Supplementary Materials

Figure S1: (A) Pathway analysis from the PRC1 gene target genes enriched within the CD RNA sequencing data set (Panther 2016, Enrichr, Ma'ayan Lab). **(B)** Immunoblot depicting BMI1 and EZH2 expression following transfection with BMI1 or EZH2 siRNA.

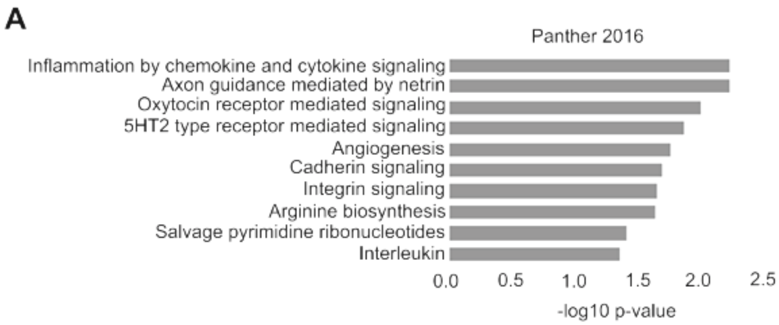

Figure S2: Heatmap depicting merged ATAC peaks in Tnaïve/Treg at day 7 (total 51,943 peaks, peak length mean = 695).

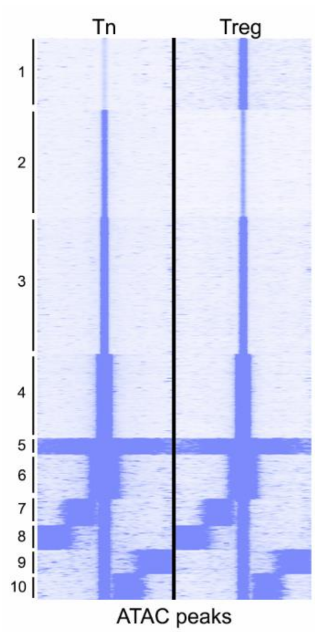

Figure S3: Increased RNA expression of CCL2 and ATP2B4 in the Jurkat T cell line upon pharmacologic inhibition of BMI1 via PTC209.

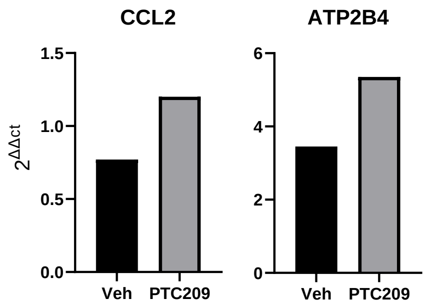

Figure S4: Box plot depicting significance of H3K27ac occupancy at TSS of Jurkat cells using genes upregulated in conditional BMI1KO mice. Enrichment was evaluated using computeMatrix function in DEEPTOOLS.

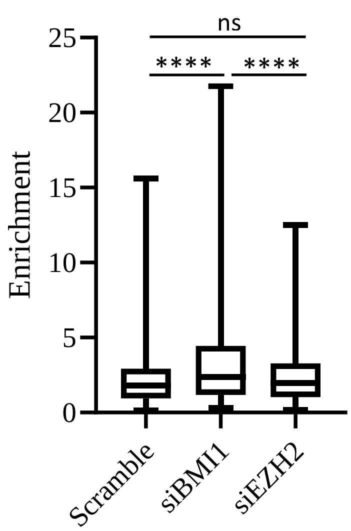

Figure S5:

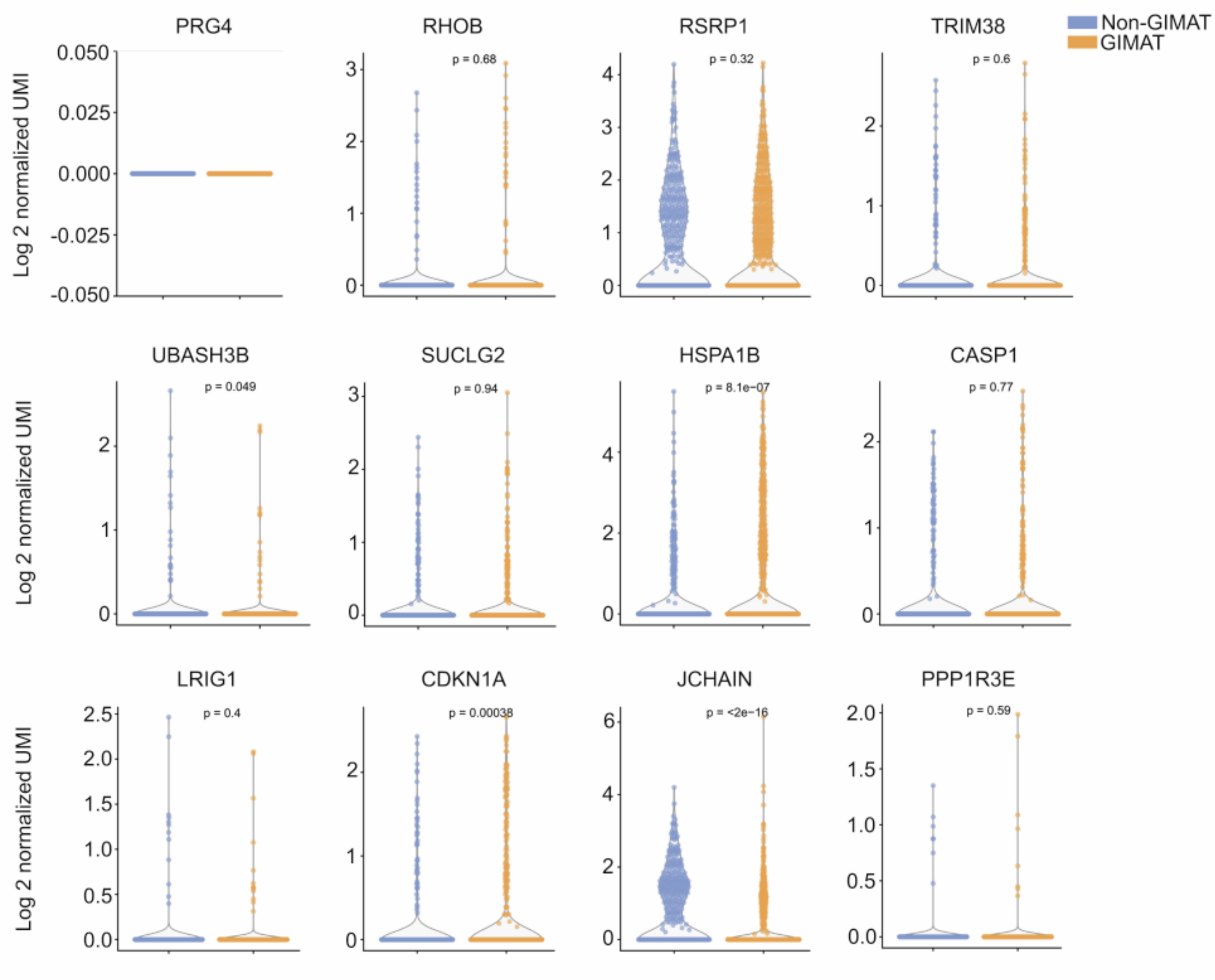

Figure S6: Top 4 DNA-binding transcription factors identified by HOMER de novo motif analysis on the open chromatin regions unique to EZH2$^{\Delta/\Delta}$ Tregs

Total target sequences = 399
Total background sequences = 48380
* - possible false positive

Rank	Motif	P-value	log P-pvalue	Best Match/Details
1	CACTAGATGGCG	1e-32	-7.371e+01	CTCF(Zf)/CD4+-CTCF-ChIP-Seq(Barski_et_al.)/Homer(0.845) More Information | Similar Motifs Found
2	AAGAGGAAGT	1e-15	-3.472e+01	ELF3(ETS)/PDAC-ELF3-ChIP-Seq(GSE64557)/Homer(0.918) More Information | Similar Motifs Found
3 *	CCGATAGA	1e-11	-2.568e+01	HOXB13/MA0901.1/Jaspar(0.642) More Information | Similar Motifs Found
4 *	TGTGGGTTAC	1e-10	-2.520e+01	RUNX1/MA0002.2/Jaspar(0.788) More Information | Similar Motifs Found

Table S1: List of upregulated CD-DEGs

chr.symbol	Symbol	logFC
chr11.MMP8	MMP8	12.34
chr17.GIP	GIP	12.28
chr10.LIPF	LIPF	12.20
chr20.BPIFB1	BPIFB1	11.95
chr6.PGC	PGC	11.15
chr1.S100A12	S100A12	10.85
chr15.AQP9	AQP9	9.41
chr2.GKN1	GKN1	9.27
chr1.S100A8	S100A8	8.58
chr6.C6orf58	C6orf58	8.56
chr6.DPCR1	DPCR1	8.43
chr17.CCL1	CCL1	7.99
chr19.CEACAM7	CEACAM7	7.84
chr4.ANXA10	ANXA10	7.45
chr19.FPR2	FPR2	7.06
chr14.GZMB	GZMB	6.94
chr1.S100A9	S100A9	6.51
chr15.DUOXA2	DUOXA2	6.45
chr17.CSF3	CSF3	6.42
chr2.MARCO	MARCO	6.30
chr9.FCN1	FCN1	6.14
chr11.TCN1	TCN1	5.93
chr17.CD300E	CD300E	5.71
chr7.INHBA	INHBA	5.68
chr11.SAA1	SAA1	5.65
chr12.AQP5	AQP5	5.63
chr19.C19orf59	C19orf59	5.63
chr16.AQP8	AQP8	5.54
chr12.KRT5	KRT5	5.51
chr11.MS4A12	MS4A12	5.50
chr21.TFF2	TFF2	5.43
chr2.GNLY	GNLY	5.32
chr7.IL6	IL6	5.27
chr8.PSCA	PSCA	5.22
chr11.MMP10	MMP10	5.20
chr19.CD177	CD177	5.13
chr11.MMP3	MMP3	5.06
chr12.IFNG	IFNG	5.04
chr3.CLDN18	CLDN18	4.98
chr12.C12orf36	C12orf36	4.96
chr19.RETN	RETN	4.96
chr10.CH25H	CH25H	4.95
chr2.TNFAIP6	TNFAIP6	4.94
chr19.FPR1	FPR1	4.84
chr17.KRT17	KRT17	4.78
chr6.TREM1	TREM1	4.67
chr19.LILRA3	LILRA3	4.60
chr15.DUOX2	DUOX2	4.56

chr4.CXCL5	CXCL5	4.55
chr7.TWIST1	TWIST1	4.55
chr6.MLN	MLN	4.52
chr16.CCL17	CCL17	4.50
chr2.SLC11A1	SLC11A1	4.49
chr11.MUC6	MUC6	4.38
chr4.CXCL11	CXCL11	4.38
chr1.IL12RB2	IL12RB2	4.37
chr4.CXCL13	CXCL13	4.36
chr12.KRT7	KRT7	4.34
chr15.GREM1	GREM1	4.31
chr12.CLEC4D	CLEC4D	4.29
chr1.MUC1	MUC1	4.24
chr8.CA2	CA2	4.22
chr5.VTRNA1-3	VTRNA1-3	4.21
chr14.RNASE2	RNASE2	4.19
chr2.IL1R2	IL1R2	4.16
chr5.CDO1	CDO1	4.14
chr11.MMP7	MMP7	4.12
chr6.FOXQ1	FOXQ1	4.10
chrX.SLC6A14	SLC6A14	4.08
chr2.IL1A	IL1A	4.05
chr12.CLEC4E	CLEC4E	4.01
chr4.CXCL10	CXCL10	4.01
chr11.MUC5B	MUC5B	3.95
chr19.AMH	AMH	3.91
chr7.SERPINE1	SERPINE1	3.91
chr4.JAKMIP1	JAKMIP1	3.89
chr10.ADAM12	ADAM12	3.88
chr16.HP	HP	3.86
chr4.S100P	S100P	3.86
chr4.IL8	IL8	3.82
chr1.FCGR3A	FCGR3A	3.82
chr11.MYEOV	MYEOV	3.81
chr14.SERPINA3	SERPINA3	3.81
chr1.TNFRSF18	TNFRSF18	3.80
chr4.SPP1	SPP1	3.80
chr2.IL1B	IL1B	3.79
chr5.CSF2	CSF2	3.77
chr19.CXCL17	CXCL17	3.77
chr19.KLK10	KLK10	3.71
chr3.CCR8	CCR8	3.69
chr16.SCNN1B	SCNN1B	3.68
chr19.C5AR1	C5AR1	3.67
chr2.GKN2	GKN2	3.66
chr1.TNFRSF8	TNFRSF8	3.59
chr11.FAM55D	FAM55D	3.56
chr7.TFPI2	TFPI2	3.54
chr22.IGLL5	IGLL5	3.50
chr9.LCN2	LCN2	3.46
chr10.IL2RA	IL2RA	3.45
chr12.IL26	IL26	3.43

