908 **Supplementary Materials**

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910 **MyD88-dependent Dendritic and Epithelial Cell Crosstalk in the**

911 **Lung Orchestrates Immune Responses to Inhaled Allergens**

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916 **Supplementary Materials and Methods**

917 **Nanostring Mouse Immunology Gene Expression**

918 Gene expression data for whole lung RNA were normalized using 14 Nanostring nSolver
919 housekeeper genes: *Alas1*, *Eef1g*, *G6pdx*, *Gapdh*, *Gusb*, *Hprt*, *Oaz1*, *Polr1b*, *Polr2a*, *Ppia*,
920 *Rpl19*, *Sdha*, *Tbp*, and *Tubb5*. Sorted EC, cDC, and AM samples were quantile normalized using
921 raw Nanostring counts. Between Groups Analysis (BGA) of the data was carried out using the
922 Bioconductor made4 package (version 1.45.0), using log2-transformed normalized expression
923 values. Genes having a group mean intensity ≥32 (ie. log2 ≥5) for at least one sample group were
924 considered to be expressed. All other genes were considered to be below the minimum intensity
925 threshold (MTI). Data analysis was performed in R version 3.2.1, using limma (version 3.27.5)
926 from Bioconductor (version 2.31.0) for statistical linear modeling, using a moderated t-test. For
927 each pairwise comparison, hits were defined using p ≤0.01, fold change ≥1.5.
928
929 Minimum threshold intensity (MTI) was determined using the positive and negative control probes
930 provided by Nanostring. We selected a constant MTI using normalized group mean ≥32 for
931 consistency across the datasets. Nanostring outliers were identified on the basis of an aberrant
932 MA plot using raw data, e.g. extremely high variability compared with other samples in the study,
933 and sample correlation which differed more than 5x median absolute deviation (MAD) from other
934 replicates in the sample group.
935

936 **Primary data processing for ATAC-seq**

937 Data were collected using 50 bp paired-end reads from NextSeq platform (Illumina). Raw reads
938 were first cleaned for adapter sequences using Trim Galore with default parameters. Cleaned
939 reads were aligned to mm9 using Bowtie with the parameters -m1, -v2 and –X1500. These
940 parameters ensured that fragments up to 1500bp (-X1500) and mismatch up to 2 (-v2) were
941 allowed to align, and that only unique aligning reads were collected (-m1) and mapped to the
942 mm9 genome. For all data files, duplicates were removed using Picard. The total number of such
943 reads per sample ranged from 19,955,634 to 85,555,024 with an average of ~40,000,000 reads,

of which 75.93% to 78.66% mapped to unique sites.

Two biology replicates for each condition were merged into one sample. Comparison of the biological replicates for each genotype and condition revealed that they were between 88.4% and 98.9% identical. Given this high degree of similarity, we pooled replicates to give between 62,978,130 and 122,040,288 reads per condition and used the combined files for peak calling. For peak calling, we adjusted the read start sites to represent the center of the transposon binding site. Previous descriptions of the Tn5 transposase show that the transposon binds as a dimer and inserts two adaptors separated by 9 bp.[51] Therefore, all reads aligning to the + strand were offset by +4 bp, and all reads aligning to the – strand were offset −5 bp.

ATAC-seq peak-calling

We used PeaKDEck[52] (Version 1.1) to call all reported ATAC-seq peaks. PeaKDEck distinguishes signal from noise by randomly sampling read densities and using kernel density estimation to generate a dataset-specific probability distribution of random background signal. PeaKDEck then uses this probability distribution to select an appropriate read density threshold for 300 bp and probability value <0.0001.

ATAC-seq differential peak identification

After peak calling for each sample, we obtained the union of peaks called from all paired conditions as the candidate regions for quantitative comparison. For each comparison, union peak lists were made by two steps: 1) Two lists of peaks were put into one file and sorted; 2) Overlapping and neighboring peaks within 100nt were merged using *mergeBed* from *bedTools* (version 2.16.2). Read counts of each union peak for each sample were calculated using *intersectBed* from *bedTools*. R (R-program project) was used to build a statistical model to detect significant peaks.

The "Z-test" method from EpiCenter[53] was applied as a statistical test to find genomic regions whose ratio (fold-change) and difference (Delta) between samples was extreme compared to the expected distribution of z-scores across the genome. Based on our observations and testing from real data, we found that log2 ratios of normalized read counts are sensitive to narrow peaks, and differences (Delta) are sensitive to broad peaks. We therefore modified the score calculation by combining both Ratios and Delta. The first, normalized count (C_{nk}, n is nth peak and k is kth samples) of peaks was calculated as Reads Per 10 Kilobase of peak per Million mapped reads. A score was calculated as follows:

$$\widehat{S_n} = \log_2 \frac{C_{n1}}{C_{n2}} * \log_2 |C_{n1} - C_{n2}|$$

A z-test was constructed by assuming a Gaussian distribution, and a p-value was computed for each peak. Regions with p≤0.05 were considered significant. This procedure was repeatedly applied to all paired comparisons. Of the 124,144 to 164,963 union peaks generated for each paired condition, 42,238 to 69,796 significant differential peaks were identified. All significant peaks were assigned to individual genes using PAVIS.[54]

Association of Differential ATAC-seq peaks with Defined Promoter Loci

To narrow the list of differential promoter-associated peaks, we restricted our analysis to peaks within ±500 bp of the TSS as well as a 1.3-fold change, p ≤0.05, and peak read depth ≥100 counts for at least one sample group.

Whole Transcriptome Microarray Amplification, Hybridization and Probe Level Analysis

Thirty-five ng total RNA from sorted cDCs was amplified using the WT-Ovation Pico RNA Amplification System protocol (Nugen, San Carlos, CA). Sense strand cDNA target was made using the Nugen Exon Module, and after fragmentation the product was labeled with the Nugen Encore Biotin module. Five μg of resulting amplified biotin-cDNAs were hybridized to the Affymetrix Mouse Whole Transcriptome Array 1.0 according to manufacturer's instructions and scanned in an Affymetrix Scanner 3000 (Affymetrix, Santa Clara, CA). Data was obtained using the GeneChip® Command Console software. Analyses of probe level and gene level data was

performed using the Affymetrix Expression Console (EC) and Transcriptome Analysis Console (TAC) software. p-values were generated using the Affymetrix Transcriptome Analysis Console (TAC) software version 3.0 using a one-way between subject ANOVA (unpaired).

Analysis of Transcriptional Regulation associated with Open Chromatin

Regions of the genome associated with differential, promoter-associated ATAC-seq peaks were matched with local transcripts from the Ensembl database. In some cases, such as bidirectional transcription, more than one gene was associated with an individual ATAC-seq peak, and were analyzed separately. Transcripts were excluded from analysis if their start sites were not within 500 bp of the ATAC-seq peak. Using the Affymetrix Transcriptome Analysis Console, 5' and 3' probes were defined for all loci examined, and only genes with at least 2 different probes were included in further analysis. The 3' probe selected excluded the 3' UTR to minimize any post-transcriptional alterations in RNA stability.

Mean values reflecting signals for all probes on the transcriptome array were calculated for each gene whose chromatin accessibility after allergic sensitization differed between lung cDCs of WT mice and those of the conditionally mutant *Myd88* mice. Genes were placed in categories based on the following criteria.

A) Expressed. Genes whose maximum mean bi-weight log2 probe signal of at least one group was ≥ 6.0. This value was used for the minimum threshold intensity (MTI).

B) No differential expression. Genes whose expression between genotypes is different by less than 1.5-fold.

C) Baseline different; not induced. Genes whose expression between genotypes at baseline (0h) is greater than 1.5-fold, but this difference does not further increase by more than 1.5 fold after allergic sensitization (6h). ie. $\frac{WT6h/Mut6h}{WT0h/Mut0h} \leq 1.5$

D) Induced. Genes that are more highly expressed (1.5-fold) after allergic sensitization (6h post-OVA/FLA) than at baseline (0h), and where that difference is dependent on MyD88. Genes

expressed above the MTI were considered to be induced when following two ratios of mean probe signal strength were greater than 1.5.

- $\frac{WT6h}{WT0h}$, where *6h* and *0h* refer to post-sensitization and steady state, respectively.
- $\frac{WT6h}{Mut6h}$, where *Mut* refers to the conditional *Myd88* mutant under study.

D1) Induced through transcription initiation. Genes whose MyD88-dependent increase in mRNA level can be measured with a 5' probe; ie. genes expressed above the MTI and for which the following ratio was ≥ 1.5.

- $\frac{5'WT6h}{5'Mut6h}$, where *5'* refers to the probe closest to the 5' end of the transcript.

D2) Induced through RNA Elongation. Genes whose MyD88-dependent increase in mRNA level is greater when measured with a 3' probe than with a 5' probe; ie. genes expressed above the MTI and for which each the following four ratios were ≥ 1.5.

- $\frac{3'WT6h}{3'WT0h}$, indicating higher gene expression in WT cDCs after allergic sensitization than at steady state, as measured with a 3' probe.
- $\frac{3'WT6h}{3'Mut6h}$, indicating *Myd88*-dependent gene expression, as measured with a 3' probe.
- $\frac{3'WT6h/3'Mut6h}{3'WT0h/3'Mut0h}$ = (3' *ratio*), indicating a greater effect of *Myd88* on gene expression after allergic sensitization than at steady state, as measured with a 3' probe.
- $\frac{3'ratio}{5'ratio}$, indicating the *Myd88*-dependent increase in expression after sensitization is greater when measured using 3' probes than with 5' probes: (5' *ratio* = $\frac{5'WT6h/5'Mut6h}{5'WT0h/5'Mut0h}$).

D3) Induced (complex). Expressed genes induced in a MYD88-dependent manner, but not fitting the criteria of categories **D1**) or **D2**).

