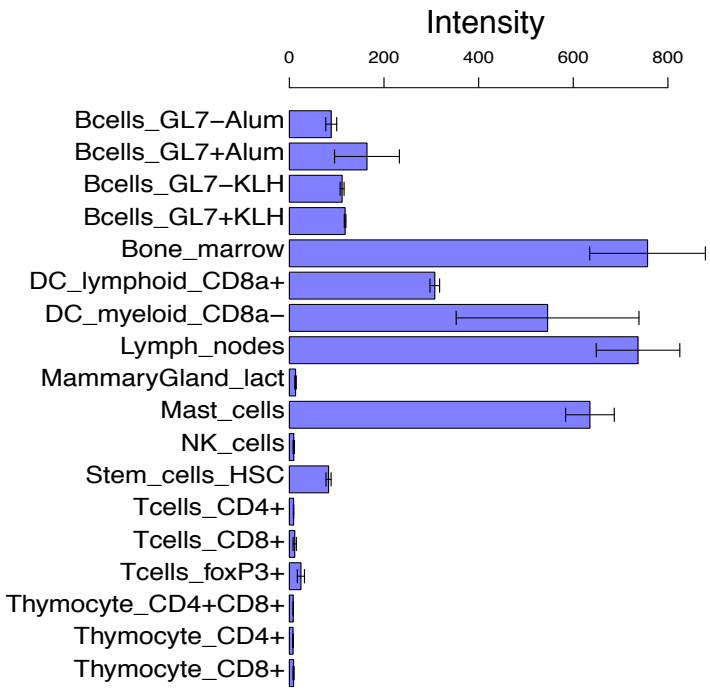
Supplementary Information for Li et al. “BATF/Jun is critical for IRF4-mediated transcription in T cells”

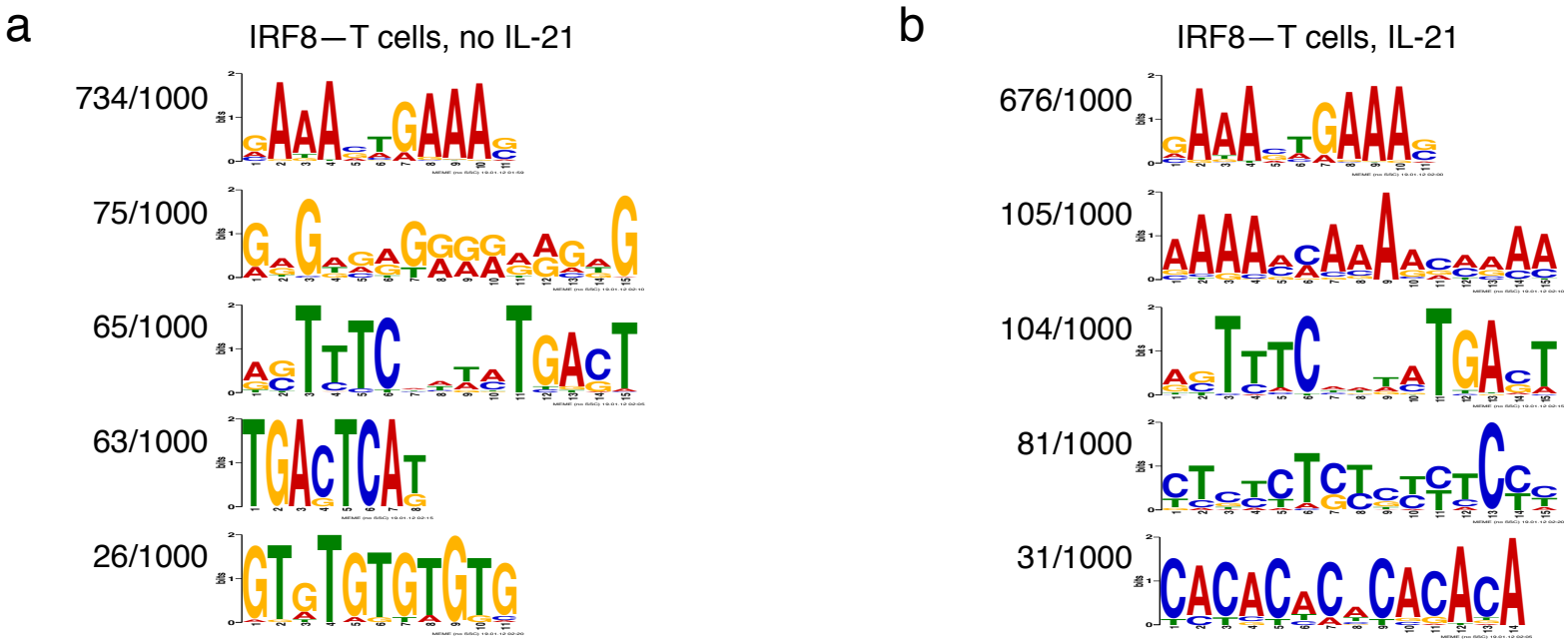
Supplementary Table 1. List of AP-1/IRF4 composite motifs identified in the top 1000 IRF4 peaks in $CD4^+$ T cells.

Supplementary Table 2. Summary of ChIP-Seq and RNA-Seq libraries used in this paper, including the total number of mapped reads and reads used (only non-redundant reads were used for ChIP-Seq analysis; all reads were used for RNA-Seq analysis), as well as the total number of binding sites identified in each ChIP-Seq library.

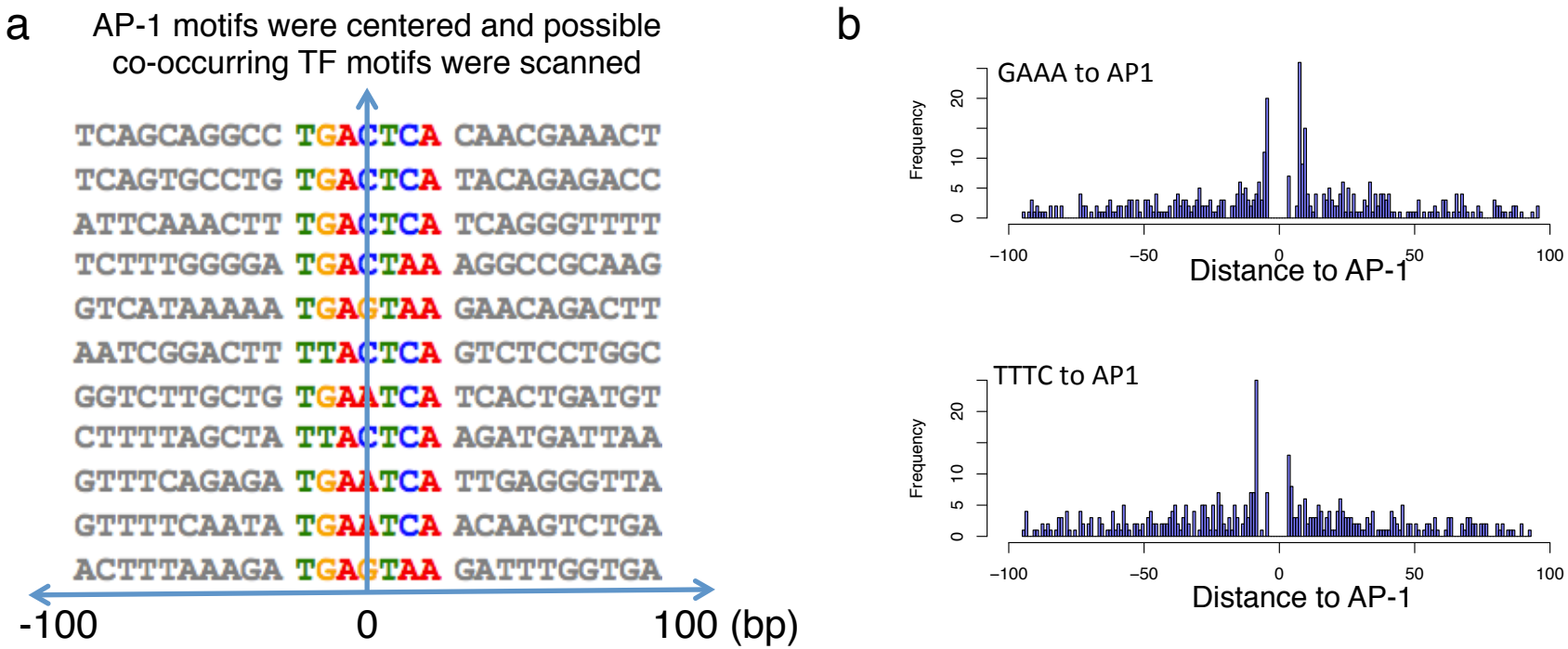
Li et al. Suppl. Fig. 1



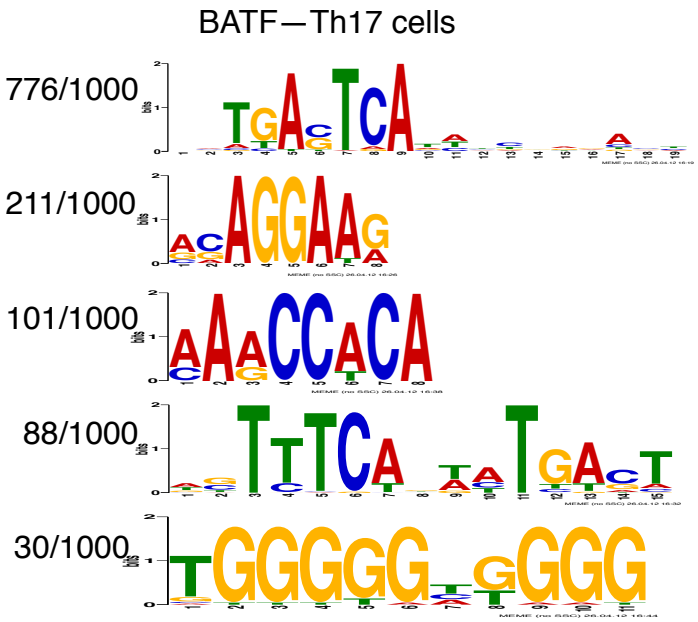
Supplementary Figure 1. PU.1 expression in a range of populations of primary cells. The data were derived from the BioGPS database.



Supplementary Figure 2. IRF8 preferentially binds DNA via classical IRF motifs. **a, b,** IRF8 ChIP-Seq data in pre-activated T cells not stimulated (**a**) or stimulated (**b**) with IL-21. The canonical IRF-family-core motif (5'-GAAA[CG][TA]GAAA[GC]-3') was consistently discovered in each library (734 out of the top 1000 peaks in WT T cells not stimulated with IL-21 and 676 out of the top 1000 peaks in WT T cells stimuilated with IL-21).

