Supplementary Materials for

PD-1 Marks Dysfunctional Regulatory T cells in Malignant Gliomas

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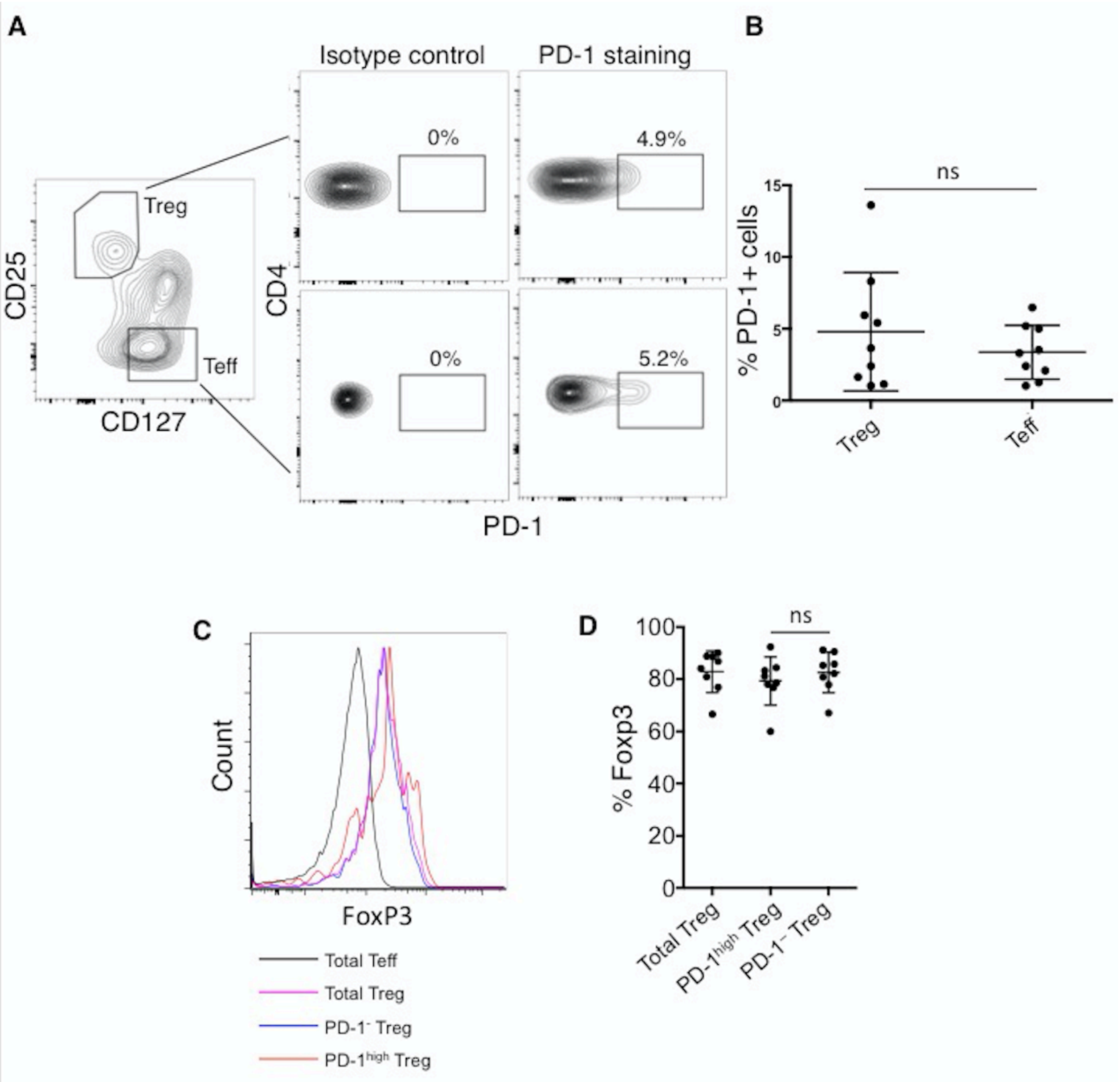
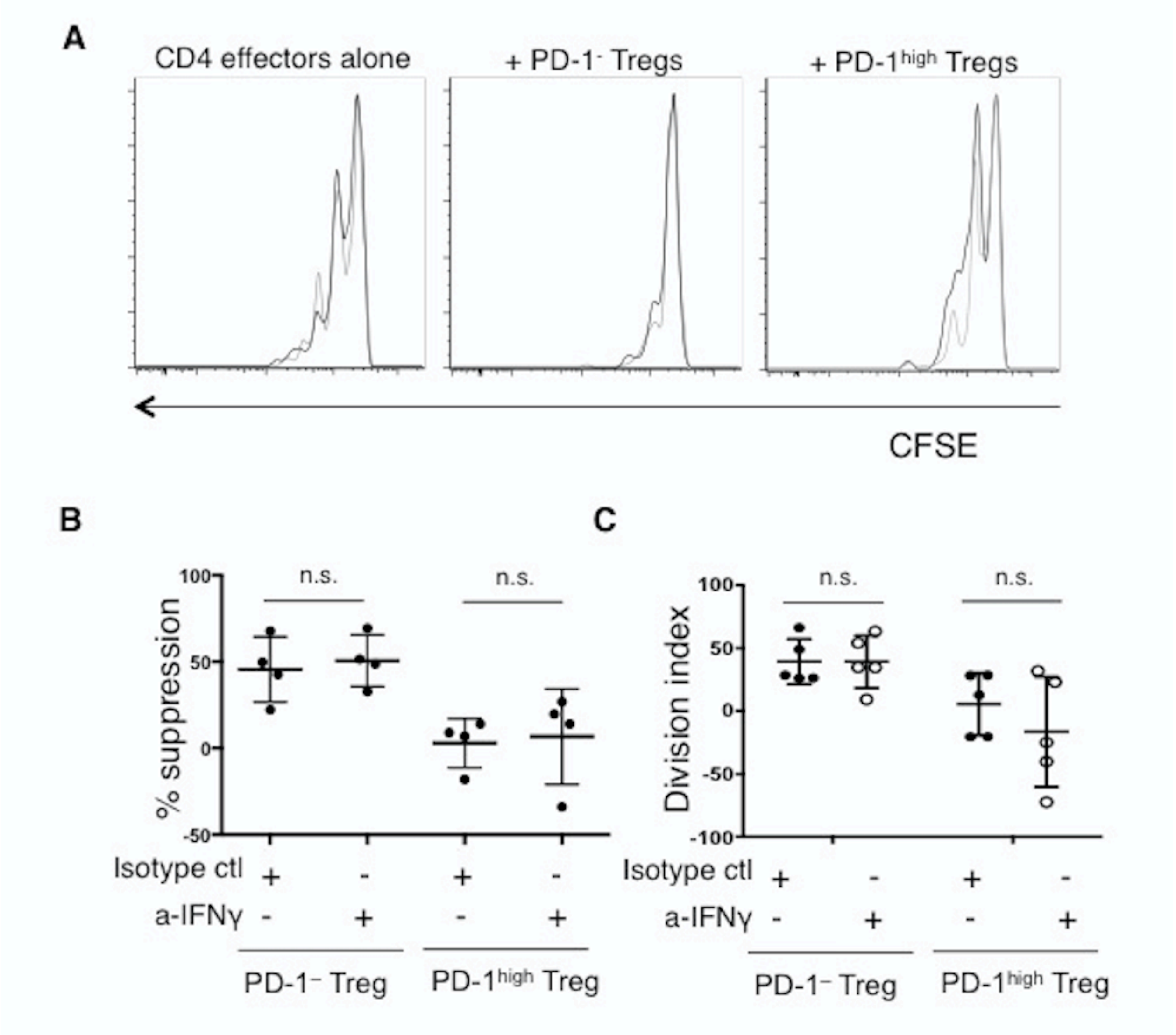
This PDF file includes:

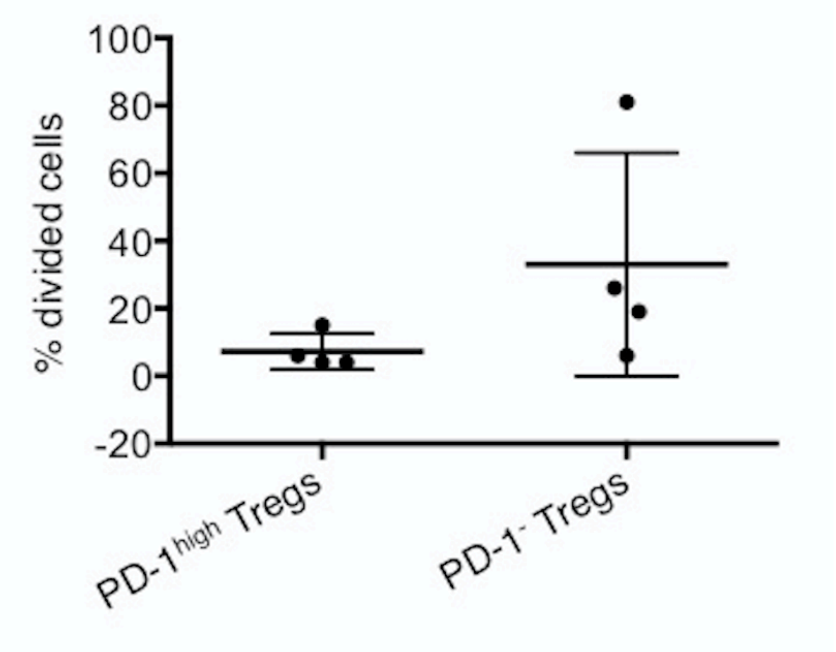
- Materials and Methods
- Supplementary Figures 1 to 17
- Supplementary Tables 1 to 11
- References (64-68)



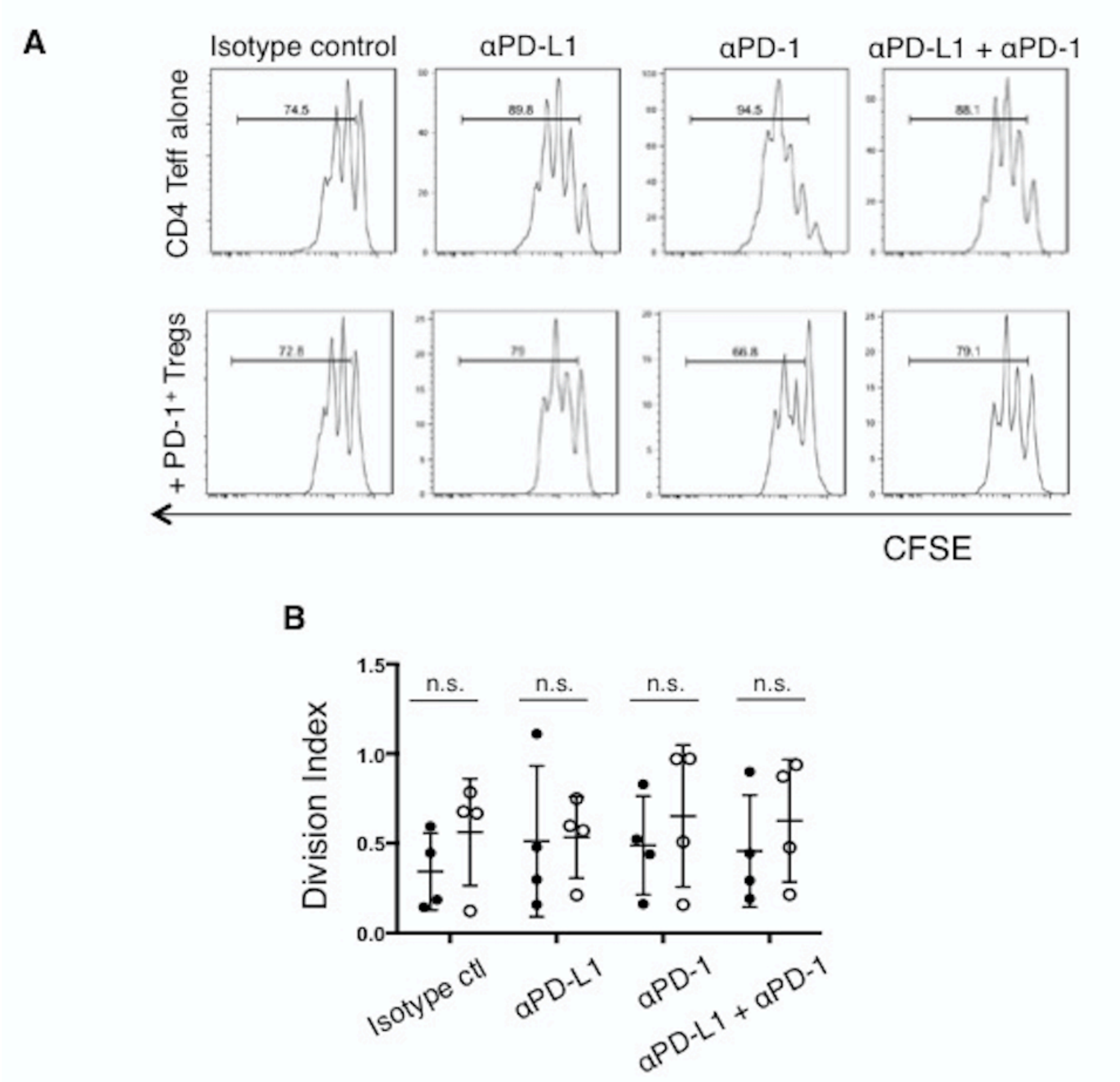
Supplementary Figure 1. Gating strategy for the isolation of Programmed cell death protein 1 (PD-1)^{high} and PD-1^{-} FoxP3^{+} Tregs. **a**, Representative plot showing gates for Tregs (CD25^{hi}CD127^{lo}) and Teffs (CD25^{lo}CD127^{+}) among total CD4^{+} cells, and gates for PD-1^{high} Tregs and Teffs based on isotype control **b**, quantification of the frequency of PD-1^{high} cells among Tregs and Teffs. N = 9, mean +/- S.D., paired Student's t test . **c**, Representative FoxP3 staining of total Teff (black line), total Tregs (purple line), PD-1- Tregs (blue line) and PD-1^{high} Tregs (red line). **d**, Frequency of Foxp3% cells among total, PD-1^{high} and PD-1^{-} Treg gates for 8 individuals, mean + S.D, paired Student's t test.



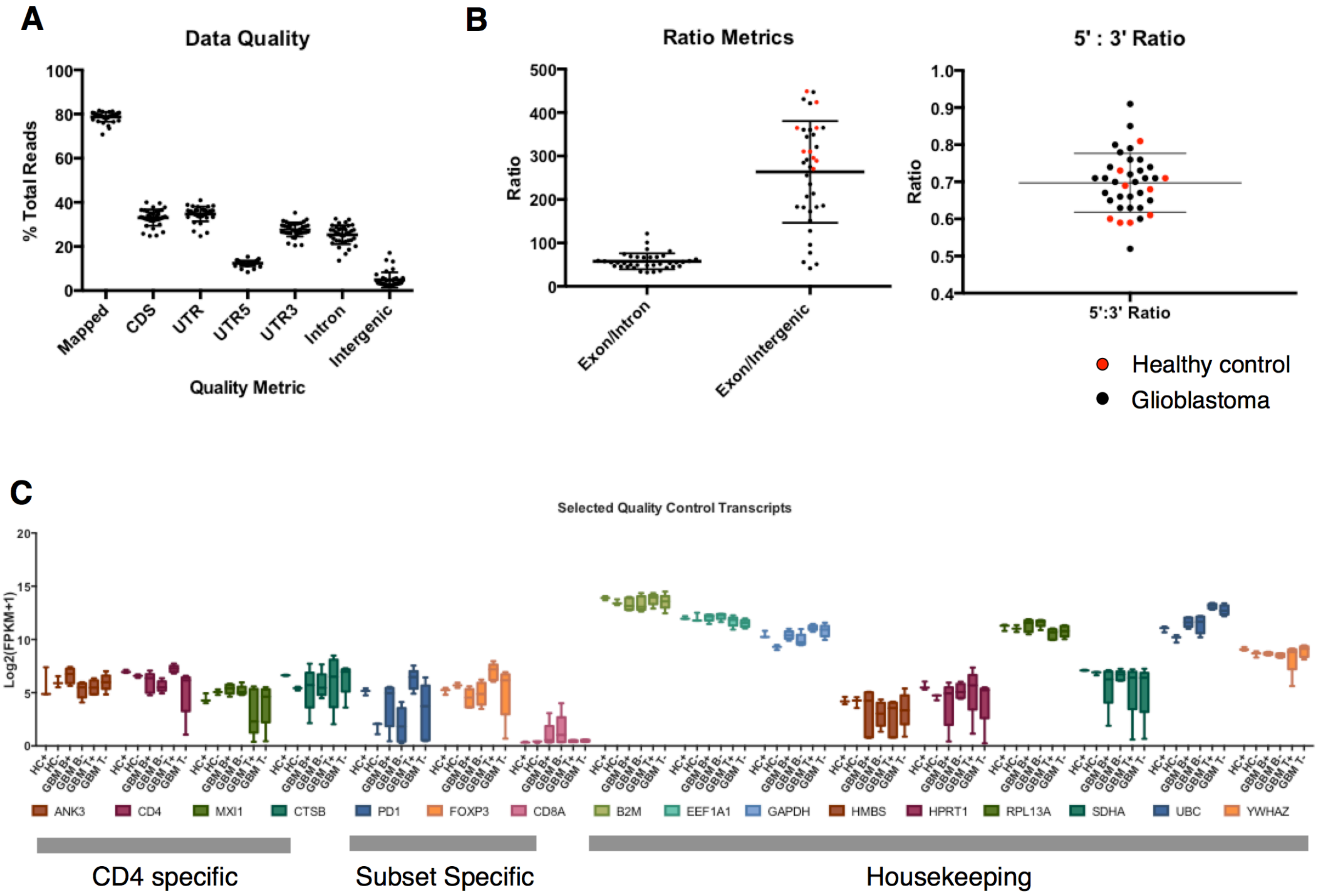
Supplementary Figure 2. Blocking IFNγ doesn't restore suppression activity in Programmed cell death protein 1 (PD-1)^{high} Tregs. **a**, Proliferation of T effectors co-cultured with PD-1^{-} or PD-1^{high} Tregs (Teff/Treg ratio 1:2) in the presence of a blocking anti-IFNγ antibody (grey line) or an isotype control (black line). Treg and Teff were stimulated for 4 days with aCD3/aCD28/aCD2. **b**, Percentage of suppression of 4 individuals calculated from the percentage of divided cells, or **c**, division index. For b, c Mean + S.D, Student's t test.



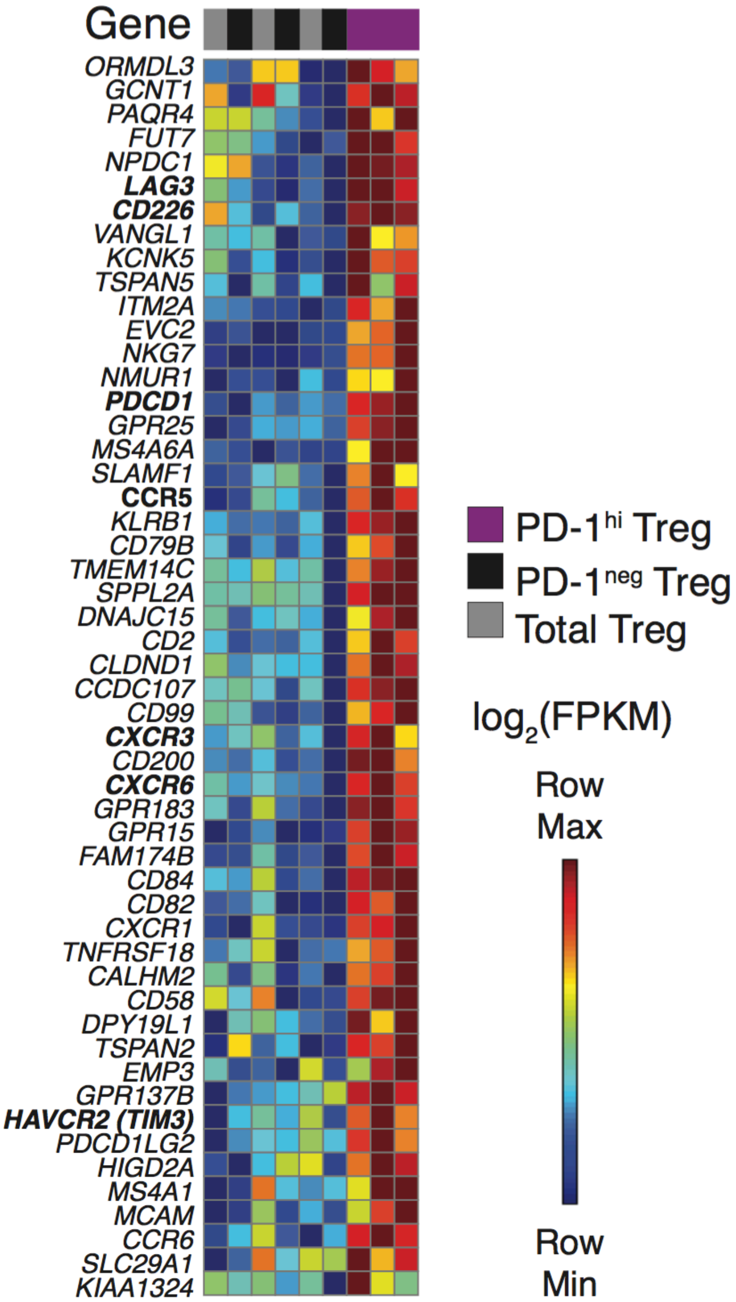
Supplementary Figure 3. Programmed cell death protein 1 (PD-1)^{high} **Tregs display reduced proliferation in vitro.** Proliferation of sorted Tregs stimulated for 4 days with aCD3/aCD28/aCD2 in the presence of IL-2, assessed as dilution of CFSE. CFSE^{low} Tregs were gated among live FoxP3^{+} cells. Mean + S.D. of 4 individuals.



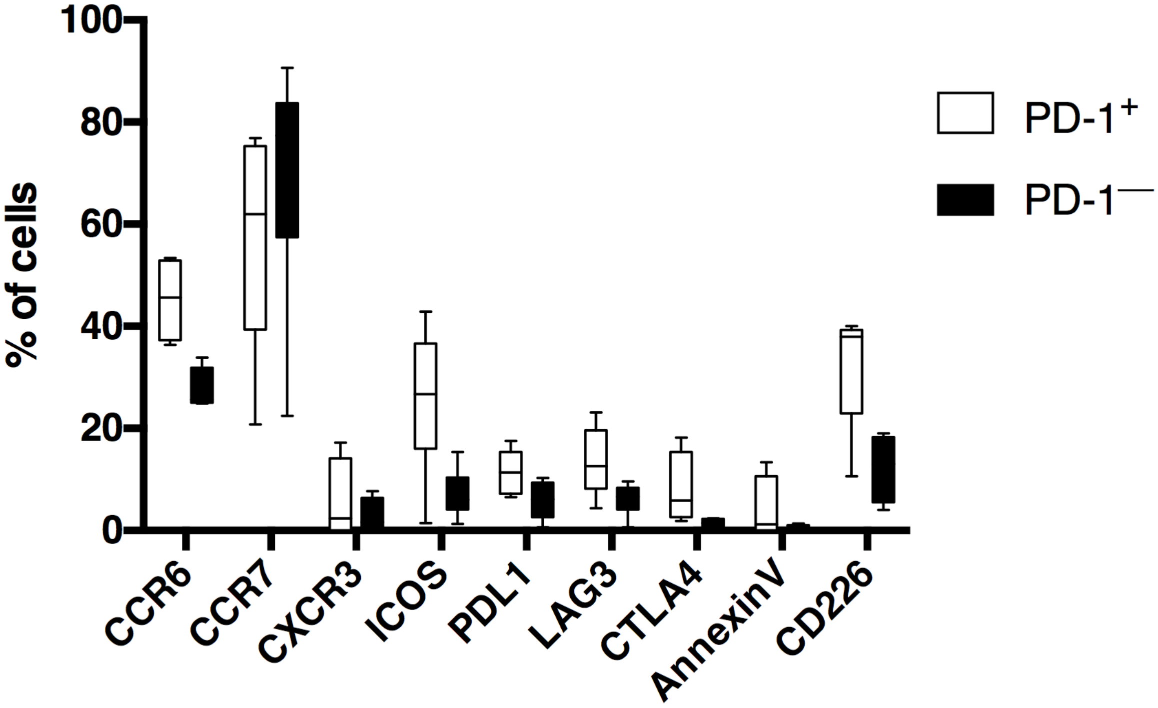
Supplementary Figure 4. **Blocking the Programmed cell death protein 1 (PD-1)-Programmed cell death ligand 1 (PD-L1) axis does not restore suppression activity in PD-1^{high} Tregs**. **a**, Proliferation of T effectors co-cultured with PD-1^{high} Tregs (Teff/Treg ratio 1:2) in the presence of blocking antibodies for PD-1, PD-L1, or both in combination. Treg and Teff were stimulated for 4 days with aCD3/aCD28/aCD2. **b**, Division index of T effectors alone (black dots) or co-cultured with PD-1^{high} Tregs (white dots) of 4 individuals. Mean + S.D., One-way Anova (b) and Two-way ANOVA (c) with Sidak multiple comparison correction.



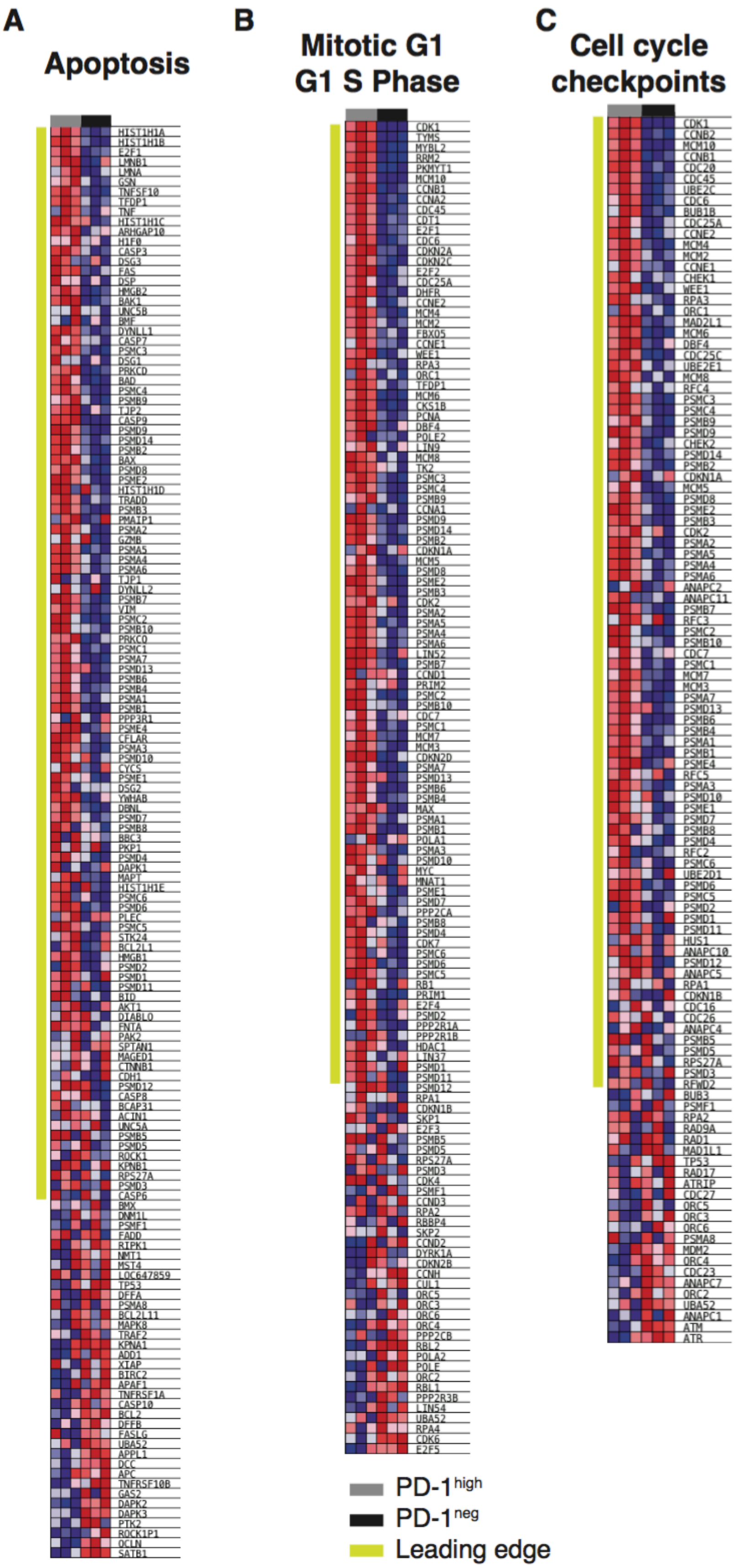
Supplementary Figure 5. Quality control metrics of RNA-sequencing libraries. a, Indicated quality metrics for each library are shown, mean and standard deviation are shown. **b**, Ratio metrics for each library are shown, where healthy control libraries are highlighted in red. Mean and standard deviation are shown. **c**, Boxplots of select transcripts are shown. Bounds of the boxes: 25th and 75th percentile; line within the box: median; top and bottom whiskers: maximum and minimum values.



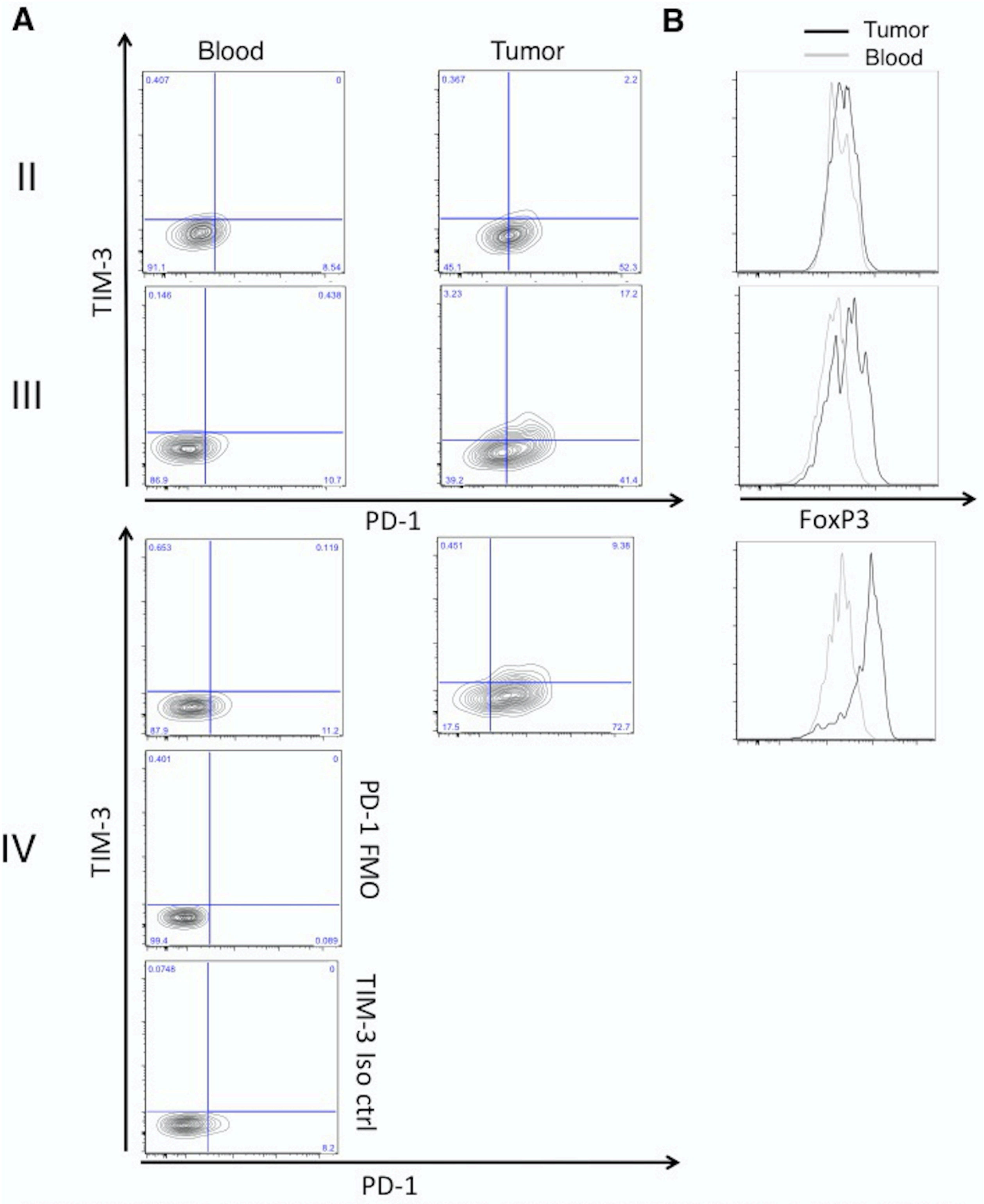
Supplementary Figure 6. Fully annotated heatmap of functional cluster shown in Figure 2B.