Whole Transcriptome Microarray Differential Gene Expression Analysis

Whole transcriptome array genes were filtered based on a bi-weight log2 average probe signal ≥7 and a ratio of ≥2 for at least one genotype and treated WT mice (reference group). DC-MyD88-dependent genes were defined as those having a ratio of ≥2 for both DC-KO/WT and KO/WT, and a ratio of <2 for EC-KO/WT. EC-MyD88-dependent genes had a ratio of ≥2 for both EC-KO/WT and KO/WT, and <2 for DC-KO/WT. Genes were ranked according to absolute fold change in DC-KO/WT or EC-KO/WT genes, respectively. Heat maps were generated using the Partek Genomic Suite software (Partek, St Louis, MO).

Pathway analysis

For pathway analysis of whole transcriptome microarray data, gene hits were defined as those with a bi-weight log2 average signal ≥7, $p \leq 0.05$, and ≥1.3 fold change as compared to WT (reference group) or bi-weight log2 average signal ≥7, no p-value restriction, and ≥2 fold change as compared to WT.

Pathway analysis was performed using the Ingenuity Pathway Analysis software to calculate the p-value of likely pathway association (Ingenuity, Redwood City, CA). The most differential pathways for DC-KO and EC-KO cDCs were ranked using a ratio of -log(p-value) of DC-KO/WT vs EC-KO/WT. In cases where the p-value was equal to zero (since no genes in the pathway were altered), the –log(p-value) for that subset was defined as 0.2 (or p=0.63) to allow ranking by –log(p-value) ratio. Heat maps were generated using the Partek Genomic Suite software (Partek, St Louis, MO).

Supplementary References

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Supplementary Figure and Table Legends.

Supplementary Figure 1. *Cd11c-cre*-mediated recombination in CD103$^+$ DCs, CD11b$^+$ DCs and AMs or *Sftpc-cre*-mediated recombination in ECs. (**a**) Flow cytometry gating strategy for lung CD11b$^+$ DCs, CD103$^+$ DCs, and AMs from *Cd11c-cre*$^+$ x ROSA-loxP-STOP-loxP *tdTomato* (RT) mice. Lung DCs were first gated on single cells that are CD11c^{hi}, nonautofluorescent, and I-A^{b+}, then divided into CD11b$^+$ or CD103$^+$ DCs. AMs were gated on CD11c^{hi} autofluorescent^{hi} cells. (**b**) Quantitation of *tdTomato* expression in the indicated cell types. Data are representative of cells from three *Cd11c-cre* x RT mice. (**c**) Flow cytometry gating strategy for EpCAM$^+$ ECs prepared from *Sftpc-cre*$^+$ x ROSA-loxP-STOP-loxP *tdTomato* (RT) mice. ECs were gated on single, live (7AAD$^-$), lineage$^-$ (CD31$^-$ CD34$^-$ CD45$^-$) EpCAM$^+$ cells. Lineage$^+$ EpCAM$^-$ cells (non-epithelial cells) express little *tdTomato*, whereas almost all lineage$^-$ EpCAM$^+$ cells (ECs) are *tdTomato*$^+$. (**d**) Quantitation of *tdTomato* expression in Lin$^+$ EpCAM$^-$ and Lin$^-$EpCAM$^+$ cells. Data shown is representative of lung cells from three *Sftpc-cre* x RT mice.

Supplementary Figure 2. IL33 adjuvant activity is independent of MyD88 in ECs or *Cd11c*-expressing cells and *Il1a* is expressed in AMs in a *Cd11c*-MyD88 dependent manner. (**a**) Schematic of OVA/IL33 mouse model of allergic asthma (top). Neutrophilic (bottom left) and eosinophilic (bottom right) inflammation of the airway in WT, DC-KO, EC-KO, and *Myd88* null mice sensitized with OVA/IL33 and challenged with OVA. Data shown are representative of two experiments, n = 11 mice per group. (**b**) Relative *Il1a* expression in purified ECs at 2h post-sensitization and cDCs and AMs at 6h post-sensitization of the indicated mouse strains. For purified AMs and cDCs, lungs from 3 mice were pooled prior to sorting each cell sample. For each sorted cell type, n = 3 (ECs), n = 3-4 (cDCs) and n = 2 (AMs) unique sorts per group. MTI = minimum threshold intensity for gene detection, ****$p < 0.0001$.

Supplementary Table 1. Genes differentially expressed at steady state in lungs of WT mice and mice having cell-specific deletion of *Myd88*.

Shown are genes whose expression in whole lung is significantly different at steady state between WT mice and the indicated strains (≥1.5 fold; p≤0.01, MTI≥32 for at least one group), as determined by Nanostring analysis. The categories shown are the same as those in the Venn diagram for the 0h time point in Figure 3b (top).

Supplementary Table 2. Genes whose expression in whole lungs of WT mice is changed by OVA/FLA. Shown are genes whose expression is either increased (orange) or decreased (blue) at 2h or at 6h post-OVA/FLA treatment (≥1.5 fold; p≤0.01, MTI≥32 for at least one group).

Supplementary Table 3. Genes whose expression in whole lung is affected at 2h post-OVA/FLA by cell-specific *Myd88* deletion. Shown are genes whose expression in whole lung at 2h post-OVA/FLA differs between WT and the indicated mouse strain(s) (≥1.5 fold; p≤0.01, MTI≥32 for at least one group). The categories shown are the same as those in the Venn diagram for the 2h time point in Figure 3b (bottom).

Supplementary Table 4. Genes whose expression in sorted ECs is affected at 2h post-OVA/FLA by cell-specific deletion of *Myd88*. Shown are genes whose expression in sorted ECs at 2h post-OVA/FLA differs between WT and the indicated mouse strain(s) (≥1.5 fold; p≤0.01, MTI≥32 for at least one group). The categories shown are the same as those in the Venn diagram for the 2h time point in Figure 3e.

Supplementary Table 5. Genes whose expression in the whole lung is affected at 6h post-OVA/FLA by cell-specific *Myd88* deletion. Shown are genes whose expression in whole lung at 6h post-OVA/FLA differs between WT and the indicated mouse strain(s) (≥1.5 fold; p≤0.01, MTI≥32 for at least one group). The categories shown are the same as those in the Venn diagram for the 6h time point in Figure 4b.

Supplementary Table 6. Genes whose expression in cDCs is affected at 6h post-OVA/FLA by cell-specific *Myd88* deletion. Shown are genes whose expression in sorted cDCs at 6h post-OVA/FLA differs between WT and the indicated mouse strain(s) (≥1.5 fold; p≤0.01, MTI≥32 for at least one group). The categories shown are the same as those in the Venn diagram for the 6h time point in Figure 4g.

Supplementary Table 7. Genes whose expression in AMs is affected at 6h post-OVA/FLA by cell-specific *Myd88* deletion. Shown are genes whose expression in sorted AMs at 6h post-OVA/FLA differs between WT and the indicated mouse strain(s) (≥1.5 fold; p≤0.01, MTI≥32 for at least one group). The categories shown are the same as those in the Venn diagram for the 6h time point in Figure 4h.

Supplementary Table 8. ATAC-seq peaks in cDCs are affected by cell-specific *Myd88* deletion. Worksheets in file show genes whose ATAC-seq peaks in cDCs significantly differ (p<0.05) for the following four comparisons: WT 0h vs DC-KO or EC-KO at 0h; and WT 6h vs DC-KO or EC-KO at 6h. Genes are assigned to each peak, and the distance from the peak to TSS is indicated.

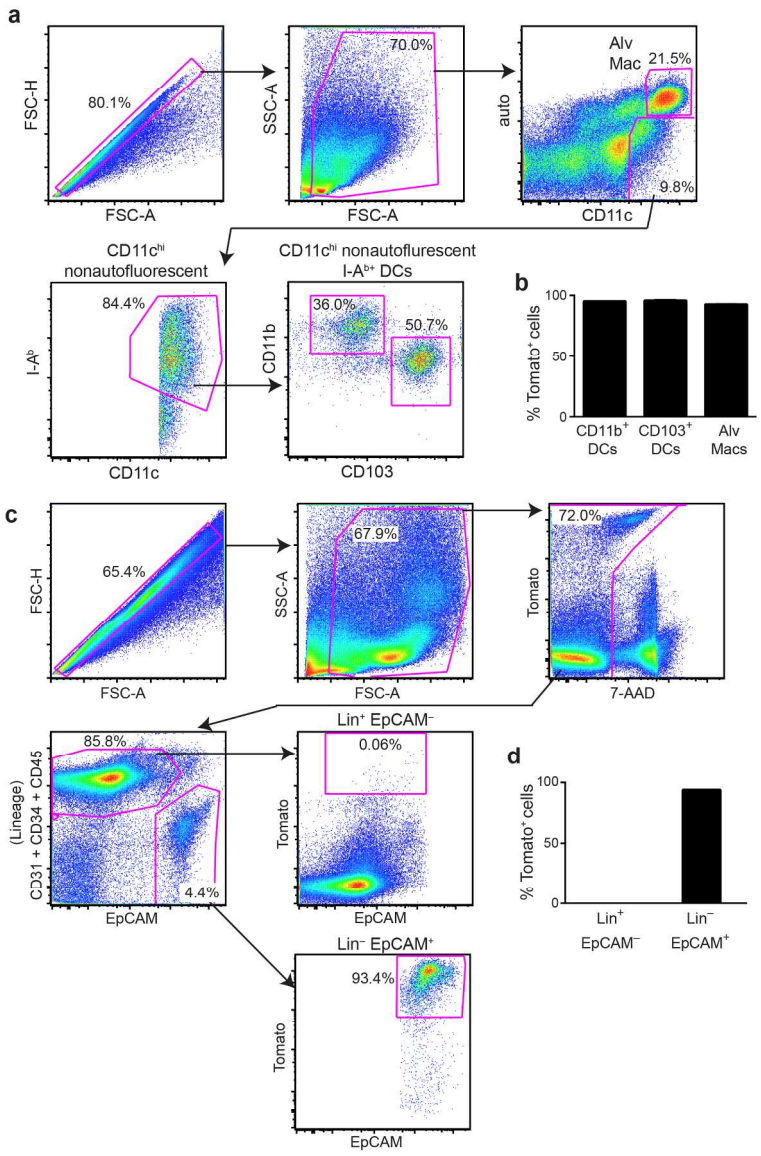
Supplementary Table 9. Mechanisms of transcriptional regulation associated with genes with MyD88-dependent, differential ATAC-seq peaks in cDCs. (**a-c**) Categories of transcriptional regulation are shown for genes associated with genotype-dependent ATAC-seq peaks at baseline (0h) and/or following 6h post-sensitization with OVA/FLA. Genes listed map to ATAC-seq peaks that are different between between WT (reference) and (**a**) DC-KO at both 0h and 6h, (**b**) DC-KO at 6h only, and (**c**) EC-KO at 6h only, as shown in Figure 5b. These genes are futher subdivided into genotypes depending on whether the genes are expressed or not, and whether they are differentially expressed at baseline, or after induction by OVA/FLA.

