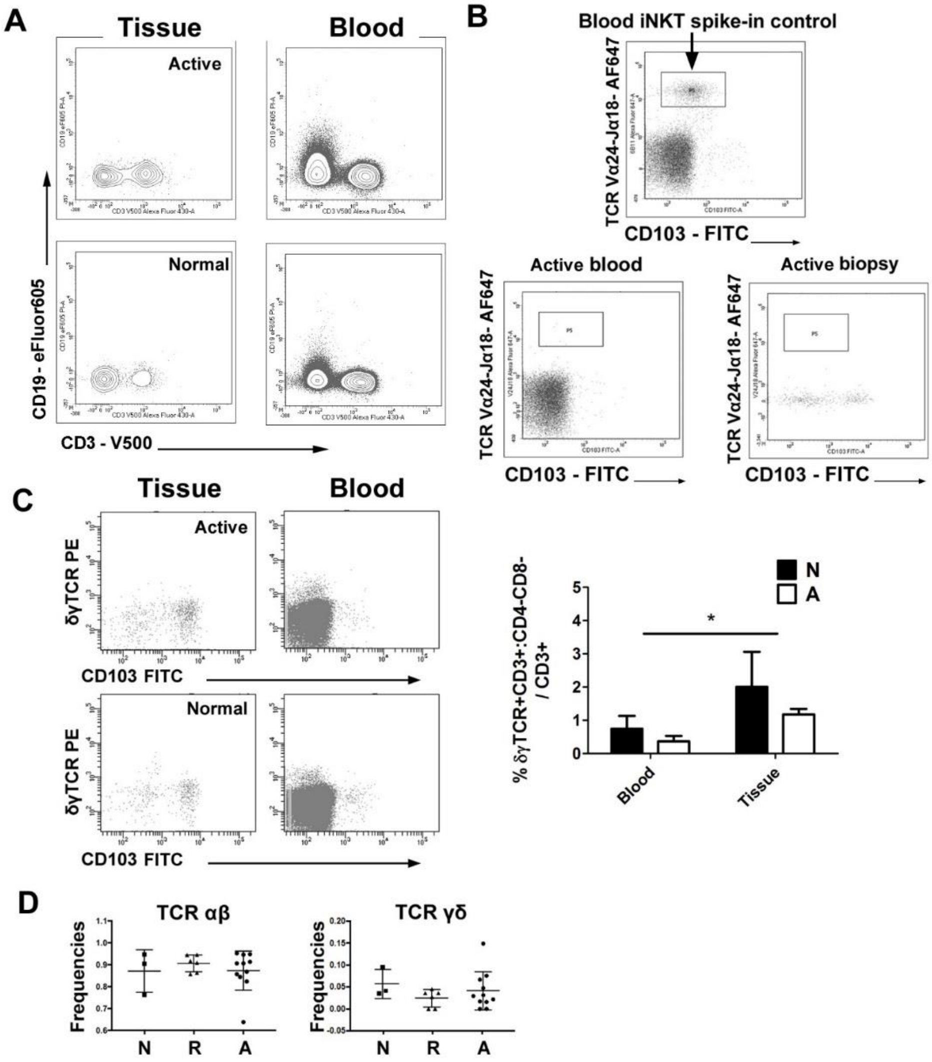
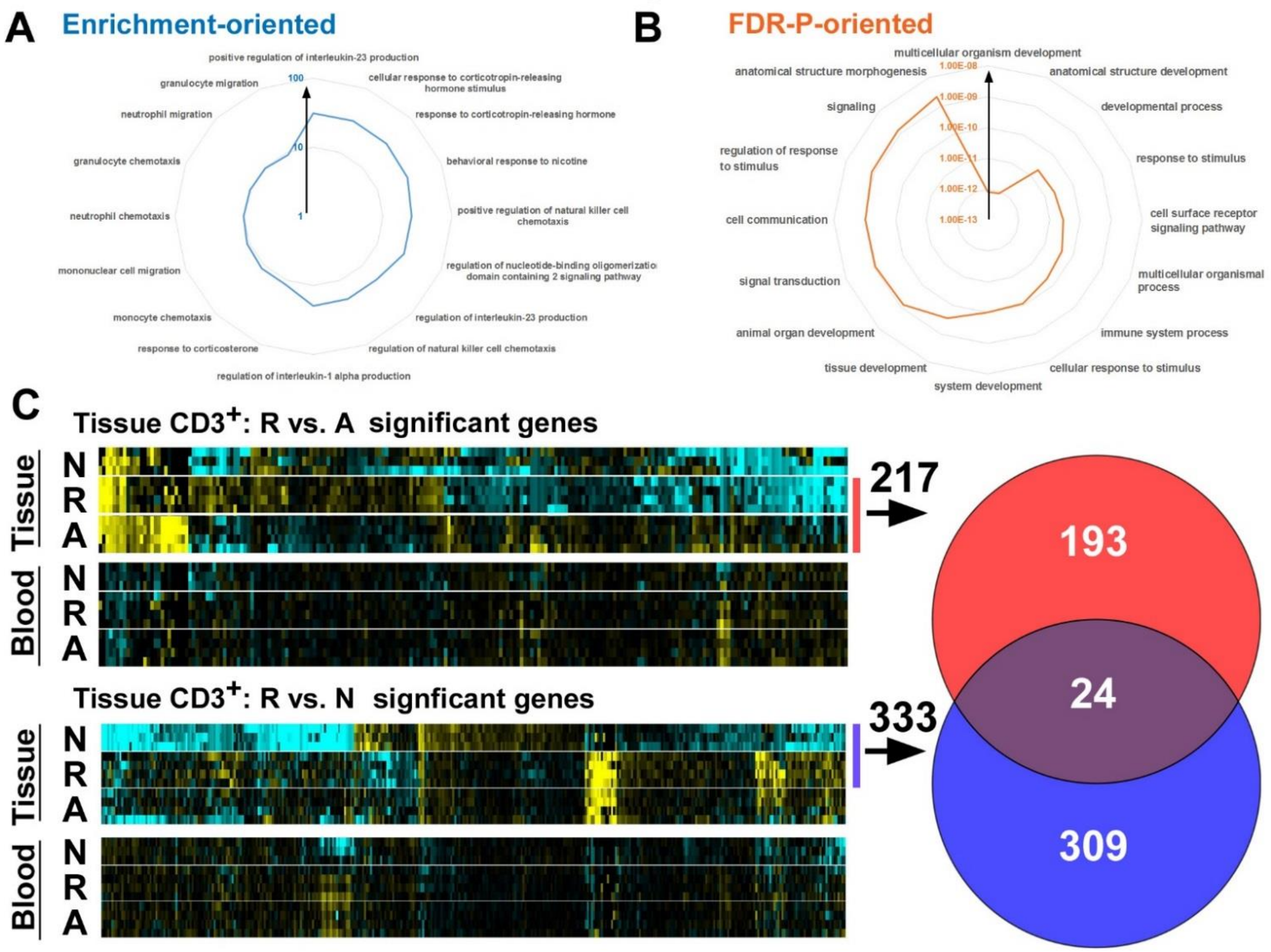
Supplementary Figures:

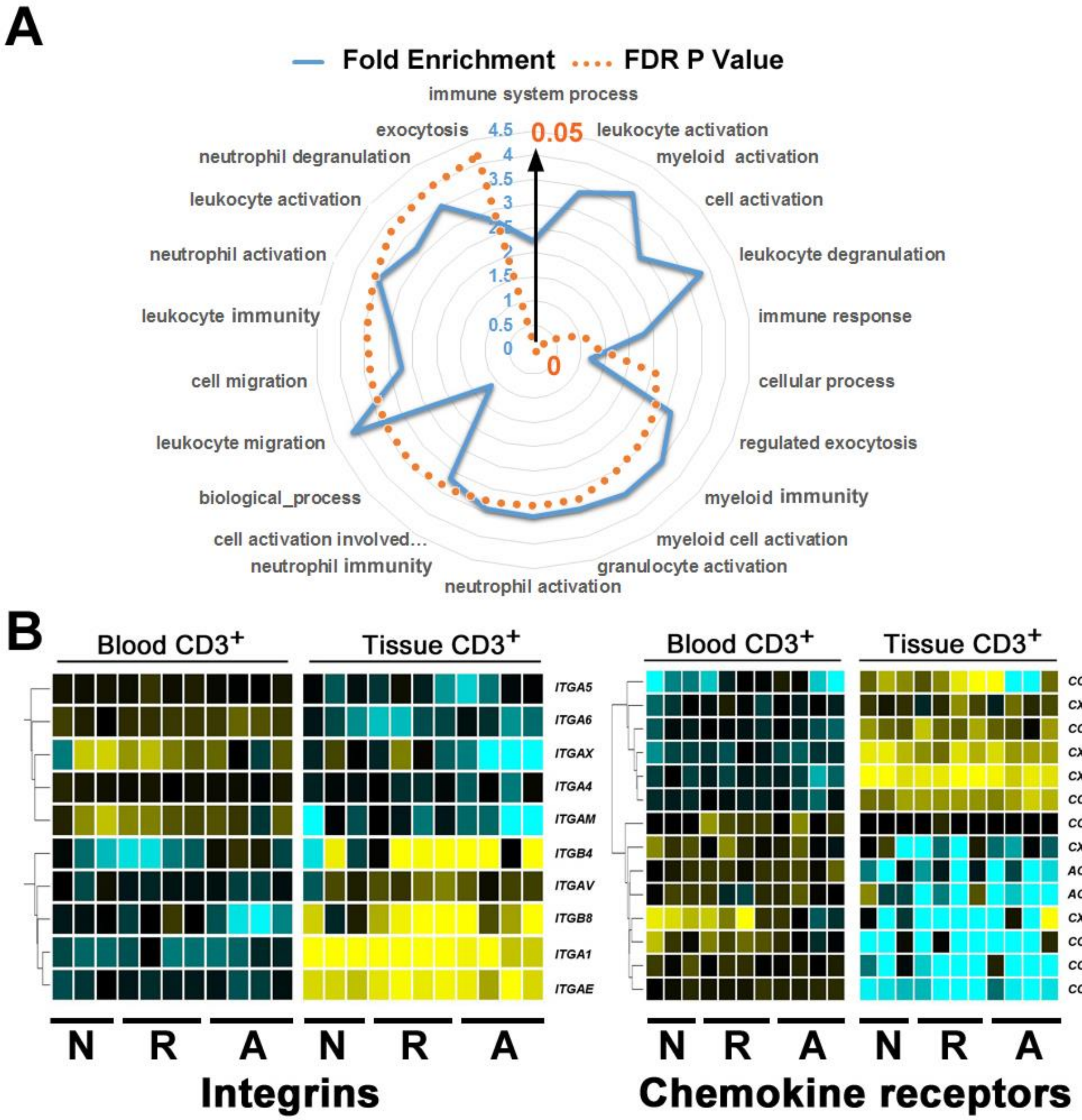


S Figure 1. Cellular and molecular presence of B cells, iNKT cells, and δγTCR T cells in allergic inflammatory tissue.

A, CD45+ events isolated from biopsy tissue and autologous blood were gated and double-plotted for CD19 (for B cells) and CD3 (for T cells) in the context of normal (N) and active disease (A). B, Cellular presence of iNKT cells, identified by the invariant TCR Vα24-Jα18, as assessed in active disease biopsy and autologous blood tissue, with a spike-in of the iNKT cell line (upper panel) as the positive staining control. C, The % CD4 frequency of δγT cells was assessed by FACS (anti-δγTCR staining) in the context of normal vs. active disease. D, The frequencies of δγT cells were also assessed by extracting the entire TCR sequence pool from scRNA-seq of the 1088 tissue T cells, followed by computerized enumeration. N, normal; R, remission; A, active EoE.

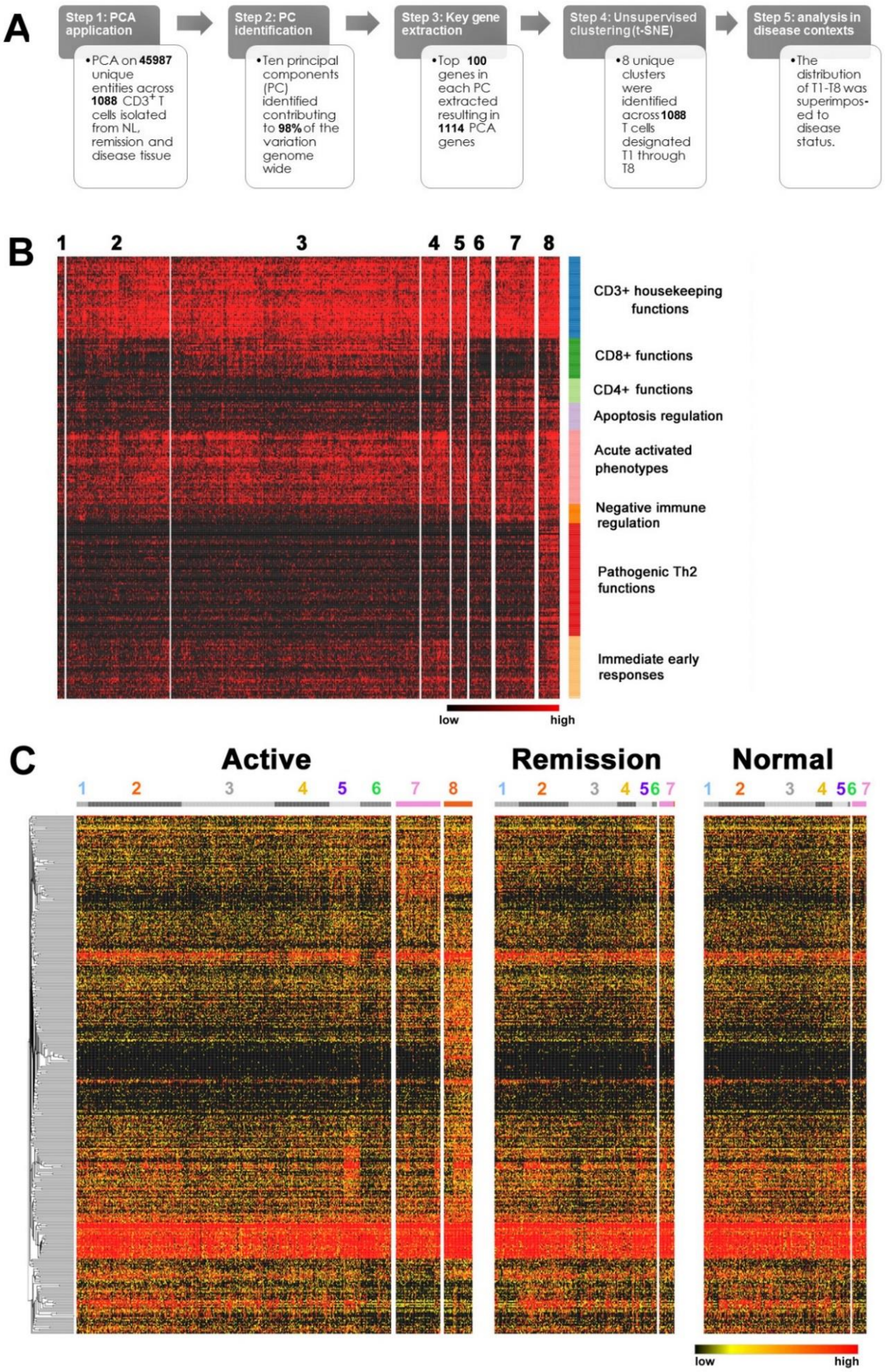


S Figure 2. Gene ontology analysis of the tissue lymphocyte-specific genes in disease context. The full list of GO function nodes shown with two approaches, namely enrichment priority (A) and FDR-adjusted p value priority (B), with the radar scanning map representing the top contributing biofunction nodes derived from the 331 tissue-specific genes. C, The signatures of remission (R) tissue lymphocytes signature were compared to those of active (A) and normal (N) tissue lymphocytes genome wide (Mann-Whitney test, FDR-adjusted $p < 0.05$, fold change > 2), resulting in 217 and 333 significant genes, respectively. Heat maps in the context of all tissue and disease activities types were shown. The Venn gram for overlapping genes between the two cohorts were exhibited on the right. The gene lists were exhibited in Table S4 A and B.

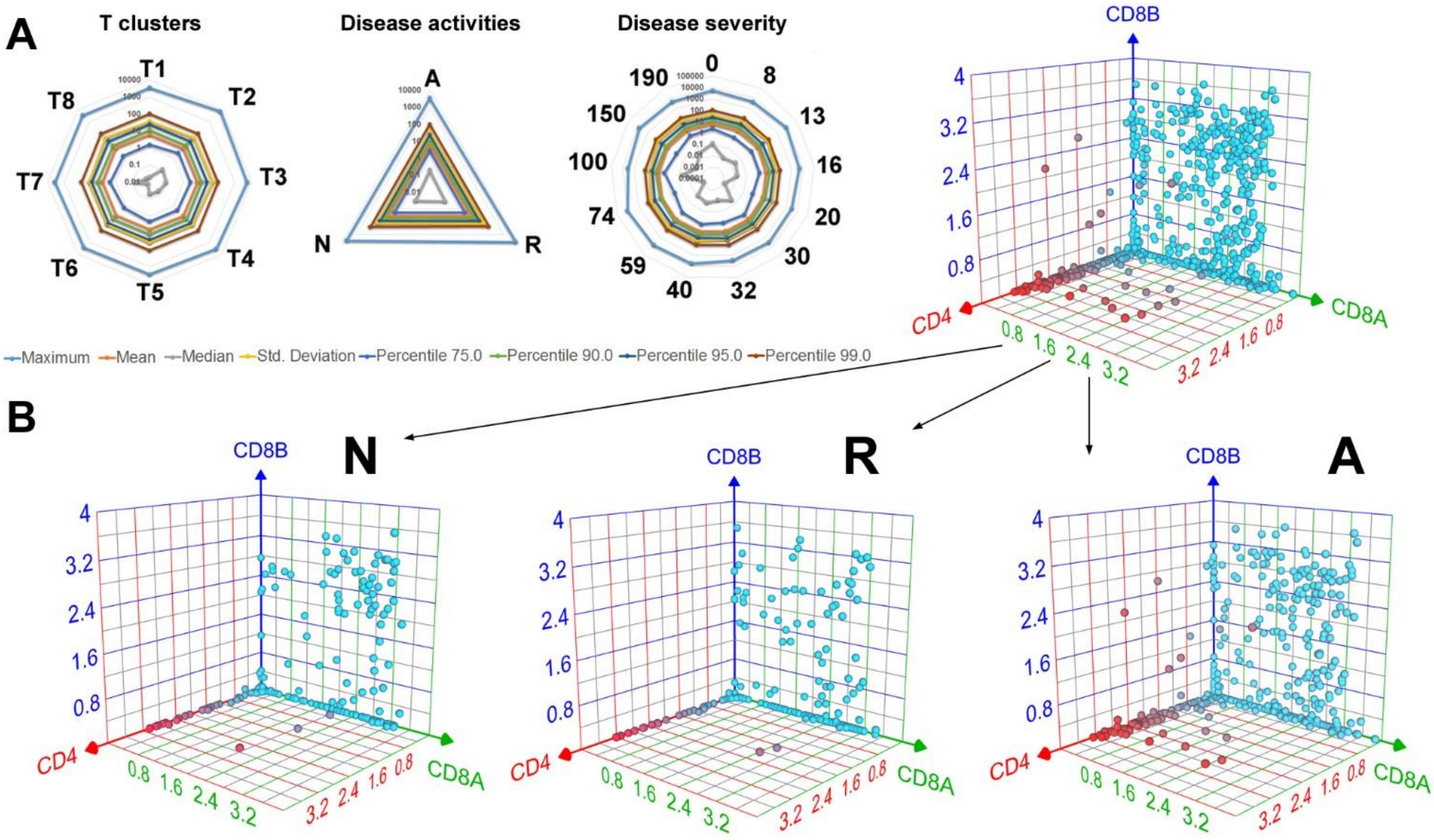


S Figure 3. Ontology analysis of tissue T cells in disease context and integrin/chemokine receptor comparison in tissue context.

A, Focusing on the 150 dysregulated genes shown in the volcano plot (147 being upregulated in $CD3^+$ cells from patients with active allergic inflammation), major gene ontology (GO) functional nodes are shown on the radar scanning map. The blue radar indicates the fold change in GO enrichment, whereas the orange radar shows the FDR-adjusted p value of the given nodes. B, A set of 14 out 23 chemokine receptors and 10 out of 27 integrin (subunit) genes are significantly different between blood and tissue as shown by the heat diagrams (2-way ANOVA; FDR-adjusted $p < 0.05$). Disease status illustrated as, N, normal, R, remission and A, active EoE.

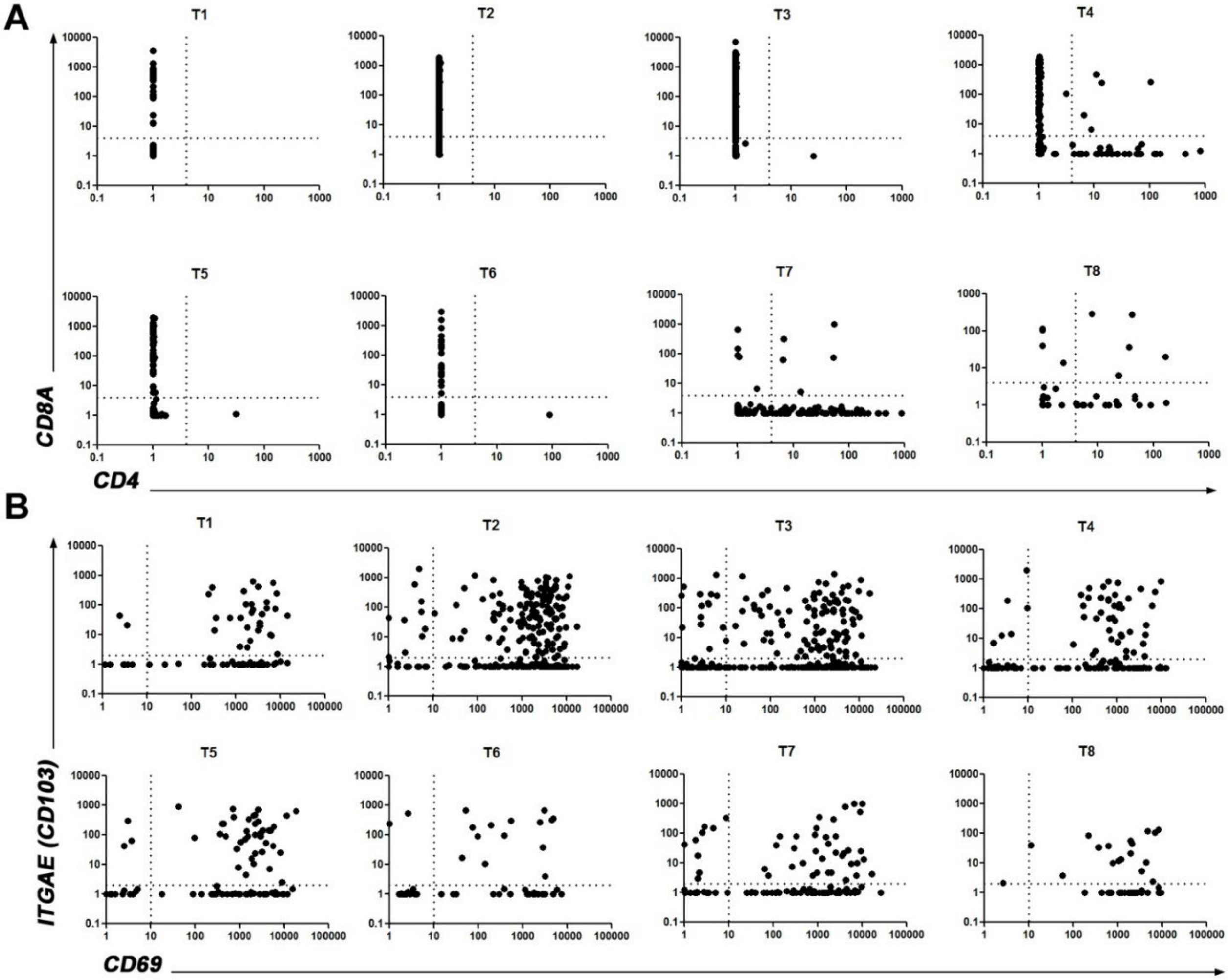

A
Step 1: PCA application
•PCA on 45987 unique entities across 1088 CD3+ T cells isolated from NL, remission and disease tissue
Step 2: PC identification
•Ten principal components (PC) identified contributing to 98% of the variation genome wide
Step 3: Key gene extraction
•Top 100 genes in each PC extracted resulting in 1114 PCA genes
Step 4: Unsupervised clustering (t-SNE)
•8 unique clusters were identified across 1088 T cells designated T1 through T8
Step 5: analysis in disease contexts
•The distribution of T1-T8 was superimposed to disease status.
B
1
2
3
4
5
6
7
8
CD3+ housekeeping functions
CD8+ functions
CD4+ functions
Apoptosis regulation
Acute activated phenotypes
Negative immune regulation
Pathogenic Th2 functions
Immediate early responses
low
high
C
Active
1
2
3
4
5
6
7
8
Remission
1
2
3
4
5
6
7
Normal
1
2
3
4
5
6
7
low
high

S Figure 4. Genetic interrogation of the expression phenotypes of T1-T8. A, A pipeline for dimensionality reduction of the genome-wide scRNA-seq data to obtain principal component (PC) genes defining T cells subsets using principal component analysis (PCA). B, Heatmap indicating the genetic separation of T1-T8 by the 1,114 PCA genes, with brief GO annotation of major gene clusters juxtaposed. C, The heatmap of the 1088 T cells stratified on disease activity based on the 1114 core genes identified by PCA. Within each disease activity bin, the T cell classification grouping is illustrated, also serving as absoluate cell counters for each cluster. T7 and T8 are separately spaced to emphasize their activated transcriptome phenotype and specific overrepresentation in the cohort with active EoE.



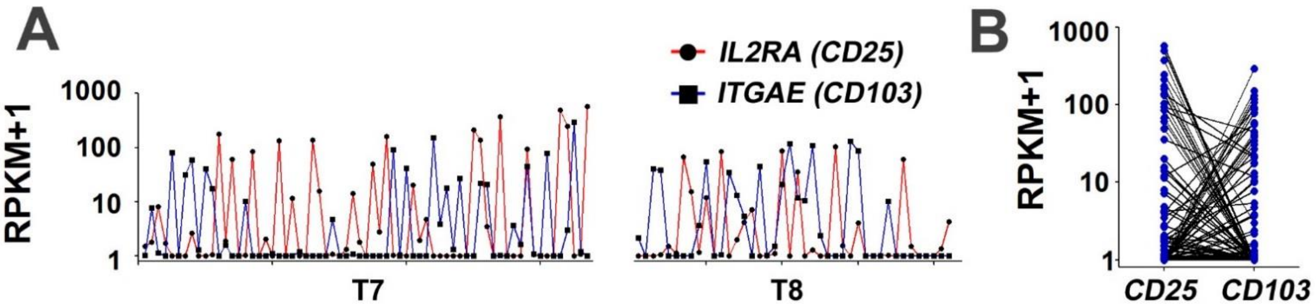
S Figure 5. Overall expression topology in the contexts of T1-T8, disease condition and severity, and CD8 dimerization component analyses.

A, Global assessment of overall genome wide expression profiles. The non-supervised (genome-wide) expression percentile were graphed as a function of the unique T1-T8 clusters, disease activities and level of esophageal eosinophilia in the unit of RPKMs. Radar plots show the RPKM percentile gradient showing the overall expression abundancy for each parameter. B, On the basis of the expression RPKMs of CD4 and the two CD8 monomers, *CD8A*, and *CD8B*, the topology of all 1088 tissue T cells were collectively exhibited in a 3-D plot (top panel, pivoting animation), which were subsequently broken down to 3 disease activities to visually reveal their individual presence (N, normal; R, remission; A, active). Each dot represents a single T cell, and the system is heat labeled on x axis (CD4) to indicate presence of the CD4 component.



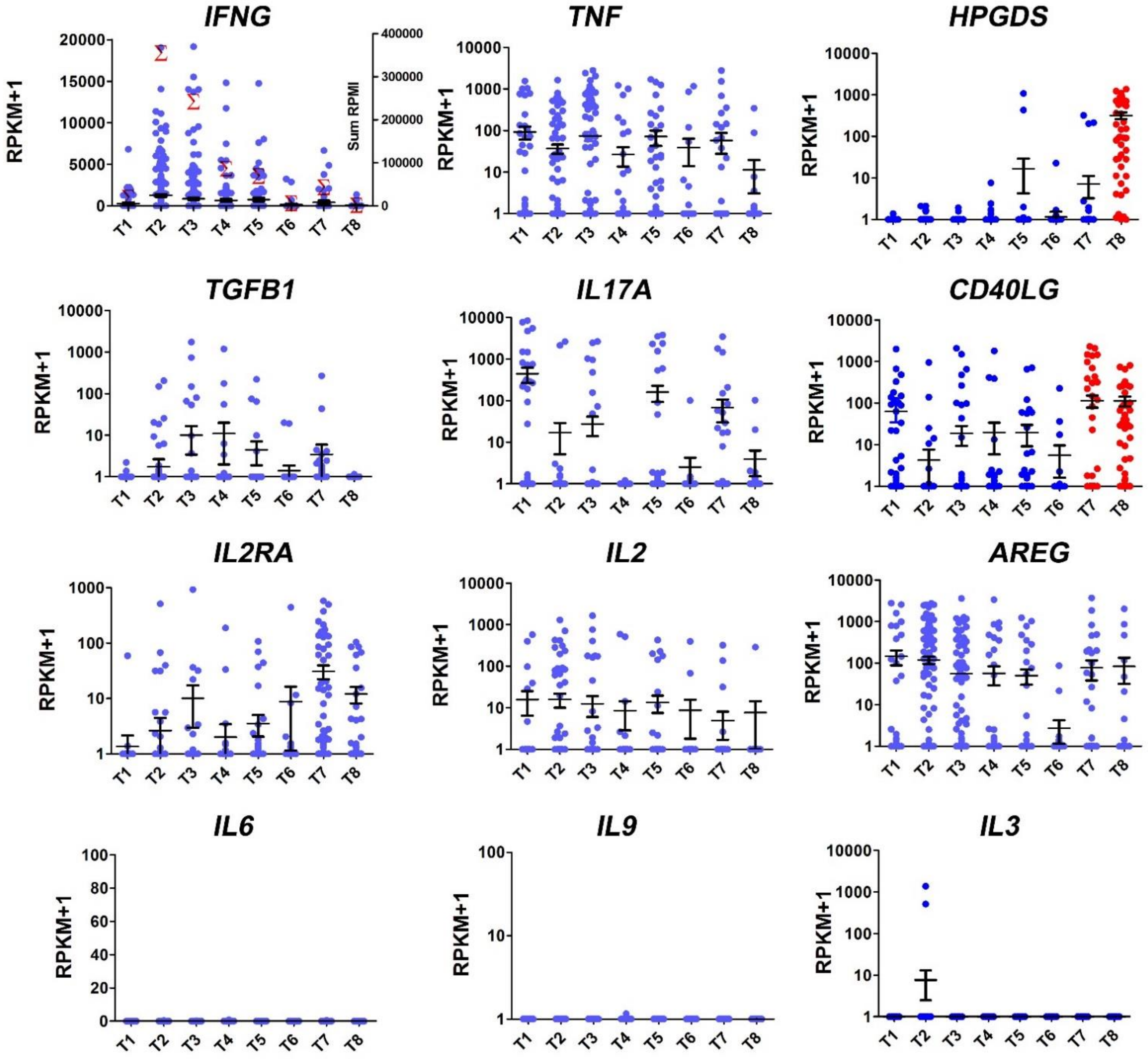
S Figure 6. CD4-CD8 and T_{RM} topology analyses of T1-T8 clusters

The CD4-CD8A distribution plots (A) and *CD69*-*ITGAE* (*CD103*) distribution plots (B) of T1-T8 are shown to illustrate their CD4-CD8A cellularity and tissue-resident memory T cell (T_{RM}) distribution, respectively. All cells were included without disease context, and each dot represents a single T cell.

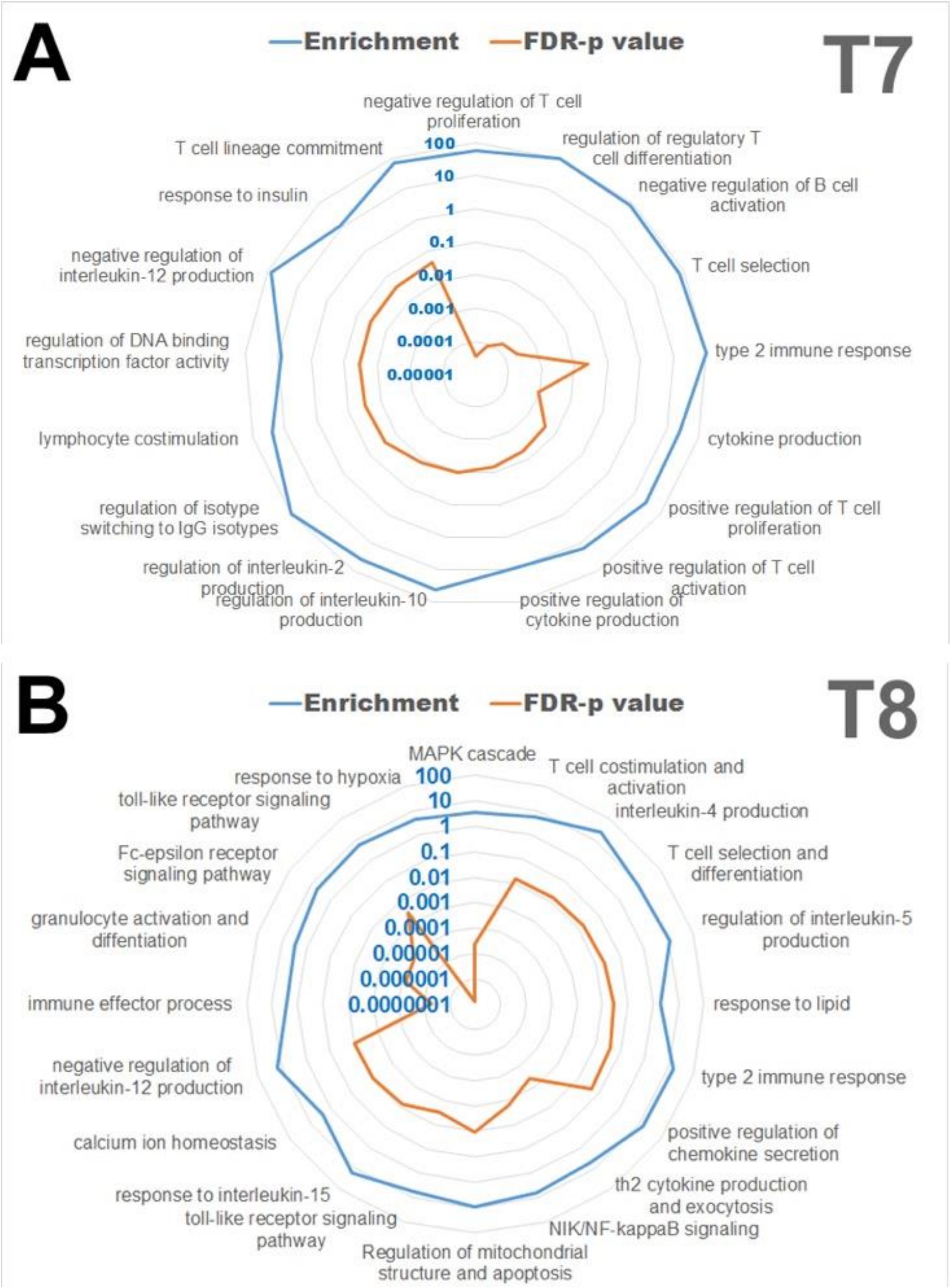


S Figure 7. The mutually exclusive pattern of CD103 and CD25 in T7 and T8

A, T7 and T8 cells were analyzed for their expression of CD25 and CD103 at the single-cell level with each data point representing a single cell. B, With each line (pairing two blue dots) representing a single T7/T8 cell, the single-cell level of CD25 and CD103 are shown with the blue data points.

