr4	1.59E+08	1.59E+08	FAM198B
chr5	1075298	1087057	SLC12A7
chr5	14187145	14208772	TRIO
chr5	34582963	34628937	nrg_RAI14;RAI14
chr5	34654891	34659501	RAI14
chr5	52300354	52328420	ITGA2
chr5	55287543	55294239	FLJ31104;IL6ST
chr5	55462757	55508531	ANKRD55
chr5	55565185	55579226	ANKRD55

chr5	55614080	55655201	nrg_ANKRD55;nrg_LOC102467147
chr5	64493607	64506158	ADAMTS6
chr5	64769552	64779355	ADAMTS6
chr5	66596817	66612001	nrg_CD180
chr5	76101235	76128436	F2RL1
chr5	77814175	77827007	LHFPL2
chr5	81682143	81703177	nrg_ATP6AP1L
chr5	1.14E+08	1.14E+08	KCNN2
chr5	1.19E+08	1.19E+08	HSD17B4;TNFAIP8
chr5	1.31E+08	1.31E+08	nrg_CSF2;IL3;CSF2
chr5	1.34E+08	1.34E+08	nrg_SAR1B;JADE2
chr5	1.36E+08	1.36E+08	nrg_TRPC7
chr5	1.44E+08	1.44E+08	YIPF5;KCTD16
chr5	1.47E+08	1.47E+08	DPYSL3;JAKMIP2-AS1
chr5	1.5E+08	1.5E+08	TNIP1
chr5	1.6E+08	1.6E+08	nrg_PTTG1
chr5	1.63E+08	1.63E+08	nrg_MAT2B
chr5	1.63E+08	1.63E+08	nrg_MAT2B
chr5	1.63E+08	1.63E+08	nrg_MAT2B
chr5	1.69E+08	1.69E+08	FAM196B
chr6	7899598	7911701	TXNDC5
chr6	7974319	7977704	PIP5K1P1
chr6	7990343	8005699	PIP5K1P1;nrg_PIP5K1P1
chr6	11207260	11225397	NEDD9
chr6	11586708	11615639	TMEM170B;nrg_TMEM170B
chr6	11649345	11654232	nrg_TMEM170B
chr6	11754770	11773339	ADTRP
chr6	17826510	17866473	KIF13A;nrg_NUP153
chr6	22880810	22893372	nrg_HDGFL1
chr6	30709517	30721096	IER3
chr6	31509108	31532325	LTA;DDX39B;NFKBIL1
chr6	31544571	31550622	LTB
chr6	32936024	32940430	BRD2
chr6	1.13E+08	1.13E+08	LAMA4
chr6	1.22E+08	1.22E+08	nrg_GJA1
chr6	1.26E+08	1.26E+08	NCOA7;HINT3
chr6	1.34E+08	1.35E+08	SGK1
chr6	1.35E+08	1.35E+08	LINC01010;nrg_LINC01010
chr6	1.38E+08	1.38E+08	nrg_TNFAIP3
chr6	1.38E+08	1.38E+08	nrg_TNFAIP3
chr6	1.38E+08	1.38E+08	LOC100130476;TNFAIP3
chr6	1.51E+08	1.51E+08	MTHFD1L
chr6	1.58E+08	1.58E+08	SYNJ2
chr6	1.58E+08	1.58E+08	SYNJ2

chr6	1.67E+08	1.67E+08	RPS6KA2
chr7	22153959	22169597	nrg_CDCA7L
chr7	22602145	22629943	nrg_LOC100506178;LOC100506178
chr7	27135202	27165008	HOTAIRM1;HOXA3;HOXA1
chr7	27169142	27176656	HOXA4;HOXA-AS3
chr7	27178437	27201223	HOXA7;HOXA6;HOXA5;HOXA-AS3
chr7	33764271	33774505	nrg_BMPER
chr7	39626571	39668068	YAE1D1;RALA
chr7	1.01E+08	1.01E+08	TRIM56;SERPINE1
chr7	1.08E+08	1.08E+08	NRCAM;nrg_NRCAM
chr7	1.16E+08	1.16E+08	nrg_TES;nrg_CAV2
chr7	1.16E+08	1.16E+08	CAV1
chr7	1.31E+08	1.31E+08	LINC-PINT;LOC100506860
chr7	1.31E+08	1.31E+08	nrg_PODXL
chr7	1.34E+08	1.34E+08	BPGM
chr7	1.55E+08	1.55E+08	nrg_INSIG1
chr8	10633902	10658040	PINX1;SOX7;nrg_SOX7
chr8	17204442	17213102	MTMR7
chr8	32180608	32193354	nrg_NRG1-IT3
chr8	39956328	39982655	nrg_C8orf4;C8orf4
chr8	40010552	40033247	nrg_C8orf4;C8orf4
chr8	55239122	55252296	nrg_SOX17
chr8	59739656	59771569	nrg_NSMAF
chr8	61815778	61823670	nrg_CHD7
chr8	70089622	70099656	nrg_LOC100505718
chr8	96693477	96716561	nrg_C8orf37
chr8	1.04E+08	1.04E+08	CTHRC1
chr8	1.06E+08	1.06E+08	ZFPM2
chr8	1.2E+08	1.2E+08	nrg_TNFRSF11B
chr8	1.2E+08	1.2E+08	COLEC10
chr8	1.29E+08	1.29E+08	nrg_TMEM75;PVT1
chr8	1.29E+08	1.29E+08	nrg_TMEM75
chr9	682644	695633	KANK1
chr9	18330561	18341111	nrg_ADAMTSL1
chr9	18356808	18361228	nrg_ADAMTSL1
chr9	21674054	21690713	nrg_MIR31HG;nrg_MTAP
chr9	33495807	33511947	SUGT1P1
chr9	1.03E+08	1.03E+08	MSANTD3
chr9	1.24E+08	1.24E+08	TRAF1
chr9	1.31E+08	1.31E+08	ENG
chr9	1.35E+08	1.35E+08	RAPGEF1
chrX	23800873	23826608	SAT1;nrg_SAT1
chrX	45556499	45576681	nrg_LINC01204

HUVEC, human umbilical vein endothelial cell.

Table SV. Super-enriched regions in the KOPT-K1 cell line.

chr	St	Ed	Genes	
chr1	8978004	9008609	CA6	
chr1	11412603	11469107	nrg_UBIAD1;nrg_PTCHD2	
chr1	21945408	21960527	RAP1GAP	
chr1	23376499	23410270	KDM1A	
chr1	25278864	25364346	RUNX3;nrg_RUNX3	
chr1	27925476	27961854	AHDC1;FGR	
chr1	32387894	32430318	PTP4A2	
chr1	42315530	42386390	HIVEP3	
chr1	54939806	54955583	nrg_ACOT11;nrg_SSBP3	
chr1	94526785	94561495	ABCA4	
chr1	1.02E+08	1.02E+08	nrg_S1PR1;nrg_LOC102606465	
chr1	1.02E+08	1.02E+08	nrg_RNU6-31P	
chr1	1.12E+08	1.12E+08	CHI3L2;DENND2D	
chr1	1.16E+08	1.16E+08	VANGL1	
chr1	1.17E+08	1.17E+08	CD58;nrg_CD58	
chr1	1.17E+08	1.17E+08	CD2	
chr1	1.5E+08	1.5E+08	HIST2H2AA3	
chr1	1.58E+08	1.58E+08	CD1B	
chr1	1.58E+08	1.58E+08	OR10T2	
chr1	1.61E+08	1.61E+08	CD48;SLAMF1	
chr1	1.68E+08	1.68E+08	RCSD1	
chr1	1.7E+08	1.7E+08	SELL	
chr1	1.81E+08	1.81E+08	KIAA1614	
chr1	1.98E+08	1.98E+08	NEK7	
chr1	1.99E+08	1.99E+08	PTPRC	
chr1	1.99E+08	1.99E+08	LINC01222;nrg_LINC01222	
chr1	1.99E+08	1.99E+08	nrg_LINC01222	
chr1	2.02E+08	2.02E+08	PTPN7	
chr1	2.08E+08	2.08E+08	nrg_CD34;CD34	
chr1	2.29E+08	2.29E+08	nrg_RAB4A	
chr1	2.34E+08	2.34E+08	nrg_COA6	
chr10	8367144	8375594	nrg_LINC00708	
chr10	11186977	11222895	CELF2	
chr10	48451983	48490859	nrg_GDF10;GDF10	
chr10	63510086	63545183	nrg_C10orf107;C10orf107;nrg_ARID5B	
chr10	73472043	73534388	C10orf54;C10orf105	
chr10	74007678	74097412	DNAJB12;DDIT4;nrg_DDIT4;nrg_DNAJB12	
chr10	80853179	80908239	ZMIZ1	
chr10	89788185	89828117	nrg_KLLN	
chr10	90134608	90152603	RNLS	
chr10	92689598	92709264	ANKRD1	
chr10	1.02E+08	1.02E+08	SEC31B	

chr10	1.21E+08	1.21E+08	SFXN4	
chr10	1.26E+08	1.26E+08	FAM53B	
chr10	1.33E+08	1.33E+08	TCERG1L	
chr11	310582	356764	IFITM3;B4GALNT4;IFITM1	
chr11	17432845	17461692	KCNJ11;ABCC8	
chr11	32436995	32456671	WT1	
chr11	33879275	33916215	LMO2	
chr11	65183628	65193213	NEAT1	
chr11	67030012	67057361	ANKRD13D;ADRBK1	
chr11	77988643	78066320	GAB2	
chr11	78125154	78143796	GAB2	
chr11	1.18E+08	1.18E+08	FXYD2	
chr11	1.18E+08	1.18E+08	CD3E	
chr11	1.18E+08	1.18E+08	CD3G	
chr11	1.23E+08	1.23E+08	UBASH3B;nrg_CRTAM	
chr11	1.28E+08	1.28E+08	ETS1	
chr12	7045541	7080678	C12orf57;PTPN6;EMG1;SCARNA12	
chr12	11911353	11967945	RNU6-19P;ETV6	
chr12	48201537	48231921	HDAC7	
chr12	51762315	51789878	GALNT6;SLC4A8	
chr12	55362107	55385749	TESPA1	
chr12	56320016	56326857	WIBG	
chr12	89410763	89445546	LOC728084	
chr12	89616252	89646723	nrg_DUSP6	
chr12	1.05E+08	1.05E+08	CHST11	
chr12	1.09E+08	1.09E+08	SELPLG	
chr12	1.13E+08	1.14E+08	RASAL1;DTX1	
chr12	1.22E+08	1.22E+08	ORAI1;MORN3	
chr12	1.22E+08	1.22E+08	SETD1B;RHOF	
chr12	1.3E+08	1.3E+08	TMEM132D	
chr12	1.33E+08	1.33E+08	CHFR;GOLGA3	
chr13	26442405	26459341	nrg_SHISA2	
chr13	30945147	30996570	nrg_HMGB1;LINC00426	
chr13	49060340	49170309	RCBTB2;LINC00462	
chr13	51463831	51486840	RNASEH2B	
chr14	22538336	22574512	nrg_OR4E2	
chr14	22630675	22653591	nrg_DAD1	
chr14	22921192	22951657	nrg_DAD1	
chr14	23018651	23039842	DAD1	
chr14	61873234	61946517	PRKCH;nrg_LOC101927780	
chr14	66291224	66357525	nrg_FUT8	
chr14	72901258	72920304	nrg_DPF3	
chr14	72933855	72949621	nrg_DPF3	
chr14	77493242	77520072	LOC283575;IRF2BPL	