Supplementary Table 10. Control of gene expression in cDCs by cell-intrinsic and -extrinsic MyD88 signaling. Shown are genes whose expression in cDCs (based on Affymetrix Whole Transcriptome Array 1.0) is dependent on MyD88 signaling in *Cd11c*-expressing cells (left) or ECs (right). Expressed genes had a minimum bi-weight log2 average probe signal ≥7. *Cd11c*-MyD88-dependent genes were defined as those having a ratio of ≥2 for both DC-KO/WT and KO/WT, and a ratio of <2 for EC-KO/WT. EC-MyD88-dependent genes had a ratio of ≥2 for both EC-KO/WT and KO/WT, and <2 for DC-KO/WT (as described in Supplementary Methods). Fold-changes and p-values are shown for each genotype compared to WT (reference) at 6h.

Supplementary Resource. Online interactive display of Nanostring data for whole lung, sorted ECs, cDCs, and AMs. Gene expression data for whole lung at various time points, as well as sorted ECs at 2h, cDCs at 6h, and AMs at 6h are included online: *https://jmw86069.github.io/myd88-asthma/*

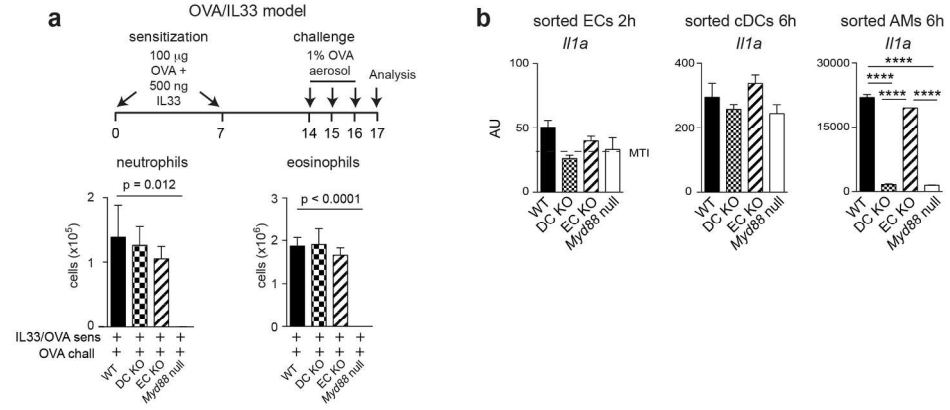
Genes with significant differences in expression between genotypes are indicated with a bar. The comparison groups, p-value, and fold-change can all be seen when hovering over this bar. Significant differences are defined as 1.5-fold difference between groups, $p<0.01$, with a normalized MTI ≥32 (indicated by the dotted line) for at least one group in the comparison.

Supplementary Figure 1



166x250mm (300 x 300 DPI)

Supplementary Figure 2



196x93mm (300 x 300 DPI)

Supplementary Table 1: Genes differentially expressed at steady state in lungs of WT mice and mice having cell-specific deletion of *Myd88*

EC-KO	EC-KO & DC-KO	DC-KO	EC-KO & *Myd88* null	EC-KO, DC-KO & *Myd88* null	DC-KO & *Myd88* null	*Myd88* null
Gzma		Cd3e	Il18rap	Stat4	Jak3	Cd109
Klra7		Cd5		Tlr9		Cfb
		Gp1bb				Il16
		Il1a				Itga5
		Itgam				Myd88
		Itgax				
		Nfatc2				

Supplementary Table 2: Genes whose expression in whole lungs of WT mice is changed by OVA/FLA

2 h vs 0 h

Decreased	Increased	
Ahr	Batf	Irgm1
Atm	Batf3	Itga5
Ccrl1	Bcl3	Itgam
Cd2	Bcl6	Jak2
Cd27	Ccl11	Jak3
Cd28	Ccl12	Lcp2
H2-Ob	Ccl19	Lif
Ikzf2	Ccl2	Lilra6
Il12a	Ccl20	Lilrb3
Il7	Ccl22	Lilrb4
Maf	Ccl3	Litaf
Ms4a1	Ccl4	Ly96
Tnfrsf13b	Ccl5	Mapk11
	Ccl7	Mapkapk2
	Ccl9	Marco
	Ccrl2	Msr1
	Cd109	Mx1
	Cd14	Myd88
	Cd274	Ncf4
	Cd44	Nfil3
	Cd69	Nfkb1
	Cd80	Nfkb2
	Cd83	Nfkbia
	Cd86	Nfkbiz
	Cdkn1a	Nod2
	Ceacam1	Notch1
	Cebpb	Pigr
	Cfb	Plaur
	Cish	Ptafr
	Clec4e	Ptger4
	Clec5a	Ptgs2
	Clu	Ptpn2
	Csf1	Rela
	Csf2	Relb
	Csf2rb	S100a8
	Csf3r	S100a9
	Cxcl1	Sele
	Cxcl10	Smad3
	Cxcl11	Socs1
	Cxcl13	Socs3
	Cxcl3	Stat2
	Cxcl9	Stat3
	Cxcr1	Stat4
	Cxcr2	Stat5a
	Ebi3	Syk
	Entpd1	Tagap
	Fas	Tbx21
	Fcgr3	Tirap
	Fcgr4	Tlr2
	Fkbp5	Tmem173
	H2-Q10	Tnf
	Hamp	Tnfaip3
	Hif1a	Tnfaip6
	Icam1	Tnfrsf11a
	Icam4	Tnfrsf1b
	Icosl	Tnfrsf9
	Ifi204	Tnfsf14
	Ifit2	Tnfsf15
	Ifitm1	Trem1
	Ifngr2	Vcam1
	Ikbke	Xbp1
	Ikzf4	
	Il10ra	
	Il10rb	
	Il12b	
	Il13ra1	
	Il17ra	
	Il18rap	
	Il1a	
	Il1b	
	Il1r1	
	Il1r2	
	Il1rn	
	Il2ra	
	Il33	
	Il4ra	
	Il6	
	Irak2	
	Irak3	
	Irf1	
	Irf5	
	Irf7	

6 h vs 0 h

Decreased	Increased		
Ahr	Batf	Il12rb2	Tagap
Atm	Batf3	Il13ra1	Tap1
Ccr6	Bcl3	Il15ra	Tbk1
Ccrl1	Bcl6	Il17ra	Tbx21
Cd19	Bid	Il18rap	Tgfbi
Cd1d1	Bst1	Il1a	Tgfbr2
Cd2	C1qbp	Il1b	Tirap
Cd209g	C3	Il1r1	Tlr2
Cd27	C8b	Il1r2	Tmem173
Cd36	Ccbp2	Il1rap	Tnf
Cd5	Ccl11	Il1rn	Tnfaip3
Cd55	Ccl12	Il23a	Tnfaip6
Cd79b	Ccl19	Il2ra	Tnfrsf11a
Cd97	Ccl2	Il2rb	Tnfrsf14
Cx3cr1	Ccl20	Il33	Tnfrsf1b
Cxcl12	Ccl22	Il4ra	Tnfrsf4
Cxcl15	Ccl3	Il6	Tnfrsf9
Cxcr3	Ccl4	Il6ra	Tnfsf14
Cxcr6	Ccl5	Il7r	Tnfsf15
Dpp4	Ccl6	Irak2	Traf3
Fcgrt	Ccl7	Irak3	Traf6
Gpr44	Ccl9	Irf1	Trem1
Gusb	Ccrl2	Irf5	Tyrobp
H2-Ob	Cd109	Irgm1	Vcam1
Hc	Cd14	Itga2b	Xbp1
Hfe	Cd244	Itga5	
Icam2	Cd24a	Itgam	
Ikzf2	Cd274	Itgax	
Il18	Cd3eap	Itgb2	
Il27ra	Cd44	Jak2	
Il7	Cd69	Jak3	
Kit	Cd80	Klra7	
Lilra5	Cd82	Lcp2	
Maf	Cd83	Lif	
Mr1	Cd86	Lilra6	
Ms4a1	Cd99	Lilrb3	
Nox4	Cdkn1a	Lilrb4	
Npc1	Ceacam1	Litaf	
Pax5	Cebpb	Ltb4r1	
Prim1	Cfb	Mapk11	
Sigirr	Cish	Mapkapk2	
Tgfb3	Clec4e	Marco	
Tnfrsf13b	Clec5a	Mbp	
Tnfsf10	Clu	Msr1	
Tnfsf12	Crlf2	Mx1	
Traf5	Csf1	Myd88	
Xcr1	Csf2	Ncf4	
	Csf2rb	Nfil3	
	Csf3r	Nfkb1	
	Ctla4	Nfkb2	
	Cxcl1	Nfkbia	
	Cxcl10	Nfkbiz	
	Cxcl13	Nod2	
	Cxcl3	Notch1	
	Cxcl9	Notch2	
	Cxcr1	Nt5e	
	Cxcr2	Pigr	
	Ebi3	Plaur	
	Entpd1	Pol1r1b	
	Fas	PbPb	
	Fcer1g	Prkcd	
	Fcgr2b	Ptafr	
	Fcgr3	Ptger4	
	Fcgr4	Ptgs2	
	Fkbp5	Ptpn2	
	Gapdh	Ptpn22	
	Gm10499	Ptprc	
	Gzmb	Rela	
	H2-Q10	Relb	
	Hamp	S100a8	
	Hcst	S100a9	
	Hif1a	Sele	
	Hprt	Sell	
	Icam1	Selpig	
	Icam4	Smad3	
	Icosl	Socs1	
	Ifi204	Socs3	
	Ifit2	Stat2	
	Ifitm1	Stat3	
	Ikbke	Stat4	
	Ikzf4	Stat5a	
	Il10ra	Syk	