Supplementary Figure 7. Characterization of Programmed cell death protein 1 (PD-1)^{high} and PD-1$^-$ CD4 Treg. Expression of selected cell markers within PD-1^{high} and PD-1$^-$ Tregs (CD4$^+$CD25$^+$CD127$^-$Foxp3$^+$). Bounds of the boxes: 25th and 75th percentile; line within the box: median; top and bottom whiskers: maximum and minimum values.

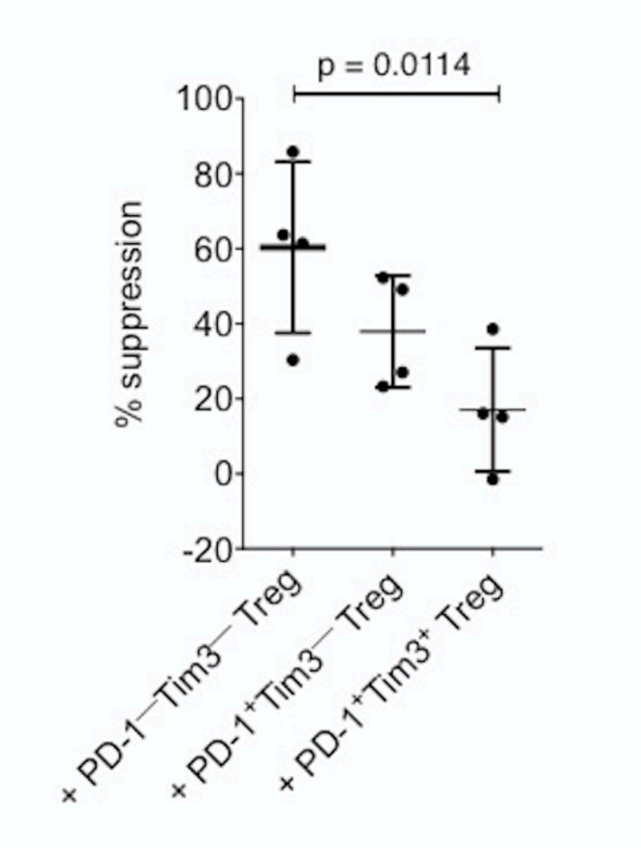


Supplementary Figure 8. Example gene sets enrichment analysis results for healthy control Programmed cell death protein 1 (PD-1)^{high} RNA-seq libraries with select genes in leading edge highlighted. **a**, Apoptosis pathway, **b**, Mitotic G1 G1 S Phase, and **c**, Cell cycle checkpoints. Leading edge is highlighted with a yellow bar, PD-1^{high} with a grey bar, and PD-1^{-}with a black bar.

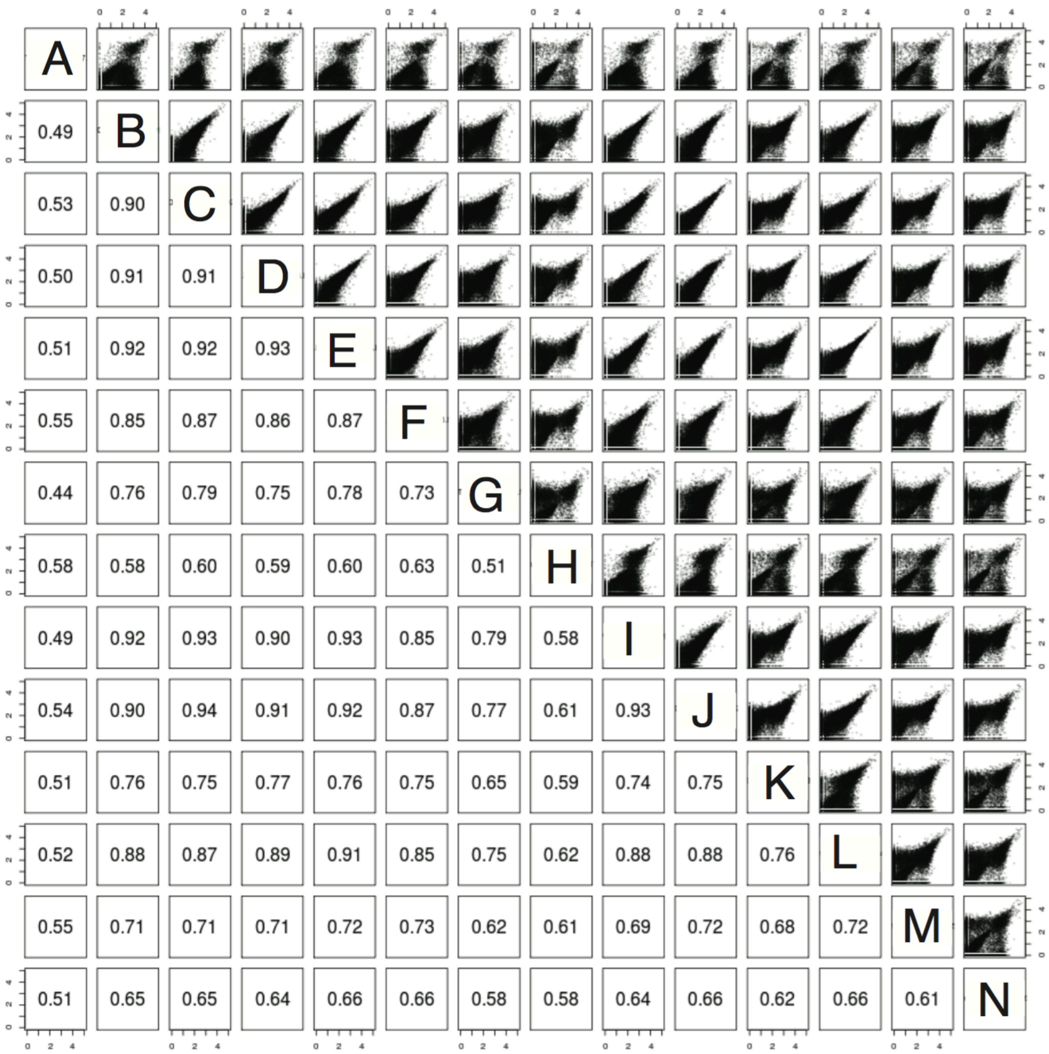


Supplementary Figure 9. Representative staining for Programmed cell death protein 1 (PD-1) and T-cell immunoglobulin and mucin domain-containing 3 (TIM-3) in the blood and

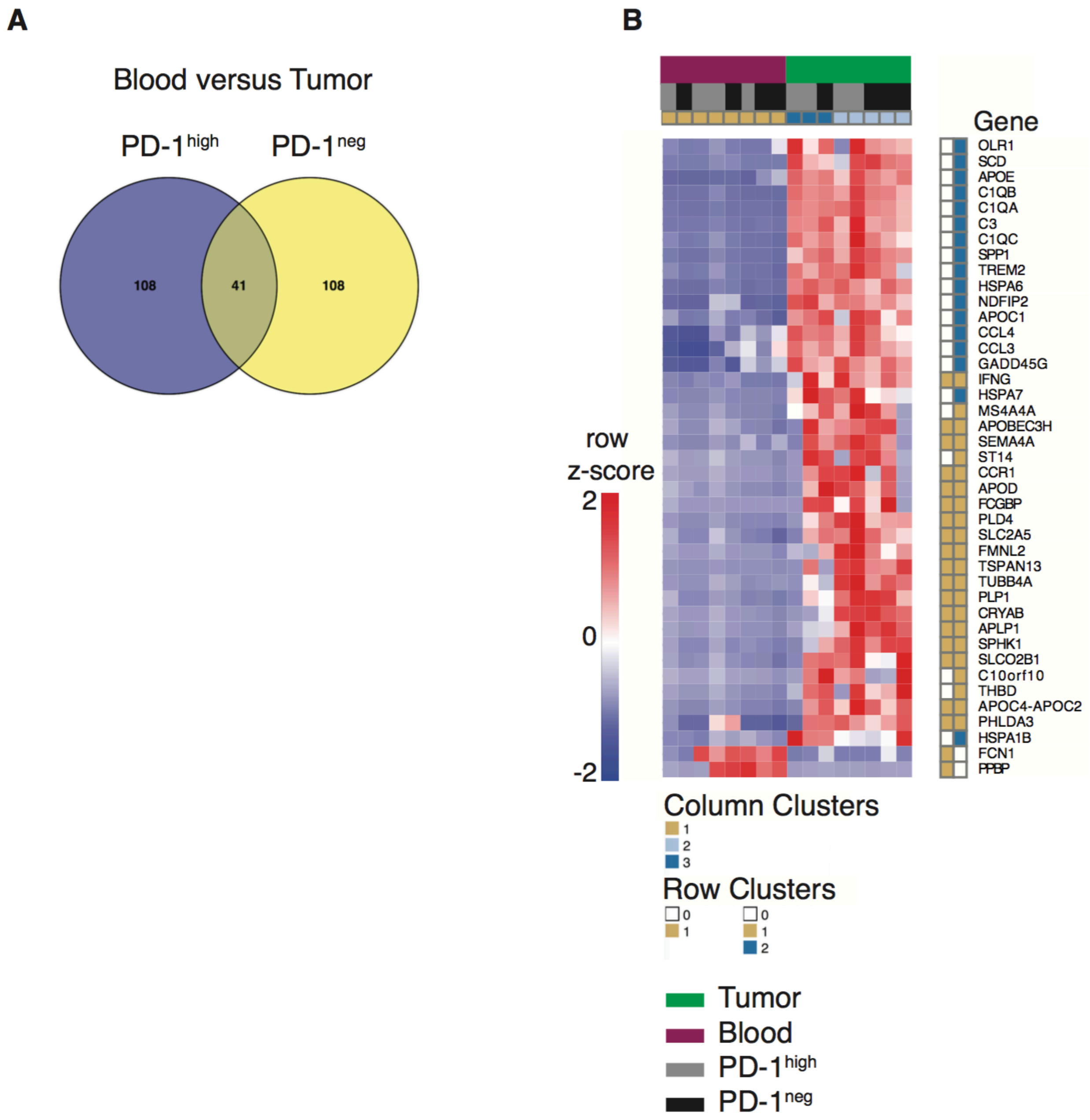
tumor infiltrate of patients with different WHO grade gliomas (grade II = G15, grade III = G11 grade IV = G3). a, Plots are gated on live CD4$^+$CD25^{hi}CD127$^-$FoxP3$^+$. **b,** Representative FoxP3 staining from the same samples. Histograms are gated on live CD4$^+$CD25^{hi}CD127$^-$



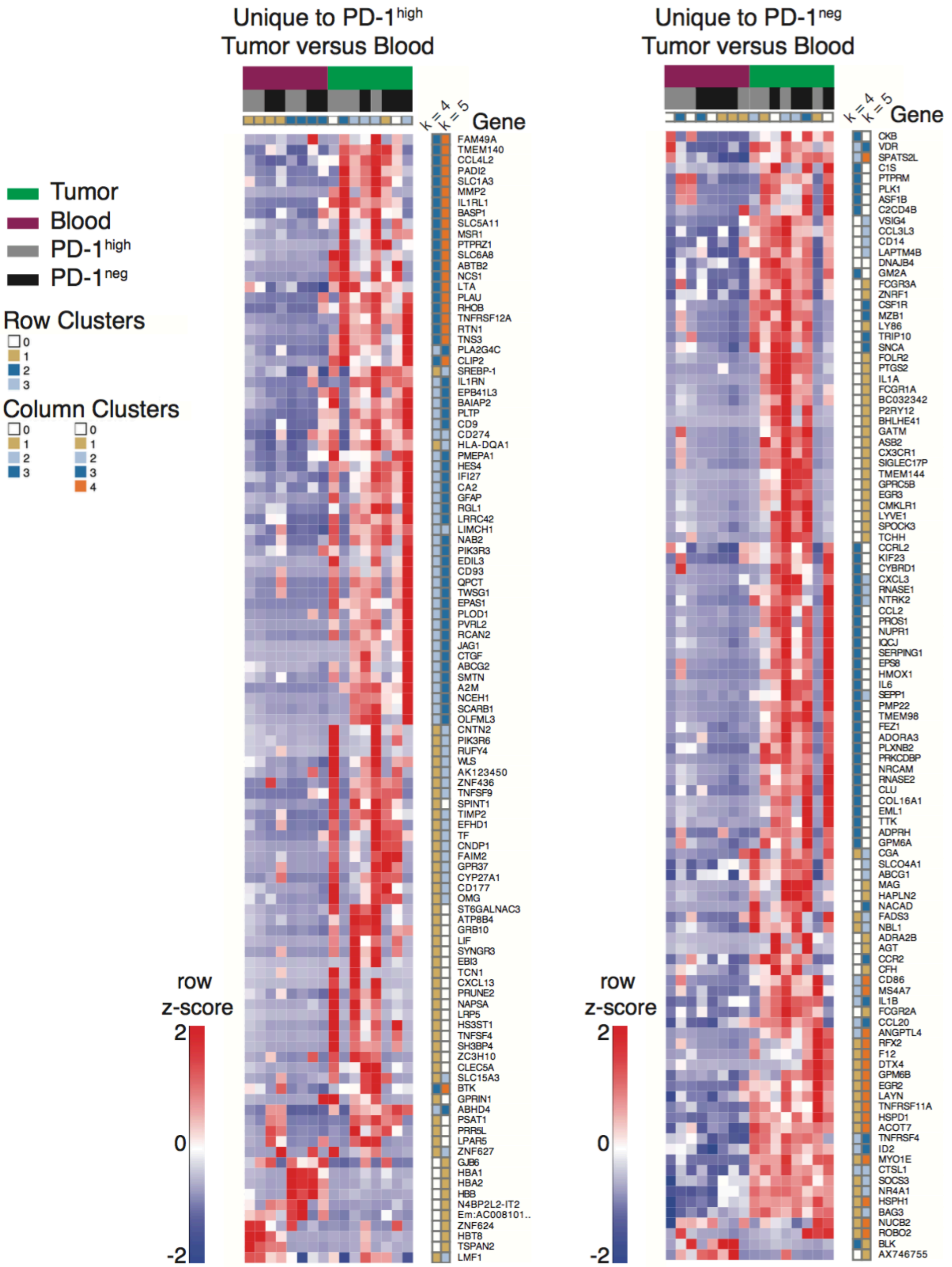
Supplementary Figure 10. Treg (CD4$^+$CD25$^+$CD127$^-$) populations from peripheral blood of glioblastoma multiforme (GBM) patients co-cultured with CD4 effectors (CD4$^+$CD25$^-$CD127$^+$). Treg and Teff were cultured at a 1:2 ratio (n=4; G37-40). Statistical analyses were performed using paired student's t-test.



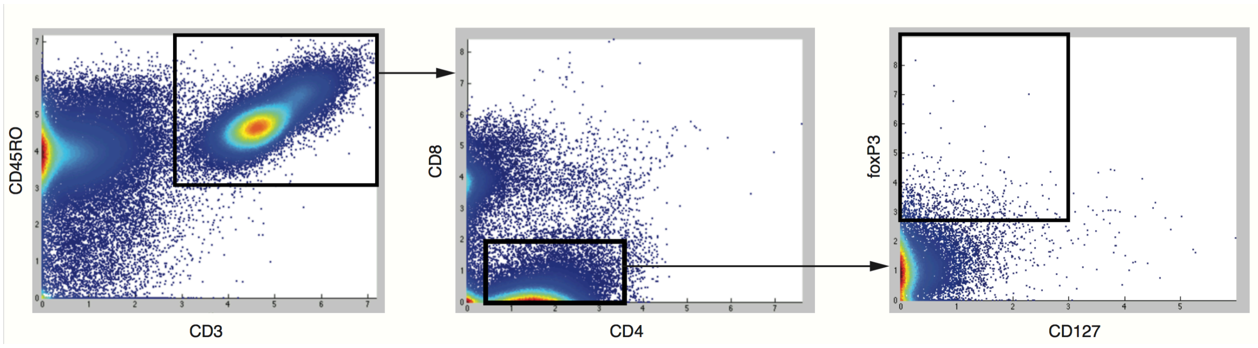
Supplementary Figure 11. Scatter plot matrix of log$_{10}$(counts + 1) and Pearson correlation coefficient for each indicated tumor-derived sample. **a,** BT229 PD-1^{-}, **b**, BT213 PD-1^{-}, **c**, BT215 PD-1^{-}, **d**, BT219 PD-1^{-}, **e**, BT220 PD-1^{-}, **f**, BT223 PD-1^{-}, **g**, BT228 PD-1^{-}, **h**, BT229 PD-1$^{\text{high}}$, **i**, BT213 PD-1$^{\text{high}}$, **j**, BT215 PD-1$^{\text{high}}$, **k**, BT219 PD-1$^{\text{high}}$, **l**, BT220 PD-1$^{\text{high}}$, **m**, BT223 PD-1$^{\text{high}}$, **n**, BT228 PD-1$^{\text{high}}$.



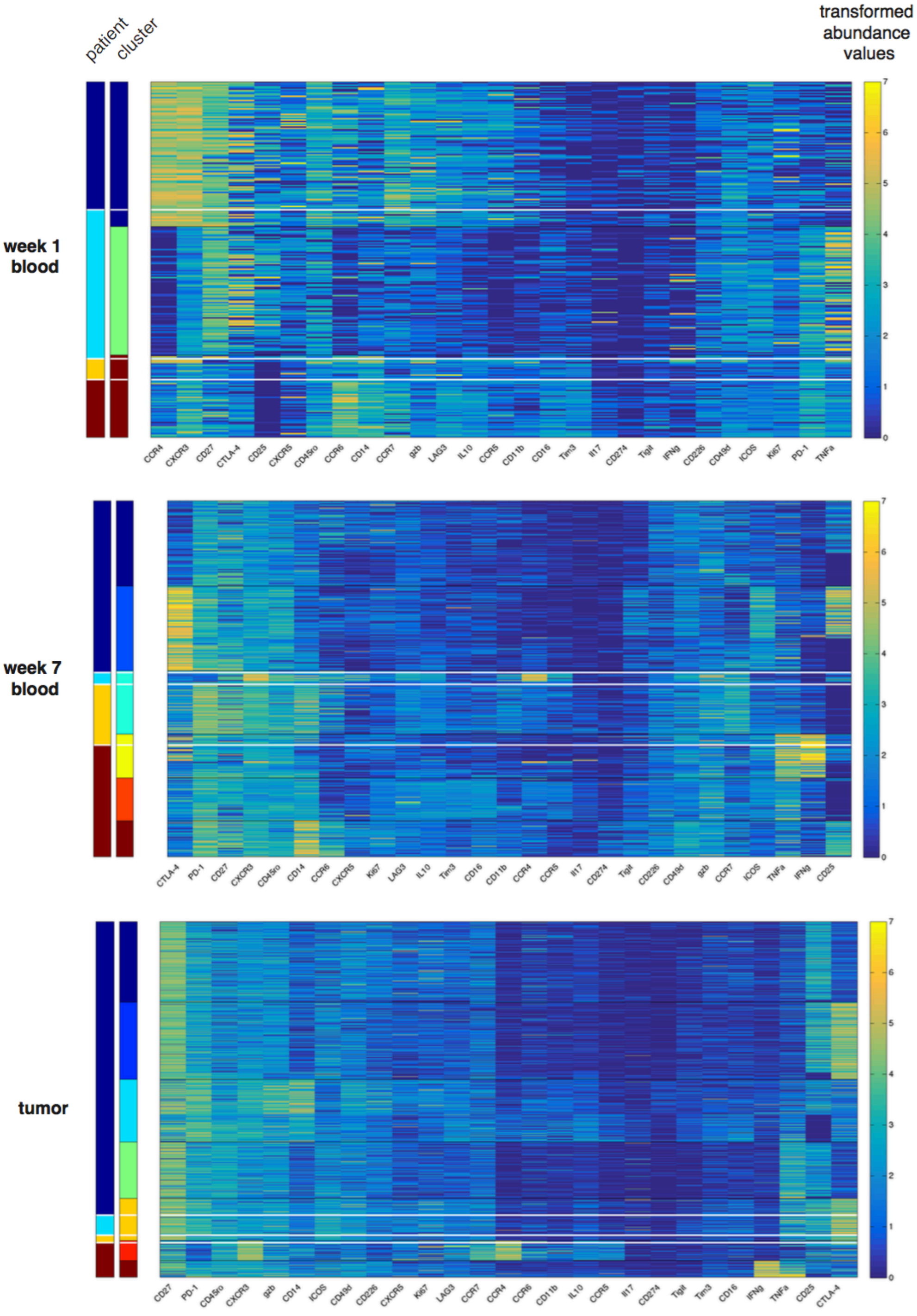
Supplementary Figure 12. Differential expression of Programmed cell death protein 1 (PD-1)^{high} or PD-1^{-} Tregs within tumor or blood. a, Venn diagram comparison of differential expression of PD-1high or PD-1—Tregs from tumor as compared to blood. Gene sets were filtered based on p-value for top differentially expressed genes and lists were compared. **b**, Heatmap of 41 common genes identified. Data was hierarchically clustered and k means clustered using GeneE.



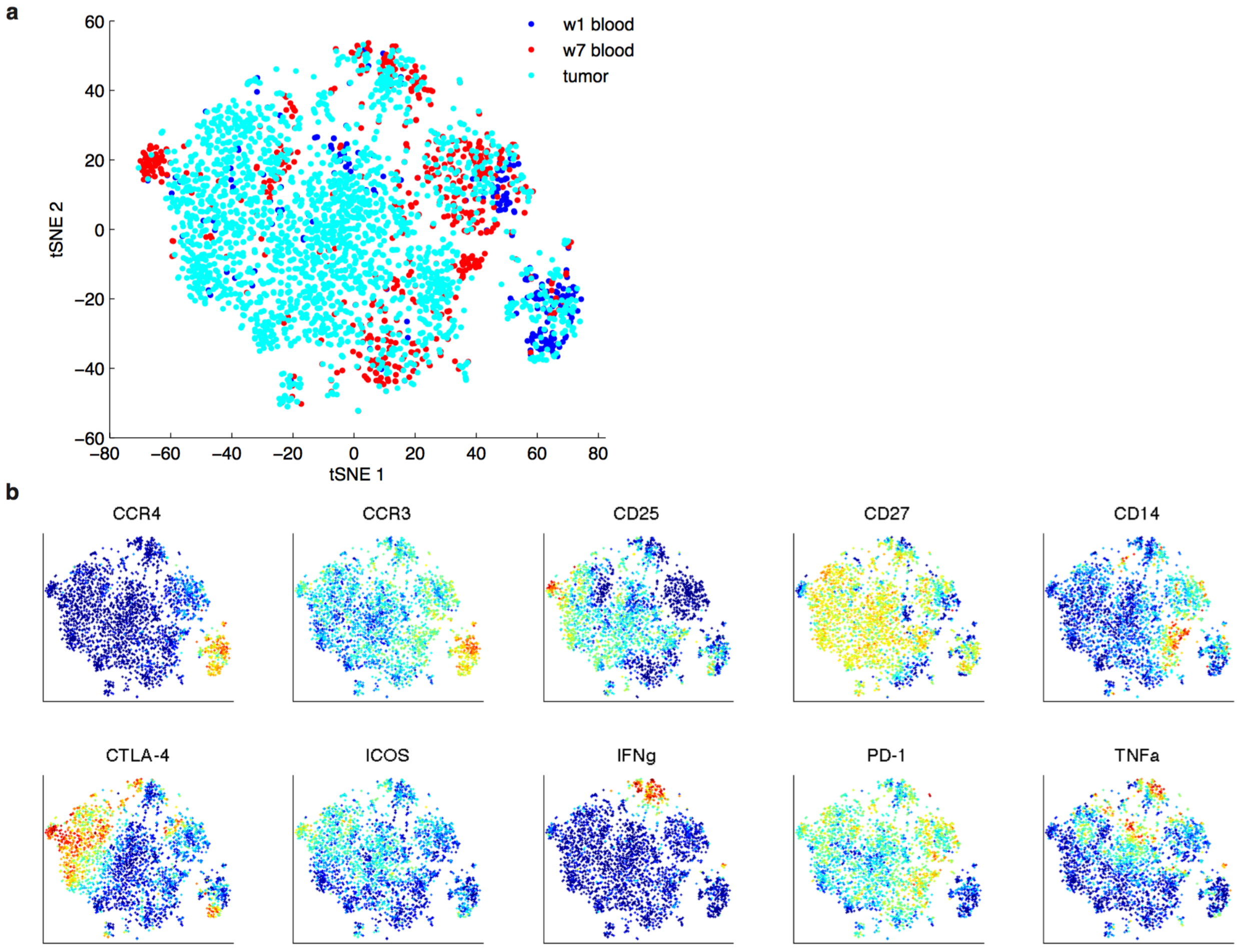
Supplementary Figure 13. Differential expression of Programmed cell death protein 1 (PD-1)^{high} or PD-1^{-} Tregs within tumor or blood, unique gene sets are shown as indicated from Supplementary Figure 10a. Data was hierarchically clustered and k means clustered using GeneE.



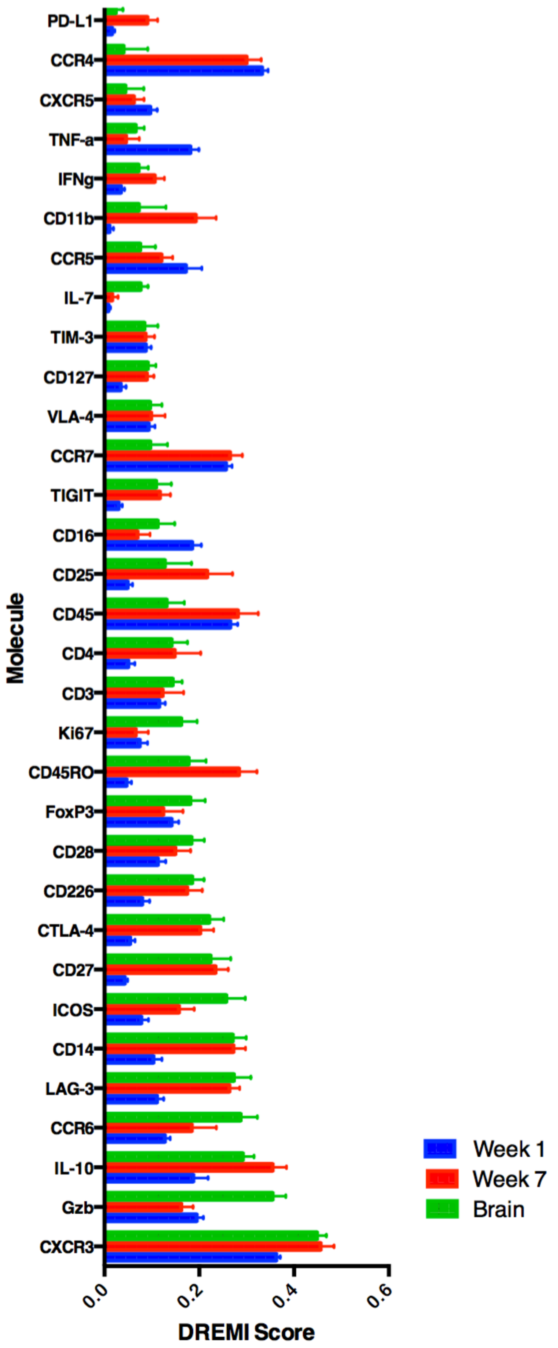
Supplementary Figure 14. **Representative gating strategy for Tregs in cytometry by time of flight (CyTOF) data.** Representative of four patients.



Supplementary Figure 15. Multi-dimensional single-cell Treg data measured by cytometry by time of flight (CyTOF). Tregs were sorted in silico as CD3$^+$CD45$^+$CD8$^-$ CD4$^+$CD127$^+$Foxp3$^+$. Single-cells organized in a nested structure by patient (shown on left colorbar) and louvain clusters (shown on right colorbar). Data for week 1 blood, week 7 blood, and tumors are shown. Transformed data represents arcsin transformed raw values.



Supplementary Figure 16. T-distributed stochastic neighbor embedding (tSNE) representation of cytometry by time of flight (CyTOF) data. a. Multidimentional tSNE plot colored according to week 1 blood, week 7 blood, or tumor. **b**. Same tSNE plots as in a, but colored according to protein.



Supplementary Figure 17. Robustness analysis of conditional-density rescaled estimate of mutual information (DREMI). DREMI was computed on measured proteins against **Programmed cell death protein 1** (PD-1) in blood from week 1, blood from week 7 and in the tumor at recurrence, in order to score and compare relationship strength. Here we compute the robustness of the DREMI scores by computing the standard deviation in DREMI scores in 100 trials where 10% of cells were randomly discarded.

Supplementary Table 1, RNA-sequencing quality control information for all samples.

Full BT and Subset Sample ID	Number of Cells	Number of reads	Mapped (%)	5'/3'
213BloodTregPD1pos	1512	1.24E+07	79.42%	0.73
213BloodTregPD1neg	5000	1.97E+07	78.37%	0.76
213TumorTregPD1pos	3900	1.49E+07	78.53%	0.63
213TumorTregPD1neg	1043	1.70E+07	78.89%	0.66
215BloodTregPD1pos	1500	1.26E+07	79.27%	0.79
215TumorTregPD1pos	1044	1.61E+07	80.38%	0.63
215TumorTregPD1neg	3617	1.35E+07	79.39%	0.71
215BloodTregPD1neg	5000	1.79E+07	79.55%	0.85
219TumorTregPD1pos	275	1.83E+07	78.32%	0.66
219TumorTregPD1neg	1728	1.79E+07	79.46%	0.65
219BloodTregPD1pos	500	1.87E+07	80.07%	0.74
219BloodTregPD1neg	2000	8.15E+05	79.21%	0.76
220TumorTregPD1pos	700	1.43E+07	80.63%	0.72
220TumorTregPD1neg	2100	1.34E+07	81.29%	0.71
220BloodTregPD1pos	700	2.23E+07	80.14%	0.78
220BloodTregPD1neg	2100	2.06E+07	79.03%	0.80
223TumorTregPD1pos	47	1.64E+07	74.60%	0.67
223TumorTregPD1neg	644	1.79E+07	77.50%	0.70
223BloodTregPD1pos	5000	1.61E+07	80.06%	0.71
223BloodTregPD1neg	185777	1.84E+07	78.96%	0.91
228BloodTregPD1pos	250	1.85E+07	78.57%	0.70
228BloodTregPD1neg	2000	3.30E+07	76.02%	0.71
228TumorTregPD1pos	76	1.76E+07	76.48%	0.65
228TumorTregPD1neg	277	1.01E+07	78.12%	0.52
229TumorTregPD1pos	27	2.00E+07	73.51%	0.67
229TumorTregPD1neg	16	1.87E+07	70.81%	0.74
229BloodTregPD1pos	378	1.28E+07	79.33%	0.60
229BloodTregPD1neg	2000	2.14E+07	79.09%	0.63
2686BloodTregPD1neg	30000	2.40E+07	81.10%	0.73
2686BloodTregtotal	30000	2.79E+07	80.43%	0.81
2686BloodTregPD1pos	20000	1.99E+07	76.67%	0.71
2687BloodTregtotal	30000	3.46E+07	79.88%	0.61
2687BloodTregPD1pos	14663	2.01E+07	77.08%	0.68
2687BloodTregPD1neg	30000	2.04E+07	80.96%	0.69

2688BloodTregPD1pos	20000	2.02E+07	80.65%	0.59
2688BloodTregtotal	30000	3.59E+07	79.55%	0.59
2688BloodTregPD1neg	30000	2.56E+07	81.61%	0.60

Supplementary Table 2, Differentially expressed genes in Programmed cell death protein 1 (PD-1)^{high} and PD-1^{-} Tregs from healthy donors.

