Control of Treg differentiation by the transcription factors Thpok and LRF.

Supplementary data

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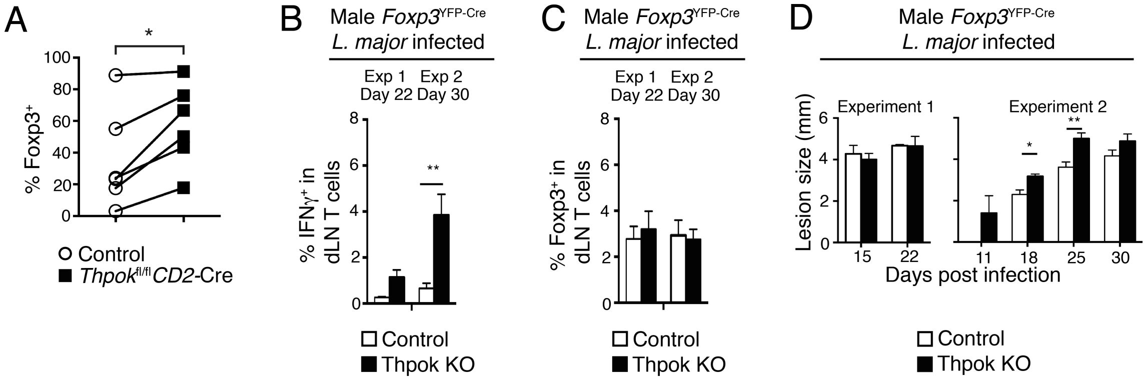

Figure S1. Thpok is dispensable for TGFβ induced Foxp3 expression and Treg response to *L. major*.

(A) Percentage of Foxp3$^+$ T cells among cells of the indicated genotypes after anti-CD3 activation and 4-day culture in the presence of IL-2 and TGFβ. Starting cell populations were sorted as CD4$^+$CD8$^-$ CD44^{lo}. Each symbol represents a distinct mouse; data is from 5 distinct experiments (*: $P<0.05$, paired t-test).

(B, C) Percentage of IFNγ$^+$ (B) or Foxp3$^+$ (C) among TCRβ$^+$ cells in draining lymph nodes (dLN) in control (open bars) or Thpok KO (closed bars) male mice infected with *L. major* (**: $P<0.01$).

(D) Time-course of progression of ear lesion size in mice analyzed in (B, C). Data (B-D) is from two independent experiments (shown on top of bar graphs in [A, B]), with at least five mice each group and analyzed either 22 or 30 days post-inoculation (*: $P<0.05$; **: $P<0.01$).

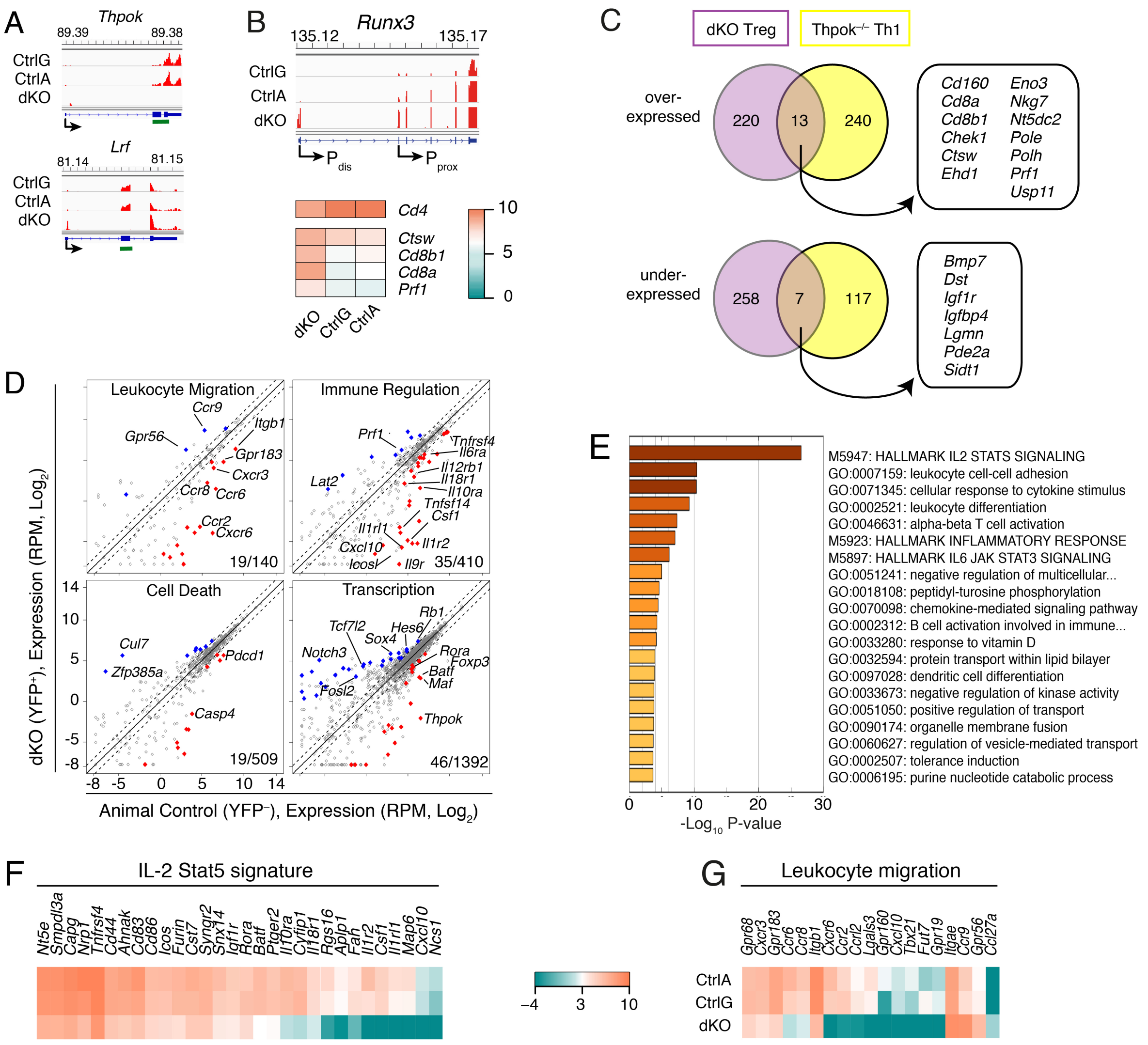

Figure S2. Transcriptome analyses of dKO Treg cells.

(A) Integrative Genomics Viewer (IGV) tracks show the distribution of RNAseq reads from dKO, genetic (CtrlG) and animal (CtrlA) control cells at *Thpok* and *Lrf* loci. Chromosomal coordinates are indicated at the top and genes schematically depicted at the bottom of each panel; thick and thin blue boxes depict coding and non-coding exonic sequences, respectively. Thick green bars underneath gene depiction indicate floxed segments in *Thpok*$^{\text{fl}}$ and *Lrf*$^{\text{fl}}$ alleles.

(B) (Top) IGV tracks, as in (A), show read distribution at the *Runx3* locus. $\mathrm{P_{dis}}$ and $\mathrm{P_{prox}}$ refer to the *Runx3* distal and proximal promoters, of which the only former gives rise to translated transcripts in T cells. (Bottom) Heat map shows expression of indicated genes in dKO, CtrlG and CtrlA cells (Log$_2$ values, color scale at right).

(C) (left) Venn diagram showing the overlap between the set of genes over-expressed (top) or under-expressed (bottom) in dKO relative to control Treg cells (purple, defined in Fig. 6A) or in *Thpok*$^{-/-}$ relative to control conventional Th1 effectors (17) (yellow). Boxes to the right list genes common to each pair of sets.

(D) Scatter plots show expression of genes from indicated Gene Ontology (GO) category (average of three samples, Log$_2$ RPM values) in animal control (CtrlA) vs. dKO Treg cells. Genes significantly ($P<0.05$) over-expressed or under-expressed in dKO cells relative to both animal and genetic controls are shown in blue or red, respectively. Dashed lines indicate 2-fold change. Relevant genes are indicated. Ratios in bottom right corner of each plot indicate the number of genes with significantly changed expression over the total number of expressed genes in each GO category.

(E) Graphical display from Metascape (metascape.org) analysis listing gene signatures with significant enrichment in the set of genes under-expressed in dKO relative to control cells. Scale at the bottom indicates P-value (-Log$_{10}$).

(F, G) Heat map shows the expression in dKO, CtrlG and CtrlA cells of genes from Metascape IL-2 Stat5 (F), or GO leukocyte migration (G) signatures and under-expressed in dKO Treg cells [Log$_2$ values, orange-green color scale between (F) and (G)].

Table S1: Over-expressed genes [1]