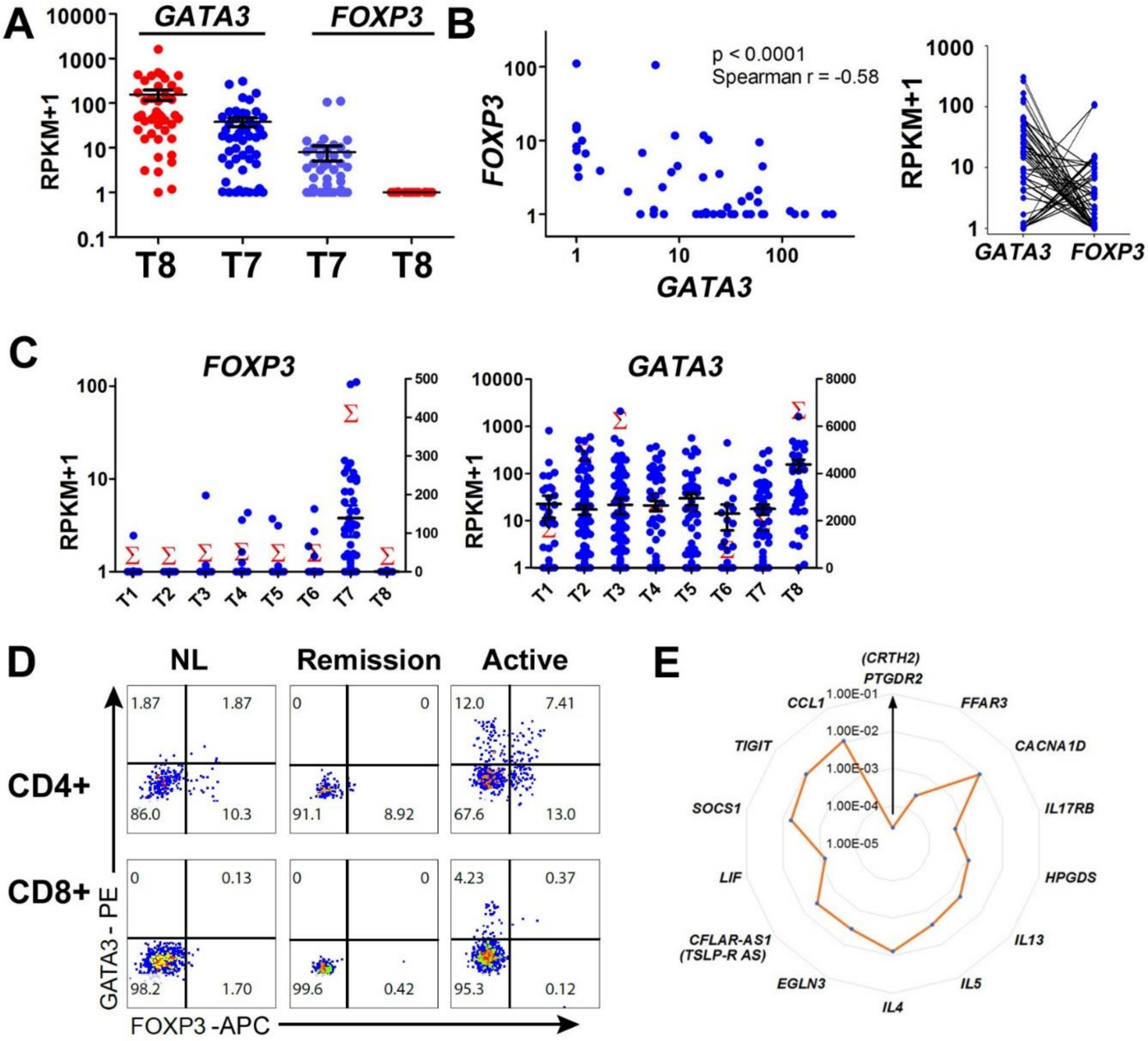


S Figure 8. Extended panel of gene expression by tissue CD3$^+$ T cells as a function of T cell cluster. Focusing on a panel of T cell cytokines relevant to allergy and Th2 activation, we analyzed their cluster-specific expression levels and patterns. In *IFNG* panel, a red Σ resembles the cumulative expression level within a given cluster referred to the right y axis. In the graphs of *HPGDS* and *CD40LG*/*CD154*, the red color was used to emphasize the unique high expression in reference to other clusters in blue. Data were graphed as Mean ± SEM with each dot representing a single T cell.



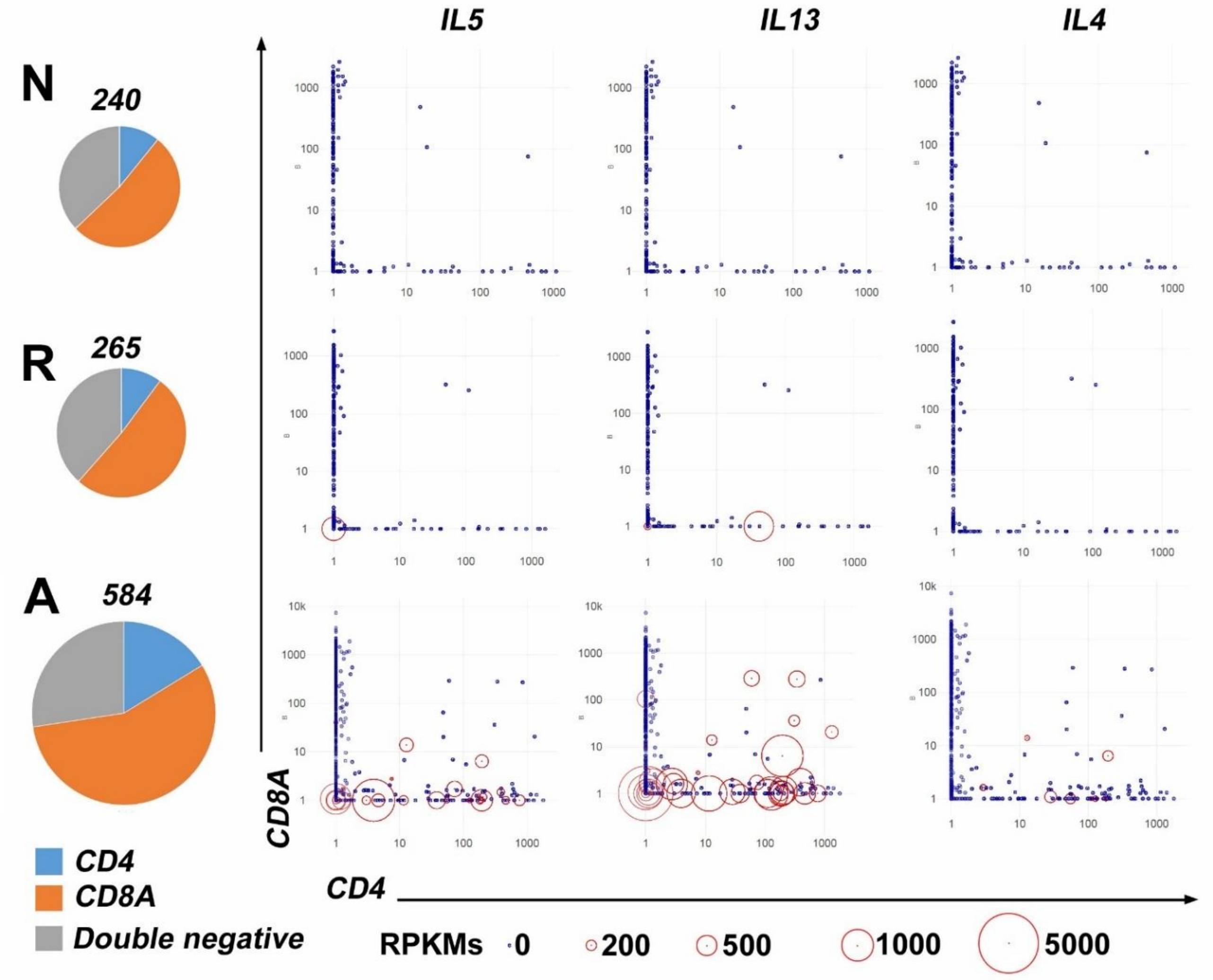
S Figure 9. Gene ontology analyses focusing on functionality of T7 and T8

Gene ontology analysis (FDR-adjusted $p < 0.05$, Fisher test–based) revealed major biological functions of T7 (A) and T8 (B) presented by radar map. The full functional lists are shown in Table S8 and S9.



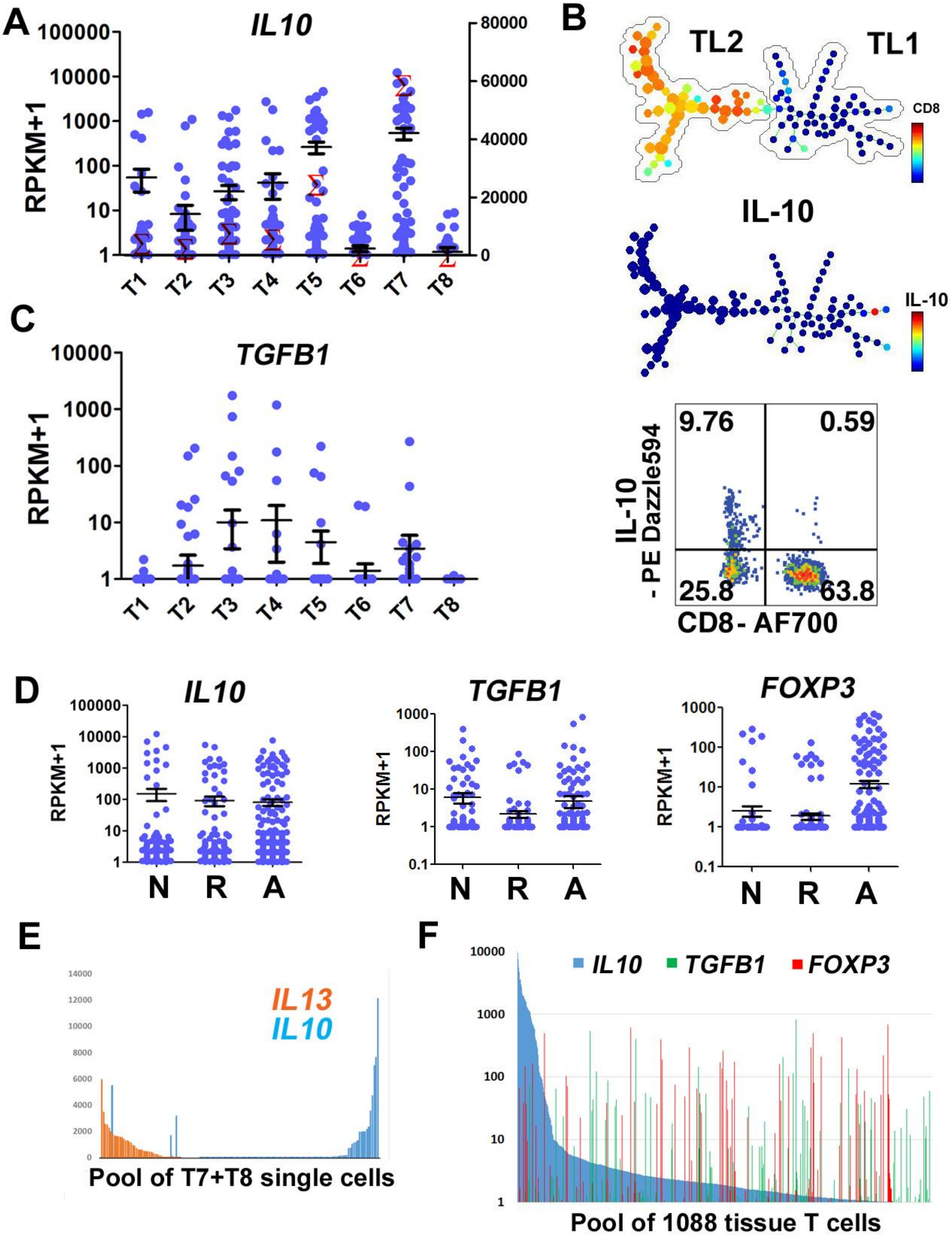
S Figure 10. Transcriptional and translational properties of T7 and T8 clusters and disease-related clinical correlating genes.

A, The expression levels of two key transcription factors determining the differentiation of T_{REG} and peTh2, FOXP3 and GATA3, respectively, within the T7 and T8 cluster, are plotted at single-cell levels to illustrate their mutually exclusive pattern. B, With T7 and T8 cells double-plotted on FOXP3 and GATA3, a negative correlation (left panel, $p < 0.0001$, spearman correlation) and a largely mutually exclusive relationship (right panel) at single-cell resolution is found. C, Expression profiles of GATA3 and FOXP3 in all T8 clusters with 1088 T cells plotted. Each cell's RPKM exhibited on left y axis and the RPKM Σ in that particular T cluster shown with the red Σ tracked to the right y axis. (Mean ± SEM) D, FACS analysis of esophageal $CD3^+$ T cells from active EoE biopsies. $CD3^+$ $CD4^+$ and $CD3^+CD8^+$ gated (internal negative control) events were double-plotted on FOXP3 and GATA3. E, A selected gene cohort whose expression correlated with EoE clinical severity (tissue eosinophilia), with the Pearson correlation p value plotted in the radar map.



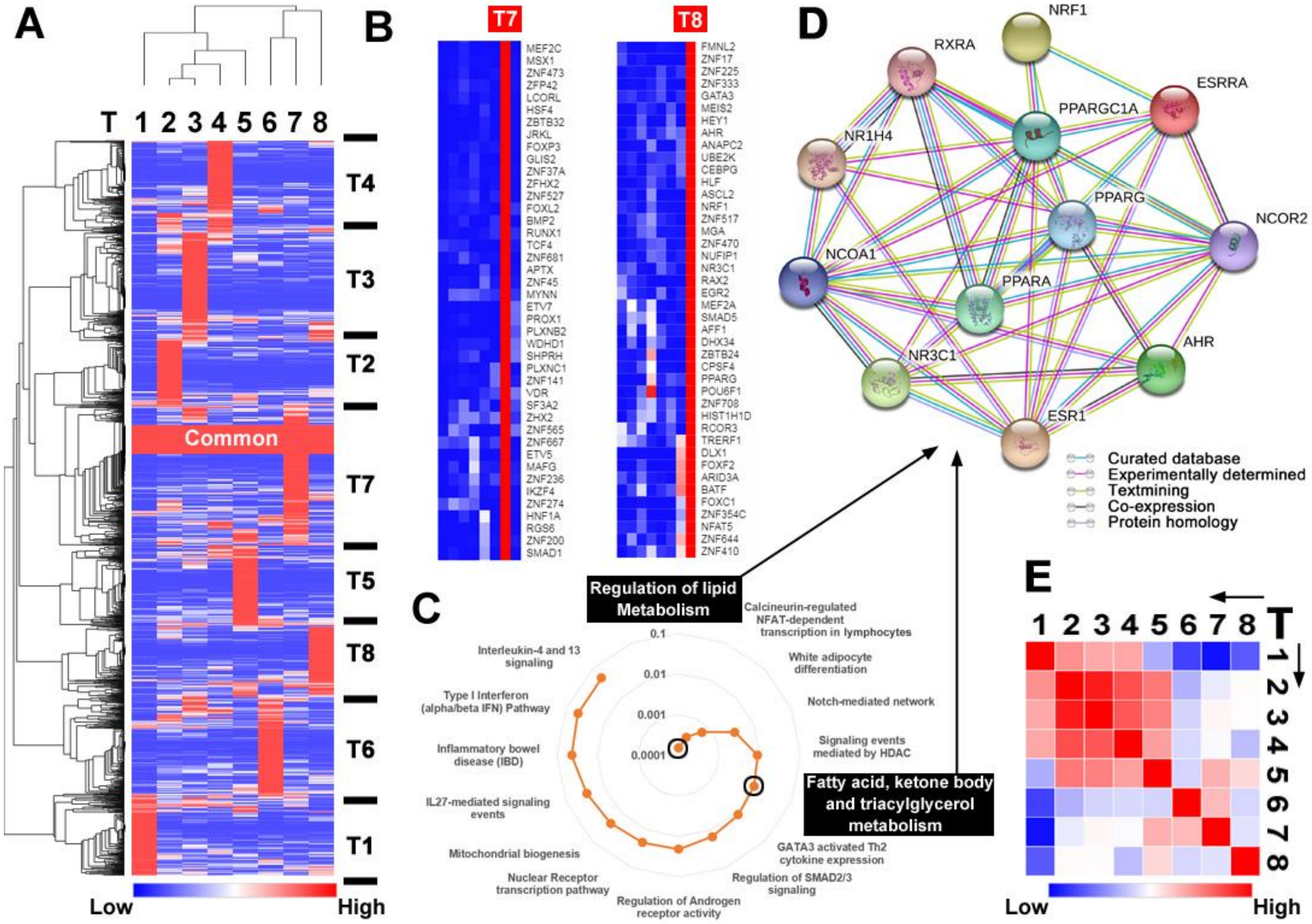
S Figure 11. 2D-TRACER analysis for single-cell Th2 cytokine expression topology

Left panel: CD3$^+$ tissue T cells from active (A), remission (R), and normal (N) were quantitatively analyzed by CD4-CD8A expressions. CD4 T cells are defined by CD4 RPKM > 2.0 per single cell as shown in blue, with CD8 T cells by CD8 RPKM > 2.0 shown in orange and non-CD4/non-CD8 cells (Double negative) defined by RPKMs < 2.0 for both shown in grey. Right panel: following the same disease activity designation on the left, Th2 cytokine–positive cells are color-traced for the given Th2 cytokine by a red circle, with the area of that circle proportional to the Th2 cytokine RPKM at the single-cell level. A scale of a series of RPKM circles is shown on the bottom.


A
IL10
RPKM+1
100000
10000
1000
100
10
1
80000
60000
40000
20000
0
T1
T2
T3
T4
T5
T6
T7
T8
B
TL2
TL1
CD8
IL-10
IL-10
9.76
0.59
25.8
63.8
IL-10 - PE Dazzle594
CD8 - AF700
C
TGFB1
RPKM+1
10000
1000
100
10
1
T1
T2
T3
T4
T5
T6
T7
T8
D
IL10
TGFB1
FOXP3
RPKM+1
100000
10000
1000
100
10
1
0.1
N
R
A
E
14000
12000
10000
8000
6000
4000
2000
0
IL13
IL10
Pool of T7+T8 single cells
F
10000
1000
100
10
1
IL10
TGFB1
FOXP3
Pool of 1088 tissue T cells

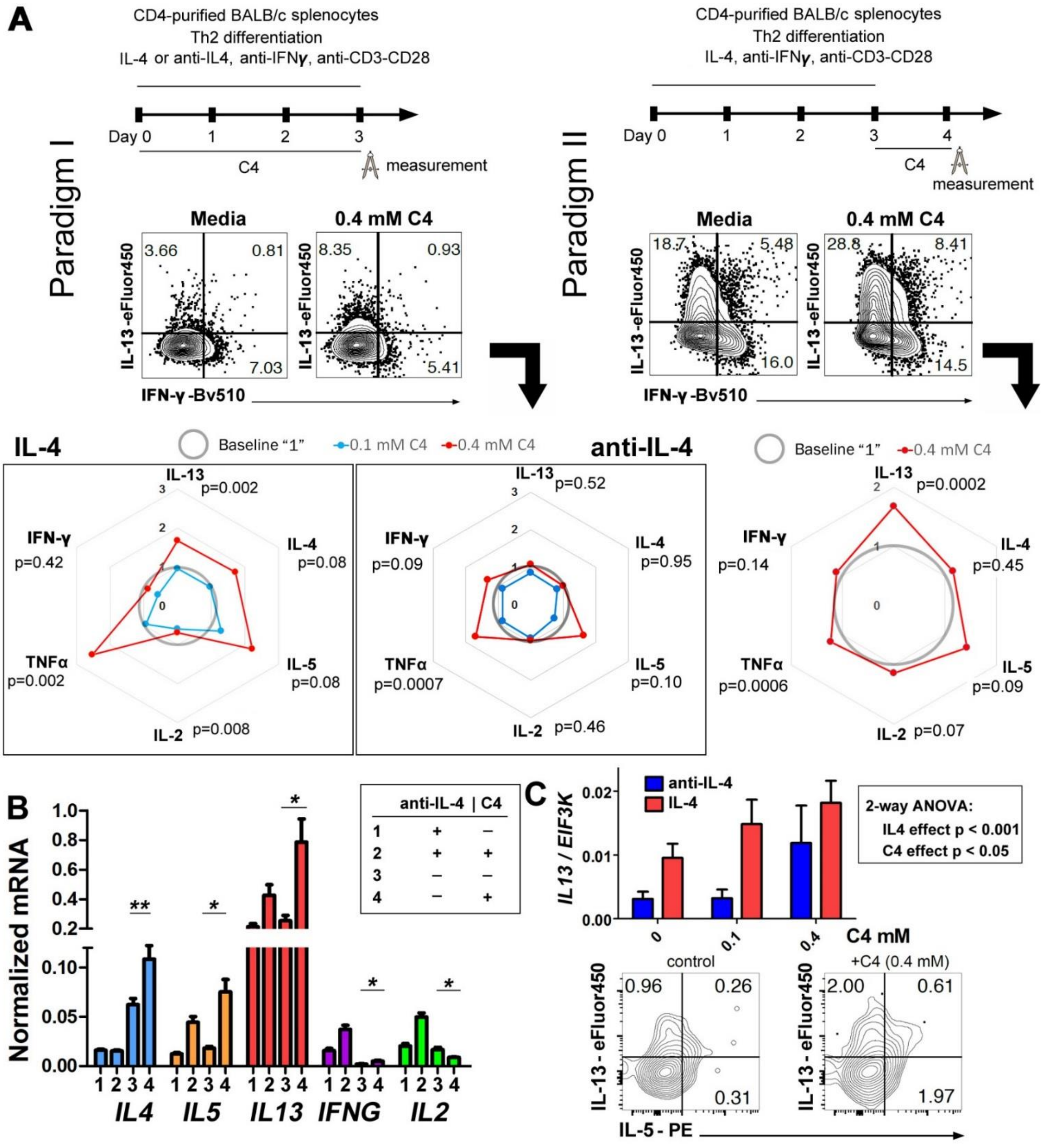
S Figure 12. The single-cell expression analysis for major T$_{\mathrm{REG}}$ anti-inflammatory cytokines

A, Across all T1-T8 clusters, expression pattern and levels of IL10 are shown at the single-cell level. Each data point represents a T cell that is tracked for RPKM expression on the left y axis. The cumulative/overall *IL10* expression for each cluster derived is graphed on the right y axis with their cumulative RPKM levels indicated by the red Σ. B, In light of the TL1-TL2 (CD4-CD8) bifurcation determined by the SPADE (Spanning-tree Progression Analysis of Density-normalized Events) analysis (Fig. 6), the developmental tree nodes of IL-10 producers were illustrated by the same tree color-scaled on *IL10* expression, with a representative double plot of IL-10/CD8 shown on the bottom. C, Scatter plots for single-cell *TGFB1* production across T1-T8 (N, normal; R, remission; A, active) are shown. D, Scatter plots for single-cell *IL10*, *TGFB1* and *FOXP3* production as a function of disease status are shown. E, The single-cell expression histogram of *IL10* and representative Th2 cytokine *IL13* for the pool of T7 and T8 combined. F, Tissue T cell pool of 1088 cells were sorted by *IL10* expression levels (blue) with highest values on the left (RPKMs), with *TGFB1* and *FOXP3* labeled by green and red on the same single-cell histogram, respectively. All data were shown as Mean ± SEM.



S Figure 13. Distinct transcription factor profiles across T1-T8

A, On the basis of the known 1391 human transcription factor as reported , the transcription factor expression profile was revealed by an averaged heatmap across T1-T8, with red being higher expression and blue being low in each row. The heatmap was clustered on the basis of transcription factor entities across T1-T8. B, A closer view of the areas where T7 and T8 selective transcription factors are enriched. C, On the basis of 133 T8 selective transcription factors, gene ontology analysis revealed major pathways related to T8 functionalities with p value shown by the radar scanning. D, Genes contributing to the two lipid activation pathways were further analyzed for protein interactions, with the interaction type legend shown beneath the diagram. E, A heat diagram of Pearson correlation among T1-T8 on the basis of the transcription factor profiling.



S Figure 14. Th2 cytokine enhancement by C4 in murine and human primary T$_H$ cells.

A, Murine splenocytes were CD4 purified (> 95% purity) followed by a Th2 or Th0 differentiations (anti-IFN-γ, anti–CD3-CD28) for 3 days with either IL-4 or anti–IL-4 supplemented, respectively. Butyrate (C4, at 0.1 or 0.4 mM) was added at different time points as schematically summarized on the top panel.

Cytokines were assessed by intracellular FACS staining at the indicated "measurement" points following a PDBU (1) and ionomycin stimulation, with representative double plots shown in the middle panel. Radar scanning map shows the C4 enhancement effects on all cytokine analyzed in two different experimental protocols; data are normalized to effect of media exposure as a grey baseline circle. B, Following the experimental protocol depicted on the left in (A), mRNA was analyzed for the T cell cytokine expression in the absence and presence of C4 and anti–IL-4 or IL-4 treatment. During CD4 cell activation, anti–IL-4 was added to neutralize endogenic secretion of IL-4 (* $p < 0.05$, ** $p < 0.01$, 2-tailed t-test IL-4 vs. IL-4+C4 [3 vs. 4]). C, Human PBMC from healthy donors were purified by CD4 positive selection and then subjected to Th2 or Th0 differentiation during culture (anti–IFN-γ and anti–CD3-CD28) in the presence of either IL-4 or anti IL-4 for 3 days, with or without C4 (0.1 or 0.4 mM). The *IL13* mRNA level was measure by qRT-PCR, and 2-way ANOVA was used to examine the IL-4 vs. anti–IL-4 effects and the C4 effect. FACS data was obtained similarly with 5 days of activation in the absence and presence of C4 (0.4 mM).

Supplementary Tables

Table S1. Significant gene list from bulk CD3+ RNA-seq of blood vs. tissue lymphocytes

Gene Symbol	Gene ID	FC ([Blood-N] vs [Tissue-N])	FC ([Blood-R] vs [Tissue-R])	FC ([Blood-A] vs [Tissue-A])
GCNT4	51301	675.2	234.6	22.5
DSC1	1823	500.7	28.5	37.7
NRCAM	4897	497.7	189.5	88.2
DCHS1	8642	458.2	83.1	16.4
VCAN	1462	438.1	2172.4	192.0
PCSK5	5125	416.8	29.8	58.9
AK5	26289	400.4	38.6	88.0
ADD2	119	363.3	123.3	60.7
TSPAN18	90139	354.6	327.1	42.7
NBEA	26960	353.9	70.8	38.6
ANKRD55	79722	349.5	103.5	17.1
AFF2	2334	347.7	147.1	25.0
VIPR1	7433	309.4	125.1	233.4
TRABD2A	129293	306.3	104.8	66.6
DACT1	51339	282.0	222.0	103.1
S1PR5	53637	247.6	11.6	23.8
ACVR1C	130399	246.7	13.6	20.2
CR2	1380	243.2	73.2	23.8
ZNF204P	7754	221.7	10.1	16.6
NCF2	4688	218.3	17.1	11.7
ZNF711	7552	209.5	15.4	49.5
SULT1B1	27284	179.2	30.5	27.7
CCR7	1236	177.7	36.9	10.8
GRIN3A	116443	165.1	11.4	13.0
HEMGN	55363	163.2	55.9	34.5
NEFL	4747	145.8	39.3	19.0
NOG	9241	145.3	72.1	82.1
MIR4697HG	283174	144.1	21.6	20.3
SLC16A10	117247	142.0	10.2	14.7
GIPC3	126326	139.4	62.6	29.3
AKR1E2	83592	136.6	34.8	23.7
S1PR1	1901	135.9	36.7	12.2
MORF4L2-AS1	340544	130.4	49.5	16.8
LINC00612	253128	125.8	10.5	21.4
RBM11	54033	118.8	13.5	11.3
LINC00282	283521	117.7	48.3	88.3

MYH3	4621	117.3	33.8	11.3
FAM87B	400728	117.2	43.6	20.2
AMIGO1	57463	113.9	54.1	10.6
LOC101928150	101928150	112.1	66.0	24.3
MSX2P1	55545	110.8	53.2	47.6
ALKBH3-AS1	100507300	110.0	14.1	26.7
CHRNB2	1141	108.8	36.8	13.4
MDS2	259283	105.3	78.2	46.0
ATP8A2	51761	103.0	24.5	22.3
HAVCR1	26762	102.3	33.5	44.2
FGFBP2	83888	98.7	46.0	31.8
SSTR3	6753	93.4	66.8	15.7
FHIT	2272	92.2	213.5	33.0
KRT73	319101	92.0	74.6	24.6
APOBEC2	10930	89.4	35.5	15.1
LEF1-AS1	641518	87.5	15.3	48.3
LINC00565	100861555	85.0	57.8	61.0
ARHGEF10	9639	84.8	54.3	24.4
TTYH2	94015	80.4	20.5	10.9
AFF3	3899	76.6	21.6	29.6
CLMP	79827	72.1	44.7	21.2
HCG27	253018	71.8	63.5	16.9
LINC00854	100874261	71.2	10.5	11.9
KCNJ10	3766	70.2	29.7	35.1
PFN2	5217	69.6	20.6	13.7
KBTBD11	9920	69.1	36.8	32.0
GP5	2814	67.4	59.5	39.8
EFHC2	80258	67.3	34.3	23.5
KLHL29	114818	67.2	48.1	10.7
CD300E	342510	67.0	1069.1	382.4
KRT72	140807	64.8	55.8	33.5
ZNF239	8187	63.9	10.7	37.1
FAM153A	285596	63.4	14.3	54.2
FAM226A	203429	63.1	20.0	13.2
C10orf2	56652	59.6	21.6	15.5
LOC101927124	101927124	59.5	10.9	19.5
CLDN20	49861	59.3	32.3	13.8
PMEL	6490	59.1	37.0	20.8
WNT7A	7476	59.1	65.9	33.1
TMEM177	80775	57.7	14.1	12.3
METTL21EP	121952	57.6	22.9	10.4

LRRN1	57633	56.7	33.5	39.8
USP44	84101	56.6	20.3	22.3
LILRA1	11024	54.9	318.4	148.1
FAM153B	202134	54.8	16.2	40.9
CFP	5199	54.5	85.8	45.4
SIGLEC9	27180	53.9	77.8	53.5
BEND5	79656	53.8	25.0	20.7
C10orf25	220979	53.6	37.8	13.4
ACE	1636	53.0	41.0	10.0
CXCR2	3579	52.7	21.2	12.3
EDAR	10913	52.6	35.6	27.6
ALK	238	52.5	16.2	17.3
SYNM	23336	52.4	15.9	10.9
CSF3R	1441	52.1	132.3	16.3
MINOS1P1	100462953	51.7	34.3	18.1
GNG7	2788	51.3	64.1	41.4
ME3	10873	51.0	11.7	37.5
MYLK4	340156	48.5	10.0	11.8
TIMD4	91937	47.8	69.3	27.0
ZNF572	137209	47.2	15.2	34.5
LOC100507387	100507387	47.0	25.7	32.6
FMO5	2330	46.8	10.3	12.8
FCN1	2219	46.8	637.5	268.6
ZSCAN23	222696	45.2	16.8	10.7
SELP	6403	44.4	13.9	14.6
REG4	83998	43.7	52.3	30.1
FLT4	2324	43.5	10.7	24.8
GAS7	8522	42.4	20.8	10.3
IFNG-AS1	100885789	42.3	59.5	27.8
HPCAL4	51440	41.4	172.1	35.1
ZFP2	80108	41.3	17.2	11.8
GDAP1L1	78997	40.8	11.1	12.2
ASRGL1	80150	39.5	41.3	17.5
S100A12	6283	39.1	12.6	124.1
ST6GALNAC1	55808	39.1	13.3	11.8
CACHD1	57685	38.8	20.5	12.2
LOC101927053	101927053	38.6	10.7	30.6
TAS2R3	50831	38.3	23.6	14.9
ZC3H12B	340554	36.0	11.9	11.5
ACSBG2	81616	34.8	13.1	10.9
NPAS2	4862	34.7	19.6	13.1

ACTG1P4	648740	34.3	38.9	50.4
SMCR5	140771	34.2	40.6	10.8
PNMA3	29944	34.2	62.9	10.2
PRAM1	84106	33.5	65.5	15.0
ASIC3	9311	32.6	29.8	20.6
LIMS2	55679	31.9	76.0	11.7
MAGEF1	64110	31.9	13.7	10.6
S1PR4	8698	31.4	14.4	10.1
DIP2C	22982	30.9	13.5	28.3
CCDC71	64925	30.7	20.2	13.7
MKRN3	7681	30.5	11.4	16.8
AQP11	282679	30.2	10.7	22.5
ZFP37	7539	29.9	15.7	10.3
HCG8	100507399	29.7	25.7	16.5
MUC6	4588	29.2	48.7	34.3
LOC653160	653160	28.9	48.1	12.5
ALDH8A1	64577	28.8	25.1	24.9
ANKRD36BP2	645784	27.8	27.4	19.8
EXOSC5	56915	27.3	12.9	11.5
DSEL	92126	27.1	12.3	10.2
KATNAL2	83473	27.1	15.4	33.3
CD79A	973	26.8	53.3	13.3
PADI4	23569	26.5	64.7	12.4
NLE1	54475	25.4	30.1	13.8
PI16	221476	24.9	16.0	30.4
PRPH2	5961	24.6	11.6	10.9
NLRC4	58484	24.0	45.3	35.0
CRISPLD2	83716	23.0	35.4	157.7
LOC441454	441454	22.6	15.9	13.1
DPPA4	55211	22.5	17.3	46.7
MFSD3	113655	22.3	31.6	11.9
CA14	23632	22.3	22.1	12.6
PELI2	57161	22.2	13.0	12.0
NPY6R	4888	22.0	23.8	17.3
SCIMP	388325	21.5	17.1	24.4
SORCS3	22986	21.0	11.1	11.8
TXNRD3	114112	20.4	11.8	24.1
LY86	9450	20.3	23.9	26.3
NUDT10	170685	20.1	12.5	27.5
NME9	347736	19.5	110.5	13.8
ZCWPW1	55063	18.9	20.4	11.3