Transcript	**Gene Symbol**	**BloodPD1negTreg_HCvsBloodPD1posTreg_HC_log2fc**	**BloodPD1negTreg_HCvsBloodPD1posTreg_HC_pvalue**	**BloodPD1negTreg_HCvsBloodPD1posTreg_HC_-log10pval**	**BloodPD1negTreg_HCvsBloodPD1posTreg_HC_fdr**
uc001qqs.3,uc001qqt.4,uc001qqu.3	LAG3	3.84	8.80E-24	23.06	1.72E-19
uc003jsh.3,uc011cqm.2,uc011cqn.2	DEPDC1B	5.15	4.04E-18	17.39	3.94E-14
uc003jpm.3	GZMA	3.76	1.29E-17	16.89	8.38E-14
uc002wcq.4,uc010fzs.3,uc010fzt.3	PDCD1	4.07	4.68E-17	16.33	1.97E-13
uc003cnx.4,uc003cny.1,uc010hiq.3,uc010hir.3	KIF15	3.83	5.05E-17	16.30	1.97E-13
uc002tgc.3,uc002tgd.2,uc010fkb.3,uc010yxh.2	BUB1	3.09	4.50E-16	15.35	1.46E-12
uc001ycb.2,uc001ycc.2,uc001ycd.3,uc001yce.1	ASB2	4.01	2.72E-15	14.57	7.12E-12
uc002qza.3	ID2	2.63	2.92E-15	14.53	7.12E-12
uc002ffm.3,uc002ffn.3	MAF	2.51	4.08E-15	14.39	8.85E-12
uc010unf.1,uc010ung.1,uc021srk.1	CTSH	3.42	2.75E-14	13.56	5.37E-11
uc001dhm.2,uc001dhn.3,uc001dho.3	AK5	-3.18	3.17E-14	13.50	5.62E-11
uc003tff.3,uc003tfg.3,uc010kxe.3,uc011kaz.2	ANLN	4.89	1.38E-13	12.86	2.24E-10
uc002bul.3,uc010bon.3,uc010boo.1,uc010urq.2,uc010urr.1,uc021sxi.1	IGF1R	-3.39	2.01E-13	12.70	3.01E-10
uc002wwp.1,uc010gdv.1	TPX2	4.44	2.62E-13	12.58	3.65E-10
uc004eqd.3,uc004eqe.3,uc010nqf.3,uc010nqg.3,uc011mtf.2,uc011mtg.2,uc011mth.2,uc011mti.2,uc011mtj.2,uc011mtl.2	PLS3	4.82	7.16E-13	12.15	9.32E-10
uc001gtu.3,uc001gtv.3,uc001gtw.4	ASPM	4.17	2.57E-12	11.59	3.14E-09
uc004eun.4,uc004eup.4,uc011muk.1,uc011mul.1	SMARCA1	-6.98	3.57E-12	11.45	4.10E-09
uc003jvm.3,uc010ixb.3,uc031sjm.1	CCNB1	4.65	4.27E-12	11.37	4.47E-09
uc001unt.3,uc001unu.3,uc001unv.3	SKA3	4.35	4.35E-12	11.36	4.47E-09
uc010dka.1,uc010dkb.1,uc010dkc.1	TYMS	6.30	4.72E-12	11.33	4.60E-09
uc002oay.3,uc002oaz.3	ZBTB32	2.88	7.68E-12	11.11	7.14E-09
uc002iup.2	NOG	-3.67	8.45E-12	11.07	7.49E-09
uc002hrg.2,uc002hrh.2,uc002hri.2,uc002hrj.1,uc002hrk.1,uc010cvr.1	PLXDC1	-2.56	9.28E-12	11.03	7.88E-09
uc010sgt.2	KLRB1	3.85	1.02E-11	10.99	8.32E-09
uc002teg.3,uc002teh.3,uc002tei.3,uc002tej.3,uc002tek.4,uc002tel.3	LIMS1	2.01	1.48E-11	10.83	1.15E-08
uc002hus.3	IGFBP4	5.11	1.54E-11	10.81	1.15E-08
uc001uvd.3,uc010abi.3,uc010tee.1,uc010tef.2,uc010teg.1,uc021ric.1,uc021rid.1	NBEA	-3.77	2.60E-11	10.59	1.88E-08
uc003iut.2,uc010irs.3	NEIL3	4.10	4.73E-11	10.33	3.30E-08
uc001hiz.4,uc009xdc.3,uc010ptb.2	DTL	5.19	6.73E-11	10.17	4.53E-08
uc002jor.1,uc002jos.4,uc010dgi.1	MYO15B	-2.25	7.69E-11	10.11	4.90E-08

uc001tnj.4,uc009zva.4,uc010sxf.3,uc031qjk.1	CORO1C	2.79	7.78E-11	10.11	4.90E-08
uc001dxx.4,uc021org.1	AMIGO1	-2.37	1.26E-10	9.90	7.66E-08
uc003sua.1,uc003sub.4,uc003sud.2,uc003sue.3,uc003suf.2,uc003suh.3,uc003sui.3,uc003suj.3,uc003suk.3,uc010kud.2,uc010kue.1,uc011jya.2,uc011jyb.2,uc011jyc.2,uc011jyd.2,uc011jye.2,uc011jyf.2	HDAC9	2.87	1.42E-10	9.85	8.39E-08
uc001tjl.3	PMCH	5.60	1.53E-10	9.81	8.81E-08
uc003qbw.4,uc003qbx.4,uc003qby.4,uc003qbz.1,uc010kfg.2,uc031spp.1	SAMD3	2.15	1.99E-10	9.70	1.11E-07
uc002huq.3,uc002hur.1	TOP2A	5.23	2.10E-10	9.68	1.14E-07
uc001rvs.2,uc001rvt.2,uc001rvu.2,uc009zlm.1	RACGAP1	2.49	2.22E-10	9.65	1.17E-07
uc003tfa.3	EEPD1	2.78	2.46E-10	9.61	1.26E-07
uc003int.3,uc003inu.1	RNF175	-4.33	2.95E-10	9.53	1.48E-07
uc002csm.3,uc002csn.3,uc002cso.3,uc002csq.3,uc010bsy.1,uc010uwn.2	PKMYT1	4.91	3.70E-10	9.43	1.81E-07
uc003lzf.3,uc003lzg.3,uc003lzh.3,uc011dem.2	HMMR	6.34	3.96E-10	9.40	1.88E-07
uc001lke.3,uc001lkf.3,uc009yav.1,uc009yaw.1	MKI67	4.50	4.67E-10	9.33	2.17E-07
uc002agk.3,uc002agl.3,uc002agm.3,uc002agn.3,uc010bgj.3,uc010uhd.2,uc021snc.1	ANXA2	2.19	5.59E-10	9.25	2.54E-07
uc003hxb.1,uc003hxc.1,uc003hxd.1	CENPE	3.09	7.80E-10	9.11	3.46E-07
uc002msy.1,uc002msz.1	ZNF433	-3.48	8.96E-10	9.05	3.89E-07
uc002kvs.4,uc002kvt.4,uc002kvu.4	TAF4B	-2.22	9.20E-10	9.04	3.90E-07
uc001jld.3,uc001jle.3,uc001jlg.3,uc010qii.2,uc021prh.1,uc031pvg.1	CDK1	6.23	1.01E-09	8.99	4.21E-07
uc002bsl.4,uc010boe.3	FAM174B	2.35	1.09E-09	8.96	4.35E-07
uc003cbh.3,uc003cbi.3,uc003cbj.3	SATB1	-1.81	1.11E-09	8.95	4.35E-07
uc002teq.4,uc010fjn.3,uc010yws.2	EDAR	-2.29	1.12E-09	8.95	4.35E-07
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uc001gvn.2	GPR25	2.45	1.16E-09	8.94	4.35E-07
uc002bnm.1,uc002bnn.1,uc002bno.3,uc002bnp.1,uc002bnq.1,uc010bnp.1	FANCI	2.04	1.18E-09	8.93	4.36E-07
uc003tir.3,uc010kxv.3	BLVRA	2.14	1.53E-09	8.82	5.51E-07
uc003ken.4	F2R	3.27	1.63E-09	8.79	5.78E-07
uc001lfg.4,uc001lfk.1,uc001lfn.5,uc001lfo.1,uc010qtl.2,uc010qtm.2,uc010qtn.2,uc010qto.2,uc010qtp.2,uc010qtq.2,uc021pzv.1,uc021pzw.1,uc021pzx.1,uc021pzy.1,uc021pzz.1,uc021qaa.1,uc021qab.1,uc021qac.1,uc031pxk.1	FGFR2	3.75	2.37E-09	8.62	8.27E-07
uc001dku.4,uc009wcm.3	SYDE2	-2.66	3.42E-09	8.47	1.17E-06
uc003wda.4	EPHA1-AS1	-2.60	3.52E-09	8.45	1.18E-06
uc002fid.3	COTL1	1.73	3.71E-09	8.43	1.23E-06
uc002iou.4,uc002iov.4,uc002iow.3	ZNF652	-1.75	3.86E-09	8.41	1.26E-06
uc001mhk.3,uc001mhl.3,uc010rbw.2,uc010rbx.2	DENND5A	-1.89	3.94E-09	8.40	1.26E-06
uc001zck.3,uc001zcl.3,uc001zcm.1,uc010azj.2,uc010uas.1,uc010uat.2	APBA2	-2.63	5.50E-09	8.26	1.72E-06

uc002kli.3	NDC80	2.20	5.56E-09	8.26	1.72E-06
uc004eji.4,uc004ejj.4,uc010nod.3,uc022cbc.1,uc022cbd.1	GPRASP1	-1.84	5.91E-09	8.23	1.75E-06
uc010ywt.1	SH3RF3	-2.76	5.92E-09	8.23	1.75E-06
uc010gce.1	ISM1	-3.16	5.93E-09	8.23	1.75E-06
uc002mbo.3,uc002mbp.3,uc010duf.3,uc010xik.2	UHRF1	5.90	6.05E-09	8.22	1.76E-06
uc003alz.3,uc003ama.3,uc010gwm.3	YWHAH	1.74	6.63E-09	8.18	1.90E-06
uc003cpo.4,uc010hjd.3,uc021wxb.1	CCR5	2.97	7.61E-09	8.12	2.15E-06
uc003cdx.4,uc003cdy.4,uc010hfn.3,uc011axc.2	EOMES	15.00	8.07E-09	8.09	2.25E-06
uc003wcz.3	EPHA1	-2.60	8.19E-09	8.09	2.25E-06
uc001tlh.4,uc031qji.1	C12orf75	1.82	9.21E-09	8.04	2.50E-06
uc003xep.1,uc003xeq.1,uc003xer.1,uc011lae.1	CDCA2	4.46	9.52E-09	8.02	2.55E-06
uc001ocp.2	CDCA5	4.84	1.10E-08	7.96	2.91E-06
uc003cpc.1,uc010hix.1,uc021www.1	CXCR6	3.20	1.15E-08	7.94	2.91E-06
uc003pnw.3,uc010kch.3,uc011eab.2	BACH2	-1.86	1.15E-08	7.94	2.91E-06
uc001wrq.3,uc010aml.3	AKAP6	-15.00	1.15E-08	7.94	2.91E-06
uc021uec.1	EPR-1	5.80	1.17E-08	7.93	2.91E-06
uc003xsq.4,uc003xsr.4,uc010lyi.3,uc010lyj.3,uc022aur.1	PLAG1	-2.46	1.18E-08	7.93	2.91E-06
uc001scj.2,uc001sck.2,uc010soe.1	ESPL1	7.35	1.44E-08	7.84	3.52E-06
uc010ppj.1,uc010ppk.1	KIF14	4.27	1.51E-08	7.82	3.63E-06
uc002ktw.3,uc002ktx.1,uc002kty.3,uc002ktz.3,uc002kua.3,uc010xap.2,uc021uid.1	RBBP8	2.19	1.58E-08	7.80	3.76E-06
uc001zoa.3,uc001zob.3,uc010bcg.2,uc010ucx.1	LTK	4.41	1.79E-08	7.75	4.22E-06
uc003zzn.4,uc010mll.4,uc010mlm.4,uc011lpm.3,uc011lpn.3,uc011lpo.3,uc011lpp.3,uc011lpq.3,uc011lpr.3,uc011lps.3,uc022bgq.2	MELK	4.27	1.90E-08	7.72	4.42E-06
uc003gzm.4,uc003gzn.3,uc011bzr.2,uc011bzs.2	USP46	2.17	2.03E-08	7.69	4.67E-06
uc001ezg.3,uc001ezh.3,uc010pdo.2,uc010pdp.2	RORC	2.97	2.21E-08	7.65	5.02E-06
uc001rdb.3,uc009zif.3,uc009zig.3,uc010shv.2	EPS8	-5.00	3.27E-08	7.49	7.33E-06
uc002jmz.1,uc002jna.1,uc002jnb.1	HN1	2.06	3.36E-08	7.47	7.46E-06
uc002jef.2	PECAM1	-2.77	4.05E-08	7.39	8.88E-06
uc003idu.4,uc003idv.4	ANXA5	1.63	4.25E-08	7.37	9.23E-06
uc003ybd.3	ZC2HC1A	1.80	4.71E-08	7.33	1.01E-05
uc003dly.2	PSMD6-AS2	-1.87	5.29E-08	7.28	1.12E-05
uc002ebq.3,uc002ebr.3,uc002ebs.1,uc010cam.1,uc010can.3,uc010vfj.1	ITGAM	2.42	6.43E-08	7.19	1.35E-05
uc001egm.3,uc001egn.3,uc001ego.1,uc001egp.4,uc010owy.2	CD58	1.68	6.87E-08	7.16	1.43E-05
uc004cyb.3,uc004cyc.3,uc004cyd.3,uc004cye.3	SCML1	-2.50	7.06E-08	7.15	1.45E-05
uc001myc.3,uc001myd.3	CD82	1.63	7.82E-08	7.11	1.59E-05
uc002mkg.3,uc010xkf.2	MYO1F	1.60	7.96E-08	7.10	1.60E-05
uc002asb.3,uc002asc.3,uc010bih.2,uc010bii.3,uc010ukc.2	KIF23	4.67	8.78E-08	7.06	1.75E-05
uc003jqp.3,uc003jqq.3,uc003jqr.3,uc010iwb.3,uc010i	IL6ST	-2.10	1.00E-07	7.00	1.96E-05

wd.3,uc010iwe.1,uc010iwf.1,uc011cqk.2					
uc002qvn.1,uc010evy.1	FAM72D	4.76	1.00E-07	7.00	1.96E-05
uc001bhe.2	E2F2	2.20	1.02E-07	6.99	1.98E-05
uc001joz.3,uc001jpa.1,uc021prx.1	SRGN	1.62	1.05E-07	6.98	2.02E-05
uc003ccg.2,uc010hfc.2	UBE2E2	-3.34	1.16E-07	6.93	2.19E-05
uc003ont.3	CCDC167	1.76	1.17E-07	6.93	2.19E-05
uc002ggi.4,uc002ggj.4,uc010cmf.3	TNK1	-1.82	1.27E-07	6.90	2.37E-05
uc002orh.1,uc010xwd.1	CEACAM4	-3.24	1.51E-07	6.82	2.77E-05
uc003ink.2,uc021xtj.1,uc021xtk.1	MND1	4.62	1.66E-07	6.78	3.00E-05
uc001iks.1,uc001ikt.3,uc001iku.3	USP6NL	-2.22	1.66E-07	6.78	3.00E-05
uc002lkm.4,uc010dqo.3,uc021uli.1	CD226	1.91	1.78E-07	6.75	3.18E-05
uc002uhq.1,uc002uhs.3,uc010zdz.1,uc010zea.1,uc010zeb.2	PDK1	-1.58	1.84E-07	6.73	3.27E-05
uc004bgf.1,uc011lwx.1	KIAA1958	-4.10	1.87E-07	6.73	3.28E-05
uc003ikc.3,uc003ikd.3,uc003ikf.3,uc010iov.3,uc011cic.2	SMAD1	3.59	1.89E-07	6.72	3.29E-05
uc002fdk.3,uc002fdl.1,uc010cgr.1,uc010vmz.1	ZNRF1	2.91	2.01E-07	6.70	3.45E-05
uc003xqk.2,uc003xql.2,uc010lxw.2,uc011ldi.2	MCM4	1.92	2.01E-07	6.70	3.45E-05
uc001fmg.3,uc010pgq.2	SYT11	1.88	2.23E-07	6.65	3.75E-05
uc003cen.3,uc003ceo.3,uc021wut.1	TGFBR2	-1.50	2.23E-07	6.65	3.75E-05
uc022cew.1,uc022cex.1	LINC00892	3.16	2.25E-07	6.65	3.75E-05
uc003xgg.3,uc003xgh.3,uc010luy.1	ESCO2	4.22	2.31E-07	6.64	3.81E-05
uc001fyz.1,uc001fza.1	FCER1G	-2.84	2.34E-07	6.63	3.84E-05
uc001dqz.4,uc010otv.2,uc010otx.2	CNN3	-3.02	2.42E-07	6.62	3.94E-05
uc001uvm.3,uc001uvn.3,uc001uvo.3,uc001uvp.2,uc001uvq.3,uc010ten.2	SPG20	-1.63	2.57E-07	6.59	4.12E-05
uc002taf.3,uc002tag.3,uc002tah.1,uc010fiq.1,uc010fir.1,uc010yvr.1	AFF3	-2.05	2.57E-07	6.59	4.12E-05
uc002wlp.3,uc002wlq.3,uc010zqs.1	PCNA	1.62	2.65E-07	6.58	4.20E-05
uc003gpp.4,uc011bxj.3	NCAPG	6.57	2.87E-07	6.54	4.52E-05
uc003gol.1,uc021xmk.1	CD38	2.69	2.90E-07	6.54	4.52E-05
uc003dyw.3,uc003dyx.3,uc003dyy.3,uc003dyz.3,uc010hqd.1	CD200	2.48	2.95E-07	6.53	4.57E-05
uc002qys.3,uc002qyu.3	RNF144A	-1.78	3.21E-07	6.49	4.93E-05
uc004ajf.1,uc004ajg.1,uc031tee.1	ANXA1	1.96	3.61E-07	6.44	5.49E-05
uc001nnl.3,uc001nnm.3,uc010rko.2,uc021qjn.1	FAM111B	2.71	3.64E-07	6.44	5.49E-05
uc003vog.3,uc003voh.3,uc003voi.3,uc003voj.4,uc003vok.2,uc010llr.1,uc010lls.1,uc010llt.3,uc010llu.1,uc010llv.1,uc010llw.1,uc011kot.1,uc011kou.1	IRF5	1.78	3.66E-07	6.44	5.49E-05
uc003ejd.2,uc011bkl.2	TXNRD3	-4.79	3.79E-07	6.42	5.64E-05
uc002xlb.1,uc010zwj.1	MYBL2	5.80	4.56E-07	6.34	6.74E-05
uc003xyx.1	MSC	2.75	4.62E-07	6.34	6.78E-05
uc003gij.3,uc003gik.3,uc011bwb.2	EVC2	2.66	4.89E-07	6.31	7.12E-05
uc001qez.3,uc001qfb.3,uc009zco.3,uc009zcp.3,uc009zcq.2	ARHGAP32	-4.21	5.01E-07	6.30	7.25E-05

uc001quy.3,uc009zgg.2	RIMKLB	-2.34	5.11E-07	6.29	7.34E-05
uc003bhl.1,uc003bhm.1,uc003bhn.3,uc011aqy.2,uc011aqz.2	GTSE1	3.26	5.67E-07	6.25	7.98E-05
uc003kgy.1,uc010jap.2,uc011ctl.2,uc011ctm.2	DHFR	1.90	5.67E-07	6.25	7.98E-05
uc003lww.3,uc003lwy.3,uc003lwz.4,uc011ddr.1,uc021ygq.1	ADAM19	2.29	5.68E-07	6.25	7.98E-05
uc003opa.3,uc003opb.3,uc003opd.3,uc003ope.3	MOCS1	-15.00	6.01E-07	6.22	8.38E-05
uc003fli.1,uc003flj.1,uc003flp.1,uc011bqr.1,uc011bqs.1	MCF2L2	1.94	6.37E-07	6.20	8.82E-05
uc021vdr.1	RRM2	4.76	6.60E-07	6.18	9.08E-05
uc003fhs.3,uc003fht.3,uc003fhu.4,uc003fhv.1	PLD1	4.16	7.17E-07	6.14	9.73E-05
uc002aco.3,uc002acp.3,uc002acq.3,uc002acr.3	RAB27A	1.57	7.18E-07	6.14	9.73E-05
uc003awr.3	APOBEC3C	1.49	7.59E-07	6.12	0.000102122
uc002qrh.2,uc002qri.2,uc002qrj.3,uc002qrk.1,uc002qrl.2,uc002qrm.2,uc010yhs.1,uc010yht.1	ZSCAN18	-1.61	7.99E-07	6.10	0.000106769
uc003xtw.1	TOX	1.54	8.89E-07	6.05	0.000118012
uc003upz.3	ARPC1B	1.42	9.00E-07	6.05	0.000118667
uc002urx.4,uc002ury.4,uc010fsb.3	INPP1	2.75	9.28E-07	6.03	0.000121562
uc001mpm.3,uc001mpn.5,uc001mpo.2,uc009yhv.3	E2F8	15.00	9.91E-07	6.00	0.000128967
uc002fnp.3,uc002fnq.3	CPNE7	4.06	1.02E-06	5.99	0.000131335
uc002icp.4,uc002icq.3,uc002ict.3,uc002icu.3,uc002idc.1,uc002idd.3,uc002ide.1,uc010cyx.3,uc010cyy.1,uc010cyz.2,uc010cza.2,uc010czc.3,uc010whl.2,uc010whm.2,uc010whn.2,uc010who.3,uc010whp.2,uc010whq.1,uc010whr.1,uc010whs.1,uc010wht.1	BRCA1	2.04	1.02E-06	5.99	0.000131335
uc002tvo.3,uc002tvp.3,uc002tvr.3,uc002tvs.3,uc002tvt.2,uc010fnn.3,uc010fno.3,uc021vqf.1,uc021vqg.1	GTDC1	1.77	1.12E-06	5.95	0.000143374
uc002tff.3,uc021vlz.1	LIMS3	2.20	1.14E-06	5.94	0.000145128
uc001hzh.3,uc009xgq.3,uc021plj.1,uc021plk.1	EXO1	3.11	1.16E-06	5.93	0.000146289
uc001stw.1	IFNG	3.77	1.17E-06	5.93	0.000146289
uc002xle.4,uc002xlf.4,uc010ggo.3,uc010ggp.3,uc010zwk.2,uc021wdz.2,uc031rtm.1	TOX2	3.94	1.24E-06	5.91	0.000153549
uc001vtv.3,uc001vtw.3,uc001vty.4,uc010agx.3,uc010tkd.2,uc010tke.2	TFDP1	1.49	1.40E-06	5.85	0.000173034
uc003srm.3,uc003srn.5,uc003sro.5,uc003srq.4,uc003srr.4,uc003srs.2,uc010ktr.3,uc010kts.4	ICA1	2.28	1.41E-06	5.85	0.000173163
uc003wnv.1,uc003wnw.1,uc003wnx.1,uc010lqu.1,uc011kwc.1,uc011kwd.1,uc011kwe.1	NCAPG2	1.81	1.42E-06	5.85	0.00017368
uc002unu.3,uc002unv.3,uc010frj.1,uc010zfl.1	ITGA4	1.39	1.46E-06	5.84	0.000177139
uc001pwf.3,uc001pwg.1	MCAM	2.98	1.47E-06	5.83	0.000177389
uc003vez.3,uc003vfa.3,uc003vfc.3,uc003vfd.3,uc003vfe.3,uc011kmj.2,uc011kmk.2,uc022aka.1	NRCAM	-15.00	1.55E-06	5.81	0.000185293
uc004dyd.1,uc004dye.1	PDZD11	1.69	1.58E-06	5.80	0.000188515
uc003pjb.4,uc003pjc.3	TTK	4.57	1.63E-06	5.79	0.000192518
uc001tyj.3,uc001tyl.3,uc001tym.3	DYNLL1	1.51	1.64E-06	5.79	0.000192914

uc003xqh.1	CEBPD	3.56	1.67E-06	5.78	0.000195246
uc004dan.3,uc004dao.3,uc004dap.3,uc004dar.3,uc004dat.1,uc011mjt.2	ACOT9	1.52	1.69E-06	5.77	0.000196458
uc001crc.1,uc001crd.1,uc001cre.1,uc001crf.1,uc001crg.1,uc010omn.1,uc010omo.1	STIL	3.36	1.77E-06	5.75	0.000204507
uc001tay.3,uc001taz.3	DUSP6	2.39	1.79E-06	5.75	0.000205404
uc001kxa.3,uc001kxb.3,uc001kxc.3,uc001kxd.1	CALHM2	1.52	1.85E-06	5.73	0.000211259
uc003qvb.1,uc003qvc.1,uc003qvd.1,uc010kkk.1,uc010kkl.1,uc011ego.1	RPS6KA2	-1.75	1.99E-06	5.70	0.000225531
uc004aqh.3	CKS2	2.51	2.14E-06	5.67	0.000241435
uc001mwo.4,uc001mwp.3,uc009ykk.3,uc010rfc.2	PRR5L	3.65	2.15E-06	5.67	0.000241694
uc002qot.3,uc002qou.3,uc010ygy.2,uc010ygz.2,uc010yha.2	ZNF772	-2.28	2.17E-06	5.66	0.000242089
uc001oht.3,uc001ohu.3,uc001ohv.3,uc009yrf.3	SLC29A2	-1.96	2.21E-06	5.66	0.000244619
uc001zci.1,uc010azf.3,uc010azg.1,uc010azh.1,uc010azi.1,uc010uap.2	WHAMMP2	-1.55	2.25E-06	5.65	0.000248428
uc003oef.4,uc011drf.2	KIFC1	5.00	2.42E-06	5.62	0.000265656
uc003giu.4,uc003giv.4,uc010idb.1,uc010idc.1,uc010idd.1,uc010ide.3,uc011bwc.2	JAKMIP1	1.53	2.59E-06	5.59	0.000282103
uc001mus.4,uc001mut.4,uc001muu.4,uc001muv.4,uc009yjx.3,uc009yjy.3,uc009yjz.3,uc009yka.3	CD59	1.73	2.80E-06	5.55	0.000303398
uc001hkm.3	CENPF	2.63	2.92E-06	5.53	0.000314967
uc003fgi.3,uc010hwq.3,uc021xhe.1	GPR160	-2.17	2.94E-06	5.53	0.000315051
uc001mlm.2,uc001mln.3,uc010rcr.2	PDE3B	-1.36	2.95E-06	5.53	0.000315051
uc002ewa.3,uc010cfe.3,uc010vlh.2	SMPD3	-1.82	3.00E-06	5.52	0.000318579
uc001lyw.4,uc009yeh.1,uc009yei.3,uc009yej.3,uc010qyc.2,uc010qyd.2	RRM1	1.40	3.06E-06	5.51	0.000323063
uc001kfr.3,uc001kfs.3,uc001kft.3,uc001kfw.3,uc009xtp.3,uc010qna.2,uc010qnb.2,uc010qnc.2,uc010qnd.2,uc010qne.2,uc031pwn.1	FAS	1.40	3.13E-06	5.50	0.000328761
uc002ffw.4,uc002ffx.2,uc002ffy.4,uc010vnl.1,uc010vnm.1	CENPN	1.83	3.24E-06	5.49	0.000337901
uc001vud.3,uc001vuf.3,uc001vug.3	GAS6	3.15	3.37E-06	5.47	0.000350247
uc001wjc.2,uc031qns.1	PPP1R3E	-1.69	3.50E-06	5.46	0.000361677
uc004edh.3,uc011mqr.2	ITM2A	1.35	3.70E-06	5.43	0.000379855
uc003wul.3,uc003wum.3,uc003wun.3,uc003wuo.3,uc003wup.3,uc003wuq.3,uc003wuu.3,uc010lsc.3,uc011kx1.2	CTSB	1.35	3.72E-06	5.43	0.000379855
uc003ype.3,uc010mdg.3	SNTB1	-1.92	3.80E-06	5.42	0.000386284
uc011jwz.2	ZNF853	-3.04	3.92E-06	5.41	0.000396007
uc001aub.3,uc001auc.3,uc001aud.4,uc001aue.1,uc009vnm.3	DHRS3	-1.65	4.02E-06	5.40	0.000404658
uc002yjx.2,uc021whl.1,uc031ruy.1,uc031ruz.1	NRIP1	-1.43	4.05E-06	5.39	0.000405549
uc001qqw.1,uc001qqx.1,uc001qqy.1,uc001qra.1,uc001qrb.1,uc009zfd.1,uc010sfn.1	GPR162	-2.97	4.14E-06	5.38	0.000412375

uc011dkv.2	ZNF204P	-1.97	4.46E-06	5.35	0.000442045
uc003idx.1	TMEM155	6.01	4.58E-06	5.34	0.000451383
uc001noq.3,uc001not.3,uc009ymv.3,uc010rla.2,uc010rlb.2	MS4A6A	4.40	4.73E-06	5.33	0.000463697
uc001cgj.3	CITED4	-1.69	4.86E-06	5.31	0.000474469
uc003cjl.3,uc021wwa.1,uc021wwb.1,uc021wwc.1,uc021wwd.1	CX3CR1	4.30	5.08E-06	5.29	0.000492891
uc001cix.3,uc001ciy.3	CDC20	5.51	5.58E-06	5.25	0.000539059
uc002ndi.2,uc002ndj.2,uc002ndk.1,uc002ndl.1	TPM4	1.33	5.96E-06	5.22	0.000573101
uc001slf.2,uc001slg.2	TIMELESS	1.78	6.12E-06	5.21	0.000585469
uc001elb.4	AK094156	-1.58	6.26E-06	5.20	0.000596231
uc001xdw.3,uc001xdx.3,uc010trv.2,uc010trw.2	DACT1	-15.00	6.52E-06	5.19	0.000617531
uc001vjt.1,uc001vju.1,uc001vjv.3,uc001vjw.1,uc001vjx.1,uc010thv.2,uc010thw.2,uc021rkq.1	LMO7	-1.69	6.67E-06	5.18	0.000629438
uc003xlp.3,uc003xlu.3,uc003xlv.3,uc003xlw.1,uc010lwf.3,uc010lwk.3,uc011lbr.2,uc011lbs.2,uc011lbt.1,uc011lbu.2,uc011lbv.2,uc011lbw.2,uc011lbx.1,uc022aua.1,uc022aub.1,uc022auc.1,uc022aud.1	FGFR1	2.27	7.40E-06	5.13	0.000694852
uc002fjz.1,uc002fka.1,uc002fkb.3	ZCCHC14	-1.56	7.50E-06	5.12	0.000700469
uc003hyt.2,uc003hyu.2,uc003hyv.2,uc003hyw.1,uc010imb.2,uc011cfj.1,uc011cfk.2	LEF1	-1.28	7.56E-06	5.12	0.000702945
uc003gxx.4,uc003gxy.1,uc010igj.3,uc011bzj.2	TXK	-1.32	7.61E-06	5.12	0.000703956
uc001xbs.3,uc001xbt.3	DLGAP5	5.20	7.77E-06	5.11	0.000715535
uc002rhr.3,uc002rhs.3,uc002rht.3	CENPA	3.90	7.82E-06	5.11	0.000716748
uc001fwf.4,uc001fwg.4,uc001fwh.4,uc001fwi.4,uc001fwj.3,uc001fwk.3,uc009wtn.3	CD84	1.35	8.25E-06	5.08	0.000749187
uc001kic.3	KIF11	3.03	8.25E-06	5.08	0.000749187
uc001ima.3,uc001imb.3,uc001imc.3	MCM10	7.94	8.42E-06	5.07	0.000760547
uc003icr.4,uc003ics.4,uc003ict.3,uc003icu.4	USP53	-1.42	8.48E-06	5.07	0.000763076
uc003gsv.4,uc011bxy.3,uc021xne.2	DTHD1	6.72	9.02E-06	5.04	0.00080757
uc002tfw.3	LIMS3	2.19	9.20E-06	5.04	0.000820281
uc001qbc.3,uc001qbd.2,uc001qbe.3,uc001qbf.1,uc010saq.2,uc010sar.2	ROBO3	-2.79	9.41E-06	5.03	0.000834929
uc004azc.3,uc004azd.3,uc004aze.3,uc011lvc.2	TGFBR1	-1.34	9.76E-06	5.01	0.000861991
uc002ckm.1	LMF1	-2.65	1.06E-05	4.98	0.000923643
uc001qmu.3,uc001qmw.3,uc009zeg.3,uc010sep.2,uc010seq.2	RAD51AP1	3.89	1.06E-05	4.98	0.000923643
uc004dau.3,uc004dav.3,uc010nfv.3,uc022bty.1,uc031tha.1	SAT1	1.32	1.08E-05	4.97	0.000941281
uc002the.2,uc002thf.4,uc010yxl.1	LOC541471	2.34	1.09E-05	4.96	0.000943879
uc002niy.3,uc002niz.3,uc010ebp.3	SSBP4	1.35	1.11E-05	4.96	0.000955213
uc003yca.2	FABP5	2.54	1.11E-05	4.95	0.000955406
uc001tqq.3	ARPC3	1.27	1.13E-05	4.95	0.000970855
uc003kdl.4,uc003kdm.4,uc010izm.3	FAM169A	-1.53	1.16E-05	4.93	0.000989986
uc002jvc.3,uc002jvd.2,uc002jve.1,uc002jvf.3,uc002jv	BIRC5	6.42	1.17E-05	4.93	0.000989986