Gene	Sample									Fold Change (Log2)		P-Value	
	CtrlA1	CtrlA2	CtrlA3	CtrlG1	CtrlG2	CtrlG3	dKO1	dKO2	dKO3	dKO vs. CtrlA	dKO vs. CtrlG	dKO vs. CtrlA	dKO vs. CtrlG
Epb4.1l5	-7.77	-4.98	-7.77	-6.58	-3.58	-5.56	5.29	5.67	4.62	12.04	10.43	2.96E-05	6.82E-05
Nt5dc2	-6.99	-7.77	-6.99	-6.58	-7.77	2.25	4.16	4.28	5.25	11.81	8.62	2.95E-04	1.54E-03
Cpxm1	-7.77	-7.77	-6.99	-7.24	-7.77	-7.77	4.57	4.06	3.85	11.66	11.75	6.80E-06	6.37E-06
Tuft1	-5.54	-7.77	-7.77	-6.58	2.68	-5.56	4.18	3.72	4.58	11.18	7.27	3.19E-04	2.77E-03
Bai2	-7.77	-7.77	-6.99	-6.58	-7.77	-7.77	2.99	3.19	4.30	11.01	10.87	2.26E-05	2.51E-05
Rcor2	-7.77	-7.77	-7.77	-7.77	-0.60	-4.15	3.47	2.44	3.74	10.98	7.37	1.09E-04	1.25E-03
Notch3	-6.99	-2.23	-7.77	-5.71	-4.81	-6.81	5.81	6.04	3.47	10.76	10.88	2.78E-03	2.64E-03
Vangl2	-2.27	-4.98	-6.99	-1.97	3.45	-4.64	5.57	6.19	5.96	10.66	6.92	2.87E-04	1.67E-03
Gm11998	-7.77	-7.77	-7.77	-1.36	-5.73	-0.76	3.08	2.58	2.00	10.32	5.18	9.89E-05	5.25E-03
Zfp385a	-7.77	-4.98	-6.99	-7.24	-7.77	-7.77	3.61	3.20	4.24	10.25	11.27	3.56E-05	1.61E-05
Mcam	-6.99	-3.38	-6.99	-6.81	-5.73	-7.77	3.58	4.02	5.75	10.23	11.23	4.95E-04	2.97E-04
Cul7	-5.33	-1.98	-6.34	4.03	4.28	1.57	5.92	5.90	5.12	10.18	2.30	3.96E-04	7.72E-03
Arhgef25	-6.99	-7.77	-7.77	-7.77	-5.73	-7.77	2.93	2.29	1.85	9.86	9.44	5.03E-05	7.23E-05
Tubb3	-3.96	-7.77	-6.99	-7.24	-7.77	-7.77	3.61	2.94	3.87	9.71	11.06	6.18E-05	2.27E-05
Bag2	-5.73	-4.98	-7.77	-7.77	-5.73	-7.77	3.44	3.97	3.06	9.65	10.59	5.58E-05	2.88E-05
2700081O15	0.64	-7.77	-7.77	-6.81	-4.81	-7.77	5.09	4.68	4.08	9.60	11.07	5.24E-04	2.51E-04
Maml3	-1.00	-7.77	-6.99	-6.58	-5.73	-6.81	4.45	3.67	4.88	9.59	10.69	2.62E-04	1.44E-04
Chrm4	-7.77	-4.98	-7.77	-6.81	-7.77	-7.77	3.54	1.35	2.82	9.38	10.00	1.86E-04	1.12E-04
Tsga10	-7.77	-7.77	-7.77	0.31	-7.77	-7.77	1.24	3.28	0.13	9.34	6.65	1.70E-03	1.05E-02
Chek1	-7.77	-4.98	-7.77	-6.58	1.32	-0.39	0.79	2.82	3.40	9.20	4.23	1.89E-03	4.81E-02
Grin2d	-7.77	-7.77	-6.34	-7.24	-4.81	-7.77	-0.54	3.57	2.41	9.15	8.46	8.03E-04	1.37E-03
Kirrel	-7.77	-7.77	-7.77	-7.77	-7.77	-7.77	0.91	-0.22	3.42	9.14	9.14	3.98E-04	3.98E-04
Olfr755-ps1	-7.77	-7.77	-7.77	-7.77	-7.77	-7.77	0.89	1.14	1.74	9.03	9.03	1.06E-04	1.06E-04
Trnp1	-7.77	-7.77	-7.77	-7.24	-7.77	-7.77	2.25	-0.56	1.97	8.97	8.80	3.06E-04	3.56E-04
Dchs1	-7.77	-7.77	-7.77	-7.24	-7.77	-6.81	3.02	-4.01	4.33	8.84	8.34	9.38E-03	1.28E-02
Pln	-7.77	-4.98	-6.34	-6.81	2.01	-5.56	1.89	2.75	2.71	8.82	5.89	1.64E-03	1.10E-02
4930513N10	-7.77	-7.77	-2.35	-7.77	-5.73	-0.65	3.88	2.98	1.56	8.76	7.52	1.73E-03	3.65E-03
Sema4c	-6.99	-7.77	-7.77	-7.77	-4.81	-6.81	4.08	-1.32	0.99	8.72	7.67	1.88E-03	4.13E-03
Efcab5	-7.77	-7.77	-6.99	-7.77	-7.77	-2.35	1.30	-0.22	2.57	8.72	7.18	9.34E-04	3.09E-03
Arhgap33	-7.77	-7.77	-7.77	-7.77	-7.77	-5.56	3.17	-4.01	3.58	8.64	7.90	8.45E-03	1.36E-02
Ppic	-6.99	-4.98	-7.77	0.04	0.27	-5.56	1.00	2.85	2.04	8.56	3.72	1.25E-03	4.79E-02
Slc6a19	-6.99	-7.77	-7.77	-7.77	-5.73	-5.56	5.09	-3.41	1.60	8.55	7.39	9.57E-03	1.93E-02
Gm16225	-7.77	-7.77	-7.77	-7.77	-7.77	-7.77	0.42	1.02	0.78	8.51	8.51	1.92E-04	1.92E-04
6030442K20	-7.77	-4.98	-7.77	1.18	-7.77	-7.77	0.24	3.45	1.12	8.47	6.43	5.03E-03	1.73E-02
Nim1k	-7.77	-4.98	-6.34	-7.24	-5.73	-7.77	2.50	3.11	0.55	8.42	8.97	5.22E-04	3.42E-04
Hcn3	-7.77	-2.67	-7.77	1.74	-5.73	-6.81	3.21	1.87	1.97	8.40	5.95	3.20E-03	1.48E-02
Ptprf	-5.54	-2.23	-6.99	3.09	-7.77	-6.81	3.39	2.46	4.36	8.30	7.24	5.38E-03	9.34E-03
RP23-463E8.	-2.58	-4.98	-6.99	1.29	-3.40	-3.73	3.08	3.53	3.41	8.20	5.30	5.39E-04	4.57E-03
Maneal	-7.77	-7.77	-7.77	-7.77	-7.77	-5.56	3.28	-5.27	3.23	8.14	7.40	1.62E-02	2.54E-02
BC035044	-6.99	2.77	-6.99	0.04	-5.73	-7.77	5.70	3.02	4.67	8.12	8.91	1.30E-02	9.20E-03
Dscc1	-5.54	-4.98	-7.77	1.18	-4.81	-5.56	2.22	1.74	1.98	8.07	5.04	1.50E-03	1.42E-02
Pianp	-7.77	-7.77	1.61	-5.71	-7.77	-7.77	2.46	4.20	3.46	8.05	10.49	3.00E-03	7.52E-04
AA413626	-7.77	-7.77	-7.77	-7.77	-7.77	1.02	-0.37	-0.44	1.42	7.98	5.06	5.94E-03	4.46E-02
Crocc	-5.33	-4.98	-4.88	-2.88	-7.77	-6.81	1.01	3.83	3.68	7.94	8.71	1.55E-03	9.50E-04
Aebp1	-7.77	-7.77	-6.99	-6.81	-7.77	-7.77	-3.13	4.06	0.21	7.93	7.87	5.99E-03	6.26E-03
Gm12247	-7.77	-4.98	-7.77	-7.77	-7.77	-5.56	0.49	1.71	1.04	7.93	8.12	6.04E-04	5.06E-04
Ptprn	-7.77	-4.98	-6.99	0.82	-7.77	-7.77	-2.51	3.23	3.15	7.91	6.26	1.67E-02	3.98E-02
Gm15743	-7.77	-7.77	-7.77	-6.81	-7.77	-4.81	-0.54	1.05	-0.17	7.89	6.59	7.07E-04	2.38E-03
Efemp2	-7.77	1.40	-6.99	-7.24	-0.06	1.70	3.82	2.33	4.26	7.87	5.31	1.02E-02	3.85E-02
2810408A11	-3.40	-7.77	-7.77	-7.77	2.79	-7.77	0.74	1.22	2.60	7.85	5.75	1.13E-02	3.78E-02
2010320M18	-7.77	-7.77	-5.56	0.18	-7.77	-7.77	0.53	-0.37	2.26	7.84	5.94	5.15E-03	1.89E-02
Gm11738	-7.77	-7.77	-6.99	-7.24	-5.73	-7.77	2.60	3.64	-5.27	7.84	7.24	1.80E-02	2.60E-02
Xpnpep2	-7.77	-7.77	-7.77	-7.77	-7.77	-7.77	-0.95	1.24	-0.41	7.74	7.74	7.45E-04	7.45E-04
Egfl7	-1.45	-7.77	-7.77	-7.77	-7.77	-7.77	1.94	1.96	2.23	7.73	9.82	1.11E-03	2.26E-04
Celsr2	-6.99	-7.77	-1.67	-5.44	-3.40	-3.73	3.21	0.81	2.76	7.72	6.42	1.87E-03	4.68E-03
Kcna2	-5.33	-2.67	-5.56	2.32	-4.81	-7.77	3.17	3.62	2.54	7.63	6.54	3.66E-03	7.15E-03
Gm28557	-5.33	-4.98	-7.77	-1.60	-7.77	-5.56	1.68	0.58	2.51	7.61	6.57	1.92E-03	4.12E-03
Pla2g7	-7.77	-7.77	-7.77	-7.77	-7.77	-7.77	1.71	-3.41	1.00	7.51	7.51	3.56E-03	3.56E-03
Gm5148	-7.77	-7.77	-7.77	-7.24	-7.77	-7.77	-4.01	1.29	1.84	7.51	7.33	5.19E-03	5.98E-03
Gm16086	-7.77	-7.77	-7.77	-7.77	-7.77	-7.77	-0.41	-1.78	1.21	7.44	7.44	1.34E-03	1.34E-03
Dmwd	2.58	-7.77	-6.99	-6.81	-4.81	-5.56	3.33	2.77	3.41	7.25	8.88	4.93E-03	1.92E-03
Sugct	-4.68	-7.77	-7.77	-7.77	-1.22	-3.96	0.81	0.77	-0.07	7.25	4.81	3.82E-03	2.54E-02
Smim3	-6.99	-1.25	-7.77	1.58	-7.77	-5.56	1.76	0.34	3.62	7.21	5.83	1.44E-02	3.19E-02
Syngr1	1.09	-7.77	-6.99	-7.77	-4.05	-0.02	2.85	3.49	1.49	7.20	6.57	1.00E-02	1.45E-02
Homer2	-7.77	-7.77	-7.77	-7.77	-7.77	-7.77	-7.77	2.52	3.11	7.11	7.11	4.21E-02	4.21E-02
Sec1	-7.77	-7.77	-7.77	-7.77	-7.77	-7.77	2.99	-7.77	2.85	7.08	7.08	4.55E-02	4.55E-02
Ercc6l	0.50	-3.38	-6.99	-7.77	2.43	-5.56	3.57	3.43	4.29	7.06	7.37	7.70E-03	6.53E-03
Hic2	-4.68	-7.77	1.23	2.95	-5.73	-5.11	1.51	4.34	3.92	7.06	5.95	1.84E-02	3.25E-02
Pvrl2	-7.77	2.76	-7.77	1.67	-4.81	-7.77	2.30	2.56	3.49	7.01	6.43	2.02E-02	2.71E-02
Vmn2r96	1.54	-7.77	-7.77	-7.77	-7.77	-7.77	2.02	2.69	2.09	6.97	10.05	6.11E-03	8.01E-04
Ncald	-7.77	-4.98	1.58	-7.77	-7.77	-6.81	3.40	2.51	3.81	6.94	10.68	3.81E-03	3.71E-04
Slc23a1	-0.47	-7.77	-7.77	-7.24	-0.35	-7.77	0.41	1.80	2.40	6.90	6.65	1.27E-02	1.49E-02
Cacng4	-7.77	-7.77	-7.77	-7.77	-7.77	-7.77	-0.95	-0.09	-1.60	6.89	6.89	1.72E-03	1.72E-03