Supplementary Table 3: Genes whose expression in whole lung is affected at 2h post-OVA/FLA by cell-specific *Myd88* deletion

EC-KO	EC-KO & DC-KO	DC-KO	EC-KO & *Myd88* null	EC-KO, DC-KO & *Myd88* null	DC-KO & *Myd88* null	*Myd88* null
Batf3		Il12b	Ccl11	Il1b	Ccl22	Batf
Ccl6		Itgax	Ccl20	Ptfar	Ccl3	Bcl3
Cd244		Marco	Cd14		Ccl4	Bid
Cd3eap			Cd44		Cxcl3	C3
Clec5a			Cd80		Ebi3	Ccl12
Tlr8			Cd83		Emr1	Ccl19
			Cdkn1a		Il1a	Ccl2
			Ceacam1		Tnf	Ccl24
			Clu		Tnfaip3	Ccl7
			Csf2			Ccl8
			Csf3r			Ccrl2
			Cxcl1			Cd53
			Cxcr2			Cebpb
			Fcgr3			Cfb
			Fcgr4			Cish
			H2-Q10			Clec4e
			Ikbke			Csf1
			Il18rap			Csf2rb
			Il1r2			Cxcr1
			Il6			Cxcr3
			Irak2			Fas
			Itgam			Gpi1
			Lilra6			Hamp
			Lilrb4			Hcst
			Nfil3			Hif1a
			Pigr			Icam1
			Plaur			Icam4
			Ptgs2			Ifitm1
			S100a8			Ifngr2
			S100a9			Ikzf4
			Sell			Il17ra
			Socs3			Il1rn
			Tnfrsf9			Il4ra
			Trem1			Il6st
			Tyrobp			Irak3
						Irf1
						Irf5
						Jak2
						Lif
						Lilrb3
						Litaf
						Mapk11
						Msr1
						Myd88
						Ncf4
						Nfkb1
						Nfkb2
						Nfkbia
						Nfkbiz
						Nod2
						Plau
						Ptger4
						Ptpn2
						Rela
						Relb
						Sele
						Smad3
						Stat5a
						Tbx21
						Tlr2
						Tmem173
						Tnfaip6
						Tnfrsf11a
						Tnfrsf1b
						Tnfsf14
						Tnfsf15
						Tslp
						Vcam1
						Xbp1

Supplementary Table 4: Genes whose expression in sorted ECs is affected at 2h post-OVA/FLA by cell-specific deletion of *Myd88*

EC-KO	EC-KO & DC-KO	DC-KO	EC-KO & *Myd88* null	EC-KO, DC-KO & *Myd88* null	DC-KO & *Myd88* null	*Myd88* null
Cd3eap			Abcb10			Atm
Ifngr1			Adal			Batf
Ikzf4			Ccl20			Bcap31
Il15ra			Ccr6			Bcl2
Irf1			Cd14			Bcl3
Stat3			Cd164			Bid
Tmem173			Cd44			C1ra
			Cd79b			C3
			Cd81			C6
			Cd83			Casp2
			Ceacam1			Casp3
			Cfp			Casp8
			Ciita			Ccl2
			Clu			Ccrl2
			Cradd			Cd274
			Csf1			Cd55
			Csf1r			Cd82
			Csf2			Cfb
			Cul9			Chuk
			Cxcl3			Cx3cl1
			Entpd1			Cxcl1
			Ets1			Cxcl10
			Fcgrt			Cxcr4
			Ifngr2			Dpp4
			Ikzf2			Fadd
			Il11ra1			Fas
			Il17re			Fyn
			Il18r1			H2-Eb1
			Il4ra			Hc
			Irak2			Hfe
			Irak4			Icam1
			Irf5			Ifitm1
			Itga6			Ifnar2
			Jak3			Igf2r
			Lif			Ikbke
			Ly96			Ikbkg
			Mapk14			Il18rap
			Mme			Il1b
			Nfil3			Il1r1
			Nfkb1			Il6ra
			Npc1			Irak1
			Pdgfb			Irak3
			Pigr			Irf3
			Ptafr			Jak1
			Ptpn6			Jak2
			Sigirr			Ltbr
			Smad5			Map4k2
			Stat5a			Map4k4
			Tfrc			Mapk1
			Tgfbr2			Mapk11
			Tlr2			Mif
			Tlr3			Myd88
			Tnf			Nfatc3
			Tnfrsf1b			Nfkb2
			Tnfrsf9			Nfkbia
			Tnfsf10			Nos2
			Tnfsf12			Notch2
			Tollip			Phlpp1
						Phlpp2
						Plau
						Pml
						Prdm1
						Prim1
						Psmb5
						Psmb7
						Psmd7
						Ptk2
						Ptpn2
						Relb
						Runx1
						Ski
						Stat1
						Tcf4
						Tgfb1
						Tlr5
						Tnfaip3
						Tnfrsf11a
						Traf1
						Ube2l3
						Zbtb7b

Supplementary Table 5: Genes whose expression in the whole lung is affected at 6h post-OVA/FLA by cell-specific *Myd88* deletion

EC-KO	EC-KO & DC-KO	DC-KO	EC-KO & *Myd88* null	EC-KO, DC-KO & *Myd88* null	DC-KO & *Myd88* null	*Myd88* null
Adal	Cr2	Btla	Cd22	Ahr	Ccl8	Batf3
Ccl12	Hamp	Cd69	Clu	Atm	Cd244	C3
Ccl7	Maf	Hcst	Gp1bb	Batf	Cd53	C8b
Ccr5	Marco	Il2rb	Il21r	Bcl3	Csf1	Ccl2
Ccr6	Prim1	Itgax	Il27ra	Bid	Cxcl3	Ccl22
Cd209g	Xcl1	Sell	Irf4	Bst1	Fcer1g	Ccl5
Cd48		Tgfb2	Lck	Bst2	Hlx	Ccl9
Cd55		Tgfb3	Ly86	Ccbp2	Icos	Cd1d1
Cd7		Tnfaip6	Pigr	Ccl11	Ifi35	Cd2
Cxcr6			Ppbp	Ccl19	Ifih1	Cfb
Fadd			Tlr9	Ccl20	Il1rl2	Cfd
Gpr183			Tnfrsf11a	Ccl3	Il33	Cfp
H2-DMb2			Tnfrsf13b	Ccl4	Il6	Cxcl13
Ikzf3			Tnfrsf13c	Ccl6	Il7r	Cxcl9
Il12b			Tnfrsf9	Ccr2	Itgb2	Dpp4
Ir1rl1				Ccrl1	Lif	Emr1
Itga2b				Ccrl2	Mapk11	Eomes
Nt5e				Cd14	Mbp	Fcgrt
Tlr1				Cd163	Ncf4	Gzma
Tyk2				Cd19	Nod2	Ifngr1
				Cd24a	Nox4	Il6st
				Cd27	Tmem173	Irgm1
				Cd44	Tslp	Jak3
				Cd79b		Klrd1
				Cd80		Lilra6
				Cd83		Ltb4r1
				Cd97		Ltbr
				Cdkn1a		Msr1
				Ceacam1		Polr1b
				Cebpb		Runx1
				Ciita		Stat5a
				Cish		Traf3
				Clec4e		
				Clec5a		
				Crlf2		
				Csf2		
				Csf2rb		
				Csf3r		
				Cx3cr1		
				Cxcl1		
				Cxcr1		
				Cxcr2		
				Cxcr3		
				Cxcr5		
				Ddx58		
				Ebi3		
				Entpd1		
				Fas		
				Fcgr1		
				Fcgr2b		
				Fcgr3		
				Fcgr4		
				Fkbp5		
				H2-Ob		
				H2-Q10		
				Hif1a		
				Icam1		
				Icam4		
				Ifit2		
				Ifitm1		
				Ikbke		
				Ikzf2		
				Ikzf4		
				Il10ra		
				Il13ra1		
				Il15ra		
				Il17ra		
				Il17re		
				Il18rap		
				Il1a		
				Il1b		
				Il1r1		
				Il1r2		
				Il1rap		
				Il1rn		
				Il23a		
				Il4ra		
				Il6ra		
				Il7		
				Irak2		
				Irak3		

AEC-KO	AEC-KO & DC-KO	DC-KO	AEC-KO & *Myd88* null	AEC-KO, DC-KO & *Myd88* null	DC-KO & *Myd88* null	*Myd88* null
				Irf7		
				Itga5		
				Itgam		
				Jak2		
				Lcp2		
				Lilrb3		
				Lilrb4		
				Litaf		
				Ltb		
				Map4k4		
				Mapkapk2		
				Ms4a1		
				Mx1		
				Myd88		
				Nfil3		
				Nfkb1		
				Nfkb2		
				Nfkbia		
				Nfkbiz		
				Notch2		
				Pax5		
				Plaur		
				Pml		
				Psmb10		
				Psmb9		
				Ptafr		
				Ptger4		
				Ptgs2		
				Ptpn2		
				Ptpn22		
				Rela		
				Relb		
				S100a8		
				S100a9		
				Smad3		
				Socs3		
				Stat1		
				Stat2		
				Stat3		
				Syk		
				Tagap		
				Tbk1		
				Tirap		
				Tlr2		
				Tlr3		
				Tnf		
				Tnfaip3		
				Tnfrsf1b		
				Tnfrsf4		
				Tnfsf10		
				Tnfsf14		
				Tnfsf15		
				Traf5		
				Traf6		
				Trem1		
				Tyrobp		
				Xbp1		
				Xcr1		

Supplementary Table 6: Genes whose expression in cDCs is affected at 6h post-OVA/FLA by cell-specific *Myd88* deletion