chr14	81420749	81454391	TSHR	
chr14	91693347	91722938	GPR68	
chr14	92979197	93009908	RIN3	
chr14	98601759	98696800	nrg_C14orf64	
chr14	99728413	99741522	BCL11B	
chr14	1.01E+08	1.01E+08	EVL	
chr14	1.02E+08	1.02E+08	nrg_MEG9	
chr14	1.07E+08	1.07E+08	nrg_LINC00226;nrg_ADAM6	
chr14	1.07E+08	1.07E+08	nrg_LINC00226	
chr14	1.07E+08	1.07E+08	nrg_LINC00226;nrg_LINC00221	
chr14	1.07E+08	1.07E+08	nrg_LINC00221	
chr15	22420355	22484875	OR4N3P;nrg_OR4N3P;nrg_REREP3	
chr15	70535046	70561574	nrg_TLE3	
chr15	70705352	70785761	nrg_UACA	
chr15	74666128	74696799	CYP11A1	
chr15	91999141	92041139	LOC101926928	
chr16	3102282	3127929	MMP25;IL32	
chr16	11139525	11252079	CLEC16A;nrg_SOCS1	
chr16	11306716	11351850	SOCS1;nrg_SOCS1	
chr16	26603578	26628188	nrg_C16orf82	
chr16	27241589	27250500	nrg_KDM8	
chr16	29018896	29041514	nrg_LAT	
chr16	57625128	57644510	GPR56	
chr16	57672901	57683669	GPR56	
chr16	68098461	68120202	NFATC3	
chr16	88847297	88871308	PIEZO1;CDT1	
chr16	89005829	89102378	nrg_CBFA2T3;CBFA2T3	
chr16	89156192	89189614	ACSF3	
chr16	89659839	89683866	CPNE7;DPEP1	
chr17	3597559	3624135	GSG2;P2RX5-TAX1BP3	
chr17	3640764	3676020	ITGAE;nrg_GSG2	
chr17	3691240	3705232	ITGAE	
chr17	33539452	33547019	SLC35G3	
chr17	37909588	37929273	IKZF3;GRB7	
chr17	38689368	38717609	nrg_CCR7;CCR7	
chr17	40457345	40475479	nrg_STAT5A	
chr17	43296078	43326665	FMNL1;MAP3K14-AS1	
chr17	43589052	43598597	LRRC37A4P	
chr17	43656900	43670252	CRHR1	
chr17	45125507	45130081	ARL17A	
chr17	54282873	54399996	ANKFN1	
chr17	55481240	55568139	nrg_LOC101927557	
chr17	55600571	55632195	LOC101927557	
chr17	55662736	55685682	nrg_LOC101927539;LOC101927539	

chr17	56405173	56422751	BZRAP1-AS1	
chr17	62092638	62106809	ICAM2	
chr17	62961007	62983088	AMZ2P1	
chr17	65417831	65449902	PITPNC1	
chr17	66339869	66353305	ARSG;nrg_PRKAR1A	
chr17	72448331	72489989	CD300A	
chr17	72732477	72748329	RAB37;SLC9A3R1	
chr17	74010174	74034920	EVPL	
chr17	74175578	74196166	FOXJ1;RNF157	
chr17	75359720	75462534	SEPT9-	
chr17	76704427	76745351	CYTH1	
chr17	78616670	78647746	RPTOR	
chr17	78694128	78766157	nrg_LOC101928855	
chr17	78792907	78822393	LOC101928855	
chr17	78860855	78873672	nrg_CHMP6;nrg_LOC101928855	
chr17	79367526	79384034	BAHCC1	
chr17	79398715	79423857	BAHCC1	
chr17	80245694	80279764	nrg_CD7;CSNK1D;CD7	
chr18	13421099	13465439	LDLRAD4-AS1	
chr18	13607791	13617288	LDLRAD4	
chr18	24279147	24297839	PCAT18	
chr18	60865100	60884836	BCL2	
chr18	77264350	77285778	NFATC1	
chr19	2598636	2637672	GNG7	
chr19	3125798	3156807	LOC100996351;GNA15	
chr19	8763805	8816804	nrg_ACTL9;ACTL9	
chr19	13260549	13283622	STX10;nrg_IER2;IER2	
chr19	15946332	15957719	UCA1	
chr19	18390026	18439661	LSM4;JUND	
chr19	52028311	52053475	SIGLEC6	
chr19	54874739	54903074	LAIR1	
chr2	1780846	1827565	nrg_PXDN;PXDN	
chr2	42865321	42890824	MTA3	
chr2	43352299	43370988	nrg_ZFP36L2;nrg_LOC102723854	
chr2	43445503	43457188	LINC01126;ZFP36L2	
chr2	46368988	46389055	nrg_EPAS1	
chr2	54784577	54825200	SPTBN1	
chr2	60318369	60334343	nrg_BCL11A	
chr2	64067212	64084605	UGP2	
chr2	70345708	70370977	nrg_PCBP1;C2orf42	
chr2	87185878	87214892	nrg_PLGLB1;RGPD1	
chr2	87755013	87848058	LINC00152;nrg_LINC00152	
chr2	88081635	88098901	RGPD2;nrg_PLGLB1	
chr2	95670080	95693867	MAL	

chr2	95715708	95744669	nrg_MRPS5;MAL	
chr2	96809909	96831203	DUSP2	
chr2	99374069	99391409	MGAT4A	
chr2	1.01E+08	1.01E+08	LONRF2	
chr2	1.12E+08	1.12E+08	nrg_BCL2L11	
chr2	1.28E+08	1.28E+08	GPR17;nrg_GPR17	
chr2	1.29E+08	1.29E+08	nrg_HS6ST1	
chr2	1.29E+08	1.29E+08	nrg_LOC101927881	
chr2	1.37E+08	1.37E+08	LCT	
chr2	1.37E+08	1.37E+08	CXCR4	
chr2	1.62E+08	1.62E+08	nrg_TANK;TANK	
chr2	1.63E+08	1.63E+08	nrg_DPP4;DPP4	
chr2	1.82E+08	1.82E+08	nrg_ITGA4	
chr2	1.82E+08	1.82E+08	nrg_ITGA4;ITGA4	
chr2	1.97E+08	1.97E+08	STK17B	
chr2	1.97E+08	1.97E+08	LOC101927482;nrg_LOC101927482	
chr2	2.02E+08	2.02E+08	CASP8	
chr2	2.05E+08	2.05E+08	CD28	
chr2	2.14E+08	2.14E+08	nrg_IKZF2	
chr2	2.14E+08	2.14E+08	IKZF2	
chr2	2.14E+08	2.14E+08	IKZF2	
chr2	2.14E+08	2.14E+08	nrg_LOC100130451	
chr2	2.32E+08	2.32E+08	nrg_LOC151475	
chr2	2.33E+08	2.33E+08	nrg_C2orf57;PTMA	
chr2	2.35E+08	2.35E+08	nrg_SPP2	
chr2	2.35E+08	2.35E+08	nrg_SPP2;nrg_ARL4C	
chr2	2.35E+08	2.35E+08	nrg_ARL4C	
chr2	2.4E+08	2.4E+08	HDAC4;nrg_MGC16025	
chr2	2.4E+08	2.4E+08	nrg_HDAC4	
chr2	2.43E+08	2.43E+08	RTP5;LINC01237	
chr20	30249102	30274952	BCL2L1;nrg_COX4I2	
chr20	31097003	31128728	nrg_LOC101929698;LOC101929698	
chr20	31533287	31580204	nrg_SUN5;SUN5	
chr20	43270711	43281995	ADA	
chr20	48206004	48228177	PTGIS	
chr20	58761891	58800551	LOC284757	
chr20	58819374	58851896	LOC284757	
chr20	61347425	61375817	nrg_LINC00659;NTSR1	
chr21	28204474	28218417	ADAMTS1	
chr21	36376835	36424337	RUNX1-IT1;nrg_RUNX1-IT1;RUNX1	
chr21	39843770	39872127	ERG	
chr21	40348101	40384821	LOC101928435	
chr22	19872480	19898036	GNB1L;COMT	
chr22	23863058	23882322	LOC388882;nrg_IGLL1	

chr22	26093651	26152248	MYO18B	
chr22	30556765	30593199	nrg_LIF;nrg_LOC101929664	
chr22	30608854	30680246	OSM;LIF;nrg_LIF;GATSL3	
chr22	30682313	30706845	GATSL3;TBC1D10A	
chr22	40296014	40353863	GRAP2	
chr22	46988039	47016057	GRAMD4	
chr3	4862064	4888090	nrg_BHLHE40-AS1;nrg_EGOT	
chr3	13109548	13134270	IQSEC1	
chr3	14920465	14933832	nrg_FGD5-AS1	
chr3	18003735	18034327	LOC339862	
chr3	31252881	31276087	nrg_STT3B	
chr3	35680109	35707747	ARPP21	
chr3	45906273	45934983	CCR9	
chr3	45949163	45971111	LZTFL1	
chr3	46578188	46600340	LRRC2-AS1	
chr3	50604645	50662202	MAPKAPK3;CISH	
chr3	53131630	53148451	RFT1	
chr3	60031648	60080865	nrg_C3orf67	
chr3	1.11E+08	1.11E+08	nrg_PVRL3;nrg_CD96	
chr3	1.52E+08	1.52E+08	MBNL1;MBNL1-AS1	
chr3	1.72E+08	1.72E+08	nrg_TNFSF10;TNFSF10	
chr3	1.96E+08	1.96E+08	MUC4	
chr3	1.96E+08	1.96E+08	nrg_ZDHHC19;ZDHHC19	
chr3	1.96E+08	1.96E+08	FBXO45;NRROS	
chr4	40185074	40207689	RHOH	
chr4	40230542	40268572	nrg_RHOH;RHOH	
chr4	40284497	40327958	nrg_CHRNA9;CHRNA9	
chr4	1.09E+08	1.09E+08	LEF1	
chr4	1.09E+08	1.09E+08	nrg_LEF1-AS1;nrg_RPL34-AS1	
chr4	1.19E+08	1.19E+08	nrg_SNHG8	
chr4	1.44E+08	1.44E+08	INPP4B	
chr4	1.46E+08	1.46E+08	HHIP-AS1	
chr4	1.78E+08	1.78E+08	nrg_NEIL3	
chr5	39177017	39218403	FYB	
chr5	40669794	40688776	PTGER4	
chr5	42990629	43020925	FLJ32255;LOC648987	
chr5	43036337	43048141	ANXA2R	
chr5	52019775	52040368	PELO;nrg_PELO	
chr5	79475454	79515432	SERINC5	
chr5	1.19E+08	1.19E+08	TNFAIP8	
chr5	1.2E+08	1.2E+08	nrg_LOC102467226	
chr5	1.32E+08	1.32E+08	nrg_IRF1;C5orf56;IRF1	
chr5	1.33E+08	1.33E+08	nrg_TCF7;VDAC1;nrg_VDAC1;TCF7	
chr5	1.51E+08	1.51E+08	CCDC69	

chr5	1.57E+08	1.57E+08	CYFIP2	
chr5	1.57E+08	1.57E+08	ADAM19	
chr5	1.57E+08	1.57E+08	ADAM19	
chr5	1.8E+08	1.8E+08	nrg_SCGB3A1	
chr6	5693115	5728068	LOC101927950	
chr6	14210650	14232887	nrg_LINC01108	
chr6	14254231	14296376	LINC01108;nrg_LINC01108	
chr6	14368287	14397859	nrg_LINC01108	
chr6	14432717	14457934	nrg_LINC01108	
chr6	21586843	21605198	SOX4	
chr6	22019273	22097216	nrg_CASC14	
chr6	22136839	22153354	CASC14	
chr6	26026065	26037091	HIST1H3B;HIST1H2AB	
chr6	26042927	26052524	HIST1H3C;HIST1H1C	
chr6	26155412	26182001	HIST1H1E;HIST1H2BE	
chr6	26195384	26208061	HIST1H4E;HIST1H3D	
chr6	27094291	27103419	HIST1H2AG	
chr6	27774192	27788810	HIST1H2BM;HIST1H3H;HIST1H4J	
chr6	27789214	27803602	HIST1H4K;HIST1H4J;HIST1H2AK	
chr6	27832151	27844647	HIST1H1B;HIST1H4L	
chr6	27856851	27871057	HIST1H3J;OR2B2	
chr6	32935162	32941364	BRD2	
chr6	35685017	35704566	FKBP5;LOC285847	
chr6	36841925	36892461	PPIL1;PI16;C6orf89	
chr6	37012407	37020676	nrg_FGD2	
chr6	37136702	37178846	nrg_PIM1;PIM1	
chr6	37225009	37283148	TMEM217;RNF8	
chr6	41888172	41911124	BYSL;CCND3	
chr6	41972785	42018762	CCND3;TAF8	
chr6	45388405	45419267	RUNX2	
chr6	53158684	53181416	nrg_RPS16P5	
chr6	74229384	74234140	EEF1A1	
chr6	1.36E+08	1.36E+08	MYB;nrg_MYB	
chr6	1.36E+08	1.36E+08	nrg_MYB;AHI1	
chr6	1.36E+08	1.36E+08	AHI1	
chr7	623101	659723	nrg_FLJ44511;PRKAR1B	
chr7	1543570	1554691	INTS1	
chr7	29368545	29383974	CHN2;nrg_CHN2	
chr7	38255130	38309443	TARP;STARD3NL;nrg_TARP	
chr7	38369656	38408205	TRG-AS1	
chr7	44113170	44146815	POLM;AEBP1	
chr7	50342827	50356418	IKZF1	
chr7	50410327	50437702	IKZF1	
chr7	92250076	92325903	FAM133B;nrg_FAM133B	