Gene	Sample									Fold Change (Log2)		P-Value	
	CtrlA1	CtrlA2	CtrlA3	CtrlG1	CtrlG2	CtrlG3	dKO1	dKO2	dKO3	dKO vs. CtrlA	dKO vs. CtrlG	dKO vs. CtrlA	dKO vs. CtrlG
Phf19	-2.32	0.94	-6.99	-7.77	-5.73	-2.17	4.26	4.56	3.49	6.88	9.34	3.12E-03	7.50E-04
AA386476	-7.77	-2.67	-7.77	-0.31	-7.77	-7.77	0.91	1.83	-0.36	6.86	6.09	1.16E-02	1.92E-02
Gipc3	-6.99	-7.77	-4.88	-7.77	-7.77	-6.81	0.36	-1.25	1.67	6.80	7.70	2.79E-03	1.24E-03
Rarb	-6.99	-7.77	-3.32	-7.24	0.70	-7.77	1.08	-0.47	1.62	6.77	5.49	1.38E-02	3.20E-02
Zfp30	-7.77	-7.77	0.74	-7.77	-4.81	-6.81	3.95	1.83	-0.33	6.74	8.25	1.58E-02	6.53E-03
Gm21992	-4.15	-7.77	-6.34	-3.25	-7.77	-7.77	-2.38	2.18	1.86	6.68	6.85	1.08E-02	9.59E-03
Pnoc	-7.77	-7.77	-7.77	-7.77	-7.77	-7.77	1.87	-7.77	2.62	6.65	6.65	4.55E-02	4.55E-02
Ccdc102a	-4.87	-1.98	2.03	-5.46	-7.77	-5.11	3.51	6.01	5.48	6.63	11.15	1.32E-02	1.86E-03
H19	-7.77	-4.98	-7.77	-7.77	-7.77	-7.77	2.79	-5.27	1.93	6.61	7.55	2.76E-02	1.48E-02
B3gnt9	-7.77	3.25	-7.77	-7.24	-5.73	2.24	1.14	2.45	3.77	6.53	6.06	3.96E-02	4.92E-02
Atad3aos	-3.71	-7.77	-7.77	-1.28	-7.77	-7.77	-1.63	0.44	1.40	6.51	5.70	1.35E-02	2.38E-02
5430402O13	0.24	-7.77	-6.99	-3.45	-7.77	-7.77	0.11	2.28	2.11	6.38	7.85	1.26E-02	4.85E-03
Gm16365	-7.77	-7.77	-7.77	-6.81	-7.77	-7.77	-2.38	0.53	-2.36	6.37	6.05	4.90E-03	6.63E-03
Pole	-5.54	-4.98	2.64	1.50	-4.05	-7.77	3.40	3.73	4.00	6.35	7.16	1.19E-02	7.46E-03
Ptpla	-4.50	-7.77	-7.77	-7.77	-7.77	-6.81	1.37	2.85	-5.27	6.34	7.11	3.16E-02	1.89E-02
Ccdc114	-7.77	3.38	-7.77	-7.24	2.11	-7.77	2.05	1.82	3.01	6.31	6.57	4.48E-02	3.94E-02
A930029G22	-7.77	-2.67	-7.77	-0.24	-7.77	-7.77	1.01	0.77	-1.32	6.21	5.42	2.28E-02	3.81E-02
Lrrn4	0.95	-4.98	0.01	1.29	-5.73	-4.81	4.38	4.92	5.14	6.20	7.92	4.01E-03	1.50E-03
Fam131a	-7.77	-7.77	-7.77	-7.77	-5.73	-7.77	-2.25	-4.01	1.46	6.17	5.49	1.24E-02	2.21E-02
3110070M22	-7.77	-7.77	-7.77	-7.77	-7.77	-7.77	-7.77	0.52	2.23	6.12	6.12	4.80E-02	4.80E-02
Lat2	1.68	-7.77	-7.77	-0.52	-7.77	-7.77	2.04	1.52	0.81	6.10	6.81	3.17E-02	2.11E-02
Zfp239	-1.56	-2.67	-2.12	-7.24	2.64	-5.11	3.60	3.44	4.85	6.08	7.17	8.44E-03	4.40E-03
Leprel4	-7.77	-7.77	-7.77	-7.77	-7.77	-7.77	1.02	-7.77	1.73	6.08	6.08	4.85E-02	4.85E-02
Clspn	-7.77	0.96	-6.99	-6.81	-2.16	-7.77	2.34	3.71	-1.60	6.06	7.06	4.09E-02	2.38E-02
Hist2h2be	-0.85	-7.77	0.01	-6.58	-0.25	-5.56	3.52	2.61	3.37	6.06	7.27	9.87E-03	4.60E-03
Arhgef40	-6.99	-4.98	-7.77	-6.81	-5.73	-6.81	1.93	-5.27	1.90	6.06	5.93	3.25E-02	3.51E-02
Kifc3	-6.99	-7.77	-6.34	-6.81	-7.77	-6.81	1.84	-4.01	-0.80	6.02	6.12	1.46E-02	1.34E-02
Spag1	-6.99	-3.38	-1.22	-7.77	0.82	-5.11	1.70	3.33	1.42	6.02	6.16	1.54E-02	1.40E-02
Rims3	1.80	-1.53	-3.25	3.17	-4.05	-5.11	4.67	5.34	4.76	5.94	6.94	5.44E-03	3.20E-03
Syde2	-6.99	-7.77	-7.77	-7.24	-7.77	-7.77	-1.35	-3.41	-0.33	5.81	5.90	8.15E-03	7.51E-03
Slc35f5	-4.64	-7.77	-6.99	-7.77	-7.77	-6.81	2.71	0.44	-5.27	5.75	6.73	3.87E-02	1.97E-02
Snora31	-4.98	-7.77	-7.77	-3.45	-7.77	-6.81	-0.85	-0.37	-2.17	5.71	4.89	1.30E-02	2.59E-02
5730480H06	-7.77	-4.98	-7.77	-7.77	-7.77	-3.12	0.23	0.31	-4.03	5.68	5.06	2.59E-02	4.06E-02
Srsf12	2.77	-7.77	0.89	1.09	-5.73	-6.81	3.66	4.91	4.03	5.65	8.04	2.65E-02	8.23E-03
Gm8817	-7.77	2.45	-7.77	-7.77	-7.77	-7.77	1.61	1.21	1.09	5.63	9.07	3.01E-02	3.25E-03
Mtap7d3	-7.77	-4.98	-6.99	-7.77	-7.77	-7.77	-5.33	1.38	1.00	5.62	6.82	3.42E-02	1.41E-02
Mdk	-7.77	-7.77	-3.25	-7.77	-7.77	-3.96	-1.67	1.31	-1.67	5.60	5.84	2.10E-02	1.75E-02
Hist4h4	-0.13	-7.77	-7.77	-7.77	-7.77	-7.77	-0.24	-0.13	1.27	5.54	8.07	2.16E-02	3.25E-03
Tubb2b	-4.64	4.51	0.79	-4.93	2.83	1.32	6.03	5.20	6.09	5.43	5.98	1.71E-02	1.46E-02
Gm12345	-6.99	-1.37	-5.11	-5.58	-7.77	-5.11	0.19	1.00	1.44	5.35	7.04	1.11E-02	2.83E-03
Adam12	-7.77	-3.38	-7.77	-5.46	-7.77	-7.77	-1.09	-0.15	-1.67	5.33	6.03	1.72E-02	9.39E-03
Gm26792	-6.99	-7.77	-6.34	-7.77	-7.77	-5.56	-4.01	-1.17	-0.10	5.28	5.28	1.93E-02	1.93E-02
Gm26908	-7.77	2.05	-7.77	-7.77	-5.73	-6.81	2.07	0.64	-0.37	5.24	7.54	4.79E-02	1.15E-02
3830403N18	0.79	-3.38	-7.77	0.21	-7.77	-6.81	1.41	2.41	1.34	5.19	6.53	3.97E-02	1.72E-02
Ap1m2	1.48	-7.77	1.79	-7.77	-4.81	1.21	3.30	3.87	3.63	5.16	7.40	3.68E-02	1.11E-02
Zfp683	-7.77	-4.98	0.06	-7.77	-7.77	-7.77	2.71	-0.69	0.48	5.04	8.59	3.14E-02	2.43E-03
Dnajc27	2.64	3.29	-5.56	1.72	1.44	2.44	5.50	5.02	5.03	5.02	3.32	1.05E-02	1.87E-02
Ccl27a	-0.69	-7.77	-4.00	-0.50	-7.77	-7.77	0.32	0.99	1.07	4.98	6.16	4.39E-02	2.00E-02
Sytl3	-1.00	-3.38	1.95	1.58	2.62	-7.77	3.91	4.01	4.36	4.94	5.25	2.83E-02	2.51E-02
A930002I21F	3.72	3.63	-4.29	2.18	3.18	0.16	5.86	6.02	5.97	4.91	4.07	8.15E-03	9.22E-03
Hdac9	-0.69	1.09	-1.36	-0.24	1.01	4.41	4.54	4.58	4.63	4.88	2.88	4.42E-03	1.41E-02
Tcf7l2	1.67	-4.98	2.05	1.75	-5.73	2.28	4.80	4.13	4.13	4.84	4.98	2.80E-02	2.63E-02
Slc30a4	-4.68	0.57	4.30	3.29	3.34	-5.11	5.04	5.34	4.35	4.80	4.35	4.35E-02	4.96E-02
Cxxc5	2.50	-3.38	1.06	1.75	2.27	0.52	3.69	5.31	5.17	4.76	3.21	1.07E-02	2.41E-02
Egfl8	-1.66	-0.74	-6.99	-0.27	-7.77	-7.77	1.23	1.60	1.90	4.70	6.86	4.27E-02	9.89E-03
Gm23346	-4.78	-7.77	-6.99	-7.77	-7.77	-7.77	-3.96	-0.41	-1.16	4.68	5.94	3.16E-02	1.02E-02
Tlr12	-4.98	4.11	2.77	0.48	-3.25	3.86	5.96	4.71	5.58	4.66	5.10	3.45E-02	2.75E-02
Slc16a5	1.52	0.81	2.44	3.41	4.38	2.02	6.07	5.60	6.93	4.63	2.88	3.45E-03	3.37E-03
Stx2	1.20	-1.67	2.96	3.90	2.07	2.87	5.70	5.58	4.61	4.51	2.38	4.89E-03	1.17E-02
Gtf2ird1	2.98	-1.81	0.19	-4.18	-3.58	3.35	4.77	4.11	5.53	4.40	6.28	1.67E-02	8.08E-03
Fosl2	-2.66	-3.38	2.25	1.81	0.15	-5.56	3.05	4.09	2.09	4.36	4.27	4.21E-02	4.48E-02
Col15a1	1.48	-1.42	-5.56	-5.58	-0.40	-3.73	3.00	2.47	1.75	4.24	5.62	3.44E-02	1.20E-02
Grifin	0.63	-4.98	2.18	-6.81	-4.81	0.07	3.02	3.91	3.27	4.19	7.27	3.30E-02	4.69E-03
Ctsl	-1.71	4.40	1.73	3.99	3.20	3.83	5.22	6.30	5.24	4.03	1.95	9.88E-03	1.76E-02
A630091E08	2.35	-2.23	3.21	1.68	2.22	2.32	4.95	4.49	5.66	3.99	2.95	8.75E-03	1.52E-02
Aldh7a1	3.08	5.31	-1.98	2.84	-2.31	3.74	5.50	6.34	6.09	3.78	4.65	2.55E-02	2.00E-02
Susd1	3.69	-2.23	1.96	1.97	-5.73	-6.81	5.01	3.92	5.35	3.69	8.28	3.60E-02	5.33E-03
Cd8a	5.08	4.23	5.67	3.72	4.76	4.66	8.47	8.61	8.48	3.56	4.13	6.30E-07	9.80E-07
Rcn3	3.20	0.56	1.88	2.79	-4.05	2.94	5.00	5.34	5.62	3.50	4.85	1.21E-02	7.33E-03
Polh	-2.58	0.88	3.59	-5.58	-4.81	-1.43	4.45	3.23	4.80	3.48	8.09	3.18E-02	2.26E-03
Ccr9	6.20	4.43	5.25	5.43	4.25	3.08	8.62	8.96	8.48	3.44	4.43	1.04E-05	2.15E-05
Ampd1	-0.22	2.92	2.17	1.75	-0.71	-5.56	5.20	4.46	5.27	3.29	6.46	1.36E-02	3.09E-03
Gpr56	3.05	2.71	3.41	2.87	4.51	2.89	6.01	6.92	5.98	3.27	2.84	1.01E-03	1.08E-03
Trpm1	3.68	3.93	3.93	5.23	5.02	4.97	7.20	6.81	6.98	3.14	1.92	7.30E-06	1.90E-05
Tfrc	5.36	-1.53	3.81	3.25	-2.82	4.26	5.71	5.35	5.46	3.13	4.05	4.84E-02	4.49E-02