chr3.PROK2	PROK2	3.41
chr11.ZBTB16	ZBTB16	3.40
chr14.GZMH	GZMH	3.38
chr9.FUT7	FUT7	3.38
chr11.FOLH1	FOLH1	3.38
chr21.ADAMTS1	ADAMTS1	3.35
chr22.MIR650	MIR650	3.35
chr19.GNG8	GNG8	3.33
chr1.CLCA4	CLCA4	3.33
chr11.MMP1	MMP1	3.32
chr8.DUSP4	DUSP4	3.31
chr3.GPR171	GPR171	3.27
chr12.SCARNA10	SCARNA10	3.25
chr2.IL1RN	IL1RN	3.25
chr22.OSM	OSM	3.24
chr1.TNFRSF4	TNFRSF4	3.22
chr11.ST3GAL4	ST3GAL4	3.21
chr6.PRDM1	PRDM1	3.20
chr12.MMP19	MMP19	3.19
chr19.CEACAM5	CEACAM5	3.17
chr4.CXCL9	CXCL9	3.16
chr14.BATF	BATF	3.14
chr19.LILRA2	LILRA2	3.13
chr8.MSC	MSC	3.12
chr9.UNQ6494	UNQ6494	3.10
chr6.PI16	PI16	3.10
chrX.ZCCHC12	ZCCHC12	3.08
chr19.CEACAM4	CEACAM4	3.07
chr11.VSIG2	VSIG2	3.06
chr4.CXCL2	CXCL2	3.04
chr16.SOCS1	SOCS1	3.04
chr1.S100A4	S100A4	3.02
chrX.FOXP3	FOXP3	3.02
chr12.OLR1	OLR1	3.02
chr11.TRIM29	TRIM29	3.01
chr6.IL17F	IL17F	3.01
chr19.LILRA4	LILRA4	3.01
chr3.CAMP	CAMP	3.01
chr3.CCK	CCK	2.97
chr4.NMU	NMU	2.96
chr12.CLEC4C	CLEC4C	2.94
chr1.FCGR2B	FCGR2B	2.93
chr16.SLC7A5	SLC7A5	2.93
chr2.LOC541471	LOC541471	2.93
chr19.GNA15	GNA15	2.91
chr19.ZBTB32	ZBTB32	2.90
chr3.LTF	LTF	2.86
chr1.CA6	CA6	2.86
chr11.NNMT	NNMT	2.85
chr10.DDIT4	DDIT4	2.83
chr2.CHN1	CHN1	2.83
chr1.RNU11	RNU11	2.83

chr4.SFRP2	SFRP2	2.83
chr13.POSTN	POSTN	2.82
chr9.CCL19	CCL19	2.80
chr19.LILRA5	LILRA5	2.79
chr5.MZB1	MZB1	2.79
chr4.AREG	AREG	2.79
chr1.LEFTY1	LEFTY1	2.79
chr3.EPHB1	EPHB1	2.78
chr5.SLC1A3	SLC1A3	2.78
chr3.CXCR6	CXCR6	2.77
chr15.HAPLN3	HAPLN3	2.75
chr9.NR4A3	NR4A3	2.75
chr8.CA1	CA1	2.75
chr2.DHRS9	DHRS9	2.75
chr19.JSRP1	JSRP1	2.75
chr1.CYR61	CYR61	2.74
chrX.TIMP1	TIMP1	2.74
chr1.SELE	SELE	2.73
chr22.APOBEC3H	APOBEC3H	2.73
chr11.LAYN	LAYN	2.72
chr3.CD80	CD80	2.71
chr19.PTGIR	PTGIR	2.70
chr2.CTLA4	CTLA4	2.70
chr1.FAM129A	FAM129A	2.68
chr22.APOBEC3A	APOBEC3A	2.68
chr3.PLA1A	PLA1A	2.68
chr3.P2RY14	P2RY14	2.67
chr8.CHRNA6	CHRNA6	2.64
chr8.CTHRC1	CTHRC1	2.64
chr6.RUNX2	RUNX2	2.63
chr1.PRG4	PRG4	2.63
chr1.GBP5	GBP5	2.62
chr12.GPR84	GPR84	2.62
chr9.CLIC3	CLIC3	2.62
chr9.TNFSF8	TNFSF8	2.62
chr7.MUC12	MUC12	2.61
chr12.BCAT1	BCAT1	2.61
chr19.CD70	CD70	2.61
chr11.MCAM	MCAM	2.60
chr5.VTRNA1-1	VTRNA1-1	2.59
chr17.CCL4	CCL4	2.59
chr5.VCAN	VCAN	2.58
chr14.ELK2AP	ELK2AP	2.57
chr6.NCR3	NCR3	2.57
chr19.COL5A3	COL5A3	2.57
chr15.C15orf53	C15orf53	2.57
chrY.CRLF2	CRLF2	2.56
chrX.CRLF2	CRLF2	2.56
chr1.FCGR2A	FCGR2A	2.56
chr20.SLPI	SLPI	2.56
chr21.TFF1	TFF1	2.56
chr1.FGR	FGR	2.56

chr19.OSCAR	OSCAR	2.56
chr4.CXCL3	CXCL3	2.55
chr12.TESC	TESC	2.54
chr4.IGJ	IGJ	2.54
chr3.CCDC80	CCDC80	2.53
chr3.ZBED2	ZBED2	2.52
chr11.LYVE1	LYVE1	2.52
chr12.HCAR3	HCAR3	2.52
chr2.LINC00152	LINC00152	2.51
chr2.IL18RAP	IL18RAP	2.48
chr2.IL1R1	IL1R1	2.48
chr4.TNIP3	TNIP3	2.47
chr19.PLAUR	PLAUR	2.47
chr8.FABP4	FABP4	2.47
chr16.CDH3	CDH3	2.46
chr8.SLA	SLA	2.45
chr4.PTPN13	PTPN13	2.45
chr12.CLEC12A	CLEC12A	2.45
chr20.SNORD17	SNORD17	2.44
chr22.RNU12	RNU12	2.43
chr6.RCAN2	RCAN2	2.42
chr3.LEPREL1	LEPREL1	2.42
chr1.RGS1	RGS1	2.42
chr19.PGLYRP1	PGLYRP1	2.39
chr10.SRGN	SRGN	2.38
chr19.LAIR2	LAIR2	2.38
chr12.OASL	OASL	2.37
chr17.ALOX15B	ALOX15B	2.36
chr2.SLC4A10	SLC4A10	2.35
chr6.FKBP5	FKBP5	2.35
chr1.PDPN	PDPN	2.35
chr19.LILRA6	LILRA6	2.34
chr2.IGFBP5	IGFBP5	2.34
chr9.GAS1	GAS1	2.33
chr1.BATF3	BATF3	2.32
chr16.SYNGR3	SYNGR3	2.32
chrX.TSC22D3	TSC22D3	2.31
chr16.MSLN	MSLN	2.31
chr3.LOC100507582	LOC100507582	2.31
chr2.ITPRIPL1	ITPRIPL1	2.31
chr5.HK3	HK3	2.30
chr11.PDE3B	PDE3B	2.29
chr12.PHLDA1	PHLDA1	2.29
chr1.F5	F5	2.28
chr5.GZMA	GZMA	2.28
chr2.IL18R1	IL18R1	2.28
chr5.IL7R	IL7R	2.27
chr11.SNORD15B	SNORD15B	2.27
chr1.IL10	IL10	2.26
chr10.ANKRD22	ANKRD22	2.26
chr17.RGS9	RGS9	2.26
chr18.PMAIP1	PMAIP1	2.25

chr6.MIR4645	MIR4645	2.25
chr19.MIA	MIA	2.25
chr4.CXCL1	CXCL1	2.24
chr1.SMAP2	SMAP2	2.23
chr1.L1TD1	L1TD1	2.22
chr4.SAP30	SAP30	2.22
chr10.CCDC3	CCDC3	2.22
chr20.THBD	THBD	2.22
chr17.P2RX5	P2RX5	2.22
chr14.GPR132	GPR132	2.21
chr1.TXNIP	TXNIP	2.21
chr3.MUC4	MUC4	2.20
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chr14.NFKBIA	NFKBIA	2.19
chr4.SOD3	SOD3	2.19
chr1.SYT11	SYT11	2.19
chr3.TM4SF1	TM4SF1	2.19
chr2.LINC00299	LINC00299	2.19
chr6.TREM2	TREM2	2.19
chr15.THBS1	THBS1	2.19
chr19.S1PR4	S1PR4	2.19
chr17.FAM20A	FAM20A	2.16
chr1.TNFRSF9	TNFRSF9	2.16
chr7.LOC100131176	LOC100131176	2.15
chr11.CEND1	CEND1	2.15
chr19.KLK7	KLK7	2.14
chr22.PIK3IP1	PIK3IP1	2.13
chr1.TRNP1	TRNP1	2.13
chr1.GPR25	GPR25	2.13
chr5.PITX1	PITX1	2.12
chr1.PDE4B	PDE4B	2.12
chr14.DACT1	DACT1	2.12
chr17.C17orf96	C17orf96	2.12
chr6.HIST1H1D	HIST1H1D	2.12
chr5.GFPT2	GFPT2	2.11
chr6.SYTL3	SYTL3	2.11
chr12.IL22	IL22	2.11
chr12.GRASP	GRASP	2.11
chr18.COLEC12	COLEC12	2.11
chr6.MGC39372	MGC39372	2.11
chr1.CSF3R	CSF3R	2.10
chr22.TYMP	TYMP	2.09
chr4.CXCL6	CXCL6	2.09
chr1.HSPA6	HSPA6	2.09
chr6.HIST1H3A	HIST1H3A	2.09
chr19.FSD1	FSD1	2.09
chr1.SH2D2A	SH2D2A	2.08
chr1.DPT	DPT	2.08
chr20.PI3	PI3	2.08
chr2.ACTG2	ACTG2	2.08

chr18.HMSD	HMSD	2.08
chr14.LINC00239	LINC00239	2.08
chr5.HAVCR2	HAVCR2	2.07
chr17.CCL3	CCL3	2.07
chr19.LILRB2	LILRB2	2.06
chr1.SLAMF6	SLAMF6	2.06
chr19.PBX4	PBX4	2.06
chr15.FURIN	FURIN	2.06
chr17.CD7	CD7	2.06
chr17.TBX21	TBX21	2.05
chr12.LAG3	LAG3	2.05
chr13.ALOX5AP	ALOX5AP	2.05
chr19.LILRB3	LILRB3	2.05
chr17.HLF	HLF	2.04
chr1.CD55	CD55	2.04
chr15.ISG20	ISG20	2.03
chr3.CCR4	CCR4	2.03
chr2.CXCR4	CXCR4	2.03
chr6.TNF	TNF	2.02
chrX.FLNA	FLNA	2.01
chr2.BCL2L11	BCL2L11	2.01
chr1.GBP1P1	GBP1P1	2.01
chr10.PFKFB3	PFKFB3	2.01
chr20.CASS4	CASS4	2.00
chr1.RGS16	RGS16	2.00
chr2.CYTIP	CYTIP	2.00
chr10.RTKN2	RTKN2	2.00
chr17.MGC12916	MGC12916	1.99
chr14.RPPH1	RPPH1	1.99
chr2.DUSP2	DUSP2	1.99
chr5.TMEM173	TMEM173	1.99
chr8.LY6E	LY6E	1.98
chr16.GPR97	GPR97	1.98
chr22.MAPK11	MAPK11	1.98
chr1.SELL	SELL	1.98
chr22.MEI1	MEI1	1.98
chr9.VLDLR	VLDLR	1.97
chr12.MGP	MGP	1.97
chr6.FAM26F	FAM26F	1.97
chr2.GPR55	GPR55	1.97
chr9.RMRP	RMRP	1.96
chr8.IDO1	IDO1	1.96
chr14.TMEM121	TMEM121	1.96
chr6.IER3	IER3	1.95
chr1.CHI3L1	CHI3L1	1.95
chr12.CD163	CD163	1.95
chr1.CD52	CD52	1.95
chrX.CXCR3	CXCR3	1.95
chr1.TNFSF4	TNFSF4	1.94
chr19.CEACAM6	CEACAM6	1.94
chr4.FGFBP1	FGFBP1	1.94
chr6.F13A1	F13A1	1.93