MCEMP1	199675	18.9	136.3	122.6
KCNJ9	3765	18.4	44.9	26.6
LOC100507053	100507053	18.3	16.5	12.4
PZP	5858	18.2	25.2	23.7
FAM66C	440078	18.2	18.4	12.8
GJA9	81025	17.4	10.8	16.3
TCF7L1	83439	16.9	12.4	16.1
RPL34-AS1	285456	16.8	29.4	23.1
LINC00908	284276	16.8	38.4	15.8
C11orf74	119710	16.7	13.1	18.6
PYGM	5837	16.4	10.6	16.6
RXFP4	339403	15.8	14.6	11.1
TREM1	54210	15.3	116.0	22.3
KNOP1	400506	15.2	25.4	18.4
ALDH1A1	216	14.8	177.2	30.4
LOC100507091	100507091	14.2	14.6	12.1
PACSIN1	29993	14.1	52.3	20.6
ZNF467	168544	13.8	16.3	21.3
AQP9	366	13.4	135.4	22.5
FBN2	2201	13.0	31.9	17.1
LINC00987	100499405	12.8	16.9	17.7
C17orf51	339263	12.2	20.4	14.1
SELL	6402	11.7	25.0	11.7
CCL27	10850	11.3	22.2	10.5
KCNQ5-AS1	100873997	11.0	10.9	14.8
GRAPL	400581	10.9	22.2	22.3
NFE2	4778	10.9	82.0	30.7
FXYD6	53826	10.2	38.9	87.0
CLCA2	9635	-10.0	-198.6	-120.1
ZNF331	55422	-10.2	-17.2	-11.2
LOC284454	284454	-10.6	-14.1	-11.6
EHF	26298	-10.6	-269.1	-414.7
KLK10	5655	-10.8	-146.1	-189.8
ESRP1	54845	-10.8	-55.8	-140.6
PAX9	5083	-11.4	-42.2	-36.9
ARHGEF12	23365	-11.5	-14.6	-14.2
PERP	64065	-11.9	-33.2	-20.6
SRGAP3	9901	-12.0	-12.8	-15.2
IL10	3586	-12.2	-38.4	-35.5
SDC4	6385	-12.5	-52.4	-26.5
DPF3	8110	-13.1	-10.9	-12.7

ZNF683	257101	-13.3	-11.9	-19.7
GPR15	2838	-13.3	-12.1	-22.8
KLRC1	3821	-13.3	-24.0	-19.3
SLC7A5	8140	-13.5	-10.8	-11.6
CXCR4	7852	-13.6	-14.2	-13.9
EGFR	1956	-13.7	-60.8	-34.9
RHCG	51458	-13.7	-155.3	-208.3
PTMS	5763	-15.2	-15.7	-10.2
S100A16	140576	-15.8	-127.8	-109.9
PDCD1	5133	-16.1	-11.3	-12.4
HSPB1	3315	-17.1	-15.2	-13.3
C1QC	714	-17.3	-92.2	-162.5
PFKFB3	5209	-17.7	-16.4	-29.3
KRT6A	3853	-17.7	-428.5	-1386.4
RASGEF1B	153020	-18.0	-38.7	-23.6
TNIP3	79931	-18.2	-12.3	-34.1
PTPRF	5792	-18.6	-324.8	-71.4
JUND	3727	-20.5	-12.5	-10.5
PXDC1	221749	-20.8	-41.7	-38.3
LAMA3	3909	-21.3	-32.7	-31.4
DDIT4	54541	-21.6	-11.2	-22.9
IL1R1	3554	-21.9	-58.8	-81.2
TMEM200A	114801	-22.1	-16.2	-44.2
SCUBE1	80274	-22.4	-78.6	-254.6
SCEL	8796	-22.9	-218.3	-131.5
GADD45A	1647	-23.3	-32.3	-33.5
GJB2	2706	-23.3	-71.2	-343.5
ERRFI1	54206	-24.1	-44.2	-27.7
CLCA4	22802	-24.5	-80.9	-139.8
PTTG1	9232	-24.9	-14.5	-11.5
ITGAE	3682	-25.5	-17.5	-16.2
SPRR2A	6700	-25.8	-122.7	-16.4
CREM	1390	-25.9	-22.2	-47.0
CD83	9308	-26.0	-37.9	-20.1
CTLA4	1493	-26.6	-26.2	-35.6
KLK13	26085	-27.0	-67.7	-54.9
LY6D	8581	-27.3	-266.6	-56.0
AREG	374	-27.9	-145.7	-151.0
FASLG	356	-29.2	-47.5	-33.5
AXL	558	-29.3	-28.5	-12.4
SPRY1	10252	-30.2	-67.9	-67.2

IL1R2	7850	-30.8	-21.1	-21.3
KIAA1217	56243	-31.0	-14.5	-18.1
SFN	2810	-31.4	-184.5	-233.8
FAM46C	54855	-32.0	-13.4	-19.2
ITGA1	3672	-33.0	-46.8	-60.4
EMP1	2012	-33.2	-343.5	-10.4
TNFAIP3	7128	-33.4	-14.9	-24.9
GADD45B	4616	-33.7	-13.9	-10.9
SNAI1	6615	-34.1	-121.9	-49.6
LMNA	4000	-35.0	-35.4	-45.5
CXCR6	10663	-35.3	-36.5	-17.3
KRT19	3880	-35.7	-88.5	-64.7
SPRR1B	6699	-37.0	-233.8	-82.0
IER5L	389792	-37.3	-10.5	-19.7
CSF1	1435	-37.8	-21.9	-75.4
CD177	57126	-38.9	-97.2	-185.6
PDGFA	5154	-41.9	-27.9	-48.3
C1orf116	79098	-42.4	-52.4	-20.0
PTN	5764	-42.5	-70.5	-54.2
BRE-AS1	100302650	-43.8	-24.1	-60.9
GADD45G	10912	-44.2	-33.9	-29.3
ATP1B1	481	-45.2	-39.2	-30.0
CCL3L3	414062	-45.5	-84.0	-72.4
DNAJB1	3337	-49.6	-20.5	-22.3
CCL3L1	6349	-50.2	-78.5	-68.3
TACC2	10579	-51.6	-32.5	-22.6
DUSP2	1844	-52.2	-11.2	-23.6
FERMT1	55612	-52.3	-67.6	-10.1
TP63	8626	-52.7	-32.2	-49.5
JUN	3725	-52.7	-31.6	-41.2
MYO7A	4647	-56.2	-24.7	-25.2
IL26	55801	-56.4	-40.6	-27.0
FAT1	2195	-57.5	-39.5	-51.6
CD69	969	-57.7	-34.5	-30.2
HTRA1	5654	-59.7	-34.7	-21.7
DUSP5	1847	-61.3	-36.2	-25.0
HES1	3280	-61.7	-260.9	-110.0
CKS2	1164	-62.9	-31.0	-24.7
CEACAM6	4680	-64.2	-49.2	-67.4
PHLDA1	22822	-69.4	-79.8	-78.8
ATF3	467	-69.8	-77.1	-195.6

PPARG	5468	-83.0	-16.2	-234.2
LAYN	143903	-83.5	-13.0	-45.3
TRIM29	23650	-91.9	-1525.5	-510.4
CSF2	1437	-97.4	-10.2	-11.0
SIK1	150094	-100.4	-45.0	-54.1
EGR3	1960	-101.3	-203.0	-56.5
RGS16	6004	-104.1	-50.5	-52.5
FPR3	2359	-115.0	-17.0	-17.3
PITX1	5307	-115.2	-93.2	-65.9
CSRNP1	64651	-118.6	-16.9	-24.1
EGR1	1958	-128.5	-102.3	-20.9
IL22	50616	-135.4	-62.4	-28.4
HSPA1A	3303	-139.8	-77.3	-52.4
KRT15	3866	-175.1	-1038.9	-469.0
XCL2	6846	-181.1	-102.3	-148.4
CCL20	6364	-181.9	-88.8	-85.7
CCL3	6348	-194.9	-390.3	-163.0
RAPGEF5	9771	-208.4	-175.0	-237.5
EGR2	1959	-241.5	-276.3	-34.3
NTRK2	4915	-255.9	-54.4	-48.6
RBM14-RBM4	100526737	-264.2	-110.4	-41.4
HSPA1B	3304	-274.2	-147.7	-96.0
TJP1	7082	-301.7	-539.4	-340.0
CCL4	6351	-312.7	-162.8	-98.2
CA10	56934	-318.6	-164.7	-53.9
TNFSF9	8744	-320.5	-521.0	-551.5
HSPA6	3310	-321.3	-21.7	-26.3
CCL4L2	388372	-322.9	-252.3	-97.3
TNFRSF9	3604	-333.3	-26.7	-11.3
LOC101929450	101929450	-360.9	-19.7	-250.6
IFNG	3458	-414.7	-337.3	-136.0
KRT5	3852	-443.5	-2374.4	-480.5
A2ML1	144568	-446.5	-154.2	-200.5
IL17A	3605	-524.0	-1149.6	-156.5
GEM	2669	-531.2	-241.5	-280.7
DSP	1832	-637.7	-873.1	-843.4
DUSP4	1846	-644.7	-199.2	-225.4
NR4A1	3164	-672.6	-147.1	-45.0
XCL1	6375	-694.4	-261.8	-237.6
NR4A3	8013	-1024.2	-1407.7	-865.5
NR4A2	4929	-1052.8	-251.7	-215.6

SPINK5	11005	-1256.4	-494.8	-626.2
KRT13	3860	-1277.0	-6039.0	-698.0
KRT4	3851	-1521.6	-640.6	-943.2
CRNN	49860	-1528.2	-569.2	-59.5
FOSB	2354	-1750.5	-505.0	-131.0
RGS1	5996	-1754.9	-729.8	-1406.9
CDKN1A	1026	-1836.5	-45.4	-29.5
SPRR3	6707	-2296.2	-1388.1	-231.6

FC: Fold change. N, normal; R, remission; A, active disease.

Table S2. Gene ontology analysis of the 331 tissue vs. blood differential genes

GO biological process complete	Fold Enrichment	FDR-adjusted p value
multicellular organism development	1.8	8.4E-13
anatomical structure development	1.8	8.6E-13
developmental process	1.7	2.0E-11
response to stimulus	1.5	2.2E-11
cell surface receptor signaling pathway	2.3	2.8E-11
multicellular organismal process	1.6	4.0E-11
immune system process	2.2	4.9E-11
cellular response to stimulus	1.6	8.7E-11
system development	1.8	9.8E-11
tissue development	2.5	2.8E-10
animal organ development	2.0	7.9E-10
signal transduction	1.7	9.1E-10
cell communication	1.6	9.5E-10
regulation of response to stimulus	1.8	1.2E-09
signaling	1.7	1.3E-09
anatomical structure morphogenesis	2.2	2.1E-09
cellular response to chemical stimulus	2.0	4.3E-09
response to external stimulus	2.3	5.5E-09
response to organic substance	2.0	6.8E-09
regulation of protein phosphorylation	2.5	8.4E-09
Unclassified	0.3	8.6E-09
cell migration	3.0	1.3E-08
positive regulation of biological process	1.6	1.4E-08
immune response	2.3	2.7E-08
regulation of cell proliferation	2.3	3.2E-08
cellular response to organic substance	2.1	3.3E-08
cell chemotaxis	6.2	3.3E-08
positive regulation of protein phosphorylation	2.8	3.5E-08
regulation of cell death	2.3	4.0E-08
regulation of phosphorylation	2.4	4.1E-08
leukocyte migration	4.3	4.1E-08
cell differentiation	1.8	4.7E-08
epidermis development	4.1	4.8E-08
positive regulation of phosphorylation	2.8	5.1E-08
locomotion	2.6	5.2E-08
regulation of multicellular organismal process	1.9	5.2E-08
cellular process	1.2	5.3E-08
positive regulation of cellular process	1.6	5.5E-08

cell adhesion	2.9	7.3E-08
positive regulation of phosphate metabolic process	2.6	7.5E-08
cell motility	2.7	7.6E-08
movement of cell or subcellular component	2.4	7.6E-08
response to stress	1.8	7.6E-08
biological adhesion	2.9	7.7E-08
positive regulation of phosphorus metabolic process	2.6	7.7E-08
localization of cell	2.7	7.7E-08
regulation of MAPK cascade	3.1	7.7E-08
leukocyte chemotaxis	7.4	8.9E-08
epithelium development	2.6	9.0E-08
cellular developmental process	1.8	1.1E-07
positive regulation of response to stimulus	2.0	1.5E-07
response to chemical	1.7	1.5E-07
regulation of immune system process	2.3	1.7E-07
regulation of molecular function	1.8	1.8E-07
regulation of apoptotic process	2.3	2.0E-07
myeloid leukocyte migration	8.1	2.3E-07
regulation of programmed cell death	2.3	2.4E-07
regulation of phosphate metabolic process	2.2	4.7E-07
granulocyte migration	9.4	4.9E-07
biological regulation	1.3	5.4E-07
regulation of protein modification process	2.1	5.5E-07
regulation of multicellular organismal development	2.1	5.5E-07
response to oxygen-containing compound	2.3	6.3E-07
positive regulation of MAPK cascade	3.4	6.6E-07
regulation of cellular protein metabolic process	1.9	7.7E-07
regulation of phosphorus metabolic process	2.1	7.8E-07
regulation of protein metabolic process	1.8	8.0E-07
granulocyte chemotaxis	10.0	8.1E-07
regulation of catalytic activity	1.9	8.1E-07
neutrophil migration	9.7	1.1E-06
positive regulation of nitrogen compound metabolic process	1.8	1.2E-06
regulation of signaling	1.7	1.3E-06
cell death	2.5	1.3E-06
programmed cell death	2.5	1.3E-06
animal organ morphogenesis	2.7	1.3E-06
positive regulation of cellular protein metabolic process	2.2	1.3E-06
regulation of cell communication	1.7	1.6E-06
positive regulation of macromolecule metabolic process	1.8	1.7E-06
positive regulation of cellular metabolic process	1.8	1.9E-06

positive regulation of catalytic activity	2.2	1.9E-06
neutrophil chemotaxis	10.3	2.1E-06
positive regulation of cell proliferation	2.6	2.4E-06
skin development	3.7	2.7E-06
positive regulation of multicellular organismal process	2.2	3.2E-06
cornification	6.9	3.5E-06
positive regulation of protein modification process	2.3	3.5E-06
positive regulation of metabolic process	1.7	4.3E-06
regulation of developmental process	1.9	4.3E-06
regulation of cell migration	2.8	4.3E-06
positive regulation of protein metabolic process	2.1	5.2E-06
response to lipid	2.6	5.3E-06
regulation of signal transduction	1.7	6.4E-06
regulation of cell motility	2.7	8.0E-06
epithelial cell differentiation	2.8	1.0E-05
positive regulation of molecular function	2.0	1.1E-05
response to endogenous stimulus	2.2	1.3E-05
regulation of cellular component movement	2.6	1.5E-05
chemotaxis	3.1	1.5E-05
taxis	3.1	1.6E-05
positive regulation of immune system process	2.4	1.7E-05
cellular response to oxygen-containing compound	2.5	1.7E-05
positive regulation of cell death	2.8	1.7E-05
response to drug	2.5	1.9E-05
regulation of biological process	1.2	2.0E-05
defense response	2.2	2.1E-05
regulation of ERK1 and ERK2 cascade	4.1	2.3E-05
response to cytokine	2.4	2.4E-05
regulation of locomotion	2.5	2.7E-05
positive regulation of programmed cell death	2.8	2.8E-05
regulation of hydrolase activity	2.2	3.2E-05
regulation of cellular process	1.3	3.6E-05
regulation of intracellular signal transduction	1.9	3.6E-05
response to growth factor	3.0	3.9E-05
positive regulation of intracellular signal transduction	2.4	3.9E-05
cellular response to endogenous stimulus	2.3	4.3E-05
response to hormone	2.4	4.3E-05
monocyte chemotaxis	11.4	4.6E-05
cell activation	2.3	5.0E-05
positive regulation of apoptotic process	2.8	6.1E-05
epidermal cell differentiation	3.7	6.1E-05

regulation of response to external stimulus	2.5	6.1E-05
mononuclear cell migration	10.9	6.2E-05
chemokine-mediated signaling pathway	7.7	7.1E-05
cellular response to lipid	3.0	7.2E-05
inflammatory response	3.0	8.8E-05
positive regulation of signal transduction	2.0	1.1E-04
cellular response to growth factor stimulus	3.0	1.2E-04
regulation of protein kinase activity	2.5	1.3E-04
negative regulation of cellular process	1.5	1.3E-04
negative regulation of biological process	1.5	1.3E-04
response to steroid hormone	3.5	1.3E-04
cellular response to cytokine stimulus	2.4	1.5E-04
response to glucocorticoid	5.2	1.7E-04
positive regulation of cell migration	3.0	2.2E-04
regulation of protein serine/threonine kinase activity	2.9	2.5E-04
response to organic cyclic compound	2.3	2.7E-04
positive regulation of cell communication	1.9	2.8E-04
regulation of interleukin-1 production	7.4	2.9E-04
positive regulation of signaling	1.9	2.9E-04
positive regulation of ERK1 and ERK2 cascade	4.3	3.0E-04
response to organonitrogen compound	2.3	3.0E-04
keratinocyte differentiation	3.7	3.0E-04
negative regulation of cell death	2.3	3.1E-04
regulation of kinase activity	2.3	3.2E-04
response to toxic substance	2.8	3.3E-04
negative regulation of apoptotic process	2.3	3.3E-04
positive regulation of cell motility	2.9	3.8E-04
positive regulation of developmental process	2.1	3.8E-04
response to peptide	2.9	3.9E-04
lymphocyte migration	8.2	4.0E-04
negative regulation of programmed cell death	2.3	4.2E-04
regulation of response to stress	2.0	4.2E-04
regulation of localization	1.7	4.3E-04
positive regulation of protein kinase activity	2.8	4.5E-04
response to corticosteroid	4.6	4.7E-04
leukocyte activation	2.3	4.7E-04
positive regulation of hydrolase activity	2.4	4.8E-04
anatomical structure formation involved in morphogenesis	2.3	5.1E-04
regulation of immune response	2.1	5.2E-04
regulation of primary metabolic process	1.4	5.3E-04
positive regulation of cellular component movement	2.9	5.4E-04

nervous system development	1.7	5.7E-04
regulation of cell differentiation	1.9	5.8E-04
regulation of nitrogen compound metabolic process	1.4	5.8E-04
regulation of biological quality	1.5	7.4E-04
response to nitrogen compound	2.1	9.0E-04
negative regulation of cell proliferation	2.4	9.3E-04
positive regulation of locomotion	2.7	1.0E-03
positive regulation of epithelial cell proliferation	4.3	1.1E-03
cytokine-mediated signaling pathway	2.6	1.1E-03
regulation of hemopoiesis	2.9	1.2E-03
regulation of MAP kinase activity	3.1	1.2E-03
regulation of transferase activity	2.1	1.3E-03
regulation of epithelial cell proliferation	3.2	1.3E-03
positive regulation of kinase activity	2.6	1.4E-03
head development	2.3	1.4E-03
cellular response to interleukin-1	5.9	1.4E-03
keratinization	3.7	1.4E-03
enzyme linked receptor protein signaling pathway	2.3	2.0E-03
rhythmic process	3.2	2.0E-03
cellular response to organic cyclic compound	2.6	2.2E-03
regulation of macromolecule metabolic process	1.3	2.2E-03
response to abiotic stimulus	2.0	2.5E-03
regulation of smooth muscle cell proliferation	4.9	2.5E-03
cellular response to hormone stimulus	2.4	2.5E-03
neurogenesis	1.8	2.7E-03
negative regulation of response to stimulus	1.8	2.8E-03
behavioral response to nicotine	29.8	3.0E-03
regulation of cell activation	2.5	3.3E-03
sensory organ development	2.5	3.5E-03
embryo development	2.1	3.5E-03
negative regulation of multicellular organismal process	2.0	3.9E-03
cellular response to steroid hormone stimulus	3.7	4.0E-03
regulation of leukocyte differentiation	3.3	4.7E-03
tube development	2.4	5.5E-03
embryonic morphogenesis	2.4	5.6E-03
myeloid leukocyte activation	2.4	5.6E-03
forebrain development	2.8	5.6E-03
circulatory system development	2.1	5.8E-03
response to peptide hormone	2.8	6.0E-03
innate immune response	2.2	6.2E-03
cell development	1.8	6.3E-03

neuron differentiation	2.0	6.5E-03
regulation of inflammatory response	2.7	6.7E-03
regulation of leukocyte activation	2.4	7.0E-03
regulation of GTPase activity	2.5	7.2E-03
response to ketone	3.7	7.7E-03
regulation of defense response	2.1	8.0E-03
regulation of epithelial cell migration	3.6	8.0E-03
central nervous system development	2.0	8.1E-03
regulation of receptor activity	2.4	8.1E-03
response to interleukin-1	4.6	8.3E-03
response to lipopolysaccharide	3.0	8.6E-03
viral entry into host cell	5.1	8.9E-03
positive regulation of transferase activity	2.2	8.9E-03
positive regulation of cell differentiation	2.1	8.9E-03
regulation of metabolic process	1.3	9.0E-03
negative regulation of protein metabolic process	1.9	9.5E-03
regulation of leukocyte cell-cell adhesion	2.8	1.0E-02
hindlimb morphogenesis	8.5	1.0E-02
localization	1.3	1.1E-02
negative regulation of cellular protein metabolic process	1.9	1.1E-02
cell-cell signaling	1.9	1.1E-02
generation of neurons	1.8	1.1E-02
regulation of cytokine production	2.3	1.1E-02
response to other organism	2.1	1.2E-02
positive regulation of gene expression	1.7	1.2E-02
response to external biotic stimulus	2.0	1.2E-02
negative regulation of molecular function	1.9	1.2E-02
negative regulation of signal transduction	1.9	1.2E-02
apoptotic process	2.0	1.3E-02
positive regulation of leukocyte migration	4.3	1.3E-02
regulation of neuron death	2.9	1.3E-02
cellular response to glucocorticoid stimulus	6.4	1.3E-02
cell-cell adhesion	2.5	1.4E-02
neuron development	2.1	1.4E-02
adult behavior	3.9	1.4E-02
appendage development	3.6	1.4E-02
negative regulation of macromolecule metabolic process	1.5	1.4E-02
limb development	3.6	1.4E-02
chemical synaptic transmission, postsynaptic	5.3	1.4E-02
regulation of cellular metabolic process	1.3	1.4E-02
appendage morphogenesis	3.9	1.4E-02

limb morphogenesis	3.9	1.4E-02
response to molecule of bacterial origin	2.8	1.4E-02
positive regulation of cellular biosynthetic process	1.7	1.5E-02
multi-organism process	1.6	1.5E-02
positive regulation of MAP kinase activity	3.0	1.5E-02
positive regulation of biosynthetic process	1.7	1.5E-02
homeostatic process	1.7	1.6E-02
regeneration	3.8	1.7E-02
embryonic appendage morphogenesis	4.1	1.7E-02
entry into host cell	4.5	1.7E-02
embryonic limb morphogenesis	4.1	1.7E-02
regulation of chemotaxis	3.5	1.7E-02
entry into host	4.5	1.8E-02
entry into cell of other organism involved in symbiotic interaction	4.5	1.8E-02
negative regulation of protein serine/threonine kinase activity	4.1	1.8E-02
cellular response to corticosteroid stimulus	6.0	1.8E-02
entry into other organism involved in symbiotic interaction	4.5	1.8E-02
myeloid leukocyte mediated immunity	2.3	1.8E-02
lymphocyte chemotaxis	7.3	1.8E-02
response to tumor necrosis factor	2.9	1.8E-02
positive regulation of chemotaxis	4.0	1.9E-02
regulation of leukocyte proliferation	3.2	1.9E-02
negative regulation of phosphorus metabolic process	2.3	1.9E-02
response to corticotropin-releasing hormone	31.3	2.0E-02
positive regulation of interleukin-23 production	31.3	2.0E-02
cellular response to corticotropin-releasing hormone stimulus	31.3	2.0E-02
cellular response to ketone	4.9	2.1E-02
positive regulation of leukocyte differentiation	3.9	2.2E-02
positive regulation of cytokine production	2.5	2.2E-02
brain development	2.1	2.2E-02
response to biotic stimulus	2.0	2.3E-02
embryonic hindlimb morphogenesis	9.0	2.3E-02
ion transport	1.7	2.4E-02
odontogenesis	4.3	2.4E-02
negative regulation of nitrogen compound metabolic process	1.5	2.4E-02
ion transmembrane transport	1.9	2.5E-02
neuron projection development	2.2	2.5E-02
calcium-mediated signaling	4.2	2.5E-02
response to oxidative stress	2.5	2.5E-02
behavior	2.3	2.5E-02

cellular response to vascular endothelial growth factor stimulus	8.7	2.5E-02
regulation of myeloid cell differentiation	3.1	2.5E-02
positive regulation of transcription by RNA polymerase II	1.8	2.6E-02
negative regulation of cell communication	1.8	2.6E-02
negative regulation of signaling	1.8	2.6E-02
leukocyte degranulation	2.3	2.7E-02
regulation of nucleotide-binding oligomerization domain containing 2 signaling pathway	26.0	2.7E-02
positive regulation of natural killer cell chemotaxis	26.0	2.7E-02
response to nicotine	6.5	2.7E-02
blood circulation	2.5	2.8E-02
humoral immune response	2.7	2.8E-02
system process	1.6	2.8E-02
face morphogenesis	8.4	2.8E-02
regulation of lymphocyte activation	2.3	2.8E-02
positive regulation of cell activation	2.5	2.8E-02
positive regulation of hemopoiesis	3.5	2.9E-02
extracellular matrix organization	2.7	2.9E-02
face development	6.4	2.9E-02
formation of primary germ layer	4.1	2.9E-02
extracellular structure organization	2.7	3.0E-02
positive regulation of protein serine/threonine kinase activity	2.6	3.0E-02
circulatory system process	2.5	3.0E-02
cellular response to nitrogen compound	2.2	3.1E-02
myeloid cell activation involved in immune response	2.2	3.1E-02
negative regulation of phosphate metabolic process	2.2	3.1E-02
response to antineoplastic agent	4.5	3.2E-02
excitatory postsynaptic potential	5.1	3.3E-02
pyrimidine nucleotide biosynthetic process	7.9	3.4E-02
positive regulation of neutrophil migration	7.9	3.4E-02
endoderm formation	6.1	3.4E-02
response to corticosterone	11.6	3.4E-02
viral life cycle	3.1	3.6E-02
positive regulation of nucleobase-containing compound metabolic process	1.6	3.6E-02
negative regulation of phosphorylation	2.3	3.6E-02
endothelial cell differentiation	5.0	3.8E-02
negative regulation of protein phosphorylation	2.4	3.9E-02
cellular response to organonitrogen compound	2.2	4.0E-02
positive regulation of smooth muscle cell proliferation	4.9	4.0E-02
hair follicle development	4.9	4.0E-02

regulation of response to cytokine stimulus	3.3	4.0E-02
positive regulation of GTPase activity	2.4	4.0E-02
muscle tissue development	2.7	4.1E-02
positive regulation of macromolecule biosynthetic process	1.6	4.1E-02
intracellular receptor signaling pathway	3.3	4.1E-02
cellular component morphogenesis	2.0	4.3E-02
leukocyte mediated immunity	2.0	4.4E-02
regulation of circadian rhythm	4.2	4.4E-02
regulation of cell adhesion	2.0	4.4E-02
regulation of cellular component biogenesis	1.9	4.4E-02
regulation of interleukin-1 alpha production	19.5	4.5E-02
odontogenesis of dentin-containing tooth	4.8	4.5E-02
regulation of lymphocyte differentiation	3.5	4.5E-02
regulation of interleukin-23 production	19.5	4.5E-02
negative regulation of protein modification process	2.1	4.5E-02
skin epidermis development	4.8	4.5E-02
regulation of natural killer cell chemotaxis	19.5	4.5E-02
endoderm development	4.8	4.5E-02
regulation of interleukin-1 beta production	5.7	4.5E-02
response to bacterium	2.1	4.6E-02
molting cycle process	4.7	4.7E-02
hair cycle process	4.7	4.7E-02
cytosolic calcium ion transport	4.7	4.7E-02
regulation of transcription by RNA polymerase II	1.6	4.8E-02
head morphogenesis	7.0	4.9E-02
animal organ regeneration	4.7	4.9E-02
digestive tract development	3.7	5.0E-02
regulation of ossification	3.2	5.0E-02
renal system development	2.7	5.0E-02
negative regulation of apoptotic signaling pathway	3.0	5.0E-02

Table S3. Significant gene list from bulk $CD3^+$ RNA-seq of NL vs. EoE tissue lymphocytes

Gene Symbol	Gene ID	Fold Change (Active Tissue vs Normal Tissue)
WRAP73	49856	44.1
APITD1	378708	38.5
PLOD1	5351	123.9
EPHB2	2048	48.2
SDC3	9672	121.0
FCGR1A	2209	44.3
S100A2	6273	322.9
PRRX1	5396	110.5
FMO2	2327	129.9
ACBD6	84320	135.1
NCF2	4688	142.0
RGL1	23179	178.5
G0S2	50486	205.2
TAF1A	9015	37.0
DISP1	84976	89.6
OPN3	23596	63.5
C2orf44	80304	259.1
CHAC2	494143	42.3
LGALSL	29094	54.6
LINC00116	205251	19.8
MERTK	10461	223.8
FARP2	9855	31.6
NICN1	84276	29.1
NAT6	24142	42.9
DNASE1L3	1776	62.1
MITF	4286	75.3
KIAA1524	57650	47.3
ZBTB20-AS1	100131117	37.8
CD86	942	156.3
SLC35G2	80723	23.0
IL20RB	53833	106.5
GPR87	53836	49.2
PPM1L	151742	44.4
ETV5	2119	168.3
TPRG1	285386	55.4
APBB2	323	63.2
CXCL1	2919	509.4
HPGDS	27306	864.3

VCAN	1462	89.3
IL5	3567	1449.0
SH3RF2	153769	320.6
SH3PXD2B	285590	198.2
GFPT2	9945	46.2
F13A1	2162	1167.0
SMIM13	221710	11.2
MRPS18B	28973	189.0
SNORD84	692199	13.0
UNC5CL	222643	57.9
TREML2	79865	170.5
VEGFA	7422	134.1
RCAN2	10231	151.5
CRISP3	10321	-200.3
COQ3	51805	106.5
MTFR2	113115	28.7
AIG1	51390	95.9
RSPH3	83861	156.7
ASL	435	44.1
NCF1	653361	68.7
NCF1C	654817	43.9
FZD1	8321	51.0
SLC25A13	10165	108.5
CYP3A5	1577	88.6
PCOLCE	5118	23.7
ALKBH4	54784	24.7
PLXNA4	91584	151.2
CLEC5A	23601	240.2
CTAGE15	441294	46.2
CTAGE6	340307	54.5
CTAGE4	100128553	81.0
LOC155060	155060	31.5
TMEM176B	28959	135.3
PRKAG2-AS1	100505483	24.1
LOC100287015	100287015	25.9
LYN	4067	249.9
CYP7B1	9420	154.9
ZNF251	90987	158.6
KLF4	9314	105.3
GSN	2934	425.1
URM1	81605	64.3

DBH	1621	20.6
PLXDC2	84898	848.4
PALD1	27143	46.1
PLAU	5328	359.1
ANKRD22	118932	26.9
BLNK	29760	61.6
CHST15	51363	303.7
SPI1	6688	20.4
TCN1	6947	389.3
CCDC85B	11007	13.1
SLCO2B1	11309	115.9
OLR1	4973	359.4
PTPRO	5800	66.3
C12orf66	144577	119.3
PITPNM2	57605	104.7
RILPL1	353116	26.9
EBPL	84650	81.7
SLC7A7	9056	253.9
EFS	10278	44.8
FOXA1	3169	51.6
RGS6	9628	131.2
STON2	85439	189.0
SERPINA1	5265	204.2
SNHG10	283596	15.1
LACTB	114294	10.2
IGF1R	3480	246.0
LRRK1	79705	117.5
STUB1	10273	19.5
ZNF174	7727	98.8
LPCAT2	54947	34.2
KATNB1	10300	198.2
ENKD1	84080	36.7
DDX28	55794	39.8
ZNF821	55565	18.5
NUDT7	283927	23.0
TIMM22	29928	109.4
RANGRF	29098	126.0
RAB34	83871	33.4
ADAP2	55803	132.9
OMG	4974	78.6
SLFN14	342618	32.5

SPPL2B	56928	29.2
EPOR	2057	56.9
ZNF333	84449	38.6
CYP4F12	66002	30.7
MEF2B	4207	15.8
CCNE1	898	37.4
KCTD15	79047	30.9
PPM1N	147699	61.8
C5AR1	728	306.2
SIGLEC10	89790	50.7
FPR1	2357	144.1
FIZ1	84922	68.2
ZNF256	10172	123.0
ZSCAN18	65982	72.4
NANP	140838	37.8
HCK	3055	93.8
ZNF341	84905	29.4
CD40	958	43.4
MIS18A	54069	69.0
PCBP3	54039	31.5
CDC45	8318	67.2
PHF5A	84844	54.2
CYP2D7	1564	26.8
TTLL12	23170	91.4
SCUBE1	80274	12.5
TLR8	51311	197.7
TRO	7216	50.9
FAM58A	92002	69.9
SPRY3	10251.chrX	35.7
IL9R	3581.chrX	66.9

Table S4A. Tissue lymphocytes differentially expressed genes: remission vs. normal