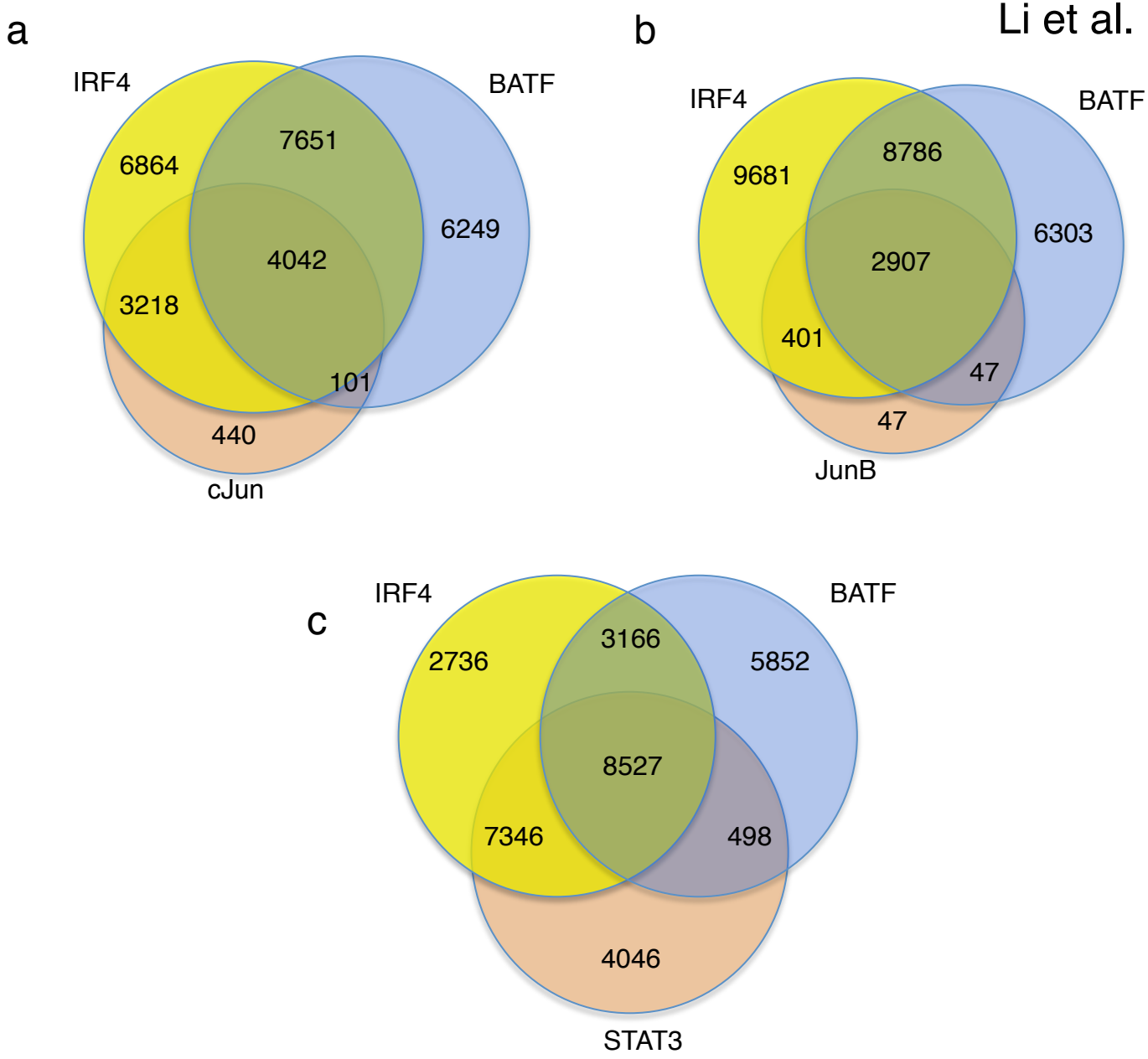


Supplementary Figure 3. Identification of closest IRF4 motifs to AP-1 motifs. a, All AP-1 motifs identified within IRF ChIP-Seq peaks were aligned. **b**, Shown are the analysis for the most proximal GAAA (upper panel) and TTTC (lower panel) motifs that were used to generate the composite figure shown in **Fig. 1g**.

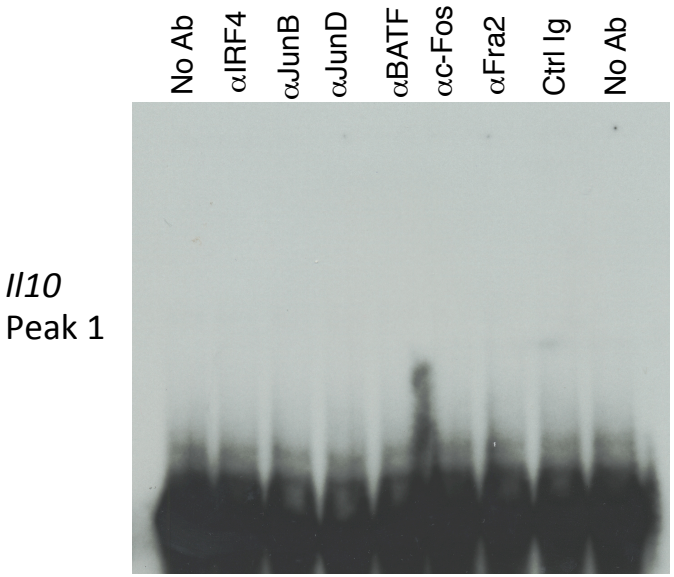


Supplementary Figure 4. Motif analysis for BATF.

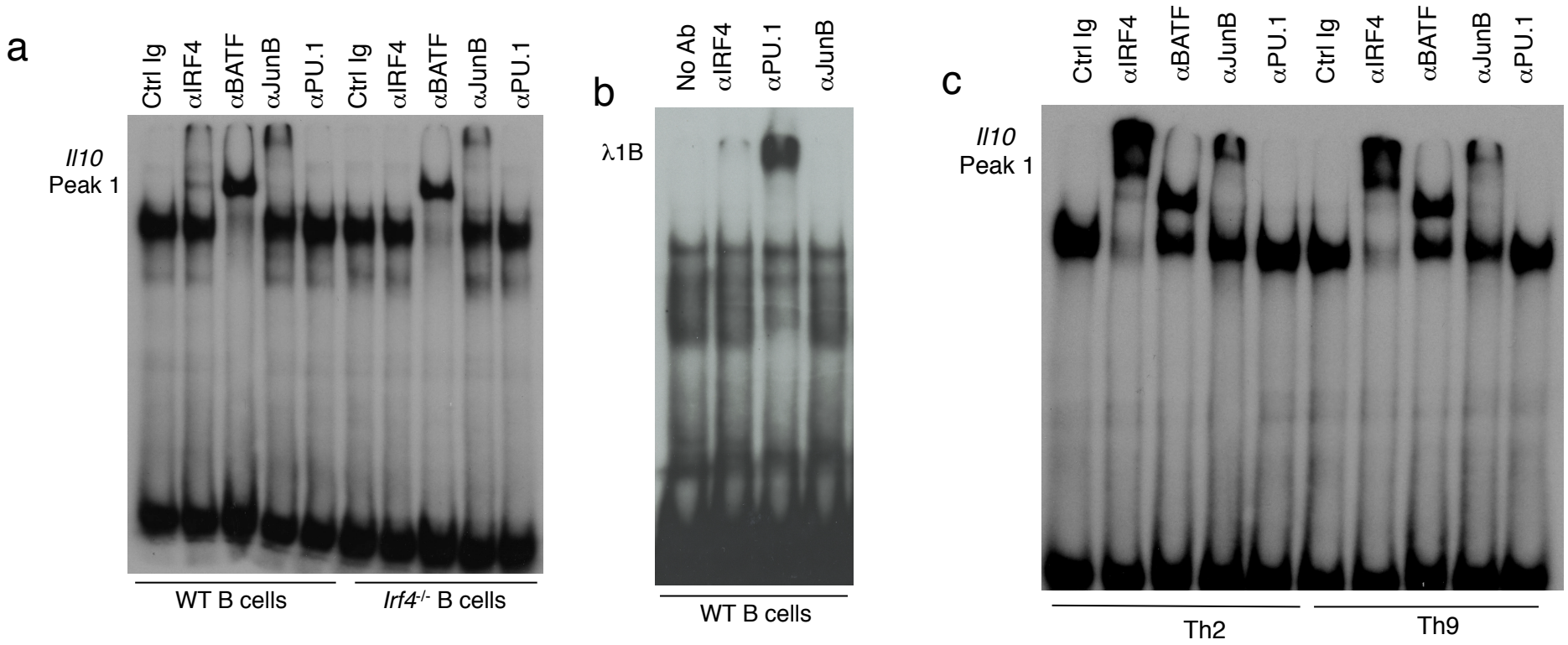
Li et al. Suppl. Figure 5



Supplementary Figure 5. Colocalization of ChIP-Seq peaks for IRF4 and BATF with STAT3 and JUN family proteins. a-c, Shown are Venn diagrams for IRF4 and BATF with cJun (**a**), JunB (**b**), and STAT3 (**c**).

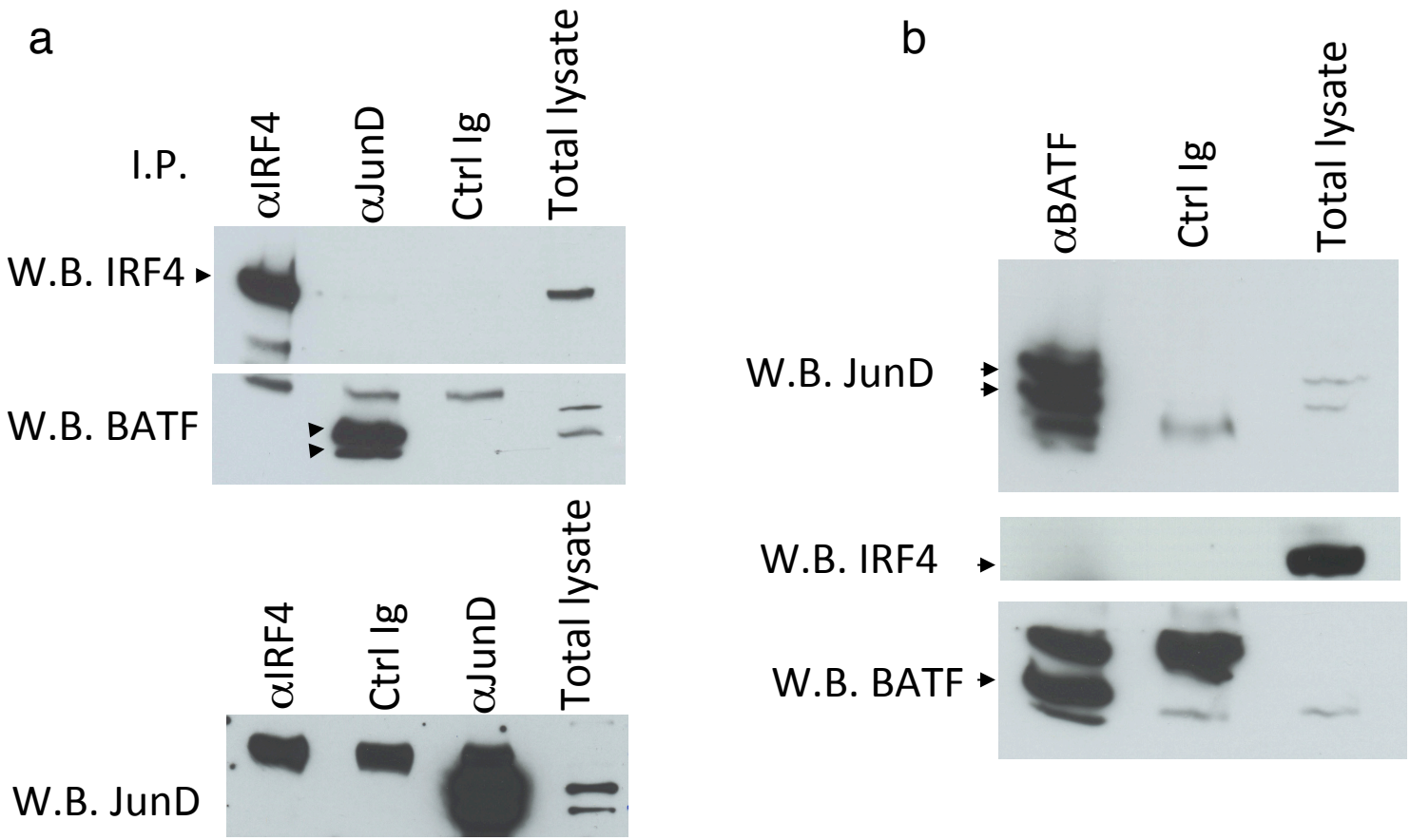


Supplementary Figure 6. Absence of supershifting when nuclear extracts were omitted.



