Supplementary Table 1 Genes in the yellow module.

Accession number	Gene symbol	Gene Name
NM_001105214	ASH2L	ASH2 like histone lysine methyltransferase complex subunit(ASH2L)
NM_004336	BUB1	BUB1 mitotic checkpoint serine
NM_001262	CDKN2C	Cyclin dependent kinase inhibitor 2C(CDKN2C)
NM_001199803	CENPO	centromere protein O(CENPO)
NM_001826	CKS1B	CDC28 protein kinase regulatory subunit 1B(CKS1B)
NM_001199741	GADD45A	growth arrest and DNA damage inducible alpha(GADD45A)
NM_001145661	GATA2	GATA binding protein 2(GATA2)
NM_005319	HIST1H1C	histone cluster 1 H1 family member c(HIST1H1C)
NM_021063	HIST1H2BD	histone cluster 1 H2B family member d(HIST1H2BD)
NM_003545	HIST1H4E	histone cluster 1 H4 family member e(HIST1H4E)
NM_001005464	HIST2H3A	histone cluster 2 H3 family member a(HIST2H3A)
NM_001142556	HMMR	hyaluronan mediated motility receptor(HMMR)
NM_182972	IRF2BP2	interferon regulatory factor 2 binding protein 2(IRF2BP2)
NM_003740	KCNK5	potassium two pore domain channel subfamily K member 5(KCNK5)
NM_006845	KIF2C	kinesin family member 2C(KIF2C)
NM_001190818	ORC1	origin recognition complex subunit 1(ORC1)
NM_001003698	RREB1	ras responsive element binding protein 1(RREB1)
NM_001034	RRM2	ribonucleotide reductase regulatory subunit M2(RRM2)
NM_014331	SLC7A11	solute carrier family 7 member 11(SLC7A11)
NM_016224	SNX9	sorting nexin 9(SNX9)
NM_001134336	STRIP2	striatin interacting protein 2(STRIP2)
NM_001031685	TP53BP2	tumor protein p53 binding protein 2(TP53BP2)
NM_178014	TUBB	tubulin beta class I(TUBB)
NM_000374	UROD	uroporphyrinogen decarboxylase(UROD)
NR_003502	ZNRF2P1	zinc and ring finger 2 pseudogene 1(ZNRF2P1)
NM_021058	Hist1h2bj	histone cluster 1 H2B family member j(HIST1H2BJ)
NR_028374	SNORA80B	small nucleolar RNA, H
NR_037864	AP4B1-AS1	AP4B1 antisense RNA 1(AP4B1-AS1)
NM_000601	HGF	Hepatocyte growth factor(HGF)
NM_001200047	NMNAT3	nicotinamide nucleotide adenylyltransferase 3(NMNAT3)
NM_016002	SCCPDH	saccharopine dehydrogenase (putative)(SCCPDH)
NM_001003794	MGLL	monoglyceride lipase(MGLL)
NM_018101	CDCA8	cell division cycle associated 8(CDCA8)
NM_018392	ZGRF1	zinc finger GRF-type containing 1(ZGRF1)
NM_003540	Hist1h4f	histone cluster 1 H4 family member f(HIST1H4F)
NM_000791	DHFR	dihydrofolate reductase(DHFR)
NM_003534	hist1h3g	histone cluster 1 H3 family member g(HIST1H3G)
NM_001142548	RAD54L	RAD54-like (S. cerevisiae)(RAD54L)