Gene	Sample									Fold Change (Log2)		P-Value	
	CtrlA1	CtrlA2	CtrlA3	CtrlG1	CtrlG2	CtrlG3	dKO1	dKO2	dKO3	dKO vs. CtrlA	dKO vs. CtrlG	dKO vs. CtrlA	dKO vs. CtrlG
Tmem108	3.59	1.03	2.05	2.56	1.76	3.09	5.01	5.33	5.53	3.13	2.85	1.77E-03	2.07E-03
Mex3a	3.75	1.34	2.14	0.67	3.03	1.94	4.58	5.30	6.24	3.03	3.48	1.04E-02	9.89E-03
Sox4	3.55	1.85	3.36	4.18	4.15	4.83	6.01	5.85	5.81	3.02	1.51	3.63E-04	1.79E-03
Prdm11	2.70	4.21	-0.85	2.58	2.06	4.56	4.84	4.96	5.24	2.95	2.00	2.13E-02	3.37E-02
Igsf23	5.19	5.15	4.83	5.41	5.31	5.85	7.56	7.98	7.98	2.79	2.33	2.35E-06	3.45E-06
Cmah	5.96	2.78	5.54	6.42	5.73	6.58	7.53	7.77	7.02	2.78	1.22	1.39E-03	1.80E-02
Fam213a	0.94	0.95	3.42	-5.34	-2.16	4.03	4.17	5.00	4.33	2.75	5.69	4.22E-02	9.63E-03
Tspan6	2.74	3.43	2.18	2.18	3.41	-1.89	5.06	5.76	5.68	2.70	4.23	6.35E-03	3.92E-03
D17H6S53E	0.86	1.69	-0.23	-0.37	0.80	2.40	3.99	3.17	3.16	2.64	2.49	2.72E-02	3.14E-02
Art4	3.46	4.93	-0.47	3.33	1.74	3.07	4.50	5.91	5.45	2.60	2.63	3.90E-02	3.36E-02
Zfp580	0.43	3.00	2.19	2.75	1.46	2.78	4.17	4.91	4.23	2.53	2.15	1.34E-02	1.77E-02
Dcaf4	1.46	3.41	4.87	3.70	4.63	3.61	5.49	5.73	6.11	2.50	1.77	4.97E-03	8.75E-03
Gm19705	0.31	2.07	1.57	-7.24	-5.73	-2.58	2.85	3.92	4.50	2.43	8.96	3.92E-02	3.11E-04
Gadd45g	3.57	2.85	3.37	3.33	3.44	3.82	5.24	5.55	6.10	2.40	2.11	1.14E-03	1.44E-03
Slc43a1	1.35	3.50	3.74	-5.58	3.14	-5.11	5.28	5.53	5.03	2.37	7.76	2.00E-02	2.11E-03
Cd8b1	4.94	6.43	4.88	3.91	5.85	4.67	7.89	7.61	7.88	2.33	2.94	1.84E-04	1.11E-04
Cd160	4.65	3.29	5.39	3.00	4.69	1.89	6.73	6.58	6.75	2.29	3.43	8.31E-04	9.07E-04
Tm6sf1	3.84	3.41	3.73	1.54	4.13	-2.28	5.93	6.50	5.34	2.29	4.74	7.09E-03	5.32E-03
Plscr3	4.89	4.12	4.01	5.28	5.82	3.37	6.44	6.37	6.79	2.21	1.67	2.57E-03	6.12E-03
Zfp850	4.16	4.24	0.49	4.74	1.58	3.64	5.18	4.96	5.43	2.20	1.94	4.14E-02	4.33E-02
Colq	4.55	4.78	3.54	5.30	5.12	5.64	6.52	6.25	6.67	2.17	1.14	2.23E-04	2.99E-03
Trim32	3.87	3.91	2.78	4.83	3.56	4.60	5.85	6.07	5.03	2.12	1.35	5.89E-03	1.76E-02
Arhgap20	2.87	4.81	5.05	5.35	3.35	6.17	6.63	5.99	6.49	2.07	1.46	1.79E-02	3.42E-02
Ehd1	6.09	5.93	4.40	5.48	4.75	5.34	7.47	7.39	7.77	2.07	2.37	2.01E-04	1.20E-04
Usp11	3.63	5.83	3.98	3.25	5.34	5.25	6.38	6.39	7.01	2.05	1.95	6.76E-03	6.85E-03
Tspyl3	5.89	3.94	5.89	6.29	5.43	4.38	7.03	7.41	7.19	2.04	1.84	2.18E-03	3.26E-03
Prf1	3.99	4.44	4.29	5.25	4.55	3.53	5.65	6.40	6.76	2.03	1.83	2.84E-03	3.63E-03
Paox	2.34	1.98	2.46	0.52	1.42	1.91	4.10	4.63	4.01	2.00	2.97	1.38E-02	4.45E-03
Timeless	2.99	5.46	3.25	3.70	5.58	2.94	5.99	6.20	5.74	1.99	1.84	1.53E-02	1.71E-02
Zswim4	4.12	3.93	1.93	5.41	2.57	3.51	5.40	5.12	5.46	1.99	1.54	2.46E-02	3.72E-02
Lysmd1	2.37	2.62	2.03	2.34	3.02	1.33	4.17	4.49	3.94	1.85	1.95	2.10E-02	1.85E-02
Eno3	5.59	4.15	5.49	5.39	4.39	6.12	6.58	6.71	7.28	1.82	1.59	3.30E-03	5.20E-03
Hmgn2	6.39	6.44	5.70	6.25	6.71	6.01	8.05	8.07	7.89	1.82	1.66	1.46E-05	2.27E-05
Gm19585	3.50	3.36	4.32	3.99	3.82	4.60	5.04	5.59	5.93	1.81	1.41	4.15E-03	8.70E-03
Anxa4	3.62	3.73	4.53	4.75	3.65	3.31	6.18	5.47	5.66	1.80	1.86	3.31E-03	2.89E-03
Nkg7	6.25	6.25	5.88	5.56	6.75	5.82	7.83	7.94	7.97	1.79	1.85	3.58E-05	3.08E-05
Wdr41	5.29	4.10	3.60	5.73	4.80	4.61	6.13	6.36	5.75	1.78	1.04	3.94E-03	2.50E-02
H2-Oa	3.10	4.17	4.44	3.61	4.58	4.53	5.06	5.90	6.10	1.77	1.45	7.74E-03	1.31E-02
Ddx31	5.11	5.42	2.13	4.74	4.08	3.62	6.07	5.85	5.97	1.71	1.81	2.29E-02	1.89E-02
Prr3	4.32	4.76	2.82	4.28	3.96	3.42	5.60	6.29	5.12	1.69	1.78	1.41E-02	1.16E-02
Hes6	5.28	4.01	5.31	4.42	5.62	4.79	6.06	6.61	6.65	1.62	1.48	3.25E-03	4.91E-03
Phc1	3.14	3.39	3.86	3.65	0.42	3.02	4.89	4.51	5.87	1.61	2.78	3.64E-02	1.25E-02
Msh3	4.39	4.47	5.51	4.12	5.30	3.64	6.82	5.85	6.48	1.58	1.98	6.25E-03	3.29E-03
Ctsw	6.48	6.96	5.95	6.87	6.90	7.22	7.86	8.18	8.13	1.58	1.07	5.62E-05	4.85E-04
Acap3	3.79	3.25	3.63	3.50	-1.32	-1.48	4.88	5.47	4.87	1.54	4.87	2.29E-02	2.34E-03
Dda1	6.94	5.31	6.14	6.88	6.32	5.98	7.18	7.77	7.85	1.52	1.21	2.30E-03	6.23E-03
Mbip	2.92	4.27	4.85	3.83	3.21	5.16	5.65	5.46	5.53	1.50	1.52	1.95E-02	1.67E-02
Cox18	3.07	4.04	4.54	3.75	3.38	2.87	5.17	5.55	5.44	1.49	2.05	7.21E-03	2.74E-03
Prnp	3.88	5.67	5.33	4.98	5.71	4.56	6.21	6.42	6.82	1.48	1.38	7.41E-03	8.99E-03
Gsn	3.64	6.05	4.86	5.11	5.62	5.19	6.29	6.03	6.82	1.46	1.06	1.43E-02	3.69E-02
Agpat4	5.26	3.64	3.25	3.73	3.75	4.13	5.63	5.70	5.05	1.45	1.60	1.51E-02	1.18E-02
Ten1	4.43	4.80	5.04	5.06	5.35	4.98	5.96	6.07	6.54	1.43	1.05	1.27E-03	4.93E-03
Tab1	6.14	3.68	3.55	4.75	3.20	4.84	5.59	6.00	5.86	1.43	1.60	3.74E-02	2.80E-02
Rras2	6.28	7.09	4.93	6.24	6.13	6.41	7.61	7.34	7.69	1.41	1.29	4.41E-03	6.08E-03
Zfp707	4.71	4.12	3.01	3.69	4.94	3.61	5.67	4.98	5.42	1.41	1.23	2.28E-02	3.44E-02
Heatr2	5.23	5.15	3.61	4.59	5.52	3.76	6.20	6.11	5.86	1.38	1.40	1.57E-02	1.55E-02
Dcun1d2	6.15	5.29	3.72	5.41	3.50	5.90	6.12	6.41	6.64	1.35	1.51	4.53E-02	3.17E-02
Arl3	3.72	2.92	3.11	2.99	2.71	2.28	4.65	4.44	4.66	1.35	1.92	2.06E-02	7.64E-03
Gm20324	4.90	4.20	3.58	3.74	4.12	3.37	5.23	5.51	5.93	1.35	1.80	9.67E-03	3.96E-03
Zfp422	4.58	5.02	4.97	5.23	4.46	4.95	6.08	6.19	6.34	1.33	1.34	1.22E-03	1.10E-03
Acp5	7.78	7.01	7.95	7.68	7.80	7.72	8.94	8.74	8.99	1.33	1.15	5.29E-05	1.26E-04
Foxn2	5.42	4.34	4.49	6.16	3.36	4.66	6.11	6.10	5.94	1.33	1.37	3.30E-02	2.88E-02
Trak2	5.58	5.65	4.14	4.93	5.56	5.33	6.19	6.57	6.47	1.28	1.13	6.77E-03	1.08E-02
Traf4	5.60	5.40	5.50	5.35	5.28	5.59	6.59	7.25	6.40	1.26	1.35	1.84E-03	1.28E-03
Acss1	6.53	5.77	6.28	6.79	6.41	5.43	7.17	7.31	7.81	1.25	1.21	3.77E-03	4.48E-03
Slc25a4	7.84	7.94	8.15	7.53	7.89	8.12	9.10	9.19	9.36	1.24	1.37	7.54E-06	3.77E-06
Rb1	6.73	4.96	6.98	6.55	6.15	6.36	7.62	7.21	7.40	1.23	1.06	1.18E-02	2.16E-02
Lphn1	4.00	4.85	4.30	4.02	3.81	3.43	6.16	5.37	5.39	1.23	1.88	1.20E-02	2.81E-03
Sbk1	7.38	7.89	6.54	7.59	7.13	7.50	8.67	8.38	8.45	1.21	1.10	1.02E-03	1.54E-03
Mvd	4.56	5.29	5.09	5.24	5.79	3.57	5.93	6.44	6.22	1.20	1.30	2.47E-02	1.94E-02
Pigp	5.01	3.89	4.54	4.60	4.41	4.54	5.73	5.31	5.89	1.19	1.13	9.77E-03	1.23E-02
Ubxn7	5.20	5.45	4.10	4.13	4.36	3.89	5.52	6.69	6.05	1.17	1.97	2.25E-02	4.28E-03
Marcksl1	3.37	4.21	3.44	3.88	2.62	3.67	4.97	4.81	4.82	1.17	1.51	3.19E-02	1.37E-02
Npc1	5.57	4.41	3.88	5.02	3.92	4.95	5.62	5.90	5.69	1.14	1.14	2.62E-02	2.59E-02
Kctd5	4.82	5.34	5.30	4.79	4.63	4.97	5.83	6.27	6.81	1.14	1.52	6.95E-03	1.99E-03

Gene	Sample									Fold Change (Log2)		P-Value	
	CtrlA1	CtrlA2	CtrlA3	CtrlG1	CtrlG2	CtrlG3	dKO1	dKO2	dKO3	dKO vs. CtrlA	dKO vs. CtrlG	dKO vs. CtrlA	dKO vs. CtrlG
Tubb2a	5.48	5.59	5.65	5.16	5.07	4.95	6.60	6.15	7.41	1.14	1.66	9.53E-03	2.04E-03
Dmap1	4.44	4.79	3.40	4.10	3.89	4.34	5.25	5.33	5.52	1.14	1.27	1.91E-02	1.24E-02
Obfc1	3.89	5.09	3.76	4.76	3.56	3.87	5.17	5.19	5.83	1.11	1.35	3.98E-02	2.05E-02
Itgae	8.13	6.98	8.42	7.78	8.04	7.26	8.80	8.85	9.06	1.10	1.20	3.86E-03	2.65E-03
Mad2l1bp	4.09	4.85	5.21	5.17	3.95	5.47	5.88	5.78	5.84	1.10	1.01	2.65E-02	3.30E-02
Cnn3	6.23	6.21	5.86	6.31	6.11	5.99	6.82	7.42	7.32	1.09	1.06	1.03E-03	1.20E-03
Tmem60	4.60	4.87	4.26	5.15	4.23	3.46	5.36	5.52	6.14	1.09	1.40	2.86E-02	1.23E-02
Aagab	5.79	6.05	5.93	6.38	3.70	5.12	6.84	6.58	7.49	1.04	1.95	3.57E-02	3.90E-03
Cdc14b	4.68	5.14	4.23	2.88	-4.81	-3.83	1.61	3.22	2.83	-2.13	4.51	3.62E-02	3.38E-02
Trip10	3.35	4.44	3.04	-7.77	-7.77	-7.77	-4.79	4.36	-2.27	-4.51	6.91	2.71E-02	2.87E-02

[1] Table S1:Genes over-expressed in dKO vs. genetic (CtrlG) or animal (CtrlA) Tregs, as defined in Fig. 6A. Normalized expression (Log2 values) is given for each gene in each of the three independent replicates for each genotype. Log2 values of Fold change (FC) and p-values are given for indicated comparisons.