g.3,uc002jvh.3,uc002jvi.3,uc010dhk.1,uc010dhl.1					
uc003nem.3,uc003nen.3,uc021ymn.1,uc021ymo.1	GMNN	1.86	1.21E-05	4.92	0.001021274
uc002juw.2	TK1	5.19	1.25E-05	4.90	0.001050015
uc001knh.3,uc010qov.2	PGAM1	1.32	1.26E-05	4.90	0.001054867
uc002dhv.3,uc002dhx.3,uc002dhy.4	LOC81691	3.99	1.29E-05	4.89	0.00107923
uc003zoe.2,uc003zof.3,uc011lne.1,uc011lnf.1	MLLT3	-1.31	1.33E-05	4.88	0.00110212
uc003eed.3,uc003eee.4	POLQ	2.81	1.35E-05	4.87	0.001119081
uc004erh.4	SLC25A5	1.59	1.36E-05	4.87	0.001119081
uc003wfb.2,uc003wfc.2,uc003wfd.2,uc011kug.2,uc011kuh.2,uc011kui.2,uc011kuj.2,uc022aov.1	EZH2	1.63	1.41E-05	4.85	0.001153665
uc001rxy.3,uc001rxz.3,uc001rya.3	POU6F1	-1.50	1.47E-05	4.83	0.001203362
uc002pwj.3,uc002pwk.3	NKG7	3.17	1.52E-05	4.82	0.001234519
uc003fid.3,uc003fie.3,uc010hwu.2,uc021xhk.1	TNFSF10	1.63	1.62E-05	4.79	0.001306677
uc001rtv.4,uc001rtw.4,uc001rtx.4,uc009zlh.3,uc031qhd.1,uc031qhe.1	TROAP	3.27	1.62E-05	4.79	0.001306677
uc001twr.2,uc009zws.1,uc010sza.1,uc010szb.1	WSB2	1.37	1.68E-05	4.78	0.001342442
uc002kag.3,uc002kak.2,uc002kal.2,uc021ufb.1	ACTG1	1.23	1.68E-05	4.78	0.001342442
uc003zyu.4,uc003zyv.3,uc003zyw.3,uc003zyx.3,uc010mle.1,uc031tdr.1	RECK	-1.40	1.72E-05	4.77	0.00136756
uc001mok.3,uc001mol.3,uc009yho.2,uc010rdc.1,uc010rdd.2,uc021qep.1	LDHA	1.25	1.76E-05	4.75	0.001395342
uc002ugy.4,uc002ugz.4,uc031rqa.1	CYBRD1	3.47	1.79E-05	4.75	0.001412545
uc001vog.3,uc021rma.1	GPR183	1.25	1.81E-05	4.74	0.001422898
uc003fay.1	PA2G4P4	-2.28	1.82E-05	4.74	0.00142713
uc004bdo.1,uc004bdp.1,uc010mts.1	CTNNAL1	2.27	1.88E-05	4.73	0.001467598
uc002qbu.2,uc010eqq.1	ZNF813	-1.68	1.95E-05	4.71	0.00151445
uc001bzi.3,uc009vux.3	CLSPN	1.85	1.98E-05	4.70	0.00152666
uc001pav.3,uc001paw.3,uc001pax.3,uc001pay.3,uc001paz.3,uc001pbb.3,uc001pbc.3,uc001pbd.3,uc001pbf.4,uc009yvj.3,uc010rte.2,uc010rtf.2,uc010rtg.2,uc010rth.2,uc010rti.2,uc010rtj.2	SYTL2	1.75	1.98E-05	4.70	0.00152666
uc003fbc.3	LINC00880	3.28	2.00E-05	4.70	0.001538288
uc001jlv.3,uc001jlw.3,uc001jlx.2,uc009xpf.1	RTKN2	-1.26	2.01E-05	4.70	0.001541486
uc001zyv.3	SPPL2A	1.34	2.07E-05	4.68	0.001580005
uc002uic.1,uc002uid.1,uc010zej.1,uc010zek.1	CDCA7	2.09	2.10E-05	4.68	0.001596511
uc001msc.2,uc001msd.3	KIF18A	2.02	2.12E-05	4.67	0.001601717
uc003ldh.3,uc003ldi.3,uc003ldj.3,uc003ldl.3,uc011cyx.2,uc011cyy.2	CTNNA1	1.49	2.13E-05	4.67	0.001601717
uc003oer.3,uc003oes.3,uc003oet.3,uc003oeu.4,uc010jvb.3	BAK1	1.28	2.13E-05	4.67	0.001601717
uc002klp.3,uc002klq.3	MYOM1	-2.11	2.21E-05	4.66	0.001652091
uc002ofq.3,uc002ofr.1	ZNF585B	-1.44	2.24E-05	4.65	0.001667656
uc003oon.3	KCNK5	3.25	2.29E-05	4.64	0.001700779
uc004ejk.3,uc004ejl.3,uc004ejm.3,uc022cay.1,uc022cbe.1,uc022cbf.1,uc022cbg.1,uc022cbh.1	GPRASP2	-2.00	2.31E-05	4.64	0.001701529

uc003vop.2,uc003voq.2	TSPAN33	-2.33	2.31E-05	4.64	0.001701529
uc002dca.4,uc002dcb.4	CPPED1	1.45	2.48E-05	4.61	0.001817503
uc002rwo.4,uc002rwp.2,uc002rws.2,uc010fbm.3,uc010yol.2,uc010yom.2,uc021vhf.1	STON1	3.35	2.49E-05	4.60	0.001817503
uc003awv.3,uc003aww.3,uc003awx.3,uc003awy.3,uc011aog.1,uc021wpr.1	APOBEC3F	1.27	2.50E-05	4.60	0.001823835
uc003fgn.1	AY940074	-1.68	2.53E-05	4.60	0.001834082
uc002xbc.2,uc002xbd.2,uc002xbe.2,uc010gey.2,uc010zum.1	ACSS2	-1.65	2.54E-05	4.60	0.001834082
uc002spl.2,uc002spm.2,uc010fgi.2,uc010fgj.1	CAPG	2.09	2.58E-05	4.59	0.001856216
uc003qvl.3,uc003qvm.4,uc003qvn.4,uc010kkm.3	CCR6	1.26	2.61E-05	4.58	0.001869499
uc001ozg.3,uc001ozh.3	GAB2	3.31	2.61E-05	4.58	0.001869499
uc002hhn.3,uc010ctc.3,uc010wca.1,uc021tux.1	CDK5R1	-1.36	2.70E-05	4.57	0.001922689
uc001xhn.1,uc001xho.1,uc001xhp.2,uc001xhq.1,uc010aqh.1	PLEKHG3	1.95	2.78E-05	4.56	0.001972743
uc002erk.1	FBXL8	1.90	2.79E-05	4.55	0.001975087
uc003mib.1,uc003mic.3,uc010jkp.1,uc021yix.1	FAM153A	-1.55	2.85E-05	4.55	0.002007802
uc001ezl.3	S100A10	1.56	2.86E-05	4.54	0.002008333
uc010efz.2,uc010ega.2,uc021utz.1,uc021uua.1,uc021uub.1,uc021uuc.1,uc021uud.1,uc021uue.1,uc021uuf.1	RASGRP4	1.99	2.87E-05	4.54	0.002008333
uc001udg.1,uc001udh.3,uc001udi.1,uc001udj.1,uc001udk.1	HIP1R	-1.31	2.89E-05	4.54	0.002012575
uc001usu.3	LINC00426	1.45	3.09E-05	4.51	0.002148519
uc002jlc.2,uc002jld.2,uc002jlk.3,uc010dfu.3,uc010wrb.2,uc010wrc.2,uc010wre.2	RAB37	1.24	3.14E-05	4.50	0.002155651
uc002ftx.3,uc031qxv.1	OVCA2	1.63	3.14E-05	4.50	0.002155651
uc001crw.4,uc001crx.4	BEND5	-3.06	3.14E-05	4.50	0.002155651
uc001jzi.3,uc001jzj.3,uc001jzk.3,uc001jzl.4,uc009xru.1	DLG5	3.04	3.15E-05	4.50	0.002155651
uc004ajv.4,uc004ajx.4	OSTF1	1.24	3.20E-05	4.50	0.002175065
uc002afz.3,uc031qsi.1	CCNB2	5.12	3.20E-05	4.50	0.002175065
uc001bkm.2,uc009vry.1	MAN1C1	-1.37	3.26E-05	4.49	0.002211425
uc002rqv.3,uc021vgb.1,uc021vgc.1	HNRPLL	1.25	3.28E-05	4.48	0.00221558
uc002iko.4,uc002iks.2,uc010wkd.1	ARL17A	-1.75	3.34E-05	4.48	0.002248412
uc003iwp.3,uc003iwq.3,uc003iwr.1	MLF1IP	3.04	3.46E-05	4.46	0.002320623
uc002dbf.3,uc021tda.1	SNN	-1.24	3.55E-05	4.45	0.002373257
uc003ita.3,uc003itb.2,uc011ckc.1	HMGB2	1.64	3.80E-05	4.42	0.002532191
uc002fgt.3,uc010chg.1	PLCG2	15.00	3.85E-05	4.41	0.002553788
uc002jfh.3,uc002jfi.3,uc002jfj.1,uc010den.1	AXIN2	-1.79	3.93E-05	4.41	0.002597729
uc004blh.4,uc004bli.4,uc011lyk.3,uc031tew.1,uc031tex.1	STOM	1.68	3.98E-05	4.40	0.002624079
uc002tzk.4,uc002tzl.4,uc010foe.3,uc010fof.3	ACVR1C	-2.98	4.05E-05	4.39	0.002659513
uc003tmg.2,uc003tmh.2,uc003tmi.1,uc003tmj.2,uc010kym.2,uc022acj.1	MYO1G	1.20	4.14E-05	4.38	0.002712531
uc003fdf.1,uc003fdg.1,uc003fdh.3,uc003fdi.3,uc003fdj	SMC4	1.60	4.28E-05	4.37	0.002793841

.3,uc003fdl.3,uc010hwc.1,uc010hwd.3					
uc003bdk.3	BIK	2.61	4.38E-05	4.36	0.002846737
uc001ffq.3	PMVK	1.78	4.45E-05	4.35	0.002889063
uc002ank.3,uc002anl.3	KIAA0101	4.64	4.48E-05	4.35	0.002893588
uc003hvn.1,uc003hvo.1	H2AFZ	1.18	4.51E-05	4.35	0.002898087
uc002ete.1,uc010vjn.1,uc010vjo.1	ATP6V0D1	1.25	4.51E-05	4.35	0.002898087
uc004cks.2,uc004ckt.2	NPDC1	1.43	4.63E-05	4.33	0.002964825
uc001efv.1,uc009wgy.1,uc021ose.1	VANGL1	2.13	4.73E-05	4.33	0.003015426
uc004ckj.1	CLIC3	4.34	4.74E-05	4.32	0.003015493
uc003kha.2,uc003khb.1,uc011ctn.2	RASGRF2	-1.45	4.77E-05	4.32	0.003023997
uc002rqy.3	GALM	1.24	5.01E-05	4.30	0.003164086
uc003cek.3,uc003cel.3,uc003cem.3,uc010hfq.3,uc010hfr.3	RBMS3	-2.06	5.22E-05	4.28	0.003287986
uc002lbu.3,uc002lbv.3	HAUS1	1.35	5.24E-05	4.28	0.00329077
uc003tvv.4,uc003tvw.4,uc003tvx.4,uc011keg.2	AUTS2	1.94	5.29E-05	4.28	0.003311743
uc003wfr.4,uc003wft.4,uc003wfu.3	LOC155060	-1.31	5.41E-05	4.27	0.003371511
uc001yvg.3,uc010ayc.3,uc010ayd.3,uc010aye.1	WHAMMP3	-1.38	5.49E-05	4.26	0.003415416
uc001gen.4,uc001geo.3,uc001gep.3,uc001geq.3,uc009wvh.3,uc031prf.1	MPZL1	-1.63	5.61E-05	4.25	0.00347845
uc004eaf.3,uc011mpx.2,uc022bys.1	CXCR3	1.89	5.63E-05	4.25	0.00347845
uc001mhs.3,uc001mht.3,uc001mhu.3	WEE1	1.36	5.69E-05	4.25	0.003501184
uc001fga.3,uc001fgb.3	CKS1B	1.50	5.78E-05	4.24	0.00354625
uc001rfs.3,uc001rft.3,uc009ziz.3	ETNK1	-1.17	5.92E-05	4.23	0.003622526
uc002eec.4	SHCBP1	3.25	5.97E-05	4.22	0.003641592
uc002jal.4,uc002jam.1,uc002jan.1,uc002jao.4,uc010wpe.2	TANC2	-2.47	6.03E-05	4.22	0.003669777
uc001gcq.1,uc001gcr.1	NUF2	2.39	6.14E-05	4.21	0.003710372
uc002xmj.3	ADA	1.23	6.14E-05	4.21	0.003710372
uc003owu.1,uc003owv.1,uc003oww.1,uc003owx.2,uc003owy.2,uc003owz.1,uc011dvp.1,uc011dvq.2,uc021yzw.1,uc021yzx.1	SLC29A1	1.84	6.18E-05	4.21	0.003721867
uc003prd.2,uc003pre.3	PRDM1	1.22	6.20E-05	4.21	0.003722154
uc003mll.1,uc003mlm.1	RNF130	-1.43	6.22E-05	4.21	0.003722195
uc001znr.4,uc001zns.4,uc001znt.4,uc001znu.4,uc001znv.4,uc001znw.4,uc010ucw.2	NUSAP1	3.37	6.53E-05	4.18	0.00390023
uc003vvh.3,uc003vvi.3,uc003vvj.3,uc010lne.3,uc011kqu.2,uc011kqv.2,uc011kqw.2,uc011kqx.1	TBXAS1	2.75	6.72E-05	4.17	0.003992714
uc003kor.1	AK021888	-4.66	6.73E-05	4.17	0.003992714
uc003iec.4	CCNA2	3.75	6.75E-05	4.17	0.003992714
uc001hce.3,uc009xbj.1	NUAK2	-1.76	6.78E-05	4.17	0.003997268
uc003kdn.3	GCNT4	-1.42	6.91E-05	4.16	0.004060651
uc003pyt.4,uc003pyu.2,uc003pyv.2	HSF2	-1.28	7.12E-05	4.15	0.004162805
uc002jdp.1,uc002jdq.1,uc002jdr.1	CD79B	1.31	7.12E-05	4.15	0.004162805
uc004cqm.3,uc004cqn.4,uc010nda.3	CD99	1.82	7.20E-05	4.14	0.004193249
uc002rmr.4,uc002rms.1,uc010ezl.3,uc010ymm.2	FAM179A	2.24	7.39E-05	4.13	0.004292992

uc002ldw.4	ACAA2	1.23	7.71E-05	4.11	0.004463885
uc002hez.2,uc010wbn.2	BLMH	1.42	7.86E-05	4.10	0.004540463
uc001ayw.4,uc001ayz.1,uc001aza.5,uc001azb.1,uc001azc.2,uc009vot.1,uc010oce.1	NBPF1	-1.35	8.26E-05	4.08	0.004754637
uc002dod.4,uc002doe.2,uc010vcl.2	ZKSCAN2	-2.10	8.35E-05	4.08	0.004791331
uc002xwf.1,uc002xwg.1,uc010gih.1	ATP9A	5.52	8.48E-05	4.07	0.004854105
uc002ilv.1	TBX21	2.12	8.56E-05	4.07	0.004882697
uc002sfr.4,uc002sfs.4,uc010yqn.1,uc010yqo.2	ANXA4	1.51	8.61E-05	4.06	0.004882697
uc003wgn.4,uc011kur.2	ATP6V0E2-AS1	-1.69	8.62E-05	4.06	0.004882697
uc003taz.3,uc003tba.3,uc003tbb.3,uc003tbc.3,uc022abe.1,uc022abf.1	GGCT	1.33	8.64E-05	4.06	0.004882697
uc002vvg.3,uc010znd.2,uc010zne.2	HJURP	4.51	8.65E-05	4.06	0.004882697
uc002ypn.2	URB1	-1.64	8.83E-05	4.05	0.004969917
uc003iwg.3,uc003iwh.3,uc003iwi.3	CASP3	1.23	8.97E-05	4.05	0.005033768
uc001xjf.3	ATP6V1D	1.32	9.01E-05	4.05	0.0050383
uc001zgw.3,uc001zgy.1,uc010ubw.1,uc010ubx.1	ARHGAP11A	1.51	9.14E-05	4.04	0.005098617
uc003ukt.1,uc003uku.1,uc003ukv.1,uc003ukx.1,uc003uky.2,uc003ukz.1,uc010les.1,uc011khl.1	CDK14	2.11	9.21E-05	4.04	0.005113406
uc001ade.3,uc001adf.3	TNFRSF4	2.22	9.22E-05	4.04	0.005113406
uc002kky.3,uc002kkz.3	YES1	-1.56	9.26E-05	4.03	0.005122089
uc002efk.2,uc021tht.1	LOC100507577	-1.30	9.37E-05	4.03	0.00516675
uc021yfx.1,uc021yfy.1,uc021yfz.1	ZNF300	-3.67	9.78E-05	4.01	0.005379848
uc001bqa.2,uc001bqb.2,uc001bqc.2,uc001bqe.2,uc001bqf.2,uc001bqg.2	RCC1	1.41	9.85E-05	4.01	0.005403454
uc002znb.3	DQ570096	-1.75	9.93E-05	4.00	0.005420556
uc002sdj.2,uc002sdk.4,uc002sdl.4,uc010yqb.1,uc010yqc.2,uc010yqd.1	CEP68	-1.22	9.94E-05	4.00	0.005420556
uc002evt.2,uc002evu.2,uc002evv.2,uc010cfb.2,uc010cfc.1	SLC7A6	-1.14	0.000101097	4.00	0.005496975
uc003kfy.4,uc010jab.4,uc010jac.4,uc010jad.4	HOMER1	-3.00	0.000102494	3.99	0.005542515
uc003keo.3	F2RL1	-1.73	0.000102633	3.99	0.005542515
uc002vsy.2	TIGD1	-1.22	0.000102786	3.99	0.005542515
uc002tuw.4	MCM6	1.22	0.000103722	3.98	0.005577567
uc003xuw.3	GGH	1.99	0.000105778	3.98	0.005660563
uc002wia.1,uc002wib.1	LZTS3	-2.03	0.000105846	3.98	0.005660563
uc004dyf.2,uc004dyg.3,uc010nkw.3	KIF4A	5.54	0.000107032	3.97	0.005708384
uc001tei.3,uc009ztf.3,uc009ztg.3	NTN4	3.71	0.000108716	3.96	0.005782391
uc001hpw.3,uc010pvl.2,uc021pjv.1	H3F3A	1.11	0.000109395	3.96	0.005802694
uc002rly.3	LOC100505716	-2.08	0.000109725	3.96	0.005804408
uc001jrv.3,uc001jrw.4,uc001jrx.4,uc001jry.3,uc001jrz.3,uc001jsc.1,uc001jsg.4,uc001jsh.4,uc001jsi.4,uc001jsj	CDH23	-1.57	0.000110088	3.96	0.0058079

.4,uc009xql.3,uc010qjr.2,uc021psl.1					
uc001xap.3,uc001xar.3,uc010aoi.1,uc010aoj.2	CDKN3	2.83	0.000110411	3.96	0.005809249
uc003lcp.1,uc003lcq.1,uc003lcr.1,uc003lcs.1,uc003lct.1,uc003lcu.1,uc010jet.1,uc011cyp.1,uc031slf.1	CDC25C	15.00	0.000112268	3.95	0.005891041
uc001oma.4,uc009yry.4,uc031qbz.1	CDK2AP2	1.19	0.000114393	3.94	0.00598644
uc003yia.3,uc010mbg.3	LAPTM4B	-1.41	0.00011484	3.94	0.005993779
uc011bds.2	DOCK3	-2.50	0.000115718	3.94	0.00602351
uc001dhg.4,uc001dhh.2,uc010orh.1	ST6GALNAC3	-2.83	0.000117316	3.93	0.006090426
uc003jpl.1	GZMK	3.92	0.000118896	3.92	0.006156103
uc002vry.4	NMUR1	2.93	0.000124159	3.91	0.006411593
uc002kyl.3,uc002kym.3,uc002kyn.1,uc002kyo.1	ZSCAN30	-1.37	0.000131752	3.88	0.00677469
uc003geu.1,uc003gev.1,uc021xko.1,uc021xkp.1	MXD4	1.15	0.000131966	3.88	0.00677469
uc002aga.4	MYO1E	4.39	0.000132231	3.88	0.00677469
uc001tuz.3,uc001tva.3,uc001tvb.3,uc001tvc.3,uc001tvd.1	SLC24A6	-1.12	0.000133819	3.87	0.006838063
uc001zht.3,uc001zhu.3,uc001zhv.3,uc001zhw.3,uc001zhx.3,uc001zhy.3,uc001zhz.3,uc001zia.3,uc001zib.3,uc001zic.3,uc001zid.3,uc010bau.3	SLC12A6	-1.13	0.00013709	3.86	0.006986948
uc003zxj.3,uc010mkx.2,uc011lox.2,uc011loy.2,uc022bgm.1	CCDC107	1.24	0.000138566	3.86	0.007043775
uc003bmb.5,uc003bmc.5,uc003bmd.5,uc003bme.5,uc010hbd.4,uc011arz.1	TYMP	2.23	0.000140164	3.85	0.007106491
uc002jgk.3,uc002jgl.3	KPNA2	1.66	0.000140995	3.85	0.007119546
uc002vpl.2,uc002vpm.2	CCL20	5.62	0.000141487	3.85	0.007119546
uc003xbv.3,uc003xbw.4,uc011kzk.1	SORBS3	-1.37	0.000141516	3.85	0.007119546
uc003ehe.3,uc003ehf.1,uc003ehg.3,uc003ehh.1,uc003ehi.3,uc003ehj.2,uc003ehk.3,uc010hru.2,uc010hrv.1,uc010hrw.2,uc011bjy.1,uc011bjz.2	KALRN	-1.48	0.00014715	3.83	0.007366973
uc001zvu.4,uc001zvv.4	SQRDL	1.16	0.000147341	3.83	0.007366973
uc003pum.3	GTF3C6	1.36	0.000147566	3.83	0.007366973
uc003utt.3,uc003utu.3,uc022aii.1	GAL3ST4	-1.38	0.000148283	3.83	0.007383898
uc003wir.2,uc003wis.2,uc022apy.1	CDK5	1.63	0.000149642	3.82	0.007423208
uc002tfc.3,uc002tfe.1,uc021vly.1	RGPD6	-2.12	0.000150165	3.82	0.007423208
uc002qzx.3	YWHAQ	1.12	0.000150491	3.82	0.007423208
uc002jfd.3,uc002jfe.3,uc002jfg.3,uc010dem.3,uc021ubw.1	RGS9	3.56	0.000150799	3.82	0.007423208
uc004ebr.1,uc010nlq.1	FTX	-1.35	0.000150974	3.82	0.007423208
uc010fhg.4	ANKRD36BP2	-3.81	0.000154371	3.81	0.007566136
uc002ohb.2,uc002ohc.2	ZNF607	-1.59	0.000154656	3.81	0.007566136
uc001nfh.2	PSMC3	1.15	0.000156004	3.81	0.007593164
uc004erq.3,uc004err.3,uc022cdk.1	NKRF	-1.34	0.000156026	3.81	0.007593164
uc001zmi.4,uc001zml.4,uc001zmm.1,uc001zmn.1,uc010bbw.3,uc010bbx.3	RAD51	3.94	0.000156376	3.81	0.007593164

uc001ywk.3	NDN	3.80	0.000157014	3.80	0.007605264
uc001lvu.3,uc021qcf.1	ASCL2	15.00	0.000157849	3.80	0.007626748
uc003xtz.1,uc003xua.1,uc003xub.3	CA8	15.00	0.000159823	3.80	0.007703064
uc003xue.3,uc003xuf.3,uc022aux.1	CHD7	-1.13	0.000160338	3.79	0.007708858
uc003hub.3,uc011cdz.2	TSPAN5	1.17	0.000164994	3.78	0.007913211
uc001vft.1,uc010tgq.1	LINC00282	-2.63	0.000166272	3.78	0.007954965
uc002owp.3,uc010eiu.1	ETHE1	1.42	0.000169277	3.77	0.008078965
uc003fsv.3,uc003fsw.3	CCDC50	1.43	0.000171534	3.77	0.008166711
uc001gpa.2,uc001gpb.2,uc001gpc.2,uc001gpd.2,uc010pnt.2,uc021pfv.1,uc021pfw.1	GLUL	-1.13	0.000175535	3.76	0.008336861
uc001dyt.2,uc001dyu.2,uc001dyw.4,uc021orj.2	CSF1	1.27	0.00018061	3.74	0.008557071
uc002lmd.3,uc021ulp.1	ZNF516	-2.66	0.000181818	3.74	0.008593426
uc001xgh.4,uc001xgi.4,uc021ruf.1,uc031qox.1	WDR89	-1.18	0.000182336	3.74	0.008597109
uc003nwr.3	CLIC1	1.28	0.000184742	3.73	0.008689548
uc003slw.3	SNX8	1.97	0.000185217	3.73	0.008690955
uc003kbk.3,uc010iyn.3,uc010jmw.1,uc011crv.1,uc011crw.1,uc011crx.1	GUSBP9	-1.33	0.000186497	3.73	0.008730009
uc001uey.1	RILPL2	1.27	0.00019147	3.72	0.008941352
uc001iig.2,uc001iih.2,uc001iii.2,uc009xic.2	ASB13	-1.44	0.000192692	3.72	0.008976968
uc001bmp.4	HMGN2	1.06	0.000197775	3.70	0.009191852
uc003yov.3	DSCC1	4.15	0.000200528	3.70	0.009297648
uc003hpi.1,uc003hpj.3,uc003hpk.3,uc003hpl.3,uc003hpm.3,uc010ikf.3	ARHGAP24	15.00	0.000205651	3.69	0.009512573
uc003yad.3,uc022awb.1	LY96	2.53	0.00021007	3.68	0.009694003
uc011bgy.3	GPR15	1.86	0.000211517	3.67	0.00973778
uc003lwk.2,uc003lwl.3	HAVCR2	1.47	0.000214983	3.67	0.00987404
uc003soq.4,uc003sor.4,uc003sot.4,uc011jwi.1	ACTB	1.05	0.000216167	3.67	0.009885146
uc001izb.4,uc001izc.4,uc001izd.2,uc009xmc.2,uc010qeu.2,uc031pue.1,uc031pug.1	ZNF248	-1.15	0.000216799	3.66	0.009885146
uc001alm.1,uc001aln.3	AJAP1	-5.34	0.000217289	3.66	0.009885146
uc001urx.3,uc001ury.3,uc001urz.3,uc010tdo.1	PAN3	-1.17	0.000217336	3.66	0.009885146
uc002ffu.3	CMC2	1.22	0.000217757	3.66	0.009885146
uc009wka.2	AK094156	-1.42	0.000221124	3.66	0.010014702
uc001oif.2,uc001oig.2,uc001oih.2,uc010rpe.2	DPP3	1.21	0.000223623	3.65	0.010104443
uc001pkb.1,uc001pkc.1,uc001pkd.4,uc001pke.2,uc001pkf.3,uc001pkg.1,uc009yxr.1,uc009yxs.1,uc009yxt.1	ATM	-1.06	0.000224864	3.65	0.010137048
uc021wps.1,uc021wpt.1,uc021wpu.1,uc021wpv.1	APOBEC3H	3.29	0.000228707	3.64	0.010248122
uc001rln.4	ALG10B	-1.26	0.000228956	3.64	0.010248122
uc002wpo.3,uc002wpp.3,uc010zrn.2,uc010zro.2	BFSP1	4.72	0.000229843	3.64	0.010248122
uc001oku.1,uc001okv.1,uc001okw.1,uc001okx.1	PPP1CA	1.05	0.000229885	3.64	0.010248122
uc003pyw.1	BC022047	-1.62	0.000229953	3.64	0.010248122
uc002xay.3,uc002xaz.1,uc002xba.1,uc010gex.3	GGT7	-1.24	0.000232462	3.63	0.010336358
uc003nac.3,uc011diq.2	HIVEP1	-1.81	0.000234288	3.63	0.010393868
uc001pkk.3,uc010rvy.2,uc010rvz.2	EXPH5	-1.88	0.000235251	3.63	0.010412933
uc003zsv.2,uc003zsx.3,uc010mju.3	AQP3	1.08	0.00023895	3.62	0.010552739

uc001bce.3,uc009vpk.3,uc010ocz.2,uc021ohr.1	CAPZB	1.06	0.000240672	3.62	0.010604785
uc002hqr.3	PSMB3	1.26	0.000245138	3.61	0.010777242
uc004ckq.2	FUT7	1.25	0.000250016	3.60	0.010966995
uc002sdh.3,uc010ypz.2,uc010yqa.2	SLC1A4	1.83	0.000251942	3.60	0.011026682
uc002qom.3,uc002qon.3	ZNF548	-1.14	0.000254054	3.60	0.011094259
uc010ydi.2,uc010ydj.2	ZNF836	-1.33	0.000257282	3.59	0.01118823
uc001blu.3	SH3BGRL3	1.25	0.000257605	3.59	0.01118823
uc001hsn.4,uc001hso.3,uc001hsp.2,uc001hsq.2,uc001hsr.1,uc009xez.2,uc009xfa.3	OBSCN	-1.33	0.000257925	3.59	0.01118823
uc003idl.2,uc003idm.2	MAD2L1	1.32	0.000258758	3.59	0.011199457
uc001dej.4,uc001dek.4,uc001del.4,uc001dem.4	DEPDC1	3.27	0.000260975	3.58	0.011270432
uc001rgc.3,uc001rgd.4,uc001rge.4,uc010six.2,uc010siy.2	BCAT1	7.15	0.000264021	3.58	0.0113768
uc002jkj.2,uc002jkk.2,uc002jkl.2,uc002jkm.4	KIF19	2.88	0.000267463	3.57	0.01145979
uc002wzu.4	E2F1	2.49	0.000268014	3.57	0.01145979
uc002ill.1,uc002ilm.3,uc002iln.3,uc010daz.1	EFCAB13	-1.73	0.000268085	3.57	0.01145979
uc002lht.3,uc010dpo.1,uc010xej.1,uc021uky.1	SEC11C	1.17	0.000268295	3.57	0.01145979
uc003nas.2,uc003nat.2,uc003nau.3,uc003nav.3,uc021ylt.1,uc021ylu.1,uc031smu.1	GFOD1	3.11	0.00026986	3.57	0.011501438
uc001nsg.3,uc021qkj.1	FEN1	1.70	0.00027049	3.57	0.011503204
uc002gaq.3,uc021tog.1	ZFP3	-1.45	0.000272001	3.57	0.011542311
uc001iou.2	VIM	1.05	0.000274524	3.56	0.011624099
uc002qbb.2,uc002qbc.2,uc010eql.2	ZNF347	-1.44	0.000277638	3.56	0.011722678
uc002vbz.2,uc002vca.2,uc010zix.2,uc031rqz.1,uc031rra.1,uc031rrb.1	KLF7	-1.57	0.000278053	3.56	0.011722678
uc001rmz.3	ZCRB1	1.24	0.000281645	3.55	0.011848529
uc002dlz.1	PLK1	4.05	0.000285567	3.54	0.011973266
uc001xkk.3,uc001xkl.3,uc001xkm.3,uc001xkn.3,uc001xko.1,uc010ttb.2,uc010ttc.2,uc010ttd.1	ACTN1	-1.05	0.000285837	3.54	0.011973266
uc002ily.3,uc002ilz.3,uc010wky.2	MRPL10	1.10	0.000291254	3.54	0.012174032
uc002flu.3	CDT1	3.25	0.000294805	3.53	0.012296156
uc003qil.2,uc003qim.2	ABRACL	1.10	0.000297001	3.53	0.012323878
uc004duu.4,uc004duv.4,uc004duw.4,uc004dux.1,uc010nkj.2,uc022bxv.1	SPIN3	-1.12	0.000297059	3.53	0.012323878
uc001tuw.3,uc001tux.3,uc010syt.1,uc010syu.2	TPCN1	-1.32	0.000297364	3.53	0.012323878
uc002ist.1	AK090674	-1.22	0.000298272	3.53	0.012335307
uc001ont.3,uc009ysg.4	LRP5	-4.97	0.000306065	3.51	0.012630844
uc002vds.3,uc002vdt.3,uc002vdv.3,uc002vdw.3,uc002vdx.1,uc002vdy.1	KANSL1L	-1.73	0.000307315	3.51	0.01265568
uc001eyn.1,uc001eyo.3,uc001eyp.3,uc021oys.1,uc031ppc.1	SNX27	-1.32	0.000309017	3.51	0.012698956
uc001cdr.3,uc010oix.2	HPCAL4	-1.46	0.000312141	3.51	0.012800399
uc003jhs.2,uc003jht.2	SUB1	1.07	0.000312877	3.50	0.012803705
uc004auw.4,uc010mrl.3	FBP1	-2.26	0.000318943	3.50	0.013024637
uc003okl.3,uc003okm.3,uc003okn.3,uc010jvv.1,uc011	PPARD	-1.20	0.000325737	3.49	0.013274275