chr7	92378170	92397410	CDK6	
chr7	92438803	92482193	CDK6	
chr7	1.16E+08	1.16E+08	TES	
chr7	1.38E+08	1.38E+08	ATP6V0A4	
chr7	1.42E+08	1.42E+08	PRSS1;nrg_MTRNR2L6	
chr7	1.42E+08	1.43E+08	nrg_PRSS2	
chr7	1.5E+08	1.5E+08	GIMAP8	
chr7	1.5E+08	1.5E+08	GIMAP7	
chr7	1.5E+08	1.5E+08	GIMAP2	
chr7	1.5E+08	1.5E+08	GIMAP5;GIMAP1-GIMAP5;nrg_GIMAP5	
chr7	1.57E+08	1.57E+08	nrg_LOC100506585;nrg_LOC101927914	
chr7	1.59E+08	1.59E+08	nrg_LINC00689	
chr8	2034160	2108343	MYOM2;nrg_MYOM2	
chr8	2139699	2171030	nrg_MYOM2	
chr8	20119968	20136112	LZTS1-AS1	
chr8	59711530	59721179	nrg_NSMAF	
chr8	66842632	66868820	nrg_DNAJC5B	
chr8	74360958	74388022	nrg_STAU2-AS1	
chr8	1.25E+08	1.25E+08	FER1L6-AS2	
chr8	1.3E+08	1.3E+08	nrg_LINC00977	
chr8	1.3E+08	1.3E+08	LINC00977;nrg_LINC00977	
chr8	1.3E+08	1.3E+08	LINC00977	
chr8	1.3E+08	1.3E+08	nrg_LINC00977	
chr8	1.3E+08	1.3E+08	nrg_LINC00977	
chr8	1.31E+08	1.31E+08	nrg_GSDMC	
chr8	1.34E+08	1.34E+08	SLA	
chr8	1.41E+08	1.41E+08	TRAPPC9	
chr9	22050479	22084962	CDKN2B;nrg_CDKN2B	
chr9	80515959	80542099	GNAQ	
chr9	1.08E+08	1.08E+08	nrg_SLC44A1	
chr9	1.13E+08	1.13E+08	AKAP2;nrg_C9orf152	
chr9	1.24E+08	1.24E+08	TRAF1;PHF19	
chr9	1.33E+08	1.33E+08	nrg_USP20;USP20	
chr9	1.39E+08	1.39E+08	NOTCH1	
chrX	2608977	2636632	CD99	
chrX	6977428	7007826	HDHD1	
chrX	12964720	13003376	TMSB4X;TLR8-AS1	
chrX	13092405	13111420	FAM9C	
chrX	38454780	38516135	TSPAN7	
chrX	40004997	40037812	BCOR	
chrX	78511958	78528665	nrg_ITM2A;nrg_GPR174	
chrX	1.29E+08	1.29E+08	SASH3;XPNPEP2	
chrX	1.36E+08	1.36E+08	LINC00892;CD40LG;nrg_CD40LG	
chrX	1.53E+08	1.53E+08	TMEM187	

chrY	2558780	2586662	CD99	
chrY	14704965	14734225	TTTY15;nrg_TTTY15	

Table SVI. Super-enriched regions in the Ly1 cell line.

chr	St	Ed	Genes
chr1	4059612	4119438	nrg_LOC728716
chr1	9122651	9145770	SLC2A5
chr1	14013482	14078668	PRDM2
chr1	23882661	23964456	MDS2;ID3
chr1	32704809	32733015	MTMR9LP;FAM167B;LCK
chr1	40839008	40870983	SMAP2
chr1	66795900	66816211	PDE4B
chr1	1.08E+08	1.08E+08	nrg_VAV3-AS1;nrg_VAV3
chr1	1.12E+08	1.12E+08	CHI3L2;DENND2D
chr1	1.45E+08	1.45E+08	nrg_NOTCH2NL;SEC22B;NOTCH2NL;nrg_SEC22B
chr1	1.68E+08	1.68E+08	RCSD1
chr1	1.79E+08	1.79E+08	nrg_C1orf220
chr1	1.83E+08	1.83E+08	RGS16;RGS8;RNASEL
chr1	1.93E+08	1.93E+08	RGS13
chr1	1.99E+08	1.99E+08	PTPRC
chr1	1.99E+08	1.99E+08	PTPRC
chr1	2.03E+08	2.03E+08	LOC100506775;BTG2;FMOD;nrg_BTG2
chr1	2.04E+08	2.05E+08	PIK3C2B;MDM4
chr1	2.05E+08	2.05E+08	nrg_NUAK2;NUAK2
chr1	2.27E+08	2.27E+08	ITPKB-IT1;nrg_ITPKB-IT1;ITPKB
chr1	2.29E+08	2.29E+08	DUSP5P1;RHOU
chr1	2.3E+08	2.3E+08	nrg_GALNT2
chr1	2.3E+08	2.3E+08	nrg_PGBD5
chr10	345339	385109	nrg_ZMYND11
chr10	540113	667081	PRR26;nrg_PRR26
chr10	1496302	1534829	ADARB2-AS1;nrg_ADARB2-AS1
chr10	6085839	6151567	IL2RA;RBM17
chr10	11704234	11741802	nrg_USP6NL;nrg_ECHDC3;ECHDC3
chr10	14687003	14716242	FAM107B;nrg_FAM107B
chr10	26726167	26771887	APBB1IP
chr10	45863359	45872320	ALOX5
chr10	62094511	62151878	ANK3
chr10	63717428	63761071	ARID5B;nrg_ARID5B
chr10	74003381	74062454	ASCC1;DDIT4;nrg_DDIT4
chr10	74076549	74100676	DNAJB12;nrg_DNAJB12
chr10	1.12E+08	1.12E+08	RBM20
chr10	1.13E+08	1.13E+08	PDCD4-AS1;nrg_PDCD4-AS1;PDCD4
chr10	1.26E+08	1.26E+08	CHST15
chr10	1.26E+08	1.26E+08	LHPP
chr10	1.26E+08	1.26E+08	LHPP;FAM53B
chr10	1.26E+08	1.26E+08	FAM53B
chr11	9683591	9724233	SWAP70

chr11	10328479	10345175	CAND1.11
chr11	48001576	48073417	PTPRJ
chr11	58844512	58875757	LOC283194;FAM111B
chr11	64611489	64662252	CDC42BPG;EHD1
chr11	65183553	65200986	NEAT1
chr11	67202329	67235179	CORO1B;PTPRCAP;CABP4;TMEM134
chr11	72852053	72869430	FCHSD2
chr11	73690871	73711220	UCP2;UCP3
chr11	76337588	76392440	nrg_LRRC32;LRRC32
chr11	1.02E+08	1.02E+08	BIRC3
chr11	1.02E+08	1.02E+08	TMEM123
chr11	1.11E+08	1.11E+08	nrg_C11orf53
chr11	1.11E+08	1.11E+08	C11orf53;COLCA1;COLCA2
chr11	1.11E+08	1.11E+08	LOC100132078;nrg_LOC100132078;POU2AF1
chr11	1.19E+08	1.19E+08	BCL9L;CXCR5
chr11	1.28E+08	1.29E+08	ETS1
chr12	2351244	2369394	CACNA1C-AS4;CACNA1C-IT3
chr12	6532500	6575199	VAMP1;CD27;TAPBPL
chr12	10539511	10560136	KLRK1;KLRC4
chr12	11898689	11920039	ETV6
chr12	11941206	11989844	RNU6-19P
chr12	12843879	12890499	CDKN1B;APOLD1;GPR19
chr12	48191054	48232942	HDAC7
chr12	57604168	57638016	SHMT2;NXPH4
chr12	70294135	70303901	nrg_RAB3IP
chr12	90249521	90276705	nrg_LINC00936
chr12	90311921	90344206	nrg_LINC00936
chr12	92531002	92567290	C12orf79;BTG1
chr12	92854729	92866083	CLLU1OS
chr12	1.11E+08	1.11E+08	TCTN1;HVCN1
chr12	1.13E+08	1.14E+08	RASAL1;DTX1
chr12	1.14E+08	1.14E+08	RITA1;TPCN1;IQCD
chr12	1.17E+08	1.17E+08	nrg_HRK;RNFT2
chr12	1.22E+08	1.22E+08	BCL7A
chr12	1.25E+08	1.25E+08	UBC
chr13	41038321	41060483	LINC00598
chr13	41146839	41172738	FOXO1;nrg_LINC00598
chr13	41547329	41595316	ELF1
chr13	42064275	42087250	nrg_RGCC
chr13	46943722	46979283	KIAA0226L
chr13	51085136	51104478	nrg_DLEU7-AS1
chr13	51160974	51173930	nrg_DLEU7-AS1
chr13	52367823	52407499	DHRS12
chr13	67566090	67571950	PCDH9-AS4

chr13	99953527	1E+08	FKSG29;GPR183
chr14	22935209	23002980	nrg_DAD1
chr14	23018666	23039942	nrg_DAD1;DAD1
chr14	61928311	61972316	nrg_LOC101927780
chr14	64660546	64705844	nrg_SYNE2;SYNE2
chr14	68732581	68773770	RAD51B
chr14	69255533	69283984	ZFP36L1
chr14	71107778	71136468	TTC9
chr14	94405794	94452023	ASB2;nrg_FAM181A
chr14	95923116	95964664	SYNE3
chr14	96118317	96174636	TCL6;TCL1A;TCL1B
chr14	1.06E+08	1.06E+08	nrg_ELK2AP;nrg_TMEM121
chr14	1.06E+08	1.06E+08	ELK2AP;nrg_ELK2AP
chr14	1.06E+08	1.06E+08	nrg_KIAA0125
chr14	1.07E+08	1.07E+08	nrg_LINC00221
chr14	1.07E+08	1.07E+08	nrg_LINC00221
chr15	40337036	40400428	SRP14-AS1;nrg_BMF;BMF;nrg_SRP14-AS1
chr15	59686239	59706332	FAM81A;MYO1E
chr15	63758701	63798379	USP3
chr15	66439617	66484433	MEGF11
chr15	75063200	75093564	LMAN1L;CSK
chr15	85986384	86029763	AKAP13
chr15	93340244	93397264	ASB9P1;nrg_ASB9P1;LOC100507217
chr15	98685644	98718391	nrg_LOC101927332
chr16	12161552	12246351	SNX29
chr16	12309214	12366473	SNX29
chr16	12383333	12443222	SNX29
chr16	21362292	21399708	SNX29P1;nrg_NPIPB3
chr16	29341417	29373257	SNX29P2
chr16	67548090	67598905	CTCF;FAM65A
chr16	81807655	81875805	PLCG2
chr16	85932305	85980699	nrg_IRF8;IRF8
chr16	89034160	89062007	CBFA2T3
chr17	1084244	1133550	ABR
chr17	18935520	18980252	GRAP;LOC388436
chr17	37930705	37957369	IKZF3
chr17	55514834	55639245	LOC101927557;nrg_LOC101927557
chr17	56394642	56422875	BZRAP1-AS1
chr17	62008343	62032672	SCN4A;CD79B
chr17	71578235	71593713	SDK2
chr17	74982299	75007819	nrg_SEC14L1
chr17	75422676	75491639	SEPT9-
chr17	78693992	78712842	nrg_LOC101928855
chr18	13607909	13630738	LDLRAD4

chr18	20804057	20823702	CABLES1
chr18	31406740	31433642	NOL4;nrg_NOL4
chr18	38957403	38973408	nrg_KC6
chr18	48332339	48348006	MRO
chr18	53082254	53184379	TCF4
chr18	53248048	53257624	TCF4
chr18	60793230	60830299	BCL2
chr18	60979644	60990950	BCL2
chr18	77195774	77289702	NFATC1
chr19	6576226	6609554	CD70
chr19	40442675	40465985	PSMC4;FCGBP
chr19	50409497	50441451	ATF5;IL4I1
chr2	8711234	8726738	LOC101929567
chr2	11967565	11977352	LPIN1
chr2	12170953	12214160	LOC100506457
chr2	12227210	12272164	LOC100506457
chr2	43352248	43369479	nrg_ZFP36L2;nrg_LOC102723854
chr2	43444650	43461159	LINC01126
chr2	47921860	47963747	nrg_MSH6;MSH6
chr2	64864236	64894798	SERTAD2
chr2	65577537	65664608	SPRED2
chr2	68936363	69003830	ARHGAP25
chr2	70297789	70370645	PCBP1-AS1;C2orf42;nrg_PCBP1;PCBP1
chr2	87785178	87826858	LINC00152
chr2	89127781	89197813	nrg_ANKRD36BP2
chr2	1.09E+08	1.09E+08	LIMS1
chr2	1.12E+08	1.12E+08	nrg_BCL2L11
chr2	1.31E+08	1.31E+08	nrg_PTPN18;PTPN18
chr2	1.35E+08	1.35E+08	MGAT5
chr2	1.37E+08	1.37E+08	LOC101928243
chr2	1.37E+08	1.37E+08	CXCR4
chr2	1.37E+08	1.37E+08	nrg_CXCR4
chr2	1.45E+08	1.45E+08	GTDC1
chr2	1.58E+08	1.58E+08	CYTIP
chr2	1.71E+08	1.71E+08	MYO3B
chr2	1.71E+08	1.71E+08	MYO3B
chr2	1.97E+08	1.97E+08	STK17B
chr2	1.97E+08	1.97E+08	LOC101927482;nrg_LOC101927482;STK17B
chr2	1.98E+08	1.98E+08	nrg_ANKRD44-IT1
chr2	2.14E+08	2.14E+08	IKZF2
chr2	2.14E+08	2.14E+08	nrg_LOC100130451
chr2	2.17E+08	2.18E+08	LINC01280;IGFBP2
chr2	2.2E+08	2.2E+08	LOC101928537;WNT10A
chr2	2.25E+08	2.25E+08	AP1S3