Table S2: Under-expressed genes [1]

Gene	Sample									Fold Change (Log2)		P-Value	
	CtrlA1	CtrlA2	CtrlA3	CtrlG1	CtrlG2	CtrlG3	dKO1	dKO2	dKO3	dKO vs. CtrlA	dKO vs. CtrlG	dKO vs. CtrlA	dKO vs. CtrlG
Il9r	3.53	4.36	3.99	3.24	3.86	1.92	-7.77	-7.77	-7.77	-11.76	-10.81	2.08E-05	5.40E-05
Fam160a1	5.13	4.28	5.78	3.70	1.21	2.63	-7.77	-7.77	-3.42	-11.36	-8.79	2.43E-04	2.43E-03
Il1r2	6.35	5.87	6.24	4.35	4.05	4.16	-6.38	-4.01	-5.27	-11.35	-9.39	9.17E-06	5.56E-05
Arc	3.75	4.16	4.70	3.78	4.91	3.36	-4.64	-7.77	-7.77	-10.94	-10.79	9.30E-05	1.07E-04
Map6	4.78	3.92	4.42	5.37	3.99	0.80	-7.77	-4.01	-7.77	-10.86	-9.94	1.50E-03	3.12E-03
Stxbp1	3.27	4.18	3.04	1.29	3.27	1.85	-6.38	-7.77	-7.77	-10.84	-9.48	4.22E-05	1.96E-04
Gcat	5.15	4.19	4.94	0.64	3.10	4.32	-7.77	-5.27	-5.27	-10.83	-8.79	2.39E-04	1.64E-03
Klrg1	6.04	5.73	4.83	1.83	3.94	5.47	-6.38	-5.27	-4.03	-10.75	-8.97	1.20E-03	4.61E-03
Ttn	3.08	3.73	4.06	4.24	5.32	4.83	-7.77	-5.27	-7.77	-10.57	-11.75	8.25E-05	2.84E-05
Gpr160	2.88	3.50	1.90	-6.81	-0.50	-0.45	-7.77	-7.77	-7.77	-10.56	-5.20	2.24E-04	4.96E-02
Ryk	4.01	3.72	1.88	-0.78	1.65	1.20	-6.38	-7.77	-7.77	-10.51	-8.01	1.27E-04	2.13E-03
Car5b	2.91	3.06	1.57	1.83	3.83	-4.81	-7.77	-7.77	-7.77	-10.30	-8.12	1.67E-03	1.26E-02
2810039B14	2.41	1.88	3.12	1.26	-5.73	1.60	-7.77	-7.77	-7.77	-10.22	-6.76	5.94E-04	1.92E-02
Cxcr6	5.81	6.38	6.59	4.56	6.30	4.85	-6.38	-2.58	-2.88	-10.21	-9.22	7.42E-04	1.60E-03
Ptpn5	4.61	3.13	0.80	3.36	4.15	4.23	-6.38	-7.77	-7.77	-10.13	-11.23	5.40E-04	1.89E-04
Pstpip2	1.67	2.64	2.64	0.52	2.79	1.89	-7.77	-7.77	-7.77	-10.11	-9.53	6.99E-05	1.40E-04
Il1rl1	4.55	3.37	4.86	3.37	3.43	3.20	-5.33	-7.77	-4.03	-9.93	-9.05	1.34E-04	3.34E-04
Lgmn	3.11	5.01	3.06	4.09	2.87	3.04	-7.77	-2.90	-7.77	-9.93	-9.46	4.77E-04	7.41E-04
Csf1	4.45	5.52	4.96	4.84	5.41	4.14	-7.77	-4.01	-2.76	-9.85	-9.66	3.11E-04	3.65E-04
Zpbp2	1.34	1.30	2.88	-7.77	2.79	1.01	-7.77	-7.77	-7.77	-9.61	-6.48	3.48E-03	4.97E-02
Lilrb4	3.15	2.86	2.00	1.66	2.49	2.69	-7.77	-7.77	-5.27	-9.60	-9.22	8.29E-05	1.32E-04
Cysltr2	2.53	2.48	0.14	2.51	2.37	-7.77	-7.77	-7.77	-7.77	-9.50	-6.85	5.87E-03	4.98E-02
Ddr1	3.88	4.11	1.01	2.42	3.21	2.80	-6.38	-5.27	-7.77	-9.50	-9.29	6.39E-04	7.86E-04
Scrn3	3.57	5.03	4.96	2.06	4.48	3.57	-1.39	-7.77	-5.27	-9.38	-8.23	1.07E-03	3.07E-03
Gdap10	4.67	4.22	3.47	4.15	3.57	-3.83	-6.38	-4.01	-5.27	-9.33	-6.57	3.74E-03	4.04E-02
Atcay	3.81	1.45	3.48	2.73	3.67	-5.11	-6.38	-7.77	-5.27	-9.32	-6.96	5.60E-03	4.09E-02
Tbx21	1.63	3.27	2.91	-2.10	1.21	2.69	-7.77	-7.77	-4.03	-9.16	-7.13	7.58E-04	6.95E-03
Crip2	2.02	3.04	2.23	2.00	3.30	2.07	-6.38	-5.27	-7.77	-8.92	-8.96	1.68E-04	1.60E-04
Axl	6.23	6.14	6.71	4.18	5.60	4.78	-5.33	3.16	-5.27	-8.81	-7.34	1.35E-03	4.77E-03
Ppm1j	2.79	5.19	5.13	4.17	4.03	3.44	-7.77	2.95	-7.77	-8.61	-8.07	7.65E-03	1.15E-02
Rnls	2.05	2.84	3.35	0.06	2.59	-0.15	-7.77	-7.77	-1.95	-8.59	-6.69	7.83E-04	7.05E-03
Zbtb7b	6.26	6.72	6.62	6.53	6.69	7.22	-1.45	-1.91	-2.76	-8.59	-8.85	1.55E-04	1.21E-04
Atxn1	4.27	4.69	1.35	2.67	4.65	2.13	-7.77	-2.24	-5.27	-8.55	-8.30	5.15E-03	6.50E-03
March3	4.90	4.15	3.74	2.30	2.60	3.90	-7.77	-7.77	3.09	-8.40	-7.07	3.46E-03	1.19E-02
Dcxr	3.07	3.87	3.72	1.31	2.02	2.34	-7.77	-5.27	-1.39	-8.38	-6.70	3.41E-04	2.80E-03
Ebi3	4.42	4.52	3.95	3.95	4.77	2.09	-6.38	2.09	-7.77	-8.31	-7.67	3.87E-03	6.91E-03
Gdpd5	4.56	5.26	4.33	3.95	2.64	4.88	-5.33	-7.77	2.96	-8.12	-7.15	4.56E-03	1.05E-02
Lgals3	3.82	5.01	3.47	1.78	5.15	3.41	-6.38	-0.09	-5.27	-8.04	-7.42	4.70E-03	8.35E-03
Atp5s	1.55	-0.60	2.26	0.17	3.99	0.36	-5.33	-7.77	-7.77	-7.99	-8.52	3.43E-03	1.99E-03
Gpr19	2.72	-2.67	3.33	1.76	2.67	2.92	-7.77	-5.27	-7.77	-7.98	-9.39	6.74E-03	1.65E-03
Ccr2	6.56	2.67	4.97	5.51	6.28	4.46	0.84	-7.77	-2.58	-7.81	-8.64	4.19E-02	2.65E-02
Cpe	-3.49	3.77	4.40	3.20	3.21	-1.22	-5.33	-5.27	-7.77	-7.79	-7.90	3.23E-02	2.93E-02
Irak3	4.60	-2.67	4.47	2.71	3.98	3.88	-5.33	-4.01	-7.77	-7.66	-9.25	2.97E-02	8.78E-03
Nr3c2	2.38	-3.38	0.88	-5.34	3.25	-0.05	-7.77	-7.77	-7.77	-7.66	-7.11	1.88E-02	3.03E-02
Tube1	2.78	-0.89	4.03	2.61	2.72	2.64	-6.38	-3.12	-7.77	-7.64	-8.42	5.34E-03	2.37E-03
Acot11	3.64	1.59	-3.17	3.13	3.88	4.08	-7.77	-7.77	-5.27	-7.61	-10.64	9.27E-03	4.58E-04
Tox2	4.76	3.82	5.08	3.84	3.50	1.89	2.75	-4.01	-7.77	-7.55	-6.12	4.69E-03	1.86E-02
Ly6d	2.48	3.07	1.14	0.99	2.57	0.22	-5.33	-2.68	-7.77	-7.51	-6.55	1.49E-03	4.89E-03
Cxcl10	2.22	2.28	1.50	2.87	0.40	1.80	-6.38	-7.77	-2.21	-7.46	-7.11	1.62E-03	2.45E-03
Sarm1	3.97	-2.67	1.82	1.71	2.05	2.13	-7.77	-4.01	-7.77	-7.46	-8.48	1.02E-02	3.76E-03
Klhl5	0.95	-1.32	3.27	3.20	3.78	4.14	-7.77	-4.01	-7.77	-7.44	-10.23	4.59E-03	2.22E-04
Pou6f1	3.31	5.16	4.10	3.45	4.64	3.34	3.68	-7.77	-5.27	-7.39	-6.99	9.18E-03	1.30E-02
A630023P12	3.90	3.88	3.80	3.43	3.43	1.66	2.57	-7.77	-5.27	-7.36	-6.37	3.77E-03	1.09E-02
Chn2	3.51	3.20	4.17	2.27	4.17	1.55	-6.38	-7.77	3.07	-7.30	-6.41	7.72E-03	1.89E-02
Tigit	4.86	4.70	5.25	3.54	4.55	1.92	-4.14	-1.53	-1.32	-7.25	-5.72	9.02E-04	5.58E-03
Tnfsf14	4.57	3.73	3.74	3.31	0.22	4.04	-3.18	-5.27	-1.26	-7.23	-5.68	2.50E-03	1.43E-02
Melk	0.78	3.23	2.12	2.30	3.07	3.88	-7.77	-7.77	0.31	-7.17	-8.16	6.89E-03	2.30E-03
Rhbdf2	-0.08	4.04	3.18	5.27	0.68	1.72	-5.33	-3.41	-5.27	-7.14	-7.16	1.61E-02	1.51E-02
Rph3al	3.06	2.44	3.05	3.54	2.49	1.72	-6.38	1.32	-7.77	-7.09	-6.85	4.50E-03	5.96E-03
Rgs16	4.21	4.46	5.23	3.66	3.35	4.17	-5.33	-5.27	3.27	-7.08	-6.15	3.29E-03	8.52E-03
RP23-392C14	2.26	3.25	-7.77	0.54	0.91	0.14	-7.77	-7.77	-7.77	-7.05	-8.31	4.36E-02	1.63E-02
Tmem191c	0.49	1.98	3.57	-0.07	3.57	2.25	-7.77	0.55	-7.77	-7.02	-6.95	1.38E-02	1.48E-02
Tnnt1	0.71	-2.67	-0.38	0.69	2.13	-2.77	-7.77	-7.77	-7.77	-6.96	-7.83	8.22E-03	3.30E-03
Chst2	5.99	5.69	5.03	5.12	4.33	1.84	2.00	-4.01	-1.98	-6.91	-5.14	6.37E-03	3.34E-02
Aplp1	4.29	3.71	2.27	3.31	2.59	3.46	2.61	-5.27	-7.77	-6.91	-6.59	7.84E-03	1.09E-02
Ncs1	1.39	2.15	0.77	-0.22	1.24	-1.04	-7.77	-0.83	-7.77	-6.90	-5.46	4.92E-03	2.41E-02
Fut7	4.21	1.51	-4.64	3.64	4.40	1.84	-7.77	-4.01	-7.77	-6.86	-9.86	4.41E-02	3.63E-03
Angptl2	4.88	4.39	4.07	0.94	3.84	3.41	0.87	-4.01	-4.03	-6.84	-5.17	2.20E-03	1.61E-02
Bivm	3.63	2.14	3.24	3.77	2.80	4.24	-7.77	4.08	-7.77	-6.76	-7.37	1.85E-02	1.05E-02
Bag3	0.28	4.47	4.71	4.50	3.45	3.59	-7.77	2.77	-5.27	-6.67	-7.24	3.32E-02	2.05E-02
Bcl7a	0.25	4.17	3.04	2.05	4.21	1.60	-7.77	-0.25	-4.03	-6.58	-6.68	1.59E-02	1.41E-02
Ddx43	-0.49	1.40	0.71	0.06	2.42	-1.28	-2.38	-7.77	-7.77	-6.55	-6.42	8.63E-03	9.93E-03
Ccrl2	4.89	2.27	2.45	4.08	4.43	2.88	3.26	-5.27	-7.77	-6.41	-7.10	2.23E-02	1.20E-02