chr5.ITK	ITK	1.92
chr1.CITED4	CITED4	1.92
chr16.TNFRSF17	TNFRSF17	1.92
chr1.THEM5	THEM5	1.92
chr20.PLTP	PLTP	1.92
chr4.HOPX	HOPX	1.91
chr10.CREM	CREM	1.91
chr5.ADAM19	ADAM19	1.91
chr11.CARD17	CARD17	1.91
chr1.LOC100132111	LOC100132111	1.90
chr12.NINJ2	NINJ2	1.90
chr1.UTS2	UTS2	1.90
chr7.STEAP4	STEAP4	1.90
chr3.CLDN1	CLDN1	1.90
chr15.C2CD4A	C2CD4A	1.90
chr4.D4S234E	D4S234E	1.89
chr1.CTSE	CTSE	1.89
chr10.PRF1	PRF1	1.88
chr5.ANKRD55	ANKRD55	1.87
chr19.GPR77	GPR77	1.87
chr8.PTP4A3	PTP4A3	1.87
chr11.FOSL1	FOSL1	1.87
chr20.EBF4	EBF4	1.86
chr5.C5orf62	C5orf62	1.86
chr2.CCL20	CCL20	1.86
chr1.DUSP10	DUSP10	1.86
chr8.LY96	LY96	1.86
chr12.ELK3	ELK3	1.85
chr6.STX11	STX11	1.85
chr20.CST7	CST7	1.85
chr5.CD14	CD14	1.84
chr7.MYO1G	MYO1G	1.84
chr19.TMIGD2	TMIGD2	1.84
chr6.CCDC167	CCDC167	1.84
chr1.IL23R	IL23R	1.84
chr12.CHST11	CHST11	1.84
chr9.KLF9	KLF9	1.83
chr21.TMPRSS3	TMPRSS3	1.83
chr2.ICOS	ICOS	1.83
chr9.NTNG2	NTNG2	1.83
chr17.COL1A1	COL1A1	1.82
chr12.SELPLG	SELPLG	1.82
chr1.TNFRSF1B	TNFRSF1B	1.82
chr1.HIST2H2AC	HIST2H2AC	1.82
chr17.CCL2	CCL2	1.82
chr6.TREML2	TREML2	1.81
chrX.CHST7	CHST7	1.81
chr22.KLHDC7B	KLHDC7B	1.81
chr11.CD3D	CD3D	1.81
chr6.HIST1H4F	HIST1H4F	1.81
chr11.PRKCDBP	PRKCDBP	1.81
chr3.CMTM7	CMTM7	1.80

chr3.LAMP3	LAMP3	1.80
chr5.PDE4D	PDE4D	1.80
chr2.COL6A3	COL6A3	1.80
chr8.PKIA	PKIA	1.80
chr17.SOCS3	SOCS3	1.79
chr19.EMP3	EMP3	1.79
chr17.HS3ST3B1	HS3ST3B1	1.79
chr19.GMFG	GMFG	1.79
chr1.CD160	CD160	1.79
chrX.RAB39B	RAB39B	1.79
chr16.IL21R	IL21R	1.79
chr17.CDK5R1	CDK5R1	1.78
chr1.PALMD	PALMD	1.78
chr18.CBX3P2	CBX3P2	1.78
chr5.KCNMB1	KCNMB1	1.78
chr1.SELP	SELP	1.77
chr21.PCBP3	PCBP3	1.77
chr1.HIVEP3	HIVEP3	1.77
chr14.PYGL	PYGL	1.77
chr6.IL17A	IL17A	1.76
chr17.TNS4	TNS4	1.76
chr7.UPP1	UPP1	1.76
chr19.GZMM	GZMM	1.76
chr5.PPP2R2B	PPP2R2B	1.76
chr12.LOC100233209	LOC100233209	1.76
chrX.PIM2	PIM2	1.76
chr6.TREML1	TREML1	1.76
chr1.GBP1	GBP1	1.75
chr4.EVC2	EVC2	1.75
chr6.ARG1	ARG1	1.75
chr1.NLRP3	NLRP3	1.75
chr2.SCARNA5	SCARNA5	1.75
chr1.SLAMF1	SLAMF1	1.74
chr9.CD274	CD274	1.74
chr6.CTGF	CTGF	1.74
chr1.FLJ27354	FLJ27354	1.74
chr12.BTG1	BTG1	1.74
chr6.PIM1	PIM1	1.74
chr4.C4orf32	C4orf32	1.74
chr6.HIST1H2AB	HIST1H2AB	1.74
chr19.CNN1	CNN1	1.74
chr11.SNORA54	SNORA54	1.74
chr19.IL12RB1	IL12RB1	1.74
chr11.ETS1	ETS1	1.73
chr20.SNORA71D	SNORA71D	1.73
chr6.RNF144B	RNF144B	1.73
chr11.IFITM2	IFITM2	1.73
chrX.XKRX	XKRX	1.73
chr6.AGPAT4	AGPAT4	1.73
chr1.C1orf38	C1orf38	1.73
chr12.LOC100507250	LOC100507250	1.72
chr14.PTGER2	PTGER2	1.72

chr1.DARC	DARC	1.72
chr10.ENTPD1	ENTPD1	1.72
chr1.IFI44	IFI44	1.72
chr13.KATNAL1	KATNAL1	1.71
chr7.LOC154761	LOC154761	1.71
chr22.APOBEC3G	APOBEC3G	1.70
chr8.LOC100130298	LOC100130298	1.70
chr1.LRRC8C	LRRC8C	1.70
chr2.VAMP5	VAMP5	1.70
chr2.FAM124B	FAM124B	1.70
chr16.ZNRF1	ZNRF1	1.70
chr1.GPX7	GPX7	1.69
chr2.MAL	MAL	1.69
chr3.CCR5	CCR5	1.69
chr1.ANKRD35	ANKRD35	1.69
chr10.ADAM8	ADAM8	1.69
chr1.IFI6	IFI6	1.69
chr4.EVC	EVC	1.69
chr6.IRF4	IRF4	1.68
chr20.SNAI1	SNAI1	1.68
chr7.PILRA	PILRA	1.68
chr17.CCL18	CCL18	1.68
chr12.LOC100506844	LOC100506844	1.68
chr20.CEBPB	CEBPB	1.68
chr12.CD69	CD69	1.68
chr20.ADA	ADA	1.68
chr4.TXK	TXK	1.68
chr11.ADM	ADM	1.67
chr17.MEOX1	MEOX1	1.67
chr2.RAB11FIP5	RAB11FIP5	1.67
chr2.IKZF2	IKZF2	1.67
chr1.AIM2	AIM2	1.67
chr2.MTHFD2	MTHFD2	1.67
chr19.FXYD7	FXYD7	1.67
chr1.S1PR1	S1PR1	1.67
chr14.LINC00341	LINC00341	1.67
chr9.CD72	CD72	1.66
chrX.RAB33A	RAB33A	1.66
chr2.KYNU	KYNU	1.66
chr2.DES	DES	1.65
chr12.MORN3	MORN3	1.65
chr1.CD53	CD53	1.65
chr13.LINC00426	LINC00426	1.65
chr3.HYAL1	HYAL1	1.65
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chr1.NCDN	NCDN	1.64
chrX.MAGEH1	MAGEH1	1.64
chr12.FAM113B	FAM113B	1.64
chr2.ASTL	ASTL	1.64
chr14.C14orf49	C14orf49	1.63
chr19.HCST	HCST	1.63
chr19.SCN1B	SCN1B	1.63

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chr3.H1FX	H1FX	1.63
chr18.ALPK2	ALPK2	1.63
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chr19.ICAM1	ICAM1	1.62
chr22.DERL3	DERL3	1.62
chr17.PIK3R5	PIK3R5	1.62
chr15.HDGFRP3	HDGFRP3	1.62
chr8.ANK1	ANK1	1.62
chr17.SPHK1	SPHK1	1.62
chr19.C19orf38	C19orf38	1.62
chr17.ASGR2	ASGR2	1.62
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chr12.IRAK3	IRAK3	1.61
chr2.GYPC	GYPC	1.61
chr10.SPOCK2	SPOCK2	1.61
chr7.ATP6V0E2	ATP6V0E2	1.61
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chr5.ANKRD33B	ANKRD33B	1.60
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chr9.SIT1	SIT1	1.60
chr19.FXYD5	FXYD5	1.59
chr11.MYO7A	MYO7A	1.59
chr6.HLA-G	HLA-G	1.58
chr10.FANK1	FANK1	1.58
chr18.EMILIN2	EMILIN2	1.58
chr4.SH3TC1	SH3TC1	1.58
chr11.FOLR2	FOLR2	1.58
chr3.BFSP2	BFSP2	1.58
chr6.LTA	LTA	1.58
chr19.LOC100287177	LOC100287177	1.58
chr9.PDCD1LG2	PDCD1LG2	1.58
chr11.B3GAT1	B3GAT1	1.58
chr8.RIPK2	RIPK2	1.58
chr4.MMRN1	MMRN1	1.58
chr6.IPCEF1	IPCEF1	1.58
chr6.TNFAIP3	TNFAIP3	1.58
chr3.SNORA63	SNORA63	1.56
chr2.ARHGAP15	ARHGAP15	1.56
chr2.STAT1	STAT1	1.56
chr1.MAD2L2	MAD2L2	1.56
chr10.O3FAR1	O3FAR1	1.56
chr1.LRP8	LRP8	1.56
chr4.ACSL1	ACSL1	1.56
chr11.CTSW	CTSW	1.55
chr18.FLJ35776	FLJ35776	1.55

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chr22.TMPRSS6	TMPRSS6	1.54
chr19.ICAM3	ICAM3	1.54
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chr4.EREG	EREG	1.54
chr4.IL2	IL2	1.54
chr22.IL2RB	IL2RB	1.54
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chr16.CCL22	CCL22	1.53
chr19.C3	C3	1.53
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chr1.CD2	CD2	1.53
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chr1.OLFML2B	OLFML2B	1.53
chr17.CCL13	CCL13	1.52
chr3.TRAT1	TRAT1	1.52
chr8.MYBL1	MYBL1	1.52
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chr22.KCTD17	KCTD17	1.52
chr6.FAM184A	FAM184A	1.51
chr2.FAM179A	FAM179A	1.51
chr10.HTRA1	HTRA1	1.51
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chrX.STARD8	STARD8	1.51
chr11.CADM1	CADM1	1.51
chr1.CD48	CD48	1.51
chr16.CORO1A	CORO1A	1.51
chr12.CLEC2B	CLEC2B	1.51
chr10.C10orf10	C10orf10	1.51
chr17.PLSCR3	PLSCR3	1.51
chr17.ERN1	ERN1	1.50
chrX.PRAF2	PRAF2	1.50
chr22.SEC14L6	SEC14L6	1.50
chr2.LOC100302650	LOC100302650	1.50
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chr12.GPR19	GPR19	1.50
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chr11.THY1	THY1	1.49
chr15.BCL2A1	BCL2A1	1.49
chr1.TRIM46	TRIM46	1.49

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chr20.LIME1	LIME1	1.49
chr17.TNFSF12	TNFSF12	1.49
chr20.HAR1A	HAR1A	1.49
chr3.BHLHE40	BHLHE40	1.49
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chr10.PSD	PSD	1.48
chr15.RORA	RORA	1.48
chr19.RINL	RINL	1.48
chr10.VIM	VIM	1.48
chr20.TNFRSF6B	TNFRSF6B	1.48
chr7.JAZF1	JAZF1	1.48
chr19.A1BG	A1BG	1.47
chr20.PTPN1	PTPN1	1.47
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chr13.TNFSF13B	TNFSF13B	1.47
chr22.CSF2RB	CSF2RB	1.47
chr6.TAGAP	TAGAP	1.47
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chr17.C17orf48	C17orf48	1.47
chr19.CDKN2D	CDKN2D	1.47
chr22.PARVB	PARVB	1.47
chrX.VSIG1	VSIG1	1.47
chr4.TSPAN5	TSPAN5	1.46
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chr6.CCR6	CCR6	1.46
chr1.GLUL	GLUL	1.46
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chr19.LILRB4	LILRB4	1.46
chr8.CYP7B1	CYP7B1	1.45
chr11.CD3E	CD3E	1.45
chr14.GPR65	GPR65	1.45
chr6.HIST1H1B	HIST1H1B	1.45
chr17.EVI2A	EVI2A	1.45
chr17.CCL8	CCL8	1.45
chr10.MRC1	MRC1	1.45
chr5.ERAP2	ERAP2	1.45
chr7.FAM115C	FAM115C	1.44
chr7.MDFIC	MDFIC	1.44
chr6.OGFRL1	OGFRL1	1.44
chr8.MYC	MYC	1.44
chr9.COL5A1	COL5A1	1.44
chrX.PPP1R3F	PPP1R3F	1.44
chr16.LDHD	LDHD	1.43
chr7.IKZF1	IKZF1	1.43
chr19.LILRA1	LILRA1	1.43
chr3.CD96	CD96	1.43
chr19.TGFB1	TGFB1	1.43
chr14.GNG2	GNG2	1.43

chr3.FAM172BP	FAM172BP	1.43
chr1.HIST3H2A	HIST3H2A	1.42
chr12.DRAM1	DRAM1	1.42
chr4.DAPP1	DAPP1	1.42
chr19.NKG7	NKG7	1.42
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chr20.PREX1	PREX1	1.42
chr22.PVALB	PVALB	1.42
chr20.TSHZ2	TSHZ2	1.42
chr20.SNTA1	SNTA1	1.41
chr3.HCLS1	HCLS1	1.41
chr22.LGALS1	LGALS1	1.41
chr17.CCR7	CCR7	1.41
chr5.ECSCR	ECSCR	1.41
chr11.CCDC85B	CCDC85B	1.41
chr4.TIFA	TIFA	1.41
chr1.FCER1G	FCER1G	1.41
chr8.PVT1	PVT1	1.41
chr12.GLIPR1	GLIPR1	1.40
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chrX.GAB3	GAB3	1.40
chr6.CCND3	CCND3	1.40
chr6.SNORA20	SNORA20	1.40
chr11.SNORA57	SNORA57	1.40
chr7.WDR86	WDR86	1.40
chr20.LAMP5	LAMP5	1.40
chr13.GPR183	GPR183	1.39
chr16.TRADD	TRADD	1.39
chr22.RAC2	RAC2	1.39
chr20.LOC79015	LOC79015	1.39
chr2.CXCR2P1	CXCR2P1	1.39
chr13.FLT3	FLT3	1.39
chr19.ZNF101	ZNF101	1.39
chr12.ARHGDIB	ARHGDIB	1.39
chrX.SH2D1A	SH2D1A	1.39
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chr9.SUSD3	SUSD3	1.39
chr1.LAPTM5	LAPTM5	1.39
chr19.GAMT	GAMT	1.39
chr14.PRKCH	PRKCH	1.38
chr4.C4orf42	C4orf42	1.38
chr1.RUNX3	RUNX3	1.38
chr11.IL10RA	IL10RA	1.38
chr3.BTLA	BTLA	1.38
chr16.SNHG9	SNHG9	1.38
chr4.HTRA3	HTRA3	1.38
chr6.C6orf226	C6orf226	1.38
chr16.C16orf74	C16orf74	1.38