dtb.2,uc011dtc.2					
uc002cgs.2	MRPL28	1.19	0.00033434	3.48	0.01359648
uc004drv.3,uc004drw.3,uc004drx.1	TSPYL2	-1.04	0.00033547	3.47	0.013614099
uc001rcu.2,uc001rcv.2,uc001rcw.2,uc001rcx.2,uc001rcy.2,uc001rcz.2,uc001rda.2	PTPRO	-2.09	0.000338695	3.47	0.013716438
uc002fxz.4,uc002fya.4,uc002fyb.4,uc010vsa.2	MYBBP1A	-1.11	0.000340078	3.47	0.013743944
uc021vlv.1	SH3RF3-AS1	-2.63	0.00034573	3.46	0.013943484
uc001uyw.2,uc001uyx.2	EPSTI1	1.34	0.000350413	3.46	0.014086411
uc003njx.3	HIST1H1B	4.27	0.000351914	3.45	0.014086411
uc001wtd.3,uc010tpt.2,uc010tpu.2	PSMA6	1.13	0.000352028	3.45	0.014086411
uc003hrv.4,uc003hrw.2,uc011cdn.2,uc011cdo.2	HERC3	-1.06	0.00035216	3.45	0.014086411
uc001ikr.1	AF007147	-1.79	0.000364554	3.44	0.014552347
uc002snd.3	HK2	-1.40	0.000365921	3.44	0.014577092
uc001pfw.1	MAML2	-1.15	0.000369888	3.43	0.014705106
uc010zhw.2,uc010zhx.2	FAM117B	-1.42	0.000371773	3.43	0.014750032
uc004avh.3,uc004avi.4,uc010mrm.1,uc011lul.1,uc022bkl.1	FANCC	-1.76	0.00037337	3.43	0.014783348
uc001kcc.4,uc001kcd.4,uc001kce.4,uc001kcf.4,uc021pux.1,uc021puy.1	FAM213A	-1.80	0.00037523	3.43	0.014810771
uc002svz.1,uc010fhu.1,uc010fhv.1,uc010yum.1,uc010yun.1	NCAPH	3.56	0.000375841	3.42	0.014810771
uc002omq.4,uc002omr.4	PSMC4	1.07	0.000376339	3.42	0.014810771
uc004ayt.3,uc004ayu.3,uc004ayv.2,uc004ayx.2,uc004ayy.2	ANKS6	-1.23	0.000382196	3.42	0.015010984
uc003dso.2,uc003dsp.3,uc003dsq.3,uc003dsr.3,uc003dss.3,uc003dst.3,uc003dsu.3,uc003dsv.3	CLDND1	1.04	0.000383417	3.42	0.015028706
uc003lbr.5,uc003lbs.1,uc010jek.3,uc010jel.1,uc010jem.1,uc010jen.2,uc011cyc.2,uc011cyd.3,uc031sle.1	KLHL3	-1.13	0.000384789	3.41	0.01505225
uc001cpl.2,uc009vye.2	RAD54L	3.65	0.000386999	3.41	0.015101893
uc001ada.3,uc001adb.3,uc001adc.3,uc001add.3	TNFRSF18	2.39	0.000387605	3.41	0.015101893
uc001tgd.2,uc001tge.2,uc001tgf.2,uc001tgg.4,uc001tgh.4,uc001tgi.3,uc001tgj.3,uc001tgk.3,uc009ztp.3,uc009ztr.3,uc009zts.2,uc009ztt.1,uc010svd.2,uc010sve.2,uc010svf.2,uc010svg.2	ANKS1B	2.71	0.000388463	3.41	0.015105192
uc001bmc.3,uc009vsg.1	CD52	1.28	0.000392976	3.41	0.015250288
uc003pfx.1	OGFRL1	1.47	0.000397398	3.40	0.0153913
uc001pxx.3,uc010rzp.1,uc010rzq.1	SORL1	-1.08	0.000405115	3.39	0.015659082
uc002zdr.4	CSTB	1.40	0.000418639	3.38	0.016149883
uc002csj.4,uc002csk.4,uc002csl.4,uc010uwm.2	PAQR4	2.58	0.000421474	3.38	0.016227154
uc001uog.2	FGF9	-3.16	0.000422773	3.37	0.01624514
uc002qpc.4,uc002qpd.4,uc002qpe.1,uc010eue.3,uc031rnf.1	ZNF550	-1.10	0.000425572	3.37	0.016320549
uc002xwx.3	PFDN4	1.25	0.000429311	3.37	0.016405676
uc001ein.4,uc009whp.3	FAM72B	4.23	0.000429472	3.37	0.016405676
uc002vhd.4,uc002vhe.3,uc002vhf.3	ARPC2	1.01	0.000430549	3.37	0.016414696

uc003cva.4,uc011bbw.2	SLC25A20	1.37	0.000436889	3.36	0.01662392
uc002hkf.3	CCL5	1.37	0.000442937	3.35	0.016821254
uc003qao.3	CENPW	3.80	0.000449125	3.35	0.016998733
uc001hyi.4,uc010pxv.1,uc010pxw.2,uc010pxx.2,uc010pxy.2	MTR	-1.06	0.000449352	3.35	0.016998733
uc003bxj.2,uc003bxk.2	CAND2	-2.68	0.000452368	3.34	0.017079731
uc001kiq.4,uc009xug.3	CEP55	4.00	0.000453922	3.34	0.017092096
uc001iwr.4,uc001iws.4,uc001iwt.4	ITGB1	1.02	0.000454447	3.34	0.017092096
uc002pzq.2,uc010epq.1,uc010epr.2	ZNF808	-1.12	0.000458467	3.34	0.017210154
uc003fuj.3	FAM43A	2.22	0.000470786	3.33	0.01763868
uc001uzf.4,uc010acg.3	LACC1	2.19	0.000478764	3.32	0.017903222
uc001bzh.1,uc021oli.1	C1orf216	1.26	0.00048879	3.31	0.018243172
uc003ejp.4,uc010hsl.3,uc011bkm.3,uc011bkn.2	MCM2	1.84	0.000490756	3.31	0.018281613
uc001slj.3,uc001slk.3,uc001sll.3,uc009zos.3,uc009zot.3,uc021qzb.1,uc021qzc.1,uc021qzd.1	GLS2	-1.68	0.000492259	3.31	0.018302667
uc003jbr.3,uc010ite.2	TRIP13	2.94	0.000502918	3.30	0.018638472
uc002jap.3,uc002jaq.3,uc002jar.3,uc002jas.3,uc002jat.3,uc010ddt.3,uc010wpf.2,uc010wpg.2	CYB561	1.86	0.000503201	3.30	0.018638472
uc002qsw.2	ZNF324	-1.18	0.000507718	3.29	0.018770181
uc004awi.3,uc004awj.3,uc004awk.3,uc004awl.3	CDC14B	-1.17	0.000512049	3.29	0.018894507
uc004ajy.2,uc004ajz.3,uc004aka.3,uc004akb.3,uc004akc.2	PCSK5	-2.84	0.000513683	3.29	0.018919032
uc003qds.3,uc003qdt.3,uc003qdv.3,uc010kgb.3,uc031sps.1,uc031spt.1	VNN2	-1.16	0.000515137	3.29	0.01893688
uc002was.3,uc002wat.1,uc002wau.1,uc010fzm.1	PPP1R7	1.07	0.000521708	3.28	0.019060882
uc001qop.2,uc021qtv.1,uc031qfw.1	GAPDH	1.34	0.000522003	3.28	0.019060882
uc001esg.4,uc010pbf.2	BC023516	-1.07	0.000522649	3.28	0.019060882
uc001wzb.4,uc001wzc.3,uc001wzd.3,uc001wze.3,uc001wzf.3,uc001wzg.3	FRMD6	-3.92	0.000522769	3.28	0.019060882
uc003kvm.2,uc003kvn.2,uc003kvo.2,uc003kvp.2,uc003kvq.3,uc003kvr.3,uc003kvs.1,uc003kvt.1,uc003kvu.3,uc010jdi.2,uc010jdj.2,uc010jdk.3,uc010jdm.1,uc011cxe.2	RAPGEF6	-1.02	0.000523393	3.28	0.019060882
uc004dnb.3,uc010nip.3,uc031tjm.1	CACNA1F	-3.65	0.00052913	3.28	0.019233907
uc004dah.3,uc011mjr.2,uc011mjs.2	PHEX	15.00	0.000533213	3.27	0.019318415
uc003ahb.3	OSM	1.94	0.000533434	3.27	0.019318415
uc003yke.3,uc003ykf.3,uc003ykg.3,uc003ykh.3,uc003yki.3,uc003ykj.3,uc003ykk.3,uc003ykl.3	NCALD	1.51	0.000535233	3.27	0.019347667
uc001npp.3,uc001npq.3,uc009ymy.1,uc009ymz.3,uc009yna.3,uc010rlc.2	MS4A1	2.23	0.000551367	3.26	0.01989404
uc002yvz.3,uc002ywa.3,uc002ywb.3,uc002ywc.3,uc002ywd.1,uc010gne.1,uc010gnf.3,uc011aed.1,uc011aee.1	TTC3	-0.99	0.000560687	3.25	0.020193011
uc001kya.3,uc021pxr.1,uc021pxs.1	GSTO1	1.12	0.000563189	3.25	0.020245767
uc002bdu.4,uc002bdv.4,uc002bdw.4,uc002bdx.4,uc010blf.3	PSMA4	1.01	0.000572696	3.24	0.020549667

uc003thy.3,uc003thz.1	PSMA2	1.01	0.000574533	3.24	0.020567393
uc001sjw.2,uc001sjx.2,uc010sqd.2,uc010sqe.2	MYL6	1.56	0.000575477	3.24	0.020567393
uc010dwa.3	KANK3	1.45	0.000576351	3.24	0.020567393
uc004fmp.2,uc010nvg.2,uc010nvh.2,uc011mzv.2,uc011mzw.2	MPP1	-1.30	0.000581063	3.24	0.020697726
uc002abk.3,uc002abl.4,uc010bfb.3	TMOD2	-1.39	0.000583398	3.23	0.020743053
uc003xdn.1,uc003xdo.3,uc003xdp.3,uc003xdq.3,uc003xdr.1	SLC25A37	-1.14	0.000589626	3.23	0.020926357
uc002nsh.4,uc002nsi.4,uc021ury.1	PLEKHF1	1.08	0.000595565	3.23	0.021098787
uc001lkm.2,uc001lkn.2,uc001lko.3,uc021qay.1	GLRX3	1.07	0.000598303	3.22	0.021157377
uc001eft.3,uc021osc.1	TSPAN2	1.38	0.000601632	3.22	0.021233081
uc003ifo.3,uc011cgs.2,uc011cgt.2	PLK4	2.39	0.000604368	3.22	0.021233081
uc002wes.3,uc002wet.3	SNPH	-1.55	0.000605343	3.22	0.021233081
uc003yek.1,uc011lgc.1,uc011lgd.1	DECR1	1.06	0.000605597	3.22	0.021233081
uc001mub.3,uc001muc.3,uc010reg.1,uc010reh.1	DEPDC7	-3.10	0.000606024	3.22	0.021233081
uc001bsb.1	MATN1-AS1	-1.63	0.00060697	3.22	0.021233081
uc010jjy.1,uc031sma.1,uc031smb.1,uc031smc.1,uc031smd.1	FAM153B	-1.55	0.000608292	3.22	0.021241266
uc003lsc.3,uc003lsd.3,uc003lse.3	CD74	1.02	0.000612526	3.21	0.021319815
uc003muf.4,uc003mug.4,uc003muh.3	SERPINB9	-1.05	0.000612932	3.21	0.021319815
uc003bzi.3,uc003bzj.4	NR2C2	-1.18	0.000613818	3.21	0.021319815
uc002qpf.3	ZNF416	-1.45	0.000621843	3.21	0.021560163
uc002mli.3,uc002mlj.3,uc002mlk.3,uc021uon.1	ZNF559-ZNF177	-2.56	0.000625658	3.20	0.021631607
uc002awc.1	LOXL1	1.88	0.00062612	3.20	0.021631607
uc002zxx.3,uc002zxy.3	MMP11	-3.00	0.000631676	3.20	0.021752322
uc001wjl.3,uc001wjm.3,uc001wjn.3,uc010akk.3,uc010akl.1	SLC22A17	-2.48	0.000631843	3.20	0.021752322
uc001nzc.3,uc001nzd.3,uc009ypk.2	BAD	1.15	0.00063436	3.20	0.021800544
uc003lcj.3,uc011cyo.2	KIF20A	15.00	0.000635803	3.20	0.02181172
uc010nko.3	ZC3H12B	-1.49	0.000637973	3.20	0.021837165
uc001coa.3,uc001cob.3,uc001coc.3,uc021omw.1	PRDX1	1.22	0.000638782	3.19	0.021837165
uc003nrl.3,uc011dmq.2	TUBB	1.18	0.000642677	3.19	0.021929653
uc001blj.4,uc009vsb.3,uc010oew.2	PDIK1L	-1.16	0.000644122	3.19	0.021929653
uc003wpx.4,uc011kwi.2	MYOM2	2.66	0.000644858	3.19	0.021929653
uc004erl.3,uc004erm.3,uc004erp.3	UBE2A	1.06	0.000647305	3.19	0.021974614
uc001iur.2	AX747507	-5.25	0.00065228	3.19	0.022105057
uc001xfl.3	TMEM30B	-1.49	0.000655545	3.18	0.022177188
uc003epn.1	BFSP2	2.73	0.000658911	3.18	0.022252497
uc002lww.3,uc010dth.3,uc010dti.3,uc010xhb.2,uc010xhc.2,uc010xhd.1	TLE2	-1.82	0.000668933	3.17	0.022551949
uc001ysv.3,uc001ysw.1,uc001ysx.1,uc021set.1,uc031qqx.1	BC042994	1.79	0.000676513	3.17	0.022768156
uc001tmj.3,uc001tmk.1,uc001tml.1,uc001tmm.1,uc009zut.1	BTBD11	-1.54	0.00067885	3.17	0.022807496

uc003kmv.1,uc003kmw.1	LNPEP	-1.01	0.000681457	3.17	0.022855738
uc002gkp.4	LINC00324	1.24	0.000683694	3.17	0.022890402
uc002diy.4	LOC100190986	-1.08	0.000684836	3.16	0.022890402
uc001plg.4	POU2AF1	2.47	0.000686761	3.16	0.022915498
uc001ctn.4,uc001cto.4,uc001ctp.4	ZFYVE9	-1.60	0.00068821	3.16	0.022924665
uc003ugd.3,uc003ugf.3,uc003ugg.1,uc011kgo.2	GSAP	-1.59	0.00069152	3.16	0.022969478
uc002hbf.2,uc010wak.2,uc021ttr.1	SLC46A1	-2.09	0.000691908	3.16	0.022969478
uc002mtb.2,uc010dym.1	ZNF844	-1.97	0.000697689	3.16	0.023114741
uc002noh.3,uc010eci.2,uc010ecj.3,uc021urk.1	ZNF506	-1.08	0.000698653	3.16	0.023114741
uc002huw.3	CCR7	-1.53	0.00070158	3.15	0.023172325
uc001zog.1,uc001zoi.3,uc010ucy.2,uc010ucz.2,uc010uda.1	MGA	-1.04	0.000704419	3.15	0.023226802
uc001qqq.3,uc001qqr.3	PTMS	3.52	0.000705652	3.15	0.023228191
uc001xbr.3,uc021rtj.1	LGALS3	1.48	0.000711502	3.15	0.02338133
uc001wqp.2,uc001wqq.4,uc001wqr.2,uc001wqt.1	COCH	3.39	0.00071491	3.15	0.023429949
uc003zpl.3	CDKN2A	3.41	0.000715382	3.15	0.023429949
uc002czc.4,uc002czd.4,uc010buh.3,uc010bui.3,uc021tcs.1	ABAT	1.36	0.000724968	3.14	0.023704144
uc009wmw.3	CGN	-2.28	0.000726315	3.14	0.023708464
uc003smc.3,uc003smd.3,uc021zyu.1,uc021zyv.1	CHST12	1.14	0.000728077	3.14	0.023726316
uc003zjg.4,uc010mho.1,uc010mhp.1,uc011lmc.2,uc011lmd.2	PDCD1LG2	15.00	0.000731159	3.14	0.023774076
uc002ywv.4,uc002yww.4,uc002ywx.4,uc021wjc.1,uc031rvj.1,uc031rvk.1,uc031rvl.1,uc031rvm.1,uc031rvn.1	KCNJ15	15.00	0.000732819	3.14	0.023774076
uc002gaa.4	PFN1	1.43	0.000733196	3.13	0.023774076
uc004cmg.1,uc004cmh.1	TUBB4B	1.71	0.000736262	3.13	0.023833884
uc002szj.1	TSGA10	-1.62	0.000738469	3.13	0.023865763
uc002ygn.4,uc002ygp.4,uc011abi.2	ZGPAT	0.96	0.000743922	3.13	0.024002253
uc002azi.4	COX5A	1.34	0.000746366	3.13	0.024022899
uc001gea.1	GPA33	-1.04	0.000747024	3.13	0.024022899
uc002zpr.3,uc002zpt.3,uc011agz.1,uc011aha.2,uc021wlg.1	CDC45	5.16	0.000749995	3.12	0.024078787
uc001ofs.3,uc001oft.3	CFL1	1.14	0.000763584	3.12	0.024474826
uc002vaz.4	INO80D	-1.02	0.000771982	3.11	0.024703422
uc002uho.1,uc002uhp.1,uc010fqk.1,uc010fql.2,uc010fqm.1,uc010zdy.1	ITGA6	-0.96	0.00077633	3.11	0.024801895
uc003qgt.1,uc003qgu.1,uc010kgp.1	MTFR2	2.85	0.000781518	3.11	0.02490416
uc001gqm.3,uc001gqo.3,uc010pof.1,uc010pog.2,uc010poh.2,uc010poi.2	RGL1	-1.97	0.000782082	3.11	0.02490416
uc002ozc.4,uc002ozd.4,uc010ejj.3,uc010xwy.2,uc010xwz.2,uc010xxa.2	ZFP112	-3.89	0.00078359	3.11	0.024911517
uc004esn.1,uc010nqm.1,uc022cdm.1	ZBTB33	-1.02	0.000791393	3.10	0.025118692
uc001wmj.3	PSME2	1.33	0.000806765	3.09	0.02556502
uc001ran.2,uc001rao.2	DUSP16	1.18	0.000812862	3.09	0.025716478

uc002blb.2,uc002blc.2,uc031qtf.1,uc031qtg.1,uc031qth.1,uc031qti.1,uc031qtj.1	SEC11A	1.01	0.000815145	3.09	0.025746974
uc001jjx.1,uc001jjy.1,uc001jka.1,uc009xoy.2,uc031pvd.1	ZWINT	2.65	0.000833922	3.08	0.02629751
uc003gmn.3,uc021xme.1,uc031sds.1	ZNF518B	-1.05	0.000837172	3.08	0.026357421
uc001kin.3,uc001kio.3,uc001kip.4,uc009xue.3,uc009xuf.2	MYOF	4.07	0.000842842	3.07	0.026493195
uc002wva.3,uc002wvc.3,uc010ztg.2	ZNF337	-1.03	0.000845194	3.07	0.02652443
uc003mzh.3,uc010joq.2,uc021ylj.1	TMEM14C	1.10	0.000850833	3.07	0.026641063
uc002xqh.3,uc002xqi.3,uc002xqj.4,uc010zxi.2	CTSA	1.00	0.000851641	3.07	0.026641063
uc003ujf.1,uc003ujg.1,uc003ujh.1,uc011khf.1	DBF4	1.09	0.000856053	3.07	0.026674452
uc031szb.1	MGC27345	-1.13	0.000858377	3.07	0.026674452
uc002bqm.4,uc002bqn.4,uc010uqs.3,uc010uqt.2	PRC1	2.56	0.000859139	3.07	0.026674452
uc003xcz.2	TNFRSF10D	-1.53	0.000859142	3.07	0.026674452
uc001rpk.3,uc001rpl.3,uc001rpm.3,uc021qxg.1	AMIGO2	-1.05	0.000859541	3.07	0.026674452
uc002nni.2,uc002nnj.2,uc010ecg.2	ZNF101	-0.98	0.000863263	3.06	0.026747448
uc002dww.3,uc002dwy.1,uc002dwz.1,uc010bzq.3,uc010vej.2	CORO1A	0.95	0.00086854	3.06	0.026868301
uc003tel.1,uc003tem.4,uc003ten.1	DPY19L1	1.22	0.000893615	3.05	0.027592198
uc002tmg.3,uc002tmh.4,uc010flk.3,uc010fll.3,uc010flm.3	EPB41L5	-1.65	0.000894768	3.05	0.027592198
uc002uwx.4,uc031rqp.1	NDUFB3	1.65	0.000896405	3.05	0.027599108
uc003arc.3	RAC2	0.95	0.000900065	3.05	0.027668154
uc001sjp.1,uc021qyw.1	ZC3H10	-1.58	0.000904414	3.04	0.027758125
uc002mye.3	ASF1B	3.08	0.000909874	3.04	0.027881863
uc003gmo.4,uc003gmp.3	CLNK	1.60	0.000917494	3.04	0.028071304
uc002xjr.1,uc002xjs.1,uc002xjt.1,uc002xju.1,uc002xjv.1,uc002xjw.1,uc010ggg.1	ZHX3	-1.16	0.000922574	3.03	0.028182527
uc004bcl.3,uc004bcm.3	ABCA1	-1.78	0.0009271	3.03	0.028276548
uc002boe.3,uc021sug.1	TICRR	15.00	0.000930673	3.03	0.028341248
uc002jib.2,uc002jic.2,uc002jid.2,uc002jie.2,uc002jif.2,uc002jig.2,uc002jih.2,uc010dfe.2	ABCA5	-1.03	0.000934211	3.03	0.028404671
uc001got.4	IER5	1.41	0.00094116	3.03	0.02857145
uc001lor.4,uc001los.1,uc001lou.4,uc001lov.4,uc010qvu.2	ATHL1	-1.02	0.000944252	3.02	0.028620803
uc002ruv.3,uc002ruw.3	EPAS1	15.00	0.000958908	3.02	0.029019975
uc002vko.2,uc002vkp.2,uc002vks.2,uc010fwf.3,uc010zky.2	STK16	1.53	0.000971083	3.01	0.029342944
uc003ktf.2,uc010jcy.3,uc011cwo.2	SNX24	2.06	0.000972835	3.01	0.029350446
uc002dkp.2,uc010vbu.1	RRN3P3	1.28	0.000978247	3.01	0.029444187
uc003com.3,uc003con.3	CDCP1	-1.81	0.000978959	3.01	0.029444187
uc001trq.1,uc001trs.2,uc001trt.1,uc010syd.1	HVCN1	-1.10	0.000985474	3.01	0.029565065
uc001sgd.2,uc001sge.3,uc001sgf.3,uc009znq.3,uc010soz.2,uc010spa.1	PDE1B	1.47	0.000986007	3.01	0.029565065
uc003ajc.4,uc003ajd.3	MORC2-AS1	-1.44	0.000988829	3.00	0.029604218

uc003bzp.2,uc003bzq.2,uc003bzr.2	SH3BP5	1.02	0.000992334	3.00	0.029663655
uc002hti.1,uc002htj.2,uc002htk.2	ORMDL3	1.39	0.00100001	3.00	0.029847378
uc003qip.2,uc021zfz.2,uc021zga.2,uc021zgb.1	CITED2	1.08	0.001003763	3.00	0.029909003
uc003mju.3	ZNF354C	-1.49	0.001005139	3.00	0.029909003
uc002erh.1,uc002eri.1,uc010vjb.1	TRADD	0.96	0.001011479	3.00	0.030032529
uc003awt.4,uc003awu.4,uc010gxu.3,uc021wpq.1	APOBEC3D	1.14	0.001012367	2.99	0.030032529
uc004akf.4,uc004akh.4,uc010mpf.3,uc010mpg.3,uc010mph.3,uc010mpi.3,uc022bif.1	GCNT1	1.22	0.001019179	2.99	0.030188737
uc001zrg.3	LCMT2	-1.41	0.001028328	2.99	0.030389704
uc001dvt.4,uc001dvu.4,uc009wer.3	HENMT1	1.05	0.001029078	2.99	0.030389704
uc004bkr.2,uc004bks.1,uc004bkt.3,uc011lyf.1	PHF19	1.62	0.001035858	2.98	0.030543724
uc003qqb.3,uc003qqe.3,uc003qqf.3,uc003qqg.3,uc003qqh.3,uc010kjj.3,uc011efl.1	TIAM2	3.13	0.00103987	2.98	0.030584786
uc002obi.1,uc002obj.1,uc002obk.1	PSENEN	1.32	0.001041443	2.98	0.030584786
uc001zme.3,uc010bbs.1,uc010bbt.1,uc010ucq.1	CASC5	2.17	0.001041951	2.98	0.030584786
uc001mdb.2,uc001mdc.1,uc001mdd.4,uc001mde.3,uc009yey.3,uc009yfa.3,uc009yfb.3,uc010rab.2,uc010rad.2,uc010rag.2,uc010rah.2,uc031pyt.1,uc031pyu.1,uc031pyv.1	APBB1	-0.95	0.001053084	2.98	0.03086516
uc002nkk.3,uc002nkl.3,uc002nkm.3	COPE	0.99	0.001056615	2.98	0.030922233
uc001lqz.3,uc001lra.3,uc010qwl.2	TALDO1	0.98	0.0010757	2.97	0.031433637
uc001hir.2,uc001his.4,uc001hit.2,uc021piq.1,uc021pir.1	NEK2	2.00	0.001084361	2.96	0.031639347
uc001fwl.4,uc001fwm.3,uc010pjk.2,uc010pjl.2,uc010pjm.2	SLAMF1	1.00	0.00110048	2.96	0.032061749
uc002pft.1,uc002pfu.1	AP2S1	1.34	0.00111372	2.95	0.032399131
uc003nok.3,uc003nol.3,uc010jrq.3,uc010klp.2,uc011dmc.2,uc011dmd.2,uc021ytz.1,uc021yua.1,uc021yub.1	HLA-A	0.97	0.001120812	2.95	0.032538938
uc003flq.2,uc021xid.1	LINC00888	1.84	0.00112186	2.95	0.032538938
uc002jmi.3,uc002jmj.4,uc002jmk.2,uc010wrs.2	HID1	-2.04	0.001124658	2.95	0.032571701
uc003kud.2,uc010jdb.2,uc011cxb.2	LMNB1	1.59	0.001128558	2.95	0.032636238
uc003gph.1,uc010ieg.3	LAP3	1.03	0.001133455	2.95	0.032729363
uc002let.3,uc002leu.3,uc010xdl.2	SKA1	1.35	0.001136341	2.94	0.032738424
uc002alx.3,uc002aly.3	RPS27L	1.25	0.001137124	2.94	0.032738424
uc003njt.1,uc003nju.1,uc003njv.3	HIST1H2BN	3.61	0.001144796	2.94	0.032910768
uc001vdv.3,uc001vdw.3,uc001vdx.3,uc001vdy.3,uc001vdz.3,uc001vea.1,uc001veb.2	DLEU2	2.07	0.00115059	2.94	0.03302871
uc002xpl.3,uc002xpm.3,uc002xpn.3,uc002xpo.3,uc002xpp.3,uc002xpq.3	UBE2C	4.57	0.001154429	2.94	0.033090227
uc003nix.2,uc021yoy.1	HIST1H2BK	1.56	0.001167864	2.93	0.033426263
uc003xkw.3,uc003xkx.3,uc022atz.1	LSM1	1.06	0.001170374	2.93	0.033449046
uc001hxt.3,uc010pxt.1	ERO1LB	-1.05	0.00117887	2.93	0.033616339
uc001ozr.3,uc001ozs.3	PRCP	1.11	0.001179672	2.93	0.033616339
uc002rqd.3,uc002rqe.1,uc002rqf.1	PRKD3	-0.99	0.001185545	2.93	0.033734472
uc002rau.3,uc002rav.3,uc002raw.3,uc010yjg.2,uc010y	PDIA6	0.94	0.00118841	2.93	0.033766757

jh.2					
uc003cyo.1,uc003cyp.1,uc003cyq.1,uc003cyr.1,uc010hlg.1,uc011bdn.2,uc031rzx.1	GNAI2	0.93	0.001193655	2.92	0.033840415
uc003fjz.3,uc003fka.3,uc003fkb.3	MRPL47	1.08	0.001195541	2.92	0.033840415
uc002ghc.4,uc002ghd.4	ZBTB4	-0.99	0.001196203	2.92	0.033840415
uc001lwf.1	CD81	1.25	0.001201604	2.92	0.033944015
uc002gec.3,uc002ged.3,uc010vti.2	RNASEK-C17orf49	1.46	0.001207291	2.92	0.034055377
uc003pfh.3,uc003pfi.3,uc003pfj.3,uc003pfk.3,uc003pfl.3,uc003pfm.1,uc003pfn.3,uc003pfo.1,uc003pfp.3,uc010kan.2	FAM135A	-1.21	0.001211023	2.92	0.034111364
uc002oii.4	PSMD8	1.05	0.001213082	2.92	0.034120116
uc001rvv.4,uc001rvw.4,uc009zln.4,uc009zlo.4,uc021qxr.2,uc031qhf.1	ASIC1	-3.60	0.001215995	2.92	0.034152831
uc010cnq.2	BC046191	-3.13	0.001224284	2.91	0.034336249
uc002qti.3,uc002qtj.3,uc002qtk.3	CHMP2A	1.24	0.001233873	2.91	0.034555537
uc002gmx.3,uc002gmy.3	TMEM220	-1.71	0.001240371	2.91	0.034687751
uc001nlf.2,uc001nlh.1,uc001nli.4,uc001nlj.4,uc001nlk.4,uc001nll.4,uc001nlm.4,uc001nln.4,uc001nlo.4,uc001nlp.4,uc001nlq.4,uc001nlr.4,uc001nls.4,uc001nlt.4,uc001nlu.4,uc001nlv.4,uc001nlw.4,uc001nlx.4,uc001nly.4,uc001nlz.4,uc001nma.4,uc001nmb.4,uc001nmc.4,uc001nmd.4,uc001nme.4,uc001nmf.4,uc001nmg.4,uc001nmh.4,uc001nmi.4,uc009ymn.3,uc021qjk.1	TMX2-CTNND1	-1.37	0.001259089	2.90	0.035124387
uc001iij.3,uc001iik.3	FAM208B	-1.03	0.001259584	2.90	0.035124387
uc001ico.3,uc001icq.1,uc009xgv.3,uc010pyv.1	ZNF496	-1.38	0.001262087	2.90	0.035143987
uc002azy.3,uc002azz.3,uc002baa.3,uc010umf.1	COMMD4	1.11	0.001276871	2.89	0.035446775
uc001jsa.2,uc001jsb.2,uc021psm.1	C10orf105	-15.00	0.001277125	2.89	0.035446775
uc002pym.3,uc002pyn.3	ZNF616	-1.28	0.001278408	2.89	0.035446775
uc002ejd.2,uc010ccg.2	BBS2	-0.96	0.001283814	2.89	0.035546175
uc002piv.2	EMP3	1.10	0.001286104	2.89	0.035559125
uc010ing.3,uc010ini.3,uc011cgj.2,uc021xrj.1	TNIP3	2.03	0.001292982	2.89	0.035698734
uc002jwu.1,uc002jwv.4,uc002jww.4,uc010wtz.1	ENGASE	-1.24	0.001295955	2.89	0.03573028
uc004alc.3,uc004ald.3,uc004ale.3,uc004alf.3,uc010mpr.3,uc010mps.3,uc011lsq.2	TLE4	-0.96	0.001297993	2.89	0.035736002
uc002ojc.1,uc002ojd.1,uc010egd.1	CAPN12	1.45	0.00130804	2.88	0.035913444
uc002rku.3,uc002rkv.3,uc010ezb.3,uc010ezc.3,uc010yls.2,uc010ylt.1	IFT172	-1.31	0.001308118	2.88	0.035913444
uc001usf.3	POMP	1.00	0.001310579	2.88	0.035930479
uc001hxq.3	GPR137B	1.28	0.001314948	2.88	0.035999692
uc002slb.3	WDR54	1.09	0.001333891	2.87	0.036467166
uc001iua.1,uc001iub.1,uc009xkz.1,uc009xla.2,uc010qdv.1	MPP7	-1.00	0.001336776	2.87	0.036494912
uc003fre.1,uc021xim.1	RPL39L	2.29	0.001346843	2.87	0.036718401
uc001bkw.1	AUNIP	2.80	0.001366339	2.86	0.037197963