NM_003531	Hist1h3c	histone cluster 1 H3 family member c(HIST1H3C)
NM_003538	Hist1h4a	histone cluster 1 H4 family member a(HIST1H4A)
NM_001003790	ERLIN2	ER lipid raft associated 2(ERLIN2)
NM_006343	MERTK	MER proto-oncogene, tyrosine kinase(MERTK)
NM_003537	Hist1h3b	histone cluster 1 H3 family member b(HIST1H3B)
NM_003535	HIST1H3J	histone cluster 1 H3 family member j(HIST1H3J)
NM_021062	HIST1H2BB	histone cluster 1 H2B family member b(HIST1H2BB)
NM_001017420	ESCO2	establishment of sister chromatid cohesion N-acetyltransferase 2(ESCO2)
NM_021064	Hist1h2ag	histone cluster 1 H2A family member g(HIST1H2AG)
NM_002491	NDUFB3	NADH:ubiquinone oxidoreductase subunit B3(NDUFB3)
NM_003539	HIST1H4D	histone cluster 1 H4 family member d(HIST1H4D)
NR_037177	LOC100294145	uncharacterized LOC100294145(LOC100294145)
NM_001198557	LMNB1	lamin B1(LMNB1)
NM_021066	Hist1h2aj	histone cluster 1 H2A family member j(HIST1H2AJ)
NM_207418	FAM72D	family with sequence similarity 72 member D(FAM72D)
NM_016448	DTL	denticleless E3 ubiquitin protein ligase homolog(DTL)
NM_053002	MED12L	mediator complex subunit 12 like(MED12L)
NM_002870	RAB13	RAB13, member RAS oncogene family(RAB13)
NM_022836	DCLRE1B	DNA cross-link repair 1B(DCLRE1B)
NM_003542	hist1h4c	histone cluster 1 H4 family member c(HIST1H4C)
NM_003544	Hist1h4b	histone cluster 1 H4 family member b(HIST1H4B)
NM_003546	hist1h4l	histone cluster 1 H4 family member l(HIST1H4L)
NM_004219	PTTG1	pituitary tumor-transforming 1(PTTG1)
NM_001002800	SMC4	structural maintenance of chromosomes 4(SMC4)
NM_000249	MLH1	mutL homolog 1(MLH1)
NM_003856	IL1RL1	interleukin 1 receptor like 1(IL1RL1)
NM_003126	SPTA1	spectrin alpha, erythrocytic 1(SPTA1)
NM_000627	LTBP1	latent transforming growth factor beta binding protein 1(LTBP1)
NR_034022	LOC100131257	zinc finger protein 655 pseudogene(LOC100131257)
NM_001195555	CLINT1	clathrin interactor 1(CLINT1)
NM_032336	GINS4	GINS complex subunit 4(GINS4)
NM_001190799	PLK4	polo like kinase 4(PLK4)
NM_003514	hist1h2am	histone cluster 1 H2A family member m(HIST1H2AM)
NM_003513	Hist1h2ab	histone cluster 1 H2A family member b(HIST1H2AB)
NM_003511	hist1h2al	histone cluster 1 H2A family member l(HIST1H2AL)
NM_003510	Hist1h2ak	histone cluster 1 H2A family member k(HIST1H2AK)
NM_018685	ANLN	anillin actin binding protein(ANLN)
NM_012412	H2AFV	H2A histone family member V(H2AFV)
NM_003519	Hist1h2bl	histone cluster 1 H2B family member l(HIST1H2BL)
NM_003518	Hist1h2bg	histone cluster 1 H2B family member g(HIST1H2BG)
NM_013296	GPSM2	G-protein signaling modulator 2(GPSM2)
NM_001017415	USP1	ubiquitin specific peptidase 1(USP1)

NM_006309	LRRFIP2	LRR binding FLII interacting protein 2(LRRFIP2)
NR_045217	GS1-24F4.2	uncharacterized LOC100652791(GS1-24F4.2)
NM_003530	Hist1h3d	histone cluster 1 H3 family member d(HIST1H3D)
NM_003525	HIST1H2BI	histone cluster 1 H2B family member i(HIST1H2BI)
NM_031271	TEX15	testis expressed 15(TEX15)
NM_003527	hist1h2bo	histone cluster 1 H2B family member o(HIST1H2BO)
NM_003520	Hist1h2bn	histone cluster 1 H2B family member n(HIST1H2BN)
NM_003523	Hist1h2be	histone cluster 1 H2B family member e(HIST1H2BE)
NM_001135822	FDPS	farnesyl diphosphate synthase(FDPS)
NM_001111101	CNRIP1	cannabinoid receptor interacting protein 1(CNRIP1)
NM_003318	TTK	TTK protein kinase(TTK)
NM_001042426	CENPA	centromere protein A(CENPA)
NM_003529	HIST1H3A	histone cluster 1 H3 family member a(HIST1H3A)
NM_001079809	TMEM183B	transmembrane protein 183B(TMEM183B)
NM_018098	ECT2	epithelial cell transforming 2(ECT2)
NM_021018	Hist1h3f	histone cluster 1 H3 family member f(HIST1H3F)
NM_001203247	EZH2	enhancer of zeste 2 polycomb repressive complex 2 subunit(EZH2)
NM_012089	abcb10	ATP binding cassette subfamily B member 10(ABCB10)
NM_000324	RHAG	Rh-associated glycoprotein(RHAG)
NM_001099286	MTFR2	mitochondrial fission regulator 2(MTFR2)
NM_024629	CENPU	centromere protein U(CENPU)
NM_018492	PBK	PDZ binding kinase(PBK)
NM_001251989	GMNN	geminin, DNA replication inhibitor(GMNN)
NM_000740	CHRM3	cholinergic receptor muscarinic 3(CHRM3)
NR_003291	ANKRD18DP	ankyrin repeat domain 18D, pseudogene(ANKRD18DP)
NM_001789	CDC25A	cell division cycle 25A(CDC25A)
NM_001080539	CCDC150	coiled-coil domain containing 150(CCDC150)
NM_002263	KIFC1	kinesin family member C1(KIFC1)
NM_003509	Hist1h2ai	histone cluster 1 H2A family member i(HIST1H2AI)
NM_000851	GSTM5	glutathione S-transferase mu 5(GSTM5)
NM_203315	BDH1	3-hydroxybutyrate dehydrogenase, type 1(BDH1)
NM_001128148	TFRC	transferrin receptor(TFRC)
NM_002358	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)(MAD2L1)
NM_175065	HIST2H2AB	histone cluster 2 H2A family member b(HIST2H2AB)
NM_003607	CDC42BPA	CDC42 binding protein kinase alpha(CDC42BPA)
NM_022809	CDC25C	cell division cycle 25C(CDC25C)
NM_001012507	CENPW	centromere protein W(CENPW)
NM_001008393	c4orf46	chromosome 4 open reading frame 46(C4orf46)
NM_198503	KCNT2	potassium sodium-activated channel subfamily T member 2(KCNT2)
NM_033211	c5orf30	chromosome 5 open reading frame 30(C5orf30)
NM_080743	SRSF12	serine and arginine rich splicing factor 12(SRSF12)
NM_001142522	FBXO5	F-box protein 5(FBXO5)