Gene Symbol	Fold change	Regulation (Normal vs. Remission)
PLOD1	91.7	down
MST1P2	12.4	down
C1QB	86.1	down
TCEA3	100.0	down
GPATCH3	16.5	down
SDC3	14.3	down
FABP3	8.5	down
MTMR9LP	27.1	down
TSSK3	50.7	down
ADPRHL2	40.1	down
ST3GAL3	32.7	down
PTCH2	28.2	down
RAD54L	10.9	down
ZFYVE9	116.8	down
ORC1	16.8	down
LRRC42	61.8	down
CYB5RL	277.7	down
GNG12	119.9	down
MCOLN3	42.5	down
ALG14	25.0	down
FAM72B	15.6	down
FAM72D	23.2	down
SV2A	20.3	down
S100A2	475.9	down
BGLAP	31.6	up
OLFML2B	100.1	down
KIAA1614	16.5	down
NCF2	65.5	down
FAM72A	15.0	down
G0S2	82.1	down
DISP1	16.5	down
OPN3	49.8	down
ZNF496	33.7	down
FAM49A	35.1	down
C2orf44	269.6	down
CENPA	10.2	down
SLC8A1	131.6	down
LOC100506142	80.2	down

MEIS1	31.7	down
PROM2	99.8	down
GPAT2	7.0	down
FNIP2	12.3	down
1-Mar	79.0	down
NEIL3	8.4	up
FRG1	3.4	up
CCDC127	17.1	down
LOC100288152	18.0	down
CLPTM1L	21.5	down
SDHAP3	4.4	up
TRIO	152.3	down
ZNF622	27.2	down
TARS	7.0	down
RAD1	18.0	down
SLC1A3	12.4	down
LOC646719	3.9	down
ZNF131	2.2	up
ARL15	3.1	down
GAPT	90.2	down
TRIM23	7.9	down
LOC647859	14.0	down
FCHO2	55.5	down
ANKRA2	19.1	down
F2RL1	21.5	down
TMEM167A	2.9	down
MEF2C	158.7	down
LYSMD3	2.2	down
SPATA9	34.6	down
WDR36	2.6	down
CEP120	2.5	up
RAPGEF6	2.0	up
ZCCHC10	9.9	down
KLHL3	9.5	up
NDUFA2	3.2	down
NR3C1	2.1	up
TCERG1	2.3	up
ABLIM3	44.9	down
SLC26A2	3.8	down
CSF1R	10.1	down
CD74	2.3	down

RPS14	2.3	down
RBM22	3.0	down
ZNF300	32.7	down
CCDC69	3.3	up
FAT2	98.1	down
SPARC	95.5	down
FNDC9	67.4	down
THG1L	4.4	down
RNF145	2.7	down
PTTG1	2.8	up
MIR146A	5.9	up
HMMR	14.7	down
FBXW11	2.2	up
SIMC1	4.5	up
CLTB	104.3	down
GRK6	2.7	up
PRR7	18.3	down
LINC00847	10.4	down
ZFP62	2.9	down
SERPINB1	28.7	down
LINC01011	5.1	up
HTATSF1P2	4.9	up
F13A1	46.7	down
SMIM13	26.3	down
NOL7	2.2	up
E2F3	4.6	down
CDKAL1	3.0	down
HIST1H1C	5.5	down
HIST1H4E	52.4	down
HIST1H2BG	29.8	up
BTN3A3	2.2	up
HIST1H2AK	16.3	up
MRPS18B	85.9	down
PPP1R18	2.0	up
LTA	4.7	up
LY6G5C	27.5	down
SNORD52	4.7	down
SKIV2L	3.8	up
FKBPL	37.3	up
PPT2	2.8	up
HLA-DQA2	5.1	down

PSMB9	6.9	down
HLA-DOA	3.6	down
RXRB	2.0	down
LEMD2	2.3	up
FANCE	30.2	down
ETV7	16.6	down
FGD2	53.6	down
GLO1	5.7	down
ADCY10P1	5.9	up
USP49	145.8	down
CNPY3	3.3	down
GTPBP2	14.2	down
VEGFA	91.7	down
ENPP5	9.0	up
RCAN2	27.8	down
RPS16P5	2.3	up
BAG2	21.2	down
PHF3	2.9	up
OGFRL1	3.4	down
C6orf147	20.0	down
DDX43	9.9	down
SLC17A5	3.2	up
HMGN3-AS1	12.8	down
RRAGD	6.5	down
MAP3K7	2.1	up
SLC16A10	10.0	down
KIAA1919	3.4	down
TRAF3IP2-AS1	13.5	down
MARCKS	18.9	down
PKIB	10.2	down
RNF217	25.1	down
SGK1	4.1	down
MAP7	27.1	down
LOC100130476	2.9	down
GPR126	20.2	down
AIG1	65.1	down
RPS18P9	47.0	up
KATNA1	4.8	down
RAET1G	8.9	down
ULBP2	55.4	down
PLEKHG1	10.5	up

TFB1M	5.8	up
ZDHHC14	4.6	down
RSPH3	44.8	down
C6orf123	3.1	up
SUN1	3.3	down
C7orf50	14.8	up
IQCE	3.0	up
RNF216P1	9.5	down
CLK2P	3.4	down
NFE2L3	2.9	up
CPVL	132.7	down
LOC646762	61.6	down
MTURN	8.2	up
LOC401320	2.6	up
AMPH	46.8	up
SNHG15	5.4	down
FKBP9L	7.5	down
14-Sep	4.3	up
MRPS17	62.5	down
ASL	97.8	down
POM121	2.0	up
NCF1	25.6	down
WBSCR16	27.7	down
NCF1C	15.4	down
STYXL1	14.5	up
ABCB4	6.7	down
FZD1	61.0	down
SLC25A13	172.7	down
ASNS	3.3	up
MGC72080	40.7	down
MIR3609	5.5	down
SMURF1	3.2	down
CPSF4	60.4	down
LAMTOR4	4.4	down
GAL3ST4	4.2	down
CLDN15	25.3	up
SYPL1	3.8	down
PRKAR2B	44.3	down
BCAP29	2.1	down
TMEM168	5.0	down
CAPZA2	2.8	down

ST7	4.6	up
ST7-OT3	14.9	up
CTTNBP2	319.2	down
NAA38	3.8	down
ARF5	26.5	down
TPI1P2	58.4	up
AKR1B1	17.3	down
CNOT4	3.0	up
C7orf73	2.6	down
C7orf55	12.5	down
TRBV7-7	9.1	down
EPHA1	14.7	down
EZH2	3.0	up
TMEM176A	74.2	down
CDK5	16.3	down
CHPF2	2.6	down
GALNT11	2.1	up
PAXIP1-AS1	12.7	down
DNAJB6	2.4	up
MCPH1	2.6	up
FAM86B3P	30.8	down
MICU3	34.8	down
BMP1	55.8	down
PIWIL2	5.3	up
SLC25A37	14.5	down
ADAM28	116.2	down
FZD3	66.4	down
UBXN8	25.7	down
FUT10	2.5	up
POLB	4.5	down
LYN	266.6	down
RAB2A	2.5	up
CYP7B1	5.0	down
RRS1	43.0	down
ADHFE1	61.8	down
SNHG6	4.8	down
GDAP1	21.1	down
ZNF704	13.8	down
IMPA1	10.6	down
SNX16	36.2	down
E2F5	5.5	down

RIPK2	11.0	down
FAM92A1	21.3	down
RBM12B-AS1	12.3	down
CCNE2	24.8	down
COX6C	3.7	down
OXR1	5.9	down
EBAG9	3.9	up
FAM84B	8.0	down
ASAP1	2.4	up
KCNQ3	85.8	down
TMEM71	18.1	down
GLI4	39.5	down
ZFP41	20.6	down
TOP1MT	32.0	down
ZNF623	3.0	up
BREA2	4.1	down
CYC1	79.2	down
SLC52A2	43.1	down
ZNF251	136.3	down
COMMD5	10.7	down
C9orf66	14.0	down
KANK1	159.8	down
AK3	5.6	down
FLJ41200	2.4	up
NFIB	79.4	down
CNTLN	11.7	down
CDKN2B-AS1	20.1	down
C9orf72	5.3	down
NDUFB6	18.7	down
UBAP1	2.2	up
UNC13B	39.0	down
RMRP	4.0	down
MGC21881	35.1	down
KGFLP2	11.4	down
APBA1	55.5	down
C9orf40	11.2	down
NMRK1	2.6	up
CDK20	61.3	up
ZNF510	2.6	down
HIATL2	18.8	up
GALNT12	29.2	down

INVS	26.1	up
TMEM246	70.5	down
GRIN3A	14.6	down
ABCA1	3.0	down
FSD1L	9.7	down
KLF4	121.8	down
PALM2-AKAP2	3.0	down
AKAP2	3.0	down
LPAR1	31.8	down
PTGR1	169.6	down
DNAJC25-GNG10	4.3	down
GNG10	3.9	down
SNX30	34.0	down
ZNF618	47.3	down
AKNA	2.3	up
TNFSF15	51.0	down
TRAF1	2.3	up
GSN	93.3	down
GGTA1P	62.4	down
C9orf16	3.9	up
CIZ1	2.4	down
SWI5	13.7	down
URM1	39.7	down
ODF2	4.5	up
USP20	3.0	down
FNBP1	2.1	up
UCK1	22.4	up
ADAMTSL2	3.0	up
SARDH	38.1	down
RXRA	3.4	down
SSNA1	57.2	down
TPRN	26.9	down
NELFB	12.3	up
ADARB2	60.8	down
PFKP	2.7	up
CALML3	66.2	down
DHTKD1	17.3	down
OPTN	2.5	up
MCM10	48.0	down
PTER	2.7	down
PLXDC2	237.4	down

LOC100130992	9.8	up
PIP4K2A	2.2	up
MASTL	21.9	down
ACBD5	2.0	up
RAB18	3.3	down
MTPAP	7.2	down
ZEB1	3.7	up
PARD3	45.9	down

Table S4B. Tissue lymphocytes differentially expressed genes: remission vs. active

Gene Symbol	Fold change	Regulation (Remission vs. Active)
ATAD3A	15.9	down
PER3	16.7	up
LZIC	2.8	up
APITD1-CORT	10.6	down
NBPF3	2.7	up
SRSF10	2.0	up
MAN1C1	4.0	down
LIN28A	6.7	down
LOC644961	24.6	down
SNORD99	4.0	down
TAF12	3.2	down
TFAP2E	32.5	down
EXO5	6.0	down
PTCH2	12.0	up
CCDC17	17.5	down
DMBX1	4.1	down
CYB5RL	38.0	up
FAM73A	2.1	up
CTBS	2.4	down
RBMXL1	2.5	up
GFI1	2.7	down
EXTL2	12.8	up
GNAT2	6.5	down
CSF1	2.2	down
DRAM2	2.1	down
TRIM45	2.2	up
ANKRD34A	12.6	down
GPR89C	2.4	down
GBA	2.3	up
ASH1L-AS1	27.7	down
KIAA0907	2.6	down
APOA1BP	10.6	down
GPATCH4	3.5	down
ISG20L2	2.1	up
FCER1A	36.7	up
CCDC19	17.7	down
USP21	12.9	down
APOA2	7.4	down

RGS5	6.4	down
MPC2	2.7	down
XCL2	2.1	up
PRRX1	46.4	down
SCARNA3	17.0	down
ZBTB41	2.2	up
TMCC2	5.7	down
CR1	15.0	down
KCTD3	5.9	up
LYPLAL1	3.6	down
DISP1	5.5	down
LOC101926980	3.2	up
LIN9	6.2	down
ABCB10	2.3	up
EDARADD	9.5	up
SMYD3	14.8	down
SH3BP5L	13.6	down
SH3YL1	2.1	up
DPYSL5	3.1	up
DHX57	2.7	down
MORN2	25.1	down
DYNC2LI1	11.3	down
SNRPG	2.7	up
LBX2-AS1	10.9	down
ANKRD23	16.7	down
TSGA10	6.0	down
LOC100499194	8.1	down
ZEB2-AS1	6.9	down
GALNT5	50.0	down
ERMN	73.2	down
FASTKD1	3.5	up
COL5A2	31.1	down
SDPR	4.7	down
GCSHP3	14.4	down
CHPF	27.3	down
MTERFD2	4.1	down
TATDN2	2.5	down
ZNF662	2.8	down
RBM5	2.2	down
CHDH	25.8	down
IL17RB	68.8	down

ASB14	3.2	down
FLNB-AS1	2.4	up
LINC00971	2.2	up
ALCAM	3.3	up
PVRL3	4.3	down
SPICE1	2.2	down
ZBTB20-AS1	21.6	down
CD80	7.9	down
SEC22A	5.5	down
TFDP2	2.8	up
GYG1	2.7	down
B3GNT5	2.9	up
KLHL6	2.2	down
MAP3K13	2.2	up
LEPREL1	12.5	up
PDE6B	5.8	down
DGKQ	5.7	down
IDUA	10.5	up
SH3BP2	2.2	up
AFAP1	2.8	down
LCORL	2.5	up
KLHL5	2.1	down
RBM47	5.3	up
GUF1	2.4	down
EXOC1	2.5	up
UTP3	2.6	down
CXCL3	14.2	down
AREG	2.3	up
C4orf21	5.0	down
TNIP3	3.0	down
SLC10A7	3.4	down
KIAA0922	2.4	down
TARS	2.3	up
ERCC8	7.2	up
ADAMTS6	26.3	down
ANKDD1B	8.0	down
ARSB	3.4	down
FER	2.6	up
MCC	2.9	up
IL5	1464.1	down
IL13	159.0	down

C5orf24	2.5	down
CD14	9.3	down
PCDHGB3	11.2	down
ABLIM3	14.1	up
HAVCR2	2.6	down
TTC1	2.3	down
SH3PXD2B	6.6	down
PRR7	10.9	up
TRIM52-AS1	2.6	up
NOL7	2.3	down
TDP2	2.2	up
GMNN	3.0	up
PGBD1	25.3	down
UBD	27.4	down
HLA-J	2.0	down
GTF2H4	4.4	down
ATP6V1G2-DDX39B	8.9	up
ABHD16A	3.1	down
DDAH2	8.1	down
PPT2	10.4	up
AGER	12.3	down
COL11A2	13.3	down
BAK1	3.8	down
TREM1	7.1	down
ENPP5	8.8	down
IL17A	10.1	up
FAM135A	2.8	up
OGFRL1	4.1	up
DCBLD1	7.6	down
AKAP7	3.3	up
OR2A4	4.6	down
CITED2	2.7	up
EPM2A	12.2	down
RSPH3	3.5	down
C7orf50	10.3	down
GPR146	10.4	down
AMZ1	19.8	down
DNAH11	16.0	down
LOC646762	19.5	up
RP9	4.7	down
AMPH	15.9	down

AEBP1	21.3	down
TMED4	3.4	up
FKBP9L	8.5	up
ZNF107	2.7	up
INTS4L2	4.0	down
PMS2P8	2.7	up
NCF1B	3.8	down
LOC441259	2.8	up
PMS2L2	6.1	up
CCL26	71.4	down
CNPY4	8.3	down
PILRA	3.5	down
GIGYF1	2.2	up
SLC12A9	4.1	up
ALKBH4	10.0	down
BCAP29	2.0	up
ST7-AS1	6.5	down
LRRC4	18.5	down
METTL2B	2.6	up
PLXNA4	49.6	down
OR2A7	7.3	down
GIMAP4	2.2	down
GIMAP2	2.0	down
VIPR2	2.7	down
CLN8	8.0	down
BMP1	2.1	up
EGR3	2.1	up
CLU	9.1	down
CYP7B1	31.5	down
LOC100132891	2.3	up
ZC2HC1A	2.8	down
SNX16	5.9	up
INTS8	2.2	up
PTDSS1	2.3	down
FLJ45248	33.9	down
SLC52A2	3.0	up
PPP1R16A	21.0	up
C9orf72	2.1	up
NDUFB6	2.1	up
CD72	4.2	up
SPAG8	5.7	down

GNE	2.2	up
LOC100132352	2.8	up
UNQ6494	38.2	down
INVS	6.6	down
FPGS	4.9	down
LOC100289019	2.8	down
SH3GLB2	5.6	up
MED27	2.2	up
SURF2	5.2	down
SNHG7	3.1	up
ARRDC1	2.4	up
MRC1	10.0	down
MRC1	12.6	down
MASTL	2.2	up
ZNF37A	2.1	down

Table S5. Demographic and clinical information of participants

	*Normal	Remission	Active
n	5	6	11
Gender (male %)	40%	83%	73%
Race (Caucasian %)	82%	83%	80%
Hispanic%	0%	0%	0%
Age (years)	12 ± 6.3	12 ± 4.6	10 ± 4.7
PPI-confirmed EoE	0% (N/A)	33%	64%
History of PPI usage	20%	83%	82%
Asthma	20%	33%	27%
Allergic rhinitis	20%	67%	45%
Hay fever	20%	17%	36%
Eczema	40%	50%	64%
Urticaria	0%	50%	55%
Food Allergy	0%	67%	64%
Food anaphylaxis	0%	33%	27%
Tissue eosinophilia (peak EOS/HPF)	0.0 ± 0.0	4.8 ± 5.6	76 ± 55
PPI	20%	83%	73%
Swallowed steroid	0%	50%	18%
H1 Block	20%	50%	27%
H2 Block	20%	0%	9%

PPI: Proton pump inhibitor; quantitative data represented in “Mean ± SD”.

EOS/HPF: Eosinophils/high power field

* The normal control were those patients with gastrointestinal symptoms without EoE history and were found to have a completely negative endoscopy and biopsy histology.

Table S6. The cohort of 1114 PCA genes contributing to the major variations of T1-T8

Gene Symbol	p value
IL1R2	3.03E-08
IL1R1	1.98E-14
FOXP3	1.04E-14
UGP2	1.44E-10
GPR15	1.32E-09
IKZF2	5.04E-06
NAB1	1.43E-07
IL10	2.48E-15
AC017002.1	2.24E-08
LINC01943	4.11E-11
CD28	6.49E-16
PELI1	2.04E-10
IL6R	1.35E-08
TBC1D4	2.61E-44
IL2RA	7.07E-14
ZC2HC1A	9.86E-18
CTLA4	5.88E-28
MAF	9.58E-47
PHACTR2	4.74E-21
PHTF2	2.13E-28
CD4	8.62E-46
CARD16	9.12E-13
CASP1	4.85E-17
TIGIT	3.83E-12
GLCCI1	1.38E-10
ICOS	1.80E-39
SLAMF1	6.45E-15
MAST4	9.90E-11
GPX1	7.72E-10
BATF	3.99E-12
NDUFV2	4.60E-15
ZNF451	0.00357
RHBDD2	9.84E-08
CENPC	0.000137
BHLHE40-AS1	1.69E-09
OAF	0.0061
EML4	4.76E-15
PPCS	0.0172

PDS5B	0.0345
CLDND1	5.23E-13
ITGAL	2.50E-08
ATG14	0.0222
LPXN	6.76E-05
PNISR	1.37E-10
TAB2	1.35E-05
ADAR	3.27E-06
ANKRD12	1.96E-13
RBPJ	4.99E-11
SERINC3	2.43E-05
ATXN1	2.84E-09
FAS	3.18E-05
DUSP10	3.81E-08
DUSP4	5.71E-14
ARID5B	4.50E-13
G3BP2	1.70E-07
UBE2B	2.64E-12
TPP1	6.39E-08
CTSC	1.84E-14
TNFRSF1B	1.24E-10
MIR4435-2HG	8.74E-11
CYTOR	5.49E-12
NAMPTP1	6.90E-07
NAMPT	4.92E-19
CNTLN	0.00551
FNTA	3.92E-08
RP11-484L7.2	0.000375
AC012668.1	2.17E-05
TLK1	9.56E-11
HNRNPLL	3.80E-12
LIMA1	0.000157
SH3BGRL	0.00105
SIRPG	1.84E-06
IL2RB	4.32E-07
MYO5A	1.70E-07
DYNC1I2	0.0388
PIM2	1.06E-17
ZIM2-AS1	8.47E-06
TTN	2.85E-12
TTN-AS1	0.0425

FOXO1	4.13E-09
NCOA1	0.000364
LAPTM4A	4.59E-06
ATP1B1	5.02E-05
TNIP3	9.07E-07
TNFRSF9	6.91E-05
ABHD17B	0.00762
CCR4	0.00241
PBXIP1	1.37E-08
SKAP1	2.10E-06
RP11-205M5.3	0.00776
POP4	0.037
KIAA0922	0.0278
GEMIN8	8.06E-08
PRDX2	7.18E-06
UBR4	7.02E-06
RDX	0.00785
ARHGAP5	0.0155
COPS3	0.021
CEP350	0.000633
COX5A	0.00863
ERI1	0.000609
RAC1	0.000346
SREK1	9.06E-05
RRS1	0.04
UBXN1	1.38E-06
CD5	3.20E-09
MTMR6	0.0302
DYNLRB1	0.00312
SPPL2A	0.000111
NUP58	0.0346
DCP2	0.015
ATAD2	0.00329
ENTPD1	0.000109
MIR205HG	0.00111
LINC01902	0.00333
RP11-473M20.5	0.00278
NDUFV2P1	0.0294
RNU6-1152P	0.000196
LINC02119	1.28E-05
JAK3	4.85E-07

IL5	7.71E-10
HPGDS	2.40E-43
IL13	8.80E-26
IL17RB	2.67E-49
EGLN3	3.96E-13
LIF	0.000292
GPR42	0.000579
FFAR3	8.77E-06
RP11-884K10.7	1.84E-11
PLN	1.22E-10
PPARG	3.54E-20
IL1RL1	2.21E-05
CHDH	1.99E-09
LINC01229	0.00336
GK	3.55E-23
RP11-242C19.2	2.69E-06
CD109	3.36E-07
GNAQ	1.75E-13
TNFRSF11A	1.52E-06
HLF	1.89E-06
TESPA1	2.39E-15
ALAS1	8.56E-07
GATA3	2.17E-44
PTGS2	0.0277
KIAA0408	0.00333
PLIN2	1.42E-65
DSE	0.000145
ACSL4	2.26E-13
YPEL2	2.47E-08
DUSP6	1.43E-22
TIMP1	4.91E-08
PDLIM5	7.84E-19
ADAM19	1.86E-33
KLRB1	7.74E-67
PTPN13	1.67E-07
CD40LG	1.55E-14
LINC00892	1.46E-12
RNA5SP493	0.00385
AC091492.2	6.86E-11
AHR	1.02E-21
GAB2	0.000215

CD38	0.00369
TNFSF10	1.36E-05
SCD	1.09E-07
EFHD2	4.78E-05
C1orf162	0.0034
IL26	2.66E-06
FURIN	5.65E-06
GPR35	8.42E-07
SESN3	1.80E-10
ST6GAL1	3.09E-08
PSMD1	7.74E-07
FAH	0.0324
HS6ST1	4.48E-11
SH3TC1	5.30E-06
LAGE3	7.31E-05
HK2	4.61E-10
GDE1	0.00635
KIF3A	3.93E-08
MAP3K8	3.73E-08
LMO4	2.69E-16
BHLHE40	4.05E-11
ALOX5AP	7.99E-37
EPC1	6.86E-06
NR3C1	5.37E-21
DGKH	0.00195
ITGAV	1.65E-10
DPY19L1	0.00484
SLC27A2	0.00138
FAM35BP	0.000925
ST13	4.08E-08
SLC5A3	1.79E-08
MRPS6	1.11E-29
SLC4A7	6.86E-11
THADA	6.32E-05
BLM	5.19E-05
MRPL14	3.46E-13
SDCBP	1.21E-10
GLO1	1.15E-11
MRFAP1	0.0187
IFNAR2	0.000578
RP11-56B16.5	0.0224

RN7SL653P	0.00353
TGFBR3	8.09E-33
IL4R	0.000295
TAB3	0.000962
FKBP2	0.00542
INPP4B	5.28E-07
RAPGEF2	0.000199
TTC17	0.000293
NDFIP2	5.79E-09
RNMT	0.00513
KIF20B	0.00319
C5orf22	0.0287
KLHL6	1.09E-06
TIMM9	4.20E-08
MGAT5	0.0101
PHLDA1	2.15E-42
STK24	1.20E-05
TOR1AIP1	5.59E-07
SEC11C	0.00486
MTSS1	0.00914
NF2	0.000367
DNAJC3	8.30E-06
NUDT4	1.08E-07
PFDN2	0.0013
HSP90B1	8.16E-13
SELENOF	0.027
C10orf128	1.42E-06
ZEB2	8.34E-16
RP11-136F16.1	8.11E-06
PPP2R2C	0.000835
DGKE	2.74E-06
RP11-107E5.3	2.08E-10
TENM4	0.014
ITGA4	2.49E-06
TBC1D15	0.0014
GMPR2	0.00376
DCAF4L1	0.00128
ITGA2	6.96E-09
GPR180	0.00113
NFATC3	7.12E-06
RP11-96D1.11	5.70E-12

CD200R1	5.73E-14
VIPAS39	3.25E-06
BFSP2	0.000221
ARHGAP18	0.0035
SOCS1	2.49E-12
TRIP12	0.000102
EAPP	0.0215
MFSD1	0.0441
RER1	5.79E-05
E2F3	0.0236
DGUOK	0.0165
CCDC86	0.00884
BAZ1A	0.00152
FNBP1	9.91E-06
STXBP3	0.0158
NDUFB4	0.0459
USP15	1.19E-08
SELENOT	1.22E-12
FILIP1L	0.0203
GAB3	0.000532
UBA6	0.0334
ELOVL5	2.00E-13
AZI2	0.0458
SRPK1	0.00997
CDK1	1.49E-05
BCL2L11	1.76E-06
DROSHA	0.00535
ZC3H11A	0.00324
MRPS31	0.000843
WBP11	0.0228
TM9SF3	0.000363
MTDH	0.000578
TIMMDC1	0.00164
TIMM23	0.00612
VEGFB	4.60E-08
TDG	0.00408
LYSMD4	0.00265
RAD23B	0.0485
SEC61G	0.00724
DENND1B	2.32E-06
LYSMD3	6.36E-20

TRIM59	0.0242
POLR3E	0.0311
FBXO34	0.000453
CFAP36	0.00164
REEP3	4.77E-07
NEK10	0.00906
PDCL3	9.49E-06
PRDX1	9.44E-08
LIMS1	2.42E-05
SPATS2L	1.11E-09
FDFT1	0.0112
DNAJC2	0.0158
COMMD1	0.0201
EIF2AK1	0.00275
RP11-643M14.1	0.00523
TMEM167A	2.98E-05
SNX5	5.08E-07
RAP1A	1.14E-07
MRPS21	0.0416
B9D2	0.0483
CCDC66	0.00382
SF3B1	3.96E-06
PPM1G	0.00585
RP1-257A7.4	0.0256
POLI	0.027
MAT2B	0.0128
PRKACB	0.000349
NCK1	0.0167
POGLUT1	0.012
FXR1	4.18E-05
FAM172A	0.0268
WDR70	0.0388
ELOF1	0.0242
SH2D6	0.00799
ABI1	0.000122
EIF4ENIF1	0.000452
SRSF11	3.12E-06
RBM39	8.29E-06
RP11-1042B17.3	0.00967
ITK	9.73E-23
EIF3D	0.00144

MOB3A	1.18E-09
DNAJC9-AS1	0.0489
PMPCB	0.00615
EHMT1	0.0221
FGFR1	0.00296
BCAM	0.0191
TMED5	9.30E-06
MARCH7	0.0119
ATP11B	0.00119
FRA10AC1	0.00161
S100A11	3.49E-11
HIGD2A	0.0111
RPL37	4.36E-23
RPS29	5.11E-06
RPS25	9.31E-09
RPS3	4.30E-06
RPS3A	3.10E-06
RPL34	9.97E-07
RPL36A	9.48E-10
RPS12	3.34E-06
RPL35A	1.17E-10
RPL9	3.46E-15
RPS18	6.13E-06
RPLP1	5.73E-10
AC010970.2	5.69E-06
RPL27A	8.24E-08
RPL31	3.18E-10
RPS28	9.16E-24
RPL23	1.82E-14
RPL39	2.10E-21
RPS7	5.37E-07
RPS15	3.03E-11
RPL27	4.86E-06
RPL32	1.03E-07
RPS11	3.58E-06
RPL15	1.51E-16
RPL30	5.65E-07
RPS20	1.28E-06
RPS15A	1.03E-09
RPS21	4.13E-14
RPL11	2.69E-16

RPL38	5.30E-08
RPS23	1.28E-13
RPLP0	1.62E-06
RPS10	1.27E-06
UBA52	1.19E-06
RPL35	2.05E-10
FAU	1.33E-07
RPL18	5.15E-13
RPS8	1.37E-06
RPL6	2.20E-11
RPL12	4.03E-06
RPS16	3.53E-19
RPL7A	4.36E-06
EEF1G	9.26E-10
RPS17	8.24E-12
RPS24	3.44E-34
RPL7	1.33E-07
RPL36	5.01E-18
RPL26	2.24E-09
SERF2	1.00E-11
AC004057.1	2.22E-07
RPS26	4.90E-08
ATP5G2	9.84E-08
RPL5	9.97E-20
RPS13	3.59E-11
ATP5L	6.47E-16
RPL4	2.50E-17
RAC2	3.09E-09
CLIC1	4.61E-09
S100A4	7.20E-13
HLA-C	6.49E-06
HLA-B	3.91E-07
HLA-A	5.61E-10
ACTB	4.21E-06
B2M	5.92E-07
IL32	2.07E-33
ACTG1	1.86E-07
EIF1	1.11E-06
PTMA	6.63E-07
TRBC1	7.49E-10
TRAC	2.34E-06

SH3BGRL3	2.14E-10
COX6A1	1.68E-08
TMA7	2.13E-06
GAPDH	8.07E-09
MYL6	2.27E-15
UBB	2.08E-10
UBC	3.07E-13
H3F3A	1.37E-06
PFN1	5.75E-10
TPM3	2.80E-08
CD3D	3.30E-06
UBL5	2.46E-07
YWHAB	1.72E-10
ARPC3	0.000167
FXYD5	9.96E-09
PPIA	1.51E-16
ELOB	2.86E-06
YBX1	0.00265
LCP1	3.80E-06
CAPZA1	2.49E-06
YWHAZ	2.83E-07
IL2RG	2.84E-09
RASSF2	0.00183
YWHAE	1.86E-07
OAZ1	3.58E-08
CALM2	1.71E-09
ARPC4	7.50E-07
ARPC1B	3.20E-06
LAPTM5	2.20E-08
NDUFA13	5.69E-07
SKP1	1.21E-06
CNBP	5.67E-07
NDUFA4	9.26E-07
TRAPPC1	0.000522
TRBC2	4.26E-06
GABARAP	2.67E-06
NDUFA1	6.09E-08
CCND2	2.16E-10
ATP5F1	0.000119
GMFG	9.16E-08
CCNI	1.54E-11

UQCR10	0.000293
NACA	4.77E-07
ENO1	4.32E-07
BUB3	2.54E-06
ACTR3	2.23E-07
NDUFB8	0.000546
CLEC2B	6.18E-07
HNRNPA2B1	1.32E-09
BRK1	0.000767
UCP2	4.93E-12
POMP	1.04E-08
PSME2	0.00905
MRPL33	5.94E-06
SSR4	2.57E-07
ISCU	0.000255
GTF3C6	0.00644
SERINC5	1.32E-09
TMBIM4	4.13E-06
FKBP1A	3.89E-17
CIB1	3.08E-06
SRP14	1.96E-07
SEC61B	5.94E-06
DCTN6	0.000173
DYNLL1	8.70E-07
RHOF	1.48E-05
CAPG	5.07E-07
OSTF1	4.42E-08
ARF6	5.08E-08
YWHAQ	7.48E-05
HMGB1	8.05E-07
HMGB1P6	0.0257
NDUFC1	0.0437
DAD1	1.11E-06
SNRPN	0.0177
UBE2V1	1.32E-07
SUMO2	1.90E-09
SURF4	0.0188
UBE2D3	1.16E-11
IQGAP1	1.75E-08
PARP1	0.00378
SETX	0.0472

DOCK8	5.76E-15
GAS5	6.64E-08
MBNL1	1.53E-15
RAB27A	5.24E-06
RAN	4.01E-07
RAB2A	0.0433
PPIB	6.01E-10
PSMA2	1.77E-05
DERL2	0.0237
MRPL18	8.00E-10
PGAM1	0.000184
ATP5J	1.40E-06
UBE2L3	0.0464
PRNP	0.0173
ZFR	0.00092
PA2G4	3.39E-05
WTAP	5.99E-06
CTBP1	6.98E-06
C6orf62	2.17E-07
ALDOA	1.30E-07
PTEN	0.0308
HIGD1A	3.20E-09
ETNK1	0.0407
ZFAS1	0.0109
SNHG8	2.46E-07
AZIN1	8.36E-08
POLR2K	0.0315
NEK1	0.00457
LAT	1.79E-08
RNASEK	2.86E-08
MEF2A	0.00492
XRCC6	3.91E-05
SUSD6	1.98E-05
PSMD12	0.000204
ITPR1	2.63E-06
ATP6V1F	0.00575
KHDRBS1	0.0179
ATP6V0E1	1.96E-07
ATP5O	0.00157
RN7SL132P	0.0476
NDUFV1	0.000708

ARF4	0.000505
CMTM3	3.18E-06
ISG15	1.37E-06
PDIA6	0.000613
WDR1	7.49E-05
CPEB4	4.07E-06
SOD1	4.78E-09
CCT8	6.63E-07
DBF4	0.0018
METTL5	0.0214
BST2	0.00401
NDUFB3	0.0306
COX8A	0.00685
UQCRQ	0.0165
DBNL	0.0304
NDUFS6	0.0176
UBE2K	1.50E-07
FAM120A	0.00747
CDV3	1.26E-09
GOLGA8B	4.15E-06
GOLGA8A	2.36E-07
PBX4	0.0107
CEBPZ	0.000412
NFKBIZ	1.11E-32
TANK	4.81E-09
FAM107B	2.03E-07
NFKB1	1.74E-07
DDX21	2.37E-06
CDK17	0.00553
ENY2	8.78E-06
NCL	7.96E-08
MT1X	0.000457
PTP4A2	1.40E-06
CSNK1A1	8.13E-06
IRF2BP2	2.09E-07
RBMS1	1.13E-06
BFAR	0.000325
CTR9	0.000486
HNRNPH3	0.0374
GPS1	3.13E-10
GOLPH3	0.00184

GNG5	0.00111
LRRC8D	0.00179
MOB4	0.000997
COX17	4.13E-07
SNRPB2	0.0291
C14orf166	0.000282
PSMB1	1.63E-05
NME2	0.000117
ORMDL3	6.17E-08
ALKBH5	0.0305
TNFAIP8	1.79E-07
PPP6C	0.0342
PRELID3B	0.000654
NDUFC2	2.13E-05
RNF6	0.00147
UBE2L6	0.0495
HNRNPM	0.00384
RRM1	0.0116
NDUFA6	0.0119
RBX1	1.03E-06
RPN2	8.91E-05
NEAT1	3.42E-07
KCTD20	0.00189
LPIN2	1.39E-05
GBP2	0.00255
GBP3	0.00413
CDKN1B	3.66E-07
PSMD14	0.0015
PPP1R18	0.016
ZRANB2	0.0152
NUDC	1.91E-06
CCT4	4.70E-12
AC107081.5	0.0429
VASP	0.00482
CTB-43P18.1	0.00397
SELENOK	7.07E-12
FTH1	1.51E-13
SAMSN1	1.23E-18
SRGN	4.09E-23
RGS1	2.05E-33
RGS2	1.64E-27