chr2	2.33E+08	2.33E+08	nrg_C2orf57;PTMA
chr20	37487446	37522966	nrg_FAM83D;PPP1R16B;FAM83D
chr20	43204600	43244552	PKIG
chr20	45964594	45990135	ZMYND8
chr20	46036384	46132299	NCOA3;nrg_NCOA3;nrg_ZMYND8
chr20	48282947	48323820	B4GALT5
chr20	49406961	49439183	BCAS4
chr20	52194963	52212364	ZNF217
chr20	52225353	52279603	nrg_ZNF217;ZNF217
chr20	52345787	52373147	nrg_SUMO1P1
chr20	52509079	52566491	nrg_SUMO1P1;SUMO1P1
chr20	55825664	55905725	BMP7;SPO11
chr20	56025015	56074375	nrg_RBM38;nrg_CTCFL;CTCFL
chr21	34732845	34756770	IFNGR2
chr21	43248599	43299929	PRDM15
chr21	45557573	45581395	C21orf33;nrg_C21orf33
chr22	22379694	22416641	nrg_TOP3B;TOP3B
chr22	22702327	22786503	nrg_BMS1P20;nrg_ZNF280B
chr22	22978548	23063433	GGTLC2;POM121L1P;nrg_GGTLC2
chr22	23182693	23301970	nrg_IGLL5;IGLL5
chr22	33961935	33976038	nrg_LARGE-AS1
chr22	39832974	39866153	LOC100506472;MGAT3
chr22	46142584	46182157	ATXN10
chr22	47154533	47174221	TBC1D22A
chr22	48466323	48502000	nrg_FAM19A5
chr3	16471710	16492218	RFTN1
chr3	16549625	16571337	LINC00690;RFTN1
chr3	31938227	32024073	nrg_ZNF860;ZNF860
chr3	35701037	35723573	ARPP21
chr3	55751873	55764472	nrg_ERC2-IT1
chr3	58309950	58342549	PXK
chr3	71465683	71515202	FOXP1;nrg_FOXP1
chr3	71612549	71636306	FOXP1
chr3	1.12E+08	1.12E+08	GCSAM
chr3	1.33E+08	1.33E+08	BFSP2;nrg_CDV3
chr3	1.52E+08	1.52E+08	nrg_MBNL1
chr3	1.52E+08	1.52E+08	MBNL1;MBNL1-AS1
chr3	1.7E+08	1.7E+08	SAMD7;SEC62
chr3	1.77E+08	1.77E+08	TBL1XR1
chr3	1.77E+08	1.77E+08	LINC00501;nrg_LINC00501
chr3	1.8E+08	1.8E+08	nrg_LOC101928790;LOC101928790;PEX5L
chr3	1.83E+08	1.83E+08	KLHL6
chr3	1.86E+08	1.86E+08	LOC253573;CRYGS;nrg_CRYGS
chr3	1.87E+08	1.87E+08	ST6GAL1

chr3	1.87E+08	1.87E+08	BCL6
chr3	1.88E+08	1.88E+08	nrg_BCL6;nrg_LPP
chr3	1.88E+08	1.88E+08	nrg_LPP;LPP
chr3	1.88E+08	1.88E+08	LPP
chr3	1.97E+08	1.97E+08	LOC220729
chr4	28663	59434	ZNF718;ZNF595
chr4	25861089	25881875	SEL1L3
chr4	37978399	38001575	nrg_PTTG2
chr4	40174652	40208653	RHOH
chr4	40281997	40327995	nrg_CHRNA9;CHRNA9
chr4	71516087	71547737	UTP3;IGJ
chr4	74454533	74486992	RASSF6
chr4	78062968	78079823	CCNG2
chr4	81529284	81540859	C4orf22
chr4	1.03E+08	1.03E+08	BANK1
chr4	1.46E+08	1.46E+08	SMAD1-AS2;SMAD1
chr4	1.54E+08	1.54E+08	KIAA0922
chr4	1.65E+08	1.65E+08	MARCH1-
chr4	1.65E+08	1.65E+08	nrg_MARCH1-
chr4	1.76E+08	1.76E+08	ADAM29
chr4	1.76E+08	1.76E+08	ADAM29
chr5	390949	447434	nrg_C5orf55;EXOC3;C5orf55
chr5	66483000	66519637	CD180
chr5	72447325	72470718	TMEM174
chr5	78013824	78032351	nrg_LHFPL2
chr5	79475693	79524304	SERINC5
chr5	1.19E+08	1.19E+08	TNFAIP8
chr5	1.24E+08	1.24E+08	ZNF608
chr5	1.24E+08	1.24E+08	ZNF608
chr5	1.24E+08	1.24E+08	nrg_LOC101927421
chr5	1.24E+08	1.24E+08	LOC101927421
chr5	1.29E+08	1.29E+08	ADAMTS19
chr5	1.43E+08	1.43E+08	nrg_NR3C1
chr5	1.51E+08	1.51E+08	GM2A;CCDC69
chr5	1.58E+08	1.58E+08	EBF1
chr5	1.73E+08	1.73E+08	LOC101928136;nrg_BOD1;nrg_LOC101928136
chr6	1848920	1873502	nrg_FOXC1
chr6	6384494	6410195	nrg_F13A1
chr6	12037793	12061967	HIVEP1
chr6	15879898	15916697	nrg_DTNBP1;nrg_MYLIP
chr6	32901165	32953119	HLA-DMB;BRD2;HLA-DMA
chr6	44038728	44064973	nrg_MRPL14
chr6	88613601	88654889	LOC101928911;nrg_SPACA1
chr6	90983878	91031642	BACH2

chr6	91079984	91124364	nrg_BACH2
chr6	1.07E+08	1.07E+08	nrg_QRSL1;LOC100422737
chr6	1.5E+08	1.5E+08	ZC3H12D
chr6	1.51E+08	1.51E+08	PLEKHG1
chr6	1.56E+08	1.56E+08	TFB1M
chr6	1.59E+08	1.59E+08	TAGAP
chr6	1.6E+08	1.6E+08	nrg_FNDC1;nrg_TAGAP;FNDC1
chr7	1014858	1085024	COX19;nrg_CYP2W1;CYP2W1;GPR146
chr7	5717460	5744648	RNF216-IT1
chr7	24851822	24888065	OSBPL3;nrg_DFNA5
chr7	30265192	30326170	nrg_ZNRF2;ZNRF2
chr7	43664810	43694433	nrg_STK17A;STK17A
chr7	45038584	45069520	CCM2
chr7	47704534	47719916	nrg_C7orf65;C7orf65
chr7	47746820	47766570	nrg_C7orf65;LINC00525
chr7	50343192	50357368	IKZF1
chr7	52567345	52578502	nrg_POM121L12
chr7	55583474	55641415	VOPP1
chr7	1.02E+08	1.02E+08	SPDYE6;SH2B2;nrg_SPDYE6
chr7	1.06E+08	1.06E+08	SYPL1;CDHR3;nrg_SYPL1
chr7	1.21E+08	1.21E+08	FAM3C
chr7	1.27E+08	1.27E+08	ZNF800
chr7	1.31E+08	1.31E+08	MKLN1
chr7	1.42E+08	1.43E+08	PRSS2;nrg_PRSS2
chr7	1.56E+08	1.56E+08	nrg_SHH;RBM33
chr8	37728369	37757703	BRF2;RAB11FIP1
chr8	59955880	59989256	TOX
chr8	66858051	66867657	nrg_DNAJC5B
chr8	66910078	66949253	DNAJC5B
chr8	81050469	81084283	TPD52
chr8	96082719	96109664	nrg_NDUFAF6;PLEKHF2
chr8	96138292	96182067	PLEKHF2
chr8	96214898	96244237	C8orf69
chr8	1.19E+08	1.19E+08	nrg_EXT1
chr8	1.24E+08	1.24E+08	ZHX2
chr8	1.29E+08	1.29E+08	MYC
chr8	1.31E+08	1.31E+08	ASAP1-IT2;nrg_ASAP1-IT2;FAM49B
chr8	1.34E+08	1.34E+08	SLA
chr8	1.36E+08	1.36E+08	ZFAT
chr8	1.42E+08	1.42E+08	DENND3
chr9	22511940	22529044	nrg_DMRTA1
chr9	35616555	35648091	SIT1;nrg_SIT1;CD72
chr9	36993637	37081451	PAX5;ZCCHC7
chr9	37137182	37147089	ZCCHC7

chr9	37281776	37309560	nrg_GRHPR
chr9	37322783	37342839	nrg_GRHPR
chr9	37364498	37431842	nrg_GRHPR;GRHPR
chr9	84694930	84749681	nrg_SPATA31D1
chr9	84783299	84802115	nrg_SPATA31D1
chr9	93557984	93593894	SYK
chr9	96023318	96067707	WNK2;nrg_C9orf129
chr9	1.13E+08	1.13E+08	nrg_AKAP2
chr9	1.13E+08	1.13E+08	nrg_AKAP2
chr9	1.13E+08	1.13E+08	AKAP2
chr9	1.25E+08	1.25E+08	TTLL11;nrg_DAB2IP
chr9	1.26E+08	1.26E+08	CRB2
chr9	1.37E+08	1.37E+08	nrg_RNU6ATAC
chr9	1.39E+08	1.39E+08	QSOX2
chr9	1.41E+08	1.41E+08	EHMT1;nrg_EHMT1-IT1
chrX	12964638	13041770	TMSB4X;nrg_TMSB4X;nrg_FAM9C;TLR8-AS1
chrX	13091875	13111468	FAM9C
chrX	33143663	33162193	DMD
chrX	33182478	33202452	DMD
chrX	38737355	38797032	nrg_MID1IP1-AS1
chrX	42791487	42815645	nrg_PPP1R2P9
chrX	1.2E+08	1.2E+08	nrg_CT47B1

Table SVII. Super-enriched regions in the MM.1S cell line.