NM_001168388	CITED2	Cbp
NM_000720	CACNA1D	calcium voltage-gated channel subunit alpha1 D(CACNA1D)
NM_001201546	SLC16A4	solute carrier family 16 member 4(SLC16A4)
NM_001114120	DEPDC1	DEP domain containing 1(DEPDC1)
NM_005733	KIF20A	kinesin family member 20A(KIF20A)
NM_001237	CCNA2	cyclin A2(CCNA2)
NM_001143674	MPC2	mitochondrial pyruvate carrier 2(MPC2)
NM_002380	MATN2	matrilin 2(MATN2)
NM_198468	MMS22L	MMS22 like, DNA repair protein(MMS22L)
NM_007027	TOPBP1	topoisomerase (DNA) II binding protein 1(TOPBP1)
NM_004499	HNRNPAB	heterogeneous nuclear ribonucleoprotein A
NR_024279	FLJ37453	uncharacterized LOC729614(FLJ37453)
NM_021052	HIST1H2AE	histone cluster 1 H2A family member e(HIST1H2AE)
NM_012081	ELL2	elongation factor for RNA polymerase II 2(ELL2)
NM_000158	GBE1	1,4-alpha-glucan branching enzyme 1(GBE1)
NM_005742	PDIA6	protein disulfide isomerase family A member 6(PDIA6)
NM_001190481	CLSPN	claspin(CLSPN)
NM_020675	SPC25	SPC25, NDC80 kinetochore complex component(SPC25)
NM_001100910	FAM72B	family with sequence similarity 72 member B(FAM72B)
NM_012347	FBXO9	F-box protein 9(FBXO9)
NM_002207	ITGA9	integrin subunit alpha 9(ITGA9)
NM_005915	MCM6	minichromosome maintenance complex component 6(MCM6)
NM_005694	COX17	COX17, cytochrome c oxidase copper chaperone(COX17)
BC096118	Hist1h2bh	histone cluster 1 H2B family member h(HIST1H2BH)
NM_033125	SLC22A16	solute carrier family 22 member 16(SLC22A16)
NM_145269	FAM92A	family with sequence similarity 92 member A(FAM92A)
NM_020242	KIF15	kinesin family member 15(KIF15)
NM_001166260	TRIP13	thyroid hormone receptor interactor 13(TRIP13)
NM_018186	c1orf112	chromosome 1 open reading frame 112(C1orf112)
NM_133331	whsc1	Wolf-Hirschhorn syndrome candidate 1(WHSC1)
NM_199420	POLQ	DNA polymerase theta(POLQ)
NM_018189	DPPA4	developmental pluripotency associated 4(DPPA4)
NM_005914	MCM4	minichromosome maintenance complex component 4(MCM4)
NM_003035	STIL	SCL
NM_001006932	RPS6KA2	ribosomal protein S6 kinase A2(RPS6KA2)
NM_024686	TTLL7	tubulin tyrosine ligase like 7(TTLL7)
NM_178229	IQGAP3	IQ motif containing GTPase activating protein 3(IQGAP3)
NM_002214	ITGB8	integrin subunit beta 8(ITGB8)