Supplementary Figure 7. EMSA from B, Th2, and Th9 cells. a, EMSA using the *Il10* peak 1 probe and nuclear extracts from WT or *Irf4*$^{-/-}$ B cells; supershifting was performed with the indicated antibodies. **b**, EMSA using a probe from the Ig λ gene (5'-GAAAAAGAGAAATAAAAGGAAGTGAAACCCAAG-3') that binds PU.1. (**c**) EMSA using the *Il10* peak 1 probes and nuclear extracts from Th2 or Th9 cells; supershifting was performed with the indicated antibodies.

Li et al. Suppl. Fig. 8



Supplementary Figure 8. Coprecipitation of BATF and Jun but not of BATF and IRF4 in Th17 cells. Lysates from Th17 cells (T cells subjected to two rounds of Th17 polarization) were prepared and immunoprecipitated with the indicated antibodies followed by western blotting as indicated.

Supplementary Table 1. List of discovered AP-1/IRF4 composite motifs from top 1000 IRF4 peaks in CD4+ T cells

position	strand	shift	pvalue	left_extension	ap1_motif	right_extension	gene	binding_to
chr6:39644055-39644155	+	57	7.60e-08	ATGTTTTATT	TGAGTCAAAATGAGA	GTGACTCATA	Braf	intron
chr7:140180883-140180983	-	53	1.04e-07	GATGGGGAGA	TGAGTCAGACTGAGA	GGCCTGATGT	Olfr527	promoter
chr13:24969714-24969814	-	54	1.45e-07	GGCACGTACC	TGAGTCAAAATGAAA	GGGAGACACG	Gpld1	intron
chr17:46653057-46653157	-	32	1.45e-07	GTTCTGAGTC	TGAGTCAAACTGAGA	CCCCTGTGTA	Trerf1	UTR_5
chr1:89965292-89965392	-	16	1.90e-07	ACAGGATTTT	TGACTCAGAATGAAA	AGAGACAAGC	Ugt1a10	intron
chr6:98958319-98958419	+	27	2.51e-07	GTCATAGCTA	TGACTCATATAGAGA	AATGGGGGTT	Foxp1	intron
chr4:133626281-133626381	+	15	3.23e-07	TCAGTGCCTG	TGACTCATACAGAGA	CCAGGAACAT	Slc30a2	UTR_3
chr6:116055068-116055168	+	80	3.23e-07	AGTCATATTA	TGACTCATAACAGGA	GCAAA	Tmcc1	intron
chr4:135132445-135132545	+	50	3.23e-07	GCTCTTAATG	TGAGTCATTCTGAAA	CTATACTGTC	Srsf10	intron
chr1:21410993-21411093	+	7	5.37e-07	TCACGGC	TGACTCAAAATGGAA	CTGAAACTCC	Kcnq5	intron
chr16:36603983-36604083	-	51	5.37e-07	GTCGTGTGAC	TGAGTCATCTCGAAA	GGAAGGTCTC	Ildr1	promoter
chr2:69892273-69892373	-	83	5.37e-07	CA	TGAGTCATAATCAGA	GCACTAACAG	Myo3b	intron
chr7:75574580-75574680	-	66	5.37e-07	AGAGAACTTT	TGAGTCATACTAGGA	ACTGGTTTAA	Akap13	intron
chr1:146009922-146010022	+	43	5.37e-07	GCTATATTAC	TGAGTCATATTGTGA	GGAAATTATG	Rgs1	intron
chr15:66628239-66628339	-	58	6.89e-07	TGTTTGGATA	TGAGTCAAAACAGGA	TGAAAGCAGA	Sla	intron
chr11:51603847-51603947	+	16	6.89e-07	GCTACTGTTA	TGAGTCATAATGTAA	ATGTCTATGT	Sar1b	promoter
chr17:3402854-3402954	+	63	6.89e-07	TGGGGAGACC	TGACTCATATCCAGA	CTTCGGGGGT	Tiam2	intron
chr11:86440641-86440741	-	15	6.89e-07	TGAGCAGGCG	TGAGTCAGAGTGAAA	CCAGCTTCCC	Vmp1	intron
chr9:88519697-88519797	+	22	8.75e-07	CTTGAGACCC	TGACTCAAAACAAAA	GCAAAGAAAC	Gm2382	promoter
chr17:44138246-44138346	-	46	8.75e-07	ACCTATCACT	TGACTCAGAAAGAAA	GTGAAGAAGA	Runx2	intron
chr4:135842083-135842183	-	63	8.75e-07	CAGCACAGAC	AGAGTCATAATGAGA	GTTTACTTAA	Kdm1a	intron
chr19:18813750-18813850	+	47	8.75e-07	AAAAGATTGA	TGACTCAAAGTGAGA	AACCTGAGCC	Trpm6	promoter
chr16:13758736-13758836	+	23	8.75e-07	TGTGGTGATA	TGAGTCAGAACAGAA	CAAGCCTGGT	Pdxdc1	intron
chr17:34289194-34289294	-	58	8.75e-07	CTCGCCGCAG	TGAGTCAGAGTGGGA	ATCTCTGGTT	Tnxb	intron
chr17:3061517-3061617	-	6	8.75e-07	CAGAGGCATC	TGACTCATTAAGAGA	GCTGTG	Scaf8	promoter
chr3:37505058-37505158	+	17	1.10e-06	GCACAGCAGA	TGAGTCAGAAAGGAA	GAAGTGTGGG	Cetn4	promoter
chr16:36860484-36860584	+	74	1.10e-06	CAGACTGAGC	TGACTCAAAACAGGA	AAAGGAAGTG	Hcls1	intron
chr11:4705086-4705186	+	12	1.10e-06	CTCTAGATAA	TGACTCAAAAAGAAA	AAGAAAGAAA	Nf2	intron
chr11:84068738-84068838	-	54	1.10e-06	GGTTTAGATT	TGAGTCAGAAAGGAA	ATGCAGGCTG	Acaca	intron
chr4:129325627-129325727	+	41	1.37e-06	GGGTATCTTC	TGACTCAGAACAGAA	GTCAGACCAC	Ptp4a2	UTR_5
chr6:128854508-128854608	+	34	1.37e-06	TCACCTCCTC	TGACTCATACCCAAA	GAGAAAGGTC	Clec2i	intron
chr1:165972865-165972965	-	68	1.37e-06	TCTTAACGAC	TTAGTCAGATCGAGA	GCGAACAGAT	Selp	intron
chr16:38277749-38277849	-	52	1.37e-06	GCAGTACTGC	TCAGTCATACTGAAA	AGGGGGAGTT	Popdc2	promoter
chr13:9766688-9766788	+	57	1.68e-06	ACCTAAACCC	TGAGTCATTTCGATA	GCTCTCCTCC	Zmynd11	promoter
chr17:87888152-87888252	+	54	1.68e-06	CTAAGACCTA	TGACTCATACTGTAA	GTCTGTTTTG	Msh6	intron
chr16:16938239-16938339	+	71	1.68e-06	GCGCAATTTT	TGAGTCATTTCCAGA	ACACTGCAGC	Mapk1	intron
chr16:76898174-76898274	-	53	2.08e-06	AAGAAGTGGT	TTAGTCAAAACGAAA	GACAAAACCC	Usp25	intron
chr17:64647617-64647717	+	46	2.08e-06	CTATGTCAGT	TGACTCATTTGGAGA	AATAAATGTG	Man2a1	intron
chr13:13259518-13259618	+	16	2.08e-06	GCTGAGAAAA	TGAGTCATATTGGGC	TTCTTGTTTT	Nid1	intron
chr14:100765739-100765839	+	74	2.08e-06	CTGTTGTATT	TGAGTCAGATTGTAA	TTTGCAGATG	Lmo7	intron
chr5:96412238-96412338	-	3	2.53e-06	GTGAGGAGCA	TGAGTCATTTTAGAA	CTA	Cnot6l	promoter