EC-KO	EC-KO & DC-KO	DC-KO	EC-KO & *Myd88* null	EC-KO, DC-KO & *Myd88* null	DC-KO & *Myd88* null	*Myd88* null
Cd36		Ahr	Bst2	Icam1	Bcl3	Arhgdib
Fcrgr3		Cx3cl1	Cd44	Myd88	Cd274	Atm
Il18r1		Il10ra	Fkbp5	Slamf1	Cd40	B2m
		Irf1	Il18rap	Tlr4	Cd53	Card9
			Itgb2		Csf2rb	Ccl22
			Pdcd1		Ctsc	Ccl3
			Psmb9		Ebi3	Ccl9
					H2-DMa	Ccr2
					Icam4	Ccr7
					Il12b	Ccrl2
					Il2ra	Cd163
					Nfkbia	Cd24a
					Nfkbiz	Cd80
					Socs3	Cd97
					Stat5a	Cx3cr1
					Traf1	Cxcl1
					Traf6	Cxcl3
						Cxcr1
						Cxcr3
						Cybb
						Entpd1
						Fas
						H2-Ob
						Icosl
						Ifngr1
						Ikzf4
						Il1b
						Il1rl1
						Il1rn
						Il22ra2
						Il23a
						Il7r
						Irf7
						Irf8
						Itga5
						Itgax
						Jak3
						Klrd1
						Ly86
						Ncf4
						Nfkb1
						Nfkb2
						Pdcd1lg2
						Prdm1
						Prim1
						Ptgs2
						Ptprc
						Sell
						Spn
						Tlr9
						Tnf
						Tnfaip3
						Tnfrsf9
						Tnfsf14

Supplementary Table 7: Genes whose expression in AMs is affected at 6h post-OVA/FLA by cell-specific *Myd88* deletion

EC-KO	EC-KO & DC-KO	DC-KO	EC-KO & *Myd88* null	EC-KO, DC-KO & *Myd88* null	DC-KO & *Myd88* null	*Myd88* null
C1qbp	Ccl6	Bst1	Batf3	Ahr	Bcl3	Abl1
C2	Cfb	Casp8	Ccr2	Ccl9	Casp3	Arhgdib
C3	Cybb	Cd244	Cd1d1	Clec4e	Ccl3	Batf
Ebi3	Fcgr2b	Cd24a	Fkbp5	Hamp	Ccr5	Bst2
Emr1	Marco	Fcgr3	Itga4	Ifit2	Ccrl2	Casp1
Gpi1	Nt5e	Il12b	Pou2f2	Ikbke	Cd164	Ccl4
Ncf4	Tgfbr1	Il17ra	S100a9	Il6	Cd2	Cish
Plaur		Il6st		Irf4	Cd40	Cx3cl1
		Irak2		Ptgs2	Cd81	Cxcl13
		Itgax		Tlr5	Cdkn1a	Cxcl9
		Lcp2		Traf1	Cfp	Ddx58
		Mif		Traf5	Ctnnb1	Entpd1
		Stat3			Ctsc	Fcgr1
		Tnfsf14			Cxcl1	Il1rn
		Xbp1			Cxcl3	Irak1
					Cxcr1	Irf7
					Cxcr2	Itga6
					Cxcr4	Itgal
					Fas	Itgb2
					Fcgr4	Lilra5
					Fcgrt	Map4k1
					H2-DMa	Msr1
					Hfe	Pecam1
					Icam1	Psmb9
					Icam4	Ptprc
					Icosl	S100a8
					Ifngr1	Serping1
					Il13ra1	Spn
					Il16	Stat1
					Il18	Syk
					Il1a	Tfrc
					Il1b	Tlr3
					Il23a	Tlr4
					Il6ra	Tlr9
					Irak3	Tnfsf12
					Irf1	Tnfsf13b
					Irf8	Traf6
					Itga5	
					Jak2	
					Lair1	
					Ly86	
					Mx1	
					Myd88	
					Nfkb1	
					Nfkb2	
					Nfkbia	
					Nfkbiz	
					Nod2	
					Npc1	
					Pdgfb	
					Pml	
					Prdm1	
					Ptafr	
					Relb	
					Runx1	
					Ski	
					Socs3	
					Tgfb2	
					Tgfbi	
					Tgfbr2	
					Tlr8	
					Tnf	
					Tnfaip3	
					Tnfrsf1b	
					Tnfsf15	
					Traf3	
					Tyrobp	

Table S9. Mechanisms of transcriptional regulation associated with genes with MyD88-dependent, differential ATAC-seq peaks in cDCs

a) DC-KO (0h & 6h)

Expressed (above MTI)									Below MTI	insufficient # of probes
58 genes										
No differential expression	Baseline different; not induced	ANOVA p-value (WT0h v CD11c0h)	Induced through Transcriptional Initiation	ANOVA p-value (WT6h v CD11c6h)	Induced by RNA elongation	ANOVA p-value (WT6h v CD11c6h)	Induced-complex	ANOVA p-value (WT6h v CD11c6h)		
24 genes	15 genes		5 genes		7 genes		7 genes		26 genes	1 gene
Apold1	Arl5c	0.010062	Ccl22	0.174339	Ankrd33b	0.055564	Car13	0.11612	1700022E09Rik	Fjx1
Cd2	Ccl5	0.190427	Cd40	0.002432	Ccr7	0.14106	Fas	0.011033	1700120G07Rik	
Ctf1	Ccrl2	0.028973	Cd69	0.198167	Ehf	0.047722	Foxp4	0.003958	1700126H18Rik	
Cxcl11	Cxcl9	0.133683	Gem	0.025731	Hamp	0.073758	Mab21l3	0.04563	5730403I07Rik	
Cxcr5	Cyba	0.623621	Pla1a	0.035857	IL4i1	0.064785	Pcgf5	0.035548	Adamts4	
Cygb	Ebi3	0.108902			Mmp25	0.008067	Sdc4	0.056201	AW495222	
Edar	H2-m2	0.62844			Nfkbiz	0.012757	St7	0.159857	Cd70	
Emr1	Optn	0.025011							Ddx25	
Fam129a	Ptgs2	0.041435							Efna2	
Gbp4	Sema4a	0.009532							Eno2	
Gm6537	Slc7a7	0.319379							Exoc3l4	
Hsd11b2	Tnfsf4	0.177463							Fam124b	
Ier3	Tnip1	0.009388							Fblim1	
Il10rb	Tpbg	0.062919							Gm11978	
Rab33a	Zhx2	0.122343							Gng4	
Scin									Gypc	
Spib									Itga2b	
Spire1									Lipg	
Stap2									Marco	
Tbc1d1									Mcpt2	
Tle2									Nlrc4	
Tnfrsf14									Ptpn3	
Vash1									Samd14	
Zfp960									Smco3	
									Sspo	
									Tmem151b	

Table S9. Mechanisms of transcriptional regulation associated with genes with MyD88-dependent, differential ATAC-seq peaks in cDCs

b) DC-KO (6h)

Expressed (above MTI)									Below MTI	insufficient # of probes
56 genes										
No differential expression	Baseline different; not induced	ANOVA p-value (WT0h v CD11c0h)	Induced through Transcriptional Initiation	ANOVA p-value (WT6h v CD11c6h)	Induced by RNA elongation	ANOVA p-value (WT6h v CD11c6h)	Induced-complex	ANOVA p-value (WT6h v CD11c6h)		
41 genes	5 genes		4 genes		5 genes		1 gene		86 genes	6 genes
1700025C18Rik	D330050G23Rik	0.019077	Cxcl2	0.032643	Adora2a	0.058721	Il10	0.325664	1700012B09Rik	1110032F04Rik
2200002D01Rik	Gm11110	0.07681	Gm15987	0.110114	Cxcl1	0.051373			1700069L16Rik	Gm17641
Abcc3	Gm13710	0.191412	Serpina3g	0.000734	Cxcl3	0.056186			4930432J09Rik	Mir7649
Akna	Tnf	0.006039	Tmem39a	0.01079	Procr	0.017349			4933401D09Rik	mir6974
Ampd2	Tnfsf9	0.003489			Slc24a1	0.041434			4933407L21Rik	Olfr49
C1qa									Adra1b	Tas2r138
C3									Afap1l2	
Cd300lh									Als2cr12	
Cd8a									Amotl1	
Clec4n									Ankrd22	
Cox4i2									Batf2	
Ctla2b									BC061237	
Dusp14									Ccr10	
Emr4									Cntnap1	
Fam114a1									Col17a1	
G530011O06Rik									Csf2	
Gm11413									D830026I12Rik	
Gm12992									Dchs1	
Gpx3									Dtx1	
H2-Q10									Epdr1	
Ifi47									Fam184a	
Igfbp4									Fam189a2	
Il15									Fcer1a	
Iqsec1									Foxh1	
Klra17									Foxq1	
Lad1									Galr1	
Mb21d2									Gipr	
Mfsd2a									Gm11627	
Ms4a1									Gm19345	
P2ry13									Gnmt	
Paqr8									Gpr110	
Phyhd1									Gprin2	
Ptplad2									Hemgn	
Serpin3f									Heyl	
Serpina3h									Hyal1	
Serpinb1b									Inhba	
Slc28a2									Irg1	
Tcea3									Kcnip2	
Tigit									Krt18	

Xlr
Zfp937

Lbp
Lbx2
Loxl4
Lrrc8e
Lta
Mapk8ip1
Mfi2
Myadml2
Mybphl
Myo5c
Nkx1-2
Nos2
Noxa1
Npb
Nrgn
Nt5c1a
Oaf
Ocln
Olfr175-ps1
Pdzk1ip1
Phlda2
Ppfia2
Prss2
Ranbp17
Rassf6
Rbm44
Rlbp1
Rln1
Rprm
Rtkn
Sapcd1
Slc1a1
Slc6a1
Sox5os3
Srd5a2
Stox2
Tex26
Tfec
Tmem119
Tmod2
Tnfrsf10b
Trib2
Trim58
Vcam1
Wnt9b
Zfp572
Zfp811

Table S9. Mechanisms of transcriptional regulation associated with genes with MyD88-dependent, differential ATAC-seq peaks in cDCs

c) EC-KO (6h)