Gene	Sample									Fold Change (Log2)		P-Value	
	CtrlA1	CtrlA2	CtrlA3	CtrlG1	CtrlG2	CtrlG3	dKO1	dKO2	dKO3	dKO vs. CtrlA	dKO vs. CtrlG	dKO vs. CtrlA	dKO vs. CtrlG
Tcrg-C4	2.69	2.44	3.01	0.83	1.82	1.82	2.02	-5.27	-7.77	-6.39	-5.18	7.29E-03	2.90E-02
Cebpa	-0.03	-3.38	-0.68	-0.64	1.07	0.06	-7.77	-7.77	-7.77	-6.39	-7.95	5.82E-03	9.27E-04
Ppap2a	2.80	3.49	-1.18	3.37	3.71	0.42	1.68	-7.77	-7.77	-6.37	-7.18	4.38E-02	2.19E-02
Plekhm3	3.80	-0.66	1.44	1.09	4.33	2.14	-6.38	-5.27	-3.12	-6.37	-7.50	1.59E-02	4.88E-03
Gm14005	-1.24	0.29	0.26	-4.18	-1.67	3.32	-4.14	-7.77	-7.77	-6.35	-5.71	2.12E-02	3.81E-02
E430018J23F	3.86	3.43	1.94	2.96	3.92	1.57	-6.38	-7.77	4.34	-6.35	-6.14	2.54E-02	3.11E-02
Ap4b1	5.20	5.23	3.36	5.02	3.61	4.99	1.79	-1.70	-5.27	-6.34	-6.24	1.20E-02	1.32E-02
Myo3b	3.39	5.68	3.15	3.31	5.26	2.09	-3.96	-5.27	2.71	-6.33	-5.80	2.83E-02	4.34E-02
Dst	1.89	1.28	1.17	1.73	1.33	1.56	1.15	-7.77	-7.77	-6.25	-6.35	1.24E-02	1.11E-02
Chil5	1.74	2.69	3.38	2.89	2.94	2.78	-0.41	-2.45	-7.77	-6.17	-6.42	4.79E-03	3.43E-03
St3gal6	2.25	2.82	4.26	2.94	4.98	4.46	-6.38	-5.27	2.58	-6.13	-7.18	2.10E-02	7.72E-03
Rasgef1b	2.90	1.89	4.49	3.17	4.76	0.95	-7.77	-4.01	2.77	-6.05	-6.03	3.54E-02	3.65E-02
Rab3a	-0.96	3.26	1.43	1.35	2.92	2.86	-4.79	-5.27	-4.03	-6.00	-7.08	8.79E-03	2.25E-03
Stx17	0.42	2.10	3.80	3.07	2.44	-0.28	-7.77	-5.27	1.41	-6.00	-5.63	2.56E-02	3.64E-02
Ell2	0.27	3.94	2.27	3.67	3.16	1.08	1.93	-7.77	-5.27	-5.96	-6.38	3.06E-02	1.99E-02
Hip1	-0.94	-4.98	0.46	-0.61	0.01	-0.53	-7.77	-7.77	-7.77	-5.93	-7.40	1.44E-02	3.05E-03
Acsl1	4.54	4.23	2.25	2.31	4.74	4.27	-0.66	1.70	-7.77	-5.92	-6.05	2.87E-02	2.55E-02
Gm13357	0.75	1.10	-0.35	-0.80	0.89	-0.58	-0.57	-7.77	-7.77	-5.89	-5.23	1.48E-02	2.99E-02
Gm16638	1.59	4.58	1.63	1.95	2.71	3.57	-1.23	0.00	-7.77	-5.68	-5.74	2.07E-02	1.90E-02
Actg2	4.75	3.70	3.58	3.29	5.02	4.05	3.01	-4.01	-4.03	-5.68	-5.85	1.14E-02	9.57E-03
Unc93b1	6.10	4.40	4.97	4.17	4.56	4.07	-4.14	3.02	-0.52	-5.62	-4.79	8.47E-03	2.11E-02
Carhsp1	5.21	5.03	5.77	5.78	5.22	5.18	1.49	3.07	-5.27	-5.56	-5.62	6.18E-03	5.75E-03
Zfp873	3.98	2.04	1.98	3.93	3.76	2.80	-7.77	-5.27	4.30	-5.53	-6.42	3.85E-02	1.64E-02
Lmna	4.40	4.18	3.81	3.07	3.56	2.99	2.23	-7.77	1.49	-5.51	-4.60	1.38E-02	3.73E-02
Mansc1	2.72	2.74	3.47	0.67	2.14	3.24	-0.71	-3.41	-3.42	-5.49	-4.53	3.20E-03	1.31E-02
Ildr1	2.96	3.46	1.87	2.35	3.75	4.57	-4.79	-7.77	4.63	-5.43	-6.21	4.86E-02	2.38E-02
Eea1	5.73	5.90	5.22	5.56	4.41	3.87	3.14	-0.09	-2.36	-5.42	-4.40	3.61E-03	1.32E-02
Pctp	3.64	3.66	4.31	2.78	5.35	2.16	-4.79	3.06	-2.88	-5.38	-5.03	2.35E-02	3.40E-02
1700028N14	-1.84	1.18	0.22	-0.78	-1.53	0.64	-7.77	-5.27	-3.42	-5.37	-4.91	1.57E-02	2.60E-02
Adap1	5.63	5.71	5.65	3.41	4.40	5.38	0.65	-4.01	4.39	-5.34	-4.07	7.55E-03	3.30E-02
Trav12d-1	-2.79	2.02	1.29	0.61	0.96	1.44	0.25	-7.77	-7.77	-5.34	-6.11	4.82E-02	2.29E-02
1700021K19	3.38	4.89	5.56	4.11	3.91	4.71	-5.33	4.55	-1.32	-5.30	-4.89	2.60E-02	3.83E-02
Casp4	4.90	2.68	3.96	3.49	3.44	4.66	-7.77	2.81	0.34	-5.29	-5.35	3.40E-02	3.22E-02
RP24-546N2.	2.55	-3.38	-0.06	2.94	-0.37	2.57	-6.38	-5.27	-5.27	-5.27	-7.29	4.51E-02	5.82E-03
Prg4	4.89	5.53	5.19	4.86	2.45	5.19	3.35	-0.64	-2.76	-5.26	-4.14	1.39E-02	4.58E-02
Farp1	3.13	2.83	3.26	3.92	4.26	1.94	-4.64	-2.51	0.54	-5.26	-5.62	1.02E-02	6.49E-03
Snx16	1.66	3.18	2.64	4.57	2.12	2.88	-1.13	-7.77	0.79	-5.25	-5.87	2.84E-02	1.41E-02
Sntb2	2.49	4.14	3.25	1.65	2.75	2.20	0.58	-1.97	-4.03	-5.16	-4.03	4.90E-03	2.49E-02
Kctd17	3.85	3.34	3.83	3.39	4.03	4.22	-7.77	1.94	1.30	-5.14	-5.37	2.04E-02	1.58E-02
Ccr6	6.40	6.56	6.98	5.42	4.38	5.79	2.15	5.20	-2.88	-5.14	-3.66	6.31E-03	3.81E-02
Fah	3.57	4.02	4.13	4.45	5.29	3.40	3.20	-0.97	-5.27	-4.95	-5.45	2.20E-02	1.28E-02
Golm1	4.42	4.12	5.73	5.64	5.49	5.16	3.31	1.39	-5.27	-4.94	-5.64	1.92E-02	9.18E-03
Il10ra	5.75	6.36	7.32	6.22	6.90	5.27	5.20	2.23	-2.66	-4.93	-4.60	2.66E-02	3.63E-02
Mthfr	3.82	4.54	4.04	5.73	4.92	3.39	3.32	-5.27	-0.16	-4.90	-5.44	3.54E-02	2.09E-02
Cyfip1	6.03	5.92	6.64	6.38	7.08	6.44	-3.52	5.51	1.74	-4.88	-5.34	1.20E-02	7.13E-03
Tmem41a	4.75	3.24	3.02	3.74	4.39	2.07	3.14	-4.01	-2.76	-4.86	-4.68	2.56E-02	3.19E-02
Prkar2a	3.98	4.26	3.64	4.28	4.58	4.43	-7.77	4.23	0.82	-4.82	-5.29	3.40E-02	2.12E-02
Gm26732	4.16	3.06	4.58	4.58	5.47	4.40	3.03	-1.70	-4.03	-4.82	-5.76	1.80E-02	6.08E-03
Evi2a	2.43	0.97	3.84	4.52	4.22	4.16	-7.77	1.02	0.13	-4.55	-6.48	4.77E-02	5.78E-03
Synpo	4.66	4.15	1.75	2.88	4.58	3.34	1.66	0.72	-5.27	-4.49	-4.61	4.60E-02	4.06E-02
Ncmap	5.34	5.49	5.80	5.51	4.40	5.24	0.81	2.33	0.11	-4.45	-3.93	1.29E-03	3.12E-03
Dnah7a	4.71	5.53	3.62	5.05	5.13	3.16	2.54	-4.01	2.26	-4.43	-4.25	3.93E-02	4.68E-02
Tmem8	4.84	4.42	5.23	4.30	3.92	5.02	1.15	1.95	-1.91	-4.42	-3.99	3.79E-03	7.35E-03
Ly6a	7.14	7.61	7.86	8.15	8.39	8.13	3.16	3.16	3.34	-4.32	-5.01	3.90E-05	9.99E-06
Sgsh	4.77	3.64	4.96	4.10	3.80	4.21	-4.79	3.09	2.54	-4.09	-3.69	2.84E-02	4.59E-02
Tbc1d30	4.49	6.05	5.79	5.61	4.58	5.21	-0.60	2.28	2.56	-4.04	-3.68	1.02E-02	1.72E-02
S100a4	4.47	4.57	4.17	3.51	4.46	3.84	0.34	0.31	0.60	-3.99	-3.54	1.66E-03	4.01E-03
Atp9a	5.91	6.21	6.80	5.81	5.82	5.68	4.22	-2.90	6.15	-3.90	-3.36	2.30E-02	4.57E-02
Fitm2	1.94	3.97	3.17	3.69	4.51	3.95	1.20	1.62	-5.27	-3.90	-4.88	4.32E-02	1.23E-02
Cep85l	4.51	2.55	3.36	2.70	3.73	4.00	1.94	-2.90	-0.17	-3.82	-3.89	2.42E-02	2.21E-02
Mettl21a	4.49	4.66	4.71	3.92	3.84	5.08	0.14	3.57	-1.13	-3.75	-3.38	8.83E-03	1.61E-02
Stk35	1.60	1.84	3.10	0.96	3.63	3.55	0.14	-2.35	-2.46	-3.74	-4.31	4.34E-02	2.02E-02
Maf	6.27	6.37	6.96	5.48	5.67	5.11	3.96	0.81	3.88	-3.69	-2.59	8.28E-04	9.76E-03
Btbd10	4.26	5.57	3.33	4.89	3.82	4.07	0.81	-1.75	3.27	-3.67	-3.48	3.15E-02	3.99E-02
Slc25a1	4.57	5.16	5.12	5.35	5.47	6.09	4.33	-2.68	2.71	-3.57	-4.23	2.19E-02	8.40E-03
Adck4	4.22	3.48	4.41	3.98	5.16	3.00	2.29	-3.12	2.49	-3.49	-3.58	4.31E-02	3.89E-02
Sdcbp2	6.50	6.62	6.15	5.56	5.60	6.23	4.71	0.52	3.82	-3.47	-2.84	1.77E-03	7.02E-03
Batf	6.69	5.90	6.54	6.06	6.22	6.32	4.82	1.27	2.91	-3.41	-3.25	1.21E-03	1.73E-03
Tmx4	5.83	6.66	5.47	5.49	4.78	6.09	4.89	0.18	2.99	-3.38	-2.80	1.13E-02	3.03E-02
Ccr8	5.15	5.43	6.29	5.13	4.44	4.65	0.65	2.74	3.30	-3.37	-2.47	3.73E-03	2.37E-02
Fbxw8	4.61	5.22	5.59	5.30	6.05	4.52	2.92	-0.51	3.17	-3.33	-3.49	1.72E-02	1.32E-02
Nrp1	9.16	9.61	9.78	8.74	8.58	8.58	5.54	6.49	6.62	-3.30	-2.40	1.57E-06	3.87E-05
Mast4	5.47	5.57	5.17	4.87	4.32	4.28	3.88	3.36	0.11	-2.97	-2.04	4.68E-03	3.86E-02
Pear1	5.30	5.66	6.63	6.43	4.94	6.81	2.49	4.41	1.70	-2.97	-3.13	3.16E-02	2.45E-02
Pde2a	7.66	8.10	7.97	6.72	7.64	7.83	4.34	6.51	3.99	-2.95	-2.43	5.33E-04	2.41E-03