uc001egu.4,uc010owz.1,uc010oxa.1	CD2	0.92	0.001378753	2.86	0.037470131
uc002tlv.3,uc002tlw.3,uc002tlx.3,uc010yyh.2,uc010yyi.2,uc010yyj.2,uc010yyk.2,uc010yyl.2,uc010yym.2,uc010yyn.2,uc010yyo.2,uc010yyp.1,uc021vnj.1	DBI	1.52	0.001380204	2.86	0.037470131
uc001xhb.3,uc010aqe.2,uc010aqf.3	MTHFD1	1.02	0.001385307	2.86	0.037470131
uc021xpq.1	AK128593	-1.11	0.001388982	2.86	0.037470131
uc003meg.3	HIGD2A	0.99	0.001389044	2.86	0.037470131
uc002uvv.4,uc002uvw.2,uc010zhd.1,uc010zhe.1	SGOL2	1.49	0.001390442	2.86	0.037470131
uc003php.3,uc003phq.3,uc010kba.3	CD109	2.47	0.001390666	2.86	0.037470131
uc001xch.3	PELI2	-1.31	0.001391693	2.86	0.037470131
uc003fih.3,uc003fii.3,uc003fij.2,uc003fik.2,uc003fil.2,uc003fim.2	ECT2	1.44	0.001396863	2.85	0.037557531
uc002gkm.4,uc002gkn.4,uc002gko.4,uc010cnu.3,uc010vuu.3,uc021tpy.1	AURKB	4.42	0.001414608	2.85	0.03797343
uc003vbc.2,uc003vbd.2,uc003vbe.2,uc003vbf.3,uc011klj.1	NAPEPLD	-1.10	0.001416222	2.85	0.03797343
uc001hts.1,uc009xfd.1	URB2	-1.15	0.001425347	2.85	0.038165677
uc003vwk.3	KIAA1147	-1.42	0.001427704	2.85	0.038176424
uc004axy.4,uc004axz.4	HEMGN	-1.58	0.00143121	2.84	0.038192904
uc002wuj.2,uc002wuk.2,uc002wul.2,uc002wum.2,uc002wuo.2,uc010gdj.1,uc010gdk.1,uc010gdl.1,uc010zsy.1,uc010zsz.1,uc010zta.1,uc010ztb.1,uc010ztc.1,uc010ztd.1	ENTPD6	-0.93	0.001432234	2.84	0.038192904
uc031qqg.1	JX073282	-2.16	0.00143514	2.84	0.038218178
uc001ftj.1	AIM2	3.17	0.001441717	2.84	0.038341028
uc004euf.4,uc004eug.4,uc004euh.4,uc004eui.4,uc010nqw.3,uc010nqx.3	SH2D1A	0.95	0.00144751	2.84	0.038442713
uc001mee.3,uc001mef.3,uc001meh.3,uc010rap.2,uc010raq.2	ILK	0.93	0.001451925	2.84	0.038481126
uc003hbz.2,uc003hca.2,uc003hcb.2,uc003hcc.2,uc003hcd.2,uc003hce.2,uc011cad.1,uc031sei.1	HOPX	2.65	0.001452899	2.84	0.038481126
uc010vyd.1,uc010vye.1	ZNF286B	-1.06	0.001460451	2.84	0.038628733
uc004cee.3,uc004cef.3,uc004ceg.3,uc011mdj.1	SLC2A6	-1.83	0.001464759	2.83	0.03869026
uc003eqc.1,uc003eqd.1	RYK	-1.01	0.001468492	2.83	0.038736435
uc003ayp.4,uc003ays.4,uc010gyb.1	ADSL	0.94	0.0014731	2.83	0.038805542
uc003caw.3,uc003cax.3,uc010her.2,uc011awb.2	OXNAD1	-0.96	0.001478699	2.83	0.038900548
uc001zkx.4,uc010ucl.1	BUB1B	2.77	0.001486181	2.83	0.039044765
uc002elg.2	PLLP	-15.00	0.001489762	2.83	0.039086221
uc003kyt.3,uc003kyu.2,uc003kyv.3,uc003kyw.3,uc003kyx.3,uc003kyy.3,uc003kyz.3,uc003kza.3,uc003kzb.3,uc010jdu.3	TCF7	-0.92	0.001491832	2.83	0.039088003
uc001bky.3,uc001bkz.3,uc001bla.3,uc001blb.3,uc001blc.3,uc010oev.2,uc021ojn.1	STMN1	2.11	0.001518109	2.82	0.039723169
uc002hsq.3	MIEN1	1.00	0.001521042	2.82	0.039740714
uc001vgt.2,uc001vgu.2,uc001vgv.2,uc010tha.1	CKAP2	1.01	0.001522851	2.82	0.039740714

uc004dvu.3,uc004dvv.3,uc004dvw.2,uc011mov.2,uc011mow.2,uc022byc.1,uc022byd.1	ZC4H2	-1.22	0.001529504	2.82	0.03986105
uc003kbw.4,uc010iyw.1,uc010iyx.1,uc010iyy.1	MAP1B	-1.84	0.001534729	2.81	0.039943874
uc001bgw.3,uc021oif.2	C1orf213	-2.31	0.001541734	2.81	0.040072761
uc001gwq.4,uc021phf.1	PHLDA3	2.68	0.001547912	2.81	0.04017984
uc001ays.2,uc001ayt.2	CROCCP3	-1.12	0.001552255	2.81	0.040239072
uc001dwr.3,uc001dws.1,uc009wex.2,uc009wey.3,uc009wez.1,uc010ovg.3,uc021orb.1,uc031pnl.1	KIAA1324	1.25	0.001563018	2.81	0.040464336
uc003vmb.2,uc010llb.2	ARF5	0.93	0.001569864	2.80	0.040587754
uc002rkl.4	PPM1G	0.93	0.001578442	2.80	0.040755548
uc003kyp.2,uc003kyq.2,uc003kyr.2,uc031slc.1	VDAC1	0.95	0.001597539	2.80	0.041194127
uc001hhr.2,uc009xcu.2	DIEXF	-1.04	0.001602912	2.80	0.04127816
uc001dmi.3,uc001dmj.3	LMO4	2.54	0.001622762	2.79	0.041734271
uc002odi.1,uc002odj.3,uc002odk.3,uc002odl.3	CAPNS1	1.07	0.001627202	2.79	0.041793388
uc001vqy.3	RAB20	-2.01	0.001631255	2.79	0.041842433
uc002oxd.2,uc002oxf.2,uc002oxg.2	PLAUR	3.22	0.001634106	2.79	0.041860565
uc003kpf.3,uc003kpg.3,uc010jbv.3	CAMK4	-0.93	0.001640269	2.79	0.041963363
uc001oup.1	UCP2	0.92	0.001643206	2.78	0.041983477
uc001tll.3,uc001tlm.3,uc001tln.3,uc001tlo.1	TCP11L2	-0.95	0.001649813	2.78	0.042097198
uc003awk.3	NPTXR	-1.68	0.001652218	2.78	0.042103521
uc002ftf.3,uc002ftg.3,uc021tni.1,uc021tnj.1,uc021tnk.1,uc021tnl.1	MIR22HG	2.11	0.001659052	2.78	0.042210097
uc003wfl.3,uc011kul.2,uc011kum.2	ZNF398	-1.00	0.001660725	2.78	0.042210097
uc001ubl.4,uc009zxj.4,uc031qjw.1,uc031qjx.1	PSMD9	0.95	0.001667392	2.78	0.042324435
uc003cbr.3,uc003cbs.3,uc003cbt.3,uc003cbu.3,uc003cbv.3,uc003cbw.3,uc003cbx.3,uc003cby.3,uc003cbz.3,uc003cca.3,uc003ccb.3,uc003ccc.3,uc010hfa.3,uc021wtx.1,uc021wty.1	SGOL1	1.65	0.00168008	2.77	0.04259112
uc003zmw.2,uc003zmx.4,uc003zmy.3,uc003zmz.2,uc010mio.3	CNTLN	1.97	0.001690572	2.77	0.042801502
uc003lal.1,uc003lam.1,uc003lan.1,uc003lao.1,uc003las.1,uc003lat.1,uc003lau.1,uc011cxz.1	H2AFY	0.93	0.001694966	2.77	0.042857169
uc001qhb.3,uc009zcz.2	JAM3	-2.22	0.001706026	2.77	0.043081006
uc002ubu.3	PSMD14	0.96	0.001732627	2.76	0.043696226
uc003ilj.4,uc003ilk.4,uc010iph.3	NR3C2	-1.28	0.001742163	2.76	0.043880028
uc001rxb.3,uc010smv.1	METTL7A	1.20	0.001748082	2.76	0.043972378
uc001uyy.3	DNAJC15	1.02	0.001754033	2.76	0.044013848
uc003wig.5,uc011kvc.2	ATG9B	-1.07	0.00175424	2.76	0.044013848
uc002box.3,uc010uqb.2,uc010uqc.2	IDH2	0.94	0.001763982	2.75	0.044201459
uc002eek.1	C16orf87	1.08	0.00176917	2.75	0.044260705
uc003zuw.1,uc003zux.1	DCTN3	1.58	0.001770882	2.75	0.044260705
uc001zue.3,uc001zuf.2,uc001zug.1,uc001zuh.1,uc001zui.1,uc010bdy.1	TRIM69	1.02	0.001778197	2.75	0.044342739
uc002prm.3,uc002prn.3,uc010ybo.2	ZNF473	-1.07	0.001778707	2.75	0.044342739
uc003dtd.3,uc003dte.3,uc003dtf.1	DCBLD2	-4.37	0.001783514	2.75	0.044405869

uc002muv.3	ASNA1	0.99	0.00179188	2.75	0.044557317
uc001utf.2,uc010tdr.2	ALOX5AP	0.98	0.001798648	2.75	0.044664069
uc003kns.3,uc003knt.3,uc003knu.3,uc003knv.3,uc003knw.3,uc003knx.1,uc003kny.1,uc003knz.3,uc011cuz.2	PAM	0.99	0.001800749	2.74	0.044664069
uc001pds.4,uc021qos.1	SMCO4	3.07	0.001804967	2.74	0.044678851
uc001fun.2,uc010piy.2,uc031pqt.1,uc031pqu.1	TAGLN2	1.05	0.001805923	2.74	0.044678851
uc010eex.2,uc010xtd.2	ZFP14	-1.07	0.001813655	2.74	0.044813344
uc001cmg.4,uc001cmh.4,uc010olb.2,uc010olc.2	KIF2C	4.41	0.001816339	2.74	0.044822918

Supplementary Table 3, Gene modules up in Programmed cell death protein 1 (PD-1)$^{\text{high}}$ Tregs from healthy donors. Differentially expressed genes that were up in PD-1$^{\text{high}}$ Tregs were analyzed with DAVID to identify functional clusters of genes.

Gene Group (Enrichment Score)	Official Gene Symbol	Gene Name
Group 1 (15.955)	ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)
	MLF1IP	MLF1 interacting protein
	POLQ	polymerase (DNA directed), theta
	CENPE	centromere protein E, 312kDa
	ANLN	anillin, actin binding protein
	TUBB	tubulin, beta; similar to tubulin, beta 5; tubulin, beta pseudogene 2; tubulin, beta pseudogene 1
	PRC1	protein regulator of cytokinesis 1
	PLK4	polo-like kinase 4 (Drosophila)
	SMC4	structural maintenance of chromosomes 4
	DSCC1	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)
	NCAPG2	non-SMC condensin II complex, subunit G2
	GTSE1	G-2 and S-phase expressed 1
	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)
	CDCA5	cell division cycle associated 5
	SKA1	chromosome 18 open reading frame 24
	CDK1	cell division cycle 2, G1 to S and G2 to M
	CDCA2	cell division cycle associated 2
	SGOL1	shugoshin-like 1 (S. pombe)
	KIF18A	kinesin family member 18A
	KIFC1	kinesin family member C1
	KIF20A	kinesin family member 20A
	DCTN3	dynactin 3 (p22)
	HAUS1	HAUS augmin-like complex, subunit 1
	DLGAP5	discs, large (Drosophila) homolog-associated protein 5
	MYO1G	myosin IG
	BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)
	FGFR2	fibroblast growth factor receptor 2
	KIF15	kinesin family member 15
	MCM2	minichromosome maintenance complex component 2
	KIF19	kinesin family member 19
	CDK14	PFTAIRE protein kinase 1
	ZWINT	ZW10 interactor

	CASC5	cancer susceptibility candidate 5
	RAD54L	RAD54-like (S. cerevisiae)
	STMN1	stathmin 1
	NUF2	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)
	ASNA1	arsA arsenite transporter, ATP-binding, homolog 1 (bacterial)
	NDC80	NDC80 homolog, kinetochore complex component (S. cerevisiae)
	PKMYT1	protein kinase, membrane associated tyrosine/threonine 1
	PMVK	phosphomevalonate kinase
	MKI67	antigen identified by monoclonal antibody Ki-67
	CENPF	centromere protein F, 350/400ka (mitosin)
	CKAP2	cytoskeleton associated protein 2
	KIF4A	kinesin family member 4B; kinesin family member 4A
	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)
	LTK	leukocyte receptor tyrosine kinase
	UBE2C	ubiquitin-conjugating enzyme E2C
	KIF14	kinesin family member 14
	NCAPH	non-SMC condensin I complex, subunit H
	MCM6	minichromosome maintenance complex component 6
	TIMELESS	timeless homolog (Drosophila)
	STK16	serine/threonine kinase 16
	PLK1	polo-like kinase 1 (Drosophila)
	CCNB2	cyclin B2
	NEK2	NIMA (never in mitosis gene a)-related kinase 2
	RCC1	regulator of chromosome condensation 1; SNHG3-RCC1 readthrough transcript
	KIF23	kinesin family member 23
	MYO1E	myosin IE
	KIF11	kinesin family member 11
	CENPN	centromere protein N
	TTK	TTK protein kinase
	KIF2C	kinesin family member 2C
	AURKB	aurora kinase B
	SGOL2	shugoshin-like 2 (S. pombe)
	NCAPG	non-SMC condensin I complex, subunit G
	CEP55	centrosomal protein 55kDa
	WEE1	WEE1 homolog (S. pombe)
	TK1	thymidine kinase 1, soluble
	MELK	maternal embryonic leucine zipper kinase
	NUSAP1	nucleolar and spindle associated protein 1

	MCM4	minichromosome maintenance complex component 4
	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)
	SKA3	chromosome 13 open reading frame 3
	RAD51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)
	BIRC5	baculoviral IAP repeat-containing 5
Group 2 (7.917)	CDK1	cell division cycle 2, G1 to S and G2 to M
	PSMB3	proteasome (prosome, macropain) subunit, beta type, 3
	BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)
	PSMA4	proteasome (prosome, macropain) subunit, alpha type, 4
	PSMD14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14
	PSMD8	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8
	PSMC4	similar to 26S protease regulatory subunit 6B (MIP224) (MB67-interacting protein) (TAT-binding protein 7) (TBP-7); proteasome (prosome, macropain) 26S subunit, ATPase, 4
	CCNB1	cyclin B1
	PSMA6	proteasome (prosome, macropain) subunit, alpha type, 6
	UBE2C	ubiquitin-conjugating enzyme E2C
	PSMD9	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9
	PSMC3	proteasome (prosome, macropain) 26S subunit, ATPase, 3
	PSMA2	proteasome (prosome, macropain) subunit, alpha type, 2
	PSME2	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)
	CDC20	cell division cycle 20 homolog (S. cerevisiae)
	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)
Group 3 (6.670)	CDC45	CDC45 cell division cycle 45-like (S. cerevisiae)
	CLSPN	claspin homolog (Xenopus laevis)
	GMNN	geminin, DNA replication inhibitor
	CDT1	chromatin licensing and DNA replication factor 1
Group 4 (5.832)	HJURP	Holliday junction recognition protein
	CENPA	centromere protein A
	H3F3A	H3 histone, family 3B (H3.3B); H3 histone, family 3A pseudogene; H3 histone, family 3A; similar to H3 histone, family 3B; similar to histone H3.3B
	HMGN2	hypothetical LOC729505; similar to hCG2040565; high-mobility group nucleosomal binding domain 2; similar to high-mobility group nucleosomal binding domain 2
	H2AFZ	H2A histone family, member Z
	MCM2	minichromosome maintenance complex component 2
	HIST1H2BN	histone cluster 1, H2bn
	HIST1H1B	histone cluster 1, H1b
	H2AFY	H2A histone family, member Y

	HIST1H2BK	histone cluster 1, H2bk
	ASF1B	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)
Group 5 (5.253)	DUSP16	dual specificity phosphatase 16
	CDC25C	cell division cycle 25 homolog C (S. pombe)
	CDKN3	cyclin-dependent kinase inhibitor 3
	DUSP6	dual specificity phosphatase 6
Group 6 (4.921)	ARPC3	similar to actin related protein 2/3 complex subunit 3; hypothetical LOC729841; actin related protein 2/3 complex, subunit 3, 21kDa
	CAPZB	capping protein (actin filament) muscle Z-line, beta
	ARPC2	actin related protein 2/3 complex, subunit 2, 34kDa
	CAPG	capping protein (actin filament), gelsolin-like
	ARPC1B	actin related protein 2/3 complex, subunit 1B, 41kDa; similar to Actin-related protein 2/3 complex subunit 1B (ARP2/3 complex 41 kDa subunit) (p41-ARC)
Group 7 (4.688)	TFDP1	transcription factor Dp-1
	E2F1	E2F transcription factor 1
	SUB1	SUB1 homolog (S. cerevisiae)
	E2F8	E2F transcription factor 8
	GTF3C6	general transcription factor IIIC, polypeptide 6, alpha 35kDa
	E2F2	E2F transcription factor 2
Group 8 (3.754)	BFSP1	beaded filament structural protein 1, filensin
	BFSP2	beaded filament structural protein 2, phakinin
	VIM	vimentin
	LMNB1	lamin B1
Group 9 (2.269)	TRIM69	tripartite motif-containing 69
	LIMS3	LIM and senescent cell antigen-like domains 3; LIMS3-LOC440895 read-through
	CA8	carbonic anhydrase VIII
	CPPED1	calcineurin-like phosphoesterase domain containing 1
	APOBEC3F	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3F
	MCM10	minichromosome maintenance complex component 10
	APOBEC3C	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3C
	LAP3	leucine aminopeptidase 3
	APOBEC3H	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3H
	APOBEC3D	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3D
	PHF19	PHD finger protein 19
	ZCRB1	zinc finger CCHC-type and RNA binding motif 1
	ETHE1	ethylmalonic encephalopathy 1

	ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)
	DBF4	DBF4 homolog (S. cerevisiae)
	DPP3	dipeptidyl-peptidase 3
Group 10 (2.067)	ETHE1	ethylmalonic encephalopathy 1
	MRPL10	mitochondrial ribosomal protein L10
	MRPL28	mitochondrial ribosomal protein L28
	MRPL47	mitochondrial ribosomal protein L47
	RPL39L	ribosomal protein L39-like
Group 11 (2.019)	ANXA1	annexin A1
	ANXA4	annexin A4
	ANXA2	annexin A2 pseudogene 3; annexin A2; annexin A2 pseudogene 1
	ANXA5	annexin A5
Group 12 (1.92)	PLEKHG3	pleckstrin homology domain containing, family G (with RhoGef domain) member 3
	MCF2L2	MCF.2 cell line derived transforming sequence-like 2
	TIAM2	T-cell lymphoma invasion and metastasis 2
	ECT2	epithelial cell transforming sequence 2 oncogene
Group 13 (1.135)	CORO1C	coronin, actin binding protein, 1C
	ARPC1B	actin related protein 2/3 complex, subunit 1B, 41kDa; similar to Actin-related protein 2/3 complex subunit 1B (ARP2/3 complex 41 kDa subunit) (p41-ARC)
	WSB2	WD repeat and SOCS box-containing 2
	DTL	denticleless homolog (Drosophila)
	WDR54	WD repeat domain 54
Group 14 (0.982)	GZMK	granzyme K (granzyme 3; tryptase II)
	PRCP	prolylcarboxypeptidase (angiotensinase C)
	CTSH	cathepsin H
	CTSB	cathepsin B
	CTSA	cathepsin A
Group 15 (0.744)	SLC25A5	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5; solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 pseudogene 8
	UCP2	uncoupling protein 2 (mitochondrial, proton carrier)
	NDUFB3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa
	SLC25A20	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20
Group 16 (0.715)	CLIC1	chloride intracellular channel 1
	KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15
	KCNK5	potassium channel, subfamily K, member 5
	CLIC3	chloride intracellular channel 3

Group 17 (0.494)	HOPX	HOP homeobox
	PRDM1	PR domain containing 1, with ZNF domain
	ZGPAT	zinc finger, CCCH-type with G patch domain
	ZBTB32	zinc finger and BTB domain containing 32
	ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
	MXD4	MAX dimerization protein 4
Group 18 (0.138)	TMEM14C	transmembrane protein 14C
	ORMDL3	ORM1-like 3 (S. cerevisiae)
	ITM2A	integral membrane protein 2A
	LAG3	lymphocyte-activation gene 3
	GPR137B	G protein-coupled receptor 137B
	GPR15	G protein-coupled receptor 15
	EVC2	Ellis van Creveld syndrome 2
	FAM174B	family with sequence similarity 174, member B
	PAQR4	progestin and adipoQ receptor family member IV
	KLRB1	killer cell lectin-like receptor subfamily B, member 1
	FUT7	fucosyltransferase 7 (alpha (1,3) fucosyltransferase)
	CD200	CD200 molecule
	NPDC1	neural proliferation, differentiation and control, 1
	NMUR1	neuromedin U receptor 1
	HAVCR2	hepatitis A virus cellular receptor 2
	CXCR3	chemokine (C-X-C motif) receptor 3
	MS4A1	membrane-spanning 4-domains, subfamily A, member 1
	NKG7	natural killer cell group 7 sequence
	SLAMF1	signaling lymphocytic activation molecule family member 1
	PDCD1	programmed cell death 1
	CCR5	chemokine (C-C motif) receptor 5
	DNAJC15	DnaJ (Hsp40) homolog, subfamily C, member 15
	CXCR6	chemokine (C-X-C motif) receptor 6
	VANGL1	vang-like 1 (van gogh, Drosophila)
	GPR25	G protein-coupled receptor 25
	TNFRSF18	tumor necrosis factor receptor superfamily, member 18
	CD2	CD2 molecule
	SPPL2A	signal peptide peptidase-like 2A
	DPY19L1	dpy-19-like 1 (C. elegans); similar to hCG1645499
	KIAA1324	KIAA1324
	CD79B	CD79b molecule, immunoglobulin-associated beta
	TSPAN5	tetraspanin 5
	CD226	CD226 molecule

	HIGD2A	HIG1 hypoxia inducible domain family, member 2A
	CLDND1	claudin domain containing 1
	GCNT1	glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylglucosaminyltransferase)
	MCAM	melanoma cell adhesion molecule
	CCDC107	coiled-coil domain containing 107
	CALHM2	calcium homeostasis modulator 2
	KCNK5	potassium channel, subfamily K, member 5
	CD58	CD58 molecule
	PDCD1LG2	programmed cell death 1 ligand 2
	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A
	CX3CR1	chemokine (C-X3-C motif) receptor 1
	EMP3	epithelial membrane protein 3
	GPR183	G protein-coupled receptor 183
	TSPAN2	tetraspanin 2
	CD84	CD84 molecule
	SLC29A1	solute carrier family 29 (nucleoside transporters), member 1
	CCR6	cyclin L2; chemokine (C-C motif) receptor 6
	CD82	CD82 molecule
	CD99	CD99 molecule

Supplementary Table 4, Gene modules down in Programmed cell death protein 1 (PD-1)^{high} Tregs from healthy donors. Differentially expressed genes that were down in PD-1^{high} Tregs were analyzed with DAVID to identify functional clusters of genes.

Gene Group (Enrichment Score)	**Official Gene Symbol**	**Gene Name**
Group 1 (7.483)	ZNF516	zinc finger protein 516
	SATB1	SATB homeobox 1
	ZNF506	zinc finger protein 506
	ZNF772	zinc finger protein 772
	ZSCAN18	zinc finger and SCAN domain containing 18
	ZBTB33	zinc finger and BTB domain containing 33
	ZNF844	zinc finger protein 844
	ZNF204P	zinc finger protein 204 pseudogene
	ZNF616	zinc finger protein 616
	NAPEPLD	N-acyl phosphatidylethanolamine phospholipase D
	ZHX3	zinc fingers and homeoboxes 3
	ZFP112	zinc finger protein 112 homolog (mouse)
	ZNF836	zinc finger protein 836
	NKRF	NFKB repressing factor
	ZFP14	zinc finger protein 14 homolog (mouse)
	ZNF652	zinc finger protein 652
	ZNF496	zinc finger protein 496
	RNF175	ring finger protein 175
	ZNF347	zinc finger protein 347
	ZNF337	zinc finger protein 337
	ZNF813	zinc finger protein 813
	ZC3H12B	zinc finger CCCH-type containing 12B
	RNF144A	ring finger protein 144A
	ZBTB4	zinc finger and BTB domain containing 4
	ZNF398	zinc finger protein 398
	ZNF548	zinc finger protein 548
	ZNF518B	zinc finger protein 518B
	ZNF585B	zinc finger protein 585B
	ZNF808	zinc finger protein 808
	PLAG1	pleiomorphic adenoma gene 1
	ZNF300	zinc finger protein 300
	ZFP3	zinc finger protein 3 homolog (mouse)
	PA2G4P4	proliferation-associated 2G4, 38kDa; proliferation-associated 2G4

		pseudogene 4
	ZNF101	zinc finger protein 101
	NR3C2	nuclear receptor subfamily 3, group C, member 2
	RNF130	ring finger protein 130
	ZNF550	zinc finger protein 550
	ZC3H10	zinc finger CCCH-type containing 10
	NR2C2	nuclear receptor subfamily 2, group C, member 2
	ZNF607	zinc finger protein 607
	HIVEP1	human immunodeficiency virus type I enhancer binding protein 1
	KLF7	Kruppel-like factor 7 (ubiquitous)
	ZNF324	zinc finger protein 324
	SH3RF3	SH3 domain containing ring finger 3
	ZNF473	zinc finger protein 473
	ZNF248	zinc finger protein 248
	ZC4H2	zinc finger, C4H2 domain containing
	ZCCHC14	zinc finger, CCHC domain containing 14
	ZNF433	zinc finger protein 433
	ZKSCAN2	zinc finger with KRAB and SCAN domains 2
	ZNF416	zinc finger protein 416
	ZNF354C	zinc finger protein 354C
Group 2 (4.99)	ZSCAN18	zinc finger and SCAN domain containing 18
	SCML1	sex comb on midleg-like 1 (Drosophila)
	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2
	MGA	MAX gene associated
	AFF3	AF4/FMR2 family, member 3
	POU6F1	POU class 6 homeobox 1
Group 3 (2.105)	WDR89	WD repeat domain 89
	TLE4	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)
	NBEA	neurobeachin
	TLE2	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)
Group 4 (1.927)	PDIK1L	PDLIM1 interacting kinase 1 like
	RYK	RYK receptor-like tyrosine kinase
	IGF1R	insulin-like growth factor 1 receptor
	RPS6KA2	ribosomal protein S6 kinase, 90kDa, polypeptide 2; hypothetical LOC100127984
	NUAK2	NUAK family, SNF1-like kinase, 2
	KALRN	kalirin, RhoGEF kinase
	TXK	TXK tyrosine kinase
	PDK1	pyruvate dehydrogenase kinase, isozyme 1
	TNK1	tyrosine kinase, non-receptor, 1

	TGFBR2	transforming growth factor, beta receptor II (70/80kDa)
	PAN3	PAN3 poly(A) specific ribonuclease subunit homolog (S. cerevisiae)
	ACVR1C	activin A receptor, type IC
	TGFBR1	transforming growth factor, beta receptor 1
	YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1
	EPHA1	EPH receptor A1
	CAMK4	calcium/calmodulin-dependent protein kinase IV
	PRKD3	protein kinase D3
Group 5 (0.991)	TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain
	AMIGO2	adhesion molecule with Ig-like domain 2
	AJAP1	adherens junctions associated protein 1
	PLXDC1	plexin domain containing 1
	GAL3ST4	galactose-3-O-sulfotransferase 4
	TMEM220	transmembrane protein 220
	JAM3	junctional adhesion molecule 3
	DCBLD2	discoidin, CUB and LCCL domain containing 2
	TSPAN33	tetraspanin 33
	CCR7	chemokine (C-C motif) receptor 7
	LNPEP	leucyl/cystinyl aminopeptidase
	GPR160	G protein-coupled receptor 160
	ST6GALNAC3	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 3
	NPTXR	neuronal pentraxin receptor
	GPA33	glycoprotein A33 (transmembrane)
	SLC7A6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6
	LMF1	lipase maturation factor 1
	SLC24A6	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6
	MPZL1	myelin protein zero-like 1
	CDCP1	CUB domain containing protein 1
	SLC29A2	solute carrier family 29 (nucleoside transporters), member 2
	NRCAM	neuronal cell adhesion molecule
	C10orf105	chromosome 10 open reading frame 105
	SLC2A6	solute carrier family 2 (facilitated glucose transporter), member 6
	PECAM1	platelet/endothelial cell adhesion molecule
	ROBO3	roundabout, axon guidance receptor, homolog 3 (Drosophila)
	LAPTM4B	lysosomal protein transmembrane 4 beta
	RNF130	ring finger protein 130

	SLC22A17	solute carrier family 22, member 17
	PTPRO	protein tyrosine phosphatase, receptor type, O
	CEACAM4	carcinoembryonic antigen-related cell adhesion molecule 4
	ALG10B	asparagine-linked glycosylation 10, alpha-1,2-glucosyltransferase homolog B (yeast)
	SLC46A1	solute carrier family 46 (folate transporter), member 1
	MAN1C1	mannosidase, alpha, class 1C, member 1
	F2RL1	coagulation factor II (thrombin) receptor-like 1
	GCNT4	glucosaminyl (N-acetyl) transferase 4, core 2 (beta-1,6-N-acetylglucosaminyltransferase)
	ENTPD6	ectonucleoside triphosphate diphosphohydrolase 6 (putative function)
	GPR162	G protein-coupled receptor 162
	TMEM30B	transmembrane protein 30B
	SNN	stannin
Group 6 (0.697)	TANC2	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2
	ANKS6	ankyrin repeat and sterile alpha motif domain containing 6
	ASB13	ankyrin repeat and SOCS box-containing 13
	BTBD11	BTB (POZ) domain containing 11

Supplementary Table 5, Gene set enrichment analysis for Programmed cell death protein 1 (PD-1)^{high} Tregs (FDR<0.05) from healthy donors, C2CP gene set database. Gene sets were categorized into the following groups: cell cycle/ proliferation (yellow), immune system / signaling (teal), metabolism (orange), and other (light blue). Gene set names in bold were chosen as representative examples in Figure 2D.