Expressed (above MTI)							Below MTI	insufficient # of probes
12 genes								
No differential expression	Baseline different; not induced	Induced through Transcriptional Initiation	ANOVA p-value (WT6h v SPC6h)	Induced by RNA elongation	ANOVA p-value (WT6h v SPC6h)	Induced-complex		
8 genes	0 genes	2 genes		2 genes		0 genes	49 genes	6 genes
Aif1		Slc24a1	0.03842	Amica1	0.098335		4930568G15Rik	Cldn9
C1qa		Sult1a1	0.001114	Slamf1	0.193368		9830107B12Rik	Gm10129
Cxcr2							A930001C03Rik	Gm24112
Dok3							Abca8a	Gm25931
Gm14341							Adra1b	Mir5123
Nfic							Ak7	Mkrn3
Serpina3f							Ankrd60	
Serpina3g							Anks1b	
							Bean1	
							Bfsp1	
							Cfb	
							Crispld1	
							D930007P13Rik	
							Dnah11	
							Dnaic2	
							Dsp	
							Fgf22	
							Fpr2	
							Fpr3	
							Gipr	
							Glis1	
							Glt28d2	
							Gm11978	
							Gm16070	
							Gm24804	
							Gnmt	
							Gpr110	
							Ica1	
							Kcnip2	
							Krt18	
							Maneal	
							Mapk12	
							Mapk8ip1	
							Mybphl	
							Nkain4	
							Nutm1	
							Pcdhga11	
							Ppl	
							Prss2	
							Rab34	
							Rhod	
							Selenbp1	
							Sgsm1	
							Slc6a1	
							Tdrd5	
							Tmem151a	
							Vwa7	
							Wnt1	
							Zfp772	

Supplementary Table 10. Control of gene expression in cDCs by cell-intrinsic and -extrinsic MyD88 signaling

Gene Symbol (Cd11c-MYD88 dep)	Fold Change (linear) (SPC-6h vs. WT-6h)	ANOVA p-value (SPC-6h vs. WT-6h)	Fold Change (linear) (CD11c-6h vs. WT-6h)	ANOVA p-value (CD11c-6h vs. WT-6h)	Fold Change (linear) (KO-6h vs. WT-6h)	ANOVA p-value (KO-6h vs. WT-6h)
Tnfsf9	-1.37	0.338717	-121.59	0.070077	-50.13	0.011913
Tnf	-1.43	0.411276	-36.66	0.005067	-40.29	0.006556
Il12b	1.09	0.587694	-35.17	0.009287	-8.06	0.003549
Gm10462	-1.05	0.953278	-31.94	0.230912	-3.43	0.2738
Nfkbiz	-1.58	0.123099	-27.98	0.012757	-14.23	0.009179
Tnfaip3	-1.69	0.128444	-25.11	0.004562	-16.42	0.005051
Nfkbia	-1.29	0.012619	-18.93	0.010888	-10.93	0.000173
Cd40	-1.69	0.210216	-15.11	0.002432	-12.8	0.002901
Dusp2	-1.6	0.230608	-12.74	0.002973	-10.08	0.005281
Orm2	-1.86	0.21424	-12.38	0.001418	-6.66	0.00145
Mmp25	-1.51	0.170102	-9.58	0.008067	-4.05	0.01137
Arl5c	-1.04	0.919909	-9.45	0.096752	-6.73	0.037522
Tgif1	-1.95	0.012248	-9.3	0.003535	-6.73	0.003026
Ptgs2	-1.03	0.895866	-9.28	0.012555	-7.17	0.039175
Ly75	-1.67	0.100231	-9.05	0.026953	-9.05	0.004559
Pik3r5	-1.44	0.058751	-8.49	0.044387	-6.31	0.010373
Ptafr	1.03	0.950332	-8.42	0.033099	-2.03	0.168514
Cd274	-1.74	0.276093	-8.04	0.089825	-16.04	0.030025
Bcl3	-1.49	0.060862	-8	0.016167	-3.21	0.003088
Ppp1r15a	-1.25	0.143701	-7.83	0.049767	-2.92	0.043507
Il1rn	-1.41	0.441123	-7.76	0.001381	-11.96	0.015136
Il2ra	1.23	0.614564	-7.52	0.002127	-6.97	0.000448
Rapgef2	1.18	0.458	-7.47	0.003527	-3.65	0.026318
Swap70	1.22	0.270471	-7.4	0.108981	-3.74	0.014074
Eid3	1.42	0.528146	-7.39	0.121127	-2.31	0.33511
Lrrc32	-1.43	0.139761	-7.22	0.070775	-3.67	0.04323
Cflar	-1.38	0.215976	-7.07	0.002845	-6.17	0.005214
Birc3	-1.19	0.300611	-7.01	0.004921	-4.37	0.008908
Sema7a	-1.23	0.700636	-6.82	0.068193	-2.05	0.31886
Kif21b	1.21	0.232408	-6.74	0.043882	-3.48	0.020164
Orm3	-1.6	0.080214	-6.63	0.017728	-9.03	0.002284
Traf1	1.04	0.654551	-6.54	0.107335	-2.64	0.004356
Tmem39a	1.05	0.760883	-6.46	0.01079	-7.71	0.014034
Nfkbid	-1.52	0.261178	-6.46	0.042764	-4.9	0.020825
Birc2	-1.15	0.558421	-6.29	0.019031	-4.1	0.035801
Plat	-1.82	0.367861	-6.27	0.057314	-4.92	0.073364
Slc41a1	-1.93	0.037108	-6.26	0.00427	-4.54	0.007697
Tank	-1.12	0.550613	-6.18	0.003724	-2.95	0.015387
Clec2d	-1.26	0.479065	-6.06	0.071442	-2.47	0.06352
Csrnp1	-1.67	0.239606	-6.06	0.088298	-2.3	0.024491
1700047I17Rik2	-1.42	0.319554	-6.05	0.043958	-6.09	0.009943
Itga5	1.04	0.887039	-5.8	0.073328	-2.36	0.041944
Zc3h12c	-1.37	0.256263	-5.74	0.004051	-4.55	0.013771
Il10ra	-1.37	0.612721	-5.72	0.080947	-4.13	0.115409
Tnfaip2	-1.72	0.092233	-5.62	0.001469	-6.02	0.000487
Stat5a	-1.32	0.089571	-5.56	0.03603	-4.5	0.004562
Uchl4	-1.12	0.561424	-5.44	0.015203	-2.48	0.080939
Ccl22	-1.19	0.321505	-5.24	0.174339	-3.36	0.002952
Sdc4	-1.49	0.161008	-5.22	0.056201	-5.79	0.016332
Gm10197	-1.84	0.345472	-5.11	0.188977	-2.79	0.278618
Myo1g	-1.11	0.43639	-5.1	0.088165	-3.09	0.000421
Tspan33	-1.94	0.070051	-4.93	0.005612	-4.82	0.002188
Pvr	-1.85	0.063348	-4.9	0.000591	-2.95	3.04E-08
Pfkfb3	-1.96	0.004891	-4.9	0.109042	-2.63	0.002607
Tk1	-1.58	0.03972	-4.87	0.072172	-2.94	0.008103
Orm1	-1.41	0.203919	-4.84	0.001298	-5.78	0.00096
Nfkb1	-1.77	0.010953	-4.82	0.028085	-4.9	0.000728
Fscn1	-1.3	0.016178	-4.82	0.261804	-3.01	0.027493
Slfn2	-1.53	0.348219	-4.79	0.027918	-3.16	0.027931
Txnrd1	-1.4	0.108912	-4.79	0.026644	-2.76	0.02185
Ehd1	-1.48	0.100189	-4.77	0.019542	-3.14	0.006773
Sowahc	-1.13	0.824642	-4.7	0.001759	-4.23	0.090005
Poglut1	1.41	0.187052	-4.7	0.04988	-3.53	0.022795
Rnf19b	-1.1	0.562647	-4.62	0.019309	-4.79	0.006342
Map3k8	-1.54	0.27055	-4.61	0.074423	-3.36	0.066248
Afmid	-1.99	0.059039	-4.51	0.088476	-3.48	0.006895
Casp4	-1.15	0.660997	-4.49	0.062415	-3.8	0.079408
Procr	-1.34	0.33016	-4.47	0.017349	-3.84	0.006676
Ccr7	-1.78	0.032485	-4.4	0.14106	-3.21	0.098743
Herpud1	1.27	0.510081	-4.37	0.097353	-2.57	0.084992