CREM	3.44E-34
LY86-AS1	2.01E-06
CNOT6L	1.14E-08
TIPARP	5.80E-05
TNFAIP3	2.34E-06
NR4A2	4.80E-12
KLF6	6.39E-07
ZFP36L2	1.04E-08
CXCR4	1.14E-12
RASGEF1B	7.27E-22
PTGER4	1.41E-16
EZR	4.67E-07
FOSL2	3.91E-07
ZNF331	2.62E-08
NR4A3	5.35E-11
REL	1.29E-09
MCL1	2.11E-06
PDE4D	4.07E-08
PER1	6.32E-09
ANXA1	7.03E-30
ANKRD28	2.10E-13
LINC01871	3.93E-13
SYTL3	2.36E-07
AUTS2	7.97E-15
ASIC4	0.000406
RGPD5	6.20E-06
RANBP2	2.45E-10
ELF1	3.17E-12
PRMT9	8.92E-07
TSC22D2	8.74E-06
PDCD4	1.76E-06
SARAF	2.14E-10
PABPC1	2.97E-08
EIF5	1.35E-08
PPP2R5C	8.81E-08
PRRC2C	4.80E-08
CLK1	1.12E-06
ADGRE5	8.06E-08
ELL2	7.70E-07
BIRC3	2.94E-07
GTF2B	9.95E-38

KDM6B	1.81E-08
VPS37B	0.00159
CCT2	3.95E-05
IRF1	4.95E-06
PPP1R16B	0.000781
RSL24D1	0.0052
GNL3	0.00353
HSPB1	6.28E-08
FKBP4	1.49E-07
BAG3	4.65E-19
HSPA6	1.36E-07
DNAJA4	2.67E-12
ZFAND2A	4.28E-15
SERPINH1	1.47E-07
CACYBP	6.39E-14
DNAJB4	1.22E-06
PPP1R15A	3.68E-07
DUSP1	9.14E-10
HSP90AA6P	5.02E-10
HSP90AA2P	4.73E-10
HSP90AA1	1.46E-12
HSPA1B	8.05E-17
HSPA1A	2.59E-22
HSPH1	8.17E-19
DNAJB1	6.42E-15
HSP90AB1	1.37E-13
HSPD1	3.00E-19
HSPE1	3.69E-23
AHSA1	6.53E-08
CHORDC1	3.77E-11
DNAJB6	1.22E-12
TCP1	2.63E-15
HSPA4	5.08E-08
NABP1	2.20E-09
TRA2B	2.41E-06
GPBP1	1.32E-14
STIP1	1.81E-07
BCAS2	0.000218
NKRF	0.005
PTGES3	8.29E-09
MAP7D3	0.00203

CDKN1A	1.43E-11
DUSP5	3.36E-12
CSRNP1	0.000183
RBM8A	7.93E-07
CKS2	2.10E-12
EGR1	1.17E-06
RP11-1100L3.8	3.73E-10
NR4A1	7.72E-12
TAGAP	6.43E-07
CD69	6.99E-09
DNAJA1	1.51E-09
HSPA8	7.96E-10
JUNB	3.65E-06
JUN	6.22E-13
DUSP2	2.81E-12
FOS	5.08E-07
FOSB	5.00E-07
BTG2	4.38E-06
YPEL5	1.96E-06
ZFP36L1	1.61E-06
CH507-42P11.8	3.96E-07
CDK2AP2	0.000436
MYLIP	0.00012
CD83	6.50E-05
NFKBIA	4.10E-07
DDIT4	3.15E-10
IER5	0.000644
ZC3H12A	0.000265
TUBB4B	6.54E-13
EIF4A2	2.95E-07
PMAIP1	2.52E-09
ROMO1	0.0118
PPP1R15B	5.78E-05
ABI3	0.00449
SLC20A1	0.00311
EPG5	2.00E-05
ZNF131	0.0213
RSRC2	2.45E-10
SMARCA2	5.19E-07
NOP58	8.88E-13
UTY	0.000332

TTTY15	0.00989
DDX3Y	0.000654
RPS4Y1	0.000511
RP11-631M6.2	9.49E-06
SF3A3	0.00717
RSBN1	0.00823
ACTR2	8.87E-06
NUFIP2	0.0132
ZYX	0.00108
DEK	0.00198
SUCO	0.0102
RASA2	0.00872
ARAP2	0.0277
SH2D1A	0.00048
PSMC5	0.00142
ETFB	0.049
IFI6	0.0172
GPR89A	0.00168
PHTF1	0.00244
EAF1	0.0167
SERPINB9	3.78E-11
SIMC1	0.0188
MRPS11	0.0311
WDR43	0.017
YY1	0.00129
ARL6IP1	9.24E-06
RAB21	0.0126
VPS26A	0.0128
ZWILCH	0.0227
BNIP3L	0.0192
PPP2CA	0.00538
TMX1	0.00181
RNF19A	4.57E-30
SPAG1	0.0137
SAT1	1.49E-12
TSPYL2	4.86E-08
CCDC47	0.0146
FKBP5	1.23E-13
IL7R	8.29E-15
SMAP2	0.00231
TXNIP	2.07E-10

PIK3IP1	0.00012
SLA	8.06E-08
RBM12	0.00753
PPP2R3C	0.0291
SREBF1	0.0205
TMED10	0.00537
BIRC2	0.00126
LINC01578	2.19E-06
IL18R1	0.00804
DEF6	0.0251
ZMAT2	4.90E-21
CWC22	0.000618
SNHG25	0.0181
PSMC2	1.04E-09
IQCB1	0.0227
ZBTB1	8.30E-07
XRN2	0.0366
BTG3	2.11E-06
JTB	0.0143
C1orf52	3.52E-18
PIGF	0.0106
TFG	0.0123
GGCT	2.88E-09
MANF	5.38E-06
ATP6V0B	0.000505
MZT1	0.00427
HINT2	1.14E-09
KIF5B	0.0101
MKL1	2.65E-07
DYNLT1	3.05E-05
YTHDF2	2.19E-09
LAMA4	0.00982
BLVRA	0.0233
USP7	2.31E-05
LYST	0.0432
TSEN54	0.000193
WDR19	0.0163
SND1	0.00418
GCC2	0.000524
ICAM2	0.00107
SRSF9	0.00352

GPSM3	0.0277
RP11-158G18.1	3.21E-05
ARHGAP30	0.00641
TSNAX	0.0083
SLC30A1	8.41E-07
FAM126B	0.000293
CACNA1D	0.00114
ERO1A	9.94E-06
SMC3	0.0223
ZNF148	0.00207
RTCA	0.0315
ACTR1A	0.0122
CIAO1	3.72E-26
SRPRA	0.00694
DCTN1	0.00739
SPTBN1	0.000649
IKBKB	0.00165
CCT7	0.0303
TROVE2	0.00077
NRDE2	0.0255
GPS2	0.0308
COPS5	0.0359
ERVK3-1	0.0137
CASP2	0.0107
SNRNP40	0.0416
DZIP3	0.000287
AP4B1	0.0234
ILF2	0.000226
PRDX3	0.00748
AHCTF1	0.0379
TERF2IP	0.00435
AC007403.3	0.0323
SIN3A	0.047
SEC14L1	0.049
RP11-297D21.4	0.0012
LAP3	0.0105
BZW1	0.0247
CCDC93	2.59E-10
JAK1	0.00032
TOP1	0.000336
WWC3	0.0248

ATP6V1A	0.00445
UBASH3B	0.0391
NCBP2	0.0211
CPNE3	0.0294
SLC35B1	0.0496
KIF13B	9.44E-07
TMEM230	0.0234
AHI1	1.32E-09
BRIX1	0.0248
HAX1	0.00034
PPP2R5E	0.0103
SQSTM1	4.59E-11
P2RY10	5.44E-06
SLC35A2	7.12E-12
EIF3J	0.000509
VDAC1	0.00425
SLC25A19	1.01E-27
SLX4IP	0.0244
ATP5G3	0.00101
PCBP1	0.00177
RBBP6	0.0287
PRKD3	0.0367
EED	0.00268
OGFOD1	0.00203
VDAC3	6.34E-05
IL10RA	5.63E-05
GPR65	2.27E-06
RP11-632C17	0.0124
RP11-641D5.1	0.0299
RNU2-2P	0.0409
RNU4ATAC	6.26E-06
UHMK1	0.00923
RP1-56K13.3	0.00305
NEDD9	3.87E-07
MKNK2	4.38E-09
CCNK	0.0185
TSTA3	0.0208
NT5DC2	0.00708
EPAS1	0.00069
CAB39	0.00178
LIMD2	0.0443

NBDY	0.00299
FAM32A	2.69E-05
POLE4	0.0147
NDUFS4	0.00519
RLF	0.0308
SP3	1.83E-29
RAD51D	0.0113
CALU	0.00013
NFU1	0.0252
DDOST	0.0407
ABCB10	3.48E-07
IL10RB	0.000583
NFAT5	0.000471
TINF2	0.00479
HIBCH	0.0221
CAMK4	4.29E-05
FLI1	0.03
LNPK	0.0226
PTBP3	7.47E-05
ARHGEF3	0.0208
SOS2	0.00993
PIGV	0.0221
IRAK4	0.0449
TVP23C-CDRT4	0.00095
NLRX1	0.0276
RC3H2	0.000848
EIF2A	0.0446
SERP1	0.022
KYAT3	2.82E-08
CD58	0.00677
KIAA1109	3.35E-06
SIPA1	0.0425
RPS7P10	2.62E-05
ITPR2	0.00447
SDF2	0.0196
RP11-1024P17.1	0.0197
PSMA1	0.00156
DHRS3	1.80E-05
PTP4A1	0.000371
RP11-545A16.4	1.12E-05
SEC62-AS1	0.0208

RORA-AS1	0.00181
CTC-505O3.3	3.46E-09
RORA	9.29E-23
CYCSP38	8.88E-06
TRIB2	1.24E-09
CXCR6	2.67E-06
PRDM1	6.24E-18
MGAT4A	1.43E-09
TBC1D31	0.02
TRNT1	0.0102
RNF4	9.66E-05
SLC30A7	0.0147
ANAPC15	0.016
HN1	0.0106
RBM4	0.00133
MYEF2	0.00866
CHKB	0.0301
TUBB	5.94E-06
SETD5	3.70E-05
ERN1	2.42E-05
CACNB3	0.00273
ABCC1	0.00159
MAP3K10	3.15E-06
DLEU1	0.00335
RP11-5O24.1	0.0476
B3GALNT1P1	0.0156
HAVCR2	0.00274
BAZ1B	0.00282
ZCCHC6	2.24E-05
USP42	8.93E-06
COL4A3BP	0.0163
NUPL2	7.94E-05
TSPAN6	0.00354
TULP4	1.98E-06
RP3-449O17.1	0.00889
KAT2B	5.09E-07
RP11-1152H15.1	0.0403
NUP62	0.0107
RP11-76I7.1	0.0245
TPMT	0.0301
SLFN5	1.61E-06

STX17	0.0152
RP5-826L7.1	0.0281
WASHC3	0.00288
GOLGA2P5	0.0117
NT5C2	0.0194
NUDT15	0.00657
FAM45A	0.045
GSDMD	0.0494
LCMT1-AS1	0.0414
IL6ST	0.00332
TBC1D8	0.0186
AC005954.4	0.0315
GALC	8.12E-12
PRKAB1	0.0159
RP11-434H14.1	0.0371
NAA16	0.0233
KAT6B	0.00814
FRYL	0.0245
PDE3B	0.0274
FBXW11	0.0249
TMA16	0.00579
AKR1A1	0.000173
RP11-113K21.6	0.0477
PTRH1	0.0312
EIF4G3	0.000141
PLD1	0.0175
PHF20	0.00175
LIX1L	0.0359
EXOSC1	0.0237
PINLYP	0.00378
ZMYM6	0.0109
UQCRC2	4.63E-05
LUC7L	0.00172
TTPAL	0.0453
RP11-703G6.1	4.97E-06
RP11-624A21.1	3.20E-06
GRIPAP1	0.000293
TBCK	0.0109
MORC3	0.00639
AP000692.9	0.0464
GALNT10	0.00501

RP11-717A5.2	0.000567
LINC01697	0.0436
PCBD2	0.0441
TRIP4	0.00551
CNOT4	0.00673
LINC00891	0.0032
ELK3	4.03E-05
RP11-304L19.11	0.0275
ATG10	0.00275
RN7SL624P	0.0315
REEP2	0.0189
KLF12	0.00668
UBE2F	0.0116
RP11-715J22.6	0.0224
GEMIN7	0.00372
ZMYM2	3.25E-07
EDEM3	0.00339
RP11-264L1.2	0.0282
RP11-806L2.2	0.000581
CRBN	0.000168
KIAA1524	0.021
MCM10	0.0335
MPV17	0.0274
TMX3	0.0028
TRIM13	0.0339
SOS1	7.53E-05
SIAH2	0.00316
MAP3K4	7.46E-05
GPR171	1.50E-11
TRGV4	8.38E-06
TRGV3	9.24E-07
TRGJP2	5.60E-07
TRGC1	8.67E-15
TRGC2	1.45E-24
TRGJ1	9.95E-38
TRGJ2	9.95E-38
TRGV10	4.12E-19
TRGV9	5.60E-09
CCL3	5.40E-07
CCL3L3	3.80E-08
RP11-230F18.5	8.91E-08

CTSW	4.50E-08
KLRD1	5.76E-09
PRF1	5.47E-09
GZMA	7.01E-16
GZMH	2.01E-16
GZMB	1.02E-26
ITGA1	1.74E-14
XCL2	4.70E-17
XCL1	4.81E-29
CCL4L2	1.19E-18
CCL4	1.59E-34
IFNG	2.12E-21
ZNF683	8.59E-22
NKG7	3.54E-22
KLRK1	8.62E-46
CCL5	5.17E-49
CD8A	2.23E-52
CD8B	1.84E-28
AOAH	1.01E-13
KLRC4	5.23E-13
KLRC4-KLRK1	4.09E-13
KLRC1	2.65E-14
KLRC3	8.48E-17
KLRC2	6.88E-17
HOPX	1.39E-08
RP11-291B21.2	5.19E-23
SLAMF7	4.59E-08
CD244	1.06E-17
CST7	2.23E-08
CRTAM	4.59E-16
FASLG	0.000502
CH17-189H20.1	5.42E-06
PARP8	1.73E-10
LINC01138	1.94E-09
LINC00869	1.92E-05
TBX21	1.62E-13
TBCD	1.25E-07
CTB-178M22.1	1.24E-09
CD55	5.77E-17
RP11-77A13.1	1.68E-14
TOB1	7.78E-06

HLA-DRB5	1.11E-06
HLA-DRB1	1.07E-06
HLA-DRB6	7.38E-09
HLA-DQB1	0.000284
HLA-DPB1	0.00015
CD63	0.0161
RP11-277P12.20	5.33E-09
STYK1	6.31E-11
RP11-73M18.8	3.82E-05
USP11	0.00937

Table S7. Genes differentially expressed between T7 and T8

Gene Symbol	Transcript ID	FDR-adjusted p values	Fold Change (absolute)	Regulation T8 vs. T7
CD40LG	NM_000074	7.50E-05	5.46E+02	down
TRERF1	NM_033502	7.85E-04	1.81E+01	down
FOXP3	NM_001114377	1.02E-03	3.74E+13	down
PRR5L	NM_001160169	1.03E-03	2.87E+01	down
ZNF92	NM_001287534	1.62E-03	9.85E+01	down
CD6	NM_006725	2.18E-03	2.83E+01	down
THADA	NM_022065	2.89E-03	2.47E+02	down
SLAMF1	NM_003037	4.50E-03	3.06E+18	down
KIF20B	NM_001284259	7.69E-03	2.77E+01	down
MBNL1	NM_207295	8.37E-03	8.27E+01	down
LUC7L	NM_201412	1.04E-02	2.59E+02	down
INPP4B	NM_001101669	1.09E-02	2.42E+10	down
TGFBR2	NM_003242	1.42E-02	2.71E+06	down
PHF6	NM_032335	1.42E-02	5.34E+03	down
TNFRSF9	NM_001561	1.42E-02	1.33E+13	down
CFL2	NM_001243645	1.65E-02	5.22E+02	down
SIRPB1	NM_001083910	1.93E-02	5.56E+03	down
ACAD11	NM_032169	2.39E-02	5.91E+02	down
IL1R1	NM_000877	2.47E-02	6.54E+15	down
PIK3R1	NM_181523	2.53E-02	2.30E+03	down
KRCC1	NM_001304526	2.59E-02	4.51E+01	down
IL1R2	NR_048564	2.96E-02	8.58E+08	down
CST7	NM_003650	3.13E-02	2.53E+31	down
RSRC2	NR_036434	3.17E-02	4.47E+03	down
STAT4	NM_003151	3.48E-02	8.46E+04	down
TINF2	NM_001099274	3.61E-02	9.67E+01	down
ALKBH5	NM_017758	3.70E-02	1.79E+05	down
PDE4D	NM_001197223	3.77E-02	3.10E+01	down
DDX50	NM_024045	3.94E-02	2.40E+14	down
LTB	NM_002341	4.16E-02	8.46E+07	down
ARHGEF3	NM_001289698	4.35E-02	9.24E+02	down
COX10-AS1	NR_049718	4.87E-02	1.59E+09	down
EGLN3	NM_001308103	0.00E+00	1.54E+24	up
LIF	NM_001257135	0.00E+00	9.09E+06	up
PLN	NM_002667	2.17E-13	3.45E+37	up
PPARG	NM_138711	1.56E-12	9.81E+19	up
PTGDR2	NM_004778	1.91E-11	6.96E+15	up
LMO4	NM_006769	2.60E-11	7.62E+06	up

TESPA1	NM_001136030	7.50E-11	1.34E+16	up
PLIN2	NR_038064	2.58E-10	3.44E+18	up
NR3C1	NM_001024094	4.27E-10	5.68E+01	up
GALC	NM_000153	6.55E-10	5.09E+01	up
CHDH	NM_018397	1.02E-09	2.91E+13	up
PTPN13	NM_080684	1.41E-09	2.26E+03	up
GNAQ	NM_002072	3.97E-09	2.14E+09	up
CACNA1D	NM_001128839	4.23E-08	1.27E+03	up
ZEB2	NM_014795	7.83E-08	6.65E+01	up
AHI1	NM_001134832	9.73E-08	1.18E+06	up
MAP3K8	NM_005204	1.45E-07	1.13E+07	up
ACSL4	NM_022977	2.23E-07	5.23E+01	up
ALOX5AP	NM_001204406	4.67E-07	1.85E+17	up
CASQ1	NM_001231	4.68E-07	9.89E+20	up
GLO1	NM_006708	8.79E-07	6.86E+20	up
TSEN54	NM_207346	1.18E-06	5.18E+10	up
BHLHE40-AS1	NR_125914	1.37E-06	1.78E+03	up
GATA3	NM_002051	1.41E-06	3.94E+23	up
GK	NM_001205019	1.42E-06	6.68E+02	up
PLCL2	NM_015184	2.43E-06	1.29E+05	up
FKBP5	NM_004117	3.43E-06	2.33E+05	up
ITPR1	NM_002222	8.77E-06	1.81E+03	up
BLM	NM_001287248	9.58E-06	1.73E+01	up
NFKBIZ	NM_031419	9.65E-06	1.80E+09	up
TNFSF11	NM_003701	1.04E-05	4.33E+05	up
ITK	NM_005546	1.15E-05	2.22E+20	up
LINC00892	NR_038461	1.18E-05	2.38E+22	up
IL1RL1	NM_016232	1.40E-05	2.48E+22	up
TNFSF10	NR_033994	1.43E-05	4.88E+06	up
ALAS1	NM_199166	1.45E-05	8.57E+26	up
CD200R1	NM_170780	1.74E-05	1.70E+03	up
LOC101928791	NR_110121	1.81E-05	1.68E+32	up
IL4	NM_000589	2.42E-05	6.49E+07	up
ST6GAL1	NM_173217	2.58E-05	2.25E+06	up
TIMP1	NM_003254	2.96E-05	9.15E+36	up
MRPS6	NM_032476	3.20E-05	1.39E+25	up
HLF	NM_002126	3.35E-05	2.17E+05	up
C5orf22	NM_018356	3.74E-05	4.14E+11	up
PFDN1	NM_002622	4.22E-05	5.23E+09	up
SOS1	NM_005633	4.22E-05	4.16E+08	up
SDCBP	NM_001007067	4.30E-05	1.64E+10	up

BAG2	NM_004282	4.70E-05	3.42E+03	up
SLC27A2	NM_001159629	5.82E-05	8.33E+03	up
BHLHE40	NM_003670	7.17E-05	2.59E+14	up
HK2	NM_000189	9.01E-05	2.13E+03	up
YPEL2	NM_001005404	9.82E-05	1.72E+03	up
C1orf162	NM_001300835	1.04E-04	1.55E+03	up
DZIP3	NM_014648	1.33E-04	1.35E+16	up
SMARCA2	NM_001289399	1.43E-04	1.18E+12	up
TAB3	NM_152787	1.58E-04	2.27E+03	up
CYSLTR1	NM_006639	1.66E-04	6.38E+09	up
DENND1B	NM_001195215	1.66E-04	3.43E+01	up
IL10RA	NM_001558	1.66E-04	4.36E+09	up
RGS9	NM_001165933	1.67E-04	5.05E+05	up
TIMMDC1	NM_016589	1.94E-04	4.44E+20	up
ADAM19	NM_033274	2.09E-04	1.64E+33	up
TMED5	NM_001167830	2.14E-04	9.28E+02	up
ATP11B	NM_014616	2.64E-04	8.05E+03	up
DUSP4	NM_001394	2.66E-04	7.44E+08	up
SLC4A7	NM_001258380	2.66E-04	2.93E+04	up
GPR35	NM_005301	3.13E-04	3.99E+13	up
BCL2L11	NM_001204107	3.69E-04	9.66E+02	up
UBE2E1	NM_001202476	4.83E-04	8.97E+02	up
PTP4A2	NM_080391	4.89E-04	2.72E+13	up
CREM	NM_182717	5.08E-04	3.11E+34	up
GAB3	NR_104114	6.13E-04	2.63E+30	up
PSMD1	NM_002807	6.34E-04	8.99E+02	up
RBPJ	NM_203284	6.47E-04	5.28E+05	up
BCAR3	NM_001308251	6.81E-04	5.03E+07	up
ITGA4	NM_000885	7.24E-04	6.48E+07	up
IL4R	NM_001257997	7.71E-04	6.54E+01	up
SLC1A4	NM_001193493	7.75E-04	2.03E+03	up
PTGER4	NM_000958	8.21E-04	9.92E+06	up
RABGAP1L	NM_001243763	8.21E-04	3.98E+02	up
IL10RB-AS1	NR_038974	8.34E-04	2.96E+09	up
FUT8	NR_038170	8.56E-04	1.51E+05	up
PDCD4	NM_014456	8.67E-04	1.61E+06	up
RNU4ATAC	NR_023343	8.73E-04	2.16E+14	up
SCD	NM_005063	9.06E-04	2.88E+24	up
DSE	NM_001080976	9.06E-04	4.22E+03	up
SERP1	NM_014445	9.86E-04	1.43E+13	up
AHR	NM_001621	1.21E-03	3.22E+18	up

NDFIP2	NM_019080	1.21E-03	2.90E+03	up
EIF2AK1	NM_014413	1.26E-03	2.04E+06	up
CRBN	NM_016302	1.28E-03	2.38E+23	up
SOCS1	NM_003745	1.34E-03	5.82E+06	up
FBXL5	NM_012161	1.34E-03	6.48E+03	up
NFATC3	NM_173165	1.37E-03	8.13E+05	up
PPIB	NM_000942	1.42E-03	2.46E+36	up
KIF13B	NM_015254	1.43E-03	6.71E+02	up
C10orf128	NM_001010863	1.46E-03	1.92E+06	up
CDC73	NM_024529	1.46E-03	7.68E+05	up
JUN	NM_002228	1.48E-03	2.50E+10	up
ZC2HC1A	NM_016010	1.50E-03	1.93E+02	up
RAD50	NM_005732	1.54E-03	2.56E+04	up
RHOQ	NM_012249	1.62E-03	1.69E+02	up
ATAD2	NM_014109	1.70E-03	2.33E+02	up
RAB33A	NM_004794	1.81E-03	2.29E+07	up
RAPGEF2	NM_014247	1.82E-03	4.10E+01	up
OGN	NM_014057	1.82E-03	3.39E+07	up
RNF19A	NM_183419	1.82E-03	3.28E+06	up
PTGS2	NM_000963	1.82E-03	1.46E+04	up
TIGIT	NM_173799	1.89E-03	9.69E+28	up
MRPS31	NM_005830	1.96E-03	1.12E+07	up
AZIN1	NM_001301668	1.96E-03	1.13E+02	up
SERINC5	NM_001174072	1.97E-03	7.20E+17	up
LACTB	NM_032857	1.98E-03	1.52E+02	up
POLK	NM_016218	2.18E-03	3.09E+07	up
TNFAIP8	NM_014350	2.19E-03	1.16E+14	up
MLEC	NM_001303627	2.19E-03	4.67E+01	up
TFG	NM_001195478	2.34E-03	3.21E+05	up
DOCK8	NM_203447	2.47E-03	5.33E+03	up
FAM193A	NR_046335	2.64E-03	6.83E+05	up
KLHL6	NM_130446	2.70E-03	3.03E+02	up
HADHA	NM_000182	2.78E-03	1.51E+10	up
SAMSN1	NM_022136	2.88E-03	9.94E+35	up
EVC2	NM_147127	2.97E-03	9.77E+01	up
SNX22	NM_024798	3.06E-03	1.74E+03	up
KDM1A	NM_015013	3.06E-03	4.43E+02	up
CCDC71L	NM_175884	3.28E-03	1.09E+03	up
IL9R	NM_002186	3.28E-03	6.78E+01	up
SOS2	NM_006939	3.40E-03	3.77E+03	up
SNHG8	NR_003584	3.42E-03	8.34E+14	up

CPEB4	NM_001308192	3.54E-03	3.33E+01	up
PXK	NM_001289101	3.60E-03	1.46E+10	up
ZFC3H1	NM_144982	3.62E-03	8.41E+04	up
RPL23P8	NR_026673	3.76E-03	1.57E+07	up
SQSTM1	NM_003900	4.06E-03	3.85E+12	up
NAA60	NM_024845	4.30E-03	1.33E+02	up
RPL37	NM_000997	4.39E-03	1.03E+24	up
WDR7	NM_052834	4.46E-03	8.84E+04	up
MLH1	NM_000249	4.47E-03	4.51E+01	up
MRPS28	NM_014018	4.50E-03	4.16E+11	up
PHYH	NM_006214	4.63E-03	2.97E+14	up
SORD	NR_034039	4.90E-03	5.54E+02	up
ZCCHC10	NM_001308129	5.16E-03	1.73E+08	up
CKAP5	NM_014756	5.33E-03	1.62E+04	up
LRMP	NM_001204127	5.44E-03	3.52E+02	up
SPTBN1	NM_003128	5.72E-03	6.75E+02	up
CYP4F22	NM_173483	5.83E-03	1.72E+03	up
FAH	NM_000137	5.85E-03	7.60E+20	up
TRA2A	NM_001282757	5.86E-03	4.27E+16	up
PRKAB1	NM_006253	6.32E-03	7.64E+27	up
POLB	NM_002690	6.62E-03	6.44E+04	up
TERF2IP	NM_018975	6.75E-03	9.22E+08	up
GMNN	NM_015895	6.80E-03	5.96E+15	up
CCDC86	NM_024098	6.80E-03	3.51E+02	up
RTN4	NM_207521	6.85E-03	2.48E+02	up
PDHB	NM_000925	6.88E-03	4.62E+10	up
OSTF1	NM_012383	6.98E-03	7.98E+17	up
UBE2D3	NM_181887	7.08E-03	2.17E+06	up
TRAM1	NM_014294	7.19E-03	3.53E+05	up
DGKE	NM_003647	7.40E-03	6.26E+10	up
ERN1	NM_001433	7.72E-03	1.60E+02	up
HENMT1	NM_001102592	7.86E-03	1.62E+10	up
CLDND1	NM_001040182	7.86E-03	3.97E+02	up
USP15	NM_001252078	8.16E-03	2.72E+02	up
ASNSD1	NM_019048	8.20E-03	5.79E+07	up
E2F3	NM_001243076	8.20E-03	1.25E+03	up
XPO1	NM_003400	8.94E-03	6.17E+15	up
NUB1	NM_001243351	8.94E-03	1.05E+03	up
NCOA1	NM_003743	8.94E-03	8.27E+01	up
ATP5F1	NM_001688	9.10E-03	8.50E+26	up
FXYD5	NM_001164605	9.14E-03	4.55E+03	up

GSTO1	NM_004832	9.15E-03	1.55E+27	up
CANX	NM_001024649	9.23E-03	2.05E+16	up
SLC5A3	NM_006933	9.88E-03	1.65E+04	up
DEK	NM_001134709	9.96E-03	3.99E+10	up
FOXP1	NM_001244812	1.03E-02	1.72E+01	up
MRPL32	NM_031903	1.06E-02	7.84E+21	up
CASP1	NM_001223	1.07E-02	1.07E+02	up
CLECL1	NM_172004	1.07E-02	1.65E+03	up
AKIRIN2	NM_018064	1.09E-02	2.28E+15	up
POLE4	NM_019896	1.17E-02	8.78E+07	up
PLA2G16	NM_001128203	1.21E-02	6.00E+01	up
FBXO34	NM_017943	1.21E-02	3.32E+01	up
TTC3	NM_001001894	1.23E-02	3.94E+03	up
LAGE3	NM_006014	1.23E-02	2.50E+01	up
NUDT4	NM_001301024	1.23E-02	3.73E+10	up
TARBP1	NM_005646	1.23E-02	1.10E+07	up
TAF1D	NM_024116	1.26E-02	1.97E+07	up
SLC38A1	NM_001077484	1.26E-02	3.50E+01	up
ANKRD44	NM_001195144	1.26E-02	5.87E+05	up
AOAH	NM_001637	1.27E-02	2.45E+03	up
DGKA	NM_201554	1.28E-02	9.23E+06	up
NAA35	NM_024635	1.30E-02	2.68E+01	up
TXNDC11	NM_015914	1.36E-02	2.49E+09	up
GPR65	NM_003608	1.36E-02	3.02E+01	up
CSNK2B	NM_001282385	1.37E-02	5.25E+01	up
TMEM173	NM_001301738	1.38E-02	1.84E+04	up
SLFN5	NM_144975	1.38E-02	1.05E+03	up
MRPL53	NM_053050	1.39E-02	9.65E+21	up
RIF1	NM_001177664	1.39E-02	6.55E+01	up
EIF3L	NM_001242923	1.42E-02	4.79E+08	up
XPNPEP1	NM_020383	1.44E-02	2.50E+11	up
SAFB	NR_037699	1.44E-02	6.37E+04	up
MRFAP1	NM_033296	1.47E-02	2.44E+08	up
POLR2G	NM_002696	1.48E-02	5.49E+08	up
PIGP	NM_153682	1.49E-02	5.55E+10	up
TMEM14B	NM_001127711	1.49E-02	5.44E+03	up
BIRC3	NM_182962	1.52E-02	1.12E+31	up
RTFDC1	NM_001283037	1.53E-02	6.70E+07	up
LIMA1	NM_001113547	1.53E-02	2.28E+27	up
RPS24	NM_033022	1.57E-02	2.49E+05	up
SPIRE1	NM_001128627	1.57E-02	1.21E+05	up

EDEM3	NM_025191	1.60E-02	3.14E+02	up
NR4A3	NM_006981	1.61E-02	1.24E+06	up
NACA	NR_045277	1.61E-02	1.60E+30	up
GDE1	NM_016641	1.61E-02	3.58E+18	up
SND1	NM_014390	1.61E-02	1.50E+02	up
CXorf65	NR_033212	1.62E-02	2.08E+01	up
UNG	NM_080911	1.63E-02	6.78E+23	up
CCDC28B	NM_024296	1.65E-02	1.17E+02	up
BTG3	NM_006806	1.65E-02	4.37E+07	up
GIMAP2	NM_015660	1.65E-02	1.68E+16	up
SLCO4C1	NM_180991	1.66E-02	2.50E+01	up
SMCO4	NM_020179	1.67E-02	8.37E+26	up
MOAP1	NM_022151	1.67E-02	1.16E+10	up
AVEN	NM_020371	1.67E-02	7.49E+04	up
RHBDD2	NM_001040457	1.67E-02	4.34E+04	up
UBE2R2	NM_017811	1.67E-02	1.89E+03	up
KRAS	NM_004985	1.67E-02	3.97E+01	up
SNAP23	NM_003825	1.67E-02	1.77E+01	up
FKBP4	NM_002014	1.70E-02	4.40E+04	up
ERO1A	NM_014584	1.72E-02	2.43E+34	up
IRF2BP2	NM_001077397	1.72E-02	8.42E+16	up
STAMBPL1	NM_020799	1.75E-02	1.22E+13	up
CD83	NM_004233	1.77E-02	1.73E+21	up
ISG15	NM_005101	1.77E-02	6.13E+15	up
DDX17	NM_006386	1.77E-02	3.44E+08	up
MS4A6A	NM_022349	1.77E-02	1.12E+02	up
ASF1A	NM_014034	1.79E-02	1.20E+16	up
CAPZA2	NM_006136	1.81E-02	1.40E+20	up
SNRPD2	NM_177542	1.82E-02	1.48E+02	up
HSPD1	NM_199440	1.83E-02	2.22E+28	up
ITCH	NM_001257138	1.83E-02	5.83E+03	up
DCTN6	NM_006571	1.88E-02	4.13E+26	up
CHCHD2	NM_016139	1.91E-02	3.29E+08	up
COX5A	NM_004255	1.94E-02	6.26E+03	up
IFNGR2	NM_005534	1.95E-02	6.56E+05	up
TIMM9	NM_012460	1.96E-02	5.72E+05	up
BAG3	NM_004281	2.02E-02	1.71E+07	up
PSMC2	NM_002803	2.07E-02	2.06E+09	up
CDR2	NM_001802	2.11E-02	1.31E+04	up
GNA13	NM_001282425	2.16E-02	2.95E+10	up
ILK	NM_004517	2.17E-02	2.30E+13	up