NM_016343	CENPF	centromere protein F(CENPF)
NM_002916	RFC4	replication factor C subunit 4(RFC4)
NM_001077511	TCF19	transcription factor 19(TCF19)
NM_145278	GCSAML	germinal center associated signaling and motility like(GCSAML)
NM_000181	GUSB	glucuronidase beta(GUSB)
NM_001193493	SLC1A4	solute carrier family 1 member 4(SLC1A4)
NM_001012409	SGO1	shugoshin 1(SGO1)
NM_000465	BARD1	BRCA1 associated RING domain 1(BARD1)
NM_001127181	CENPL	centromere protein L(CENPL)
NM_006402	LAMTOR5	late endosomal
NM_001206846	ASPM	abnormal spindle microtubule assembly(ASPM)
NM_001130675	CLGN	calmegin(CLGN)
NM_001134420	CDC7	cell division cycle 7(CDC7)
NM_020120	UGGT1	UDP-glucose glycoprotein glucosyltransferase 1(UGGT1)
NM_004462	FDFT1	farnesyl-diphosphate farnesyltransferase 1(FDFT1)
NM_001564	ING2	inhibitor of growth family member 2(ING2)
NM_033050	SUCNR1	succinate receptor 1(SUCNR1)
NM_006816	LMAN2	lectin, mannose binding 2(LMAN2)
NM_006810	PDIA5	protein disulfide isomerase family A member 5(PDIA5)
NM_001048249	SMIM15	small integral membrane protein 15(SMIM15)
NM_024037	AUNIP	aurora kinase A and ninein interacting protein(AUNIP)
NR_033423	DHFRP3	dihydrofolate reductase pseudogene 3(DHFRP3)
NM_021908	ST7	suppression of tumorigenicity 7(ST7)
NM_182776	MCM7	minichromosome maintenance complex component 7(MCM7)
NM_017760	NCAPG2	non-SMC condensin II complex subunit G2(NCAPG2)
NM_022145	CENPK	centromere protein K(CENPK)
NM_000589	IL4	interleukin 4(IL4)
NM_001193557	ENY2	ENY2, transcription and export complex 2 subunit(ENY2)
NM_007270	FKBP9	FK506 binding protein 9(FKBP9)
NM_001870	CPA3	carboxypeptidase A3(CPA3)
BC096123	Hist1h2bf	histone cluster 1 H2B family member f(HIST1H2BF)
NM_017898	2-Mar	mitochondrial amidoxime reducing component 2(MARC2)
NM_152515	CKAP2L	cytoskeleton associated protein 2 like(CKAP2L)
NM_001145208	depdc1b	DEP domain containing 1B(DEPDC1B)
NM_003575	ZNF282	zinc finger protein 282(ZNF282)
NM_018410	HJURP	Holliday junction recognition protein(HJURP)
NM_001042762	FIGNL1	fidgetin like 1(FIGNL1)
NM_001130172	MYB	MYB proto-oncogene, transcription factor(MYB)
NM_022346	NCAPG	non-SMC condensin I complex subunit G(NCAPG)

NM_080596	hist1h2ah	histone cluster 1 H2A family member h(HIST1H2AH)
NM_198566	C5orf34	chromosome 5 open reading frame 34(C5orf34)
NM_080593	Hist1h2bk	histone cluster 1 H2B family member k(HIST1H2BK)
NM_001018115	FANCD2	Fanconi anemia complementation group D2(FANCD2)
NM_001005739	VPS54	VPS54, GARP complex subunit(VPS54)
NM_001432	EREG	epiregulin(EREG)
NM_022778	CEP85	centrosomal protein 85(CEP85)
NM_003686	EXO1	exonuclease 1(EXO1)
NM_004526	MCM2	minichromosome maintenance complex component 2(MCM2)
NM_004528	MGST3	microsomal glutathione S-transferase 3(MGST3)
NM_001130688	HMGB2	high mobility group box 2(HMGB2)
NM_001144999	ITGAV	integrin subunit alpha V(ITGAV)
NM_001123168	FAM72A	family with sequence similarity 72 member A(FAM72A)
NM_001813	CENPE	centromere protein E(CENPE)
NM_030920	ANP32E	acidic nuclear phosphoprotein 32 family member E(ANP32E)
NM_005048	PTH2R	parathyroid hormone 2 receptor(PTH2R)
NM_018132	CENPQ	centromere protein Q(CENPQ)
NM_001127383	CYBRD1	cytochrome b reductase 1(CYBRD1)
NM_031942	CDCA7	cell division cycle associated 7(CDCA7)
NM_014875	KIF14	kinesin family member 14(KIF14)
NM_014049	ACAD9	acyl-CoA dehydrogenase family member 9(ACAD9)
BC025376	CHAC2	ChaC cation transport regulator homolog 2(CHAC2)
NM_001134656	ZNF662	zinc finger protein 662(ZNF662)
BC012827	CDC20	cell division cycle 20(CDC20)
NM_005431	XRCC2	X-ray repair cross complementing 2(XRCC2)
NM_033296	MRFAP1	Morf4 family associated protein 1(MRFAP1)
NM_014485	HPGDS	hematopoietic prostaglandin D synthase(HPGDS)
NM_018725	IL17RB	interleukin 17 receptor B(IL17RB)
NM_020890	KIAA1524	KIAA1524(KIAA1524)
NM_001136570	fam47e	family with sequence similarity 47 member E(FAM47E)
NM_001123375	hist2h3d	histone cluster 2 H3 family member d(HIST2H3D)
NM_001199199	AK2	adenylate kinase 2(AK2)
NM_001162900	TMEM217	transmembrane protein 217(TMEM217)
NM_000097	CPOX	coproporphyrinogen oxidase(CPOX)
NM_152562	CDCA2	cell division cycle associated 2(CDCA2)
NM_022757	CCDC14	coiled-coil domain containing 14(CCDC14)
NM_022897	RANBP17	RAN binding protein 17(RANBP17)
NM_001160033	SGO2	shugoshin 2(SGO2)
NM_001204182	NEK2	NIMA related kinase 2(NEK2)
NM_005321	HIST1H1E	histone cluster 1 H1 family member e(HIST1H1E)
NM_031423	NUF2	NUF2, NDC80 kinetochore complex component(NUF2)
NM_005517	HMGN2	high mobility group nucleosomal binding domain