chr8.CSGALNACT1	CSGALNACT1	1.38
chr20.SIRPG	SIRPG	1.38
chr5.IRGM	IRGM	1.37
chr19.BST2	BST2	1.37
chr21.MIR155HG	MIR155HG	1.37
chr14.IFI27L2	IFI27L2	1.37
chr9.CTSL1	CTSL1	1.37
chr1.MNDA	MNDA	1.37
chr2.MIR4772	MIR4772	1.37
chr19.PDE4A	PDE4A	1.37
chr1.TNFRSF25	TNFRSF25	1.37
chr6.SAMD3	SAMD3	1.37
chr19.LINGO3	LINGO3	1.37
chr15.SLCO3A1	SLCO3A1	1.37
chr10.FGFBP3	FGFBP3	1.37
chr16.C16orf86	C16orf86	1.37
chr1.GJA4	GJA4	1.36
chrX.CFP	CFP	1.36
chr10.PRKCQ	PRKCQ	1.36
chr1.SH3BGRL3	SH3BGRL3	1.36
chr1.KCNAB2	KCNAB2	1.36
chr15.FLJ10038	FLJ10038	1.36
chr17.PLD6	PLD6	1.36
chr3.LOC339894	LOC339894	1.36
chr16.SNORD68	SNORD68	1.36
chr6.HIST1H3J	HIST1H3J	1.35
chr4.CPLX1	CPLX1	1.35
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chr1.ADAMTS4	ADAMTS4	1.35
chr3.LMCD1	LMCD1	1.35
chr11.GDPD5	GDPD5	1.35
chrX.TSPYL2	TSPYL2	1.35
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chr17.FAM195B	FAM195B	1.35
chr14.TNFAIP2	TNFAIP2	1.35
chr6.TRERF1	TRERF1	1.35
chr19.SNORA68	SNORA68	1.35
chr6.PDE7B	PDE7B	1.35
chr1.PTGS2	PTGS2	1.35
chr2.TUBA4A	TUBA4A	1.35
chr16.CPNE7	CPNE7	1.35
chr18.CD226	CD226	1.35
chr16.CMTM3	CMTM3	1.34
chr20.SPAG4	SPAG4	1.34
chr1.C1orf162	C1orf162	1.34
chr6.FYN	FYN	1.34
chr3.SH3BP5	SH3BP5	1.34
chr6.CD83	CD83	1.34
chr1.GBP2	GBP2	1.34
chr22.LOC100144603	LOC100144603	1.34
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chr5.C5orf39	C5orf39	1.34

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chr1.ALPL	ALPL	1.34
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chr10.CALHM2	CALHM2	1.33
chr13.GTF3A	GTF3A	1.33
chr7.GIMAP5	GIMAP5	1.33
chr1.LAX1	LAX1	1.33
chr21.ITGB2	ITGB2	1.33
chr16.SNORA78	SNORA78	1.33
chr12.EID3	EID3	1.33
chr19.FLT3LG	FLT3LG	1.32
chr10.PLAU	PLAU	1.32
chr10.FAS-AS1	FAS-AS1	1.32
chr2.ATP6V1E2	ATP6V1E2	1.32
chr3.PPM1M	PPM1M	1.32
chr1.C1QB	C1QB	1.32
chr4.PDE6B	PDE6B	1.32
chr7.C7orf50	C7orf50	1.31
chr16.B3GNT9	B3GNT9	1.31
chr17.HOXB2	HOXB2	1.31
chr8.LZTS1	LZTS1	1.31
chr12.IKZF4	IKZF4	1.31
chr13.SLAIN1	SLAIN1	1.31
chr3.TIGIT	TIGIT	1.31
chrX.MSN	MSN	1.31
chr15.BLM	BLM	1.30
chr1.THEM4	THEM4	1.30
chr11.CD6	CD6	1.30
chrX.TLR8	TLR8	1.30
chr14.WARS	WARS	1.30
chr22.ODF3B	ODF3B	1.30
chrX.IL2RG	IL2RG	1.30
chr6.HIST1H2AH	HIST1H2AH	1.30
chr11.FLI1	FLI1	1.30
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chr5.ANXA6	ANXA6	1.30
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chr18.TTC39C	TTC39C	1.29
chr6.PLA2G7	PLA2G7	1.29
chr12.CD4	CD4	1.29
chr6.SERPINB9	SERPINB9	1.29
chr1.IFI44L	IFI44L	1.29
chr3.CD86	CD86	1.29
chr1.HIST2H3D	HIST2H3D	1.29
chr6.GPSM3	GPSM3	1.29
chr22.LOC100506714	LOC100506714	1.29
chr19.ARRDC2	ARRDC2	1.29
chr4.LOC100130872	LOC100130872	1.29

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chr22.ADORA2A	ADORA2A	1.29
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chr1.SV2A	SV2A	1.28
chr19.MAP4K1	MAP4K1	1.28
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chr6.THEMIS	THEMIS	1.28
chrX.WAS	WAS	1.28
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chr10.ITPRIP	ITPRIP	1.28
chr9.ST6GALNAC6	ST6GALNAC6	1.28
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chr17.CEP112	CEP112	1.28
chr11.CD3G	CD3G	1.28
chr2.RNU4ATAC	RNU4ATAC	1.27
chr2.SP140	SP140	1.27
chr7.SNHG15	SNHG15	1.27
chr15.ANKDD1A	ANKDD1A	1.27
chr9.CDKN2A	CDKN2A	1.27
chrX.BEX5	BEX5	1.27
chr4.CCDC109B	CCDC109B	1.27
chrX.BGN	BGN	1.26
chr8.DOK2	DOK2	1.26
chr2.RBMS1	RBMS1	1.26
chr12.RHEBL1	RHEBL1	1.26
chr12.SLC2A3	SLC2A3	1.26
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chr15.AEN	AEN	1.26
chr12.BIN2	BIN2	1.26
chr16.C16orf45	C16orf45	1.26
chr19.CEACAM21	CEACAM21	1.26
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chr4.TMEM156	TMEM156	1.26
chr11.MMP12	MMP12	1.25
chrX.PRPS1	PRPS1	1.25
chr16.ZG16B	ZG16B	1.25
chr19.MYO1F	MYO1F	1.25
chr9.LOC100129250	LOC100129250	1.25
chr12.LOC256021	LOC256021	1.25
chr1.FBXO2	FBXO2	1.25
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chr3.C3orf18	C3orf18	1.25
chr17.ITGAE	ITGAE	1.25
chr22.MFNG	MFNG	1.25
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chr8.DENND3	DENND3	1.24

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chr15.NMB	NMB	1.24
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chr9.GLIPR2	GLIPR2	1.24
chr2.CD8A	CD8A	1.24
chr7.CARD11	CARD11	1.24
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chr4.CDKL2	CDKL2	1.23
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chr14.GPR68	GPR68	1.23
chr3.SATB1	SATB1	1.23
chr2.CD28	CD28	1.23
chr16.NETO2	NETO2	1.23
chr3.LRRC33	LRRC33	1.23
chr17.RHBDF2	RHBDF2	1.23
chr1.RCAN3AS	RCAN3AS	1.23
chr16.NHLRC4	NHLRC4	1.23
chr16.CKLF	CKLF	1.23
chr3.RFTN1	RFTN1	1.23
chr8.TRPS1	TRPS1	1.23
chr11.CCDC88B	CCDC88B	1.23
chr5.SGTB	SGTB	1.23
chr20.LOC100270804	LOC100270804	1.23
chr12.ABCD2	ABCD2	1.22
chr20.SLC17A9	SLC17A9	1.22
chr7.SNX10	SNX10	1.22
chr11.IFITM1	IFITM1	1.22
chr1.PTPN7	PTPN7	1.22
chr1.POLR3GL	POLR3GL	1.22
chr1.C2CD4D	C2CD4D	1.22
chr13.LPAR6	LPAR6	1.22
chr6.HIST1H2AL	HIST1H2AL	1.22
chr22.SSTR3	SSTR3	1.22
chr6.TAP1	TAP1	1.22
chr11.UCP2	UCP2	1.22
chr15.RASGRP1	RASGRP1	1.22
chr3.GYG1	GYG1	1.22
chr11.UBASH3B	UBASH3B	1.22
chr13.RASA3	RASA3	1.21
chr11.TRIM22	TRIM22	1.21
chr19.EBI3	EBI3	1.21
chr11.UBE2L6	UBE2L6	1.21
chr2.RSAD2	RSAD2	1.21
chr2.THADA	THADA	1.21
chr6.ZC3H12D	ZC3H12D	1.21
chr19.SIGLEC14	SIGLEC14	1.21
chrX.F8	F8	1.21

chr2.COL3A1	COL3A1	1.21
chr12.CD27	CD27	1.21
chr1.SLC2A1	SLC2A1	1.21
chr12.DTX3	DTX3	1.21
chr4.HMGB2	HMGB2	1.21
chr11.RDX	RDX	1.21
chr21.RUNX1	RUNX1	1.21
chr15.FBN1	FBN1	1.21
chr7.IMPDH1	IMPDH1	1.21
chr4.TLR2	TLR2	1.21
chr10.CELF2	CELF2	1.20
chr17.DHX58	DHX58	1.20
chr7.COL1A2	COL1A2	1.20
chr16.CBFB	CBFB	1.20
chr1.CTSK	CTSK	1.20
chr1.ATP2B4	ATP2B4	1.20
chr1.PHTF1	PHTF1	1.20
chr16.SNX29	SNX29	1.20
chr22.PIM3	PIM3	1.20
chr7.GIMAP7	GIMAP7	1.20
chr11.SLC36A4	SLC36A4	1.20
chr3.SUCNR1	SUCNR1	1.20
chr6.SYNGAP1	SYNGAP1	1.19
chr6.ETV7	ETV7	1.19
chr11.SNORD22	SNORD22	1.19
chr19.KCNN4	KCNN4	1.19
chr10.TET1	TET1	1.19
chr16.COTL1	COTL1	1.19
chr19.NAT14	NAT14	1.19
chr12.C3AR1	C3AR1	1.19
chr3.COLQ	COLQ	1.19
chr19.ATP1A3	ATP1A3	1.19
chr19.PLEKHF1	PLEKHF1	1.19
chr6.HLA-E	HLA-E	1.19
chr1.PYHIN1	PYHIN1	1.19
chr5.CAMK4	CAMK4	1.19
chr7.GIMAP2	GIMAP2	1.19
chr8.LOC100130231	LOC100130231	1.18
chr2.QPCT	QPCT	1.18
chr19.APOE	APOE	1.18
chr17.GNGT2	GNGT2	1.18
chr11.TBC1D10C	TBC1D10C	1.18
chr2.STAT4	STAT4	1.18
chr21.C21orf63	C21orf63	1.18
chr7.PHTF2	PHTF2	1.18
chr14.OTUB2	OTUB2	1.18
chr17.SLFN13	SLFN13	1.18
chr1.LOC100129196	LOC100129196	1.18
chr7.ZYX	ZYX	1.17
chr3.ITPR1	ITPR1	1.17
chr1.SRM	SRM	1.17
chr3.IQCG	IQCG	1.17