chr17:32206671-32206771	+	32	2.53e-06	CGCAGAGGGA	TGAGTCAACTTGAAA	CTCCCAGAAC	Cyp4f39	intron
chr9:122026351-122026451	-	15	2.53e-06	ATTCATGCTT	TTAGTCATAAAGAGA	GTCTAAAAGT	Ano10	intron
chr8:97129520-97129620	-	51	2.53e-06	TACTAAGAGT	TGACTCAAAGCAAGA	GATAAACTCA	Nup93	intron
chr1:132838179-132838279	+	70	3.08e-06	TCAGCAGGCC	TGACTCACAACGAAA	CTGCAACCTC	Il10	promoter
chr1:13140741-13140841	-	15	3.08e-06	TCAGACTTGT	TGATTCATATTGAAA	ACAGCAGAAT	Ncoa2	intron
chr10:62565005-62565105	+	46	3.08e-06	ATACAAGCTT	TGAGTCAGAATGCGA	AGTAAACCTT	Mypn	intron
chr13:20118861-20118961	+	24	3.08e-06	TGGAAAGCCA	TGAGTCATTTCTGAA	ACTGTGTTAG	Elmo1	UTR_5
chr19:57878646-57878746	+	18	3.08e-06	CAAAGTCCCA	TTAGTCAGATTGAAA	GTTTGACTCC	Atrnl1	intron
chr2:90291299-90291399	-	35	3.08e-06	AGTAGCAGGC	TTAGTCATAGTGAGA	TATCTGTGGC	Ptprj	intron
chr3:142296431-142296531	+	57	3.08e-06	TTTTAGTGTG	TGAGTCAAACTGTAA	GCAATTTAAC	Pdlim5	intron
chr8:15013515-15013615	+	55	3.71e-06	TGTGTATCTT	AGACTCAAAATGAGA	GAAAGATATG	Kbtbd11	UTR_5
chr7:143522214-143522314	+	56	3.71e-06	CATGCTGAGC	TGAGTCAACCCGGAA	ACCGAACCAC	Osbpl5	intron
chr7:89048318-89048418	-	35	4.44e-06	TTCAGGTTGC	TGATTCAAAACGAAA	TTGTTTCAAA	Tmem135	intron
chr4:129330012-129330112	-	53	4.44e-06	TTTAAAGATA	TGACTCACAATGAAA	ATGAAAGGTG	Ptp4a2	UTR_5
chr9:84572086-84572186	+	21	4.44e-06	TGTGGGAGGG	TGACTCATTCTGATA	AACCAAGTGC	4930554C24R	UTR_5
chr13:36542284-36542384	+	0	4.44e-06		TTAGTCATTTTGAAA	GTATACAGTT	Fars2	intron
chr4:131302956-131303056	+	8	5.32e-06	TATGGATA	TGACTCATAACCTGA	CACCATCAAA	Epb4.1	UTR_5
chr3:60691278-60691378	-	5	5.32e-06	TCCACCTTTG	TGACTCAATCCTAGA	AATGT	Mbnl1	intron
chr19:55803936-55804036	-	28	5.32e-06	CCATGAGCTA	TGAGTCAAAGCTGGA	TCGTTAGCTT	Tcf7l2	intron
chr4:88515421-88515521	+	70	5.32e-06	AAAGAGAATG	TGAGTCAGATAGATA	CTCTGACATA	Gm12603	promoter
chr6:119658491-119658591	+	62	5.32e-06	AGTACAGAGA	TGAGTCATCCCTAAA	CAGTGGGGGT	Erc1	intron
chr15:66534038-66534138	+	51	5.32e-06	TTACTGGGAT	TGACTCATTGAGAAA	GTAGCATTTG	Tg	intron
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chr11:51919977-51920077	+	31	6.35e-06	AGAATGAAAC	TGTGTCATAAAGAGA	GTCTCAGGAC	Cdkl3	UTR_3
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chr6:31425591-31425691	+	44	6.35e-06	AAAGAACCAC	TGACTCATCTCAGAA	TTTAACCACT	Mkln1	intron
chr10:67435162-67435262	-	20	6.35e-06	TCTGCATGAG	TGACTCATTTAAAAA	CCAACCAAGC	Rtkn2	intron
chr1:140106594-140106694	-	69	7.58e-06	TCTGGGAAAA	TGAGTCATTCAGTGA	CAAAGATATG	Atp6v1g3	Downstream_TES
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chr12:52952687-52952787	+	21	8.97e-06	TAGAAAAAAA	TGACTCATAAGTGAA	GCTCTGAGAG	Gpr33	promoter
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chr9:78172829-78172929	-	1	1.06e-05	CGACCCGGAA	TGAGTCACATCTAGA	A	Ddx43	promoter
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chr8:125914007-125914107	+	53	1.46e-05	ATGCTAGGCT	TGAGTCACAATGTGA	ATGCGGAATC	Ankrd11	UTR_5
chr7:106009676-106009776	-	27	1.46e-05	AACAAATGGT	TCAGTCATTTCAGAA	AATGCCATGT	Gm4070	promoter
chr2:115327808-115327908	+	75	1.46e-05	CATGTAATTT	TGACTCAAAACAACA	GTTCTCTTTA	Mir1951	promoter
chr7:35454084-35454184	+	6	1.46e-05	GGCTGG	TGACTCAGAAAGGGC	CTCTCATTTC	Dpy19l3	intron
chr7:125292166-125292266	-	81	1.46e-05	TCAG	TGAGTCAACTTGATA	CTTTCTTTTC	Nsmce1	promoter
chr12:86482247-86482347	+	34	1.46e-05	TTAGACTCGG	TGACTCAAACGGTGA	ACTCGTGGCT	Jdp2	promoter
chr1:39141355-39141455	+	69	1.46e-05	TTCCATTTGG	TGATTCAGAACAGGA	ATGAGAGTTT	Npas2	UTR_5
chr18:14968839-14968939	+	34	1.72e-05	TGAAAGTAAG	AGACTCAAAGTGAAA	GTGCCTAGGG	Taf4b	intron
chr5:139557448-139557548	+	21	1.72e-05	AAAACCACCA	TGAGTAAAACCAAGA	CACTTGTGAA	Adap1	intron
chr5:53834809-53834909	-	27	1.72e-05	CTGAGCCGAA	TGAATCATTTTGAGA	AAAAAAAAAA	Rbpj	promoter
chr6:145080907-145081007	-	30	1.72e-05	TTCAAGTGTC	TGACTCAGAACTCGA	GAGGCCTGGG	Lrmp	UTR_5
chr16:50209270-50209370	+	57	1.72e-05	GTTAGGAGCA	TGAGTAATAATGATA	AAGACAGCGG	Bbx	UTR_5
chr14:17128917-17129017	-	61	1.72e-05	AGGGTGACCT	AGACTCAAATAGAAA	GCAAAGAATG	Ube2e1	promoter
chr5:107889201-107889301	-	19	2.01e-05	CTCACACATC	TGATTCATTTTAAGA	ACCGAGCAGG	Rpap2	intron
chr12:80547355-80547455	+	33	2.01e-05	TTCAGAAACC	TGAGTCAAATCAGCA	GTCTCTAGGA	Rad51l1	intron
chr7:107455637-107455737	+	79	2.01e-05	ACTTTCATAA	TCAGTCATAGCCAAA	GGCCAC	Ppfibp2	intron
chr9:3851636-3851736	+	7	2.01e-05	AGGCCAT	TGAGTCATTCTCTGA	AACACAGTAC	Gucy1a2	intron
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chr5:32289963-32290063	+	74	2.01e-05	GAGGGGGCTG	TGAGTCAGACCTACA	GTCAATGTAG	Bre	intron
chr13:97579858-97579958	-	46	2.01e-05	ACAGATGAAG	TGAGTAAAAACTAGA	AACAAGTAAA	Ankdd1b	promoter
chr11:98321154-98321254	+	39	2.33e-05	TCTGTGCTTA	CCAGTCAAAACGAGA	AAGGTCACAT	Ikzf3	intron
chr2:19446821-19446921	+	16	2.33e-05	TGTGAGGTCA	TGAGTCAAATCAAAG	CTAACAAGCC	4921504E06R	intron
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chr11:72137167-72137267	-	26	2.33e-05	TTAACCAAGA	TGACTCAAACTCTGA	AAGACTGAAG	Fbxo39	Downstream_TES
chr11:66864845-66864945	+	75	2.33e-05	TGTGTCATAC	TGATTCATCCTGAAA	CTCCTTTCAG	2310004I24Rik	UTR_5
chr1:140420615-140420715	-	62	2.33e-05	GACATAAGTT	AGAGTCATTTGGAAA	GGGAAAACCA	Nek7	UTR_5
chr1:134958285-134958385	-	61	2.33e-05	TCATCCCTAG	TGAATCATAGTGAAA	CTGAATCACT	Ppp1r15b	promoter
chr6:146142879-146142979	-	50	2.33e-05	ACAGTCTGTG	TGAGTCAGCTCATGA	CAACTTTATG	Itpr2	intron
chr8:125245565-125245665	-	84	2.33e-05	C	TGACTCAAATTCATA	GTCACCCCAC	Trhr2	intron
chr19:53854021-53854121	-	61	2.33e-05	TAGGCCTCTG	TGACTAATTTCAAGA	TTACCGGGTC	Rbm20	intron
chr1:173521742-173521842	-	13	2.70e-05	AAAACCCTGA	TGAGTCAAAGTTTGA	ATGCGTGCAT	Cd48	intron
chr14:39858802-39858902	-	85	2.70e-05		TGAATCATTCTGAAA	GCCTCTGCTT	Tspan14	UTR_5
chr4:149388833-149388933	-	62	2.70e-05	GAGAAGAGGC	TGACTCAGAATCGTA	CAAAACAGAA	Rere	intron
chr17:28425921-28426021	+	26	2.70e-05	TTCCATCTGG	TGATTCAGATCTGGA	AAGGATGACA	Mapk14	intron
chr1:54224401-54224501	-	39	2.70e-05	GCTGACACAG	TGACTCAAATCAGCA	GCCCTAAGTG	Ccdc150	intron
chr9:48155779-48155879	+	36	2.70e-05	GGTCCAACAC	TCAGTCATAAATGAA	AAAAGTAATC	Fam55d	Downstream_TES