		2(HMGN2)
NM_014176	UBE2T	ubiquitin conjugating enzyme E2 T(UBE2T)
NM_015341	NCAPH	non-SMC condensin I complex subunit H(NCAPH)
NM_005322	HIST1H1B	histone cluster 1 H1 family member b(HIST1H1B)
NM_004172	SLC1A3	solute carrier family 1 member 3(SLC1A3)
NM_001145319	PLS1	plastin 1(PLS1)
NM_005218	DEFB1	defensin beta 1(DEFB1)
NR_036501	LINC00997	long intergenic non-protein coding RNA 997(LINC00997)
NM_005216	DDOST	dolichyl-diphosphooligosaccharide--protein glycosyltransferase non-catalytic subunit(DDOST)
NM_005021	ENPP3	ectonucleotide pyrophosphatase
NM_001005476	PKP4	plakophilin 4(PKP4)
NM_001184988	NDUFC1	NADH:ubiquinone oxidoreductase subunit C1(NDUFC1)
NM_031966	CCNB1	cyclin B1(CCNB1)
NR_034134	LINC01249	long intergenic non-protein coding RNA 1249(LINC01249)

Supplementary Table 2 Super-enhancer and super-enhancer-associated genes.

Number of peaks stitched

chromsome	start	end	#	size_of_SE	H3K27Ac signal	Closet Gene
chr18	3584895	3627819	9	27294	205348.416	FLJ35776
chr2	87752833	87845197	11	54043	193964.4	NCRNA00152
chr2	112162711	112254789	11	54069	193584.7872	LOC541471
chr20	45933086	46022732	18	38779	165755.454	ZMYND8
chr16	85556307	85655033	12	51384	166698.851	KIAA0182
chr17	40417284	40476119	12	43073	156765.8575	STAT5A
chr4	10166375	10206865	7	25589	140848.514	WDR1
chr11	65215458	65276607	15	36812	142000.2078	MALAT1
chr1	144982173	145043585	6	35426	163478.744	PDE4DIP
chr10	74003490	74088372	17	34358	131719.8876	DDIT4
chr6	147176267	147238222	8	39378	125613.7625	LOC729176
chr6	43592191	43608659	2	11142	106574.3088	MAD2L1BP
chrX	65205408	65251756	6	36395	108940.974	MIR223
chr6	31700911	31709354	1	8444	103121.9577	CLIC1
chr20	30249019	30312368	18	46752	106724.0603	BCL2L1
chr6	7105653	7181303	11	41531	108656.095	RREB1
chr1	36837033	36878274	6	16504	98446.3911	LSM10
chr18	9866678	9930980	12	36046	104728.6674	TXNDC2
chr6	68590803	68609434	3	15179	92337.0991	BAI3
chr6	26282603	26337859	14	32884	99118.2128	HIST1H4H
chr1	12488053	12572179	13	42107	105123.8496	SNORA59A
chr17	56405255	56418628	1	13374	88265.8119	MIR142
chr19	52044324	52077248	5	18970	90886.702	ZNF175

chrX	11358836	11456926	19	47960	95039.401	AMELX
chr6	28907272	28965455	10	26801	93540.8091	ZNF311
chr1	11845077	11868656	4	20774	87048.9522	MTHFR
chr2	158113089	158127195	2	11081	85294.7502	GALNT5
chr7	104649175	104657921	1	8747	84551.0804	LOC100216545
chr6	26020338	26035931	1	15594	84467.281	HIST1H4B
chr9	123627538	123641853	4	12953	84223.734	PHF19
chr7	12751801	12788319	4	26295	82483.2066	ARL4A
chr11	85844599	85914490	16	46192	88328.2458	EED
chr3	5017361	5066247	7	31070	86283.79	BHLHE40
chr3	45082598	45186417	20	39928	94641.4004	CDCP1
chr10	49663868	49715981	8	24591	85282.9245	MAPK8
chr9	132617654	132654924	7	25404	83555.613	USP20
chr7	106616676	106698255	16	34749	94786.6401	PRKAR2B
chr1	161498968	161565699	8	22026	95391.9645	FCGR3A
chr1	38462462	38482537	5	17013	78969.0275	FHL3
chr7	154996190	155000905	1	4716	75586.6365	INSIG1
chr1	45267402	45297550	4	8958	78110.4532	BTBD19
chr21	31006791	31032951	6	21779	79283.112	NCRNA00258
chr1	31228916	31256855	5	23060	78220.8183	LAPTM5
chr11	59303885	59334531	6	18980	76587.4186	OR4D9
chr8	130564240	130604476	9	28218	79550.5956	GSDMC
chr6	37137869	37178977	11	27632	78314.8508	PIM1
chr8	41644725	41687236	9	23518	78437.0461	ANK1
chr11	65170931	65198508	2	16150	75174.902	NEAT1
chr6	32934257	32942983	1	8727	73177.9812	BRD2
chr16	70437702	70473065	10	22556	74555.8129	ST3GAL2
chr22	19464660	19469047	1	4388	72135.8797	UFD1L
chr10	52070487	52096551	5	23687	77165.0784	ASAH2
chr20	326798	365790	12	26592	72599.2048	TRIB3
chr1	161580609	161618191	5	14994	80316.4922	FCGR3B
chr10	71068193	71095961	7	15515	73923.9696	HK1
chr8	37937339	37966322	4	17726	71330.0613	ASH2L
chr6	28676456	28785728	20	38070	84019.2408	LOC401242
chr7	150644932	150674880	6	18753	70210.0912	KCNH2
chr20	52194861	52241194	9	23041	70023.0629	ZNF217
chr18	3245029	3266545	4	12456	66972.8532	MYL12B
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chr6	16257721	16278547	4	8784	26213.6862	GMPR
chr14	91263707	91274101	4	8718	24160.853	TTC7B
chr19	788472	801637	3	10051	24697.54	PTBP1
chr4	40238973	40242212	1	3240	23680.9768	RHOH
chr19	15938540	15950458	5	10275	24164.9368	UCA1
chr3	193554268	193573127	4	9338	25838.7159	LOC100128023
chr12	108953184	108959072	1	5889	24075.4432	ISCU