chrX.ITM2A	ITM2A	1.17
chr16.PRSS21	PRSS21	1.17
chr7.FLJ43663	FLJ43663	1.17
chr8.ST3GAL1	ST3GAL1	1.17
chr11.IFITM3	IFITM3	1.17
chr1.PTPN22	PTPN22	1.17
chr19.CFD	CFD	1.17
chr19.IFI30	IFI30	1.17
chr1.GBP4	GBP4	1.17
chr22.SLC35E4	SLC35E4	1.17
chr3.NFKBIZ	NFKBIZ	1.17
chr1.NCF2	NCF2	1.17
chr15.CRTC3	CRTC3	1.17
chr1.FAM91A2	FAM91A2	1.17
chr19.EID2B	EID2B	1.16
chr21.CBR3	CBR3	1.16
chr1.CD84	CD84	1.16
chr2.STK17B	STK17B	1.16
chrX.LOC100128420	LOC100128420	1.16
chr19.CD37	CD37	1.16
chr11.SLC43A3	SLC43A3	1.16
chr11.SLC37A2	SLC37A2	1.16
chr3.TCTEX1D2	TCTEX1D2	1.16
chr19.R3HDM4	R3HDM4	1.16
chr11.TSPAN18	TSPAN18	1.15
chr10.CSGALNACT2	CSGALNACT2	1.15
chr18.MALT1	MALT1	1.15
chr16.PARD6A	PARD6A	1.15
chr2.FN1	FN1	1.15
chr10.BAG3	BAG3	1.15
chr22.ASPHD2	ASPHD2	1.15
chr6.DEF6	DEF6	1.15
chr22.CACNA1I	CACNA1I	1.15
chr9.MED27	MED27	1.15
chr8.NCALD	NCALD	1.15
chr4.NAP1L5	NAP1L5	1.15
chr22.APOL3	APOL3	1.15
chr19.IL4I1	IL4I1	1.15
chr12.LOC100131733	LOC100131733	1.15
chr1.PTAFR	PTAFR	1.15
chr1.RPS27	RPS27	1.14
chr12.CPM	CPM	1.14
chr10.OBFC1	OBFC1	1.14
chr2.GTDC1	GTDC1	1.14
chr5.CCDC69	CCDC69	1.14
chr15.CHST14	CHST14	1.14
chr1.RIMS3	RIMS3	1.14
chr6.HLA-F	HLA-F	1.14
chr20.SMOX	SMOX	1.14
chr7.LOC401431	LOC401431	1.14
chr6.ELOVL5	ELOVL5	1.14
chr10.ZEB1	ZEB1	1.14

chr17.RPL27	RPL27	1.14
chr3.SLC9A9	SLC9A9	1.13
chr11.FAM89B	FAM89B	1.13
chr3.CMTM6	CMTM6	1.13
chr16.LOC554206	LOC554206	1.13
chr4.CNOT6L	CNOT6L	1.13
chr2.DTNB	DTNB	1.13
chr1.AGTRAP	AGTRAP	1.13
chr19.UBE2S	UBE2S	1.13
chr6.HCP5	HCP5	1.13
chr1.ADAMTSL4	ADAMTSL4	1.13
chr1.FAM46C	FAM46C	1.13
chr18.NPC1	NPC1	1.13
chr12.C1R	C1R	1.13
chr16.LAT	LAT	1.13
chr1.KCNA3	KCNA3	1.13
chr19.JAK3	JAK3	1.13
chr16.SNAI3	SNAI3	1.12
chr4.RPS3A	RPS3A	1.12
chr16.NLRC5	NLRC5	1.12
chr12.KLRB1	KLRB1	1.12
chr20.STMN3	STMN3	1.12
chr11.TSPAN4	TSPAN4	1.12
chr17.STAT5A	STAT5A	1.12
chr6.CMAHP	CMAHP	1.12
chr12.SNORA34	SNORA34	1.12
chr14.TMED8	TMED8	1.12
chr9.TLE1	TLE1	1.12
chr22.APOBEC3C	APOBEC3C	1.12
chr12.GTSF1	GTSF1	1.12
chr1.SUSD4	SUSD4	1.12
chr17.LIMD2	LIMD2	1.11
chr8.RNF19A	RNF19A	1.11
chr3.GNAI2	GNAI2	1.11
chr6.SUPT3H	SUPT3H	1.11
chr17.PER1	PER1	1.11
chr3.CDV3	CDV3	1.11
chr16.KIAA0513	KIAA0513	1.11
chr1.RASSF5	RASSF5	1.11
chr11.CD248	CD248	1.11
chr5.PRR7	PRR7	1.11
chr6.HLA-H	HLA-H	1.11
chr10.FAM53B	FAM53B	1.11
chr9.SLC31A2	SLC31A2	1.11
chr1.ARHGAP30	ARHGAP30	1.11
chr17.FMNL1	FMNL1	1.11
chr3.OXNAD1	OXNAD1	1.10
chr10.LOC619207	LOC619207	1.10
chr17.TBKBP1	TBKBP1	1.10
chr17.FAM100B	FAM100B	1.10
chr22.MIAT	MIAT	1.10
chr6.HIST1H2AK	HIST1H2AK	1.10

chr2.C2orf48	C2orf48	1.10
chr8.LETM2	LETM2	1.10
chr8.ZC2HC1A	ZC2HC1A	1.10
chr17.TRPV2	TRPV2	1.10
chr14.C14orf64	C14orf64	1.10
chr17.CCL5	CCL5	1.10
chr19.LILRB1	LILRB1	1.10
chr7.LOC100506776	LOC100506776	1.10
chr1.PPT1	PPT1	1.10
chr17.CD79B	CD79B	1.10
chr1.CR1	CR1	1.10
chr3.CBLB	CBLB	1.10
chr10.SFMBT2	SFMBT2	1.10
chrY.CSF2RA	CSF2RA	1.10
chrX.CSF2RA	CSF2RA	1.10
chrX.SRPX	SRPX	1.10
chr2.WIPF1	WIPF1	1.10
chr2.TMEM169	TMEM169	1.09
chr8.TP53INP1	TP53INP1	1.09
chr1.CSF1	CSF1	1.09
chrX.VSIG4	VSIG4	1.09
chr16.CYBA	CYBA	1.09
chr15.GABPB1	GABPB1	1.09
chr5.F2R	F2R	1.09
chr1.ST3GAL3	ST3GAL3	1.09
chr1.SRGAP2P2	SRGAP2P2	1.09
chr3.H1FX-AS1	H1FX-AS1	1.09
chr19.PKN1	PKN1	1.09
chr17.C17orf90	C17orf90	1.09
chr8.EGR3	EGR3	1.09
chr16.LITAF	LITAF	1.09
chr19.SIGLEC9	SIGLEC9	1.09
chr2.EHD3	EHD3	1.09
chr5.LCP2	LCP2	1.08
chr6.HIST1H2BI	HIST1H2BI	1.08
chr16.SNORA10	SNORA10	1.08
chr19.LRRC25	LRRC25	1.08
chr2.POMC	POMC	1.08
chr17.C17orf107	C17orf107	1.08
chr15.PSTPIP1	PSTPIP1	1.08
chr3.RPSA	RPSA	1.08
chr1.PBXIP1	PBXIP1	1.08
chrX.ARHGEF6	ARHGEF6	1.08
chrX.SEPT6	SEPT6	1.08
chr5.C5orf56	C5orf56	1.08
chr19.SSBP4	SSBP4	1.08
chr7.TBXAS1	TBXAS1	1.08
chr19.TYROBP	TYROBP	1.08
chr18.TAF4B	TAF4B	1.08
chr4.C4orf26	C4orf26	1.08
chr12.CERS5	CERS5	1.08
chr12.OAS2	OAS2	1.07

chr11.PACS1	PACS1	1.07
chr3.RPL22L1	RPL22L1	1.07
chrX.PORCN	PORCN	1.07
chr9.RPL35	RPL35	1.07
chr20.NXT1	NXT1	1.07
chr7.GIMAP6	GIMAP6	1.07
chr4.RBPJ	RBPJ	1.07
chr6.AKIRIN2-AS1	AKIRIN2-AS1	1.07
chr15.LOC100287616	LOC100287616	1.07
chr4.KIAA0922	KIAA0922	1.07
chr17.SLFN5	SLFN5	1.07
chr6.HLA-B	HLA-B	1.07
chr11.SNORD25	SNORD25	1.07
chr1.RCAN3	RCAN3	1.07
chr9.LINC00092	LINC00092	1.07
chr8.PPP3CC	PPP3CC	1.07
chr9.FNBP1	FNBP1	1.07
chr19.DNASE2	DNASE2	1.07
chr1.SLAMF8	SLAMF8	1.07
chr7.BLVRA	BLVRA	1.07
chr10.MAP3K8	MAP3K8	1.06
chr8.RRS1	RRS1	1.06
chr1.C1QA	C1QA	1.06
chr1.IFI16	IFI16	1.06
chr2.GPR155	GPR155	1.06
chr2.ARL4C	ARL4C	1.06
chr6.CITED2	CITED2	1.06
chr20.COMMD7	COMMD7	1.06
chr16.SNX20	SNX20	1.06
chr17.AMZ2P1	AMZ2P1	1.06
chr11.CD44	CD44	1.06
chr1.MAPKAPK2	MAPKAPK2	1.05
chr19.ZNF826P	ZNF826P	1.05
chr19.CA11	CA11	1.05
chr16.FBXL8	FBXL8	1.05
chrX.AP1S2	AP1S2	1.05
chr12.PFDN5	PFDN5	1.05
chr8.TMEM66	TMEM66	1.05
chr7.NAMPT	NAMPT	1.05
chr6.DSE	DSE	1.05
chr20.PRNP	PRNP	1.05
chr19.CD97	CD97	1.05
chr2.DYSF	DYSF	1.05
chr1.SNHG3	SNHG3	1.05
chr6.MICB	MICB	1.05
chr9.GPSM1	GPSM1	1.05
chr9.B4GALT1	B4GALT1	1.05
chr20.SLCO4A1	SLCO4A1	1.05
chr2.LOC375190	LOC375190	1.05
chr11.DENND5A	DENND5A	1.05
chr7.FAM40B	FAM40B	1.05
chr6.GABBR1	GABBR1	1.05

chr10.IDI2-AS1	IDI2-AS1	1.05
chr19.GMIP	GMIP	1.04
chr10.ZNF25	ZNF25	1.04
chr6.C6orf1	C6orf1	1.04
chr1.ADC	ADC	1.04
chr1.FAM159A	FAM159A	1.04
chr2.ZFP36L2	ZFP36L2	1.04
chr19.GRAMD1A	GRAMD1A	1.04
chr2.PLEK	PLEK	1.04
chrX.P2RY10	P2RY10	1.04
chr20.CD40	CD40	1.04
chr6.HIST1H3I	HIST1H3I	1.04
chr10.ZEB1-AS1	ZEB1-AS1	1.04
chr12.C12orf57	C12orf57	1.04
chr10.PIP4K2A	PIP4K2A	1.04
chr9.DPP7	DPP7	1.04
chr6.FAM65B	FAM65B	1.04
chr19.CNN2	CNN2	1.04
chr11.FADS2	FADS2	1.03
chr4.TMEM154	TMEM154	1.03
chr10.FAS	FAS	1.03
chr2.HK2	HK2	1.03
chr3.ARHGEF3	ARHGEF3	1.03
chrX.SASH3	SASH3	1.03
chr2.MIR4785	MIR4785	1.03
chr19.LOC147727	LOC147727	1.03
chr21.COL18A1	COL18A1	1.03
chr1.IL24	IL24	1.03
chr22.NCF4	NCF4	1.03
chr9.DNAJB5	DNAJB5	1.03
chr4.CRMP1	CRMP1	1.03
chr7.GLCCI1	GLCCI1	1.03
chr11.AIP	AIP	1.03
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chr6.PSMB9	PSMB9	1.02
chr1.SLAMF7	SLAMF7	1.02
chr10.ACTA2	ACTA2	1.02
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chr3.CSRNP1	CSRNP1	1.02
chr14.EVL	EVL	1.02
chr7.CHST12	CHST12	1.02
chr2.NCAPH	NCAPH	1.02
chr11.LOC100507392	LOC100507392	1.02
chr9.SLC2A6	SLC2A6	1.02
chr3.RAB43	RAB43	1.02
chr3.PLXND1	PLXND1	1.02
chr12.ERP27	ERP27	1.02
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chr4.LEF1	LEF1	1.02
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chr7.PCOLCE	PCOLCE	1.01
chr11.FERMT3	FERMT3	1.01
chr1.SLC41A1	SLC41A1	1.01
chr6.MB21D1	MB21D1	1.01
chr3.LOC100505687	LOC100505687	1.01
chr4.RPL9	RPL9	1.01
chr14.SLC22A17	SLC22A17	1.01
chr6.AKIRIN2	AKIRIN2	1.01
chr11.STIM1	STIM1	1.01
chr19.FCAR	FCAR	1.01
chr18.PSTPIP2	PSTPIP2	1.01
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chr14.CFL2	CFL2	1.01
chr11.ANKRD13D	ANKRD13D	1.01
chr17.PITPNC1	PITPNC1	1.01
chr17.ZNF287	ZNF287	1.01
chr16.MEFV	MEFV	1.01
chr3.MUSTN1	MUSTN1	1.01
chr10.C10orf128	C10orf128	1.01
chr5.DOCK2	DOCK2	1.01
chr12.CCDC65	CCDC65	1.01
chrX.RPL39	RPL39	1.01
chr9.FAM78A	FAM78A	1.01
chr16.MYH11	MYH11	1.01
chr6.HLA-F-AS1	HLA-F-AS1	1.01
chr2.WDR54	WDR54	1.01
chr7.SMARCD3	SMARCD3	1.01
chr15.TARSL2	TARSL2	1.00
chr21.BTG3	BTG3	1.00
chr19.CERS4	CERS4	1.00
chr6.HIST1H1E	HIST1H1E	1.00
chr11.RASGRP2	RASGRP2	1.00
chr2.ARHGAP25	ARHGAP25	1.00
chr17.AMZ2	AMZ2	1.00
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chr17.UNC13D	UNC13D	1.00
chr8.EEF1D	EEF1D	1.00
chr2.BIN1	BIN1	1.00
chr8.WDR67	WDR67	1.00
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chr1.RPA2	RPA2	1.00
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chr14.PNMA1	PNMA1	0.98
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chr16.ATF7IP2	ATF7IP2	0.98
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chr3.CISH	CISH	0.98
chr7.SAMD9L	SAMD9L	0.98
chr3.ARL6IP5	ARL6IP5	0.98
chr5.JAKMIP2	JAKMIP2	0.98
chr3.FAM55C	FAM55C	0.98
chr3.C3orf71	C3orf71	0.98
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chr11.LPXN	LPXN	0.98
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chr17.SLC16A6	SLC16A6	0.97
chr12.CDKN1B	CDKN1B	0.97
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chrX.SH3KBP1	SH3KBP1	0.97
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chr6.LY6G5C	LY6G5C	0.97
chr6.HECA	HECA	0.96
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chr15.RPL4	RPL4	0.96