chr5:107995243-107995343	-	46	2.70e-05	CAATCTGATA	TGACTCAACCTTGGA	AACTTACTGC	Evi5	intron
chr1:36270553-36270653	-	56	2.70e-05	TCAGAGTCAC	TGACTCAGAAGGCAA	GGTAAAGGGT	Arid5a	Downstream_TES
chr3:96845306-96845406	+	32	2.70e-05	GGAAATGCAT	TGAGTAAGAAGGAAA	GTATATGTGG	Rnf115	intron
chr9:79843468-79843568	-	40	2.70e-05	CACACTATGG	TGACTCATTCCTGTA	ATCCTGGTAT	Senp6	promoter
chr10:89019852-89019952	+	21	3.12e-05	AAAACCTCCC	TGAGTCATAAACAAC	CATTGCTACT	Slc17a8	intron
chr17:83392304-83392404	+	64	3.12e-05	TGAGGTAGAC	TTTGTCATATTGAAA	CTGAAATACC	Eml4	Downstream_TES
chr2:157139408-157139508	-	16	3.12e-05	AGGCCCTGAA	TTAGTCATCTTAAAA	CTTCCCTTAA	Src	UTR_5
chr2:44167507-44167607	-	18	3.12e-05	ACACCATTTC	TGACACAAAATGAGA	ATAGAGTTCA	Arhgap15	intron
chr16:49901942-49902042	-	18	3.12e-05	GGGACTCAGC	ACACTCATTATGAGA	CAGGCTGTTA	Gm6936	UTR_5
chr8:84762945-84763045	-	48	3.12e-05	TGAACACAGA	TGACTCAAAAATTGA	AGAGAAAACT	Inpp4b	intron
chr4:152981082-152981182	+	68	3.12e-05	TGCCACACTG	TTACTCATAAGTAGA	GTTGTTGTCA	Trp73	UTR_5
chr13:109018096-109018196	-	84	3.12e-05	C	AGATTCATATTGAAA	AACTTTACAT	Zswim6	promoter
chr10:93451561-93451661	-	36	3.12e-05	CTAAGAAGGA	ATAGTCATTTTGAGA	GAAAGGTTTC	Vezt	intron
chr8:83628185-83628285	+	72	3.12e-05	GGGGAGGTGT	CTAGTCATACTGAAA	CTTGGTATGT	Smarca5	intron
chr13:95255307-95255407	-	72	3.12e-05	CATCGCGGTG	TGAGTCATAGCCACA	AACCGTTGAT	Lhfpl2	UTR_5
chr12:42011229-42011329	-	78	3.12e-05	TTATGGA	TCAGTCATCTCTAAA	CTGTGAGTTG	Immp2l	intron
chr3:123559525-123559625	+	51	3.12e-05	AGTTGTCATC	ACAGTCATAAAGAAA	CTCGCAGCAT	Ndst3	intron
chr12:112032277-112032377	-	45	3.12e-05	CAGATGATTA	TGATTCATAGCAGAA	ACAAAATTAG	Mark3	intron
chrX:73885155-73885255	-	18	3.60e-05	TTAATCATCT	TGAGTAATAGCTAAA	AGGTGCAGGT	Tbl1x	UTR_5
chr16:27315191-27315291	+	22	3.60e-05	TGAGGCTGTC	TTTGTCAGAATGAGA	GGGGTAGTTG	Ccdc50	intron
chr9:123447851-123447951	+	30	3.60e-05	AATGGATATG	TTTGTCAGAATGAGA	GGTGTTATGA	Slc6a20b	intron
chr5:29913163-29913263	-	34	3.60e-05	TTAGAAACAC	TTACTCAATCCAAAA	CTTGCACTTA	Ube3c	intron
chr5:103682632-103682732	-	73	3.60e-05	GAGAATCTGG	TTACTCATCTAGAAA	CTCAAAGACT	Ptpn13	UTR_5
chr7:96942447-96942547	+	20	3.60e-05	TCCTAACTGC	TGAGTCATCTCTGTA	GCCCCATAAA	Nars2	Downstream_TES
chr14:19765907-19766007	-	65	3.60e-05	CTGCACGTAT	ACACTCAAAATGAAA	ACTCTGACCA	Vcl	intron
chr15:66624999-66625099	-	70	3.60e-05	AGTCACTAAA	TGAGTAAGTATAAGA	TGTAATCCAG	Sla	intron
chr3:135603236-135603336	-	10	3.60e-05	CCTGCCAAGG	ACAGTCATTTTGAAA	GTGTCTCATG	Nfkb1	intron
chr12:15846837-15846937	-	48	3.60e-05	TCACCTTTTA	ACAGTCATACTAAGA	ATCACCTTGT	Trib2	promoter
chr1:93949792-93949892	+	28	3.60e-05	AGAACTGCTA	TGAGTCAGATCTGGG	GCAGCCTGAG	Hdac4	intron
chr15:39184848-39184948	+	2	4.14e-05	TA	TGAATCATAATGTAA	ATGCCTACAT	Rims2	intron
chr17:6426659-6426759	-	47	4.14e-05	TACGCAAATT	TGAGTCACTCCTAAA	CTCGAAACGA	Dynlt1b	promoter
chr7:46767606-46767706	-	77	4.14e-05	GAAGGATC	TTACTCAAAACATGA	GTTGATGATG	Tsg101	intron
chr2:128119721-128119821	+	20	4.14e-05	GTTAGGTTGC	TGACTCATTCTTAAC	CCGGGAAGCC	Gm14005	UTR_3
chr3:136680308-136680408	+	58	4.14e-05	ATGCAATCAA	CGACTCAAACCCAGA	AACCAGTGTG	Ppp3ca	intron
chr10:90458924-90459024	-	67	4.14e-05	CACTCCCTGG	TGACTAATAACATGA	TGCATGAATT	Apaf1	intron
chr3:36112632-36112732	+	2	4.14e-05	TT	CCAGTCATTTTGAGA	AAGACAACTT	Dcun1d1	exon
chr13:49569030-49569130	+	28	4.14e-05	GCTACTGTTA	TGAATCATAATGTAA	AAATCTGTGG	Cenpp	intron
chr10:53715273-53715373	+	60	4.14e-05	TGGCCACAGG	TGACTAAAATCCAGA	AAAACAAAAG	Man1a	intron
chr14:59839873-59839973	-	29	4.14e-05	ACCTTTCCTG	TGAGTCACTTAGGAA	GGGAGTTTCA	Mipep	intron
chr4:101891642-101891742	-	40	4.14e-05	TTAGAATAAG	TGACTCAGCCAGTGA	CTCACCACAC	Pde4b	intron
chr13:103993991-103994091	+	3	4.75e-05	GTC	ACACTCATTTTGAAA	ATGCCAGTTA	Mast4	intron
chr3:129932997-129933097	-	59	4.75e-05	GCCTGGAGTC	TGAGTGATTCAGAGA	GTTTCTATGA	Ccdc109b	intron
chr15:85217867-85217967	+	40	4.75e-05	GCCCATGGAA	TGAGTAAGAATGGTA	TCTCTGATTG	Atxn10	intron
chr13:60905489-60905589	+	44	4.75e-05	AGCTGAACAC	TTAGTCAAACAGTGA	ACTGCATGTT	Ctla2b	UTR_3

chr9:88754662-88754762	-	22	4.75e-05	CTTCCTCTTC	TGATTCAGTTTAAAA	GTCAAAAATG	Bcl2a1a	promoter
chr9:88529800-88529900	+	50	4.75e-05	CTTCCTCTTC	TGATTCAGTTTAAAA	GTCAAAAATG	Bcl2a1d	promoter
chr9:70436088-70436188	-	15	4.75e-05	ATTTGCATTA	TGATTCATAACAGTA	GCAAAATTAC	Fam63b	intron
chr10:84325666-84325766	-	45	4.75e-05	ATGAATAGCG	TGAGTCATAACACAC	AAGAACAGTC	Rfx4	intron
chr9:88996971-88997071	-	22	4.75e-05	CTTCCTCTTC	TGATTCAGTTTAAAA	GTCAAAAATG	Bcl2a1b	promoter
chr8:82170047-82170147	+	60	4.75e-05	AAGTCAGTTG	TTAGTCATCTTTAAA	TAGCACTCAT	Mmaa	intron
chr8:72849324-72849424	-	38	4.75e-05	GCTGGGATGC	TGAGTGATACTGATA	GCAGTGACAT	Gatad2a	intron
chr2:128092885-128092985	+	73	5.43e-05	AGCTACACGC	TGTGTCATCTCAGGA	AGGTTACCTC	Gm14005	UTR_3
chr11:93915084-93915184	-	27	5.43e-05	TGTACACATC	TGAGTCATTACTGAG	AAAATGAGGC	Spag9	exon
chr1:55355411-55355511	-	8	5.43e-05	GCCTCTCTGC	TGAGTCATAACTTGG	TCATGAGT	Plcl1	intron
chr11:54031474-54031574	-	50	5.43e-05	AAGAAATCAT	ACAGTCATTTTGGAA	GATAGTTTGG	4933405E24R	UTR_3
chr1:188936017-188936117	+	36	5.43e-05	TTTAATACTG	TGTCTCAGAGCAAAA	ATGTGTGGTT	Gpatch2	intron
chr6:48340192-48340292	-	56	5.43e-05	CAGGCTGGTT	TTACTCATCAGGGGA	AACTAAAATG	Krba1	intron
chr14:26211109-26211209	-	83	5.43e-05	AG	TTAGTCATAAAGAGG	CTACTCAAAA	Arhgef3	intron
chr11:21002782-21002882	+	37	5.43e-05	CAAAGTACCC	TGAGTCATAATGGTT	AAACTCTGAA	Peli1	UTR_5
chr14:8933236-8933336	+	48	5.43e-05	GGGTAAAAGC	ATACTCATAAAGGGA	AATGTGAACC	Fhit	intron
chr1:89266466-89266566	-	33	5.43e-05	CCAAAATAAA	CGACTCAACTTGAAA	GTTCTTTCTA	Gigyf2	intron
chr14:118100920-118101020	-	39	5.43e-05	GGAAGTGGGA	TGTCTCATACATAGA	AAAGGAAAGC	Dnajc3	intron
chr16:58441128-58441228	+	77	5.43e-05	TCAAACTGTA	TCTGTCATAACAGGA	TCTTTATA	St3gal6	UTR_5
chr9:63536508-63536608	-	41	5.43e-05	GAAATGACAG	TTATTCATTCTGAGA	GTTTCAGAAT	Smad3	intron
chr8:117860692-117860792	+	10	5.43e-05	GCCTTTTTGA	TGAGTAAAATTGAGC	CTTTTTTTTT	Wwox	intron
chr16:34585449-34585549	-	22	6.20e-05	AACTCTAGGG	ACAGTCATACCTGGA	AAGGCCACAA	Ropn1	UTR_5
chr16:45061457-45061557	-	31	6.20e-05	TCAAGAGTGA	TGACTCAGATGACGA	CACTTTATAA	Slc35a5	exon
chr7:115286010-115286110	-	17	6.20e-05	TCACCAAATC	TTACTCATCTTTAAA	GTTGAAAGTG	Sox6	intron
chr1:97420721-97420821	-	30	6.20e-05	CAACATGAAC	TTACTCATAGAGTGA	CTTACTGACT	St8sia4	UTR_3
chr6:108244896-108244996	+	8	6.20e-05	GTTCCAGT	TTACTCATTTAGTGA	GTGGCAGTTA	Itpr1	intron
chr8:97522813-97522913	-	54	6.20e-05	TCAAGTGCTG	TGAGTGATAAGAAGA	CAGCTTCAGC	Rspry1	intron
chr6:108304487-108304587	+	20	7.05e-05	TGGACGGCTT	TGACTCAGAGCTGAC	CAGATCATTA	Itpr1	intron
chr12:32787370-32787470	-	57	7.05e-05	TCCAACTAAA	TGACTCATTGCTGGC	TAAAATGGTC	Pik3cg	intron
chr3:126652831-126652931	-	12	7.05e-05	CAGGAAACTC	TGACTGAAAACCAGA	CAGGTTCCTG	Camk2d	intron
chr3:85032424-85032524	-	62	7.05e-05	GTTACAACAT	ACACTCATACCAGAA	CTGATACATA	Fbxw7	intron
chr12:80355920-80356020	+	28	7.05e-05	TACTTGTCAG	TGAATCAGACCTGGA	TACATTCTGT	Rad51l1	intron
chr4:102596612-102596712	+	72	7.05e-05	TGAGAAACAA	TGAGTCAAGTCAAAA	GCTCTGGGGG	Wdr78	intron
chr19:5878095-5878195	-	44	8.02e-05	CCACCTATGC	CTAGTCAGAATAAGA	ATAACCCAAA	Frmd8	promoter
chr16:24442717-24442817	-	40	8.02e-05	GTTTCGCATT	TCACTCAACTCAGAA	CTCCACGTTT	Lpp	UTR_5
chr3:38169567-38169667	+	9	8.02e-05	CTAGGCAAA	TGACTAAATCAGAAA	ATGACAGACT	LOC626410	UTR_5
chr2:18581906-18582006	-	45	8.02e-05	CTATAGGAAA	GTAGTCATTTCGAAA	GCAAACATCC	Commd3	promoter
chr1:140790141-140790241	-	66	8.02e-05	ACCCACTTGA	TGTGTCATTTGAAGA	GTTGGGGGGG	Dennd1b	UTR_5
chr7:104188647-104188747	+	56	8.02e-05	TCTACAGTTT	TGAATCATAATATGA	ATGTATGACA	Trim12a	UTR_5
chr15:76950159-76950259	-	85	8.02e-05		GTACTCATAACAAGA	ATGTTTTGTA	Rbfox2	intron
chr2:6237577-6237677	-	38	8.02e-05	AGTGTTTTGT	TGACTCAAAAAGTCA	GTTCCAATAT	A230108P19R	UTR_5
chr9:50674716-50674816	-	64	8.02e-05	GACAGCTATA	TGACTCAGCTTCTGA	GGCCCAGTTG	Sik2	intron
chr5:58262381-58262481	+	19	8.02e-05	GAAACTCTCT	TGAGTAATAATACGA	CCAGATGCAT	Pcdh7	intron
chr11:100824355-100824455	+	53	8.02e-05	GAAGGAAGTG	ACAGTCATTGTGAAA	TACTTGGCAG	Atp6v0a1	promoter