Category	Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val
Other	BIOCARTA_ACTINY_PATHWAY	20	0.432	2.268	0.000	0.004	0.307
	KEGG_OLFACTORY_TRANSDUCTION	377	0.307	6.991	0.000	0.000	0.000
	KEGG_PARKINSONS_DISEASE	111	0.475	5.831	0.000	0.000	0.000
	KEGG_ALZHEIMERS_DISEASE	155	0.366	5.391	0.000	0.000	0.000
	KEGG_HUNTINGTONS_DISEASE	170	0.326	5.011	0.000	0.000	0.000
	KEGG_PROTEASOME	44	0.567	4.440	0.000	0.000	0.000
	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	123	0.341	4.396	0.000	0.000	0.000
	REACTOME_DESTABILIZATION_OF_MRNA_BY_AUF1_HNRNP_D0	50	0.512	4.224	0.000	0.000	0.000
	REACTOME_HIV_INFECTION	187	0.241	3.828	0.000	0.000	0.000
	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICATION	99	0.325	3.807	0.000	0.000	0.000
	KEGG_ALLOGRAFT_REJECTION	33	0.544	3.715	0.000	0.000	0.000
	REACTOME_PREFOLDIN_MEDIATED_TRANSFER_OF_SUBSTRATE_TO_CCT_TRIC	27	0.584	3.656	0.000	0.000	0.000
	KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	267	0.190	3.574	0.000	0.000	0.000
	REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS	118	0.279	3.535	0.000	0.000	0.000
	KEGG_TYPE_I_DIABETES_MELLITUS	38	0.490	3.533	0.000	0.000	0.000
	KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	55	0.401	3.453	0.000	0.000	0.000
	REACTOME_HEMOSTASIS	443	0.136	3.405	0.000	0.000	0.000
	REACTOME_AMYLOIDS	73	0.327	3.303	0.000	0.000	0.000
	BIOCARTA_MPR_PATHWAY	33	0.483	3.234	0.000	0.000	0.000
	REACTOME_INFLUENZA_LIFE_CYCLE	132	0.235	3.130	0.000	0.000	0.000
	NABA_CORE_MATRISOME	274	0.164	3.106	0.000	0.000	0.000
	KEGG_LEISHMANIA_INFECTION	67	0.318	3.087	0.000	0.000	0.000
	REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS	290	0.152	3.010	0.000	0.000	0.001
	KEGG_VIRAL_MYOCARDITIS	65	0.312	2.962	0.000	0.000	0.001

	KEGG_GRAFT_VERSUS_HOST_DISEASE	32	0.416	2.825	0.000	0.000	0.003
	NABA_SECRETED_FACTORS	335	0.130	2.778	0.000	0.000	0.006
	NABA_ECM_GLYCOPROTEINS	195	0.154	2.487	0.002	0.001	0.073
	BIOCARTA_CDC42RAC_PATHWAY	15	0.515	2.435	0.000	0.001	0.101
	REACTOME_DEVELOPMENTAL_BIOLOGY	382	0.108	2.407	0.000	0.002	0.128
	KEGG_GAP_JUNCTION	86	0.222	2.402	0.000	0.002	0.128
	REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	180	0.152	2.345	0.000	0.003	0.196
	KEGG_AUTOIMMUNE_THYROID_DISEASE	48	0.284	2.326	0.000	0.003	0.219
	KEGG_CELL_ADHESION_MOLECULES_CAMS	128	0.173	2.316	0.000	0.003	0.225
	REACTOME_BASIGIN_INTERACTIONS	23	0.392	2.292	0.000	0.003	0.253
	KEGG_ASTHMA	27	0.375	2.287	0.000	0.003	0.264
	REACTOME_L1CAM_INTERACTIONS	84	0.205	2.280	0.000	0.004	0.285
	NABA_ECM_REGULATORS	226	0.128	2.272	0.002	0.004	0.301
	REACTOME_ENOS_ACTIVATION_AND_REGULATION	18	0.445	2.258	0.000	0.004	0.330
	REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2_	80	0.208	2.209	0.000	0.006	0.434
	REACTOME_AXON_GUIDANCE	242	0.122	2.190	0.002	0.006	0.472
	KEGG_TIGHT_JUNCTION	129	0.162	2.167	0.000	0.008	0.537
	REACTOME_KINESINS	24	0.367	2.155	0.002	0.008	0.565
	KEGG_CARDIAC_MUSCLE_CONTRACTION	73	0.212	2.150	0.000	0.008	0.579
	SIG_PIP3_SIGNALING_IN_CARDIAC_MYOCTES	67	0.216	2.104	0.004	0.011	0.672
	BIOCARTA_MTA3_PATHWAY	19	0.401	2.093	0.006	0.012	0.704
	REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES	25	0.353	2.090	0.000	0.012	0.714
	REACTOME_DARPP_32_EVENTS	23	0.361	2.070	0.006	0.013	0.761
	KEGG_BLADDER_CANCER	42	0.271	2.049	0.006	0.015	0.804
	REACTOME_MRNA_SPLICING_MINOR_PATHWAY	42	0.267	2.034	0.006	0.016	0.839
	BIOCARTA_MCALPAIN_PATHWAY	24	0.341	2.020	0.006	0.017	0.860
	KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION	68	0.204	2.020	0.002	0.017	0.860
	REACTOME_FACTORS_INVOLVED_IN_MEGAKARYOCYTE_DEVELOPMENT_AND_PLATELET_PRODUCTION	123	0.155	2.006	0.008	0.018	0.873
	BIOCARTA_FMLP_PATHWAY	36	0.283	1.997	0.004	0.018	0.891
	REACTOME_TRANSCRIPTION_COUPLED_N	43	0.258	1.985	0.010	0.020	0.908

	ER_TC_NER						
	REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_MRNA	131	0.151	1.983	0.014	0.020	0.912
	REACTOME_SMOOTH_MUSCLE_CONTRACTION	23	0.340	1.947	0.000	0.024	0.948
	BIOCARTA_P53_PATHWAY	16	0.407	1.944	0.008	0.024	0.954
	BIOCARTA_ERK_PATHWAY	27	0.319	1.940	0.008	0.024	0.954
	ST_PHOSPHOINOSITIDE_3_KINASE_PATHWAY	35	0.270	1.923	0.006	0.027	0.964
	REACTOME_FANCONI_ANEMIA_PATHWAY	21	0.351	1.918	0.018	0.027	0.966
	BIOCARTA_CHREBP2_PATHWAY	40	0.255	1.902	0.008	0.030	0.978
	REACTOME_SIGNALLING_TO_P38_VIA_RIT_AND_RIN	15	0.398	1.894	0.002	0.031	0.981
	REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WALL	83	0.179	1.892	0.010	0.031	0.982
	KEGG_MAPK_SIGNALING_PATHWAY	258	0.099	1.877	0.010	0.034	0.991
	REACTOME_GLOBAL_GENOMIC_NER_GG_NER	32	0.276	1.859	0.006	0.036	0.994
	BIOCARTA_RHO_PATHWAY	32	0.282	1.846	0.012	0.038	0.997
	BIOCARTA_GCR_PATHWAY	19	0.352	1.843	0.014	0.039	0.998
	REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION	23	0.318	1.821	0.010	0.042	1.000
	REACTOME_LIGAND_GATED_ION_CHANNEL_TRANSPORT	21	0.330	1.815	0.016	0.044	1.000
	BIOCARTA_HSP27_PATHWAY	15	0.382	1.809	0.024	0.044	1.000
	KEGG_MELANOMA	69	0.183	1.807	0.015	0.045	1.000
	KEGG_PROTEIN_EXPORT	23	0.305	1.791	0.018	0.048	1.000
Metabolism	REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE_ODC	48	0.577	4.729	0.000	0.000	0.000
	BIOCARTA_PPARA_PATHWAY	54	0.239	2.025	0.006	0.017	0.850
	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS_	78	0.596	6.218	0.000	0.000	0.000
	REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT	114	0.481	5.936	0.000	0.000	0.000
	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	64	0.625	5.837	0.000	0.000	0.000
	KEGG_OXIDATIVE_PHOSPHORYLATION	114	0.438	5.534	0.000	0.000	0.000

	REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES	194	0.222	3.594	0.000	0.000	0.000
	REACTOME_METABOLISM_OF_RNA	247	0.186	3.363	0.000	0.000	0.000
	REACTOME_METABOLISM_OF_NUCLEOTIDES	67	0.251	2.429	0.000	0.001	0.106
	REACTOME_GLUCOSE_METABOLISM	61	0.251	2.289	0.000	0.003	0.260
	KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM	31	0.348	2.262	0.002	0.004	0.325
	KEGG_GLYOXYLATE_AND_DICARBOXYLATE_METABOLISM	16	0.444	2.119	0.006	0.010	0.642
	REACTOME_AMINE_LIGAND_BINDING_RECEPTORS	37	0.280	2.011	0.004	0.018	0.868
	REACTOME_METABOLISM_OF_PROTEINS	418	0.189	4.427	0.000	0.000	0.000
	REACTOME_METABOLISM_OF_MRNA	204	0.220	3.599	0.000	0.000	0.000
	REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT	48	0.410	3.394	0.000	0.000	0.000
	KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS	15	0.635	2.978	0.000	0.000	0.001
	KEGG_CITRATE_CYCLE_TCA_CYCLE	30	0.442	2.947	0.000	0.000	0.001
	KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION	43	0.348	2.735	0.000	0.000	0.008
	REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE	19	0.516	2.668	0.000	0.000	0.011
	KEGG_PEROXISOME	76	0.234	2.389	0.000	0.002	0.142
	REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE	40	0.289	2.209	0.002	0.006	0.433
	REACTOME_METABOLISM_OF_CARBOHYDRATES	229	0.120	2.100	0.000	0.011	0.689
	REACTOME_PEROXISOMAL_LIPID_METABOLISM	20	0.390	2.089	0.006	0.012	0.715
	REACTOME_GLUCONEOGENESIS	29	0.321	2.026	0.006	0.017	0.850
	REACTOME_CHOLESTEROL_BIOSYNTHESIS	21	0.364	2.009	0.004	0.018	0.871
	KEGG_PYRIMIDINE_METABOLISM	93	0.176	1.955	0.006	0.023	0.943
	REACTOME_FATTY_ACID_TRIACYLGLYCEROL_AND_KETONE_BODY_METABOLISM	165	0.130	1.954	0.008	0.023	0.943
	REACTOME_METABOLISM_OF_LIPIDS_AND_LIPOPROTEINS	462	0.078	1.914	0.014	0.028	0.967
	REACTOME_GLYCOLYSIS	26	0.303	1.849	0.016	0.038	0.995
	KEGG_ONE_CARBON_POOL_BY_FOLATE	17	0.369	1.844	0.010	0.039	0.998

	KEGG_PROPANOATE_METABOLISM	32	0.274	1.838	0.023	0.040	0.999
	KEGG_PURINE_METABOLISM	153	0.124	1.831	0.008	0.041	0.999
Immune System / Signalling	BIOCARTA_DC_PATHWAY	22	0.365	2.085	0.000	0.012	0.722
	REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G	48	0.539	4.447	0.000	0.000	0.000
	REACTOME_ANTIGEN_PROCESSING_CROSS_PRESENTATION	70	0.483	4.756	0.000	0.000	0.000
	REACTOME_ACTIVATION_OF_NF_KAPPAB_IN_B_CELLS	62	0.388	3.632	0.000	0.000	0.000
	REACTOME_MHC_CLASS_II_ANTIGEN_PRESENTATION	89	0.275	3.067	0.000	0.000	0.000
	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	252	0.164	3.008	0.000	0.000	0.001
	BIOCARTA_NO2IL12_PATHWAY	17	0.537	2.708	0.000	0.000	0.009
	REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY	60	0.293	2.648	0.000	0.000	0.013
	REACTOME_INTERFERON_GAMMA_SIGNALING	57	0.259	2.304	0.000	0.003	0.239
	ST_FAS_SIGNALING_PATHWAY	63	0.247	2.303	0.002	0.003	0.239
	KEGG_CHEMOKINE_SIGNALING_PATHWAY	184	0.139	2.223	0.000	0.005	0.408
	REACTOME_INTERFERON_SIGNALING	149	0.153	2.206	0.000	0.006	0.438
	BIOCARTA_IL12_PATHWAY	22	0.350	1.986	0.004	0.020	0.906
	REACTOME_INTERFERON_ALPHA_BETA_SIGNALING	61	0.214	1.957	0.004	0.023	0.941
	REACTOME_PD1_SIGNALING	16	0.397	1.924	0.008	0.027	0.964
	REACTOME_CTLA4_INHIBITORY_SIGNALING	21	0.339	1.850	0.012	0.038	0.995
	BIOCARTA_GATA3_PATHWAY	15	0.389	1.824	0.015	0.042	1.000
	BIOCARTA_CTLA4_PATHWAY	19	0.340	1.794	0.023	0.047	1.000
	BIOCARTA_SPPA_PATHWAY	22	0.354	1.997	0.004	0.019	0.890
	BIOCARTA_STEM_PATHWAY	15	0.436	2.001	0.006	0.018	0.882
	REACTOME_NEGATIVE_REGULATORS_OF_RIG_I_MDA5_SIGNALING	30	0.413	2.664	0.000	0.000	0.012
	REACTOME_ER_PHAGOSOME_PATHWAY	56	0.505	4.553	0.000	0.000	0.000
	REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES	47	0.556	4.538	0.000	0.000	0.000
	REACTOME_ADAPTIVE_IMMUNE_SYSTEM	495	0.172	4.471	0.000	0.000	0.000

	REACTOME_SIGNALING_BY_THE_B_CELL_RECEPTOR_BCR	121	0.268	3.532	0.000	0.000	0.000
	REACTOME_GPCR_LIGAND_BINDING	390	0.139	3.236	0.000	0.000	0.000
	BIOCARTA_NKT_PATHWAY	29	0.498	3.140	0.000	0.000	0.000
	REACTOME_DOWNSTREAM_SIGNALING_EVENTS_OF_B_CELL_RECEPTOR_BCR	92	0.281	3.127	0.000	0.000	0.000
	REACTOME_G_ALPHA_I_SIGNALLING_EVENTS	189	0.189	3.028	0.000	0.000	0.000
	BIOCARTA_INFLAM_PATHWAY	28	0.457	2.861	0.000	0.000	0.003
	REACTOME_INNATE_IMMUNE_SYSTEM	258	0.142	2.738	0.000	0.000	0.007
	REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRESENTATION	229	0.158	2.733	0.000	0.000	0.008
	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	44	0.339	2.649	0.000	0.000	0.013
	KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	71	0.256	2.559	0.000	0.001	0.041
	REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	54	0.276	2.399	0.000	0.002	0.128
	REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION_PROTEASOME_DEGRADATION	194	0.143	2.294	0.000	0.003	0.252
	BIOCARTA_CYTOKINE_PATHWAY	21	0.410	2.284	0.000	0.003	0.276
	BIOCARTA_TH1TH2_PATHWAY	18	0.427	2.210	0.000	0.006	0.431
	KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	100	0.187	2.184	0.000	0.007	0.491
	REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION	195	0.135	2.180	0.002	0.007	0.500
	KEGG_HEMATOPOIETIC_CELL_LINEAGE	82	0.186	1.999	0.006	0.018	0.885
	REACTOME_GPVI_MEDIATED_ACTIVATION_CASCADE	31	0.296	1.989	0.006	0.019	0.902
	REACTOME_TRIF_MEDIATED_TLR3_SIGNALING	70	0.199	1.974	0.004	0.021	0.925
	KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	74	0.192	1.935	0.006	0.025	0.956
	REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	255	0.103	1.906	0.006	0.029	0.977
	REACTOME_ACTIVATED_TLR4_SIGNALLING	88	0.170	1.878	0.010	0.033	0.988
	REACTOME_TOLL_RECEPTOR_CASCADES	111	0.150	1.867	0.004	0.035	0.992
	REACTOME_RIG_I_MDA5_MEDIATED_IND	72	0.182	1.813	0.011	0.044	1.000

	UCTION_OF_IFN_ALPHA_BETA_PATHWAYS						
	KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	71	0.182	1.810	0.021	0.044	1.000
	KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	114	0.143	1.808	0.016	0.045	1.000
	BIOCARTA_NFAT_PATHWAY	51	0.211	1.808	0.015	0.044	1.000
CellCycle/Prolif	REACTOME_ACTIVATION_OF_BH3_ONLY_PROTEINS	16	0.470	2.180	0.002	0.007	0.500
	BIOCARTA_MCM_PATHWAY	18	0.435	2.151	0.000	0.008	0.577
	REACTOME_AUTODEGRADATION_OF_CDH1_BY_CDH1_APC_C	56	0.505	4.475	0.000	0.000	0.000
	REACTOME_MITOTIC_G1_G1_S_PHASES	129	0.449	5.912	0.000	0.000	0.000
	REACTOME_SYNTHESIS_OF_DNA	90	0.494	5.698	0.000	0.000	0.000
	REACTOME_CELL_CYCLE_CHECKPOINTS	111	0.405	5.010	0.000	0.000	0.000
	REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1_S_TRANSITION_	62	0.533	4.968	0.000	0.000	0.000
	REACTOME_SCFSKP2_MEDIATED_DEGRADATION_OF_P27_P21	53	0.537	4.575	0.000	0.000	0.000
	REACTOME_REGULATION_OF_APOPTOSIS	56	0.487	4.297	0.000	0.000	0.000
	REACTOME_CYCLIN_A_B1_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION	15	0.628	2.951	0.000	0.000	0.001
	REACTOME_APOPTOTIC_EXECUTION_PHASE	53	0.335	2.812	0.000	0.000	0.004
	REACTOME_DNA_REPAIR	103	0.206	2.487	0.000	0.001	0.073
	BIOCARTA_CELLCYCLE_PATHWAY	23	0.405	2.390	0.000	0.002	0.140
	REACTOME_EXTENSION_OF_TELOMERES	27	0.380	2.345	0.000	0.002	0.196
	REACTOME_CELL_CYCLE	394	0.321	7.424	0.000	0.000	0.000
	REACTOME_CELL_CYCLE_MITOTIC	306	0.348	7.115	0.000	0.000	0.000
	REACTOME_DNA_REPLICATION	187	0.427	6.644	0.000	0.000	0.000
	REACTOME_MITOTIC_M_M_G1_PHASES	167	0.415	6.287	0.000	0.000	0.000
	REACTOME_G1_S_TRANSITION	106	0.501	6.199	0.000	0.000	0.000
	REACTOME_S_PHASE	106	0.482	5.927	0.000	0.000	0.000
	REACTOME_APOPTOSIS	144	0.362	5.179	0.000	0.000	0.000
	REACTOME_M_G1_TRANSITION	78	0.483	4.957	0.000	0.000	0.000
	REACTOME_ORC1_REMOVAL_FROM_CHR	65	0.511	4.929	0.000	0.000	0.000

	OMATIN						
	REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX	63	0.505	4.821	0.000	0.000	0.000
	REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE	77	0.457	4.763	0.000	0.000	0.000
	REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_MITOTIC_PROTEINS	65	0.489	4.716	0.000	0.000	0.000
	REACTOME_APC_C_CDH1_MEDIATED_DEGRADATION_OF_CDC20_AND_OTHER_APC_C_CDH1_TARGETED_PROTEINS_IN_LATE_MITOSIS_EARLY_G1	64	0.487	4.673	0.000	0.000	0.000
	REACTOME_P53_INDEPENDENT_G1_S_DNA_DAMAGE_CHECKPOINT	48	0.539	4.427	0.000	0.000	0.000
	REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF_CDC6	46	0.553	4.407	0.000	0.000	0.000
	REACTOME_P53_DEPENDENT_G1_DNA_DAMAGE_RESPONSE	53	0.498	4.292	0.000	0.000	0.000
	REACTOME_SIGNALING_BY_WNT	61	0.465	4.271	0.000	0.000	0.000
	REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_ORIGIN_COMPLEX	54	0.486	4.259	0.000	0.000	0.000
	REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAINING_NUCLEOSOMES_AT_THE_CENTROMERE	59	0.461	4.245	0.000	0.000	0.000
	REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF_EMI1	49	0.510	4.243	0.000	0.000	0.000
	REACTOME_TRANSLATION	142	0.299	4.219	0.000	0.000	0.000
	REACTOME_G1_S_SPECIFIC_TRANSCRIPTION	17	0.839	4.200	0.000	0.000	0.000
	REACTOME_AUTODEGRADATION_OF_THE_E3_UBIQUITIN_LIGASE_COP1	47	0.505	4.136	0.000	0.000	0.000
	REACTOME_CHROMOSOME_MAINTENANCE	115	0.332	4.105	0.000	0.000	0.000
	REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_BIND_AU_RICH_ELEMENTS	80	0.387	4.081	0.000	0.000	0.000
	REACTOME_RNA_POL_I_PROMOTER_OPENING	54	0.470	4.053	0.000	0.000	0.000
	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	106	0.339	4.032	0.000	0.000	0.000

	REACTOME_TELOMERE_MAINTENANCE	72	0.387	3.886	0.000	0.000	0.000
	KEGG_RIBOSOME	84	0.354	3.827	0.000	0.000	0.000
	REACTOME_MITOTIC_PROMETAPHASE	85	0.348	3.711	0.000	0.000	0.000
	BIOCARTA_PROTEASOME_PATHWAY	28	0.583	3.700	0.000	0.000	0.000
	REACTOME_MEIOTIC_RECOMBINATION	76	0.357	3.680	0.000	0.000	0.000
	KEGG_CELL_CYCLE	124	0.270	3.608	0.000	0.000	0.000
	REACTOME_DNA_STRAND_ELONGATION	30	0.552	3.546	0.000	0.000	0.000
	REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION	102	0.298	3.498	0.000	0.000	0.000
	REACTOME_PEPTIDE_CHAIN_ELONGATION	83	0.333	3.490	0.000	0.000	0.000
	REACTOME_RNA_POL_I_TRANSCRIPTION	79	0.336	3.480	0.000	0.000	0.000
	REACTOME_TRANSCRIPTION	190	0.217	3.425	0.000	0.000	0.000
	REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION	33	0.495	3.375	0.000	0.000	0.000
	REACTOME_G2_M_CHECKPOINTS	41	0.435	3.308	0.000	0.000	0.000
	REACTOME_MEIOSIS	104	0.274	3.284	0.000	0.000	0.000
	REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMEDIATES_BY_CCT_TRIC	21	0.576	3.142	0.000	0.000	0.000
	REACTOME_PACKAGING_OF_TELOMERE_ENDS	45	0.395	3.136	0.000	0.000	0.000
	KEGG_DNA_REPLICATION	36	0.430	3.078	0.000	0.000	0.000
	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXON_JUNCTION_COMPLEX	103	0.255	3.056	0.000	0.000	0.000
	REACTOME_MEIOTIC_SYNAPSIS	68	0.307	2.964	0.000	0.000	0.001
	KEGG_P53_SIGNALING_PATHWAY	67	0.300	2.915	0.000	0.000	0.001
	REACTOME_PROTEIN_FOLDING	51	0.341	2.909	0.000	0.000	0.001
	REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS	35	0.401	2.859	0.000	0.000	0.003
	REACTOME_RNA_POL_I_RNA_POL_III_AND_MITOCHONDRIAL_TRANSCRIPTION	112	0.231	2.846	0.000	0.000	0.003
	REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX	30	0.433	2.845	0.000	0.000	0.003
	REACTOME_POST_CHAPERONIN_TUBULIN_FOLDING_PATHWAY	18	0.566	2.843	0.000	0.000	0.003
	REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS	29	0.442	2.815	0.000	0.000	0.004
	REACTOME_FORMATION_OF_THE_TERNA	47	0.344	2.803	0.000	0.000	0.004

	RY_COMPLEX_AND_SUBSEQUENTLY_THE_43S_COMPLEX						
	KEGG_SPLICEOSOME	120	0.216	2.771	0.000	0.000	0.006
	KEGG_OOCYTE_MEIOSIS	109	0.222	2.766	0.000	0.000	0.006
	REACTOME_G0_AND_EARLY_G1	23	0.471	2.700	0.000	0.000	0.010
	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELLULAR_PROTEINS	39	0.343	2.601	0.000	0.000	0.027
	BIOCARTA_G2_PATHWAY	24	0.422	2.497	0.000	0.001	0.068
	KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	208	0.150	2.495	0.000	0.001	0.068
	REACTOME_MRNA_SPLICING	103	0.205	2.445	0.000	0.001	0.095
	REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP_BINDING_COMPLEX_AND_EIFS_AND_SUBSEQUENT_BINDING_TO_43S	54	0.276	2.389	0.000	0.002	0.143
	REACTOME_RNA_POL_II_TRANSCRIPTION	94	0.209	2.368	0.000	0.002	0.167
	REACTOME_LAGGING_STRAND_SYNTHESIS	19	0.436	2.317	0.000	0.003	0.225
	REACTOME_MITOTIC_G2_G2_M_PHASES	78	0.220	2.220	0.000	0.005	0.413
	REACTOME_RNA_POL_II_TRANSCRIPTION_PRE_INITIATION_AND_PROMOTER_OPENING	40	0.288	2.195	0.000	0.006	0.461
	REACTOME_PHOSPHORYLATION_OF_THE_APC_C	17	0.412	2.053	0.006	0.015	0.796
	BIOCARTA_RAS_PATHWAY	23	0.355	2.034	0.004	0.016	0.839
	REACTOME_RNA_POL_II_PRE_TRANSCRIPTION_EVENTS	55	0.233	2.004	0.008	0.018	0.878
	BIOCARTA_RACCYCD_PATHWAY	26	0.318	1.937	0.008	0.025	0.955
	REACTOME_INHIBITION_OF_THE_PROTEOLYTIC_ACTIVITY_OF_APC_C_REQUIRED_FOR_THE_ONSET_OF_ANAPHASE_BY_MITOTIC_SPINDLE_CHECKPOINT_COMPONENTS	18	0.369	1.906	0.007	0.029	0.977
	REACTOME_NUCLEOTIDE_EXCISION_REPAIR	48	0.235	1.891	0.010	0.031	0.982
	KEGG_MISMATCH_REPAIR	22	0.326	1.873	0.002	0.034	0.991
	REACTOME_PROCESSING_OF_CAPPED_INTRONLESS_PRE_MRNA	22	0.338	1.870	0.014	0.034	0.992
	REACTOME_FORMATION_OF_RNA_POL_II_ELONGATION_COMPLEX_	39	0.246	1.867	0.010	0.035	0.992
	KEGG_NUCLEOTIDE_EXCISION_REPAIR	42	0.244	1.851	0.013	0.038	0.994

	BIOCARTA_BARRESTIN_SRC_PATHWAY	15	0.399	1.844	0.006	0.039	0.998
	BIOCARTA_CASPASE_PATHWAY	23	0.314	1.836	0.006	0.040	0.999
	REACTOME_ELONGATION_ARREST_AND_RECOVERY	27	0.295	1.833	0.014	0.041	0.999
	REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_CYCLIN_B	19	0.349	1.828	0.016	0.041	1.000
	REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION	180	0.116	1.797	0.016	0.047	1.000
	REACTOME_APC_CDC20_MEDIATED_DEGRADATION_OF_NEK2A	21	0.327	1.794	0.012	0.047	1.000

Supplementary Table 6, T cell subset, activation, and exhaustion gene signatures derived from the literature. Symbols were cross-checked using HGNC symbol checker.

Gene Set	Description	Reference	Genes
Th17 cytokines	Cytokines secreted by Th17 cells.	(65)	IL23R, IL9, IL17R, IL17A, IL24, IL12RB1, IL17F, LIF, IL10, TNFRSF8, IL21, IL1R1
Th17 core	Combinatorial core of transcription factor targets involved in Th17 cell specification.	(65) Figure 6D	STAT3, IRF4, RORC, MAF, BATF, FOSL2, CYSLTR2, CCL5, HIF1A, IL18RAP, IL17A, IL17F, CCL20, CCR8, IL2, CXCR3, TBX21, CCL4, CCL3, CCR6, IL1R1, GPR15, IL18R1, IL21RB1, IL7R, IL2RA, LTB4R1, IL12RB2, LTB, IL10RA, SMAD3, IL23A, CCR7, IL24, IL4RA, IL21, CXCL10, IL6RA, IL16
Th1	Th1-specific gene signature derived from C57BL/6 mice.	(66)	See Supplementary Table 4.
Th2	Th2-specific gene signature derived from C57BL/6 mice.		
iTreg	iTreg-specific gene signature derived from C57BL/6 mice.		
IFN-responsive	Exhaustion-specific genes associated with CD4+ T cell dysfunction during chronic infection in mice	(24) Figure 3C	MX2, MX1, ISG20, ISG15, IRF7, IFRD1, IFITM3, IFITM1 IFIT3, IFIT1, IFIH1, IFI44, IFI30, AIM2
Co-inhibitory exhaustion		(24) Supplemental Table 2	BTLA, CD160, CD200, CD200R1, CD200R1L, CD244, CD274, CTLA4, HAVCR2, LAG3, LAIR1, LILRB4, PDCD1, PDCD1LG2, PILRA, SIRPB1, TIGIT
Core exhaustion		(24) Supplemental Table 3	ARAP2, CCNA2, CCNB2, CCNYL1, CD86, CENPE, CRLF3, DEPDC1, DPH5, DTL, ENTPD5, EOMES, FAM105A, GPI, GPR141, GRAP2, HSPA4L, IDH2, IFI44, IFIH1, IRF4, ISG20, KIF15, KLHL6, KLHL7, LAG3, MKI67, MLF1, MLKL, MX1, NAB1, NAP1L3, NCAPG, NLK, NSMAF, NUDT15, PLOD2, PON3, PRR11, RCBTB1, RSAD2, SATB1, SCARNA17, SETBP1, SH2D1A, SNORD35B, TAF1A, TINF2, TMEM140, TMEM2,

			TNFSF4, TPX2, TXNIP, USP18
Anergic	Differentially expressed genes found in early anergic T cell clones (A.E7 CD4$^+$)	(67) Table 1	EGR2, ETV6, FOXP1, HLF, IRF4, JARID2, NFATC1, NOTCH1, NR4A2, NR4A3, ZFP36L1, ACTN4, AGT, ANGPTL2, ANKRD28 ANP32A, RCBTB1, S100A5, SFRP4, SOCS4, GCH1, KIFC3, PFKP, PLA2G10, ARFIP1, BNIP3, CCRN4L, DTNA, CCL1, CCL3, CSF1, TNFSF11, TNFSF9, FBXO34, GADD45B, HEBP2, DDR1, FYN, JAK3, ADORA2A, ADORA2B, F2R, GABRA4, KCNJ11, KCNK5, KCNQ5, CASP4, CTSE, FURIN, TINAG, GGA2, SLC29A3, STX11, CDC14A, DUSP6, HIF1AN, HSPA1A, IER3, JUP, LAG3, LRRC3, MARCH2, MMD, MYH14, MYL7, MYO1C, MYO1E, NDRG1, OAZ3, AGAP1, TEKT2, TNFRSF19, TNFRSF4, RNF19A, SOCS6, KIF15, CLEC4E, CD40LG, MPZL2, ADGRE5, LPAR4, SRGN
Activated Treg (up)	Genes identified by RNAseq in activated and unactivated Tregs (CD4$^+$CD25^{hi}) and Th (CD4$^+$CD25$^-$)	(38)	Table S1, Treg specific, >2FC CD25 activated v unactivated
Activated Treg (down)			Table S1, Treg specific, <2FC CD25 activated v unactivated
Activated Teff (up)			Table S1, Teff specific, >2FC CD4 activated v unactivated
Activated Teff (down)			Table S1, Teff specific, <2FC CD4 activated v unactivated
PD-1^{hi} up	Sorted CD8 CCR7lo PD1hi and PD1lo and naïve cells from humans were profiled with microarrays (Table I and Table II)	(68)	CD28, CD27, CTLA4, RGS1, SIRPG, MEGF6, PASK, ZNF512B, CXCR6 CXCR4, GZMK, ITM2A, SGPP2, TTC9, MBOAT1
PD-1^{hi} down			SH2D1B, TRA/TRD, LYN, LAT2, RAP2A, VAV3, KIR3DL2, KLRC3, KIR3DL1/KIR3DS1, KIR2DL2/3, KIR2DS1/2/4/5, KLRC1/2, KLRF1, KLRC4, IR2DS3, KLRD1, KIR2DL1, KIR2DL4, NCR1, KIR2DL5A, NCAM1, ITGAM, PALLD, ITGAX, IKZF2, KLF11, ZNF683, TFCP2L1, METTL7A, GNLY, GZMB, MYO6, GOLIM4, IL8RB, IL7, CMKLR1, CTBP2 BOK, RASSF4, PDGFD, GPR56, HDGFRP3, ADRB1, PRSS23, GOLM1, GLB1L2, TM6SF1,

			RHOBTB3, SYNGR1, OSBPL5, TSPAN2, TMCC3, LILRB1, DOCK5, ARRB1, PTGDS FCGR3B, CES1, BNC2, SSX2IP, MXRA7
TF exhaustion	Gene sets associated with CD8 T cell dysfunction in acute versus chronic CMV infection in mice. Set identified through network analysis of transcription factors associated with Tbet.	(39)	See Supplemental Table 7, 242 gene signature of transcription factor 'neighbors' in acute and chronic networks
Exhausted up, memory down	Gene sets associated with progressive stimulation of CD8 T cells with antigen, identified by comparing CD8 from primary to quaternary antigen exposure.	(22) Table S6 blue module	FIGNL1, CTLA4, PLSCR1, ART3, PRC1, TOP2A, PLK4, MKI67, HIST1H2AE, CD160, EOMES, PGLYRP1, CDC6, MYB, CKS2
Exhausted up, memory up		(22) STable 6 orange module	ADGRG1, CCL3, CCL4, CD244, ENTPD1, FGL2, GPD2, GZMA GZMB, GZMK, IRF4, LAG3, LGALS3, MAD2L1, NR4A2, PBX3 PDCD1, PERP, PON2, PRDM1, RGS16, WBP5
Exhausted down, memory down		(22) STable 6 yellow module	ARHGAP1, ATP6V0B, CCR7, CEBPB. CRLF3, CTSW, DGKA, DUSP1, DUSP12, EEF1D, EEF2, ELOVL5, EPHB4, EVL, FOSB, GARS, GM2A, GZMM, IL7R, IMPDH2, KCNN4, KCTD12, KLF3, LEF1, LGALS13 LTB, MBP, MRPL13, PDLIM1, PIK3CD, PLAC8, PRG2, PSMD1, RPL10A, RPL13, RPL8, RPLP1, RPN2, RPS3, RPS5, SELL, SLC3A2, SMAD1, SMAD7
Repeat antigen exposure, up	Gene sets associated with progressive stimulation of CD8 T cells with antigen,	(22) Table S5, >2FC	ALCAM, ANXA1, ARHGEF12 ,BHLHE40 ,BHLHE40, CAPG, CAPN2, CARNS1, CCDC109B, CCR5, CD244, CD80, CDC20B, CDHR1,CHN2, CMKLR1, CRYBG3, CX3CR1, DDX28, DENND5A, EMP1, ERN1, ESM1, FASLG, FBXL2,FCGR2B,

	compared quaternary to primary antigen exposure.		GABARAPL1, GALNT3,GNA15, GSAP,GSTM5,GZMB,HAVCR2, IFIT2, IL12RB2,IL18RAP,IL1RL1, IL2RA,INPP4A,ITGAM,KCNJ8,KLRC2, KLRC3,KLRG1, LAMC1,LONRF3, LPIN1,LPP, MBD3L2, MMP25, MS4A4A, MT2A, MYL10, NEBL,OSBPL3, PIK3AP1,PLK3, PLSCR4,REEP5,RNF216,RORA, S1PR5, SAR1B, SETBP1,SLAMF1,SLAMF7, SPATS2,SRXN1, SYTL3,TCF4, TCF7L2, TEF,TMBIM1, TMEM97, TSPAN2, TTC39C, ZEB2
Repeat antigen exposure, down		(22) Table S5, <2FC	ACTN1 AFF3 ATP6V0D2 AXIN2 CAPN11 CCDC64 CCNE1 CCR7 CD55 CDCA7L CDH1 COTL1 CTSE CXCR3 DAPL1 DDX21 DENND2D DPP4 ECE2 EIF5AP4 ENTPD5 EOMES EYA2 F2RL1 FA2H FAAH FAM101B FAM134B FAM169B FAM46A FAM46C FCHSD2 FZR1 HOOK1 IL2 INADL INSR ITGAX KBTBD11 LARP1 LTB LY6E LYST MAP3K5 MAPK11 MBOAT1 MDN1 METTL2A METTL2B MGST2 MYB MYC NEDD4L NHP2 PDE2A PDK1 PDLIM1 PDPK1 PECAM1 PGLYRP1 PLA2G16 PLEKHA1 PRKCSH QPCT QTRTD1 RANBP10 RAPGEF4 RASSF2 RCN3 RGS10 RLTPR RNF122 RNF144A RPLP1 RPP38 RRAGA RRP15 SATB1 SELL SIDT1 SLAMF6 SLC11A2 SLC25A40 SLFN5 SMYD2 SNHG1 SPIN2A SSBP2 TCF7 TFDP1 THG1L TLR1 TNFSF8 TREML2 TSR1 TTC27 UBALD1 VIPR1 VWA5A WBSCR27 WDR3 WDR77 WFIKKN2 XCL1

Supplementary Table 7, Data for patients used in this study.