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chr16.CYLD	CYLD	0.96
chr3.PARP9	PARP9	0.96
chr3.WDR53	WDR53	0.96
chr3.TMEM110	TMEM110	0.96
chr3.SERPINI1	SERPINI1	0.96
chr4.NOP14-AS1	NOP14-AS1	0.96
chr6.SCML4	SCML4	0.96
chr8.SNHG6	SNHG6	0.96
chr5.PTGER4	PTGER4	0.95
chr19.ZNF331	ZNF331	0.95
chr2.ID2	ID2	0.95
chr2.CDC42EP3	CDC42EP3	0.95
chr2.FAM49A	FAM49A	0.95
chr10.C10orf54	C10orf54	0.95
chr2.SP110	SP110	0.95
chr19.TSHZ3	TSHZ3	0.95
chr16.LOC100505865	LOC100505865	0.95
chr19.RPL18A	RPL18A	0.95
chr17.TMEM107	TMEM107	0.95
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chrX.PDZD4	PDZD4	0.95
chr6.RPS10	RPS10	0.95
chr1.NUDT17	NUDT17	0.95
chr1.FAIM3	FAIM3	0.95
chrX.CYBB	CYBB	0.95
chr6.PPP1R18	PPP1R18	0.95
chr1.CDC42SE1	CDC42SE1	0.95
chr19.RASAL3	RASAL3	0.95
chr2.ITGA4	ITGA4	0.95
chr17.PECAM1	PECAM1	0.95
chr1.SRGAP2	SRGAP2	0.94
chr22.GATSL3	GATSL3	0.94
chr8.FAM49B	FAM49B	0.94
chr5.LOC648987	LOC648987	0.94
chr19.WDR88	WDR88	0.94
chr1.HES4	HES4	0.94
chr1.MCOLN2	MCOLN2	0.94
chr17.ACAP1	ACAP1	0.94
chr5.ARRDC3	ARRDC3	0.94
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chr1.TOR1AIP1	TOR1AIP1	0.62
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chr10.ADK	ADK	0.62
chr22.RPL3	RPL3	0.62
chr12.RARG	RARG	0.62
chrX.CXorf40B	CXorf40B	0.62
chr19.MEF2BNB	MEF2BNB	0.62
chr7.OSBPL3	OSBPL3	0.62
chr19.EIF3G	EIF3G	0.62
chr7.NFE2L3	NFE2L3	0.62
chr12.PRH1-PRR4	PRH1-PRR4	0.62
chr6.TXLNB	TXLNB	0.62
chr12.KANSL2	KANSL2	0.62
chr18.SMCHD1	SMCHD1	0.62
chr19.PRMT1	PRMT1	0.62
chr10.FAM204A	FAM204A	0.62
chr1.FAM69A	FAM69A	0.62
chr8.EPB49	EPB49	0.62
chr19.SLC27A5	SLC27A5	0.62
chr13.SETDB2	SETDB2	0.62
chr3.CHCHD6	CHCHD6	0.62
chr1.PRDX6	PRDX6	0.62
chr15.SNAPC5	SNAPC5	0.62
chr17.CBX4	CBX4	0.62
chr12.UBE2N	UBE2N	0.62
chr6.RNASET2	RNASET2	0.62
chr15.KLF13	KLF13	0.62
chr9.LOC100288842	LOC100288842	0.62
chr17.MSI2	MSI2	0.62
chr17.MXRA7	MXRA7	0.62
chr9.NPDC1	NPDC1	0.62
chr1.MIER1	MIER1	0.62

chr4.HELQ	HELQ	0.62
chr1.YRDC	YRDC	0.62
chr17.CCDC137	CCDC137	0.62
chr20.SAMD10	SAMD10	0.62
chr16.IL4R	IL4R	0.61
chr2.LOC254128	LOC254128	0.61
chr16.METTL9	METTL9	0.61
chr11.PELI3	PELI3	0.61
chr16.CMC2	CMC2	0.61
chr16.METRN	METRN	0.61
chr7.EZH2	EZH2	0.61
chr19.ELL	ELL	0.61
chr17.PGS1	PGS1	0.61
chr1.MKNK1	MKNK1	0.61
chr19.SLC39A3	SLC39A3	0.61
chr8.ERICH1	ERICH1	0.61
chr10.ARL3	ARL3	0.61
chr1.ACBD6	ACBD6	0.61
chr18.PTPRM	PTPRM	0.61
chrX.PIGA	PIGA	0.61
chr2.DUSP28	DUSP28	0.61
chr5.TMED9	TMED9	0.61
chr12.KLRAP1	KLRAP1	0.61
chr17.ALYREF	ALYREF	0.61
chr20.NFATC2	NFATC2	0.61
chr7.TTC26	TTC26	0.61
chr2.RBM43	RBM43	0.61
chr12.MYL6	MYL6	0.61
chr12.ARPC3	ARPC3	0.61
chr3.EAF2	EAF2	0.61
chr5.DIAPH1	DIAPH1	0.61
chr6.TAP2	TAP2	0.61
chr5.ACSL6	ACSL6	0.61
chr14.BAZ1A	BAZ1A	0.61
chr4.DCTD	DCTD	0.61
chr16.ARL2BP	ARL2BP	0.61
chr15.ZSCAN2	ZSCAN2	0.61
chr14.STYX	STYX	0.61
chr8.EIF2C2	EIF2C2	0.61
chr3.TATDN2	TATDN2	0.61
chr12.C12orf45	C12orf45	0.61
chr1.ZNF362	ZNF362	0.61
chr1.ARID4B	ARID4B	0.61
chr11.ADRBK1	ADRBK1	0.61
chr2.DOK1	DOK1	0.61
chr7.CCDC71L	CCDC71L	0.61
chr8.OSGIN2	OSGIN2	0.61
chr17.LLGL1	LLGL1	0.60
chrX.MCART6	MCART6	0.60
chr2.EEF1B2	EEF1B2	0.60
chr12.C12orf66	C12orf66	0.60
chr2.R3HDM1	R3HDM1	0.60

chr17.SLC16A3	SLC16A3	0.60
chr19.UBA2	UBA2	0.60
chr1.MAP3K6	MAP3K6	0.60
chr14.KIAA0391	KIAA0391	0.60
chr5.PIK3R1	PIK3R1	0.60
chr6.RRP36	RRP36	0.60
chr1.SMYD3	SMYD3	0.60
chr19.ZNF653	ZNF653	0.60
chr17.AATF	AATF	0.60
chr10.STAM	STAM	0.60
chr16.ST3GAL2	ST3GAL2	0.60
chr7.RPA3	RPA3	0.60
chr13.PSPC1	PSPC1	0.60
chr15.AKAP13	AKAP13	0.60
chr3.PCBP4	PCBP4	0.60
chr2.IAH1	IAH1	0.60
chr4.KLHL5	KLHL5	0.60
chr7.CASD1	CASD1	0.60
chr8.TSTA3	TSTA3	0.60
chr3.EDEM1	EDEM1	0.60
chr4.MRFAP1L1	MRFAP1L1	0.60
chr14.CHURC1	CHURC1	0.60
chr12.RAN	RAN	0.60
chr20.C20orf27	C20orf27	0.60
chr5.C5orf55	C5orf55	0.60
chr11.SLC3A2	SLC3A2	0.60
chr9.CNTRL	CNTRL	0.60
chrX.IDS	IDS	0.60
chr10.DNAJC9	DNAJC9	0.60
chr7.C7orf60	C7orf60	0.60
chr15.LCMT2	LCMT2	0.60
chr16.THAP11	THAP11	0.60
chr1.CDC14A	CDC14A	0.60
chr22.APOBEC3D	APOBEC3D	0.60
chr21.IFNAR2	IFNAR2	0.60
chr17.ZNF18	ZNF18	0.60
chr1.PFDN2	PFDN2	0.60
chr12.SENP1	SENP1	0.60
chr19.RPL18	RPL18	0.60
chr17.MMD	MMD	0.60
chr10.BLOC1S2	BLOC1S2	0.60
chr3.RASSF1	RASSF1	0.60
chr7.NOD1	NOD1	0.59
chrX.FAM50A	FAM50A	0.59
chr1.CAP1	CAP1	0.59
chr10.ZFAND4	ZFAND4	0.59
chr16.FHOD1	FHOD1	0.59
chr1.C1orf96	C1orf96	0.59
chrX.FLJ44635	FLJ44635	0.59
chr11.TSSC4	TSSC4	0.59
chr7.PRKRIP1	PRKRIP1	0.59
chr3.ISY1	ISY1	0.59

chr6.FRS3	FRS3	0.59
chr19.RPS28	RPS28	0.59
chr6.TUBB	TUBB	0.59
chr4.ANAPC10	ANAPC10	0.59
chr17.SGSH	SGSH	0.59
chr2.CAPN10	CAPN10	0.59
chr17.RFFL	RFFL	0.59
chr8.SLC25A32	SLC25A32	0.59
chr17.C17orf89	C17orf89	0.59
chr2.TTC32	TTC32	0.59
chrX.EMD	EMD	0.59
chr10.DDX21	DDX21	0.59
chr17.YPEL2	YPEL2	0.59
chr7.GIMAP8	GIMAP8	0.59
chr18.SETBP1	SETBP1	0.59
chr11.PRKRIR	PRKRIR	0.59
chr17.CHMP6	CHMP6	0.59
chr6.CYB5R4	CYB5R4	0.59
chr13.TBC1D4	TBC1D4	0.59
chr14.RPL36AL	RPL36AL	0.59
chr1.ILF2	ILF2	0.59

Table S2: Suppressive regulatory factors identified via patient transcription profiles and ATAC data integration identified by the ReMAP tool.

Transcription Factor	Observed Overlap	Expected Overlap	E-value
EED	787	30.827	780.773
MTA3	628	22.019	652.45
BCL6	632	25.553	618.959
JMJD1C	595	25.635	567.077
RCOR1	653	37.319	546.06
RNF2	486	15.593	523.378
REST	675	48.074	504.003
BCOR	378	13.071	395.509
CBX3	412	18.106	389.735
KDM5B	490	34.674	367.564
CBX1	365	15.783	347.895
KDM1A	452	34	328.05
SIN3A	458	35.707	325.809
HDAC2	429	30.061	323.689
HDAC1	371	20.743	314.219
SUZ12	268	17.083	213.023
EZH1	203	7.389	208.687
SIN3B	171	4.833	194.181
KDM4B	167	4.552	192.223
MTA2	219	11.714	190.034
DNMT3B	117	2.732	142.702
HDAC8	158	8.784	134.958

JARID2	172	16.105	110.682
KDM4A	156	13.519	105.278
MTA1	108	4.586	104.661
MBD1	89	2.355	104.122
EZH2	352	106.382	77.772
TGIF2	67	2.448	69.558
SETDB1	149	22.216	69.507
SFMBT1	62	2.11	66.294
KDM4C	98	9.108	63.865
PRDM14	91	10.583	51.435
BMI1	46	1.806	46.702
ASXL1	36	1.251	38.6
ZMYND11	42	2.746	33.889
MBD3	37	3.855	23.085
KDM5A	30	2.74	20.441
PRDM1	18	0.7	18.885
RYBP	8	0.387	8.057
L3MBTL2	9	0.589	7.857
MBD2	11	1.176	7.291
HDAC6	6	0.299	6.113
CBX2	36	15.27	5.358
CHD4	4	0.152	4.704
TLE3	9	1.742	4.066
HDAC3	7	1.396	3.214
CBX4	2	0.293	1.452
MBD4	3	0.826	1.291

Table S3: Patient characteristics from CD ileal CD4+ RNAseq dataset

	Healthy	**Crohn's Disease**		
		All	33%	66%
Age median (y)	54	32	45.5	31
Age range (y)	18-70	18-76	20-69	18-76
Female	6/12 (50%)	12 (57%)	4 (57%)	8 (57%)
Male	6/12 (50%)	9 (43%)	3 (43%)	6 (43%)
Medications at time of surgery	N/A			
Anti-TNF		15/21 (71%)	4/7 (57%)	11/14 (79%)
Prednisone		9/21 (43%)	5/7 (71%)	4/14 (29%)
Budesonide		3/21 (14%)	0/7 (0%)	3/14 (21%)
6-mercaptopurine		2/21 (10%)	1/7 (14%)	1/14 (7%)
Methotrexate		2/21 (10%)	1/7 (14%)	1/14 (7%)
Antibiotics		2/21 (10%)	1/7 (14%)	1/14 (7%)
Mesalamine		1/21 (5%)	0/7 (0%)	1/14 (7%)

Table S4: List of TSS associated with genes upregulated upon BMI1 KO in mice.