Gene	Sample									Fold Change (Log2)		P-Value	
	CtrlA1	CtrlA2	CtrlA3	CtrlG1	CtrlG2	CtrlG3	dKO1	dKO2	dKO3	dKO vs. CtrlA	dKO vs. CtrlG	dKO vs. CtrlA	dKO vs. CtrlG
Ass1	6.86	6.93	6.82	6.33	6.76	6.66	3.22	4.36	4.19	-2.94	-2.65	2.32E-05	6.12E-05
Pck2	5.20	6.06	5.61	5.60	5.72	4.95	2.84	3.10	2.26	-2.91	-2.70	1.73E-03	2.98E-03
Ly6c1	6.66	7.05	6.77	7.17	7.55	7.65	4.73	3.40	3.96	-2.83	-3.45	8.35E-05	1.26E-05
Ampd3	5.43	4.52	5.73	5.92	5.48	4.86	2.75	0.54	3.94	-2.82	-3.04	1.64E-02	1.06E-02
Il12rb1	5.05	5.68	6.50	5.88	6.31	4.89	4.49	4.51	-0.09	-2.79	-2.75	3.55E-02	3.78E-02
Cd83	8.27	8.64	8.67	7.70	7.51	7.56	5.95	5.17	6.20	-2.77	-1.82	1.38E-06	9.18E-05
Gpr183	7.68	7.17	7.89	7.09	8.17	7.69	5.01	4.82	4.60	-2.76	-2.86	3.33E-04	2.47E-04
Slc22a5	6.39	6.14	5.53	6.19	5.77	5.90	0.97	3.63	5.10	-2.74	-2.67	6.14E-03	7.19E-03
Arhgap5	4.94	5.90	5.99	5.21	5.51	4.71	1.35	4.28	3.05	-2.70	-2.22	6.86E-03	2.10E-02
Chsy1	4.35	3.07	4.40	3.79	3.58	3.74	0.48	0.33	2.93	-2.65	-2.45	2.48E-02	3.67E-02
Itgb1	8.71	9.19	9.17	8.93	9.14	8.81	6.49	6.41	6.29	-2.65	-2.58	8.60E-07	1.13E-06
Ptger2	4.92	5.65	6.39	5.67	5.63	6.49	3.92	2.27	3.06	-2.61	-2.86	8.86E-03	4.85E-03
Ank	6.28	5.69	6.10	5.79	5.64	6.50	4.22	3.63	2.48	-2.58	-2.53	1.53E-03	1.74E-03
Atp10a	6.44	5.21	4.39	5.09	5.49	5.14	3.25	1.52	3.57	-2.57	-2.49	2.07E-02	2.41E-02
Tmem154	7.30	7.58	8.03	6.75	7.07	7.53	4.48	5.38	5.35	-2.56	-2.03	8.50E-05	6.48E-04
Ighmbp2	4.20	5.33	4.82	4.27	4.73	4.23	1.66	1.48	3.66	-2.55	-2.16	9.97E-03	2.51E-02
Fbxl17	6.48	6.49	6.32	5.39	6.37	6.16	4.86	5.70	1.12	-2.53	-2.09	1.12E-02	3.16E-02
Ahnak	8.08	7.70	7.54	7.13	7.21	7.52	5.72	4.64	5.58	-2.47	-1.98	1.93E-05	1.53E-04
Furin	7.24	6.56	6.35	6.22	6.42	6.87	4.81	4.89	3.11	-2.44	-2.23	1.03E-03	2.04E-03
Snx14	5.80	6.57	6.17	5.51	4.98	5.15	3.91	4.02	3.39	-2.43	-1.43	3.54E-04	1.54E-02
Pard6g	4.57	6.42	5.37	5.48	6.19	6.09	4.35	4.67	0.24	-2.42	-2.84	4.82E-02	2.22E-02
Plekha1	5.78	5.31	5.80	5.85	4.78	5.63	4.48	4.71	0.46	-2.41	-2.18	2.22E-02	3.57E-02
Il18r1	5.24	3.75	4.78	5.10	4.48	3.70	2.15	1.38	2.92	-2.40	-2.29	2.86E-02	3.62E-02
Glrx	5.93	6.13	6.66	5.69	6.37	5.67	4.67	2.41	4.87	-2.29	-1.97	3.40E-03	9.16E-03
Cxcr3	5.79	5.95	7.44	6.21	6.13	6.16	2.58	5.16	4.46	-2.28	-2.06	1.17E-02	2.08E-02
Fuca2	5.62	5.30	5.14	5.46	5.57	5.92	3.60	3.38	2.29	-2.26	-2.56	2.08E-03	7.92E-04
S100a6	6.40	6.63	5.93	4.97	6.21	5.20	3.53	4.39	4.27	-2.26	-1.41	1.34E-03	2.74E-02
Ube2l6	5.36	6.03	6.07	5.91	6.64	6.05	3.56	4.69	2.46	-2.25	-2.63	4.66E-03	1.51E-03
Tmem243	6.35	6.55	6.41	5.78	5.99	6.21	4.47	4.68	3.58	-2.19	-1.75	1.26E-04	8.85E-04
Lgals1	7.11	7.02	7.48	6.79	7.47	7.12	4.97	4.91	5.21	-2.17	-2.11	6.39E-05	8.37E-05
Capg	8.97	9.27	9.29	8.60	8.67	9.02	6.92	7.00	7.17	-2.15	-1.73	5.90E-07	5.88E-06
Fam101b	6.09	4.95	6.07	5.77	6.36	5.99	4.56	2.77	3.45	-2.11	-2.49	8.32E-03	2.75E-03
Cpd	4.48	5.07	4.34	5.55	4.69	5.45	4.19	0.20	3.44	-2.09	-2.65	4.73E-02	1.40E-02
Tspan31	5.78	5.42	6.18	5.35	6.08	5.35	4.62	1.97	4.67	-2.07	-1.90	1.07E-02	1.75E-02
Bmp7	4.49	5.05	5.39	4.38	4.93	4.34	3.36	2.90	2.62	-2.04	-1.61	6.40E-03	2.48E-02
Rilpl2	5.64	6.32	6.54	5.66	5.90	5.95	2.89	4.35	5.17	-2.02	-1.68	3.38E-03	1.12E-02
Lax1	5.77	6.29	6.67	6.78	6.42	5.91	5.39	4.46	2.96	-2.00	-2.12	6.29E-03	4.22E-03
Osbpl5	5.28	5.46	5.00	5.13	6.01	5.93	5.03	1.09	3.84	-1.99	-2.44	3.27E-02	1.09E-02
Iqgap2	5.25	6.05	4.40	6.34	5.92	6.29	4.86	3.67	1.36	-1.98	-2.90	4.12E-02	4.88E-03
Icos	6.43	6.20	6.57	5.99	5.83	5.88	4.47	3.99	4.85	-1.96	-1.47	1.36E-04	1.58E-03
Pdcd1	8.13	7.31	7.50	7.77	7.03	7.30	5.72	5.68	5.61	-1.96	-1.68	2.26E-04	8.21E-04
Psen2	7.11	7.47	7.54	6.83	6.80	7.05	5.12	5.79	5.33	-1.96	-1.47	2.21E-05	3.16E-04
Arhgap26	5.79	6.55	4.95	6.08	5.50	5.29	4.31	4.91	2.27	-1.96	-1.79	2.44E-02	3.76E-02
Cd44	7.24	7.47	7.99	7.12	7.70	7.55	5.10	5.02	6.78	-1.94	-1.83	1.13E-03	1.75E-03
Ccnc	5.99	5.04	5.56	5.03	4.81	5.29	5.10	2.93	2.87	-1.91	-1.44	1.01E-02	4.45E-02
Smpdl3a	8.40	8.81	8.88	8.54	8.63	8.21	6.50	6.81	7.14	-1.89	-1.65	1.06E-05	4.10E-05
Fam210b	5.45	5.94	5.32	4.92	5.91	5.20	3.00	4.64	3.46	-1.86	-1.64	7.34E-03	1.55E-02
Nt5e	8.82	8.54	8.86	8.51	8.61	8.15	6.69	6.98	6.94	-1.86	-1.56	3.06E-06	1.83E-05
Ldlrad4	5.59	5.48	6.43	5.84	6.08	6.75	5.16	2.67	4.25	-1.84	-2.23	1.62E-02	4.92E-03
Endod1	5.97	7.33	6.16	5.84	6.82	6.92	5.23	4.94	3.91	-1.84	-1.85	1.27E-02	1.20E-02
Sh3bgrl	7.53	7.98	7.88	7.14	7.11	6.92	5.61	5.81	6.53	-1.82	-1.07	3.28E-05	2.98E-03
Ermp1	6.85	6.47	6.86	6.93	6.33	5.97	5.67	3.81	5.42	-1.77	-1.47	3.12E-03	1.09E-02
Abcb1a	6.21	6.01	5.42	5.47	5.75	4.82	3.56	4.03	4.78	-1.74	-1.23	4.39E-03	3.33E-02
Stard3nl	5.64	5.72	4.95	5.09	5.67	5.72	5.03	4.51	1.61	-1.74	-1.80	3.60E-02	3.04E-02
Cst7	7.15	6.72	7.79	6.23	6.68	6.58	5.46	5.72	5.23	-1.73	-1.03	7.81E-04	2.51E-02
Fam117b	6.58	7.10	6.80	6.01	6.66	6.32	5.84	5.31	4.21	-1.73	-1.23	1.19E-03	1.25E-02
Nabp2	5.67	6.13	5.07	4.66	5.53	5.21	4.06	3.77	3.94	-1.72	-1.23	5.96E-03	3.83E-02
H2-Q6	8.70	8.62	8.56	8.22	8.07	8.11	6.45	7.52	6.79	-1.69	-1.20	1.17E-05	3.03E-04
Abhd6	4.87	5.83	5.39	4.62	5.40	5.71	3.01	3.95	4.10	-1.69	-1.55	1.41E-02	2.22E-02
Ube2o	5.35	4.51	4.30	5.31	4.95	5.45	4.18	3.53	1.39	-1.68	-2.20	4.41E-02	1.06E-02
Igf1r	5.58	5.13	5.47	5.25	5.27	4.98	3.72	4.16	3.26	-1.66	-1.45	3.03E-03	7.58E-03
Tyk2	6.44	7.52	6.69	6.66	6.56	6.78	5.02	5.21	5.53	-1.66	-1.41	1.23E-03	4.03E-03
S100a11	6.24	6.35	6.34	5.60	6.24	5.65	4.54	4.42	5.07	-1.64	-1.17	5.34E-04	6.60E-03
Nbn	4.23	5.01	5.27	4.83	4.91	4.63	3.54	4.06	2.07	-1.62	-1.57	2.59E-02	3.06E-02
Trib1	5.41	4.60	5.84	5.43	4.71	5.92	3.94	3.03	3.99	-1.62	-1.69	2.92E-02	2.33E-02
Clip1	6.66	6.59	6.45	7.28	6.39	5.81	5.32	5.93	3.59	-1.61	-1.54	1.77E-02	2.24E-02
Slc48a1	6.29	6.75	6.55	6.29	6.82	6.81	5.16	4.61	5.08	-1.60	-1.70	5.83E-04	3.39E-04
Tesc	5.25	5.36	5.72	5.56	6.37	5.85	4.39	3.87	3.34	-1.59	-2.09	8.05E-03	1.15E-03
Ptpn7	8.14	8.16	8.34	8.29	7.53	8.46	7.01	6.31	6.62	-1.57	-1.44	3.92E-04	8.17E-04
Cd86	5.92	6.61	6.14	6.04	5.89	5.82	4.54	4.88	4.58	-1.57	-1.24	7.79E-04	4.38E-03
Mettl2	5.06	4.87	5.39	4.43	4.45	5.42	3.59	3.05	4.01	-1.56	-1.21	1.36E-02	4.86E-02
Mtif2	5.04	5.45	5.69	5.08	4.90	5.20	3.84	3.11	4.65	-1.55	-1.20	7.51E-03	3.08E-02
Anxa2	6.38	6.31	6.60	5.33	6.81	6.37	4.64	4.91	5.09	-1.54	-1.31	5.79E-03	1.60E-02
Plekhb2	7.35	7.77	7.81	6.84	7.74	7.46	6.00	6.11	6.24	-1.54	-1.24	3.63E-04	2.00E-03
Lats2	6.95	7.11	7.47	7.14	6.76	7.97	6.49	6.31	4.14	-1.54	-1.63	1.96E-02	1.39E-02