MSTO1	NR_046294	2.18E-02	3.54E+03	up
LINC00657	NR_027451	2.18E-02	3.45E+01	up
APLP2	NM_001142278	2.23E-02	2.58E+05	up
IL10RB	NM_000628	2.24E-02	4.63E+02	up
FKBP2	NM_004470	2.26E-02	1.31E+04	up
SH2D2A	NM_003975	2.26E-02	1.42E+03	up
INPP1	NM_002194	2.27E-02	3.47E+04	up
PRELID3B	NM_001256403	2.29E-02	2.52E+10	up
SLC25A20	NM_000387	2.29E-02	1.68E+07	up
LRRC8C	NM_032270	2.29E-02	2.12E+03	up
SLC39A8	NM_001135146	2.29E-02	4.39E+01	up
FAM76B	NM_144664	2.30E-02	2.55E+04	up
PFDN2	NM_012394	2.30E-02	3.28E+05	up
DNAJC2	NM_001129887	2.35E-02	8.51E+02	up
RPL22	NM_000983	2.37E-02	4.24E+06	up
CAPG	NM_001256139	2.37E-02	6.03E+31	up
RDX	NM_001260493	2.37E-02	2.66E+06	up
SPCS2	NM_014752	2.37E-02	1.10E+08	up
CD226	NM_001303619	2.38E-02	5.33E+03	up
SGK1	NM_005627	2.38E-02	9.76E+01	up
CLEC2D	NM_001004419	2.42E-02	1.07E+10	up
SEPHS2	NM_012248	2.44E-02	1.67E+01	up
OGT	NM_181673	2.45E-02	1.52E+11	up
MCOLN2	NM_153259	2.45E-02	4.46E+01	up
APEX1	NM_080648	2.47E-02	4.07E+06	up
P4HB	NM_000918	2.48E-02	1.95E+22	up
SF3B1	NM_012433	2.50E-02	4.24E+21	up
FAM120A	NM_001286722	2.51E-02	4.88E+01	up
FAM35BP	NR_027632	2.52E-02	2.03E+01	up
RMRP	NR_003051	2.53E-02	4.03E+06	up
ADD1	NM_001119	2.53E-02	1.02E+03	up
ACADVL	NM_000018	2.54E-02	1.70E+01	up
PSMA5	NM_001199773	2.56E-02	1.73E+02	up
SESN3	NM_001271594	2.56E-02	8.18E+01	up
ELF1	NM_172373	2.62E-02	1.79E+02	up
ZNF217	NM_006526	2.62E-02	2.62E+01	up
NEK1	NM_001199399	2.66E-02	2.46E+04	up
TM2D2	NM_078473	2.69E-02	7.85E+02	up
FNBP4	NM_015308	2.71E-02	8.58E+02	up
FURIN	NM_001289823	2.72E-02	1.96E+03	up
COX7B	NM_001866	2.75E-02	1.17E+38	up

SEC61G	NM_014302	2.75E-02	5.52E+15	up
NDUFV1	NM_007103	2.78E-02	4.19E+12	up
SIAH2	NM_005067	2.80E-02	1.25E+05	up
RHOH	NM_001278364	2.83E-02	7.00E+01	up
SNORA84	NR_003704	2.86E-02	1.18E+06	up
MIR3651	NR_037424	2.86E-02	2.49E+01	up
RPN1	NM_002950	2.89E-02	4.61E+01	up
MIER1	NM_001077704	2.90E-02	9.45E+05	up
DNAJA4	NM_001130183	2.91E-02	9.19E+23	up
MRPS11	NM_022839	2.91E-02	2.68E+08	up
DNTTIP2	NM_014597	2.92E-02	1.78E+28	up
MT1F	NM_005949	2.94E-02	1.67E+20	up
SEMA4D	NM_006378	2.94E-02	1.56E+05	up
RRAGA	NM_006570	2.95E-02	3.45E+02	up
PABPC1L	NM_001124756	2.96E-02	1.85E+07	up
ZFAND5	NM_001278244	3.02E-02	8.81E+08	up
MRPS12	NM_033362	3.03E-02	5.35E+05	up
USP22	NM_015276	3.05E-02	1.46E+16	up
IL16	NM_004513	3.05E-02	6.12E+07	up
STRIP1	NM_001270768	3.06E-02	1.03E+13	up
GPR171	NM_013308	3.09E-02	3.88E+09	up
HMOX2	NM_001286271	3.12E-02	7.22E+05	up
SRSF9	NM_003769	3.17E-02	8.68E+12	up
YY1	NM_003403	3.17E-02	8.73E+03	up
TSEN15	NM_052965	3.17E-02	4.96E+03	up
NCEH1	NM_001146278	3.21E-02	7.47E+01	up
UBE2K	NM_005339	3.28E-02	4.05E+03	up
SETD5	NM_001292043	3.35E-02	1.82E+02	up
ZC3H12A	NM_025079	3.36E-02	4.23E+06	up
SREK1	NM_001077199	3.37E-02	2.16E+02	up
USP9Y	NM_004654	3.38E-02	9.70E+02	up
DNAJC3	NM_006260	3.40E-02	5.81E+16	up
FGFR1	NM_001174066	3.43E-02	1.26E+08	up
LDB1	NM_001113407	3.49E-02	2.60E+02	up
TBC1D15	NM_001146213	3.49E-02	5.94E+04	up
CDK2AP1	NM_001270433	3.49E-02	6.66E+04	up
FAM118A	NM_017911	3.51E-02	8.26E+14	up
ZFAS1	NR_003604	3.51E-02	4.37E+07	up
EML4	NM_001145076	3.55E-02	1.46E+20	up
C21orf33	NM_004649	3.61E-02	9.43E+04	up
DNAJC15	NM_013238	3.62E-02	9.29E+02	up

PELI1	NM_020651	3.65E-02	8.55E+03	up
RBM39	NR_040724	3.65E-02	1.55E+03	up
JTB	NM_006694	3.66E-02	7.78E+11	up
NFKBID	NM_139239	3.69E-02	2.23E+03	up
RAB6A	NM_002869	3.73E-02	2.71E+06	up
KIF3A	NM_007054	3.74E-02	2.09E+04	up
PPCS	NM_001077447	3.75E-02	9.02E+08	up
WDR36	NM_139281	3.76E-02	4.81E+03	up
CNOT2	NR_037615	3.76E-02	7.74E+01	up
FBXO7	NM_001033024	3.80E-02	2.73E+07	up
ACTR3	NM_001277140	3.80E-02	9.34E+06	up
IFNAR2	NM_000874	3.82E-02	1.96E+10	up
LINC00852	NR_026829	3.83E-02	1.61E+06	up
SRP54	NM_003136	3.84E-02	1.83E+05	up
FAM102B	NM_001010883	3.85E-02	4.29E+01	up
MRPL14	NM_032111	3.89E-02	6.72E+17	up
LGALS8	NM_006499	3.89E-02	1.88E+01	up
TADA2A	NM_001291918	3.89E-02	3.00E+08	up
TDG	NM_003211	3.89E-02	3.34E+03	up
NDUFA11	NM_175614	3.93E-02	3.11E+07	up
AGGF1	NM_018046	3.94E-02	1.87E+05	up
BNIP1	NM_001205	3.98E-02	1.82E+10	up
PAPOLA	NM_001293632	3.98E-02	1.05E+09	up
MTHFD2	NM_006636	3.98E-02	3.68E+05	up
NFU1	NR_045631	3.98E-02	3.18E+02	up
CHMP6	NM_024591	3.98E-02	2.83E+02	up
PRPS2	NM_002765	4.04E-02	8.66E+13	up
MLLT3	NM_001286691	4.07E-02	2.07E+05	up
PLEKHO1	NM_001304723	4.11E-02	3.14E+01	up
IL32	NM_001308078	4.14E-02	2.87E+23	up
PCBP2	NM_005016	4.14E-02	3.20E+05	up
PSMB9	NM_002800	4.15E-02	1.93E+32	up
PPM1A	NM_177951	4.17E-02	1.84E+01	up
TRAPPC2L	NM_016209	4.17E-02	3.11E+16	up
EFHD2	NM_024329	4.19E-02	6.47E+03	up
DUSP10	NR_111939	4.21E-02	1.51E+06	up
TSPAN13	NM_014399	4.27E-02	3.46E+03	up
ZNF326	NM_182975	4.27E-02	9.17E+01	up
NR1H2	NM_001256647	4.27E-02	2.21E+01	up
RBM48	NM_032120	4.28E-02	4.67E+13	up
MRPL33	NM_145330	4.28E-02	6.39E+10	up

TMEM167A	NM_174909	4.28E-02	3.59E+08	up
HIST1H1D	NM_005320	4.28E-02	1.96E+11	up
CLTB	NM_001834	4.31E-02	1.30E+22	up
CCDC47	NM_020198	4.35E-02	1.10E+08	up
SAMD9	NM_001193307	4.35E-02	1.87E+06	up
NXT2	NM_001242618	4.35E-02	2.60E+02	up
VEGFB	NM_003377	4.38E-02	2.29E+01	up
BATF	NM_006399	4.47E-02	2.08E+19	up
STX17	NM_017919	4.48E-02	6.23E+02	up
SRI	NM_003130	4.52E-02	9.88E+03	up
PRKD3	NM_005813	4.53E-02	4.80E+04	up
NOMO3	NM_001004067	4.53E-02	2.01E+01	up
PBDC1	NM_001300888	4.59E-02	3.31E+03	up
NASP	NM_002482	4.63E-02	1.11E+07	up
PDCD11	NM_014976	4.65E-02	7.15E+02	up
SERPINB9	NM_004155	4.71E-02	1.26E+38	up
MGA	NM_001164273	4.94E-02	8.93E+01	up
DENND4C	NM_017925	4.94E-02	2.28E+01	up
DYNLT1	NM_006519	4.97E-02	2.90E+35	up
RPS3	NM_001005	4.97E-02	2.45E+02	up

Table S8. Full gene ontology analysis of T7

(FDR-adjusted $p < 0.05$ by Fisher)

GO biological process complete	Enrichment	FDR-adjusted p value
regulation of leukocyte proliferation (GO:0070663)	24.3	6.6E-06
regulation of mononuclear cell proliferation (GO:0032944)	25.3	7.4E-06
negative regulation of cell activation (GO:0050866)	26.4	1.2E-05
negative regulation of T cell activation (GO:0050868)	39.9	1.3E-05
regulation of lymphocyte proliferation (GO:0050670)	25.4	1.4E-05
regulation of cell-cell adhesion (GO:0022407)	13.7	1.5E-05
negative regulation of leukocyte cell-cell adhesion (GO:1903038)	37.1	1.7E-05
regulation of lymphocyte activation (GO:0051249)	12.2	3.3E-05
negative regulation of T cell proliferation (GO:0042130)	58.0	3.4E-05
positive regulation of leukocyte activation (GO:0002696)	13.9	7.6E-05
regulation of regulatory T cell differentiation (GO:0045589)	> 100	8.1E-05
immune response (GO:0006955)	5.2	8.4E-05
regulation of leukocyte activation (GO:0002694)	10.7	8.6E-05
positive regulation of cell activation (GO:0050867)	13.5	8.8E-05
negative regulation of cell-cell adhesion (GO:0022408)	25.5	9.5E-05
negative regulation of response to external stimulus (GO:0032102)	16.6	1.2E-04
regulation of cell activation (GO:0050865)	10.0	1.2E-04
negative regulation of B cell activation (GO:0050869)	79.7	1.7E-04
regulation of B cell activation (GO:0050864)	22.4	1.7E-04
T cell selection (GO:0045058)	70.9	2.4E-04
regulation of cell adhesion (GO:0030155)	8.6	3.7E-04
positive regulation of lymphocyte activation (GO:0051251)	13.4	4.0E-04
negative regulation of inflammatory response (GO:0050728)	29.0	4.7E-04
regulation of T cell differentiation (GO:0045580)	25.7	8.0E-04
positive regulation of biological process (GO:0048518)	2.5	8.6E-04
negative regulation of cell adhesion (GO:0007162)	16.1	8.8E-04
regulation of inflammatory response (GO:0050727)	11.7	8.8E-04
positive regulation of lymphocyte proliferation (GO:0050671)	24.3	9.2E-04
positive regulation of mononuclear cell proliferation (GO:0032946)	24.2	9.3E-04
cytokine production (GO:0001816)	23.6	9.5E-04
negative regulation of immune system process (GO:0002683)	11.2	9.7E-04
negative regulation of cytokine secretion (GO:0050710)	44.8	9.7E-04
positive regulation of leukocyte proliferation (GO:0070665)	23.3	9.7E-04
regulation of response to external stimulus (GO:0032101)	7.3	9.9E-04
regulation of leukocyte differentiation (GO:1902105)	15.1	1.0E-03

positive regulation of cell-cell adhesion (GO:0022409)	14.9	1.1E-03
regulation of B cell proliferation (GO:0030888)	41.1	1.2E-03
regulation of hemopoiesis (GO:1903706)	10.6	1.2E-03
negative regulation of B cell proliferation (GO:0030889)	> 100	1.3E-03
regulation of lymphocyte differentiation (GO:0045619)	21.1	1.4E-03
regulation of cytokine production (GO:0001817)	8.2	1.4E-03
regulation of interleukin-2 biosynthetic process (GO:0045076)	> 100	1.4E-03
positive regulation of cellular process (GO:0048522)	2.6	2.0E-03
negative regulation of defense response (GO:0031348)	18.9	2.1E-03
regulation of gene expression (GO:0010468)	2.6	2.9E-03
negative regulation of interleukin-1 production (GO:0032692)	79.7	2.9E-03
positive regulation of RNA metabolic process (GO:0051254)	4.7	3.1E-03
positive regulation of gene expression (GO:0010628)	4.2	3.1E-03
regulation of immune system process (GO:0002682)	4.6	3.6E-03
immune system process (GO:0002376)	3.5	3.8E-03
positive regulation of T cell proliferation (GO:0042102)	27.1	4.3E-03
regulation of cytokine biosynthetic process (GO:0042035)	26.6	4.5E-03
regulation of cell proliferation (GO:0042127)	4.4	4.7E-03
regulation of isotype switching (GO:0045191)	63.8	4.7E-03
positive regulation of macromolecule metabolic process (GO:0010604)	3.2	4.7E-03
regulation of RNA metabolic process (GO:0051252)	2.8	5.0E-03
positive regulation of T cell activation (GO:0050870)	14.9	5.2E-03
lymphocyte differentiation (GO:0030098)	14.7	5.4E-03
positive regulation of immune system process (GO:0002684)	5.5	5.4E-03
regulation of defense response (GO:0031347)	6.5	5.5E-03
positive regulation of leukocyte cell-cell adhesion (GO:1903039)	14.3	5.9E-03
regulation of multi-organism process (GO:0043900)	9.8	6.9E-03
positive regulation of cell adhesion (GO:0045785)	9.7	7.1E-03
response to organic substance (GO:0010033)	3.2	7.1E-03
negative regulation of protein secretion (GO:0050709)	22.4	7.2E-03
positive regulation of cytokine production (GO:0001819)	9.6	7.2E-03
regulation of response to stimulus (GO:0048583)	2.7	7.6E-03
negative regulation of cytokine production (GO:0001818)	13.1	8.2E-03
negative regulation of peptide secretion (GO:0002792)	21.3	8.2E-03
regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043122)	12.9	8.4E-03
regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains (GO:0002822)	20.9	8.6E-03
positive regulation of nucleobase-containing compound metabolic process (GO:0045935)	4.0	8.7E-03
positive regulation of metabolic process (GO:0009893)	2.9	9.0E-03
negative regulation of response to biotic stimulus (GO:0002832)	45.6	9.0E-03

regulatory T cell differentiation (GO:0045066)	> 100	9.1E-03
negative regulation of chronic inflammatory response (GO:0002677)	> 100	9.2E-03
T cell differentiation (GO:0030217)	20.2	9.2E-03
adaptive immune response (GO:0002250)	8.8	9.9E-03
regulation of interleukin-10 production (GO:0032653)	42.5	1.0E-02
regulation of adaptive immune response (GO:0002819)	19.2	1.1E-02
positive regulation of leukocyte differentiation (GO:1902107)	19.2	1.1E-02
negative regulation of immune response (GO:0050777)	19.0	1.1E-02
regulation of interleukin-1-mediated signaling pathway (GO:2000659)	> 100	1.1E-02
regulation of B cell mediated immunity (GO:0002712)	40.7	1.1E-02
regulation of immunoglobulin mediated immune response (GO:0002889)	40.7	1.1E-02
negative regulation of cell proliferation (GO:0008285)	6.8	1.1E-02
regulation of nucleobase-containing compound metabolic process (GO:0019219)	2.5	1.1E-02
regulation of molecular function (GO:0065009)	2.8	1.2E-02
regulation of cellular process (GO:0050794)	1.7	1.2E-02
regulation of interleukin-2 production (GO:0032663)	37.5	1.3E-02
cell surface receptor signaling pathway (GO:0007166)	3.4	1.6E-02
leukocyte differentiation (GO:0002521)	10.5	1.7E-02
regulation of signal transduction (GO:0009966)	2.9	1.7E-02
regulation of immunoglobulin production (GO:0002637)	33.6	1.7E-02
negative regulation of cellular process (GO:0048523)	2.4	1.8E-02
negative regulation of biological process (GO:0048519)	2.3	1.8E-02
regulation of nitrogen compound metabolic process (GO:0051171)	2.1	1.9E-02
CD4-positive, alpha-beta T cell lineage commitment (GO:0043373)	> 100	1.9E-02
positive regulation of hemopoiesis (GO:1903708)	15.4	2.0E-02
negative regulation of multi-organism process (GO:0043901)	15.0	2.2E-02
regulation of cytokine secretion (GO:0050707)	14.9	2.2E-02
regulation of chronic inflammatory response (GO:0002676)	> 100	2.2E-02
regulation of multicellular organismal process (GO:0051239)	3.0	2.2E-02
type 2 immune response (GO:0042092)	> 100	2.4E-02
alpha-beta T cell lineage commitment (GO:0002363)	> 100	2.5E-02
regulation of T cell tolerance induction (GO:0002664)	> 100	2.5E-02
cytokine-mediated signaling pathway (GO:0019221)	7.1	2.5E-02
regulation of primary metabolic process (GO:0080090)	2.1	2.5E-02
regulation of macromolecule metabolic process (GO:0060255)	2.1	2.5E-02
negative regulation of secretion by cell (GO:1903531)	14.3	2.5E-02
regulation of transcription, DNA-templated (GO:0006355)	2.6	2.5E-02
regulation of nucleic acid-templated transcription (GO:1903506)	2.6	2.6E-02
regulation of interleukin-1 production (GO:0032652)	27.3	2.6E-02
lymphocyte activation (GO:0046649)	9.2	2.6E-02
regulation of RNA biosynthetic process (GO:2001141)	2.6	2.6E-02

regulation of isotype switching to IgG isotypes (GO:0048302)	> 100	2.7E-02
positive regulation of interleukin-2 biosynthetic process (GO:0045086)	> 100	2.7E-02
regulation of DNA recombination (GO:0000018)	26.6	2.7E-02
positive regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043123)	13.5	2.8E-02
CD4-positive or CD8-positive, alpha-beta T cell lineage commitment (GO:0043369)	98.1	2.9E-02
negative regulation of interleukin-1 secretion (GO:0050711)	98.1	2.9E-02
negative regulation of lipopolysaccharide-mediated signaling pathway (GO:0031665)	98.1	3.0E-02
regulation of alpha-beta T cell activation (GO:0046634)	25.5	3.0E-02
T cell costimulation (GO:0031295)	25.2	3.0E-02
cellular response to cytokine stimulus (GO:0071345)	5.4	3.0E-02
positive regulation of transcription by RNA polymerase II (GO:0045944)	4.6	3.0E-02
lymphocyte costimulation (GO:0031294)	24.8	3.1E-02
biological regulation (GO:0065007)	1.5	3.1E-02
response to other organism (GO:0051707)	5.3	3.1E-02
positive regulation of transcription, DNA-templated (GO:0045893)	4.0	3.1E-02
positive regulation of RNA biosynthetic process (GO:1902680)	4.0	3.1E-02
response to external biotic stimulus (GO:0043207)	5.3	3.1E-02
positive regulation of nucleic acid-templated transcription (GO:1903508)	4.0	3.1E-02
positive regulation of nitrogen compound metabolic process (GO:0051173)	2.8	3.1E-02
positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains (GO:0002824)	24.5	3.1E-02
cellular response to organic substance (GO:0071310)	3.3	3.1E-02
negative regulation of protein transport (GO:0051224)	12.6	3.1E-02
regulation of cell communication (GO:0010646)	2.7	3.1E-02
negative regulation of macromolecule metabolic process (GO:0010605)	3.0	3.2E-02
negative regulation of secretion (GO:0051048)	12.5	3.2E-02
positive regulation of adaptive immune response (GO:0002821)	23.3	3.3E-02
negative regulation of establishment of protein localization (GO:1904950)	12.3	3.3E-02
positive regulation of lymphocyte differentiation (GO:0045621)	23.3	3.3E-02
regulation of biological process (GO:0050789)	1.6	3.3E-02
negative regulation of response to stimulus (GO:0048585)	3.9	3.4E-02
regulation of signaling (GO:0023051)	2.6	3.4E-02
regulation of cellular metabolic process (GO:0031323)	2.1	3.4E-02
regulation of DNA binding transcription factor activity (GO:0051090)	8.2	3.5E-02
positive regulation of cell proliferation (GO:0008284)	5.1	3.5E-02
negative regulation of interleukin-12 production (GO:0032695)	79.7	3.5E-02
leukocyte activation (GO:0045321)	5.1	3.5E-02
response to insulin (GO:0032868)	11.9	3.6E-02

response to biotic stimulus (GO:0009607)	5.1	3.6E-02
T cell activation (GO:0042110)	11.7	3.7E-02
regulation of tolerance induction (GO:0002643)	75.0	3.8E-02
positive regulation of cellular metabolic process (GO:0031325)	2.7	3.9E-02
T cell lineage commitment (GO:0002360)	70.9	4.2E-02
response to cytokine (GO:0034097)	4.9	4.6E-02
defense response to protozoan (GO:0042832)	67.1	4.6E-02
regulation of protein secretion (GO:0050708)	7.5	4.7E-02
antigen receptor-mediated signaling pathway (GO:0050851)	10.8	4.8E-02
response to protozoan (GO:0001562)	63.8	4.9E-02

Table S9. Full gene ontology analysis of T8 biological functions

(FDR-adjusted $p < 0.05$ by Fisher)

GO biological process complete	Enrichment	FDR-adjusted p value
cellular process (GO:0009987)	1.28	3.26E-17
positive regulation of biological process (GO:0048518)	1.89	3.36E-17
regulation of cellular protein metabolic process (GO:0032268)	2.5	7.55E-16
immune system process (GO:0002376)	2.48	8.68E-16
negative regulation of biological process (GO:0048519)	1.93	8.81E-16
biological regulation (GO:0065007)	1.39	1.34E-15
regulation of protein metabolic process (GO:0051246)	2.39	1.71E-15
response to organic substance (GO:0010033)	2.38	2.65E-15
regulation of biological process (GO:0050789)	1.41	8.03E-15
regulation of response to stimulus (GO:0048583)	2.02	1.10E-14
positive regulation of cellular process (GO:0048522)	1.88	1.52E-14
cellular response to chemical stimulus (GO:0070887)	2.37	2.40E-14
regulation of metabolic process (GO:0019222)	1.69	2.46E-14
regulation of cellular metabolic process (GO:0031323)	1.73	3.47E-14
regulation of macromolecule metabolic process (GO:0060255)	1.73	4.63E-14
regulation of cellular process (GO:0050794)	1.43	6.65E-14
regulation of immune system process (GO:0002682)	2.89	1.28E-13
negative regulation of cellular process (GO:0048523)	1.92	1.42E-13
regulation of molecular function (GO:0065009)	2.11	1.53E-13
signal transduction (GO:0007165)	1.84	2.16E-13
cellular response to organic substance (GO:0071310)	2.49	3.44E-13
regulation of catalytic activity (GO:0050790)	2.41	4.09E-13
regulation of primary metabolic process (GO:0080090)	1.7	6.03E-13
regulation of immune response (GO:0050776)	3.32	6.76E-13
regulation of nitrogen compound metabolic process (GO:0051171)	1.71	1.36E-12
positive regulation of immune system process (GO:0002684)	3.25	5.08E-12
cellular response to stimulus (GO:0051716)	1.65	5.45E-12
positive regulation of metabolic process (GO:0009893)	2.06	5.58E-12
negative regulation of macromolecule metabolic process (GO:0010605)	2.26	6.05E-12
response to cytokine (GO:0034097)	3.41	6.86E-12
cell surface receptor signaling pathway (GO:0007166)	2.35	7.30E-12
positive regulation of macromolecule metabolic process (GO:0010604)	2.11	8.06E-12
negative regulation of metabolic process (GO:0009892)	2.16	1.08E-11
symbiont process (GO:0044403)	3.72	1.89E-11

cellular response to cytokine stimulus (GO:0071345)	3.51	2.09E-11
interspecies interaction between organisms (GO:0044419)	3.62	2.42E-11
signaling (GO:0023052)	1.73	2.42E-11
cell communication (GO:0007154)	1.71	3.58E-11
response to chemical (GO:0042221)	1.86	5.12E-11
positive regulation of response to stimulus (GO:0048584)	2.31	7.10E-11
negative regulation of protein metabolic process (GO:0051248)	3	8.76E-11
response to stimulus (GO:0050896)	1.5	9.35E-11
positive regulation of cellular metabolic process (GO:0031325)	2.04	1.39E-10
response to stress (GO:0006950)	1.97	1.39E-10
organonitrogen compound metabolic process (GO:1901564)	1.68	1.52E-10
Unclassified (UNCLASSIFIED)	0.26	2.34E-10
biological_process (GO:0008150)	1.15	2.39E-10
regulation of cell communication (GO:0010646)	1.96	2.40E-10
regulation of signal transduction (GO:0009966)	2.02	2.75E-10
negative regulation of cellular protein metabolic process (GO:0032269)	3	3.19E-10
negative regulation of nitrogen compound metabolic process (GO:0051172)	2.2	3.66E-10
transport (GO:0006810)	1.8	3.72E-10
establishment of localization (GO:0051234)	1.78	3.99E-10
regulation of signaling (GO:0023051)	1.94	4.84E-10
localization (GO:0051179)	1.67	5.71E-10
cell activation (GO:0001775)	3.02	5.81E-10
cellular response to stress (GO:0033554)	2.51	8.20E-10
regulation of protein modification process (GO:0031399)	2.42	8.46E-10
negative regulation of programmed cell death (GO:0043069)	3.22	8.58E-10
positive regulation of nitrogen compound metabolic process (GO:0051173)	2.02	8.64E-10
viral process (GO:0016032)	3.6	1.38E-09
negative regulation of cell death (GO:0060548)	3.07	1.38E-09
regulation of intracellular signal transduction (GO:1902531)	2.39	1.40E-09
response to abiotic stimulus (GO:0009628)	2.86	1.48E-09
negative regulation of apoptotic process (GO:0043066)	3.2	1.57E-09
multi-organism process (GO:0051704)	2.15	1.91E-09
response to oxygen levels (GO:0070482)	4.7	2.62E-09
protein folding (GO:0006457)	5.99	3.28E-09
positive regulation of signal transduction (GO:0009967)	2.5	3.66E-09
regulation of programmed cell death (GO:0043067)	2.5	3.80E-09
regulation of cell death (GO:0010941)	2.43	4.41E-09
negative regulation of cellular metabolic process (GO:0031324)	2.08	4.46E-09

positive regulation of cell communication (GO:0010647)	2.41	5.90E-09
establishment of localization in cell (GO:0051649)	2.49	6.08E-09
regulation of apoptotic process (GO:0042981)	2.49	6.39E-09
positive regulation of molecular function (GO:0044093)	2.34	6.40E-09
positive regulation of signaling (GO:0023056)	2.4	6.58E-09
immune response (GO:0006955)	2.37	6.76E-09
leukocyte activation (GO:0045321)	3.06	9.24E-09
regulation of multicellular organismal process (GO:0051239)	1.99	9.99E-09
regulation of cytokine production (GO:0001817)	3.55	1.00E-08
regulation of biological quality (GO:0065008)	1.83	1.31E-08
phosphorus metabolic process (GO:0006793)	2.14	1.42E-08
negative regulation of protein modification process (GO:0031400)	3.46	3.44E-08
phosphate-containing compound metabolic process (GO:0006796)	2.15	3.50E-08
positive regulation of immune response (GO:0050778)	3.18	3.73E-08
immune response-regulating signaling pathway (GO:0002764)	3.69	3.75E-08
intracellular signal transduction (GO:0035556)	2.35	4.47E-08
positive regulation of protein metabolic process (GO:0051247)	2.34	4.84E-08
response to decreased oxygen levels (GO:0036293)	4.52	4.87E-08
positive regulation of catalytic activity (GO:0043085)	2.43	7.19E-08
positive regulation of cellular protein metabolic process (GO:0032270)	2.37	7.23E-08
regulation of protein localization (GO:0032880)	2.73	7.50E-08
regulation of response to stress (GO:0080134)	2.42	7.81E-08
apoptotic process (GO:0006915)	2.87	8.87E-08
regulation of leukocyte cell-cell adhesion (GO:1903037)	4.51	1.03E-07
T cell receptor signaling pathway (GO:0050852)	6.88	1.13E-07
cellular localization (GO:0051641)	2.1	1.21E-07
response to hypoxia (GO:0001666)	4.46	1.25E-07
cellular metabolic process (GO:0044237)	1.38	1.25E-07
phosphorylation (GO:0016310)	2.48	1.61E-07
regulation of establishment of protein localization (GO:0070201)	2.94	1.71E-07
regulation of T cell activation (GO:0050863)	4.54	1.82E-07
regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043122)	5.18	1.95E-07
cellular protein metabolic process (GO:0044267)	1.74	2.96E-07
cellular response to oxygen levels (GO:0071453)	5.56	3.49E-07
nitrogen compound metabolic process (GO:0006807)	1.39	3.50E-07
regulation of lymphocyte activation (GO:0051249)	3.7	3.51E-07
immune response-activating signal transduction (GO:0002757)	3.6	3.56E-07
homeostatic process (GO:0042592)	2.33	3.94E-07
regulation of cell-cell adhesion (GO:0022407)	3.89	4.22E-07

negative regulation of molecular function (GO:0044092)	2.52	4.42E-07
positive regulation of intracellular signal transduction (GO:1902533)	2.7	4.64E-07
regulation of leukocyte activation (GO:0002694)	3.46	4.65E-07
regulation of cell activation (GO:0050865)	3.34	5.69E-07
regulation of transcription from RNA polymerase II promoter in response to stress (GO:0043618)	7.65	6.93E-07
regulation of proteolysis (GO:0030162)	2.83	7.12E-07
protein localization (GO:0008104)	2.09	7.45E-07
regulation of transferase activity (GO:0051338)	2.61	8.08E-07
positive regulation of leukocyte cell-cell adhesion (GO:1903039)	5.21	8.65E-07
protein transport (GO:0015031)	2.35	8.80E-07
cotranslational protein targeting to membrane (GO:0006613)	8.22	9.37E-07
establishment of protein localization (GO:0045184)	2.3	9.68E-07
macromolecule localization (GO:0033036)	1.98	9.68E-07
immune response-regulating cell surface receptor signaling pathway (GO:0002768)	3.72	9.78E-07
negative regulation of catalytic activity (GO:0043086)	2.74	1.01E-06
activation of immune response (GO:0002253)	3.31	1.11E-06
myeloid leukocyte activation (GO:0002274)	3.3	1.17E-06
regulation of DNA-templated transcription in response to stress (GO:0043620)	7.27	1.18E-06
protein targeting (GO:0006605)	4.6	1.18E-06
regulation of gene expression (GO:0010468)	1.61	1.18E-06
protein targeting to ER (GO:0045047)	7.98	1.22E-06
intracellular transport (GO:0046907)	2.39	1.43E-06
translational initiation (GO:0006413)	6.5	1.51E-06
regulation of cysteine-type endopeptidase activity involved in apoptotic process (GO:0043281)	5.28	1.52E-06
cytokine-mediated signaling pathway (GO:0019221)	3.33	1.56E-06
protein metabolic process (GO:0019538)	1.61	1.62E-06
leukocyte activation involved in immune response (GO:0002366)	3.17	1.66E-06
peptide transport (GO:0015833)	2.31	1.67E-06
regulation of macromolecule biosynthetic process (GO:0010556)	1.64	1.67E-06
establishment of protein localization to endoplasmic reticulum (GO:0072599)	7.68	1.78E-06
cell activation involved in immune response (GO:0002263)	3.14	1.87E-06
antigen receptor-mediated signaling pathway (GO:0050851)	4.91	1.88E-06
protein localization to endoplasmic reticulum (GO:0070972)	6.92	1.90E-06
positive regulation of T cell activation (GO:0050870)	5.16	1.99E-06
establishment of protein localization to organelle (GO:0072594)	3.91	2.17E-06
amide transport (GO:0042886)	2.27	2.30E-06

establishment of protein localization to membrane (GO:0090150)	5.09	2.40E-06
protein localization to organelle (GO:0033365)	3.1	2.40E-06
regulation of cellular macromolecule biosynthetic process (GO:2000112)	1.64	2.61E-06
cell death (GO:0008219)	2.49	2.86E-06
SRP-dependent cotranslational protein targeting to membrane (GO:0006614)	8.13	2.94E-06
regulation of biosynthetic process (GO:0009889)	1.6	3.07E-06
cellular protein localization (GO:0034613)	2.3	3.16E-06
programmed cell death (GO:0012501)	2.52	3.19E-06
protein targeting to membrane (GO:0006612)	6.56	3.39E-06
cellular macromolecule localization (GO:0070727)	2.29	3.61E-06
regulation of transcription from RNA polymerase II promoter in response to hypoxia (GO:0061418)	8.83	4.26E-06
positive regulation of lymphocyte activation (GO:0051251)	4.03	4.44E-06
response to unfolded protein (GO:0006986)	5.89	4.59E-06
metabolic process (GO:0008152)	1.31	4.91E-06
primary metabolic process (GO:0044238)	1.33	5.37E-06
immune effector process (GO:0002252)	2.49	5.44E-06
positive regulation of cell-cell adhesion (GO:0022409)	4.52	5.70E-06
regulation of peptide transport (GO:0090087)	2.7	5.82E-06
positive regulation of leukocyte activation (GO:0002696)	3.8	5.98E-06
regulation of transport (GO:0051049)	2.04	6.24E-06
positive regulation of cytokine production (GO:0001819)	3.65	6.50E-06
regulation of hydrolase activity (GO:0051336)	2.34	7.79E-06
regulation of cysteine-type endopeptidase activity (GO:2000116)	4.62	8.66E-06
immune response-activating cell surface receptor signaling pathway (GO:0002429)	3.59	8.74E-06
protein phosphorylation (GO:0006468)	2.52	8.96E-06
positive regulation of cell activation (GO:0050867)	3.7	9.19E-06
mitochondrion organization (GO:0007005)	3.46	9.39E-06
organic substance metabolic process (GO:0071704)	1.31	1.02E-05
cellular response to decreased oxygen levels (GO:0036294)	5.12	1.03E-05
signal transduction by protein phosphorylation (GO:0023014)	3.54	1.10E-05
leukocyte mediated immunity (GO:0002443)	2.76	1.12E-05
translation (GO:0006412)	3.64	1.16E-05
regulation of localization (GO:0032879)	1.81	1.16E-05
cellular component organization or biogenesis (GO:0071840)	1.49	1.16E-05
viral gene expression (GO:0019080)	6.36	1.18E-05
positive regulation of defense response (GO:0031349)	3.51	1.21E-05
negative regulation of response to stimulus (GO:0048585)	2.16	1.21E-05