Chrom	ChromStart	ChromEnd	Name	Score	Strand
chr1	20486235	20486236	CAMK2N1	0	-
chr1	21651855	21651856	RAP1GAP	0	-
chr1	21669380	21669381	RAP1GAP	0	-
chr1	21669380	21669381	RAP1GAP	0	-
chr1	21669380	21669381	RAP1GAP	0	-
chr1	21669380	21669381	RAP1GAP	0	-
chr1	21669380	21669381	RAP1GAP	0	-
chr1	21669380	21669381	RAP1GAP	0	-
chr1	21669380	21669381	RAP1GAP	0	-
chr1	21669380	21669381	RAP1GAP	0	-
chr1	31409563	31409564	SERINC2	0	+
chr1	31410172	31410173	SERINC2	0	+
chr1	31413114	31413115	SERINC2	0	+
chr1	31413811	31413812	SERINC2	0	+
chr1	31413811	31413812	SERINC2	0	+
chr1	34929585	34929586	DLGAP3	0	-
chr1	54801268	54801269	TTC22	0	-
chr1	54801268	54801269	TTC22	0	-
chr1	55039474	55039475	PCSK9	0	+
chr1	55040220	55040221	PCSK9	0	+
chr1	65792508	65792509	PDE4B	0	+
chr1	65792508	65792509	PDE4B	0	+
chr1	65793171	65793172	PDE4B	0	+
chr1	65913243	65913244	PDE4B	0	+
chr1	65992614	65992615	PDE4B	0	+
chr1	66332106	66332107	PDE4B	0	+
chr1	66354376	66354377	PDE4B	0	+
chr1	97921059	97921060	DPYD	0	-
chr1	97921059	97921060	DPYD	0	-
chr1	115338236	115338237	NGF	0	-
chr1	151511384	151511385	CGN	0	+
chr1	169630139	169630140	SELP	0	-
chr1	185734549	185734550	HMCN1	0	+
chr1	228644645	228644646	RHOU	0	+
chr1	228735075	228735076	RHOU	0	+
chr10	48493649	48493650	ARHGAP22	0	-
chr10	48605131	48605132	ARHGAP22	0	-
chr10	48605131	48605132	ARHGAP22	0	-
chr10	48605131	48605132	ARHGAP22	0	-
chr10	48605131	48605132	ARHGAP22	0	-
chr10	48605131	48605132	ARHGAP22	0	-
chr10	48605131	48605132	ARHGAP22	0	-
chr10	48605131	48605132	ARHGAP22	0	-
chr10	48605131	48605132	ARHGAP22	0	-
chr10	48605131	48605132	ARHGAP22	0	-
chr10	48652516	48652517	ARHGAP22	0	-
chr10	48656265	48656266	ARHGAP22	0	-
chr10	48656265	48656266	ARHGAP22	0	-

chr10	48656265	48656266	ARHGAP22	0	-
chr10	84194633	84194634	CDHR1	0	+
chr10	84194633	84194634	CDHR1	0	+
chr10	90921275	90921276	ANKRD1	0	-
chr10	107164708	107164709	SORCS1	0	-
chr10	107164708	107164709	SORCS1	0	-
chr10	107164708	107164709	SORCS1	0	-
chr10	107164708	107164709	SORCS1	0	-
chr10	107164708	107164709	SORCS1	0	-
chr10	107164708	107164709	SORCS1	0	-
chr10	122461523	122461524	HTRA1	0	+
chr11	2137288	2137289	IGF2	0	-
chr11	2138974	2138975	IGF2	0	-
chr11	2141124	2141125	IGF2	0	-
chr11	2141124	2141125	IGF2	0	-
chr11	2149603	2149604	IGF2	0	-
chr11	44950208	44950209	TP53I11	0	-
chr11	44950208	44950209	TP53I11	0	-
chr11	44950904	44950905	TP53I11	0	-
chr11	44950904	44950905	TP53I11	0	-
chr11	44950904	44950905	TP53I11	0	-
chr11	44950904	44950905	TP53I11	0	-
chr11	44950904	44950905	TP53I11	0	-
chr11	44950904	44950905	TP53I11	0	-
chr11	44950904	44950905	TP53I11	0	-
chr11	44951306	44951307	TP53I11	0	-
chr11	44951306	44951307	TP53I11	0	-
chr11	44951306	44951307	TP53I11	0	-
chr11	44951306	44951307	TP53I11	0	-
chr11	44951306	44951307	TP53I11	0	-
chr11	57597552	57597553	SERPING1	0	+
chr11	57598230	57598231	SERPING1	0	+
chr11	117199292	117199293	TAGLN	0	+
chr11	117199292	117199293	TAGLN	0	+
chr11	119317130	119317131	MCAM	0	-
chr12	47079951	47079952	AMIGO2	0	-
chr12	47079951	47079952	AMIGO2	0	-
chr12	49295124	49295125	PRPH	0	+
chr12	52233168	52233169	KRT7	0	+
chr12	54000117	54000118	HOXC9	0	+
chr12	57216793	57216794	NXPH4	0	+
chr12	57738246	57738247	AGAP2	0	-
chr12	57742161	57742162	AGAP2	0	-
chr12	112906775	112906776	OAS1	0	+
chr12	112906775	112906776	OAS1	0	+
chr12	112906775	112906776	OAS1	0	+
chr12	112906775	112906776	OAS1	0	+
chr14	105168824	105168825	JAG2	0	-
chr14	105168824	105168825	JAG2	0	-
chr15	39581077	39581078	THBS1	0	+
chr15	43592855	43592856	CKMT1B	0	+
chr15	43592855	43592856	CKMT1B	0	+

chr15	43593832	43593833	CKMT1B	0	+
chr15	43593832	43593833	CKMT1B	0	+
chr15	43593832	43593833	CKMT1B	0	+
chr15	43593832	43593833	CKMT1B	0	+
chr15	43692784	43692785	CKMT1A	0	+
chr15	43692784	43692785	CKMT1A	0	+
chr15	43693431	43693432	CKMT1A	0	+
chr15	43693689	43693690	CKMT1A	0	+
chr15	43693689	43693690	CKMT1A	0	+
chr15	43693938	43693939	CKMT1A	0	+
chr15	77632527	77632528	LINGO1	0	-
chr15	77696148	77696149	LINGO1	0	-
chr15	77696495	77696496	LINGO1	0	-
chr15	77707507	77707508	LINGO1	0	-
chr15	77720751	77720752	LINGO1	0	-
chr15	77787014	77787015	LINGO1	0	-
chr15	77819524	77819525	LINGO1	0	-
chr15	77819524	77819525	LINGO1	0	-
chr15	77819524	77819525	LINGO1	0	-
chr15	77820102	77820103	LINGO1	0	-
chr15	77820332	77820333	LINGO1	0	-
chr15	77820900	77820901	LINGO1	0	-
chr16	280604	280605	ARHGDIG	0	+
chr16	3046679	3046680	MMP25	0	+
chr16	66925536	66925537	RRAD	0	-
chr16	66925536	66925537	RRAD	0	-
chr16	68448506	68448507	SMPD3	0	-
chr16	81779256	81779257	PLCG2	0	+
chr17	2025345	2025346	RTN4RL1	0	-
chr17	34255275	34255276	CCL2	0	+
chr17	34270214	34270215	CCL7	0	+
chr17	38605930	38605931	SRCIN1	0	-
chr17	40443422	40443423	IGFBP4	0	+
chr17	43530435	43530436	ETV4	0	-
chr17	43545937	43545938	ETV4	0	-
chr17	43545937	43545938	ETV4	0	-
chr17	43546432	43546433	ETV4	0	-
chr17	43546432	43546433	ETV4	0	-
chr17	48614939	48614940	HOXB8	0	-
chr17	48626473	48626474	HOXB9	0	-
chr17	78187204	78187205	TK1	0	-
chr17	78187204	78187205	TK1	0	-
chr18	63753045	63753046	SERPINB7	0	+
chr18	63775373	63775374	SERPINB7	0	+
chr18	63775373	63775374	SERPINB7	0	+
chr18	63777775	63777776	SERPINB7	0	+
chr19	33621953	33621954	CHST8	0	+
chr19	33621965	33621966	CHST8	0	+
chr19	33684526	33684527	CHST8	0	+
chr19	43639839	43639840	CADM4	0	-
chr19	44809057	44809058	BCAM	0	+
chr19	44809057	44809058	BCAM	0	+

chr19	48513189	48513190	LMTK3	0	-
chr19	51311846	51311847	IGLON5	0	+
chr2	26786012	26786013	CENPA	0	+
chr2	26786013	26786014	CENPA	0	+
chr2	101151447	101151448	TBC1D8	0	-
chr2	101151447	101151448	TBC1D8	0	-
chr2	101151447	101151448	TBC1D8	0	-
chr2	119431868	119431869	TMEM37	0	+
chr2	169067033	169067034	DHRS9	0	+
chr2	169067033	169067034	DHRS9	0	+
chr2	169072573	169072574	DHRS9	0	+
chr2	169081105	169081106	DHRS9	0	+
chr2	174847618	174847619	CHN1	0	-
chr2	175005253	175005254	CHN1	0	-
chr2	175005379	175005380	CHN1	0	-
chr2	175005379	175005380	CHN1	0	-
chr2	216632826	216632827	IGFBP2	0	+
chr2	216632826	216632827	IGFBP2	0	+
chr2	216633402	216633403	IGFBP2	0	+
chr2	216659616	216659617	IGFBP2	0	+
chr2	218859821	218859822	WNT6	0	+
chr20	32052186	32052187	HCK	0	+
chr20	32052186	32052187	HCK	0	+
chr20	32052186	32052187	HCK	0	+
chr20	32052186	32052187	HCK	0	+
chr20	32052186	32052187	HCK	0	+
chr20	32052186	32052187	HCK	0	+
chr20	46021688	46021689	SLC12A5	0	+
chr20	46029180	46029181	SLC12A5	0	+
chr20	62367312	62367313	LAMA5	0	-
chr22	37519203	37519204	CARD10	0	-
chr22	38201930	38201931	MAFF	0	+
chr22	38201930	38201931	MAFF	0	+
chr22	38201930	38201931	MAFF	0	+
chr22	38203018	38203019	MAFF	0	+
chr22	45502837	45502838	FBLN1	0	+
chr22	45502837	45502838	FBLN1	0	+
chr22	45502837	45502838	FBLN1	0	+
chr22	45502837	45502838	FBLN1	0	+
chr3	8501805	8501806	LMCD1	0	+
chr3	8501805	8501806	LMCD1	0	+
chr3	8501805	8501806	LMCD1	0	+
chr3	8501805	8501806	LMCD1	0	+
chr3	24494822	24494823	THRB	0	-
chr3	24494822	24494823	THRB	0	-
chr3	24494822	24494823	THRB	0	-
chr3	24494822	24494823	THRB	0	-
chr3	24494822	24494823	THRB	0	-
chr3	24494822	24494823	THRB	0	-
chr3	24494822	24494823	THRB	0	-
chr3	24495005	24495006	THRB	0	-
chr3	24495005	24495006	THRB	0	-

chr3	24495005	24495006	THRB	0	-
chr3	24495005	24495006	THRB	0	-
chr3	24495281	24495282	THRB	0	-
chr3	49198426	49198427	CCDC36	0	+
chr3	49199498	49199499	CCDC36	0	+
chr3	53495047	53495048	CACNA1D	0	+
chr3	53495047	53495048	CACNA1D	0	+
chr3	53495047	53495048	CACNA1D	0	+
chr3	156120546	156120547	KCNAB1	0	+
chr3	156120546	156120547	KCNAB1	0	+
chr3	156142960	156142961	KCNAB1	0	+
chr3	156290985	156290986	KCNAB1	0	+
chr3	156291035	156291036	KCNAB1	0	+
chr3	184230427	184230428	VWA5B2	0	+
chr3	184233414	184233415	VWA5B2	0	+
chr3	186717307	186717308	KNG1	0	+
chr3	186717307	186717308	KNG1	0	+
chr3	186717307	186717308	KNG1	0	+
chr4	5887813	5887814	CRMP1	0	-
chr4	5888616	5888617	CRMP1	0	-
chr4	5890226	5890227	CRMP1	0	-
chr4	5893083	5893084	CRMP1	0	-
chr4	41256879	41256880	UCHL1	0	+
chr4	74933073	74933074	PARM1	0	+
chr4	78057568	78057569	FRAS1	0	+
chr4	78057568	78057569	FRAS1	0	+
chr4	78551586	78551587	ANXA3	0	+
chr4	88592421	88592422	HERC3	0	+
chr4	88592421	88592422	HERC3	0	+
chr4	88592421	88592422	HERC3	0	+
chr4	123396793	123396794	SPRY1	0	+
chr4	123396793	123396794	SPRY1	0	+
chr4	123398384	123398385	SPRY1	0	+
chr4	123399488	123399489	SPRY1	0	+
chr4	176792745	176792746	VEGFC	0	-
chr5	32710635	32710636	NPR3	0	+
chr5	32711330	32711331	NPR3	0	+
chr5	32711330	32711331	NPR3	0	+
chr5	157266078	157266079	CYFIP2	0	+
chr5	157266078	157266079	CYFIP2	0	+
chr5	157266078	157266079	CYFIP2	0	+
chr5	157269340	157269341	CYFIP2	0	+
chr5	169301129	169301130	SLIT3	0	-
chr5	169301129	169301130	SLIT3	0	-
chr5	171419661	171419662	FGF18	0	+
chr6	2903312	2903313	SERPINB9	0	-
chr6	12716654	12716655	PHACTR1	0	+
chr6	12716654	12716655	PHACTR1	0	+
chr6	12716654	12716655	PHACTR1	0	+
chr6	12718307	12718308	PHACTR1	0	+
chr6	12718697	12718698	PHACTR1	0	+
chr6	12957354	12957355	PHACTR1	0	+