chr	St	Ed	Genes
chr14	1.06E+08	1.06E+08	nrg_TMEM121
chr3	1.41E+08	1.41E+08	ZBTB38;nrg_RASA2
chr14	1.06E+08	1.06E+08	ELK2AP
chr22	23264578	23298654	nrg_IGLL5
chr6	1.09E+08	1.09E+08	FOXO3
chr6	291352	337186	DUSP22
chr4	1.85E+08	1.85E+08	LOC728175;IRF2;nrg_LOC728175
chr1	1.18E+08	1.18E+08	nrg_FAM46C;FAM46C
chr20	32398604	32473612	CHMP4B;nrg_CHMP4B
chr1	2.03E+08	2.03E+08	LINC01136;LOC100506775;BTG2;FMOD;nrg_BTG2
chr17	32688296	32720861	CCL1
chr2	37535856	37586308	QPCT;PRKD3
chr6	7893440	7919576	TXNDC5
chr22	23224168	23249074	nrg_IGLL5;IGLL5
chr21	45552582	45595739	C21orf33;nrg_C21orf33
chrX	58211531	58278982	nrg_ZXDA
chrX	58107196	58167196	nrg_ZXDA
chr22	29186119	29225930	XBP1
chr2	99054999	99132139	INPP4A
chr10	1.26E+08	1.26E+08	CHST15
chr7	1.02E+08	1.02E+08	ORAI2;ALKBH4
chr20	30278958	30312192	BCL2L1
chr16	11771988	11837370	SNN;nrg_SNN;TXNDC11
chr2	20390902	20426497	SDC1
chr4	1.85E+08	1.85E+08	nrg_ENPP6;nrg_LOC728175
chr17	34598035	34640485	TBC1D3H;CCL4L1;CCL3L3;CCL3L1;nrg_CCL3L3
chr11	22677444	22704845	GAS2
chr1	1.5E+08	1.5E+08	HIST2H2AA3;HIST2H4A
chr18	9055076	9084860	NDUFV2
chr5	1311330	1321163	TERT
chr15	90563062	90646513	IDH2;nrg_IDH2;ZNF710
chr4	90211000	90239692	GPRIN3
chr22	24179396	24192311	DERL3
chr9	93670822	93706903	nrg_SYK
chr12	53590072	53616036	RARG;ITGB7
chr6	1.07E+08	1.07E+08	PRDM1
chr2	97191211	97220597	ARID5A
chr11	65183594	65192752	NEAT1
chr4	1.85E+08	1.85E+08	IRF2
chr10	11202970	11222828	CELF2
chr13	1.15E+08	1.15E+08	RASA3
chr15	31546948	31560302	LOC283710

chr18	46439791	46479757	SMAD7
chr19	2595302	2637674	GNG7
chr6	26341453	26367505	BTN3A2
chr5	1.32E+08	1.32E+08	nrg_IRF1;IRF1
chr3	1.94E+08	1.94E+08	HES1;nrg_HES1;nrg_LOC647323;LOC647323
chr17	16863937	16895297	TNFRSF13B
chr3	1.72E+08	1.72E+08	FNDC3B
chr17	34509855	34539628	CCL4L1;CCL3L3;CCL3L1;nrg_CCL3L3
chr15	68569293	68599527	FEM1B;nrg_FEM1B
chr8	1.21E+08	1.21E+08	DEPTOR
chr6	32935593	32941207	BRD2
chrX	56789891	56815922	nrg_UQCRBP1;UQCRBP1
chr20	25261276	25300791	nrg_PYGB;PYGB
chr4	71525754	71554807	UTP3;IGJ
chr7	55598752	55641127	VOPP1
chr12	4378037	4386712	CCND2
chr14	91816615	91866721	CCDC88C
chr1	2.26E+08	2.26E+08	nrg_H3F3AP4;nrg_ACBD3
chrX	1.31E+08	1.31E+08	FIRRE
chr17	56405858	56422757	BZRAP1-AS1;BZRAP1
chr3	1.77E+08	1.77E+08	TBL1XR1
chr1	1.5E+08	1.5E+08	HIST2H2AA3
chr1	2.29E+08	2.29E+08	DUSP5P1;RHOU
chr11	10323941	10345062	CAND1.11
chr6	26233051	26252894	HIST1H1D;HIST1H3F;HIST1H4F
chr1	1.55E+08	1.55E+08	PBXIP1;PMVK
chr13	78676133	78712423	RNF219-AS1
chr12	12873911	12881972	APOLD1
chr12	94541522	94603104	PLXNC1;nrg_PLXNC1
chr5	55437508	55464486	ANKRD55
chr13	1.15E+08	1.15E+08	GAS6
chr3	1.94E+08	1.94E+08	HES1
chr12	1.09E+08	1.09E+08	SELPLG
chrX	39953353	39969542	BCOR
chr16	56944226	56967234	HERPUD1
chr5	1.32E+08	1.32E+08	C5orf56
chr1	2.35E+08	2.35E+08	IRF2BP2
chr5	1.8E+08	1.8E+08	MGAT1;HEIH
chr3	1.77E+08	1.77E+08	nrg_LINC00501
chr10	43890956	43916860	HNRNPF
chr6	90059805	90085843	UBE2J1
chr8	2028582	2050311	MYOM2
chr7	1.5E+08	1.5E+08	LOC728743;LINC00996
chr7	25980165	26008996	nrg_RNU6-16P

chr6	26188072	26200834	HIST1H3D;HIST1H4D
chr18	9102085	9121314	NDUFV2;LOC101927275
chr19	16676827	16711280	SLC35E1
chr2	2.33E+08	2.33E+08	nrg_COPS7B
chr21	43480758	43498735	UMODL1
chr2	43444695	43457261	LINC01126;ZFP36L2
chr10	1.12E+08	1.12E+08	nrg_SMNDC1
chr2	2.02E+08	2.02E+08	CFLAR
chr8	27208986	27263628	nrg_CHRNA2;PTK2B
chr2	2.32E+08	2.32E+08	ITM2C
chr2	2.33E+08	2.33E+08	PTMA
chr11	1.29E+08	1.29E+08	SENCR
chr9	1.34E+08	1.34E+08	FAM78A;nrg_FAM78A
chr1	1.55E+08	1.55E+08	ZBTB7B
chr22	37610547	37641974	SSTR3;RAC2
chr6	52393302	52423437	TRAM2
chr17	75131619	75146518	SEC14L1
chr2	1.12E+08	1.12E+08	nrg_ANAPC1
chr6	1.07E+08	1.07E+08	nrg_PRDM1
chr2	47526417	47550823	LOC101927043
chrX	40012574	40036900	BCOR
chr1	27018618	27029917	ARID1A
chr2	2.2E+08	2.2E+08	LOC101928537;WNT10A
chr15	69109304	69136658	MIR548H4;ANP32A
chr20	37498994	37505525	nrg_FAM83D
chr9	94182917	94195853	NFIL3
chr2	70311884	70317158	PCBP1-AS1;PCBP1
chr18	60805014	60830463	BCL2
chr3	46227950	46256813	CCR1;nrg_CCR1
chr1	1.51E+08	1.51E+08	ADAMTSL4-AS1;MCL1
chr3	46317767	46363556	nrg_CCR2;nrg_CCR3;CCR2;CCR3
chr20	52198161	52212259	ZNF217
chr16	23334200	23362581	SCNN1B
chr1	1.56E+08	1.56E+08	MEF2D
chr10	11279335	11313174	CELF2
chr6	42738117	42752086	TBCC
chr14	81930665	81955880	LOC100506700
chr5	88175631	88186449	MEF2C-AS1
chr15	93351508	93388926	nrg_ASB9P1;LOC100507217
chr1	1.56E+08	1.56E+08	MIR7851;SEMA4A
chr1	1.54E+08	1.54E+08	IL6R
chr1	1.5E+08	1.5E+08	HIST2H2AC
chr11	65263815	65277820	MALAT1
chr11	19451355	19465514	nrg_NAV2-AS5

chr19	2445871	2479956	LMNB2;GADD45B
chr19	2082828	2097398	MOB3A
chr19	1648075	1672886	TCF3
chr6	1.38E+08	1.38E+08	nrg_LOC100130476
chr19	39888037	39901262	MED29;ZFP36
chr2	42327791	42360898	nrg_PKDCC;nrg_EML4;EML4
chr7	1.05E+08	1.05E+08	KMT2E-AS1
chr6	26155492	26184703	HIST1H2BD;HIST1H2BE
chr22	27005578	27014689	CRYBB1
chrX	1.53E+08	1.53E+08	TMEM187
chrX	10050567	10090886	WWC3;nrg_CLCN4;CLCN4
chr12	48201066	48214695	HDAC7
chr2	2.39E+08	2.39E+08	PER2;HES6
chr10	1.12E+08	1.12E+08	DUSP5
chr3	1.83E+08	1.83E+08	KLHL6
chr17	34409813	34431321	CCL3;CCL4
chr17	20205121	20224848	CCDC144CP
chr11	72851978	72869148	FCHSD2
chr15	70769887	70805655	nrg_UACA
chr6	11827411	11837121	nrg_ADTRP
chr1	2.09E+08	2.09E+08	nrg_MIR205HG
chr15	70387870	70394439	TLE3
chr9	93953031	93957332	nrg_LOC100129316
chr14	77488283	77500944	IRF2BPL
chr17	36856677	36862880	MLLT6
chr15	75063201	75093054	LMAN1L;CSK
chr2	2.41E+08	2.42E+08	DUSP28;RNPEPL1;CAPN10-AS1
chr6	7958678	7977932	PIP5K1P1
chr12	53845264	53869543	PCBP2-OT1;PCBP2
chr6	27857804	27871364	HIST1H2AM;OR2B2
chr16	89033192	89045988	CBFA2T3
chr4	1.05E+08	1.05E+08	CXXC4
chr7	78114340	78128111	nrg_RPL13AP17
chr21	41325336	41342529	nrg_PCP4
chr16	67578646	67600899	CTCF;FAM65A
chr20	40710840	40727092	nrg_CHD6
chr17	42276266	42299366	UBTF;ATXN7L3
chr20	56047951	56057905	nrg_CTCFL
chr17	37909648	37914892	nrg_GRB7;GRB7
chr15	31636865	31654467	KLF13
chr2	70335628	70370893	nrg_PCBP1;C2orf42
chr12	1.22E+08	1.22E+08	SETD1B;LINC01089;RHOF
chr7	1.5E+08	1.5E+08	ZNF775;REPIN1
chr5	1335612	1346164	CLPTM1L

chr21	45195422	45207076	CSTB;RRP1
chr18	42258629	42263207	SETBP1
chr4	1.85E+08	1.85E+08	LOC728175;nrg_LOC728175
chr3	5223104	5255949	EDEM1
chr9	1.24E+08	1.24E+08	PHF19
chr6	26520385	26573298	ABT1;HMGN4;HCG11
chr21	44725485	44746307	nrg_LINC00322;LINC00322
chr16	66550104	66559464	TK2
chr3	1.24E+08	1.25E+08	nrg_UMPS
chr12	26266593	26280006	BHLHE41
chr18	9134313	9149526	ANKRD12;LOC101927275
chr10	45914122	45931887	ALOX5
chr4	1.3E+08	1.3E+08	JADE1
chr22	38782570	38795666	CSNK1E
chr11	67033407	67057414	ANKRD13D;ADRBK1
chr1	1.45E+08	1.45E+08	TXNIP;POLR3GL
chr22	39632279	39663573	PDGFB
chr17	75079431	75106687	SEC14L1;SCARNA16;nrg_SCARNA16
chr22	39823868	39845158	LOC100506472;MGAT3
chr20	62359336	62371880	LIME1
chr1	16160597	16176439	SPEN
chr4	38307631	38322127	nrg_TBC1D1
chr11	1.11E+08	1.11E+08	POU2AF1
chr8	1.35E+08	1.35E+08	ST3GAL1
chr22	48491951	48509227	nrg_FAM19A5
chr15	89647048	89674731	ABHD2
chr12	89738152	89748802	DUSP6
chr13	1.15E+08	1.15E+08	RASA3
chr12	7057739	7074793	SCARNA12;PTPN6
chr5	6476057	6496766	UBE2QL1
chr6	26270257	26274990	HIST1H3G
chr22	23478107	23500751	RTDR1;RAB36
chr2	86220250	86227820	nrg_POLR1A
chr14	1.06E+08	1.06E+08	nrg_KIAA0125
chr17	76712722	76744706	CYTH1
chr5	1.73E+08	1.73E+08	CPEB4
chr12	46120433	46131955	LINC00938;ARID2
chr6	26054328	26057812	HIST1H1C
chr15	1.02E+08	1.02E+08	nrg_CHSY1
chr10	81001694	81021418	nrg_PPIF
chr21	36237526	36262975	RUNX1
chr3	13050489	13061405	IQSEC1;nrg_IQSEC1
chr17	43505176	43531691	ARHGAP27
chr3	1.33E+08	1.33E+08	BFSP2;nrg_CDV3