chr17:3036136-3036236	+	14	9.11e-05	CATCCCCACA	TGAGTGAGAGAGAAA	GAAACTCTAC	Pisd-ps2	UTR_3
chr3:37140116-37140216	-	70	9.11e-05	AGAACTGAAA	TGACTCAGCTTAACA	ACTTAAAACT	4932438A13R	intron
chr6:142780445-142780545	-	24	9.11e-05	ACCTGCCTTT	TGAGTCATACTCTCA	AGATGAGTTA	St8sia1	UTR_3
chr10:26048314-26048414	-	10	9.11e-05	GAAAGACTGT	CTAGTCAAAGTGAGA	TGAGTCGATC	L3mbtl3	UTR_5
chr13:52998371-52998471	+	9	9.11e-05	AAAACCATT	TTACTAAGAACAAGA	GATGACACAT	Nfil3	promoter
chr11:43017968-43018068	-	22	9.11e-05	CAGAGTATAC	TGTTTCATTTTGAGA	AGTGATACAG	Atp10b	intron
chr7:99708034-99708134	+	48	1.03e-04	AACATAGCCT	ACAGTCATCTCAAGA	AAGTCTCACT	Neu3	promoter
chr5:103759657-103759757	+	56	1.03e-04	TGTCTTTTAG	TGACTAAAAAAGATA	CTGAGAGCTG	Ptpn13	intron
chr12:100027333-100027433	+	59	1.03e-04	AAGGAGAAAA	TGACTAAGAGTCAGA	GAATAGCTAT	1700064M15R	UTR_3
chr7:46867115-46867215	+	21	1.03e-04	TCTAGAGAGC	TGTGTCAAATGAGGA	AGTCATCTAA	Spty2d1	intron
chr1:88225566-88225666	+	71	1.03e-04	TGAGTGTAGA	CCAGTCATTTCAAAA	CTGGAAGATA	Nmur1	promoter
chr7:92009686-92009786	-	17	1.03e-04	TGGAAACTTC	CGAGTCAGAAAGCGA	TGCCTGCTTC	Dlg2	intron
chr6:43350077-43350177	+	44	1.16e-04	CACAGAGGAG	TCACTAAAAACAAAA	CTGGAAGTCA	Tpk1	intron
chr2:132380147-132380247	+	69	1.16e-04	GCTTGTTGAG	TGAGTAATCGAGAAA	CTATATTTGT	1110034G24R	promoter
chr4:97353117-97353217	-	61	1.16e-04	AGCGGAAATA	TGACTAATACAGAAC	TTAACACACA	Nfia	intron
chr1:129181855-129181955	-	56	1.16e-04	CATCAAAAGC	AGAGTAAAAACAAAA	GCTAGAACTC	Mgat5	intron
chr9:79592112-79592212	+	36	1.16e-04	CATTTTTCAT	CCAGTCATTTAGAAA	CCAAAGTAAG	4930429F24R	Downstream_TES
chr16:4418819-4418919	+	28	1.16e-04	CCTGACTTGC	GCACTCATTTTGAAA	GATGAGTATC	Srl	intron
chr3:75996407-75996507	-	64	1.16e-04	ATGCACAGAC	TTAATCATTCTGAGA	AATGCTTTCA	Golim4	intron
chr8:108518606-108518706	-	68	1.31e-04	AAGAAGTTAC	TTATTCAAAACCAGA	ACGAAACACA	Ctcf	promoter
chr6:99022733-99022833	+	37	1.31e-04	CAGGGTTGAG	CGAGTCATCTGAAGA	CATGAAACTG	Foxp1	intron
chr3:142498696-142498796	-	46	1.31e-04	ATTTGAAGTC	TGTTTCAGTATGAGA	AGTTTGCCGG	Gbp3	UTR_5
chr5:108211421-108211521	+	58	1.31e-04	GGCCTGGCAA	GGATTCATAGTGAGA	TCTTGTCTAA	Fam69a	intron
chr4:32916258-32916358	+	8	1.31e-04	AGCATGAT	ACACTCAAACCCAGA	GAGAGAAAGC	Bach2	Downstream_TES
chr11:106918644-106918744	+	30	1.31e-04	AGAAATGAAA	TTACTCAAACCTGTA	GTAATTGCAT	Bptf	intron
chr10:107575054-107575154	+	34	1.31e-04	CACGTTGTCA	TGTGTCATATAGGCA	TTTCTGAAAT	Ppp1r12a	intron
chr9:88178167-88178267	-	14	1.31e-04	CGGTTGGTGG	TGAGTCACTGTGAGC	TGTTTCATAT	Snx14	intron
chr8:131306620-131306720	+	74	1.48e-04	GTCATAAAAA	TGAGTAAGAACAGAC	TTTCATTTTC	Nrp1	intron
chr5:121489956-121490056	+	19	1.48e-04	CAGCTGGAGA	TGAGTAAGAACAGAC	TCCAGGGAAG	Gm15800	intron
chr12:87031679-87031779	+	23	1.48e-04	CAGGTTGTGC	TGAGTCACTCCAGTA	CTGAAGTGAG	1700019E19R	intron
chr7:117926778-117926878	+	19	1.48e-04	GAATTGAAAA	TCACTAAGAACCAGA	AAGGACACAT	Arl6ip1	promoter
chr5:96463367-96463467	-	83	1.48e-04	AA	TGAGTGAAAACATAA	AATATGGCAT	Mrpl1	intron
chr6:129542925-129543025	+	13	1.48e-04	TTTAAGACAC	TTAGTGATTCTGAAA	GTCTGGCCTG	Klre1	promoter
chr19:16322472-16322572	-	84	1.48e-04	C	TGACTGAATCAGAAA	CCAACACCTC	Gnaq	intron
chr19:4304347-4304447	-	85	1.48e-04		TTTCTCAAAACAGGA	ACTAGACTGA	Adrbk1	UTR_5
chrX:164541035-164541135	+	85	1.48e-04		CAAAACATCA	TTACTGATTATGA	Arhgap6	intron
chr19:47560621-47560721	-	44	1.48e-04	ATAACGAAAT	CCAGTCATCTCAAGA	AACCCTTGAG	Obfc1	intron
chr9:108013004-108013104	-	26	1.66e-04	AGCCTTTCAC	GGTCTCAGACCGAAA	CTCTGAACCT	Bsn	intron
chr4:97351266-97351366	-	20	1.66e-04	CCCAAACTGA	ACAGTCAGAAAGTGA	CATGGCTGGG	Nfia	intron
chr14:51022247-51022347	-	41	1.66e-04	CAGTTTCAGT	TGAGTCATATGGTTC	TCTAGATTTT	Hnrnpc	UTR_5
chr6:8686583-8686683	-	47	1.66e-04	TTCTAATTGA	TGATTCATGTTGAAA	CCAGCAAAAC	Ica1	intron
chr2:50146916-50147016	+	4	1.66e-04	TCGC	CCAGTCATAAGAAAA	GTGTAAGTTC	Gm13483	UTR_5
chr2:11560464-11560564	+	18	1.66e-04	ACACAAAAAA	GGACTCATAAGTGAA	GCCTGATCCT	Il2ra	promoter
chr16:22479011-22479111	+	73	1.66e-04	CTTTCAGTTT	ACAGTCATTATTGAA	CCTGACTATG	Dgkg	intron