regulation of phosphorylation (GO:0042325)	2.15	1.35E-05
regulation of cellular biosynthetic process (GO:0031326)	1.57	1.35E-05
intracellular protein transport (GO:0006886)	2.73	1.36E-05
cellular homeostasis (GO:0019725)	2.64	1.37E-05
Fc receptor signaling pathway (GO:0038093)	4.44	1.41E-05
cellular macromolecule catabolic process (GO:0044265)	2.59	1.49E-05
myeloid cell activation involved in immune response (GO:0002275)	3.17	1.54E-05
regulation of peptidase activity (GO:0052547)	3.45	1.56E-05
response to topologically incorrect protein (GO:0035966)	5.25	1.61E-05
regulation of protein transport (GO:0051223)	2.66	1.66E-05
myeloid leukocyte mediated immunity (GO:0002444)	3.15	1.69E-05
regulation of catabolic process (GO:0009894)	2.52	1.72E-05
regulation of cell proliferation (GO:0042127)	2.09	1.76E-05
viral transcription (GO:0019083)	6.63	1.96E-05
nitrogen compound transport (GO:0071705)	2.05	1.97E-05
protein stabilization (GO:0050821)	5.48	2.25E-05
regulation of protein phosphorylation (GO:0001932)	2.18	2.25E-05
MAPK cascade (GO:0000165)	3.6	2.27E-05
positive regulation of gene expression (GO:0010628)	1.98	2.27E-05
regulation of proteolysis involved in cellular protein catabolic process (GO:1903050)	4.26	2.31E-05
organonitrogen compound biosynthetic process (GO:1901566)	2.14	2.41E-05
response to oxygen-containing compound (GO:1901700)	2.13	2.59E-05
chaperone-mediated protein folding (GO:0061077)	9.38	2.68E-05
regulation of protein catabolic process (GO:0042176)	3.44	2.74E-05
cellular response to hypoxia (GO:0071456)	5	2.76E-05
protein localization to membrane (GO:0072657)	3.43	2.83E-05
regulation of cell adhesion (GO:0030155)	2.77	3.16E-05
regulation of protein modification by small protein conjugation or removal (GO:1903320)	3.97	3.17E-05
peptide biosynthetic process (GO:0043043)	3.4	3.17E-05
peptide metabolic process (GO:0006518)	3.03	3.19E-05
regulation of protein ubiquitination (GO:0031396)	4.15	3.20E-05
leukocyte degranulation (GO:0043299)	3.11	3.21E-05
apoptotic signaling pathway (GO:0097190)	3.95	3.26E-05
cellular chemical homeostasis (GO:0055082)	2.75	3.57E-05
purine nucleotide metabolic process (GO:0006163)	3.47	3.85E-05
negative regulation of gene expression (GO:0010629)	2.02	4.09E-05
neutrophil degranulation (GO:0043312)	3.13	4.57E-05
negative regulation of cell communication (GO:0010648)	2.19	4.78E-05

neutrophil activation involved in immune response (GO:0002283)	3.12	4.88E-05
negative regulation of signaling (GO:0023057)	2.18	4.95E-05
regulated exocytosis (GO:0045055)	2.7	4.99E-05
regulation of endopeptidase activity (GO:0052548)	3.39	5.45E-05
cellular macromolecule metabolic process (GO:0044260)	1.4	5.62E-05
positive regulation of cell adhesion (GO:0045785)	3.38	5.63E-05
positive regulation of establishment of protein localization (GO:1904951)	3	5.77E-05
regulation of innate immune response (GO:0045088)	3.27	5.82E-05
mitochondrial membrane organization (GO:0007006)	5.86	6.13E-05
neutrophil activation (GO:0042119)	3.07	6.27E-05
neutrophil mediated immunity (GO:0002446)	3.05	6.95E-05
regulation of cellular response to stress (GO:0080135)	2.76	7.05E-05
granulocyte activation (GO:0036230)	3.04	7.14E-05
regulation of phosphate metabolic process (GO:0019220)	1.96	7.75E-05
cellular component organization (GO:0016043)	1.47	8.03E-05
positive regulation of innate immune response (GO:0045089)	3.69	8.18E-05
regulation of cellular protein catabolic process (GO:1903362)	3.85	8.42E-05
negative regulation of transferase activity (GO:0051348)	3.4	8.62E-05
regulation of nucleobase-containing compound metabolic process (GO:0019219)	1.54	8.69E-05
posttranscriptional regulation of gene expression (GO:0010608)	2.92	9.13E-05
positive regulation of macromolecule biosynthetic process (GO:0010557)	1.96	9.14E-05
cellular nitrogen compound metabolic process (GO:0034641)	1.47	9.41E-05
Fc-epsilon receptor signaling pathway (GO:0038095)	4.76	9.57E-05
organic substance transport (GO:0071702)	1.85	1.13E-04
regulation of phosphorus metabolic process (GO:0051174)	1.94	1.20E-04
positive regulation of transport (GO:0051050)	2.32	1.31E-04
regulation of cellular catabolic process (GO:0031329)	2.52	1.34E-04
purine nucleoside triphosphate metabolic process (GO:0009144)	4.08	1.38E-04
regulation of defense response (GO:0031347)	2.51	1.38E-04
negative regulation of protein ubiquitination (GO:0031397)	5.36	1.41E-04
mitochondrial transport (GO:0006839)	4.07	1.44E-04
purine-containing compound metabolic process (GO:0072521)	3.17	1.46E-04
activation of innate immune response (GO:0002218)	4.05	1.50E-04
regulation of cellular localization (GO:0060341)	2.39	1.51E-04
positive regulation of proteolysis (GO:0045862)	3.25	1.59E-04
purine ribonucleoside monophosphate metabolic process (GO:0009167)	4.02	1.64E-04
nucleoside monophosphate metabolic process (GO:0009123)	3.82	1.64E-04

negative regulation of signal transduction (GO:0009968)	2.17	1.70E-04
purine nucleoside monophosphate metabolic process (GO:0009126)	4	1.71E-04
response to organonitrogen compound (GO:0010243)	2.37	1.72E-04
positive regulation of RNA metabolic process (GO:0051254)	2.01	1.72E-04
organelle organization (GO:0006996)	1.63	1.75E-04
response to nitrogen compound (GO:1901698)	2.27	1.77E-04
purine ribonucleotide metabolic process (GO:0009150)	3.34	1.81E-04
secretion by cell (GO:0032940)	2.3	1.92E-04
positive regulation of nucleobase-containing compound metabolic process (GO:0045935)	1.9	2.10E-04
cation homeostasis (GO:0055080)	2.64	2.23E-04
chemical homeostasis (GO:0048878)	2.28	2.23E-04
innate immune response-activating signal transduction (GO:0002758)	4.12	2.31E-04
cellular cation homeostasis (GO:0030003)	2.73	2.65E-04
positive regulation of cellular biosynthetic process (GO:0031328)	1.87	2.84E-04
negative regulation of protein modification by small protein conjugation or removal (GO:1903321)	4.94	2.94E-04
ATP metabolic process (GO:0046034)	4.27	2.95E-04
ribonucleoside monophosphate metabolic process (GO:0009161)	3.82	2.95E-04
lymphocyte activation (GO:0046649)	3.34	2.95E-04
ribonucleotide metabolic process (GO:0009259)	3.2	3.13E-04
amide biosynthetic process (GO:0043604)	2.91	3.27E-04
inorganic ion homeostasis (GO:0098771)	2.58	3.28E-04
cellular component biogenesis (GO:0044085)	1.69	3.28E-04
response to temperature stimulus (GO:0009266)	4.88	3.29E-04
nucleoside triphosphate metabolic process (GO:0009141)	3.77	3.31E-04
purine ribonucleoside triphosphate metabolic process (GO:0009205)	3.96	3.50E-04
nucleotide metabolic process (GO:0009117)	2.8	3.78E-04
regulation of peptide secretion (GO:0002791)	2.96	3.81E-04
cellular ion homeostasis (GO:0006873)	2.66	3.93E-04
regulation of hemopoiesis (GO:1903706)	3.04	4.04E-04
cytokine production (GO:0001816)	5.17	4.25E-04
exocytosis (GO:0006887)	2.41	4.31E-04
positive regulation of transcription, DNA-templated (GO:0045893)	1.99	4.32E-04
positive regulation of RNA biosynthetic process (GO:1902680)	1.99	4.32E-04
regulation of multi-organism process (GO:0043900)	3.12	4.33E-04
positive regulation of nucleic acid-templated transcription (GO:1903508)	1.99	4.34E-04
'de novo' protein folding (GO:0006458)	11	4.38E-04
nucleoside phosphate metabolic process (GO:0006753)	2.77	4.38E-04

positive regulation of multicellular organismal process (GO:0051240)	1.95	4.38E-04
ribonucleoside triphosphate metabolic process (GO:0009199)	3.86	4.50E-04
positive regulation of biosynthetic process (GO:0009891)	1.84	4.51E-04
mRNA catabolic process (GO:0006402)	4.07	4.66E-04
nucleobase-containing compound catabolic process (GO:0034655)	3.21	4.67E-04
immune system development (GO:0002520)	2.62	4.70E-04
macromolecule catabolic process (GO:0009057)	2.22	4.71E-04
RNA catabolic process (GO:0006401)	3.83	4.86E-04
cellular catabolic process (GO:0044248)	1.88	4.88E-04
positive regulation of transferase activity (GO:0051347)	2.53	4.89E-04
response to endoplasmic reticulum stress (GO:0034976)	3.81	5.03E-04
positive regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043123)	4.31	5.05E-04
ribose phosphate metabolic process (GO:0019693)	3.07	5.10E-04
cellular amide metabolic process (GO:0043603)	2.51	5.10E-04
cellular response to tumor necrosis factor (GO:0071356)	3.8	5.23E-04
regulation of cellular protein localization (GO:1903827)	2.6	5.27E-04
positive regulation of protein modification process (GO:0031401)	2.08	5.59E-04
regulation of transcription by RNA polymerase II (GO:0006357)	1.79	6.03E-04
cellular response to oxygen-containing compound (GO:1901701)	2.25	6.28E-04
protein refolding (GO:0042026)	20.76	6.32E-04
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)	5.37	6.55E-04
hydrogen ion transmembrane transport (GO:1902600)	5.37	6.57E-04
regulation of protein stability (GO:0031647)	3.69	7.09E-04
homeostasis of number of cells (GO:0048872)	4.15	7.11E-04
regulation of proteasomal protein catabolic process (GO:0061136)	4.45	7.30E-04
negative regulation of protein phosphorylation (GO:0001933)	2.98	7.74E-04
regulation of cellular response to heat (GO:1900034)	6.71	7.91E-04
ion homeostasis (GO:0050801)	2.48	8.04E-04
negative regulation of ubiquitin protein ligase activity (GO:1904667)	6.62	8.63E-04
negative regulation of phosphorylation (GO:0042326)	2.85	8.93E-04
cellular response to interleukin-4 (GO:0071353)	12.46	9.60E-04
regulation of kinase activity (GO:0043549)	2.26	1.05E-03
proton transport (GO:0015992)	4.62	1.06E-03
positive regulation of hydrolase activity (GO:0051345)	2.36	1.06E-03
cellular component assembly (GO:0022607)	1.69	1.09E-03
aromatic compound catabolic process (GO:0019439)	2.89	1.13E-03
cellular nitrogen compound biosynthetic process (GO:0044271)	1.53	1.15E-03
regulation of protein secretion (GO:0050708)	2.88	1.20E-03

tumor necrosis factor-mediated signaling pathway (GO:0033209)	4.96	1.25E-03
response to tumor necrosis factor (GO:0034612)	3.5	1.26E-03
cellular protein modification process (GO:0006464)	1.56	1.42E-03
protein modification process (GO:0036211)	1.56	1.42E-03
enzyme linked receptor protein signaling pathway (GO:0007167)	2.36	1.45E-03
response to interleukin-4 (GO:0070670)	11.25	1.52E-03
negative regulation of ubiquitin-protein transferase activity (GO:0051444)	6.08	1.52E-03
NIK/NF-kappaB signaling (GO:0038061)	6.08	1.53E-03
leukocyte differentiation (GO:0002521)	3.26	1.60E-03
regulation of protein kinase activity (GO:0045859)	2.3	1.60E-03
secretion (GO:0046903)	2.06	1.61E-03
activation of cysteine-type endopeptidase activity involved in apoptotic process (GO:0006919)	6.01	1.63E-03
positive regulation of cellular protein localization (GO:1903829)	2.9	1.63E-03
macromolecule metabolic process (GO:0043170)	1.29	1.63E-03
negative regulation of cytokine production (GO:0001818)	3.57	1.69E-03
regulation of developmental process (GO:0050793)	1.66	1.70E-03
negative regulation of phosphate metabolic process (GO:0045936)	2.51	1.72E-03
negative regulation of phosphorus metabolic process (GO:0010563)	2.51	1.76E-03
response to other organism (GO:0051707)	2.22	1.76E-03
interaction with host (GO:0051701)	4.33	1.77E-03
response to external biotic stimulus (GO:0043207)	2.21	1.81E-03
macromolecule modification (GO:0043412)	1.52	1.91E-03
heterocycle catabolic process (GO:0046700)	2.86	1.93E-03
negative regulation of cysteine-type endopeptidase activity involved in apoptotic process (GO:0043154)	5.81	2.02E-03
positive regulation of transcription by RNA polymerase II (GO:0045944)	2.03	2.04E-03
cellular nitrogen compound catabolic process (GO:0044270)	2.84	2.05E-03
positive regulation of cell death (GO:0010942)	2.4	2.06E-03
circulatory system development (GO:0072359)	2.23	2.13E-03
nucleobase-containing small molecule metabolic process (GO:0055086)	2.48	2.15E-03
negative regulation of macromolecule biosynthetic process (GO:0010558)	1.89	2.18E-03
regulation of symbiosis, encompassing mutualism through parasitism (GO:0043903)	3.67	2.26E-03
positive regulation of protein localization to membrane (GO:1905477)	5.05	2.27E-03
metal ion homeostasis (GO:0055065)	2.51	2.35E-03
response to biotic stimulus (GO:0009607)	2.18	2.35E-03
regulation of RNA metabolic process (GO:0051252)	1.47	2.35E-03

negative regulation of proteolysis (GO:0045861)	3.01	2.40E-03
regulation of interleukin-12 production (GO:0032655)	7.82	2.50E-03
positive regulation of organelle organization (GO:0010638)	2.43	2.52E-03
regulation of ubiquitin protein ligase activity (GO:1904666)	5.57	2.64E-03
myeloid cell differentiation (GO:0030099)	3.84	2.64E-03
positive regulation of protein transport (GO:0051222)	2.62	2.64E-03
proteasomal protein catabolic process (GO:0010498)	3.1	2.68E-03
mitochondrial ATP synthesis coupled proton transport (GO:0042776)	13.84	2.70E-03
regulation of proteasomal ubiquitin-dependent protein catabolic process (GO:0032434)	4.93	2.70E-03
organic cyclic compound catabolic process (GO:1901361)	2.69	2.71E-03
protein polyubiquitination (GO:0000209)	3.23	2.73E-03
nuclear-transcribed mRNA catabolic process (GO:0000956)	3.8	2.84E-03
positive regulation of peptidase activity (GO:0010952)	4.08	2.85E-03
regulation of cell differentiation (GO:0045595)	1.8	2.85E-03
cellular metal ion homeostasis (GO:0006875)	2.59	2.96E-03
toll-like receptor signaling pathway (GO:0002224)	5.45	2.97E-03
viral life cycle (GO:0019058)	3.78	2.97E-03
pattern recognition receptor signaling pathway (GO:0002221)	4.8	3.19E-03
MyD88-independent toll-like receptor signaling pathway (GO:0002756)	9.43	3.23E-03
regulation of calcium-mediated signaling (GO:0050848)	6.2	3.23E-03
proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)	3.16	3.34E-03
nucleobase-containing compound metabolic process (GO:0006139)	1.41	3.36E-03
negative regulation of intracellular signal transduction (GO:1902532)	2.56	3.54E-03
stimulatory C-type lectin receptor signaling pathway (GO:0002223)	4.73	3.57E-03
positive regulation of apoptotic process (GO:0043065)	2.42	3.57E-03
positive regulation of cysteine-type endopeptidase activity involved in apoptotic process (GO:0043280)	4.69	3.77E-03
regulation of T cell differentiation (GO:0045580)	4.69	3.78E-03
response to endogenous stimulus (GO:0009719)	1.87	3.79E-03
cellular response to external stimulus (GO:0071496)	3.12	3.80E-03
myeloid cell homeostasis (GO:0002262)	5.23	3.84E-03
positive regulation of programmed cell death (GO:0043068)	2.39	3.88E-03
regulation of cellular component organization (GO:0051128)	1.62	3.88E-03
innate immune response activating cell surface receptor signaling pathway (GO:0002220)	4.61	4.20E-03
hematopoietic or lymphoid organ development (GO:0048534)	2.46	4.29E-03
ATP hydrolysis coupled cation transmembrane transport (GO:0099132)	7.02	4.30E-03
positive regulation of cellular component organization (GO:0051130)	1.94	4.41E-03

regulation of translation (GO:0006417)	2.74	4.42E-03
drug metabolic process (GO:0017144)	2.36	4.42E-03
membrane organization (GO:0061024)	2.16	4.43E-03
positive regulation of endopeptidase activity (GO:0010950)	4.15	4.56E-03
organic substance catabolic process (GO:1901575)	1.76	4.56E-03
negative regulation of transport (GO:0051051)	2.57	4.57E-03
defense response (GO:0006952)	1.9	4.73E-03
regulation of nucleic acid-templated transcription (GO:1903506)	1.46	4.82E-03
negative regulation of cellular macromolecule biosynthetic process (GO:2000113)	1.86	4.96E-03
vesicle-mediated transport (GO:0016192)	1.72	4.99E-03
inner mitochondrial membrane organization (GO:0007007)	8.51	5.01E-03
negative regulation of biosynthetic process (GO:0009890)	1.8	5.10E-03
regulation of cellular amide metabolic process (GO:0034248)	2.62	5.12E-03
cellular aromatic compound metabolic process (GO:0006725)	1.39	5.29E-03
interleukin-4-mediated signaling pathway (GO:0035771)	43.6	5.88E-03
regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process (GO:2000058)	4.89	5.89E-03
positive regulation of interleukin-5 production (GO:0032754)	17.89	5.91E-03
regulation of cellular amino acid metabolic process (GO:0006521)	6.56	6.00E-03
regulation of adaptive immune response (GO:0002819)	4.37	6.01E-03
positive regulation of leukocyte differentiation (GO:1902107)	4.37	6.02E-03
T cell activation (GO:0042110)	3.47	6.02E-03
regulation of transcription, DNA-templated (GO:0006355)	1.45	6.02E-03
organophosphate metabolic process (GO:0019637)	2	6.04E-03
cellular biosynthetic process (GO:0044249)	1.39	6.04E-03
regulation of RNA biosynthetic process (GO:2001141)	1.46	6.05E-03
regulation of organelle organization (GO:0033043)	1.89	6.06E-03
regulation of MAPK cascade (GO:0043408)	2.24	6.07E-03
negative regulation of immune response (GO:0050777)	4.34	6.26E-03
heterocycle metabolic process (GO:0046483)	1.39	6.30E-03
macromolecular complex subunit organization (GO:0043933)	1.71	6.47E-03
proteolysis involved in cellular protein catabolic process (GO:0051603)	2.42	6.50E-03
protein complex subunit organization (GO:0071822)	1.85	6.52E-03
positive regulation of cysteine-type endopeptidase activity (GO:2001056)	4.31	6.55E-03
cellular calcium ion homeostasis (GO:0006874)	2.72	6.58E-03
ubiquitin-dependent protein catabolic process (GO:0006511)	2.48	6.75E-03
regulation of protein serine/threonine kinase activity (GO:0071900)	2.48	6.77E-03
macromolecular complex assembly (GO:0065003)	1.78	6.77E-03

negative regulation of cysteine-type endopeptidase activity (GO:2000117)	4.76	6.78E-03
regulation of leukocyte differentiation (GO:1902105)	3.2	7.11E-03
response to interleukin-15 (GO:0070672)	16.61	7.13E-03
regulation of interleukin-10 production (GO:0032653)	7.75	7.37E-03
detection of stimulus involved in sensory perception (GO:0050906)	< 0.01	7.37E-03
cellular response to endogenous stimulus (GO:0071495)	1.93	7.38E-03
negative regulation of nucleobase-containing compound metabolic process (GO:0045934)	1.79	7.40E-03
regulation of DNA metabolic process (GO:0051052)	2.69	7.46E-03
endoplasmic reticulum unfolded protein response (GO:0030968)	4.67	7.55E-03
sensory perception of chemical stimulus (GO:0007606)	< 0.01	7.58E-03
regulation of hematopoietic progenitor cell differentiation (GO:1901532)	5.28	7.71E-03
positive regulation of peptide secretion (GO:0002793)	3.17	7.82E-03
positive regulation of NF-kappaB transcription factor activity (GO:0051092)	4.18	7.86E-03
transmembrane receptor protein tyrosine kinase signaling pathway (GO:0007169)	2.47	7.96E-03
energy coupled proton transport, down electrochemical gradient (GO:0015985)	10.02	8.43E-03
ATP synthesis coupled proton transport (GO:0015986)	10.02	8.45E-03
TRIF-dependent toll-like receptor signaling pathway (GO:0035666)	10.02	8.47E-03
modulation by symbiont of host cellular process (GO:0044068)	10.02	8.49E-03
cellular response to nutrient levels (GO:0031669)	3.52	8.58E-03
biosynthetic process (GO:0009058)	1.37	8.73E-03
calcium ion homeostasis (GO:0055074)	2.64	8.92E-03
mitochondrial ATP synthesis coupled electron transport (GO:0042775)	5.11	9.30E-03
positive regulation of interleukin-10 production (GO:0032733)	9.69	9.58E-03
positive regulation of interleukin-2 production (GO:0032743)	9.69	9.60E-03
regulation of lymphocyte proliferation (GO:0050670)	3.47	9.64E-03
cellular protein catabolic process (GO:0044257)	2.31	9.64E-03
negative regulation of G2/M transition of mitotic cell cycle (GO:0010972)	5.05	9.80E-03
response to organic cyclic compound (GO:0014070)	2.05	9.81E-03
ATP synthesis coupled electron transport (GO:0042773)	5.05	9.82E-03
regulation of production of molecular mediator of immune response (GO:0002700)	4.47	9.83E-03
positive regulation of protein modification by small protein conjugation or removal (GO:1903322)	3.45	9.91E-03
regulation of mononuclear cell proliferation (GO:0032944)	3.45	9.93E-03
regulation of multicellular organismal development (GO:2000026)	1.67	1.01E-02
negative regulation of interleukin-12 production (GO:0032695)	14.53	1.02E-02

cellular macromolecular complex assembly (GO:0034622)	2.07	1.02E-02
response to cold (GO:0009409)	7.12	1.04E-02
gene expression (GO:0010467)	1.43	1.04E-02
detection of chemical stimulus (GO:0009593)	< 0.01	1.04E-02
regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway (GO:1900739)	9.38	1.05E-02
intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress (GO:0070059)	9.38	1.05E-02
cristae formation (GO:0042407)	9.38	1.05E-02
regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway (GO:1901028)	7.12	1.05E-02
ATP hydrolysis coupled ion transmembrane transport (GO:0099131)	5.81	1.05E-02
cellular divalent inorganic cation homeostasis (GO:0072503)	2.6	1.05E-02
positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway (GO:1900740)	9.38	1.06E-02
cellular response to unfolded protein (GO:0034620)	4.4	1.06E-02
protein complex assembly (GO:0006461)	1.89	1.09E-02
modification-dependent protein catabolic process (GO:0019941)	2.46	1.10E-02
protein complex biogenesis (GO:0070271)	1.89	1.10E-02
catabolic process (GO:0009056)	1.64	1.10E-02
animal organ development (GO:0048513)	1.5	1.10E-02
positive regulation of protein secretion (GO:0050714)	3.19	1.12E-02
modulation of programmed cell death in other organism (GO:0044531)	29.06	1.16E-02
modulation by symbiont of host programmed cell death (GO:0052040)	29.06	1.16E-02
modulation by organism of apoptotic process in other organism involved in symbiotic interaction (GO:0052433)	29.06	1.17E-02
modulation of programmed cell death in other organism involved in symbiotic interaction (GO:0052248)	29.06	1.17E-02
modulation of apoptotic process in other organism (GO:0044532)	29.06	1.17E-02
positive regulation of kinase activity (GO:0033674)	2.32	1.18E-02
regulation of inclusion body assembly (GO:0090083)	13.68	1.19E-02
response to purine-containing compound (GO:0014074)	3.9	1.19E-02
regulation of transporter activity (GO:0032409)	3.16	1.19E-02
modification-dependent macromolecule catabolic process (GO:0043632)	2.41	1.19E-02
positive regulation of phosphorylation (GO:0042327)	1.95	1.19E-02
organic substance biosynthetic process (GO:1901576)	1.36	1.19E-02
regulation of interleukin-2 production (GO:0032663)	6.84	1.20E-02
SCF-dependent proteasomal ubiquitin-dependent protein catabolic process (GO:0031146)	5.57	1.25E-02
placenta development (GO:0001890)	3.88	1.25E-02
positive regulation of protein catabolic process (GO:0045732)	2.98	1.25E-02

regulation of leukocyte proliferation (GO:0070663)	3.32	1.28E-02
regulation of lymphocyte differentiation (GO:0045619)	3.85	1.30E-02
regulation of secretion by cell (GO:1903530)	2.17	1.30E-02
I-kappaB kinase/NF-kappaB signaling (GO:0007249)	5.5	1.34E-02
response to superoxide (GO:0000303)	12.92	1.39E-02
detection of chemical stimulus involved in sensory perception (GO:0050907)	< 0.01	1.39E-02
regulation of ubiquitin-protein transferase activity (GO:0051438)	4.19	1.40E-02
positive regulation of DNA binding transcription factor activity (GO:0051091)	3.1	1.40E-02
purine ribonucleoside triphosphate biosynthetic process (GO:0009206)	6.58	1.41E-02
myeloid leukocyte differentiation (GO:0002573)	4.7	1.41E-02
positive regulation of cell proliferation (GO:0008284)	2	1.41E-02
regulation of response to endoplasmic reticulum stress (GO:1905897)	5.43	1.42E-02
hemopoiesis (GO:0030097)	2.35	1.42E-02
cellular protein complex assembly (GO:0043623)	2.5	1.46E-02
oxidative phosphorylation (GO:0006119)	4.65	1.48E-02
mRNA metabolic process (GO:0016071)	2.14	1.48E-02
positive regulation of protein ubiquitination (GO:0031398)	3.47	1.50E-02
T cell costimulation (GO:0031295)	5.35	1.51E-02
regulation of mitochondrial membrane permeability (GO:0046902)	5.35	1.51E-02
negative regulation of T-helper 1 type immune response (GO:0002826)	24.91	1.52E-02
purine nucleoside triphosphate biosynthetic process (GO:0009145)	6.46	1.52E-02
cellular response to hyperoxia (GO:0071455)	24.91	1.53E-02
interleukin-4 production (GO:0032633)	24.91	1.53E-02
membrane fusion involved in viral entry into host cell (GO:0039663)	24.91	1.53E-02
fusion of virus membrane with host plasma membrane (GO:0019064)	24.91	1.54E-02
multi-organism membrane fusion (GO:0044800)	24.91	1.54E-02
lymphocyte costimulation (GO:0031294)	5.28	1.60E-02
positive regulation of proteolysis involved in cellular protein catabolic process (GO:1903052)	3.44	1.60E-02
lymphocyte differentiation (GO:0030098)	3.21	1.60E-02
divalent inorganic cation homeostasis (GO:0072507)	2.47	1.62E-02
regulation of cytosolic calcium ion concentration (GO:0051480)	2.87	1.70E-02
T cell selection (GO:0045058)	8.07	1.75E-02
regulation of protein localization to membrane (GO:1905475)	3.66	1.79E-02
regulation of mRNA stability (GO:0043488)	3.66	1.79E-02
entry into host cell (GO:0030260)	4.47	1.80E-02
reactive oxygen species metabolic process (GO:0072593)	4.47	1.80E-02
positive regulation of lymphocyte proliferation (GO:0050671)	3.99	1.80E-02

negative regulation of cellular biosynthetic process (GO:0031327)	1.71	1.80E-02
entry into other organism involved in symbiotic interaction (GO:0051828)	4.47	1.81E-02
entry into cell of other organism involved in symbiotic interaction (GO:0051806)	4.47	1.81E-02
entry into host (GO:0044409)	4.47	1.81E-02
regulation of hematopoietic stem cell differentiation (GO:1902036)	5.15	1.82E-02
negative regulation of cell cycle G2/M phase transition (GO:1902750)	4.47	1.82E-02
small molecule metabolic process (GO:0044281)	1.63	1.83E-02
positive regulation of mononuclear cell proliferation (GO:0032946)	3.96	1.89E-02
sensory perception of smell (GO:0007608)	< 0.01	1.95E-02
regulation of secretion (GO:0051046)	2.08	1.96E-02
multi-organism membrane organization (GO:0044803)	21.8	1.99E-02
cellular response to cold (GO:0070417)	21.8	1.99E-02
negative regulation of proteolysis involved in cellular protein catabolic process (GO:1903051)	6.01	2.03E-02
IRE1-mediated unfolded protein response (GO:0036498)	6.01	2.03E-02
erythrocyte homeostasis (GO:0034101)	5.02	2.03E-02
regulation of cellular amine metabolic process (GO:0033238)	5.02	2.03E-02
positive regulation of protein phosphorylation (GO:0001934)	1.93	2.05E-02
response to oxygen radical (GO:0000305)	11.07	2.09E-02
negative regulation of cell killing (GO:0031342)	11.07	2.09E-02
positive regulation of macrophage activation (GO:0043032)	11.07	2.09E-02
regulation of macrophage activation (GO:0043030)	7.65	2.09E-02
negative regulation of peptidase activity (GO:0010466)	2.93	2.09E-02
negative regulation of immune system process (GO:0002683)	2.48	2.09E-02
regulation of interleukin-5 production (GO:0032674)	11.07	2.10E-02
ribonucleoside triphosphate biosynthetic process (GO:0009201)	5.91	2.17E-02
regulation of tumor necrosis factor-mediated signaling pathway (GO:0010803)	5.91	2.17E-02
cellular response to extracellular stimulus (GO:0031668)	3.07	2.19E-02
cellular response to topologically incorrect protein (GO:0035967)	3.85	2.23E-02
negative regulation of adaptive immune response (GO:0002820)	7.45	2.29E-02
positive regulation of hemopoiesis (GO:1903708)	3.5	2.31E-02
response to external stimulus (GO:0009605)	1.6	2.31E-02
positive regulation of leukocyte proliferation (GO:0070665)	3.82	2.33E-02
regulation of cytokine-mediated signaling pathway (GO:0001959)	3.48	2.38E-02
regulation of RNA stability (GO:0043487)	3.48	2.38E-02
regulation of membrane permeability (GO:0090559)	4.84	2.39E-02
regulation of protein complex assembly (GO:0043254)	2.45	2.39E-02
positive regulation of protein kinase activity (GO:0045860)	2.27	2.39E-02

positive regulation of protein complex assembly (GO:0031334)	3.03	2.40E-02
regulation of nucleotide-binding oligomerization domain containing signaling pathway (GO:0070424)	19.38	2.49E-02
negative regulation of lipid localization (GO:1905953)	7.27	2.49E-02
positive regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway (GO:1901030)	7.27	2.49E-02
regulation of sequestering of calcium ion (GO:0051282)	4.19	2.50E-02
negative regulation of protein catabolic process (GO:0042177)	4.19	2.50E-02
negative regulation of multicellular organismal process (GO:0051241)	1.84	2.50E-02
organic cyclic compound metabolic process (GO:1901360)	1.33	2.50E-02
respiratory electron transport chain (GO:0022904)	4.15	2.63E-02
response to lipid (GO:0033993)	1.95	2.65E-02
regulation of immune effector process (GO:0002697)	2.42	2.66E-02
detection of chemical stimulus involved in sensory perception of smell (GO:0050911)	< 0.01	2.66E-02
multi-organism cellular process (GO:0044764)	10.11	2.70E-02
ATP biosynthetic process (GO:0006754)	7.09	2.71E-02
purine-containing compound biosynthetic process (GO:0072522)	3.71	2.72E-02
regulation of cytokine secretion (GO:0050707)	3.4	2.74E-02
protein catabolic process (GO:0030163)	2.1	2.74E-02
regulation of calcium ion transmembrane transporter activity (GO:1901019)	4.68	2.79E-02
positive regulation of cellular protein catabolic process (GO:1903364)	3.15	2.82E-02
developmental process (GO:0032502)	1.3	2.84E-02
cation transport (GO:0006812)	1.93	2.85E-02
positive regulation of cytokine secretion (GO:0050715)	4.08	2.86E-02
heart development (GO:0007507)	2.3	2.86E-02
regulation of T cell differentiation in thymus (GO:0033081)	9.69	3.04E-02
regulation of establishment or maintenance of cell polarity (GO:0032878)	9.69	3.05E-02
response to peptide hormone (GO:0043434)	2.45	3.09E-02
regulation of response to cytokine stimulus (GO:0060759)	3.32	3.18E-02
intracellular receptor signaling pathway (GO:0030522)	3.3	3.30E-02
positive regulation of multi-organism process (GO:0043902)	3.3	3.31E-02
cellular response to organonitrogen compound (GO:0071417)	2.25	3.37E-02
regulation of endoplasmic reticulum unfolded protein response (GO:1900101)	9.3	3.45E-02
positive regulation of protein serine/threonine kinase activity (GO:0071902)	2.51	3.45E-02
modification by symbiont of host morphology or physiology (GO:0044003)	6.61	3.50E-02
system development (GO:0048731)	1.35	3.57E-02

regulation of binding (GO:0051098)	2.5	3.63E-02
viral entry into host cell (GO:0046718)	4.42	3.67E-02
extrinsic apoptotic signaling pathway (GO:0097191)	4.42	3.67E-02
type 2 immune response (GO:0042092)	15.85	3.78E-02
negative regulation of inclusion body assembly (GO:0090084)	15.85	3.79E-02
regulation of mRNA catabolic process (GO:0061013)	3.23	3.80E-02
positive regulation of cytosolic calcium ion concentration (GO:0007204)	2.82	4.00E-02
negative regulation of endopeptidase activity (GO:0010951)	2.82	4.00E-02
positive regulation of MAPK cascade (GO:0043410)	2.2	4.05E-02
regulation of pancreatic stellate cell proliferation (GO:2000229)	58.13	4.13E-02
negative regulation of dendritic cell cytokine production (GO:0002731)	58.13	4.13E-02
regulation of cell cycle (GO:0051726)	1.75	4.13E-02
regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains (GO:0002822)	3.81	4.14E-02
negative regulation of cellular protein catabolic process (GO:1903363)	5.05	4.15E-02
regulation of cell killing (GO:0031341)	5.05	4.16E-02
inflammatory response (GO:0006954)	2.26	4.22E-02
response to drug (GO:0042493)	1.85	4.25E-02
ATP hydrolysis coupled proton transport (GO:0015991)	8.61	4.30E-02
nucleoside triphosphate biosynthetic process (GO:0009142)	4.98	4.42E-02
sensory perception (GO:0007600)	0.31	4.48E-02
protein localization to nucleus (GO:0034504)	3.14	4.50E-02
chaperone cofactor-dependent protein refolding (GO:0051085)	14.53	4.53E-02
negative regulation of transcription from RNA polymerase II promoter in response to stress (GO:0097201)	14.53	4.53E-02
positive regulation of chemokine secretion (GO:0090197)	14.53	4.54E-02
positive regulation of secretion by cell (GO:1903532)	2.43	4.54E-02
negative regulation of hydrolase activity (GO:0051346)	2.35	4.54E-02
multicellular organism development (GO:0007275)	1.32	4.57E-02
ribonucleoprotein complex biogenesis (GO:0022613)	2.24	4.60E-02
positive regulation of cell differentiation (GO:0045597)	1.89	4.60E-02
positive regulation of T cell differentiation (GO:0045582)	4.91	4.64E-02
energy coupled proton transmembrane transport, against electrochemical gradient (GO:0015988)	8.3	4.74E-02
negative regulation of proteasomal ubiquitin-dependent protein catabolic process (GO:0032435)	8.3	4.75E-02
regulation of interleukin-4 production (GO:0032673)	8.3	4.76E-02
regulation of ion transmembrane transporter activity (GO:0032412)	2.91	4.79E-02
regulation of intrinsic apoptotic signaling pathway (GO:2001242)	3.35	4.83E-02