chr12	12866917	12873459	CDKN1B
chr8	95953888	96004071	NDUFAF6;TP53INP1
chr19	1241361	1270192	MIDN;CIRBP;ATP5D
chr3	46129130	46151553	nrg_XCR1
chr3	39248246	39276783	XIRP1
chr7	1.5E+08	1.5E+08	ZNF775
chr2	64863003	64895326	SERTAD2
chr12	98884633	98912213	LOC643770;TMPO
chr9	98255828	98274213	PTCH1
chr14	69259303	69263504	ZFP36L1
chr7	1.05E+08	1.05E+08	nrg_LINC01004;LHFPL3-AS2
chr9	93909800	93937874	nrg_LOC100129316
chr5	87955219	87976807	LINC00461
chr15	46994755	47008901	nrg_SEMA6D
chr11	67758157	67778232	UNC93B1;ALDH3B1
chr1	23850992	23858463	E2F2;LOC101928163
chr9	1.01E+08	1.01E+08	ANP32B
chr8	29205269	29210509	DUSP4
chr17	43298549	43307099	FMNL1
chr11	1.26E+08	1.26E+08	RPUSD4;nrg_RPUSD4
chr6	27094778	27102941	HIST1H2AG;HIST1H2BJ
chr20	55958758	55975271	RBM38
chr20	46386566	46415883	SULF2
chr5	1.39E+08	1.39E+08	MZB1;PROB1
chr2	1.29E+08	1.29E+08	nrg_HS6ST1
chr17	73860185	73875492	WBP2;TRIM47
chr3	1.94E+08	1.94E+08	LINC00887
chr3	1.63E+08	1.63E+08	nrg_LINC01192
chr10	74007312	74034979	DDIT4
chr6	37122238	37140537	PIM1
chr21	44581609	44598017	CRYAA
chr20	45980044	45987192	ZMYND8
chr20	42569567	42585080	TOX2
chr6	1.09E+08	1.09E+08	nrg_LINC00222
chr14	1.06E+08	1.06E+08	nrg_ELK2AP
chr17	75229391	75243784	SEPT9-
chr2	1.06E+08	1.06E+08	NCK2
chr19	47614125	47617362	ZC3H4
chr6	1.58E+08	1.58E+08	nrg_SNX9;ZDHHC14
chr8	1.42E+08	1.42E+08	DENND3
chr10	1.12E+08	1.12E+08	nrg_DUSP5
chr6	1.2E+08	1.2E+08	LOC285762
chr2	1.1E+08	1.1E+08	nrg_SH3RF3-AS1
chr10	1.05E+08	1.05E+08	WBP1L

chrX	1.29E+08	1.29E+08	SASH3
chr21	45660011	45664610	ICOSLG
chr1	39973609	39992253	PPIEL;BMP8A
chr1	2.07E+08	2.07E+08	RASSF5
chr17	43209904	43250847	HEXIM2;HEXIM1;ACBD4
chr9	73027954	73036383	KLF9
chr12	4216328	4229209	nrg_CCND2
chr22	26975064	26991916	TPST2
chr1	1606417	1625346	SLC35E2B
chr12	1.09E+08	1.09E+08	ISCU
chr17	80307955	80330005	UTS2R;TEX19
chr6	12008352	12013831	HIVEP1
chr5	32571996	32587028	SUB1
chrX	48793862	48816425	OTUD5
chr6	45387027	45394806	RUNX2
chr3	1.7E+08	1.7E+08	SKIL
chr6	20401666	20410217	E2F3
chr2	2.36E+08	2.36E+08	AGAP1
chr1	87793484	87801646	LMO4
chr6	25403687	25414368	LRRC16A
chr17	78873652	78886306	nrg_CHMP6
chr9	93782527	93799793	nrg_LOC100129316
chr18	42289431	42306556	SETBP1
chr11	1.29E+08	1.29E+08	BARX2
chr20	42684390	42709896	TOX2;nrg_JPH2
chr19	47728801	47766147	BBC3;CCDC9
chr16	79631825	79640177	MAF
chr16	23412782	23418987	COG7
chr2	1.75E+08	1.75E+08	SP3
chr15	40389712	40408522	BMF
chr11	1.15E+08	1.15E+08	CADM1
chr2	1.82E+08	1.82E+08	nrg_ITGA4
chr18	20804066	20823807	CABLES1
chr1	1.11E+08	1.11E+08	KCNA2
chr17	6063989	6071332	nrg_WSCD1
chr9	1.17E+08	1.17E+08	AKNA
chr19	2031929	2062368	MKNK2;BTBD2
chr9	1.33E+08	1.33E+08	nrg_USP20;USP20
chr7	1.14E+08	1.14E+08	FOXP2
chr3	98480380	98495371	ST3GAL6
chr11	1.15E+08	1.15E+08	CADM1
chr1	1.68E+08	1.68E+08	RCSD1
chr20	61273001	61284636	SLCO4A1
chr3	1.69E+08	1.69E+08	TERC;MYNN;ACTRT3

chr5	55273492	55291686	IL6ST
chr17	74721806	74734514	METTL23;SRSF2
chr15	23660888	23682206	nrg_GOLGA8S
chr2	10259934	10263768	RRM2
chr1	2.45E+08	2.45E+08	COX20
chr5	1.79E+08	1.79E+08	SQSTM1
chr7	1.15E+08	1.15E+08	MDFIC
chr17	4268347	4281153	UBE2G1
chr10	7512340	7535209	nrg_SFMBT2
chr2	65158341	65174075	LOC400958
chr6	31694739	31708772	MSH5;DDAH2;CLIC1
chr6	26042702	26046970	HIST1H3C
chr9	1.4E+08	1.4E+08	TRAF2
chr17	76116863	76137048	C17orf99;TMC6;TMC8
chr16	68389892	68419235	PRMT7;SMPD3;nrg_PRMT7
chr1	1.56E+08	1.56E+08	ARHGEF2
chr9	9605767	9615822	nrg_PTPRD
chr4	1194073	1213754	SPON2;CTBP1-AS
chr17	80448163	80478867	FOXK2
chr5	1.51E+08	1.51E+08	LOC100652758;ATOX1
chr3	13455518	13470278	NUP210
chr18	48677949	48691592	MEX3C;nrg_MEX3C
chr17	17712187	17744299	SREBF1
chr2	37598866	37623685	nrg_QPCT;QPCT
chr10	3823467	3828712	KLF6
chr17	56697456	56710099	TEX14
chr9	93732799	93738288	nrg_LOC100129316
chr10	74078356	74095821	DNAJB12;nrg_DNAJB12
chr1	24513220	24519537	IFNLR1
chr10	21805234	21824273	SKIDA1;MLLT10
chr21	43283747	43300506	PRDM15
chr19	56330237	56351420	NLRP4;NLRP11
chr8	1.29E+08	1.29E+08	MYC
chr5	1.39E+08	1.39E+08	CXXC5
chr6	26031134	26034889	HIST1H3B
chr1	2.12E+08	2.12E+08	RD3

Table SVIII. Super-enriched regions in the U-87 cell line.

chr	St	Ed	Genes
chr1	7306956	7328639	nrg_CAMTA1
chr1	7358144	7375242	nrg_VAMP3
chr1	8064982	8108976	ERRFI1
chr1	8136990	8158663	nrg_ERRFI1
chr1	16275173	16293659	ZBTB17
chr1	33893492	33901769	ZSCAN20
chr1	39849820	39877140	KIAA0754
chr1	56534395	56566896	nrg_PPAP2B
chr1	59309642	59352182	LINC01135
chr1	66696626	66767337	nrg_PDE4B;PDE4B
chr1	77999182	78012174	nrg_ZZZ3
chr1	79296349	79309732	nrg_ELTD1
chr1	95175368	95206002	LINC01057
chr1	1.19E+08	1.2E+08	TBX15
chr1	1.45E+08	1.45E+08	PDE4DIP;SEC22B
chr1	1.45E+08	1.45E+08	SEC22B;nrg_SEC22B
chr1	1.45E+08	1.45E+08	NOTCH2NL
chr1	1.7E+08	1.71E+08	GORAB
chr1	1.83E+08	1.83E+08	NMNAT2
chr1	1.86E+08	1.86E+08	nrg_PRG4
chr1	2.01E+08	2.01E+08	nrg_PHLDA3;PHLDA3;TNNI1
chr1	2.07E+08	2.07E+08	FAIM3;IL24
chr1	2.13E+08	2.13E+08	ATF3
chr1	2.2E+08	2.2E+08	nrg_RNU5F-1
chr1	2.22E+08	2.22E+08	nrg_C1orf140
chr1	2.22E+08	2.22E+08	nrg_DUSP10
chr1	2.22E+08	2.22E+08	nrg_DUSP10
chr1	2.24E+08	2.24E+08	CAPN2
chr1	2.24E+08	2.24E+08	FBXO28;nrg_FBXO28
chr1	2.25E+08	2.25E+08	nrg_CNIH3;nrg_WDR26
chr1	2.25E+08	2.25E+08	CNIH3
chr1	2.35E+08	2.35E+08	IRF2BP2;LINC00184
chr1	2.36E+08	2.36E+08	LYST
chr1	2.4E+08	2.4E+08	FMN2
chr1	2.45E+08	2.45E+08	C1orf100
chr10	3870820	3930703	KLF6;nrg_KLF6
chr10	4981845	5006024	AKR1C1
chr10	5325301	5340095	nrg_UCN3
chr10	17027773	17131088	CUBN
chr10	17241080	17273093	VIM-AS1;TRDMT1
chr10	24717171	24755926	KIAA1217
chr10	29909890	29948960	SVIL

chr10	31274780	31297334	ZNF438
chr10	33246237	33275584	ITGB1
chr10	33417899	33446786	nrg_ITGB1;nrg_NRP1
chr10	33619229	33631116	NRP1
chr10	33643868	33671491	NRP1
chr10	49797118	49848926	ARHGAP22
chr10	50369388	50396847	C10orf128
chr10	73019523	73032824	UNC5B-AS1;SLC29A3
chr10	73343981	73365135	nrg_C10orf105
chr10	74020173	74038649	DDIT4
chr10	74055000	74097385	DNAJB12;nrg_DDIT4;nrg_DNAJB12
chr10	79107429	79121151	KCNMA1
chr10	79138253	79176733	KCNMA1
chr10	79260281	79274259	KCNMA1
chr10	79997635	80024056	LINC00856;LINC00595
chr10	80732041	80738573	ZMIZ1-AS1
chr10	81076282	81098531	PPIF
chr10	93347626	93415405	LOC100188947;PPP1R3C
chr10	95218249	95243212	MYOF
chr10	1.12E+08	1.12E+08	nrg_DUSP5;nrg_SMNDC1
chr10	1.28E+08	1.28E+08	nrg_FANK1-AS1
chr10	1.29E+08	1.29E+08	FAM196A
chr10	1.3E+08	1.3E+08	nrg_MKI67
chr11	9774290	9787749	SBF2-AS1;LOC440028
chr11	10370198	10397570	CAND1.11
chr11	12087457	12109647	MICAL2
chr11	12178500	12260623	MICAL2;MICALCL;nrg_MICALCL
chr11	27923858	27957061	nrg_BDNF;nrg_KIF18A
chr11	34655312	34678222	EHF
chr11	35600758	35621077	FJX1
chr11	57173906	57202730	SLC43A3;PRG2
chr11	58340583	58347843	LPXN
chr11	61716633	61741319	BEST1;FTH1
chr11	65185754	65194133	NEAT1
chr11	65238700	65275602	MALAT1
chr11	65665662	65685023	FOSL1;C11orf68
chr11	69063731	69090076	MYEOV;nrg_MYEOV
chr11	1.22E+08	1.22E+08	BLID;MIR100HG
chr12	2340925	2378865	CACNA1C-AS4;CACNA1C-IT3
chr12	13250797	13257910	GSG1
chr12	13349114	13378735	EMP1
chr12	14409000	14427568	nrg_ATF7IP
chr12	24859973	24881866	nrg_LINC00477
chr12	27701892	27728923	PPFIBP1

chr12	46942204	46957227	nrg_SLC38A2
chr12	52575202	52616256	KRT80;LINC00592;KRT7;C12orf80
chr12	53222023	53273778	nrg_KRT8;KRT79;KRT78
chr12	57503959	57565919	STAT6;LRP1
chr12	63095736	63138962	nrg_C12orf61
chr12	63176809	63188341	PPM1H
chr12	64553475	64581862	C12orf66;nrg_C12orf66
chr12	65985263	66093876	nrg_HMGA2
chr12	66214844	66226572	RPSAP52;HMGA2
chr12	66260724	66287354	RPSAP52;nrg_RPSAP52
chr12	66334109	66350850	nrg_RPSAP52
chr12	76141015	76185929	nrg_PHLDA1;nrg_KRR1
chr12	76363253	76393111	nrg_PHLDA1
chr12	76411662	76426880	PHLDA1
chr12	89549810	89560822	nrg_LOC728084
chr12	90118723	90128631	nrg_LINC00936
chr12	1.22E+08	1.22E+08	SETD1B;LINC01089;RHOF
chr12	1.25E+08	1.25E+08	UBC
chr12	1.28E+08	1.28E+08	nrg_LOC101927592
chr12	1.28E+08	1.28E+08	nrg_LOC101927616;nrg_LOC101927592
chr12	1.28E+08	1.28E+08	nrg_LOC101927616
chr13	43376146	43423217	nrg_FAM216B
chr13	44874988	44892354	nrg_SERP2
chr13	45751923	45781071	nrg_KCTD4;KCTD4
chr13	80604478	80630430	LINC01080;nrg_LINC01080
chr13	1.01E+08	1.01E+08	nrg_PCCA-AS1
chr13	1.02E+08	1.02E+08	nrg_LINC00411
chr13	1.02E+08	1.02E+08	NALCN
chr13	1.02E+08	1.02E+08	ITGBL1
chr13	1.02E+08	1.02E+08	ITGBL1
chr13	1.08E+08	1.08E+08	nrg_FAM155A-IT1
chr13	1.08E+08	1.08E+08	nrg_FAM155A-IT1
chr14	35833993	35875015	NFKBIA;nrg_NFKBIA
chr14	62013773	62053699	LOC101927780
chr14	65672926	65725757	LOC100128233
chr14	69001835	69022565	nrg_ZFP36L1
chr14	69130015	69182472	nrg_ZFP36L1
chr14	69246364	69267656	ZFP36L1
chr14	73104349	73133913	DPF3;nrg_DPF3
chr14	73924808	73944889	C14orf169;NUMB
chr14	77413308	77429149	nrg_IRF2BPL
chr14	85982773	85999983	FLRT2
chr14	91691375	91720259	GPR68
chr14	96552160	96597684	nrg_C14orf132;nrg_BDKRB2;C14orf132