chr5:20357075-20357175	+	50	1.66e-04	GGAAGCCAGT	TCAGTCATTTAAGTA	CTTGCCTTGA	Phtf2	intron
chr19:30990191-30990291	-	43	1.86e-04	AATTCACAAC	TTTCTCATTGTGAAA	CTGAGAGCAA	Prkg1	intron
chr17:16825965-16826065	+	27	1.86e-04	GTGGGATCTG	CCAGTCATAAGAGGA	GGGTGTTTCT	Zfp97	UTR_5
chr1:132850247-132850347	-	31	1.86e-04	CAAAAGTGGA	GCAGTCATTTAGAAA	CTGCCAGAGA	Il10	intron
chr18:50191460-50191560	-	44	1.86e-04	TGGAAAATGG	TTAGTCATATCTATC	CTAAACACTT	Tnfaip8	intron
chr9:44162781-44162881	-	67	1.86e-04	AGTGAAACCA	TTAATCAATTTGAGA	AACTTACAAC	Ccdc84	intron
chr13:48514417-48514517	-	70	1.86e-04	AAAGCCACTA	CGAGTCATTGAGATA	GCAAATTAGT	Zfp169	intron
chr13:45935636-45935736	+	58	1.86e-04	ACATGGGAAA	TGACTCACCGCTAAA	GAGATGGAGG	Atxn1	UTR_5
chr6:42320507-42320607	-	50	1.86e-04	TGTGTGTTTC	TTAGTCATTTGGAGG	AAGAAAGGGA	Tas2r143	promoter
chr16:55832168-55832268	-	36	1.86e-04	CCCCTGGAGA	GTAGTCAAAGTGAAA	CTAAAACTTC	Cep97	intron
chr1:60843941-60844041	-	43	1.86e-04	TTTCTAAAGG	TTACTCAGTTGTGGA	GTAGCTAAAT	Ctla4	promoter
chr12:77869257-77869357	-	74	1.86e-04	CAAAGGAAAT	TGACTCATTCTTGAT	TTGAATTGCA	Max	intron
chr18:12304871-12304971	-	26	2.08e-04	TAAAAGCCTT	TGAGTCACACAGTTA	TAATCAAGCC	3110002H16Ri	promoter
chr18:68352372-68352472	+	70	2.08e-04	TGAAAACTGC	ATAGTAAAATCGAGA	GTTCTGGTTT	D18Ertd653e	intron
chr14:120801937-120802037	-	77	2.08e-04	GTTGGGCT	ACAGTCATAACACAA	CTAACTTGTA	Dock9	intron
chr8:114453189-114453289	-	34	2.08e-04	AGCATGGTTT	CCACTCATAGTGTGA	CTTGTGTGAG	Znrf1	intron
chr9:122937044-122937144	-	41	2.33e-04	CAGTCTACCC	TGAGTCAACTCCTTA	GTCTATTCTC	Zdhhc3	intron
chr3:8828922-8829022	+	56	2.33e-04	GAGCCTTTTC	ACAGTAAGAATGAAA	GATGCTTCTG	Mrps28	intron
chr4:128562397-128562497	-	35	2.33e-04	ACCACATCTC	CGAGTAATTTAGAAA	CTCAGTGAGG	Rnf19b	intron
chr1:182228930-182229030	+	7	2.33e-04	GAATTTA	CCAGTAATATTGAAA	CCAAGATGGC	Itpkb	intron
chr3:104120500-104120600	+	80	2.33e-04	TCAGTTCTGT	TGGCTCAATCTGAGA	TGATT	Phtf1	intron
chr10:53310129-53310229	-	78	2.33e-04	ATGCCTC	TGACTCAGAACAGCG	TGTGAAGATG	Mcm9	intron
chr10:117575721-117575821	-	51	2.33e-04	TATTGGACAT	ACAGTCATTCATAGA	GCAAGCTTGC	Mdm1	Downstream_TES
chr5:110169861-110169961	-	8	2.33e-04	ATCACAGAGA	TGAGTCAGTTATTTA	AGACTATT	LOC10064216	promoter
chr5:110240933-110241033	-	8	2.33e-04	ATCACAGAGA	TGAGTCAGTTATTTA	AGACTATT	Zfp932	intron
chr11:53500423-53500523	+	79	2.33e-04	GAGAAAGAAA	TGACTCAACATAAAT	ACGTCT	Rad50	intron
chr12:81710081-81710181	-	41	2.59e-04	ATATGTAGTT	ACAGTAAAACCGAAA	CAAAACAGGA	4933426M11R	UTR_5
chr9:94501329-94501429	+	52	2.59e-04	AGCTACTATG	TGACTAAGACTTGTA	AGAATGTTAA	Slc9a9	intron
chr7:114147789-114147889	-	70	2.59e-04	AGTACACAGA	AGTTTCATAATGAAA	CTTTAAACCA	4933406I18Rik	UTR_3
chr6:39111544-39111644	-	62	2.59e-04	TCTTTCAAGC	ACACTCATTTAAGGA	CGCAAATTCT	Jhdm1d	intron
chr9:59158718-59158818	-	84	2.59e-04	C	TGACACAGAATATGA	GTTTACAAAA	Bbs4	promoter
chr18:39618207-39618307	+	7	2.59e-04	TTGGGGG	ATACTCAATTCTAAA	TAAAACTCAT	Nr3c1	promoter
chr1:156963610-156963710	-	38	2.59e-04	CATATCACAC	CTAGTCAGATAAGGA	GATTGGTTAG	Stx6	intron
chr15:8367344-8367444	-	55	2.59e-04	AAAAAGAATG	ATAGTCATAGCAATA	GTGTTAATTT	Nipbl	UTR_5
chr11:34406464-34406564	+	11	2.59e-04	GTTAATACTA	TGAATCATCATGACA	TTCAGTTACG	Dock2	intron
chr17:84343531-84343631	-	49	2.89e-04	CATATCACTT	ACAGTCATTTTGAGG	TTTTAAAGAT	Thada	intron
chr2:34861196-34861296	+	78	2.89e-04	TTTTATGTCC	TCTCTCAATCCAAAA	AAGGCAT	Hc	exon
chr5:8430690-8430790	-	12	2.89e-04	ATACCTTACA	TGACACATAATGAGT	CTAACATGGT	Dbf4	promoter
chr5:105594433-105594533	+	46	2.89e-04	CCTATTTTGC	TGACACAAAATGCAA	CTGAGTTCCT	Gbp11	promoter
chr3:32629868-32629968	+	57	2.89e-04	TAACCACAAA	ATACTCATTTCATGA	CCTACCTGCT	Pik3ca	intron
chr11:54035728-54035828	+	80	2.89e-04	GATTGGAGGA	TGACACAAAATGCAA	AAAGA	4933405E24Ri	UTR_3
chr12:53704547-53704647	-	42	2.89e-04	TTGTTCCCAC	TTAGTCATTTACAGC	AGCTACAAAA	Akap6	UTR_5
chr15:67113080-67113180	-	41	2.89e-04	TTCAGTTATG	TGAGTAAAACTGTAC	TTTTTCAAGA	1700012I11Rik	UTR_5
chr1:60716437-60716537	-	69	2.89e-04	ACCCGCCTGT	TGGTTCATACCGAGA	GCGAAAGGCT	Cd28	UTR_3

chr6:122493315-122493415	+	73	2.89e-04	TCTGGGTTCC	TGAGTAAGAGCTGTA	GTTGACTTCG	Mfap5	intron
chr7:114023161-114023261	-	39	2.89e-04	TAGTATAGCA	TGACTAAAAAATTGA	CAGAGAAATA	Copb1	intron
chr7:23790869-23790969	-	63	3.21e-04	GAGCCACTCA	CGACTCAGCGTCAGA	ACGAAACTGT	Zfp180	UTR_5
chr11:74970496-74970596	-	53	3.21e-04	CACTAGGGTG	ACAGTAAAACTGAAA	GGGCATGCCT	Smg6	intron
chr17:46978793-46978893	-	31	3.21e-04	GTGGTCTGGC	TGATTCATCCAGGGC	TCCACAGATA	Ccnd3	UTR_5
chr14:60125160-60125260	+	13	3.21e-04	TTGCTGCCTG	CCAGTCAATATGTAA	CAGGAAATGT	Sacs	intron
chr13:113579631-113579731	-	25	3.21e-04	TGTGGTCGCC	TGAGTCATTTTCGTG	ATTTTACTCT	Il6st	promoter
chr9:40199492-40199592	+	19	3.21e-04	TAGAGATGCC	AGAGTCAGTTAGGGG	CTGACAAAGA	Gramd1b	intron
chr15:5186126-5186226	-	27	3.21e-04	AACTGGAAGT	GGACTCATTAAATGA	TCGCATGAGT	Ptger4	intron
chr4:146877793-146877893	-	32	3.21e-04	AGCGCTGAGC	CTAGTCATTACAATA	GCATTACAAT	Clcn6	intron
chr1:167032511-167032611	+	17	3.21e-04	TGGTTAAGAG	ACACTCAGATCAGTA	GTGTTCATAA	Sft2d2	promoter
chr16:44130121-44130221	+	19	3.21e-04	GGTTATCAGT	GCAGTAATACTGAGA	AGCCCCTCCC	Gm608	intron
chr9:38484741-38484841	-	43	3.21e-04	CTTTCTCTCT	GGTCTCAAAACAAAA	GTCACAACTG	Vwa5a	intron
chr9:119566195-119566295	+	11	3.21e-04	TTGGCTTCTG	TTACTCAAATTATGC	ATCTGTGACT	Scn10a	UTR_5
chr9:14505150-14505250	+	66	3.21e-04	TTAAGTTGGT	ACAGTCAATAGAAGA	ATGTGTTCTG	Fut4	promoter
chr7:35451188-35451288	-	58	3.21e-04	GCAGAGCATT	TGACTCATCTGTGCA	TGCCCGGGTT	Dpy19l3	intron
chr7:127079196-127079296	+	26	3.56e-04	ATCCTGGTGG	TGACACATTTTGCAA	ATCATGTTGC	Itgal	promoter
chr5:115522997-115523097	-	46	3.56e-04	AGGATAGAAA	TCAGTCATCATTAAG	TTCTACAAAG	Rnf10	intron
chr1:129124528-129124628	+	17	3.56e-04	TTTGTGGTTA	CTAGTCAGTTCTGAA	GTGAGTACTT	Mgat5	UTR_5
chr2:68199220-68199320	+	48	3.56e-04	TTACCTCCAC	TTAGTAATTTCATGA	CCAGCCACAG	Stk39	exon
chr18:89567498-89567598	+	62	3.56e-04	GGAGCAGAAA	TGACTCAGAGAATCA	CTAAGGCTCA	Dok6	intron
chr1:129061007-129061107	+	7	3.56e-04	TCTGTTC	TTAGTCATATCCTGG	TGTCTGATCA	Mgat5	UTR_5
chr16:24340384-24340484	-	78	3.56e-04	CATCGTT	TGAGTCACTTACTGA	CAGTGGGTTC	Lpp	UTR_5
chr13:20379911-20380011	+	32	3.56e-04	ACCTTGTGAT	GTACTCATTTCTGGA	AATGCCTTTA	Elmo1	intron
chr16:50218218-50218318	-	22	3.56e-04	GAAACTCTCT	TTACTGATTACCAGA	TTGTCAATGT	Bbx	UTR_5
chr15:74826322-74826422	+	82	3.56e-04	TCTGAGCAGC	TTAGTCACCACCAAA	TCT	Ly6a	promoter
chr7:117220068-117220168	+	12	3.56e-04	AGAAATATAA	TGATTCATTTCGTAG	GACGTGTGTT	Xylt1	intron
chr17:30939613-30939713	-	25	3.56e-04	TTGCTTGTGA	TGTCTCATTATGCTA	GGAAGTGGGG	Ubash3a	intron
chr14:102235978-102236078	-	83	3.94e-04	GT	GGTCTCATTACAGGA	CGACAGTATG	Mycbp2	promoter
chr3:20293347-20293447	-	72	3.94e-04	AGACATGCTT	TTACTCAGCATGTGC	CTTGTCTAAA	Hltf	intron
chr10:23982286-23982386	+	72	3.94e-04	AAGGGTTAGA	TGACTCATTTTCTGT	ACACATACTT	Moxd1	intron
chr1:60853340-60853440	-	69	3.94e-04	GATGGAAAAT	GTACTCAACTTGAAA	CTGAAGCTTC	Ctla4	promoter
chr6:99306534-99306634	+	59	3.94e-04	CTCACATGCA	TGACACAGATGCAGA	AAGACATCAC	Foxp1	UTR_5
chr18:70701496-70701596	-	28	3.94e-04	GTGAATGATA	TTAGTCATTTTCAGT	TTGCTCTGAC	Mbd2	intron
chr6:48677480-48677580	-	38	4.36e-04	GTGCAGTGTG	ACTGTCATAACCAAA	CTCAGCAAAA	Gimap1	Downstream_TES
chr11:46297046-46297146	-	18	4.36e-04	GTGCCCAGGC	TGTGTAATTTCTGAA	AACCTGGTGG	Havcr2	promoter
chr1:82748583-82748683	-	77	4.36e-04	GCACAGAC	CGACTAAGAAAAAAA	GACTAGGCAG	Agfg1	intron
chr14:102146270-102146370	-	59	4.36e-04	ATGGGCTCTA	TGTGTCAACAGTGGA	GAACAACTCA	Mycbp2	intron
chr1:162081485-162081585	+	21	4.82e-04	TGGTGATCTT	TGTTTCAGAAACAGA	CTCACTTGTG	Rabgap1l	intron
chr12:17399197-17399297	+	56	4.82e-04	AAGGCGCTCA	TGACTCAGTACTCAG	CCCGCCTAGC	Nol10	intron
chr19:32249003-32249103	+	36	4.82e-04	TTTCCATTGC	CCTGTCATTCTGAAA	ATAATGTTCT	Sgms1	UTR_5
chr7:67187218-67187318	-	85	4.82e-04		ATACTCATAGCAAAC	TCCACATGTG	Mef2a	intron
chr9:69786870-69786970	+	33	5.31e-04	TCATGTTCTG	TTACTAAAATGAGGA	AACTCAAGAC	Bnip2	promoter
chr18:39263576-39263676	-	60	5.31e-04	TTAAGTAGTA	ATACTCATATATATA	ACTGCCGCTT	Arhgap26	intron