T cell differentiation (GO:0030217)	3.69	4.84E-02
negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle (GO:0051436)	4.84	4.90E-02
cell redox homeostasis (GO:0045454)	4.84	4.91E-02

Table S10. The cohort of 865 genes correlating with tissue eosinophilia (disease severity marker)

Gene Symbol	P values
PTGDR2	2.62E-05
SNORD127	0.00015
AB231711	0.000184
FLJ00050	0.000202
FFAR3	0.000259
DTX2P1-UPK3BP1-PMS2P11	0.000312
ASAH2B	0.000342
BC127952	0.000399
CHCHD10	0.00047
IL17RB	0.000508
SCXA	0.000518
LINC00879	0.00057
KIAA1524	0.000581
GPR137C	0.000595
ST3GAL5	0.000639
LIF	0.000722
RP11-345M22.2	0.000798
CES1P2	0.000843
PTPRN2	0.000987
ZNF710	0.00104
TSEN54	0.0011
RNF19A	0.00113
SLC4A7	0.00118
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TIGD5	0.00121
TPSB2	0.00122
AY190091	0.00123
LOC100130705	0.00131
CNIH2	0.00132
DMD	0.00137
CCDC64	0.00138
TMEM132D	0.00156
CLIP4	0.00182
IL13	0.00195
NBEAL2	0.00217

ZBTB24	0.00218
INPPL1	0.00225
CHPF	0.00227
SSX4	0.00231
SSX4B	0.00231
SH3TC1	0.00233
IRS2	0.00235
U85052	0.00237
SLC25A20	0.00239
GOLGA8DP	0.00242
MAP3K8	0.00243
SOS1	0.00251
IL5	0.00259
LINC00623	0.0026
PDE4A	0.00262
TMEM44-AS1	0.00264
SUCLG2	0.00265
CES2	0.00265
AFAP1	0.00271
BC064371	0.00277
INTS4L2	0.00296
RIPK3	0.00299
SH2D2A	0.00302
CPNE3	0.00306
RGCC	0.00306
LINC00654	0.00308
AK127124	0.00316
AY124781	0.00327
RNU5F-1	0.00327
HES4	0.00334
C2orf66	0.00339
EGLN3	0.00349
SLC35G5	0.00349
CORO2B	0.00363
VLDLR	0.00384
CFLAR-AS1	0.00384
RP11-345M22.1	0.00385
U39123	0.00403
DUSP16	0.0041
CDYL2	0.00411
ENGASE	0.00422

CYP11A1	0.00425
ASIC1	0.00444
GPR89C	0.00444
TMPO-AS1	0.00445
AX747643	0.00447
RND1	0.00447
AY190112	0.00464
ZBTB1	0.00467
LRIF1	0.00487
AK309215	0.00491
UBXN10-AS1	0.00501
CCDC177	0.00507
FAM186A	0.00513
SAMD5	0.00516
ETV7	0.00528
LOC100287534	0.00533
GPR34	0.00533
GSTA4	0.00539
ATAD2B	0.00542
AKAP11	0.0055
CASQ1	0.00556
EGR4	0.00562
TRPC3	0.00576
P4HA2-AS1	0.00576
AF387757	0.00592
TM4SF18	0.00599
PLN	0.00607
SOCS1	0.00608
BC034612	0.00614
ADM5	0.00616
PMCH	0.00628
TTTY16	0.00629
GIPR	0.0063
CSK	0.00635
SMARCA5-AS1	0.00652
ARC	0.00667
MIR4651	0.00669
SNCB	0.00669
FAM84A	0.00674
LRRC45	0.00674
RP11-432I5.1	0.00675

LENG1	0.0068
LINC00858	0.00682
GLRX	0.00682
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YY1	0.00707
AX747832	0.00727
ERMN	0.00729
GNB1L	0.00733
AQP7P1	0.00739
AF279783	0.0074
TNRC6B	0.00757
LMF2	0.00773
MAFA	0.00774
MFSD6	0.00779
IL4	0.00782
TRIM39	0.0079
LOC100287632	0.00796
BZRAP1	0.00803
MGAT5	0.00806
RAB3A	0.00815
PHKA2-AS1	0.00818
FGFR1OP2	0.00822
ZMAT2	0.00855
RNU6-69P	0.00857
CXorf65	0.00867
TCRBV18S1	0.00868
BC016831	0.00869
SLC7A4	0.00871
CYSLTR1	0.00872
EHMT1	0.00878
KAT6B	0.0089
TIGIT	0.00902
C20orf197	0.00905
CACNA1D	0.00905
FAM222A	0.00927
FAM50A	0.0093
UBL3	0.00936
AX748049	0.00939
DHH	0.00939
TAF9B	0.00943

CMTR1	0.00944
GC	0.00948
FOXI2	0.00949
ZNF727P	0.00957
F10	0.00973
SIRT6	0.0098
POLG	0.00982
MOSPD1	0.00987
CPLX2	0.00988
SERF1B	0.00989
GQ502877	0.00991
TCRBV20S1A1N2	0.00993
DBNL	0.0102
INVS	0.0102
CBX6	0.0103
TMEM160	0.0104
C10orf128	0.0104
SLC35F2	0.0104
LRRC37A5P	0.0104
TANK	0.0105
PET112	0.0105
ZC2HC1A	0.0105
FOLR2	0.0106
MARCH9	0.0106
ARL2	0.0106
GABPB1-AS1	0.0107
AVL9	0.0107
TARSL2	0.0108
FLI1	0.0108
TAAR2	0.0109
OR5B2	0.0109
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GDNF-AS1	0.0109
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IGCH	0.0109
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CBR3	0.0125
PGAP1	0.0126
MGARP	0.0126
FAM78B	0.0126
RORA	0.0127
TM6SF2	0.0128
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ACSL4	0.0131
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CHPF2	0.0131
SEC31B	0.0133
GPR152	0.0133
Ig+kappa	0.0134
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MARCH1	0.0137
STK39	0.0137
MCF2	0.0138
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ANKUB1	0.014
BCL7C	0.0141
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GRM5-AS1	0.0142
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CDKN1B	0.0142
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U80770	0.0143
MORC2-AS1	0.0144
APITD1-CORT	0.0144
LOC646214	0.0144
SETSIP	0.0145
ENTPD4	0.0146
NOX4	0.0147
AK128525	0.0147
CT45A2	0.0147
F2	0.0147
IRF4	0.0148
ELOVL2	0.0148
AK299452	0.0148
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BC041646	0.015
GALR2	0.015
LOC100130238	0.0152
ARHGEF25	0.0152
FSTL4	0.0153
SARNP	0.0155
FOXN3-AS2	0.0156
GCM2	0.0157
TNNI2	0.0158
HPN-AS1	0.0158
OR1A1	0.0158
CALN1	0.0159
HVCN1	0.0159

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USP8	0.0161
SKINTL	0.0161
RP5-1033H22.2	0.0161
C20orf78	0.0161
LOC400940	0.0161
GLYATL3	0.0161
ASB2	0.0162
LPIN1	0.0163
USP51	0.0163
STAG1	0.0163
MDFI	0.0164
AC093627.10	0.0164
MIR761	0.0164
KCNK5	0.0164
SORBS3	0.0165
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SCARNA17	0.0165
FAM181A	0.0165
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MIR3124	0.0166
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BC041947	0.0167
CCL17	0.017
BC037384	0.017
OR4S2	0.0171
SHANK1	0.0171
SMIM2-IT1	0.0171
COL26A1	0.0171
SSX9	0.0171
LEMD2	0.0172
RP3-377D14.1-001	0.0174
MIR6750	0.0174
NT5C1A	0.0174
BC050343	0.0175

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KRT10	0.0175
SRSF11	0.0176
DMRTC1B	0.0176
DIRC3	0.0177
CLTB	0.0177
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PPM1G	0.0177
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AY927512	0.0178
AK302306	0.0178
ZBTB9	0.0178
LINC00304	0.0179
AK294825	0.018
MISP	0.0181
FKBP4	0.0181
IQCF1	0.0182
PRELID1	0.0182
LCN10	0.0182
DNAJA4	0.0183
ZNF217	0.0183
RORB	0.0184
CCDC89	0.0186
NUTM2A-AS1	0.0186
BC034416	0.0186
TANGO6	0.0186
LMAN2	0.0186
TIAM2	0.0187
NSUN2	0.0187
PLB1	0.0188
GIPC1	0.0189
MRPL41	0.0189
ZCCHC2	0.019
WASH3P	0.019
PNLDC1	0.0192
NUDT3	0.0192
NGFR	0.0192
PPARG	0.0192
PGGT1B	0.0192
RGS2	0.0193
CARKD	0.0193

FAM71D	0.0194
DL491012	0.0195
SNX25	0.0196
RNU4ATAC	0.0198
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PDP1	0.0201
SSSCA1-AS1	0.0201
ZBTB22	0.0202
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BRD1	0.0202
EPX	0.0203
FANCD2	0.0204
ADORA1	0.0206
X07060	0.0207
GIMAP6	0.0209
MIR548T	0.0209
P4HA2	0.021
RBMS1	0.021
PLA2G15	0.0211
C1orf173	0.0211
ZNF17	0.0211
SNTG2	0.0212
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OR4N2	0.0213
IPO5	0.0213
MANSC4	0.0214
MIR7848	0.0214
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ACAD11	0.0216
CREB3L3	0.0216
RP11-300J18.1	0.0216
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DMRTC1	0.0217
SERP2	0.0218
HSPA7	0.0219
ERICH1-AS1	0.022
GTF3C2	0.022
NAGLU	0.022
ARID4B	0.0222
SDF4	0.0222
MRPS6	0.0222

PPCDC	0.0222
C10orf76	0.0224
MYADM	0.0224
BCL2L11	0.0224
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TTC31	0.0227
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HEXDC	0.0227
BRF1	0.0227
E10222	0.0228
EVI2B	0.0228
BTAF1	0.0228
TMEM185A	0.0228
C14orf164	0.0229
SEC22C	0.0229
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CD79A	0.0229
PTPRD	0.023
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GIMAP2	0.0231
C9orf142	0.0231
C2orf81	0.0232
HIC1	0.0232
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PSPH	0.0241
GDPGP1	0.0241
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AB231702	0.0243
GSG2	0.0244
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DUSP4	0.0246
HS3ST1	0.0246
CDCP2	0.0247
RASSF5	0.0247
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AK097437	0.0249
EHBP1L1	0.0251
ABCC9	0.0251
CLYBL-AS2	0.0251
TPT1-AS1	0.0252
SMG1	0.0252
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ABCD2	0.0253
SACS	0.0253
ACLY	0.0253
MIR3140	0.0254
RNVU1-3	0.0254
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FAM195A	0.0254
GGT2	0.0255
ICOS	0.0257
DNAJC17	0.0257
RNU6-63P	0.0258
CIDEB	0.0259
CDR2	0.0259
DQ573434	0.0259
GGT6	0.026
METTL4	0.0261
DQ589229	0.0262
MIR320D1	0.0262
PPP1CC	0.0263
THEGL	0.0263
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SALL2	0.0263
PPIAL4F	0.0264
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CCDC81	0.0266
SCNM1	0.0266
OIP5-AS1	0.0267

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CR936711	0.0267
ABCC8	0.0268
AK024119	0.0268
ASNA1	0.0268
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CLDND1	0.0272
RNA28S5	0.0273
AJ606316	0.0273
SLC24A4	0.0274
TTTY6	0.0275
AB306073	0.0275
PHLDA2	0.0276
CMTM2	0.0276
AK124930	0.0277
GPR65	0.0278
NCOR1P1	0.0278
TBC1D10C	0.0279
DQ586658	0.0279
MRPL53	0.028
YIPF1	0.028
ARID1A	0.0281
DEFB132	0.0281
JUN	0.0281
BC094860	0.0282
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PLAT	0.0283
GTF2A1L	0.0283
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HAX1	0.0284
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HSF5	0.0287
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VKORC1L1	0.0288
HLF	0.0288

IL10RA	0.0288
DUSP2	0.0288
SYCP1	0.0289
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BX248253	0.029
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SEPHS2	0.0292
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EVA1A	0.0293
IZUMO4	0.0294
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PRB1	0.0298
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AK130329	0.0298
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HSF2BP	0.03
DOK4	0.0302
KRBA2	0.0304
FGF13-AS1	0.0305
ASAH2	0.0305
HSF4	0.0306
AK093356	0.0307
SCARNA5	0.0308
AB305671	0.0308
CYB5R4	0.0309
PAPD7	0.0309
OFD1	0.031
HOXD8	0.031
MIR590	0.031
TNFRSF10D	0.0311
KRT2	0.0311
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LOC115110	0.0312
CYB561	0.0312
RNU4-2	0.0312
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BC043356	0.0313
ADORA2B	0.0314
SP3	0.0314

UCHL1-AS1	0.0315
LINC00552	0.0316
MXD4	0.0317
S1PR4	0.0317
PAF1	0.0317
TLR10	0.0318
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ATP6V0E2	0.0319
TAF10	0.0319
GRK6	0.032
HDDC3	0.0322
WWC1	0.0323
TCR+BV9	0.0324
MIDN	0.0324
ADCY9	0.0324
CR627206	0.0325
AF327297	0.0326
PDLIM2	0.0326
PTMS	0.0327
LOC100130354	0.0327
MLANA	0.0328
PWARSN	0.0329
SERP1	0.0331
SLC5A3	0.0335
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EIF4B	0.0335
KIR2DL4	0.0336
ACTR1B	0.0337
C4BPA	0.0337
NDUFS6	0.0337
AK124197	0.0338
ORM2	0.0339
ZNF214	0.034
CHD1	0.034
LMO4	0.034
WASH1	0.0342
CDKL4	0.0342
EME2	0.0343
FOXN3-AS1	0.0344
GIT1	0.0345
CD82	0.0346

IFT46	0.0346
MFN1	0.0346
PTGER3	0.0346
BC032415	0.0346
SNX18	0.0347
C19orf24	0.0348
ARL17A	0.0349
TBC1D25	0.0351
NDNF	0.0352
B3GAT1	0.0352
ESRP2	0.0354
AK126744	0.0355
LOC284454	0.0356
DCAF8L2	0.0357
PPP2R5C	0.0358
KIF22	0.0358
BX537783	0.0359
ANKRD9	0.036
FAM149A	0.0362
HADH	0.0363
C2orf74	0.0364
C21orf2	0.0364
TCRBV17S1A1T	0.0364
FSHR	0.0364
AIP	0.0364
RTN2	0.0365
C11orf80	0.0366
CMTM8	0.0366
PWWP2B	0.0366
MIR4741	0.0366
UBN1	0.0367
SEPT9	0.0367
EFHC1	0.0367
ULK3	0.0367
AK302451	0.0369
C17orf107	0.037
PTPN13	0.0371
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LOC100287704	0.0371
BC131596	0.0371

LOC100093631	0.0373
ZNF667	0.0374
REXO1	0.0374
MBD1	0.0375
CCDC78	0.0375
AK055364	0.0376
NT5C2	0.0376
SOWAHD	0.0377
ATAD3C	0.0377
GFER	0.0377
LAMP1	0.0378
SIRT4	0.0381
PLCB2	0.0382
ACAA1	0.0384
FAM181A-AS1	0.0384
NUDC	0.0385
OSM	0.0385
LINC00601	0.0386
GABRG2	0.0386
CYP2E1	0.0386
SPDYE3	0.0386
PRC1-AS1	0.0387
DNTT	0.0387
MSL3	0.0387
ZNF429	0.0388
ASTN2	0.0388
ZNF282	0.039
ADAM5	0.039
CASP1	0.0391
SCAMP1	0.0391
HMHB1	0.0392
ACBD3	0.0392
KLRF1	0.0394
MRPL1	0.0394
AC007038.7	0.0394
EFCAB14	0.0394
CR627148	0.0394
LOC100288778	0.0398
AK307061	0.0398
KIAA1549	0.0399
MROH7	0.0399

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HSPE1-MOB4	0.0401
SLCO2A1	0.0401
PPDPF	0.0402
GPBAR1	0.0402
GULP1	0.0402
TMEM14E	0.0403
PRR22	0.0404
SCD5	0.0404
HSPB9	0.0404
AK056623	0.0404
NPIPB3	0.0405
ASCC3	0.0405
C12orf5	0.0407
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LINC00161	0.0411
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CHODL	0.0414
CYTIP	0.0415
SAMD9L	0.0418
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RALGPS2	0.0419
EDN3	0.042
SMAGP	0.042
INSL3	0.0421
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MLLT1	0.0421
OR4F17	0.0423
BC067230	0.0424
NR4A2	0.0424
RPL41	0.0425
TMEM196	0.0427
hADV29S1	0.0428
TRIM52-AS1	0.0428
BC036830	0.0429
GRHL3	0.0431

LOC339166	0.0431
TSPAN32	0.0431
MMAB	0.0431
SYT5	0.0433
EIF4ENIF1	0.0434
GCKR	0.0435
REXO4	0.0435
TPTE2P1	0.0436
TMEM41B	0.0439
FAM109A	0.0439
SAMSN1	0.0441
ANKRD32	0.0442
CBLN2	0.0443
PKD2L1	0.0443
SEPT3	0.0443
SLC2A4RG	0.0444
MGC57346	0.0445
TRBV4-2	0.0445
AK126852	0.0445
MIR548AM	0.0446
SNORA37	0.0446
RRAS	0.0448
LOC101927697	0.0448
FBXL15	0.045
FAM197Y2	0.0451
LINC00476	0.0453
TLR9	0.0453
UBALD2	0.0453
ASXL2	0.0456
LOC644189	0.0456
IL18R1	0.0456
BAGE3	0.0457
MYO1E	0.0457
VMP1	0.0457
TMEM8A	0.0458
GTF2F1	0.0458
SMC3	0.0458
TRIM54	0.0459
pp8961	0.0459
SPINK4	0.0459
KCNC3	0.0459

CHDH	0.046
BC110795	0.0461
P2RY10	0.0461
HP	0.0463
BMP8B	0.0463
CEACAM7	0.0464
CAB39	0.0464
NUDT16P1	0.0465
NPDC1	0.0465
UTRN	0.0465
SLC51B	0.0466
ADAMTS7P1	0.0466
PPIG	0.0468
CYCS	0.047
RFWD3	0.0471
CITED2	0.0472
SCARA3	0.0473
ZNF773	0.0473
IL6R	0.0473
TMEM69	0.0474
PDE4C	0.0475
GLT8D2	0.0475
MIR548X2	0.0477
PELP1	0.0478
BC043293	0.0479
ZAK	0.0479
AF086102	0.048
SLC38A9	0.048
MED24	0.048
SGOL1-AS1	0.0481
IFI16	0.0482
C2CD4D	0.0482
AC113607.2	0.0484
SLC8A1-AS1	0.0485
RPS6KA5	0.0486
UBXN2B	0.0486
ABCD1	0.0487
USP33	0.0488
RP5-1159O4.2	0.0488
R3HDM4	0.0489
LPPR3	0.0491

TAS2R4	0.0493
ZNF567	0.0495
SPATA3-AS1	0.0495
ETAA1	0.0496
ARHGEF15	0.0496
PAAF1	0.0496
HSPA1L	0.0497
MPST	0.0497
SCO2	0.0498
CDCA7L	0.0499

Supplemental Materials and Methods

Patient inclusion. With the overall goal of targeting normal controls and active EoE subjects, biopsies and blood samples were acquired at the Allergy and Gastroenterology outpatient clinics (Cincinnati Children's Hospital Medical Center [CCHMC]) systemically from patients who were having an endoscopy for EoE or related symptoms. EoE was defined by a histological finding of ≥ 15 eosinophils per microscopic high-power field (HPF) with clinical symptoms and a failed proton pump inhibitor (PPI) trial. EoE remission (inactive EoE control) was defined as any patient (with EoE history) whose tissue eosinophil count was < 15 eosinophils/HPF. Normal controls were defined as patients without history of EoE and a negative endoscopy with 0 eosinophils/HPF. The normal control were those patients with gastrointestinal symptoms without EoE history and were found to have a completely negative endoscopy and biopsy histology.

Surface phenotype FACS analyses. The pellet was carefully re-suspended in 50-100 µL FACS buffer (0.5% BSA, 0.1%NaN3 in PBS). FACS staining was performed following the manufacturer's suggested protocol. The cell suspension was stained on ice for 30 minutes in the dark, washed by ice-cold PBS once, reconstituted in 80-100 µL FACS buffer, and kept on ice before the immediate FACS analysis. Five-color FACS analysis was performed with a FACS CANTO III (Becton, Dickinson and Company) equipped with 405-nm, 488-nm, and 633-nm excitation lasers. The FACS data were analyzed by the FACS Diva software (Becton, Dickinson and Company) and FlowJo software to enumerate and phenotype each cell population of interest.

Bulk RNA-seq on CD3-sorted blood and tissue lymphocytes. Single-cell suspensions were made from freshly obtained biopsies as described above. Autologous circulating blood samples (collected in heparin tubes) were processed for PBMC with ficoll sedimentation. Blood and tissue samples were stained for CD3 (HIT3a)-AF647, CD45 (2D1)-APC-H7, and Zombie Violet viability dyes and subjected to a 3 color FACS sorting by a MoFlo XDP machine (Beckman Coulter) under BSL2 conditions at the Research Flow Cytometry Core of CCHMC. Blood and tissue T cell events were logically defined as $FSC_{low}SSC_{low}CD45^{+}CD3^{+}$live singlet events. T cells were sorted into RPMI1640 supplemented with 10% FCS to confirm the presence of a visible pellet before lysing for RNA extraction (Qiagen #74104 RNeasy Mini Kit). The initial cDNA amplification step for all samples was performed at CCHMC RNA Expression Core with the NuGEN Ovation RNA-Seq System v2 Assay, which contains both random hexamers and the Oligo dT primer. The Nextera XT DNA Sample Preparation Kit (Illumina) was used to create the cDNA libraries, which were subsequently processed by the CCHMC DNA Core for RNA-seq at 30M read depth, 75 bp x 2 pair-ended NGS by Illumina's HiSeq 2500 machine. Raw reads were aligned to hg19 annotation (GRCh37/hg19) and the subsequent quantification and analysis were performed using the Strand NGS software (Agilent Inc.).

scRNA-seq platform (C1 Fluidigm). Single-cell suspensions were generated from biopsies, and FACS staining for T cells were performed the same as described above. Tissue T cells, defined as $FSC^{low}SSC_{l}^{ow}CD45^{+}CD3^{+}$ live singlet events, were sorted by MoFlo X machine. Three biopsies collected from the distal esophagus typically yielded ~2,500-10,000 T cells, which were subsequently adjusted to 300 cells/µL and loaded onto the Fluidigm® C1™ 5-10–µm chip designed to capture small-diameter leukocytes such as lymphocytes. Fluidigm® C1™ capture was robotically performed at the CCHMC Gene Expression Core, and all T cells loaded on the micro-chamber chip were manually examined with a dissecting microscope to ensure single-cell capture of live events of the expected size without debris contamination. Multiple-cell capture, dead/late apoptotic events, clogged chamber, debris/empty chambers were removed from the final analysis by expunging their chamber ID from the final analysis. The overall capture rate during the C1 project averaged around 70% (single-cell capture with satisfactory cDNA yield). Single-cell reverse transcription and cDNA libraries were robotically generated with the SMARTer® Ultra® Low RNA Kit for the Fluidigm® C1™ System (CloneTech) designed to enrich in poly-A transcript without any reading bias regarding 5' or 3' ends. Each single cell was assigned a unique barcode for a series of pulled NGS targeting at 2M read depth per cell in a 75-bp x2 pair-ended fashion. Raw reads were aligned to hg19 annotation. The TCR sequences were extracted from the same library on which the rest of the analyses relied. The entire NGS data generated during the study will be available in a public repository upon publication.

Single-cell RNA sequencing quality control. All NGS datasets discussed herein were sequenced by Illumina HiSeq 2500 system. For C1 Fluidigm single-cell system, 2M pair-ended reads (4M both directions) is the targeted read depth. In reality, we obtained 1.8M ± 0.5M (1SD) reads per cell on average. During the C1 acquisition period, we excluded doublets and erroneous/anomalous/suspicious events as below:

a. Under an inverted phase-contrast microscope, we manually evaluated each cell chamber, cell by cell, after C1 capture, for the presence of live or dead cells, levels of debris, and singlet selection. A consensus amongst two reviewers was needed to proceed to cDNA library generation for each particular cell. Our consensus rate was > 98% and QC dropout rate was about 30%. The C1 system uniquely offers the opportunity to do this as compared to other higher-throughput systems, part of the reason we chose it.

b. With 1 year of pilot experiments, we optimized the C1 system by using their small cell capture fluidic chip aiming to capture cells of 7-10 µM in diameter. We found that the small sized chip yielded the highest chamber capture rate and the lowest dropout rate.

c. Finally, we also used bioinformatic approaches to screen for anomalous RNA composition at single cell level. We only identified one cell suspected to be a doublet, demonstrating the success of our manual microscopic screening in a.

Murine and human CD4 T cell purification. Murine splenic CD4$^+$ T cells were purified using CD4$^+$ beads (Miltenyi Biotec) and activated with 5 μg/ml plate-bound anti-CD3 and 2 μg/ml soluble anti-CD28 in the presence of 10 μg/ml soluble anti–IFN-γ and/or anti-IL-4 (10 μg/ml). Each of these antibodies were obtained from BioXcell. CD4$^+$ T cells were additionally stimulated with C4 (0.4 mM) in the presence or absence of IL-4 (20 ng/ml) (PeproTech). Human T helper cells were isolated by Ficoll gradient centrifugation and then purified using CD4$^+$ T cell isolation kits (Miltenyi Biotec) from whole blood of healthy or EoE donors. Purified cells (95-98% purity) were activated with 5 μg/ml soluble anti-CD3, 2 μg/ml anti-CD28 (BioXcell), and 5 μg/ml anti–IFN-γ (BioLegend) in the presence or absence of anti–IL-4 (5 μg/ml, BioLegend), IL-4 (40 ng/ml) (PeproTech), or C4 (0.1 or 0.4 mM, SIGMA)

Murine and human Th2 cytokine intracellular FACS staining. For intracellular staining of cytokines, murine CD4$^+$ T cells and human PBMC were stimulated with 500 ng/ml PDBU (Sigma), 1 μM ionomycin (Sigma) and BrefeldinA (eBioscience) for 4 (murine) and 5.5 (human) hours. In this substudy, some normal controls (< 2 eosinophils/HPF) had a history of EoE. Harvested cells were fixed and permeabilized using Cytofix/Cytoperm kit (BD Biosciences) and stained with anti-murine or anti-human antibodies PE–anti–IL-5 (BioLegend), APC–anti–IL-4 (BioLegend), eFluor450–anti–IL-13 (eBioscience), BV711–anti–IFN-γ (BioLegend), BV510–anti-TNFα (BioLegend), and PerCP–anti–IL-2 (BioLegend). Human PBMC also were stained with FITC–anti-CD3, APC-Cy7–anti-CD4, and AF700–anti-CD8 (all from BioLegend).

For detailed clone and vender catalog information of the FACS antibodies used, see table below:

FACS Antibodies	Reactivity	Vender	Clone	Catalog #	Application
APC/Cy7-CD4	mouse	Biolegend	GK1.5	100414	ICS
FITC-CD44	mouse	Biolegend	IM7	103006	ICS
PE-IL-5	mouse	eBioscience	TRFK5	12-7052	ICS
APC-IL-4	mouse	eBioscience	11N11	17-7041	ICS
eFluor450-IL-13	mouse	eBioscience	eBio13A	48-7133	ICS
BV711-IFNγ	mouse	Biolegend	XMG1.2	505835	ICS
BV510-TNFα	mouse	Biolegend	MP6-XT22	506339	ICS
PerCP/Cy5.5-IL-2	mouse	Biolegend	JES6-5H4	503822	ICS
BV510-CD4	mouse	Biolegend	RM4-5	100553	live
AF700-CD44	mouse	Biolegend	IM7	103026	live
FITC-CD3	human	Biolegend	UCHT1	561806	ICS
APC/Cy7-CD4	human	Biolegend	SK3	344615	ICS
AF700-CD8a	human	Biolegend	HIT8a	300920	ICS
PE-IL-5	human	Biolegend	JES1-39D10	500903	ICS
APC-IL-4	human	Biolegend	MP4-25D2	500811	ICS
BV421-IL-13	human	BD Biosciences	JES10-5A2	563580	ICS
BV510-IFNγ	human	Biolegend	4S.B3	502543	ICS
BV711-TNFα	human	Biolegend	MAb11	502939	ICS
PerCP/Cy5.5-IL-2	human	Biolegend	MQ1-17H12	500321	ICS
PE/Dazzle594-IL-10	human	Biolegend	JES3-19F1	506811	ICS
PE-GATA3	human	eBioscience	TWAJ	12-9966	ICS
APC-FOXP3	human	eBioscience	PCH101	17-4776	ICS

ICS, intracellular cytokine staining; live, live surface staining.

Experimental asthma model. A bolus of 100 µg aspergillus fumigatus (GREER, Lenoir, NC) was dissolved in sterile saline and administered intranasally every other day into IL4-eGFP reporter mice (BALB/c, a gift from Dr. Yui-Hsi Wang) in the presence and absence of 1 mg sodium butyrate co-administrated; a total of five challenges were given, and the animals were sacrificed 48 hours after the last challenge. Lung tissue and bronchoalveolar lavage fluid (BALF) were subjected to Th2 cytokine analyses at mRNA and protein levels, respectively; and WBC differential count were derived from total BALF cells by conventional Cytospin and Diff-Quik histologic procedures. All rodent animal studies complied with Institutional Animal Care and Use Committee-approved protocols at CCHMC.

Tissue lymphocyte development path analysis by SPADE. Following the originator's recommended protocol(2, 3), SPADE (Spanning-tree Progression Analysis of Density-normalized Events) was employed to computationally identify T cell sub-populations from multidimensional intracellular cytokine FACS dataset obtained from the diseased tissue. ~50,000 CD3+ tissue T cells were pooled from 12 EoE individuals for the collective SPADE analysis on active tissue T cells. On the basis of the cytokines of interest, SPADE identifies development stage nodes and individual populations and then projects their expression pattern and level onto a tree, which was auto-annotated by the first-degree CD8 differential expression dividing the T cell population into CD8+ and CD4+ for further analyses.

Miscellaneous bioinformatic methodology.

The T8 clustering was determined by unsupervised PCA analyses summarized in Fig. S4A chart. Briefly, 1114 PCA variation-contributing genes (Table S6) were identified and cells were categorized on the differential expression of these genes, resulting in 8 major clusters. The best heat diagram focusing on the T1-T8 difference is exhibited in Fig. S4B.

Gene ontology and pathway analysis were carried out by the Fisher-test-based GENEONTOLOGY modules publicly available at www.pantherdb.org. In some cases, the functional node selection for radar map was supervised by biological relevance and significance. Clinical correlation was performed on per-subject basis. For any given gene, an average RPKM was first derived from all cells isolated from that patient, and then this value was correlated with the eosinophil count for that subject. Pearson correlation was used, and corresponding FDR-adjusted p values were used for screening.

Protein-protein interaction network was performed by STRING – Multiple-proteins modules as available at https://string-db.org. In the transcription factor analysis, the averaging heatmap was generated by taking an average value of the Log2 normalized values for any given T clusters, and relative heatmapping was adopted to apply the full color scale to each entity row.

The radar scanning map depicts specifically categorized activities of T1-T8 based on closeness to major relevant T cell functional modules, namely tissue Th2 properties, T_{REG} activity, T cell chemotaxis factors (migration), and CD8+ cytotoxic T cell activity. For each T cluster, the radar polar coordination axis delineates the logarithmic expression levels; the encircled area under the curve indicates the activity index in each activity module.

The 2D-TRACER analysis on Th2 cytokine source was performed by Graph Maker in 2D space (https://plot.ly/create/). CD4 and CD8A RPKMs were log-plotted on the x and y axis, respectively; and those Th2 cytokine–positive events were color-coded red with the diameter of the surrounding halo representing their specific cytokine expression RPKM values.

Statistical overview. The investigators were blinded to the group allocation during the experiment. Simple statistical analyses were performed using GraphPad Prism software. A 2-tailed student t-test was used for 2-group comparisons with regression analyses performed by the Pearson or Spearman method depending on parametric features. One-way or two-way ANOVA was employed to compare more than two groups with Bonferroni post-test used for specific group pair comparison. Statistical significance was defined by a 2-tailed p value < 0.05.

References:

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