chr14	96712290	96752569	BDKRB1;nrg_BDKRB1
chr14	97570095	97587400	nrg_LINC00618
chr14	97630194	97648005	nrg_LINC00618
chr14	1E+08	1E+08	EML1
chr14	1.05E+08	1.05E+08	CDCA4
chr15	28061841	28074491	OCA2
chr15	33116772	33165300	nrg_GREM1
chr15	51168904	51178643	AP4E1
chr15	51515458	51546168	CYP19A1
chr15	63766242	63807588	USP3
chr15	65165021	65198206	PLEKHO2;ANKDD1A
chr15	79965084	79980720	nrg_MTHFS
chr15	92079287	92116153	nrg_LOC101926928
chr15	1.01E+08	1.01E+08	nrg_ASB7
chr16	55504258	55522742	MMP2
chr16	56639708	56649077	MT1L;MT2A
chr16	70834266	70840917	VAC14
chr16	77307381	77342636	nrg_SYCE1L
chr16	77608398	77644868	nrg_NUDT7;nrg_ADAMTS18
chr16	77681500	77694878	nrg_NUDT7
chr16	82659735	82692177	CDH13
chr16	86609055	86624640	FOXL1
chr16	86686884	86715375	nrg_FOXL1
chr17	8812704	8858216	PIK3R5
chr17	13240959	13269333	nrg_HS3ST3A1
chr17	13434586	13466434	HS3ST3A1
chr17	18964442	18997083	GRAP;LOC388436
chr17	29876058	29924728	nrg_RAB11FIP4
chr17	38169818	38183786	SNORD124
chr17	38251937	38279255	NR1D1;MSL1
chr17	43220959	43250830	HEXIM1;HEXIM2
chr17	46124361	46134304	NFE2L1
chr17	48124459	48142660	LOC284080;ITGA3
chr17	57882151	57926624	nrg_TUBD1
chr17	66373709	66381318	PRKAR1A
chr17	67753378	67763719	LOC101928122
chr17	76309929	76349721	LOC100996291;nrg_SOCS3;SOCS3
chr18	3446493	3454510	TGIF1
chr18	3592961	3626391	nrg_DLGAP1-AS2;DLGAP1-AS1;DLGAP1-AS2
chr18	3643412	3666826	nrg_DLGAP1-AS2
chr18	9705078	9788245	RAB31
chr18	14758352	14770212	ANKRD30B
chr18	14841468	14853681	ANKRD30B;nrg_LOC400644
chr18	14964345	14977563	LOC400644

chr18	21153716	21175087	NPC1
chr18	43354902	43408718	SIGLEC15;nrg_SLC14A1
chr18	52425594	52444518	nrg_RAB27B
chr18	55872399	55911701	NEDD4L
chr18	67986376	68005075	SOCS6
chr18	68024330	68065518	nrg_LOC101060542;LOC101060542
chr19	13729963	13749230	nrg_CCDC130;nrg_CACNA1A
chr19	13947496	13973531	NANOS3
chr19	18474803	18526904	GDF15;LRRC25;SSBP4
chr19	39554430	39585031	PAPL
chr19	42612499	42637730	POU2F2
chr19	43297404	43357354	PSG10P;PSG8;LOC100289650
chr19	43378661	43494058	PSG6;PSG7;nrg_PSG11;PSG1
chr19	52225687	52254329	FPR1;HAS1
chr2	10418189	10443437	HPCAL1
chr2	17822975	17854811	VSNL1;SMC6
chr2	20093084	20112241	TTC32
chr2	33351940	33384462	LTBP1
chr2	33434831	33445813	LTBP1
chr2	37788228	37814033	nrg_CDC42EP3
chr2	37846815	37881566	CDC42EP3;nrg_CDC42EP3
chr2	39694823	39758212	LOC728730
chr2	46541970	46564288	EPAS1
chr2	47074125	47109924	nrg_MCFD2;LINC01119;nrg_LINC01119
chr2	55326513	55347321	RTN4;nrg_RTN4
chr2	65034229	65093293	nrg_LOC101927438;LOC101927438
chr2	67713359	67754153	nrg_ETAA1
chr2	85632067	85673828	CAPG;SH2D6
chr2	97845681	97884168	ANKRD36;nrg_LOC100506076
chr2	1E+08	1E+08	AFF3
chr2	1.02E+08	1.02E+08	RFX8
chr2	1.09E+08	1.09E+08	SULT1C3;SULT1C2
chr2	1.09E+08	1.09E+08	LIMS1
chr2	1.09E+08	1.09E+08	LIMS1
chr2	1.14E+08	1.14E+08	IL1B
chr2	1.14E+08	1.14E+08	IL37;IL1B
chr2	1.14E+08	1.14E+08	IL36RN
chr2	1.44E+08	1.44E+08	KYNU
chr2	1.45E+08	1.45E+08	LOC101928455;ZEB2-AS1
chr2	1.45E+08	1.45E+08	TEX41
chr2	1.51E+08	1.51E+08	RND3
chr2	1.51E+08	1.51E+08	RND3;nrg_LOC101929260
chr2	1.51E+08	1.51E+08	LOC101929260
chr2	1.51E+08	1.51E+08	LOC101929282

chr2	1.52E+08	1.52E+08	nrg_LOC101929282
chr2	1.53E+08	1.53E+08	FMNL2
chr2	1.59E+08	1.59E+08	ACVR1
chr2	1.61E+08	1.61E+08	ITGB6
chr2	1.74E+08	1.74E+08	ZAK
chr2	2.07E+08	2.07E+08	NRP2
chr2	2.08E+08	2.08E+08	KLF7
chr2	2.08E+08	2.08E+08	LOC101927865
chr2	2.08E+08	2.08E+08	nrg_LOC101927865
chr2	2.08E+08	2.08E+08	nrg_LOC101927865;nrg_CREB1
chr2	2.27E+08	2.27E+08	LOC646736
chr2	2.27E+08	2.27E+08	nrg_LOC646736
chr2	2.29E+08	2.29E+08	CCL20
chr2	2.29E+08	2.29E+08	nrg_SPHKAP
chr2	2.3E+08	2.3E+08	PID1
chr2	2.3E+08	2.3E+08	nrg_PID1
chr2	2.3E+08	2.3E+08	nrg_PID1
chr2	2.3E+08	2.3E+08	nrg_PID1
chr2	2.3E+08	2.3E+08	DNER
chr2	2.35E+08	2.35E+08	nrg_SPP2
chr2	2.36E+08	2.36E+08	nrg_ARL4C
chr2	2.38E+08	2.38E+08	nrg_COPS8;COL6A3;nrg_COL6A3
chr2	2.38E+08	2.38E+08	COL6A3;MLPH
chr2	2.39E+08	2.39E+08	ASB1
chr2	2.4E+08	2.4E+08	nrg_TWIST2
chr20	7821629	7840538	nrg_HAO1
chr20	13003163	13024466	SPTLC3
chr20	23123086	23142750	LINC00656
chr20	30283728	30315935	BCL2L1
chr20	33890230	33917908	FAM83C
chr20	36701485	36738954	nrg_TGM2;RPRD1B
chr20	38413887	38429856	nrg_LOC100505663
chr20	38478046	38526354	nrg_LOC100505663
chr20	43687340	43696768	nrg_KCNS1
chr20	45943617	45965761	ZMYND8
chr20	45978332	45990120	ZMYND8
chr20	49031954	49077839	nrg_PTPN1;PTPN1;nrg_LINC01271
chr20	49252268	49278313	LOC100506175;FAM65C
chr20	51554117	51576382	TSHZ2
chr20	52195166	52213405	ZNF217
chr20	52443953	52452573	nrg_SUMO1P1
chr20	52482286	52577332	nrg_SUMO1P1;SUMO1P1
chr21	28448195	28453883	nrg_ADAMTS5
chr21	28936834	28955453	nrg_LINC00113

chr21	29017311	29023841	nrg_LINC00113
chr21	35312209	35349848	nrg_LOC400863;LOC400863
chr21	36143556	36218533	LOC100506385;RUNX1;nrg_LOC100506385
chr21	39630708	39725162	LOC102724678;nrg_LOC102724678;KCNJ15
chr21	44912766	44943072	LINC00313
chr21	45177160	45199485	CSTB;nrg_CSTB
chr21	45590615	45630173	nrg_ICOSLG;nrg_C21orf33
chr21	47458556	47481504	COL6A2;nrg_COL6A1
chr22	24819480	24833072	ADORA2A
chr22	30591037	30609788	nrg_LIF
chr22	30624370	30676116	OSM;LIF;nrg_LIF;GATSL3
chr22	36935528	36943584	EIF3D
chr22	37035928	37070323	CACNG2
chr22	45973764	46009217	nrg_FBLN1;nrg_ATXN10
chr22	46449299	46477095	MIRLET7BHG;PRR34
chr22	50968956	50995634	KLHDC7B;TYMP;SYCE3
chr3	4435449	4469153	SUMF1
chr3	5018612	5037886	BHLHE40
chr3	10230878	10248264	IRAK2
chr3	11313698	11333605	ATG7
chr3	15309298	15352591	SH3BP5;SH3BP5-AS1;nrg_SH3BP5-AS1
chr3	16768802	16785425	nrg_DAZL
chr3	23689988	23728180	nrg_UBE2E1
chr3	27562722	27596766	nrg_SLC4A7;SLC4A7
chr3	45081976	45113116	CLEC3B;nrg_CLEC3B
chr3	45125696	45225464	CDCP1;nrg_CLEC3B
chr3	45239932	45268246	nrg_TMEM158;TMEM158
chr3	46121910	46169597	nrg_XCR1;nrg_CCR1
chr3	55177085	55239079	nrg_LRTM1
chr3	55510468	55523153	WNT5A
chr3	71105361	71161967	FOXP1
chr3	72025228	72061205	nrg_LINC00877
chr3	73759307	73777354	nrg_PDZRN3
chr3	73814956	73841181	nrg_PDZRN3
chr3	81772651	81794305	GBE1
chr3	98680442	98705575	nrg_DCBLD2
chr3	1.01E+08	1.01E+08	ABI3BP
chr3	1.02E+08	1.02E+08	LOC152225
chr3	1.12E+08	1.12E+08	CCDC80;LINC01279
chr3	1.12E+08	1.12E+08	LOC101929694
chr3	1.16E+08	1.16E+08	nrg_GAP43;nrg_LSAMP-AS1
chr3	1.19E+08	1.19E+08	nrg_POPDC2;POPDC2
chr3	1.27E+08	1.28E+08	nrg_ABTB1;MGLL
chr3	1.4E+08	1.4E+08	nrg_CLSTN2-AS1