Gene Symbol (EC-MYD88 dep)	Fold Change (linear) (SPC-6h vs. WT-6h)	ANOVA p-value (SPC-6h vs. WT-6h)	Fold Change (linear) (CD11c-6h vs. WT-6h)	ANOVA p-value (CD11c-6h vs. WT-6h)	Fold Change (linear) (KO-6h vs. WT-6h)	ANOVA p-value (KO-6h vs. WT-6h)
S100a8	-12.27	0.144594	-1.42	0.894939	-23.95	0.054409
Vdr	-4.79	0.019396	-1.88	0.08659	-2.85	0.135368
Rnf169	-3.46	0.088161	-1.59	0.516802	-3.64	0.073889
Fkbp5	-3.4	0.005372	-1.77	0.036819	-3.72	0.006858
Plet1	-3.27	0.013284	-1.09	0.63972	-4.62	0.008493
Lifr	-3.2	0.016174	1.38	0.533181	-2.21	0.029484
Amica1	-3.08	0.098335	-1.96	0.153183	-3.68	0.055816
Mt2	-2.98	0.118165	-1.8	0.125033	-2.54	0.091858
Ap1s2	-2.93	0.002965	1.19	0.623445	-2.33	0.007934
Ppap2a	-2.46	0.196149	-1.08	0.930773	-3.64	0.029661
Gm15250	-2.4	0.075904	-1.74	0.134552	-2.74	0.023943
Gda	-2.36	0.120692	-1.35	0.43064	-2.29	0.207234
Enah	-2.35	0.005795	-1.02	0.964515	-2.5	0.003034
Acvr2a	-2.3	0.071394	-1.11	0.829294	-2.44	0.092053
S100a9	-2.28	0.451309	-1.49	0.701988	-4.99	0.206339
Glul	-2.28	0.094752	-1.4	0.348867	-2.06	0.081919
Tns1	-2.26	0.060063	-1.63	0.138554	-2.89	0.042981
Gpr141	-2.25	0.01897	-1.34	0.090127	-2.14	0.116632
Hist2h2aa1	-2.19	0.33546	-1.2	0.842145	-2	0.380619
Kmo	-2.18	0.181872	-1.8	0.208579	-3.11	0.126679
Tsc22d3	-2.14	0.024438	-1.97	0.037144	-2.33	0.040248
Bcar3	-2.07	0.126715	-1.95	0.028399	-3	0.007825
St7	-2.05	0.003135	-1.82	0.159857	-4	0.002427
Pfkp	-2.05	0.052389	-1.74	0.131646	-2.1	0.058564
Gm10800	-2.05	0.085435	1.17	0.787973	-2.32	0.199616
Il7r	-2.04	0.126853	-1.2	0.728577	-2.2	0.223597
Stk39	-2.03	0.226896	-1.98	0.101046	-2.36	0.036083
Clec2f	-2.02	0.082392	-1.79	0.11266	-2.13	0.123341
Klri2	2	0.093163	1.75	0.267655	2.44	0.058892
Nucb2	2	0.12523	1.76	0.006415	3.16	0.027355
Hexa	2.02	0.02216	-1.27	0.726247	2.63	0.020292
Plcb2	2.05	0.043005	1.37	0.460786	2.86	0.006549
Cxx1b	2.13	0.146912	1.81	0.57297	2.97	0.124759
Pilrb1	2.14	0.045441	1.51	0.413764	3.01	0.034387
Emr4	2.2	0.178944	-1.31	0.150212	2.38	0.036056
Klri1	2.2	0.144267	1.79	0.267904	3.56	0.068929
Hpgds	2.21	0.13636	1.45	0.211565	3.59	0.01792
Anapc13	2.21	0.0776	1.86	0.3083	3.49	0.016559
Myo1f	2.24	0.002737	-1.11	0.909299	3.22	0.000864
Ddit3	2.24	0.007279	1.31	0.389306	2.48	0.074195
Card11	2.27	0.014247	1.04	0.962019	2.76	0.004117
Gm14274	2.28	0.001223	1.23	0.417879	2.13	0.031427
Gbp8	2.33	0.010032	-1.11	0.625122	2.62	0.057464
Ctsc	2.34	0.021735	1.86	0.080842	3.46	0.016164
Nlrp1c-ps	2.35	0.09946	-1.01	0.980693	2.27	0.162255
Arsb	2.36	0.174733	1.49	0.452782	3.03	0.108669
Pgap1	2.43	0.026876	1.45	0.508756	2.09	0.131286
Ccnd1	2.47	0.001567	1.22	0.429878	4.07	0.014298
Abcg3	2.49	0.000246	1.24	0.48	3.42	0.000389
F2rl2	2.49	0.046562	1.65	0.028696	2.47	0.010013
Lgals1	2.5	0.080914	-1.03	0.880055	2.33	0.118759
Tnfsf13b	2.53	0.040712	1.67	0.343904	2.66	0.043214
Smim15	2.56	0.20632	1.84	0.289155	2.49	0.126415
Gm13772	2.59	0.077993	1.33	0.625202	2.06	0.138187
Cd44	2.63	0.009851	1.19	0.699789	4.19	0.007267
H2-M2	2.68	0.08985	-1.3	0.437257	2.7	0.087552
Bst2	2.91	0.157318	-1.84	0.598001	5.97	0.018271
Pilra	3.11	0.061444	1.71	0.307113	2.35	0.104983
Pdlim1	3.49	0.014926	1.7	0.029581	5.05	0.012516
Hspa1b	4.13	0.120222	1.65	0.629732	2.26	0.372598
Hsph1	4.48	0.027696	1.3	0.804563	2.58	0.065623
Gm20481	4.65	0.200778	-1.28	0.884221	3.04	0.52542
Gm15428	5.3	0.283414	-1.06	0.883248	2.11	0.184829
Hspa1a	5.31	0.051175	1.25	0.854198	2.84	0.461267

Clec4a1	1.62	0.007827	-4.34	0.153479	-2.19	0.044963
3110043O21Rik	-1.2	0.313208	-4.29	0.015067	-3.22	0.011674
Il1b	-1.3	0.19188	-4.26	0.006276	-4.43	0.044471
Etv3	-1.01	0.937106	-4.23	0.06884	-2.25	0.040407
Tlr13	1.13	0.886176	-4.21	0.019211	-3.15	0.011862
Nfkb2	1.01	0.931852	-4.21	0.05568	-2.81	0.001444
Bcl2l1	-1.44	0.436838	-4.16	0.101566	-2.48	0.005872
Mllt6	-1.47	0.224135	-4.1	0.032772	-4.43	0.004594
Clcf1	-1.95	0.020693	-4.07	0.018989	-3.87	0.006762
Rab21	-1.49	0.305213	-3.98	0.038908	-3.09	0.058014
Bhlhe40	-1.17	0.435442	-3.98	0.141267	-2.1	0.021912
Sema4a	-1.13	0.085358	-3.97	0.109354	-2.52	0.00531
Slc2a6	1.37	0.240711	-3.97	0.085795	-2.34	0.025095
Irak2	-1.71	0.149913	-3.97	0.090889	-2.3	0.078751
Ehf	1.24	0.634354	-3.96	0.047722	-4.08	0.078401
Tbc1d4	1.05	0.72393	-3.88	0.027651	-3.09	0.0073
Tspan3	-1.23	0.520859	-3.88	0.007489	-2.37	0.006426
Crtc2	-1.6	0.145825	-3.83	0.018408	-3.53	0.00119
Gm614	-1.59	0.024354	-3.78	0.075601	-2.74	0.007091
Ccrl2	-1.26	0.325342	-3.74	0.049408	-2.67	0.153424
Rab8b	-1.44	0.010047	-3.71	0.077022	-2.09	0.031139
Nup62-il4i1	1.07	0.825022	-3.69	0.064785	-3.48	0.037234
Nrp2	-1.25	0.533116	-3.66	0.013419	-4.73	0.002236
Cacfd1	1.39	0.282125	-3.59	0.002407	-3.04	0.017777
Zbtb18	-1.16	0.62877	-3.59	0.040897	-2.21	0.081992
Traf6	-1.48	0.07614	-3.54	0.013578	-3.97	0.015032
Aebp2	-1.52	0.053059	-3.54	0.033717	-3.82	0.005702
Tmem63b	1.27	0.162016	-3.54	0.010143	-2.63	0.030224
Tmem19	-1.47	0.436409	-3.51	0.098763	-2.79	0.039183
Cx3cl1	-1.78	0.025217	-3.5	0.005365	-2.65	0.022681
Adora2a	-1.11	0.714937	-3.47	0.058721	-3	0.028417
Mmp14	-1.78	0.11591	-3.46	0.006981	-3.97	0.018483
Aldh1a2	-1.66	0.328105	-3.44	0.237952	-5.29	0.011629
Bcl2a1c	-1.81	0.144633	-3.42	0.008064	-5.03	0.007255
Car13	1.68	0.337471	-3.4	0.11612	-4.54	0.056321
Il6	-1.09	0.871534	-3.38	0.079342	-3.02	0.017246
Nfkbib	-1.06	0.843313	-3.37	0.057766	-2.57	0.019385
Srp54c	-1.23	0.078371	-3.37	0.010979	-2.23	0.003039
Tle3	-1.39	0.346752	-3.37	0.041387	-2.12	0.011635
Jak2	-1.56	0.110713	-3.36	0.002273	-3.34	0.004445
Gm9320	-1.48	0.062869	-3.36	0.005783	-2.32	0.060527
Mki67	-1.26	0.437477	-3.33	0.035802	-3.61	0.024619
Mab21l3	-1.21	0.347413	-3.32	0.045363	-3.95	0.006256
Tnip1	1.21	0.028809	-3.32	0.000954	-3.02	0.006373
Gem	-1.99	0.209297	-3.31	0.025731	-4.8	0.040364
Gm20689	-1.6	0.066889	-3.31	0.056542	-2.33	0.038839
Myd88	-1.5	0.278233	-3.3	0.00746	-3.1	0.003199
Dennd4b	-1.38	0.196745	-3.27	0.164872	-2.1	0.028587
Mreg	1.08	0.728661	-3.23	0.025466	-3.34	0.034323
Apaf1	-1.54	0.056277	-3.21	0.024936	-2.91	0.01574
4932438H23Rik	-1.74	0.007309	-3.19	0.12022	-4.45	0.023671
Zfp703	-1.44	0.129199	-3.18	0.233111	-2.48	0.063595
Apobec3	-1.89	0.039826	-3.16	0.00648	-3.54	0.005308
Sema4c	-1.9	0.029429	-3.16	0.008856	-2.61	0.022933
Ncf1	-1.1	0.688112	-3.1	0.153276	-2.18	0.043764
Cxcr4	-1.81	0.096682	-3.09	0.267997	-2.6	0.040439
Zfp36l1	-1.34	0.270102	-3.08	0.133891	-2.68	0.033073
1700034J05Rik	1.28	0.235299	-3.07	0.013059	-2.26	0.07213
Rap2a	-1.61	0.238634	-3.05	0.065537	-3.5	0.053621
Htr7	-1.8	0.228808	-2.98	0.107787	-4.25	0.032364
Spred1	-1.32	0.476775	-2.98	0.026416	-3.16	0.052984
Slc9a3r1	1.03	0.856616	-2.94	0.058624	-2.34	0.036226
Osgin2	1.04	0.874938	-2.94	0.025874	-2.08	0.116116
Cpeb4	-1.22	0.412288	-2.93	0.030109	-2.73	0.008934
Prdm1	-1.5	0.529514	-2.92	0.097405	-5.22	0.043852
Lamtor3	-1.98	0.038598	-2.92	0.053323	-2.34	0.008835
Slc24a1	-1.52	0.038242	-2.9	0.041434	-3.4	0.017945
Tmem120b	-1.56	0.461036	-2.86	0.108325	-2.45	0.12316
Clec2j	-1.44	0.283195	-2.86	0.004514	-2.32	0.050442
4932442E05Rik	1.48	0.226809	-2.86	0.079413	-2.04	0.057709
Sdhaf1	-1.73	0.208362	-2.84	0.065086	-2.71	0.044587
Rel	-1.39	0.00362	-2.84	0.002078	-2.36	0.00117
Snd1	-1.6	0.072982	-2.83	0.138141	-2.69	0.040901
Ggta1	-1.23	0.141605	-2.82	0.193385	-4.52	0.001486
Malt1	-1.49	0.087032	-2.82	0.004404	-3.01	0.020178