chr1	108813220	108817898	1	4679	25193.8368	NBPF4
chr5	10351108	10358779	2	6678	24719.0304	43530
chr5	130969281	130973104	1	3824	23788.2352	RAPGEF6
chr9	113016833	113020972	1	4140	23689.5665	TXN
chr17	41320581	41324943	1	4363	24196.4502	NBR1
chr1	12661366	12680307	3	9481	26379.1307	DHRS3
chr6	28888066	28893641	1	5576	24318.15	TRIM27
chr1	212203857	212212019	2	6090	24660.6668	INTS7
chr6	109700805	109705303	1	4499	23920.8138	CD164
chr5	33439238	33443654	1	4417	24101.2032	TARS
chr10	30830941	30843788	2	4925	24337.3568	LYZL2
chr1	149830207	149834871	1	4665	24702.876	HIST2H2BC
chr1	149802074	149806539	1	4466	24628.4935	HIST2H4B
chr11	113533494	113562388	5	10156	26227.0838	TMPRSS5
chr17	44260582	44273113	2	8035	26285.0256	KIAA1267
chr1	150944108	150952685	1	8578	24048.1926	LASS2
chr1	36600318	36628755	4	12883	27569.6715	TRAPPC3
chr20	22382545	22395750	3	7678	24467.5445	LOC284788
chr19	52299063	52333444	6	11270	26679.656	FPR3
chr19	48746573	48763282	3	9037	25825.4304	CARD8
chr11	62309955	62342883	6	12738	26694.7296	AHNAK
chr10	17684838	17726558	5	9028	28498.932	STAM
chrX	41190190	41195597	1	5408	23257.1291	DDX3X
chr15	91191252	91210895	5	9030	25009.4676	BLM
chr14	81882416	81903806	5	14524	24782.454	STON2
chr14	23747210	23772797	5	12105	25760.9916	HOMEZ
chr2	178075377	178080548	1	5172	23768.5015	HNRNPA3
chr3	176911376	176917553	1	6178	23357.0901	TBL1XR1
chr1	235489466	235495680	1	6215	23852.439	GGPS1
chr3	101347922	101362766	3	13844	23558.9124	LOC100009676
chr8	144359527	144377323	4	11606	24958.89	ZNF696
chr3	44480493	44484772	2	4131	23555.0392	ZNF445
chr16	23831319	23852363	4	13199	25578.982	PRKCB
chr19	55714768	55729567	3	6583	24169.7268	PTPRH
chr10	93367072	93391040	4	6177	24416.2016	LOC100188947
chr1	193080510	193092671	3	9835	24697.7749	CDC73
chr6	20403921	20426309	6	14638	26599.1828	E2F3
chr1	117366705	117371118	1	4414	23414.9367	CD2
chr20	44598649	44612647	2	4652	24181.545	ZNF335
chr8	102137963	102172312	5	11038	26764.7408	ZNF706
chr6	27774034	27781531	1	7498	24147.837	HIST1H3H
chr15	64384233	64389440	1	5208	23224.7821	FAM96A
chr9	119224416	119234977	3	8679	24075.9117	LOC100128505
chr16	87885277	87905547	4	7734	23547.659	SLC7A5