chr3	1.41E+08	1.41E+08	ZBTB38
chr3	1.49E+08	1.49E+08	WWTR1
chr3	1.55E+08	1.55E+08	MME
chr3	1.66E+08	1.66E+08	nrg_ZBBX
chr3	1.7E+08	1.7E+08	nrg_SLC7A14;nrg_RPL22L1
chr3	1.71E+08	1.71E+08	nrg_RPL22L1
chr3	1.72E+08	1.72E+08	FNDC3B
chr3	1.78E+08	1.78E+08	LOC102724550
chr3	1.88E+08	1.88E+08	LPP
chr3	1.94E+08	1.94E+08	ATP13A3;LINC00884
chr3	1.94E+08	1.94E+08	TMEM44-AS1
chr4	5731784	5771455	EVC
chr4	13883411	13923990	nrg_LINC01085
chr4	13967741	13993575	nrg_LINC01085
chr4	21880676	21907918	KCNIP4-IT1;KCNIP4
chr4	26198031	26208715	nrg_RBPJ
chr4	38968320	38997976	TMEM156
chr4	40992082	40998478	nrg_APBB2
chr4	74526986	74610541	nrg_IL8;nrg_RASSF6;IL8;RASSF6
chr4	74748692	74789644	nrg_CXCL1
chr4	74870935	74910232	nrg_CXCL3;CXCL3;CXCL5
chr4	74959423	75000521	MTHFD2L;CXCL2
chr4	75071690	75098608	MTHFD2L
chr4	75230078	75244956	EREG
chr4	75387930	75412760	nrg_AREG
chr4	1.14E+08	1.14E+08	CAMK2D;nrg_CAMK2D
chr4	1.2E+08	1.2E+08	MYOZ2
chr4	1.24E+08	1.24E+08	BBS12;nrg_BBS12;FGF2
chr4	1.48E+08	1.48E+08	nrg_EDNRA
chr4	1.58E+08	1.58E+08	PDGFC
chr4	1.78E+08	1.78E+08	VEGFC
chr4	1.78E+08	1.78E+08	nrg_VEGFC
chr4	1.78E+08	1.78E+08	nrg_VEGFC
chr4	1.89E+08	1.89E+08	LOC100506272
chr4	1.89E+08	1.89E+08	nrg_LINC01060;nrg_TRIML1
chr4	1.89E+08	1.89E+08	nrg_LINC01060;LINC01060
chr5	14399065	14420848	nrg_FAM105A
chr5	33772128	33811464	ADAMTS12
chr5	34561360	34610101	nrg_RAI14;RAI14
chr5	37711011	37740787	nrg_GDNF
chr5	42985044	43018641	FLJ32255;LOC648987
chr5	52656212	52675108	nrg_FST
chr5	52692509	52727114	nrg_FST;FST
chr5	64485378	64506178	ADAMTS6

chr5	66596365	66649834	nrg_CD180
chr5	77800231	77847344	LHFPL2
chr5	77862341	77907138	LHFPL2
chr5	86408991	86423904	LOC101929380
chr5	90591625	90610812	LUCAT1
chr5	97643210	97650881	nrg_RGMB
chr5	1.06E+08	1.06E+08	nrg_LOC102467213
chr5	1.31E+08	1.31E+08	nrg_CSF2;IL3;CSF2
chr5	1.32E+08	1.32E+08	C5orf56
chr5	1.32E+08	1.32E+08	nrg_IRF1
chr5	1.49E+08	1.49E+08	ABLIM3
chr5	1.5E+08	1.5E+08	SMIM3;DCTN4
chr5	1.68E+08	1.68E+08	nrg_PANK3;nrg_CTB-174D11.1
chr5	1.71E+08	1.71E+08	nrg_FGF18
chr5	1.72E+08	1.72E+08	DUSP1;LOC101928093
chr5	1.72E+08	1.72E+08	LOC100268168;nrg_LOC100268168;ERGIC1
chr5	1.73E+08	1.73E+08	nrg_STC2;nrg_LOC285593
chr6	30736382	30751080	IER3
chr6	32935782	32940489	BRD2
chr6	43877205	43896007	nrg_C6orf223
chr6	43958538	44044921	C6orf223;nrg_MRPL14;nrg_C6orf223
chr6	85820951	85845580	nrg_NT5E
chr6	86157695	86179893	NT5E
chr6	93631941	93656726	nrg_EPHA7
chr6	1.06E+08	1.06E+08	nrg_PREP
chr6	1.12E+08	1.12E+08	WISP3
chr6	1.12E+08	1.12E+08	WISP3
chr6	1.14E+08	1.14E+08	nrg_MARCKS
chr6	1.14E+08	1.14E+08	MARCKS
chr6	1.2E+08	1.2E+08	nrg_LOC285762
chr6	1.33E+08	1.33E+08	VNN2;VNN3
chr6	1.49E+08	1.49E+08	SASH1
chr6	1.56E+08	1.56E+08	NOX3
chr6	1.56E+08	1.56E+08	NOX3;nrg_NOX3
chr6	1.58E+08	1.58E+08	SYNJ2
chr7	14019441	14032209	ETV1
chr7	17560805	17586960	LOC101927630
chr7	17718695	17737183	nrg_LOC101927630
chr7	18898748	18914094	nrg_TWIST1
chr7	22599291	22651415	nrg_LOC100506178;LOC100506178
chr7	22686805	22711875	nrg_IL6
chr7	22734189	22742702	IL6
chr7	22756071	22772803	IL6
chr7	24814196	24829120	DFNA5

chr7	73115750	73136242	STX1A
chr7	73493274	73513614	LIMK1
chr7	77037837	77095774	LOC101927243;GSAP
chr7	81229723	81270775	nrg_HGF
chr7	81291585	81355647	HGF;nrg_HGF
chr7	93632716	93699313	BET1;nrg_BET1
chr7	1.01E+08	1.01E+08	TRIM56;SERPINE1
chr7	1.05E+08	1.05E+08	LINC01004
chr7	1.05E+08	1.05E+08	KMT2E
chr7	1.06E+08	1.06E+08	NAMPT
chr7	1.06E+08	1.06E+08	nrg_NAMPT
chr7	1.06E+08	1.06E+08	nrg_NAMPT
chr7	1.16E+08	1.16E+08	CAV2;CAV1
chr7	1.31E+08	1.31E+08	LINC-PINT
chr7	1.31E+08	1.31E+08	MKLN1
chr7	1.31E+08	1.31E+08	MKLN1
chr7	1.34E+08	1.34E+08	AKR1B1
chr7	1.38E+08	1.38E+08	DGKI
chr7	1.55E+08	1.55E+08	nrg_INSIG1
chr8	11305569	11369002	FAM167A;BLK
chr8	13209781	13235084	DLC1
chr8	16606074	16612723	nrg_FGF20
chr8	18983857	18999491	nrg_LOC100128993;nrg_PSD3
chr8	19024366	19080730	nrg_LOC100128993;LOC100128993
chr8	23193263	23214624	LOC100507156
chr8	23375930	23405937	SLC25A37
chr8	23602444	23621428	NKX2-6;nrg_NKX2-6
chr8	24050162	24087600	nrg_ADAM28
chr8	25530780	25548902	nrg_CDCA2
chr8	25749706	25783682	EBF2
chr8	25846295	25867484	EBF2
chr8	32175046	32219768	nrg_NRG1-IT3
chr8	49185823	49237422	nrg_UBE2V2;nrg_LOC101929268
chr8	59504317	59530017	NSMAF;nrg_SDCBP
chr8	59654745	59681977	nrg_NSMAF
chr8	62620952	62647606	ASPH
chr8	62668779	62686314	ASPH;nrg_ASPH
chr8	72740051	72779472	MSC;LOC100132891
chr8	1.04E+08	1.04E+08	nrg_AZIN1
chr8	1.04E+08	1.04E+08	FZD6
chr8	1.07E+08	1.07E+08	nrg_OXR1
chr8	1.16E+08	1.16E+08	TRPS1
chr8	1.17E+08	1.17E+08	TRPS1
chr8	1.17E+08	1.17E+08	LINC00536

chr8	1.17E+08	1.17E+08	nrg_LINC00536
chr8	1.19E+08	1.19E+08	nrg_MED30
chr8	1.19E+08	1.19E+08	EXT1
chr8	1.23E+08	1.23E+08	nrg_HAS2
chr8	1.23E+08	1.23E+08	nrg_ZHX2
chr8	1.23E+08	1.23E+08	nrg_ZHX2
chr8	1.23E+08	1.23E+08	nrg_ZHX2
chr8	1.29E+08	1.29E+08	nrg_TMEM75;TMEM75;PVT1
chr8	1.29E+08	1.29E+08	nrg_TMEM75
chr8	1.33E+08	1.33E+08	nrg_EFR3A;EFR3A
chr8	1.35E+08	1.35E+08	ST3GAL1
chr8	1.35E+08	1.35E+08	nrg_ST3GAL1
chr8	1.35E+08	1.35E+08	nrg_ST3GAL1
chr9	3842604	3881861	nrg_GLIS3-AS1;GLIS3-AS1
chr9	3894501	3918249	nrg_GLIS3-AS1;GLIS3-AS1
chr9	3951507	3973412	nrg_GLIS3-AS1
chr9	18473649	18494307	ADAMTSL1
chr9	19156502	19186899	PLIN2;DENND4C
chr9	75730731	75770219	ANXA1
chr9	1.02E+08	1.02E+08	GALNT12;nrg_GALNT12
chr9	1.02E+08	1.02E+08	COL15A1;TGFBR1;nrg_TGFBR1
chr9	1.03E+08	1.03E+08	MSANTD3
chr9	1.07E+08	1.07E+08	nrg_SMC2
chr9	1.08E+08	1.08E+08	ABCA1
chr9	1.08E+08	1.08E+08	nrg_ABCA1
chr9	1.14E+08	1.14E+08	MUSK
chr9	1.15E+08	1.15E+08	nrg_UGCG
chr9	1.15E+08	1.15E+08	nrg_UGCG;SUSD1
chr9	1.16E+08	1.16E+08	nrg_RGS3
chr9	1.18E+08	1.18E+08	TNFSF8;nrg_TNFSF8
chr9	1.18E+08	1.18E+08	nrg_TNFSF8
chr9	1.18E+08	1.18E+08	DEC1-
chr9	1.18E+08	1.18E+08	nrg_LOC101928775
chr9	1.18E+08	1.18E+08	nrg_LOC101928775
chr9	1.19E+08	1.19E+08	PAPPA
chr9	1.19E+08	1.19E+08	LOC100128505;nrg_LOC100128505
chr9	1.3E+08	1.3E+08	FAM129B
chr9	1.32E+08	1.32E+08	LINC00963
chr9	1.33E+08	1.33E+08	PTGES
chrX	43817582	43836005	NDP
chrX	45364121	45383983	LINC01204
chrX	45555863	45578239	nrg_LINC01204
chrX	45602326	45641863	nrg_LINC01204
chrX	45656128	45668932	nrg_LINC01204

Table SIX. Core set of JQ1 regulatory genes.

Symbol	EntrezID	JQ1 regulation	TF
ADORA2A	135	-2	1
ANP32A	8125	-1	1
BCL6	604	1	1
BCOR	54880	-1	1
E2F3	1871	-1	1
ETV6	2120	-1	1
HES1	3280	-1	1
HEXIM1	10614	2	1
HEXIM2	124790	-1	1
ID3	3399	-1	1
IRF2BP2	359948	-1	1
JMJD6	23210	-1	1
MLLT10	8028	-1	1
MLLT6	4302	-1	1
MYC	4609	-1	1
SOX4	6659	-1	1
SQSTM1	8878	1	1
TBL1XR1	79718	-1	1
TLE3	7090	-1	1
ZFP91	386607	-1	1
ARID2	196528	-1	1
HIVEP1	3096	-2	1
IKZF3	22806	-1	1
PRDM15	63977	-2	1
REPIN1	29803	-1	1
SKIL	6498	1	1
SREBF1	6720	-1	1
SUB1	10923	-1	1
TCF4	6925	-1	1
TMPO	7112	-1	1
UBTF	7343	-1	1
ZFAT	57623	-1	1
ZFP36	7538	1	1
BCL2L1	598	-1	0
BIRC3	330	-1	0
CFLAR	8837	-2	0
DNAJB12	54788	-1	0
DUSP6	1848	-1	0
IER3	8870	1	0
NFKBIL1	4795	-1	0
PTPN6	5777	-1	0
TGFBR2	7048	-1	0

THADA	63892	-1	0
TRAF1	7185	-1	0
ANP32B	10541	-1	0
APOLD1	81575	2	0
C2CD2	25966	-2	0
DARS	1615	-1	0
DGKA	1606	-1	0
DHX37	57647	-1	0
EIF2AK4	440275	-1	0
EMG1	10436	-2	0
FCHSD2	9873	-1	0
FLAD1	80308	-1	0
FLOT1	10211	-1	0
GRAP	10750	-2	0
HNRNPF	3185	-1	0
MAPKAPK3	7867	-1	0
MKNK2	2872	1	0
MSL1	339287	-1	0
NSMCE1	197370	-1	0
PPIL1	51645	-2	0
PTPN18	26469	-1	0
PWP2	5822	-1	0
RASA3	22821	-2	0
RGS16	6004	-2	0
RNASEH2B	79621	-1	0
RPTOR	57521	-1	0
ST3GAL1	6482	-1	0
STX10	8677	-1	0
TRIM47	91107	-1	0
TRIM65	201292	-1	0
ZC3H4	23211	-1	0
ZC3H7B	23264	-1	0
ZMYND8	23613	-2	0