chr6	12957484	12957485	PHACTR1	0	+
chr6	12957484	12957485	PHACTR1	0	+
chr6	13013654	13013655	PHACTR1	0	+
chr6	26240424	26240425	HIST1H4F	0	+
chr6	47309947	47309948	TNFRSF21	0	-
chr6	150599863	150599864	PLEKHG1	0	+
chr6	150599863	150599864	PLEKHG1	0	+
chr6	150599863	150599864	PLEKHG1	0	+
chr6	150599863	150599864	PLEKHG1	0	+
chr6	150599863	150599864	PLEKHG1	0	+
chr6	150599863	150599864	PLEKHG1	0	+
chr6	150599863	150599864	PLEKHG1	0	+
chr6	150599863	150599864	PLEKHG1	0	+
chr6	150633106	150633107	PLEKHG1	0	+
chr6	150683601	150683602	PLEKHG1	0	+
chr6	150683601	150683602	PLEKHG1	0	+
chr6	150720931	150720932	PLEKHG1	0	+
chr6	150720931	150720932	PLEKHG1	0	+
chr6	150720931	150720932	PLEKHG1	0	+
chr6	150720931	150720932	PLEKHG1	0	+
chr7	1709160	1709161	ELFN1	0	+
chr7	23246695	23246696	GPNMB	0	+
chr7	23246695	23246696	GPNMB	0	+
chr7	23470376	23470377	IGF2BP3	0	-
chr7	48088601	48088602	UPP1	0	+
chr7	48088601	48088602	UPP1	0	+
chr7	48089138	48089139	UPP1	0	+
chr7	48089210	48089211	UPP1	0	+
chr7	48089252	48089253	UPP1	0	+
chr7	48089252	48089253	UPP1	0	+
chr7	76302556	76302557	HSPB1	0	+
chr7	128937030	128937031	IRF5	0	+
chr7	128937935	128937936	IRF5	0	+
chr7	128937935	128937936	IRF5	0	+
chr7	128937935	128937936	IRF5	0	+
chr7	128938215	128938216	IRF5	0	+
chr7	128940668	128940669	IRF5	0	+
chr7	131556617	131556618	PODXL	0	-
chr7	131556617	131556618	PODXL	0	-
chr7	149773479	149773480	ZNF467	0	-
chr7	149773479	149773480	ZNF467	0	-
chr7	150800533	150800534	TMEM176B	0	-
chr7	150800533	150800534	TMEM176B	0	-
chr7	150800533	150800534	TMEM176B	0	-
chr7	150800764	150800765	TMEM176A	0	+
chr7	150801360	150801361	TMEM176B	0	-
chr8	94208587	94208588	CDH17	0	-
chr8	94217303	94217304	CDH17	0	-
chr8	98944401	98944402	OSR2	0	+
chr8	98944401	98944402	OSR2	0	+
chr8	98944401	98944402	OSR2	0	+
chr8	143018483	143018484	LY6E	0	+

chr8	143018483	143018484	LY6E	0	+
chr8	143553385	143553386	GSDMD	0	+
chr8	143558305	143558306	GSDMD	0	+
chr9	97501178	97501179	TMOD1	0	+
chr9	97501637	97501638	TMOD1	0	+
chr9	130444705	130444706	ASS1	0	+
chr9	130444705	130444706	ASS1	0	+
chr9	135075241	135075242	OLFM1	0	+
chr9	135075255	135075256	OLFM1	0	+
chr9	135087258	135087259	OLFM1	0	+
chr9	135087666	135087667	OLFM1	0	+
chrX	16946689	16946690	REPS2	0	+
chrX	16946689	16946690	REPS2	0	+
chrX	54920561	54920562	TRO	0	+
chrX	54920561	54920562	TRO	0	+
chrX	54920561	54920562	TRO	0	+
chrX	54920561	54920562	TRO	0	+
chrX	54920561	54920562	TRO	0	+
chrX	54920561	54920562	TRO	0	+
chrX	54920561	54920562	TRO	0	+
chrX	54920822	54920823	TRO	0	+
chrX	69616065	69616066	EDA	0	+
chrX	69616065	69616066	EDA	0	+
chrX	69616065	69616066	EDA	0	+
chrX	69616065	69616066	EDA	0	+
chrX	69616065	69616066	EDA	0	+
chrX	100731534	100731535	SYTL4	0	-
chrX	100731534	100731535	SYTL4	0	-
chrX	100732148	100732149	SYTL4	0	-
chrX	105822541	105822542	NRK	0	+
chrX	131058240	131058241	ARHGAP36	0	+
chrX	131058240	131058241	ARHGAP36	0	+
chrX	131082433	131082434	ARHGAP36	0	+
chrX	152914440	152914441	ZNF185	0	+
chrX	152914440	152914441	ZNF185	0	+
chrX	152914440	152914441	ZNF185	0	+
chrX	152914440	152914441	ZNF185	0	+
chrX	152914440	152914441	ZNF185	0	+
chrX	152914440	152914441	ZNF185	0	+
chrX	152917863	152917864	ZNF185	0	+
chrX	152941669	152941670	ZNF185	0	+

Table S5: Pathways enriched within the BMI1KO unique peak associated genes.

Term	Overlap	P-value	Adjusted p-value	Odds Ratio	Combined Score
Osteoclast differentiation	54/128	1.07E-09	3.23E-07	2.2280169	46.02822914
T cell receptor signaling pathway	42/101	1.20E-07	1.82E-05	2.196153072	35.00079299
Th1 and Th2 cell differentiation	37/87	3.38E-07	3.41E-05	2.246038322	33.46619976
Th17 cell differentiation	39/102	4.10E-06	3.10E-04	2.019292005	25.0492007
Pathways in cancer	140/535	1.96E-05	0.001186884	1.382002868	14.98190497
B cell receptor signaling pathway	29/72	2.16E-05	0.001092308	2.127160168	22.84875466
Gastric acid secretion	29/74	3.97E-05	0.001719385	2.069669352	20.97322515
Oxytocin signaling pathway	48/154	1.78E-04	0.006743725	1.64609618	14.21146289
VEGF signaling pathway	23/58	1.97E-04	0.006636906	2.094278976	17.86758746
Fluid shear stress and atherosclerosis	45/143	2.19E-04	0.006642413	1.661924028	14.00242082
Notch signaling pathway	20/49	3.22E-04	0.008860952	2.155602141	17.33522015
Cholinergic synapse	37/113	3.23E-04	0.008163461	1.729250744	13.89783818
Platelet activation	40/125	3.25E-04	0.007572441	1.689992078	13.57405567
Glycosaminoglycan biosynthesis	21/53	3.74E-04	0.008084472	2.092560946	16.51550717
Longevity regulating pathway	34/102	3.82E-04	0.007725409	1.760408415	13.85251845
AMPK signaling pathway	40/126	3.90E-04	0.007388562	1.676579443	13.15941546
Primary immunodeficiency	16/36	4.03E-04	0.007176795	2.34721122	18.3491401
cGMP-PKG signaling pathway	51/172	4.38E-04	0.007378401	1.565944695	12.10876033
Thyroid hormone signaling pathway	37/115	4.75E-04	0.007567935	1.699176818	13.00401924
Human cytomegalovirus infection	70/255	5.37E-04	0.008138695	1.449748106	10.91533605
Hepatitis B	48/163	7.50E-04	0.01082084	1.555207434	11.19048227
Wnt signaling pathway	47/160	8.97E-04	0.012350207	1.551359916	10.8855401
Adrenergic signaling in cardiomyocytes	44/148	9.81E-04	0.012924882	1.570093992	10.87578917
Tuberculosis	51/178	0.001037446	0.01309776	1.513160042	10.39691212
Renin secretion	26/76	0.001154119	0.013987922	1.806734952	12.22151047
PI3K-Akt signaling pathway	91/357	0.001265395	0.014746718	1.34619467	8.982310306
Neurotrophin signaling pathway	37/121	0.001367185	0.015342857	1.614920116	10.65040006
Aldosterone synthesis and secretion	32/102	0.001761417	0.019061044	1.656854979	10.50717265
GnRH signaling pathway	29/90	0.001798636	0.018792642	1.701728134	10.75615873
Inflammatory bowel disease (IBD)	21/59	0.001904027	0.019230668	1.879758138	11.77439975
Parathyroid hormone synthesis, secretion and action	33/107	0.002064177	0.020175662	1.628789094	10.07084185
Adipocytokine signaling pathway	24/71	0.002109455	0.019973902	1.785202899	10.99921646
cAMP signaling pathway	57/211	0.002471147	0.022689619	1.426681701	8.564474395
Fc epsilon RI signaling pathway	23/68	0.002561508	0.022827556	1.786296774	10.65911715
Proteoglycans in cancer	55/203	0.00271371	0.023492971	1.430873835	8.455661266
MAPK signaling pathway	75/294	0.003129001	0.02633576	1.347251338	7.769654297
TNF signaling pathway	33/110	0.003375922	0.027646064	1.584367573	9.016773365
Phosphatidylinositol signaling system	30/98	0.003629578	0.028941109	1.616701605	9.083662487
Human papillomavirus infection	89/360	0.003656611	0.028409053	1.305636241	7.326210325
Hematopoietic cell lineage	29/94	0.003702125	0.028043598	1.629314171	9.122282813
Hepatocellular carcinoma	47/171	0.003921299	0.028979359	1.451564833	8.043602932
Fc gamma R-mediated phagocytosis	27/87	0.004557996	0.032882684	1.639000938	8.835644696
Toxoplasmosis	32/108	0.004745618	0.033440052	1.56480748	8.372555051
Breast cancer	41/147	0.005116739	0.035235726	1.472994796	7.770398017
Rap1 signaling pathway	55/209	0.005264665	0.035448747	1.389796117	7.291895659
Small cell lung cancer	28/92	0.005293657	0.03486909	1.607329422	8.424408785

Regulation of lipolysis in adipocytes	19/56	0.005609413	0.03616281	1.791844279	9.287682999
Amphetamine addiction	22/68	0.005756851	0.036340124	1.708631697	8.812036644
Dopaminergic synapse	38/135	0.005815958	0.035963984	1.486567106	7.651583585
Natural killer cell mediated cytotoxicity	34/118	0.005951026	0.036063221	1.521708969	7.797528247
Phospholipase D signaling pathway	41/149	0.006578602	0.039084634	1.453223054	7.300895328
Axon guidance	48/180	0.006687898	0.038969865	1.408326732	7.052133752
Protein digestion and absorption	27/90	0.0075223	0.043004846	1.584367573	7.747372655
Focal adhesion	52/199	0.007546466	0.04234406	1.380018657	6.743703889
Insulin secretion	26/86	0.007728673	0.042577965	1.596649492	7.76421596
Chagas disease (American trypanosomiasis)	30/103	0.00796209	0.043080592	1.538220945	7.434319971
JAK-STAT signaling pathway	44/164	0.008137469	0.043257074	1.41691409	6.81716482
Oocyte meiosis	33/116	0.008181617	0.042741898	1.502417526	7.220416427
C-type lectin receptor signaling pathway	32/112	0.008517317	0.043741476	1.508921498	7.190997597
Apelin signaling pathway	38/138	0.008540226	0.043128143	1.45425043	6.926547911
Melanogenesis	29/100	0.009559407	0.04748361	1.531555321	7.122083933
Leishmaniasis	21/67	0.010194795	0.049822951	1.655309405	7.591046922

Table S6: EZH2 peak enriched pathways

Term	Overlap	P-value	Adjusted P-value	Odds Ratio	Combined Score
Glycerophospholipid metabolism	7/97	0.005591	1	3.280225	17.01308
Glycerolipid metabolism	5/61	0.010924	1	3.725782	16.82866
Th1 and Th2 cell differentiation	6/87	0.01239	1	3.134796	13.76447
Thyroid hormone signaling pathway	7/115	0.013664	1	2.766798	11.87792
Axon guidance	9/180	0.018431	1	2.272727	9.076621
Ether lipid metabolism	4/47	0.019575	0.988556	3.868472	15.21657
B cell receptor signaling pathway	5/72	0.021152	0.915561	3.156566	12.17185
Glycosaminoglycan biosynthesis	4/53	0.029025	1	3.430532	12.14275
Valine, leucine and isoleucine degradation	4/56	0.034605	1	3.246753	10.92132