chr11	65657251	65680013	8	11643	24803.7514	FOSL1
chr7	64457832	64467939	2	8542	23586.7059	ERV3
chr3	185528804	185544411	3	11172	24080.0403	IGF2BP2
chr8	101961079	101966971	1	5893	22922.826	YWHAZ
chr7	138775358	138809977	5	13791	28934.5602	ZC3HAV1
chr16	70321177	70325383	1	4207	22401.9972	AARS
chr6	27112356	27116527	1	4172	23082.314	HIST1H2BK
chr17	80817056	80846034	5	10080	25265.9182	ZNF750
chr7	12423615	12444898	2	10013	24907.4949	VWDE
chr3	196225688	196256418	6	10825	24842.132	C3orf43
chr2	55836218	55858001	4	5934	24335.9676	SMEK2
chr12	54691340	54696956	1	5617	22813.8768	NFE2
chr9	4848139	4866973	5	14524	24378.7296	MIR101-2
chr14	70151153	70170320	4	9570	23598.4104	SRSF5
chr6	41038316	41043411	1	5096	23082.8975	NFYA
chr1	228673777	228679095	1	5319	22731.2592	RNF187
chr7	106296190	106302423	1	6234	23772.662	FLJ36031
chr17	40667672	40707634	8	14163	26906.4146	NAGLU
chr3	45311067	45316497	2	4497	23073.699	TMEM158
chr1	243415619	243433588	2	8059	24764.8758	SDCCAG8
chr1	180572135	180582357	2	5058	24229.2066	XPR1
chr11	34065929	34075965	2	6725	23347.7504	CAPRIN1
chr1	202771890	202780903	2	8566	23658.2237	KDM5B
chr12	56545023	56554678	2	8736	22983.7275	MYL6
chr3	31563202	31575828	2	5328	23608.0948	STT3B
chr8	30600755	30603818	1	3064	22130.175	UBXN8
chr7	5588651	5615306	7	11809	24266.712	FSCN1
chr2	26980126	26995721	4	9772	23564.045	C2orf18
chr15	89611392	89636252	6	14238	25046.45	ABHD2
chr8	144988635	145031500	6	13694	24167.287	PLEC
chr1	116947556	116977247	5	12360	27562.1553	ATP1A1OS
chr16	28832962	28837858	1	4897	22282.1856	ATXN2L
chr12	57911766	57914528	1	2763	22129.4202	DDIT3
chr3	197679818	197689623	2	7302	22858.3965	IQCG
chr11	64035190	64041884	2	5965	22201.9898	GPR137
chr12	116989163	117000221	3	7114	22874.5788	MAP1LC3B2
chr17	61496971	61525725	5	9599	24659.4304	CYB561
chr7	128466496	128473938	2	7280	23106.6658	FLNC
chr2	85640609	85666386	5	11196	24343.7988	SH2D6
chr21	47739826	47746505	1	6680	22396.0228	C21orf58
chr2	198791105	198800197	1	9093	22635.4432	PLCL1
chr16	89552607	89575775	4	9984	23798.1696	ANKRD11
chr1	100811715	100831876	4	13204	24273.844	CDC14A
chr1	1675329	1679079	1	3751	22453.5	SLC35E2

chr5	179124074	179128676	1	4603	22056.9258	CANX
chr22	19708733	19713532	1	4800	22997.7678	GP1BB
chr12	56519719	56524932	1	5214	22287.1389	ESYT1
chr3	151984013	151991968	1	7956	22758.4595	LOC401093
chr1	1617573	1625443	2	4037	22911.931	SLC35E2B
chr1	245131864	245136008	1	4145	22137.6624	EFCAB2
chr2	70349785	70354071	1	4287	21946.8916	LOC100133985
chr2	25013009	25042080	5	9037	24454.5252	CENPO
chr9	224282	275398	7	14038	25271.7504	DOCK8
chr4	6731913	6736950	1	5038	22052.4897	CNO
chr17	57856148	57866044	2	6460	22706.372	MIR21
chrX	100638498	100648000	3	8310	21933.4666	BTK
chr12	48166379	48172121	1	5743	21948.2208	SLC48A1
chr1	21995334	22016562	5	10366	25061.7768	RAP1GAP
chr1	55644511	55683922	8	14210	26961.0651	USP24
chr2	55272728	55280464	2	7722	22702.8392	RTN4
chr2	55450381	55463703	4	7834	22813.925	RPS27A
chr11	36111674	36137434	6	12421	24090.752	LDLRAD3
chr5	139065657	139090723	4	12323	24166.1306	CXXC5
chr12	51410886	51427728	3	10479	23183.013	SLC11A2
chr7	5460610	5469989	3	9089	22069.7249	TNRC18
chr5	40831479	40836892	1	5414	22186.8044	RPL37
chr7	150752822	150760921	1	8100	22979.2927	SLC4A2
chr12	131704992	131727745	5	9334	24065.8481	LOC116437
chr10	25184737	25219550	6	11839	25016.6218	PRTFDC1
chr2	86215178	86230702	3	11255	23413.2968	LOC90784
chr5	163762933	163788438	4	9723	24229.75	MAT2B
chr16	30074640	30082329	2	7654	21922.8768	ALDOA
chrX	135960827	135993696	8	12630	22929.4144	RBMX
chr2	168795308	168820047	4	11464	24894.8557	B3GALT1
chr9	3526014	3529579	1	3566	21104.4435	RFX3
chr1	1582432	1594930	3	7414	24221.124	MMP23A
chr2	220365720	220392333	8	15800	22759.4376	ACCN4
chr19	50264374	50280199	5	9234	22686.72	AP2A1
chr15	55688425	55701291	2	10879	22611.995	CCPG1
chr19	13042300	13052209	2	7422	22243.7232	CALR
chr15	52297676	52315844	6	10871	22969.8024	MAPK6
chr6	135626980	135648948	3	10856	24579.9952	MYB
chr17	49198364	49211284	3	3860	22187.516	SPAG9
chr8	102204769	102220195	4	10811	22953.888	ZNF706
chr19	59064944	59072017	1	7074	21659.6479	UBE2M
chrX	151304762	151347300	7	11962	24068.0004	MAGEA10
chr10	70714601	70718078	1	3478	21260.4642	DDX21
chr4	127650795	127665230	5	13112	22466.634	INTU