Slc30a4	-1.7	0.294514	-2.82	0.13418	-2.44	0.147586
Gm15953	1.09	0.822934	-2.81	0.0012	-2.24	0.015786
Rras2	-1.34	0.2569	-2.8	0.021541	-3.55	0.119767
Rab12	-1	0.994061	-2.8	0.055346	-2.29	0.110199
2610024D14Rik	-1.8	0.219594	-2.79	0.072255	-2.06	0.076878
Mxd1	-1.08	0.515864	-2.76	0.096936	-2.42	0.008768
Sbds	-1.9	0.069259	-2.76	0.045058	-2.05	0.069643
Foxp4	-1.05	0.543509	-2.75	0.003958	-3.18	0.010813
Ccnd2	-1.99	0.088219	-2.73	0.001851	-4.43	0.003917
Tspo	1.28	0.743259	-2.73	0.30167	2.41	0.343832
Gnai3	-1.27	0.000657	-2.72	0.104385	-2.03	0.035555
Itga4	-1.34	0.354288	-2.68	0.002039	-2.79	0.006884
Flnb	-1.16	0.216247	-2.66	0.066819	-2.13	0.000312
Ndrg1	-1.46	0.309567	-2.63	0.04784	-4.31	0.020215
E130208F15Rik	-1.8	0.079458	-2.6	0.081641	-2.77	0.030035
Pus10	-1.21	0.125942	-2.59	0.12639	-3.03	0.005222
Tarm1	-1.46	0.332511	-2.58	0.152738	-3.91	0.011307
St8sia4	-1.07	0.69868	-2.58	0.041638	-2.25	0.039365
Dennd4a	-1.41	0.007072	-2.57	0.00503	-2.06	0.009343
Gpr55	-1.65	0.173368	-2.56	0.034136	-3.09	0.01145
Lrrk1	-1.48	0.080737	-2.56	0.070545	-2.22	0.009779
Skil	-1.42	0.017101	-2.55	0.002264	-2.11	0.002826
Galnt7	-1.8	0.127317	-2.53	0.009547	-2.57	0.026874
Fabp5	1.29	0.301466	-2.51	0.070207	-5.16	0.014445
Otulin	-1.34	0.199147	-2.5	0.177039	-2.01	0.078134
Etv6	-1.02	0.733932	-2.48	0.00365	-2.12	0.009344
Slc22a15	-1.92	0.103323	-2.47	0.016523	-2.63	0.01931
Tmem131	-1.3	0.383255	-2.47	0.147385	-2.48	0.005778
Trim35	-1.22	0.091419	-2.47	0.234327	-2.47	0.008183
Casc3	-1.06	0.77239	-2.46	0.153887	-2.03	0.052108
Slc11a2	-1.56	0.12756	-2.42	0.071131	-2.22	0.041097
Clec2g	-1.4	0.154611	-2.41	0.003314	-2.16	0.055897
Med10	-1.07	0.844899	-2.4	0.032068	-3.44	0.203557
Zfc3h1	-1.28	0.00183	-2.4	0.003372	-3.41	0.010417
Stat5b	-1.13	0.393427	-2.4	0.07458	-2.36	0.008851
Stard7	-1.28	0.225127	-2.39	0.079283	-2.36	0.061448
Stx6	-1.12	0.68314	-2.39	0.078409	-2.28	0.042177
Ncoa7	-1.64	0.032859	-2.38	0.012466	-2.89	0.009267
Kcnk6	-1.34	0.019648	-2.38	0.009938	-2.65	0.003528
Pdlim7	-1.1	0.489306	-2.38	0.01747	-2.05	0.051679
Ms4a4a	-1.91	0.05383	-2.36	0.179286	-3.43	0.012455
Stx19	-1.48	0.264375	-2.34	0.036915	-2.19	0.069147
Cacnb3	1.29	0.191048	-2.34	0.37036	-2.09	0.070579
Ktn1	-1.34	0.459703	-2.31	0.009222	-3.3	0.00123
Actn1	-1.07	0.548571	-2.29	0.098653	-2.24	0.00421
Timp1	-1.47	0.219581	-2.28	0.052217	-2.42	0.209583
Ccl9	-1.56	0.002277	-2.28	0.088202	-2.33	0.224681
Rcl1	-1.36	0.35252	-2.27	0.027262	-2.63	0.002773
Abtb2	-1.65	0.145069	-2.27	0.014541	-2.36	0.002795
Synj1	-1.52	0.057894	-2.27	0.016063	-2.35	0.009551
Gpr52	1.08	0.521895	-2.27	0.079446	-2.27	0.078947
Large	-1.63	0.155299	-2.26	0.0003	-4.56	0.000304
Gpr126	1.09	0.883325	-2.22	0.265049	-2.55	0.17682
Dph5	-1.15	0.708492	-2.2	0.037553	-2.7	0.003776
Cblb	-1.31	0.260172	-2.2	0.038204	-2.09	0.027167
Rgs1	-1.77	0.143424	-2.19	0.074352	-3.58	0.098304
Adam23	-1.42	0.241832	-2.18	0.014301	-3.5	0.011552
Rhoc	-1.48	0.160066	-2.17	0.024133	-2.29	0.098234
Tagap	1.08	0.796212	-2.16	0.259518	-2.27	0.112062
Stxbp3b	-1.86	0.175575	-2.14	0.07409	-2.04	0.070228
Ext1	-1.75	0.183123	-2.13	0.043877	-2.43	0.045791
Tet2	-1.67	0.132462	-2.12	0.065349	-2.54	0.07321
Tbc1d17	-1.03	0.891847	-2.12	0.03188	-2.21	0.009981
Pla1a	-1.49	0.280974	-2.1	0.035857	-3.2	0.015692
Plxna1	-1.94	0.102049	-2.1	0.02743	-2.15	0.020903
Samsn1	-1.24	0.526048	-2.09	0.009963	-2.19	0.003493
Nfat5	-1.36	0.154197	-2.09	0.018994	-2.01	0.018848
Dnajc10	-1.61	0.045071	-2.08	0.015578	-2.77	0.059053
Mpp5	-1.24	0.269634	-2.08	0.023544	-2.29	0.007562
Pde1b	-1.54	0.01748	-2.07	0.169938	-2.45	0.009921
Pdcd1lg2	-1.69	0.450188	-2.04	0.271269	-4.57	0.097529
Gm16147	-1.72	0.028979	-2.04	0.036294	-2.6	0.026365
Fas	-1.25	0.500999	-2.03	0.011033	-7.65	0.004485
Marcks	-1.26	0.067674	-2.03	0.015036	-2.11	0.047331
Hamp2	-1.64	0.263669	-2.01	0.056292	-2.05	0.001093

Iscu	-1.28	0.615635	-2	0.03611	-3.12	0.006883
Ikzf4	-1.53	0.006507	-2	0.002659	-2.39	0.009089
Zc3h12a	-1.01	0.796173	-2	0.014607	-2.04	0.039299
Sycp2	-1.44	0.175309	2	0.278179	2.57	0.191571
Cx3cr1	1.36	0.383245	2	0.245252	3.67	0.020306
Klf4	1.26	0.465684	2.01	0.265342	3.9	0.039225
Mef2c	1.34	0.07415	2.02	0.02843	2.43	0.012475
Gfod1	1.87	0.028467	2.02	0.019758	2.57	0.088447
Dhrs9	1.36	0.389582	2.1	0.089414	2.84	0.040289
Med7	1.5	0.016722	2.11	0.054564	2.13	0.036974
Arl11	1.12	0.842092	2.12	0.377808	2.17	0.005693
Il1rl1	-1.23	0.541406	2.12	0.047355	2.44	0.270442
Emp1	1.03	0.80338	2.16	0.012535	3.38	0.038449
Pigf	1.13	0.686386	2.23	0.220686	2.18	0.094369
Tm6sf1	-1.15	0.602218	2.27	0.036823	2.7	0.081507
Hdgfrp3	1.24	0.207412	2.35	0.086406	2.5	0.008417
Arrdc3	1.65	0.185997	2.38	0.091185	2.12	0.098666
Rnase6	1.57	0.101951	2.38	0.076038	2.54	0.006488
Tiparp	-1.32	0.443198	2.39	0.012473	4.27	0.020412
Cd84	1.59	0.503396	2.41	0.121272	2.3	0.164235
Lst1	1.76	0.53054	2.41	0.016147	5.12	0.03509
Dpep2	1.13	0.26156	2.46	0.018717	2.31	0.041074
D130062J21Rik	1.26	0.729859	2.46	0.0708	2.75	0.213829
Hepacam2	1.24	0.195519	2.48	0.015766	2.63	0.022667
Klrd1	1.28	0.22382	2.58	0.154897	2.82	0.03888
Hcst	1.71	0.131739	2.9	0.134892	2.43	0.011948
Al467606	-1.29	0.416194	3.16	0.309792	2.13	0.343779
Fam71a	1.96	0.098672	3.32	0.095472	3.18	0.024282
Gm4199	1.43	0.524246	3.34	0.0254	2.03	0.276348
Cd200r1	1.6	0.011408	3.45	0.114452	2.25	0.039032
Dcstamp	1.31	0.25373	3.87	0.071401	5.48	0.091184
Gm10337	1.69	0.176968	4.59	0.024781	3.31	0.246686