Gene	Sample									Fold Change (Log2)		P-Value	
	CtrlA1	CtrlA2	CtrlA3	CtrlG1	CtrlG2	CtrlG3	dKO1	dKO2	dKO3	dKO vs. CtrlA	dKO vs. CtrlG	dKO vs. CtrlA	dKO vs. CtrlG
Cd82	9.22	9.29	9.75	9.06	9.32	9.33	7.93	7.81	7.99	-1.51	-1.33	9.31E-06	3.24E-05
Blvra	6.09	4.94	5.82	5.57	5.78	5.28	4.24	4.65	3.33	-1.50	-1.47	1.51E-02	1.72E-02
Fam49a	6.57	6.75	5.44	6.71	7.25	7.00	5.59	2.97	5.85	-1.50	-2.23	4.97E-02	5.59E-03
Acot7	6.07	6.45	6.98	6.50	5.54	6.71	5.62	4.03	5.46	-1.49	-1.21	1.46E-02	4.12E-02
Atp2b1	7.54	7.97	7.87	7.70	6.90	7.76	6.67	6.25	6.04	-1.49	-1.12	5.72E-04	4.74E-03
Ccdc50	5.74	6.03	6.24	6.31	5.35	6.61	4.80	3.87	5.01	-1.46	-1.51	1.39E-02	1.09E-02
Ezh2	5.84	5.17	5.31	5.26	5.53	5.75	4.08	3.22	4.66	-1.45	-1.54	1.07E-02	7.42E-03
Rbl1	5.59	6.67	6.83	6.96	6.66	6.43	4.60	5.72	4.55	-1.41	-1.71	1.32E-02	3.80E-03
Cldn25	6.49	7.05	7.49	6.58	6.97	6.72	5.23	5.71	5.90	-1.40	-1.14	1.80E-03	7.23E-03
Unc119	4.56	5.73	5.21	5.26	5.59	5.60	3.43	3.17	4.82	-1.39	-1.69	3.06E-02	1.06E-02
Gpr68	5.54	6.32	6.62	6.42	6.56	6.05	4.83	4.97	4.54	-1.39	-1.57	5.97E-03	2.54E-03
Jade1	6.19	5.47	5.34	5.98	5.73	5.65	3.57	3.96	5.25	-1.38	-1.52	1.53E-02	8.63E-03
Gbp5	6.88	6.46	7.42	6.60	6.80	6.68	4.97	5.82	5.78	-1.37	-1.16	2.49E-03	7.68E-03
B3gnt1	4.87	4.13	5.19	4.88	5.33	5.38	2.46	3.24	4.26	-1.37	-1.87	4.98E-02	1.01E-02
Rfc1	6.24	7.01	5.78	6.44	5.98	5.88	4.81	5.82	4.35	-1.36	-1.09	1.57E-02	4.63E-02
Serpinb6b	5.10	5.84	4.81	5.50	5.48	5.35	4.60	2.65	4.58	-1.36	-1.53	3.59E-02	1.95E-02
Tmem109	6.41	5.92	6.04	5.92	6.80	6.15	5.25	5.07	3.99	-1.35	-1.54	1.04E-02	4.29E-03
Igfbp4	7.70	7.41	7.29	7.56	8.06	8.56	5.64	6.83	5.84	-1.34	-1.94	6.63E-03	3.98E-04
Sidt1	7.75	7.48	7.49	7.75	7.31	7.13	5.91	6.42	6.36	-1.33	-1.16	2.44E-04	7.90E-04
Cd4	9.68	9.75	9.95	10.00	9.41	9.80	8.57	8.36	8.47	-1.33	-1.26	2.53E-05	4.16E-05
Syngr2	6.52	6.66	7.15	6.65	6.75	6.84	5.98	5.44	5.09	-1.28	-1.25	1.43E-03	1.72E-03
Trat1	6.48	6.56	6.76	6.73	6.92	6.46	4.94	5.41	5.61	-1.27	-1.39	1.00E-03	4.91E-04
Il6ra	7.18	6.90	6.91	6.87	6.91	7.00	5.75	6.08	5.31	-1.27	-1.21	3.57E-04	5.41E-04
Tmub1	6.22	5.01	6.45	5.71	5.92	6.19	4.93	4.14	4.77	-1.26	-1.34	2.99E-02	2.22E-02
Sypl	7.05	6.94	7.24	6.75	7.14	6.59	5.94	5.86	5.69	-1.24	-1.01	3.74E-04	2.00E-03
Ezh1	6.85	7.53	6.86	6.78	7.22	6.71	5.50	5.88	6.18	-1.24	-1.05	2.23E-03	6.61E-03
Zfand5	6.51	6.27	6.25	6.19	7.13	6.52	5.80	5.09	4.47	-1.23	-1.52	1.20E-02	2.97E-03
Sfxn1	5.98	6.40	5.88	6.17	6.64	5.70	5.68	3.45	5.63	-1.21	-1.30	4.85E-02	3.47E-02
Tnfrsf4	9.57	9.53	9.64	9.85	9.05	9.53	8.36	8.25	8.56	-1.19	-1.07	1.86E-04	4.49E-04
Tk2	5.68	6.91	6.79	6.49	7.13	6.02	5.07	5.65	5.22	-1.17	-1.25	3.17E-02	2.23E-02
Arl5a	6.94	7.63	7.40	6.86	7.87	7.78	6.93	5.16	6.51	-1.16	-1.33	2.82E-02	1.34E-02
Cdc25b	5.95	5.94	6.04	6.37	6.11	5.41	4.80	4.18	5.50	-1.16	-1.16	1.65E-02	1.68E-02
Gltscr1l	5.65	7.03	6.85	6.77	6.37	6.38	5.21	5.20	5.74	-1.16	-1.12	2.05E-02	2.37E-02
Bcap29	6.59	7.01	7.03	6.50	6.43	7.34	5.24	5.78	6.15	-1.16	-1.02	7.26E-03	1.52E-02
Topors	6.10	6.62	7.22	6.63	6.60	6.77	6.12	5.41	5.03	-1.14	-1.16	1.10E-02	1.02E-02
Ncf4	5.99	5.83	6.42	6.10	6.33	5.95	4.05	5.09	5.69	-1.11	-1.17	1.87E-02	1.40E-02
Rora	5.15	6.06	5.38	6.11	6.20	5.69	4.77	4.32	4.27	-1.11	-1.56	2.19E-02	2.43E-03
Samhd1	9.34	9.39	9.28	9.41	9.26	9.32	8.22	8.17	8.31	-1.11	-1.09	6.10E-07	6.70E-07
Egln1	6.75	6.76	6.81	7.20	6.72	7.22	4.54	6.45	5.98	-1.09	-1.35	2.00E-02	5.53E-03
Ap1g2	6.30	7.07	5.61	7.14	6.69	6.73	5.86	4.62	5.38	-1.08	-1.58	4.19E-02	5.03E-03
Cd28	6.56	6.14	6.56	6.76	6.41	6.56	5.70	5.19	5.10	-1.08	-1.25	3.21E-03	1.12E-03
Mtg2	5.61	5.06	5.69	4.92	5.69	5.68	4.10	4.65	4.41	-1.04	-1.04	2.86E-02	2.90E-02
6330416G13	5.43	5.26	5.84	5.99	6.48	6.46	4.09	4.39	4.92	-1.03	-1.85	2.48E-02	4.67E-04

[1] Table S2:Genes under-expressed in dKO vs. genetic (CtrlG) or animal (CtrlA) Tregs, as defined in Fig. 6A. Normalized expression (Log2 values) is given for each gene in each of the three independent replicates for each genotype. Log2 values of Fold change (FC) and p-values are given for indicated comparisons.