chr1	249150061	249154682	1	4622	21493.1952	ZNF692
chr1	165796565	165812401	5	7509	23529.1288	UCK2
chr5	43037398	43043708	2	6176	21991.612	C5orf39
chr2	114643946	114653391	3	8116	22107.9115	ACTR3
chr11	122929447	122935348	2	5398	21454.8558	HSPA8
chrX	38660095	38677022	2	8152	22010.1781	MID1IP1
chr10	51561689	51578440	3	10243	23774.6943	NCOA4
chr6	27437440	27448040	2	7050	22805.9	ZNF184
chr10	43139618	43152681	3	8033	23309.6172	ZNF33B
chr1	152006119	152021615	2	6069	22610.2136	S100A11
chr14	100838444	100855228	2	5896	21609.4	WDR25
chr1	12585349	12613663	6	11584	25094.6982	SNORA59A
chr10	70090366	70093975	1	3610	21282.9948	HNRNPH3
chr6	31788435	31791423	1	2989	21498.0624	HSPA1B
chr6	170858700	170865071	2	5848	21930.8933	PSMB1
chr15	55527695	55543727	2	6673	22847.2032	RAB27A
chr1	15868325	15872314	1	3990	21445.2629	DNAJC16
chr19	38801968	38813155	4	8825	21586.4352	YIF1B
chr3	186647474	186674781	6	14293	23937.3162	ST6GAL1
chr1	29505177	29510205	1	5029	21346.8768	SRSF4
chr6	31792875	31800393	1	7519	22908.8496	HSPA1B
chr15	93420513	93428912	2	8369	21742.4913	LOC100507217
chr5	137672179	137675837	1	3659	20966.9244	FAM53C
chr1	26601913	26616267	2	13302	23237.6906	SH3BGRL3
chr3	171515536	171532508	3	10720	23025.9124	PLD1
chr10	21812283	21818628	1	6346	21382.65	C10orf140
chr3	39188064	39220241	5	12772	24361.2067	CSRNP1
chr2	26284086	26310003	6	11197	23641.4874	RAB10
chr12	28342266	28345527	1	3262	20857.6821	CCDC91
chr10	76967151	76972405	2	4741	21210.398	VDAC2
chr6	139763143	139771811	1	8669	22177.078	LOC645434
chr6	26214419	26219653	1	5235	21228.5806	HIST1H2AE
chr1	26395733	26406277	2	3766	21908.3232	TRIM63
chr6	13978179	13993747	4	9313	23113.8096	RNF182
chr4	174252927	174258067	1	5141	21003.068	HMGB2

Supplementary Table 3 Pathway enrichment analysis.

GO	Description	-LogP value	
		Super-enhancer	Yellow module
GO:0030219	Megakaryocyte differentiation	-9.333276497	-18.73113275
R-HSA-56898 80	Ub-specific processing proteases	-6.57488244	-19.40729718
R-HSA-10958	Hemostasis	-7.975552982	-6.257211463

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ID	Name		
R-HSA-1640170	Cell Cycle	-7.128956794	-72.69283418
GO:0033044	Regulation of chromosome organization	-5.742909567	-7.793615648
R-HSA-449147	Signaling by Interleukins	-5.692293323	-4.023213426
GO:0034508	Centromere complex assembly	-2.247093182	-20.5181339
hsa04110	Cell cycle	-3.99589127	-13.92977409
GO:0006281	DNA repair	0	-15.57087478
R-HSA-68877	Mitotic Prometaphase	0	-18.09648047
GO:0007051	Spindle organization	0	-10.03164282
GO:0007059	Chromosome segregation	0	-20.5366308
M14	PID AURORA B PATHWAY	0	-9.749985902
M46	PID ATR PATHWAY	0	-9.749985902
GO:0002227	Innate immune response in mucosa	0	-8.481736012
GO:0008608	Attachment of spindle microtubules to kinetochore	0	-7.524258171
GO:0035967	Cellular response to topologically incorrect protein	-7.197470088	0
R-HSA-170834	Signaling by TGF-beta Receptor Complex	-7.46973446	0
R-HSA-199991	Membrane Trafficking	-6.077936425	0
GO:1903827	Regulation of cellular protein localization	-7.278026488	0