Glioma (G)	Age	Sex	Diagnosis	WHO grade	Previous Treatments	Time from First Diagnosis/MRI to Tumor Resection				Ki67	IDH1 R132H mutation	MGMT promoter methylation
						Years	Months	Weeks	Days			
G1	45-49	F	Glioblastoma Multiforme	IV	Dexamethosone		4			10%	negative	unmethylated
G2	65-69	F	Glioblastoma Multiforme	IV	Dexamethosone				4	40%	negative	partially methylated
G3	60-64	M	Glioblastoma Multiforme	IV	Dexamethasone				3	80%	negative	unmethylated
G4	30-34	F	Secondary Glioblastoma Multiforme	IV	Dexamethasone, Avastin				N/A	10-20%		
G5	70-74	F	Glioblastoma Multiforme	IV	Dexamethasone		10			20%	not recorded	methylated
G6	60-64	M	Glioblastoma Multiforme with Oligodendroglial Component	IV	Dexamethasone				3	>25%		
G7	45-49	M	Glioblastoma Multiforme	IV	Dexamethasone		1			>15%		
G8	60-64	M	Glioblastoma Multiforme	IV	Dexamethasone			1		>10%	not recorded	unmethylated
G9	60-64	M	Glioblastoma Multiforme	IV	Dexamethasone				10	>25%		
G10	45-49	M	Glioma with Prominent Oligodendrogliomatous Differentiation	III	Dexamethasone			2		12%	positive	not recorded
G11	30-34	F	Anaplastic Oligodendroglioma	III	Dexamethasone				16	20%	positive	methylated
G12	60-64	F	Anaplastic Oligodendroglioma	III	Dexamethasone	12				20%	positive	methylated
G13	45-49	M	Astrocytoma	II	Dexamethosone				5	<4%	positive	methylated
G14	55-59	M	Oligoastrocytoma	II	Dexamethasone	14				<3%	positive	methylated
G15	40-44	M	Oligodendroglioma	II	Dexamethasone		3			5%	positive	not recorded
G16	55-59	F	Oligodendrogli	II	Dexamethasone			6		NR	not	not

			oma								recorded	recorded
G17	35-39	F	Oligoastrocytoma	II	Dexamethasone			6		4-6%	negative	partially methylated
G18	35-39	M	Astrocytoma	II	Dexamethasone				6	5-6%		
G19	60-64	M	Glioblastoma Multiforme	IV	Dexamethosone			2		>50 %	not recorded	methylated
G20	55-59	M	Glioblastoma Multiforme	IV	Dexamethasone		1			20%	not recorded	methylated
G21	45-49	F	Glioblastoma Multiforme	IV	Dexamethasone				1	20%	negative	methylated
G22	45-49	M	Glioblastoma Multiforme	IV	Dexamethasone			1		10%	not recorded	unmethylated
G23	50-54	F	Glioblastoma Multiforme	IV	Dexamethasone				5	15%	negative	unmethylated
G24	70-74	M	Gliosarcoma	IV	Dexamethasone			2		10%	not recorded	not recorded
G25	75-79	M	Glioblastoma Multiforme	IV	Dexamethasone				1	>20 %	negative	partially methylated
G26	75-79	F	Glioblastoma Multiforme	IV	Dexamethasone		2			highly elevated	negative	unmethylated
G27	15-19	F	Glioblastoma Multiforme	IV	N/A			1		40%	negative	unmethylated
G28	70-74	F	Glioblastoma Multiforme	IV	Dexamethasone				2	25%	negative	methylated
G29	80-84	F	Glioblastoma Multiforme	IV	Dexamethasone				3	15%	negative	unmethylated
G30	60-64	M	Glioblastoma Multiforme	IV	Prednisone				1	15%	positive	methylated
G31	60-64	M	Glioblastoma Multiforme	IV	Dexamethasone				1	20%	negative	methylated
G32	65-69	M	Glioblastoma Multiforme	IV	Dexamethasone		1			40%	not recorded	unmethylated
G33	55-59	M	Glioblastoma Multiforme	IV	Dexamethasone				6	20%	negative	unmethylated
G34	65-69	M	Glioblastoma Multiforme	IV	Dexamethasone		1			>60 %	not recorded	methylated
G35	50-54	F	Glioblastoma Multiforme	IV	Dexamethasone		1			5%	not recorded	partially methylated
G36	55-59	M	Recurrent Glioblastoma Multiforme	IV	Dexamethasone				N/A	NR		
G37	70-74	M	Glioblastoma	IV	Dexamethasone			1		NR	not	unmethyla

			Multiforme								recorded	ted
G38	45-49	M	Glioblastoma Multiforme	IV	Dexamethasone			5		40%	negative	unmethylated
G39	65-69	F	Glioblastoma Multiforme	IV	Dexamethasone				3	40%	negative	methylated
G40	80-84	M	Glioblastoma Multiforme	IV	N/A			1		15%	positive	methylated
BT 213	79	F	Glioblastoma	IV	None (Keppra)				5	"scattered mitotic figures"	negative	unmethylated
BT 215	76	F	Glioblastoma	IV	Dexamethasone				8	"numerous mitotic figures"	negative	methylated
BT 219	56	F	Anaplastic Oligoastrocytoma	III	Dexamethasone (and Keppra)				3	25-30%	negative	partially methylated
BT 220	63	M	Recurrent Residual Glioblastoma	IV	Partial brain XRT + dexamethasone (and Keppra)		5			10-15%	negative	partially methylated
BT 223	84	F	Glioblastoma	IV	Dexamethasone (and Keppra)		2			>30%	negative	methylated
BT 228	40	F	Glioblastoma	IV	Dexamethasone *				12*	>25%	negative	methylated
BT 229	61	M	Glioblastoma	IV	Dexamethasone (and Keppra)				8	>10%	negative	methylated
Patient 3 (CyTOF)	69	F	Glioblastoma	-	Nivolumab	-	-	-	-	-	-	-
Patient 6 (CyTOF)	67	F	Glioblastoma	-	Nivolumab	-	-	-	-	-	-	-
Patient 11 (CyTOF)	58	M	Glioblastoma	-	Nivolumab	-	-	-	-	-	-	-
Patient 14 (CyTOF)	43	M	Glioblastoma	-	Nivolumab	-	-	-	-	-	-	-

*Note: 10 years prior, oligoastrocytoma (WHO grade 2) in same location (cerebellum) treated with surgery, temozolomide, radiation therapy, and dexamethasone.

Supplementary Table 8, Differentially expressed genes in Programmed cell death protein 1 (PD-1)^{high} and PD-1^{-} Tregs from healthy donors compared to all GBM patients.

Comparison	Gene	Log2FC	p-value	FDR
PD1- GBM blood versus PD1- HC blood	NOG	8.19	3.37E-15	6.87E-11
	XIST	-12.80	1.95E-11	1.99E-07
	PRDM1	-3.38	1.07E-10	7.30E-07
	GIMAP4	2.59	4.06E-09	2.07E-05
	DQ786258	4.15	1.51E-07	6.17E-04
	ARHGEF11	2.81	2.76E-07	8.09E-04
	AK125960	-20.00	2.78E-07	8.09E-04
	FAM171A1	5.98	3.33E-07	8.48E-04
	ESYT1	2.03	4.75E-07	9.78E-04
	GIMAP8	3.15	4.80E-07	9.78E-04
	LINC00282	5.68	6.73E-07	1.25E-03
	PRKY	2.82	1.11E-06	1.86E-03
	USP9Y	3.00	1.26E-06	1.86E-03
	ARHGAP32	3.43	1.28E-06	1.86E-03
	ZNF248	2.74	2.14E-06	2.90E-03
	DENND2D	2.29	2.71E-06	3.45E-03
	INPP4A	1.88	3.07E-06	3.69E-03
	TCF7	1.79	3.73E-06	4.23E-03
	RNASEL	2.23	7.01E-06	7.52E-03
	NUAK2	2.11	1.13E-05	1.16E-02
	GPA33	2.07	1.37E-05	1.33E-02
	C20orf112	2.17	1.56E-05	1.39E-02
	HIVEP2	2.01	1.59E-05	1.39E-02
	BTBD11	2.08	1.64E-05	1.39E-02
	ZNF30	2.58	1.73E-05	1.39E-02
	DQ593252	1.88	1.77E-05	1.39E-02
	ZHX2	2.11	2.25E-05	1.68E-02
	CISH	2.52	2.41E-05	1.68E-02

	GIMAP6	1.99	2.52E-05	1.68E-02
	RAB10	1.92	2.53E-05	1.68E-02
	ST6GAL1	1.96	2.56E-05	1.68E-02
	AMIGO1	2.99	2.91E-05	1.86E-02
	DDIT4	-1.92	3.15E-05	1.94E-02
	DYRK2	1.64	3.45E-05	2.05E-02
	AK056689	2.08	3.60E-05	2.05E-02
	BCL9	2.81	3.61E-05	2.05E-02
	TMEM204	2.31	3.73E-05	2.06E-02
	PAQR8	2.46	3.83E-05	2.06E-02
	HERPUD1	-2.58	4.42E-05	2.29E-02
	EPHA1	2.81	4.50E-05	2.29E-02
	SH2D3C	2.04	4.74E-05	2.36E-02
	RBMS3	2.02	5.16E-05	2.50E-02
	CAD	2.00	6.45E-05	3.06E-02
	ZNF792	2.60	7.14E-05	3.31E-02
	TOB1	-1.86	8.58E-05	3.87E-02
	ABLIM1	1.59	8.73E-05	3.87E-02
	FAM203A	2.67	9.55E-05	4.15E-02
	PLAG1	3.89	1.05E-04	4.39E-02
	NIPAL3	1.56	1.05E-04	4.39E-02
	ITGA6	1.74	1.11E-04	4.54E-02
	ZNF146	1.73	1.17E-04	4.65E-02
	ZNF28	2.47	1.18E-04	4.65E-02
PD1+ GBM Blood versus PD1+ HC Blood	ADCK1	20.00	2.58E-06	3.30E-02
	ZNF823	7.91	4.94E-06	3.30E-02
	ZNF443	20.00	3.86E-06	3.30E-02
	MAN1C1	5.32	7.82E-06	3.93E-02

Supplementary Table 9, Gene sets enrichment analysis (GSEA) results for exhaustion gene sets in Programmed cell death protein 1 (PD-1)^{high} and PD-1^{-} tumor and blood-derived Tregs.

Comparison	Enriched in	Gene Set NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX
PD-1 positive versus PD-1 negative - Blood	PD1p	01_TH17 CYTOKINES	11	0.4451	1.7659	0.0182	0.0574	0.1840	7211
	PD1n	02_TH17_CORE	35	-0.2388	-1.7133	0.0200	0.0292	0.2230	17260
	PD1n	03_TH1	66	-0.2419	-2.2892	0.0000	0.0013	0.0060	17830
	PD1p	04_TH2	71	0.1204	1.1679	0.2711	0.3096	0.9590	13120
	PD1n	05_ITREG	32	-0.2564	-1.7170	0.0327	0.0314	0.2200	15807
	PD1n	06_IFN_RESPONSIVE_CD4	14	-0.3729	-1.6558	0.0297	0.0365	0.2870	14198
	PD1p	07_CO_INHIB_EXHAUSTIONCD4	16	0.2871	1.3985	0.1091	0.1604	0.6970	13422
	PD1n	08_CORE_EXHUASTION	52	-0.2107	-1.7966	0.0139	0.0242	0.1590	18696
	PD1n	09_ANERGIC	78	-0.0941	-0.9681	0.5041	0.4841	0.9980	19214
	PD1n	10_UP_ACTIVATEDTREGSPECIFIC	95	-0.2205	-2.4676	0.0000	0.0000	0.0000	18853
	PD1n	11_DOWN_ACTIVATEDTREGSPECIFIC	84	-0.2330	-2.5361	0.0000	0.0000	0.0000	17176
	PD1n	12_UP_ACTIVATEDTEFFSPECIFIC	45	-0.3123	-2.4646	0.0000	0.0000	0.0000	7930
	PD1n	13_DOWN_ACTIVATEDTEFFSPECIFIC	52	-0.2571	-2.2123	0.0020	0.0016	0.0090	13092
	PD1n	14_PD1UP	15	-0.3975	-1.8834	0.0082	0.0157	0.0970	15394
	PD1p	15_PD1DOWN	50	0.1284	1.1031	0.3234	0.3212	0.9820	13582
	PD1n	16_TF_EXHAUSTED	232	-0.2374	-4.0790	0.0000	0.0000	0.0000	16228
	PD1p	17_EXHAUSTEDUP_MEMORYDOWN	15	0.3458	1.6061	0.0473	0.0835	0.3720	13307
	PD1n	18_EXHAUSTED_UPMEMORYUP	21	-0.2489	-1.3658	0.1196	0.1393	0.7490	17972
	PD1n	19_EXHAUSTEDDOWN_MEMORYDOWN	44	-0.3302	-2.6110	0.0000	0.0000	0.0000	15379
	PD1n	20_UPINQUATERNARYCD8	75	-0.1059	-1.0855	0.3198	0.3609	0.9810	18075
	PD1n	21_DOWNINQUARTERNARYCD8	103	-0.2383	-2.8905	0.0000	0.0000	0.0000	9312
PD-1 positive versus PD-1 negative - Tumor	PD1p	01_TH17 CYTOKINES	11	0.4853	1.9680	0.0020	0.0165	0.0810	6185
	PD1p	02_TH17_CORE	35	0.4310	2.9988	0.0000	0.0000	0.0000	7249
	PD1p	03_TH1	66	0.2259	2.1529	0.0020	0.0078	0.0290	2758
	PD1p	04_TH2	71	0.1124	1.0970	0.3140	0.3487	0.9820	6488

	PD1p	05_ITREG	32	0.1844	1.2424	0.1894	0.2550	0.9090	4075
	PD1p	06_IFN_RESPONSIVE_CD4	14	0.3855	1.7228	0.0280	0.0435	0.2350	6576
	PD1p	07_CO_INHIB_EXHAUSTIONCD4	16	0.3909	1.8945	0.0104	0.0201	0.1100	10771
	PD1p	08_CORE_EXHUASTION	52	0.1804	1.5659	0.0379	0.0800	0.4430	13573
	PD1p	09_ANERGIC	78	0.1545	1.6079	0.0401	0.0707	0.3760	6869
	PD1p	10_UP_ACTIVATEDTREGSPECIFIC	95	0.2349	2.7122	0.0000	0.0009	0.0010	6656
	PD1n	11_DOWN_ACTIVATEDTREGSPECIFIC	84	-0.0724	-0.7831	0.7545	0.7427	1.0000	13968
	PD1n	12_UP_ACTIVATEDTEFFSPECIFIC	45	-0.1932	-1.5590	0.0518	0.2051	0.4370	15505
	PD1n	13_DOWN_ACTIVATEDTEFFSPECIFIC	52	-0.1376	-1.1730	0.2795	0.3369	0.9480	2879
	PD1p	14_PD1UP	15	0.4844	2.2133	0.0000	0.0065	0.0170	6364
	PD1p	15_PD1DOWN	50	0.1147	0.9838	0.4306	0.4574	0.9980	4737
	PD1p	16_TF_EXHAUSTED	232	0.1216	2.1654	0.0040	0.0073	0.0230	15854
	PD1p	17_EXHAUSTEDUP_MEMORYDOWN	15	0.3363	1.5652	0.0565	0.0740	0.4440	15250
	PD1p	18_EXHAUSTED_UPMEMORYUP	21	0.3755	2.0439	0.0096	0.0123	0.0540	3795
	PD1n	19_EXHAUSTEDDOWN_MEMORYDOWN	44	-0.1632	-1.2505	0.1799	0.3851	0.8860	16154
	PD1p	20_UPINQUATERNARYCD8	75	0.2252	2.3055	0.0000	0.0033	0.0070	14695
	PD1p	21_DOWNINQUARTERNARYCD8	103	0.1043	1.2244	0.2154	0.2538	0.9180	15694
PD-1 positive - Tumor versus Blood	tumor	01_TH17 CYTOKINES	11	0.3875	1.5456	0.0630	0.0856	0.4870	8680
	tumor	02_TH17_CORE	35	0.4097	2.8994	0.0000	0.0000	0.0000	2684
	tumor	03_TH1	66	0.3505	3.3756	0.0000	0.0000	0.0000	4615
	tumor	04_TH2	71	0.2272	2.2446	0.0038	0.0031	0.0180	3206
	tumor	05_ITREG	32	0.2178	1.4552	0.0943	0.1076	0.6210	9607
	tumor	06_IFN_RESPONSIVE_CD4	14	0.7082	3.2406	0.0000	0.0000	0.0000	5637
	tumor	07_CO_INHIB_EXHAUSTIONCD4	16	0.4188	2.0286	0.0100	0.0078	0.0540	6868
	tumor	08_CORE_EXHUASTION	52	0.3269	2.7007	0.0000	0.0002	0.0010	4927
	tumor	09_ANERGIC	78	0.3306	3.4225	0.0000	0.0000	0.0000	6644
	tumor	10_UP_ACTIVATEDTREGSPECIFIC	95	0.3367	3.7802	0.0000	0.0000	0.0000	6487
	blood	11_DOWN_ACTIVATEDTR	84	-0.2147	-2.3146	0.0019	0.0017	0.0080	7609

		EGSPECIFIC							
	tumor	12_UP_ACTIVATEDTEFFSPECIFIC	45	0.1793	1.4101	0.0992	0.1210	0.6770	9615
	tumor	13_DOWN_ACTIVATEDTEFFSPECIFIC	52	0.2610	2.1839	0.0039	0.0038	0.0250	10045
	tumor	14_PD1UP	15	0.2418	1.1087	0.2928	0.3473	0.9790	5746
	tumor	15_PD1DOWN	50	0.2984	2.4519	0.0000	0.0008	0.0040	5674
	tumor	16_TF_EXHAUSTED	232	0.1363	2.4209	0.0000	0.0007	0.0040	6567
	tumor	17_EXHAUSTEDUP_MEMORYDOWN	15	0.2088	0.9710	0.4918	0.5038	0.9970	4885
	tumor	18_EXHAUSTED_UPMEMORYUP	21	0.5715	3.1163	0.0000	0.0000	0.0000	6090
	blood	19_EXHAUSTEDDOWN_MEMORYDOWN	44	-0.1339	-1.0625	0.3386	0.3697	0.9890	13420
	tumor	20_UPINQUATERNARYCD8	75	0.3036	3.1216	0.0000	0.0000	0.0000	5889
	tumor	21_DOWNINQUARTERNARYCD8	103	0.1313	1.5418	0.0568	0.0807	0.4910	10296
PD-1 negative - Tumor versus Blood	tumor	01_TH17 CYTOKINES	11	0.4675	1.8527	0.0095	0.0334	0.1290	8959
	tumor	02_TH17_CORE	35	0.1668	1.1764	0.2440	0.3179	0.9450	14717
	blood	03_TH1	66	-0.0944	-0.8903	0.5833	0.5876	0.9980	18491
	tumor	04_TH2	71	0.1887	1.8408	0.0080	0.0281	0.1300	11020
	blood	05_ITREG	32	-0.2165	-1.4720	0.0513	0.1008	0.5880	16825
	tumor	06_IFN_RESPONSIVE_CD4	14	0.4368	1.9924	0.0020	0.0192	0.0580	10740
	tumor	07_CO_INHIB_EXHAUSTIONCD4	16	0.3653	1.7804	0.0202	0.0365	0.1870	11425
	tumor	08_CORE_EXHUASTION	52	0.1295	1.1089	0.3074	0.3619	0.9700	14379
	tumor	09_ANERGIC	78	0.2249	2.3321	0.0000	0.0039	0.0030	14899
	tumor	10_UP_ACTIVATEDTREGSPECIFIC	95	0.1576	1.7515	0.0258	0.0369	0.2130	15614
	blood	11_DOWN_ACTIVATEDTREGSPECIFIC	84	-0.3785	-4.0418	0.0000	0.0000	0.0000	7089
	blood	12_UP_ACTIVATEDTEFFSPECIFIC	45	-0.1410	-1.1400	0.3036	0.3260	0.9670	3784
	tumor	13_DOWN_ACTIVATEDTEFFSPECIFIC	52	0.1570	1.3335	0.1354	0.2007	0.7980	14661
	blood	14_PD1UP	15	-0.3891	-1.8274	0.0197	0.0209	0.1350	7096
	tumor	15_PD1DOWN	50	0.2418	2.0034	0.0020	0.0234	0.0530	13245
	blood	16_TF_EXHAUSTED	232	-0.1788	-3.2143	0.0000	0.0000	0.0000	16061
	tumor	17_EXHAUSTEDUP_MEMO	15	0.2218	1.0334	0.3848	0.3934	0.9910	14768

		RYDOWN							
	tumor	18_EXHAUSTED_UPMEMORYUP	21	0.2604	1.4245	0.1091	0.1523	0.6750	14027
	blood	19_EXHAUSTEDDOWN_MEMORYDOWN	44	-0.2984	-2.3490	0.0020	0.0023	0.0080	6324
	tumor	20_UPINQUATERNARYCD8	75	0.2057	2.1349	0.0021	0.0123	0.0200	14171
	blood	21_DOWNINQUARTERNARYCD8	103	-0.1806	-2.1833	0.0020	0.0037	0.0200	16482

Supplementary Table 10, Co-correlation analysis with Programmed cell death protein 1 (PD-1) for PD-1^{high} Tregs from tumors and blood. Shown here are the genes filtered for Pearson correlation coefficient greater than 0.8 for tumor-infiltrating lymphocytes.

Symbol	TIL_Tregs_p-values	TIL_Tregs_Correlation	Blood_Tregs_p-values	Blood_Tregs_Correlation
PDCD1	0.0E+00	1.00	0.00E+00	1.00
STAT4	1.1E-07	0.99	2.27E-01	0.48
ICOS	5.8E-06	0.97	8.56E-01	0.08
BC127952	2.9E-05	0.95	7.81E-01	-0.12
ERI1	3.9E-05	0.94	6.17E-01	0.21
POLD4	4.1E-05	0.94	7.90E-02	-0.65
PMF1	5.6E-05	0.94	7.76E-01	-0.12
EAF1	5.6E-05	0.94	4.24E-01	0.33
TNFAIP8	6.0E-05	0.94	1.98E-01	0.51
LPCAT4	6.1E-05	0.94	5.08E-02	-0.71
PYCARD	7.4E-05	0.93	4.58E-01	0.31
COL9A2	7.5E-05	0.93	8.50E-01	0.08
TNFRSF4	8.7E-05	0.93	7.48E-01	0.14
LAG3	8.9E-05	0.93	9.19E-02	0.63
PSPC1	1.3E-04	0.92	3.30E-01	0.40
PPIL4	1.5E-04	0.92	1.80E-01	-0.53
LPXN	1.5E-04	0.92	3.76E-01	0.36
DNAJC8	1.8E-04	0.92	4.51E-01	-0.31
LAMTOR5	1.9E-04	0.92	9.38E-01	-0.03
SLC35A4	2.1E-04	0.91	2.04E-01	0.50
SPOCK2	2.1E-04	0.91	4.46E-01	0.32
APOL6	2.2E-04	0.91	2.01E-01	-0.51
SS18L2	2.5E-04	0.91	3.75E-01	-0.36
NRBF2	2.7E-04	0.91	9.55E-02	-0.63
ARAP2	2.7E-04	0.91	2.33E-01	0.48
ORAI1	2.9E-04	0.91	7.29E-02	-0.66
ERAP1	3.3E-04	0.90	3.02E-01	0.42
CD3G	3.5E-04	0.90	3.31E-01	0.40
INPP5K	3.5E-04	0.90	1.67E-01	0.54
GOLGA8B	3.7E-04	0.90	2.76E-01	-0.44
SUMO3	3.8E-04	0.90	1.33E-01	-0.58

NOL8	4.0E-04	0.90	2.64E-01	0.45
AX748212	4.1E-04	0.90	1.47E-01	0.56
C3orf37	4.8E-04	0.89	3.52E-01	0.38
LINC00598	4.9E-04	0.89	9.48E-01	0.03
BC041998	4.9E-04	0.89	1.52E-01	0.56
IFFO2	5.0E-04	0.89	2.86E-01	0.43
COG1	5.3E-04	0.89	3.41E-01	0.39
RNF213	5.7E-04	0.89	1.16E-01	-0.60
PLAA	5.8E-04	0.89	5.63E-01	-0.24
METRNL	5.9E-04	0.89	8.79E-01	0.06
MASP2	6.3E-04	0.89	5.51E-01	-0.25
RABGAP1L	6.4E-04	0.89	6.11E-01	-0.21
KCTD9	6.5E-04	0.89	6.18E-01	0.21
IL18R1	6.8E-04	0.88	7.87E-02	0.65
MAPK14	7.7E-04	0.88	1.83E-01	0.52
DNAJB14	7.7E-04	0.88	6.17E-01	0.21
AK095621	8.1E-04	0.88	5.53E-01	0.25
PDCL3	8.2E-04	0.88	4.21E-01	-0.33
SURF2	8.2E-04	0.88	2.83E-01	-0.43
C19orf55	8.9E-04	0.88	4.25E-01	-0.33
CXCR6	9.2E-04	0.88	4.38E-01	0.32
LTB	9.6E-04	0.87	3.03E-01	-0.42
PROSC	9.6E-04	0.87	6.65E-01	0.18
EXOC5	1.1E-03	0.87	9.20E-01	0.04
RASSF2	1.1E-03	0.87	1.76E-01	0.53
LOC595101	1.1E-03	0.87	6.89E-01	0.17
HCST	1.1E-03	0.87	2.75E-01	-0.44
STK17B	1.1E-03	0.87	2.85E-01	-0.43
CD96	1.2E-03	0.87	3.37E-02	-0.75
KMT2C	1.2E-03	0.87	1.87E-01	0.52
GATA3	1.2E-03	0.87	9.22E-01	-0.04
EIF3M	1.3E-03	0.86	1.86E-01	-0.52
CCDC53	1.3E-03	0.86	2.63E-01	-0.45
AX747182	1.3E-03	0.86	1.81E-02	-0.80
PTPN22	1.3E-03	0.86	1.70E-01	0.54
SLC7A5P2	1.3E-03	0.86	9.72E-02	0.63

NDRG1	1.3E-03	0.86	4.07E-01	-0.34
SLC35B2	1.3E-03	0.86	5.38E-01	-0.26
ANXA6	1.4E-03	0.86	6.37E-01	-0.20
IL12RB2	1.4E-03	0.86	8.11E-01	-0.10
CCDC130	1.5E-03	0.86	3.45E-01	-0.39
TNFRSF9	1.5E-03	0.86	4.99E-01	-0.28
GZMM	1.6E-03	0.86	3.69E-01	0.37
LOC728730	1.7E-03	0.85	8.30E-01	-0.09
RAPGEF6	1.8E-03	0.85	9.77E-01	-0.01
PTPN4	1.8E-03	0.85	1.04E-01	-0.62
MAP4K3	1.8E-03	0.85	3.77E-01	0.36
CD53	1.9E-03	0.85	8.05E-01	0.11
FAM177A1	2.0E-03	0.85	7.20E-01	0.15
WAS	2.1E-03	0.84	4.45E-02	-0.72
EMBP1	2.2E-03	0.84	5.02E-01	-0.28
ZC3H12A	2.3E-03	0.84	1.37E-01	0.57
LRCH4	2.3E-03	0.84	2.10E-01	-0.50
KSR1	2.3E-03	0.84	3.30E-01	0.40
ADSS	2.4E-03	0.84	2.26E-01	0.48
LSP1	2.4E-03	0.84	8.80E-01	0.06
CAPN2	2.5E-03	0.84	1.16E-01	-0.60
SLC5A6	2.5E-03	0.84	2.13E-01	0.49
AL049935	2.6E-03	0.84	6.13E-01	0.21
DIP2B	2.6E-03	0.84	3.90E-01	0.35
OXNAD1	2.6E-03	0.84	7.08E-01	0.16
RGPD1	2.7E-03	0.83	7.71E-02	-0.66
LOC100506023	2.7E-03	0.83	4.54E-01	-0.31
BC016143	2.9E-03	0.83	6.18E-01	-0.21
ITPR3	2.9E-03	0.83	9.24E-01	-0.04
TTC39C	3.0E-03	0.83	3.57E-01	-0.38
ABI1	3.1E-03	0.83	4.60E-01	-0.31
ADAM8	3.1E-03	0.83	3.15E-01	0.41
PSMA2	3.1E-03	0.83	8.67E-01	-0.07
FBXO33	3.3E-03	0.83	4.91E-01	-0.29
SLAMF1	3.3E-03	0.82	7.82E-01	0.12
FKSG56	3.4E-03	0.82	5.65E-04	-0.94

IL2RB	3.4E-03	0.82	4.06E-01	-0.34
EDEM3	3.4E-03	0.82	2.88E-01	0.43
CBLB	3.5E-03	0.82	2.98E-01	0.42
RAF1	3.5E-03	0.82	1.51E-01	-0.56
ATPAF1	3.6E-03	0.82	3.65E-01	0.37
ZBTB25	3.6E-03	0.82	5.81E-01	-0.23
TYMP	3.6E-03	0.82	7.90E-01	0.11
C17orf85	3.6E-03	0.82	6.67E-01	0.18
ACBD5	3.6E-03	0.82	3.61E-01	0.37
STPG1	3.8E-03	0.82	8.42E-01	0.08
BRE	3.8E-03	0.82	3.58E-02	-0.74
DLG1	3.8E-03	0.82	4.20E-01	0.33
CES4A	3.8E-03	0.82	8.29E-01	-0.09
TERF2IP	3.9E-03	0.82	2.47E-01	0.46
ADRBK1	3.9E-03	0.82	1.51E-01	0.56
PSMB9	3.9E-03	0.82	9.30E-01	0.04
TBX21	4.0E-03	0.82	7.92E-01	0.11
RAB11FIP4	4.0E-03	0.82	2.96E-01	-0.42
SLC25A38	4.1E-03	0.81	6.92E-01	0.17
SLC35B1	4.1E-03	0.81	2.46E-01	0.46
BCL2L11	4.1E-03	0.81	1.38E-01	-0.57
TNFSF14	4.2E-03	0.81	4.03E-01	-0.34
TCRA	4.3E-03	0.81	9.20E-01	-0.04
PDE4D	4.3E-03	0.81	8.87E-01	0.06
TMEM194B	4.5E-03	0.81	5.46E-01	0.25
PACS1	4.6E-03	0.81	9.03E-01	0.05
KCNN4	4.6E-03	0.81	1.09E-01	-0.61
SPDYE1	4.7E-03	0.81	3.87E-01	-0.36
UQCRB	4.8E-03	0.81	9.31E-02	-0.63
KCTD10	4.8E-03	0.81	6.92E-02	-0.67
HAUS3	4.9E-03	0.81	7.23E-01	0.15
CARD11	4.9E-03	0.81	8.84E-02	-0.64
RALGDS	4.9E-03	0.81	1.45E-01	-0.56
DEDD2	5.0E-03	0.81	1.25E-01	-0.59
PI4KAP1	5.1E-03	0.80	1.92E-01	-0.51
TBC1D5	5.1E-03	0.80	7.29E-02	-0.66

P2RX5-TAX1BP3	5.2E-03	0.80	2.00E-01	-0.51
PITHD1	5.2E-03	0.80	5.19E-01	-0.27
IKBKE	5.2E-03	0.80	9.95E-01	0.00
ITGAL	5.2E-03	0.80	7.18E-01	-0.15
AK074476	5.3E-03	0.80	8.02E-01	0.11
S100A4	5.3E-03	0.80	5.27E-01	-0.26
AL832007	5.3E-03	0.80	2.69E-01	-0.45
COPS7B	5.3E-03	0.80	2.25E-01	0.48
THAP6	5.4E-03	0.80	4.17E-01	0.34

Supplementary Table 11. Antibodies used for cytometry by time of flight (CyTOF).

metal conjugate isotope	antigen marker
102,104,105,106,108,110Pd	MCB
89Y	CD45
141Pr	CCR6
142Nd	CD19
143Nd	CD127
144Nd	CCR5
145Nd	CD4
146Nd	CD8
147Sm	CD20
148Nd	CD16
149Sm	CD25
150Nd	Ki67
151Eu	CD278
152Sm	TNFa
153Eu	Tim3
154Sm	CXCR5
155Gd	CD27
156Gd	CD14
158Gd	CCR4
159Tb	CCR7
160Gd	CD28
161Dy	CD152
162Dy	FoxP3
163Dy	CXCR3
164Dy	CD45RO
165Ho	IFNg
166Er	CD223
167Er	Granzyme B
168Er	CD49d
169Tm	IL17
170Er	CD3
171Yb	CD226

172Yb	CD274
173Yb	TIGIT
174Yb	HLA-DR
175Lu	CD279
176Yb	IL10
209Bi	CD11b
191Ir	DNA
193Ir	DNA

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