chr3:19439140-19439240	-	73	5.31e-04	GAGTCATTTA	TTATTCATAGTGAAG	CTTTTACTAC	Pde7a	intron
chr13:63284094-63284194	-	79	5.31e-04	GTGGGT	ACAATCATTTTGAAA	CAGTTTCGAA	2010111I01Rik	intron
chr7:84621043-84621143	+	3	5.31e-04	ACA	TTACTAAGTCAAAGA	GTTGACACAA	2610206C17R	UTR_5
chr18:89569773-89569873	-	45	5.31e-04	TTCAGTTCTG	TGAGTCATTTCTGCT	CTTGTTAGTA	Dok6	intron
chr7:46972046-46972146	+	57	5.31e-04	CCTGGACTCC	TGAGTAAAAAACACA	GTAAGATAAT	Ptpn5	intron
chr4:35195598-35195698	+	54	5.31e-04	GCTAAGCACC	TGATTCATTTAGCTA	CTGTTTAGTA	Mob3b	intron
chr11:84943086-84943186	+	61	5.85e-04	TATTTTTGCA	ACACTGAAATTGAAA	ATGAAACCAC	Usp32	intron
chr5:137786726-137786826	+	61	5.85e-04	TCAAATTCCA	TGATTCATTTTACTA	ATTTCATCTT	Actl6b	intron
chr12:98671529-98671629	-	42	5.85e-04	TAGTGTCAGC	TGTGACAAAGTGAAA	CGTCTGTACT	Gpr65	UTR_5
chr1:44044511-44044611	+	85	5.85e-04		ATCTCTGTAC	ATAGTCATTACTC	1700029F09Ri	UTR_5
chr9:55902640-55902740	-	19	5.85e-04	CCCAGTGAAA	TGACTCATGAAGGAG	GCTATACACT	Pstpip1	intron
chr15:66474810-66474910	-	80	6.43e-04	AAAAC	TGACTCATTACCTCC	ATGACTTACA	Phf20l1	UTR_3
chr6:142782794-142782894	+	29	6.43e-04	TACTGAAGTG	TGATTAAAATCAAGC	AGCAGCCGCC	St8sia1	UTR_3
chr15:59625595-59625695	+	64	6.43e-04	GCTGGGCTCC	TTATTAAAACCAAGA	GACAGCTCAG	Gm19510	promoter
chr10:115891163-115891263	+	15	6.43e-04	ATGGCAGAGA	ACAGTCATTTAAAGC	CACAGAGTGG	Cnot2	UTR_3
chr13:76298898-76298998	-	36	6.43e-04	GAGATTCAGT	TTGCTCATTCTGAAA	CTAGAACTAT	Glrx	promoter
chr7:82239828-82239928	+	47	6.43e-04	CTGTACTGTT	TGATTCATTTTAGTC	AGGAGTTCTT	Adamtsl3	intron
chr5:105755997-105756097	+	72	6.43e-04	GAGAAGATTC	TGAGTAAAACCCTGC	CGGTGGTTTT	Lrrc8c	promoter
chr15:62075127-62075227	+	38	7.06e-04	TAGACCTTGA	TGACACATCCCAAGC	CCTACAGAGA	Pvt1	UTR_5
chr6:115445812-115445912	+	30	7.06e-04	TGGCACCTAA	ACACTAAAAACCAGA	GAGCTGGGGG	Pparg	intron
chr7:100322689-100322789	+	15	7.06e-04	ACAGGTCTGC	AGTTTCATTTCAAGA	ACATGACTCA	C2cd3	intron
chr1:186235362-186235462	-	83	7.06e-04	AT	TGAGTCAACATTATT	CTAACACCTT	1700112H15Ri	UTR_3
chr9:59457515-59457615	-	1	7.06e-04	GAAAGACAAA	TGAGTCATTTTCCTC	T	Pkm2	UTR_5
chr11:48761277-48761377	+	16	7.06e-04	ACTAAATGGC	TGATACATACTTGAA	AATTTACTCG	Gm12185	UTR_5
chr11:65611148-65611248	+	53	7.06e-04	CCAAAGTGGC	TGAGTCATTTGTATT	CTCAGAATAC	Map2k4	promoter
chr2:172085269-172085369	-	47	7.74e-04	AGAGCAAAGC	TTTCTCATTCCAAAC	CTGCCTGCCA	Cass4	intron
chr18:65447983-65448083	-	41	7.74e-04	TCCCCCACAC	TGTGTCATTTCTGTC	CCCGTGAAGC	Alpk2	intron
chr10:20681474-20681574	-	19	7.74e-04	TGGTACGCGG	TGACTAAACTTTGTA	TTACTAGATG	Ahi1	intron
chr12:80441305-80441405	-	51	7.74e-04	ATAAGTGGGC	ACAGTAAAATCCAAA	CCTTCCTGCA	Rad51l1	intron
chr16:21585984-21586084	+	67	7.74e-04	AGCCACCACA	GGACTCATAACAGCC	TTTCAGGCAA	2510009E07R	intron
chr1:167638606-167638706	-	34	7.74e-04	TGAATAGAGA	TGTCTGAAACTCAGA	TCAAGCCCCA	Cd247	intron
chr13:30887893-30887993	+	74	7.74e-04	TCTTTCCTGC	ACAATCAGACCAAAA	CCAGTTTGTG	Exoc2	intron
chr17:6363331-6363431	+	37	7.74e-04	TCTTAACTGC	TGATTCATCTCACTA	GGCCCTCTCT	Dynlt1e	promoter
chr4:87458339-87458439	+	60	7.74e-04	TACATGTGAG	AAAGTCATAATGAAA	CCATCATTAC	Mllt3	intron
chr16:49895840-49895940	+	44	7.74e-04	CTTCATGTCA	ACACTCATATCCTTA	CATGTGTGCT	Gm6936	promoter
chr2:181306853-181306953	-	78	8.47e-04	CTAAGGC	TGACAGAAATCAAGA	GGAAATGTGG	Zgpat	intron
chr6:91080499-91080599	-	8	8.47e-04	AGTTTCCCCC	TTACTCAACCGGAAG	CTGGTCTG	Nup210	intron
chr14:25746347-25746447	+	0	8.47e-04		TGAGTCATCTTTCAT	GTCTCAGCTC	Asb14	Downstream_TES
chr5:107505242-107505342	+	66	8.47e-04	AAAGAAAAAA	AGAATCAATAAAAAA	CATTAAGAAC	Tgfbr3	intron
chr13:36295194-36295294	-	80	9.26e-04	ATGTT	ATATTCATCTAGAAA	GTTCTTTCTG	Fars2	intron
chr17:17550247-17550347	+	47	9.26e-04	GTCAGTGACT	TGACTAAGTGCTGAC	TAAATTGGCA	Has1	intron
chr9:114626814-114626914	-	55	9.26e-04	TTTGGGGTGA	TGACTGAAACGGTTA	AAAGTTGTGG	Cmtm7	intron
chr3:106913191-106913291	-	47	9.26e-04	GAAGAAATTA	TGATTCATGACAGTA	GCAGAATTAC	Cd53	UTR_5
chr11:114624255-114624355	+	39	9.26e-04	AGTGGCAGGA	TTGCTCAAAGTGAAA	GTTGATTTCT	Gpr142	Downstream_TES

Supplementary Table 1

chr7:37946487-37946587	+	23	9.26e-04	TTGGTCTCTG	ACACTCAATCCTGTA	GCAAGTCAAC	Plekhf1	promoter	
chr2:69795754-69795854	-	84	9.26e-04	G	AGATTAAAAACAGAA	CACAACCTAA	Ubr3	intron	
chr15:35669338-35669438	+	31	9.26e-04	TGTTTTGGTT	GTATTCATTTAGAGA	GAGAGTGATA	Vps13b	intron	

Supplementary Table 2. Summary of all ChIP-Seq and RNA-Seq libraries

ChIP-Seq

Cell Type		Antibodies	Treatment	apped Reads	Reads Used	Peaks	Platform (Illumina)
B cells	Wild Type	IgG	none	3314435	3013751	N/A	Genome Analyzer
		IRF4	none	3909994	3486911	4009	Genome Analyzer
			+IL21	4750741	4101841	4593	Genome Analyzer
CD4+ T cells	Wild Type	IgG	none	13361277	4660224	N/A	Genome Analyzer II
		IRF4	none	14525747	4411076	10704	Genome Analyzer II
			+IL21	15766886	7138955	14838	Genome Analyzer II
		IRF8	none	14213861	9997943	7907	Genome Analyzer II
			+IL21	14832642	6807042	5882	Genome Analyzer II
		Stat3	none	17397798	3066585	674	Genome Analyzer II
			+IL21	18179256	4828533	4470	Genome Analyzer II
		Pan-JUN	none	21650927	10852816	8771	Genome Analyzer II
			+IL21	19829695	9992342	14659	Genome Analyzer II
		BATF	+IL21	29912814	7690689	5193	HiSeq2000
	IRF4KO	IRF4	+IL21	7232501	2786179	N/A	Genome Analyzer II
		Pan-JUN	+IL21	33605219	22027542	2697	HiSeq2000
		BATF	none	20655264	5584947	1063	HiSeq2000
			+IL21	10914964	2891506	1248	HiSeq2000
	BatFKO	BatF	+IL21	13845107	1142773	N/A	HiSeq2000
		IRF4	none	15167473	4227433	305	HiSeq2000
			+IL21	9746865	4595948	1994	HiSeq2000
Th17 cells		IgG	2x polarized	12280127	3985198	N/A	HiSeq2000
		IRF4	2x polarized	43921346	4936551	21775	HiSeq2000
		BatF	2x polarized	16476875	6122656	18043	HiSeq2000
		JunB	2x polarized	12201272	1208946	3402	HiSeq2000
		JunD	2x polarized	37459268	16071474	23409	HiSeq2000
		cJun	2x polarized	14838399	2181698	7801	HiSeq2000
		Stat3	2x polarized	39434725	5207636	20417	HiSeq2000

(peaks calling: MACS 1.3.7.1, thresholds: pvalue 1e-10)

RNA-Seq

Cell Type		Library	Treatment	apped Reads	Reads Used	rm (Illumina)
B cells	Wild Type	proB	none	45735029	45735029	HiSeq2000
		preB	none	40297073	40297073	HiSeq2000
CD4+ T cells	Wild Type	WT CD4T	none	24825191	24825191	me Analyzer II
		WT CD4T	IL21	24106589	24106589	me Analyzer II
	IRF4KO	IRF4KO CD4T	none	20089886	20089886	me Analyzer II
		IRF4KO CD4T	IL21	24806630	24806630	me Analyzer II
Th1 cells		Th1	none	53920164	53920164	HiSeq2000
Th2 cells		Th2	none	22677326	22677326	HiSeq2000
Th9 cells		Th9	none	32867510	32867510	HiSeq2000
Th17 cells		Th17	none	19804905	19804905	HiSeq2000
Treg cells		Treg	none	48849695	48849695	HiSeq2000