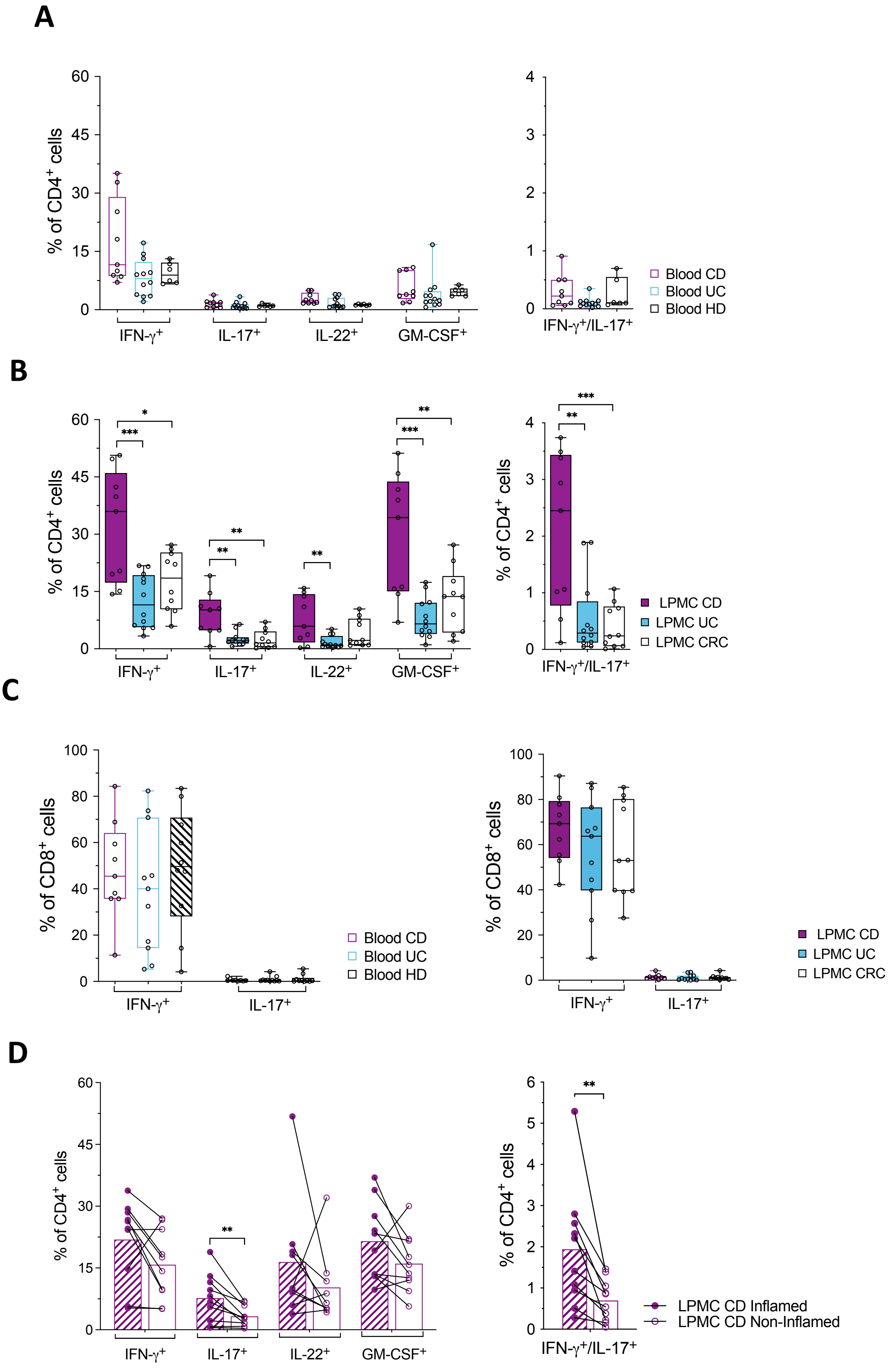
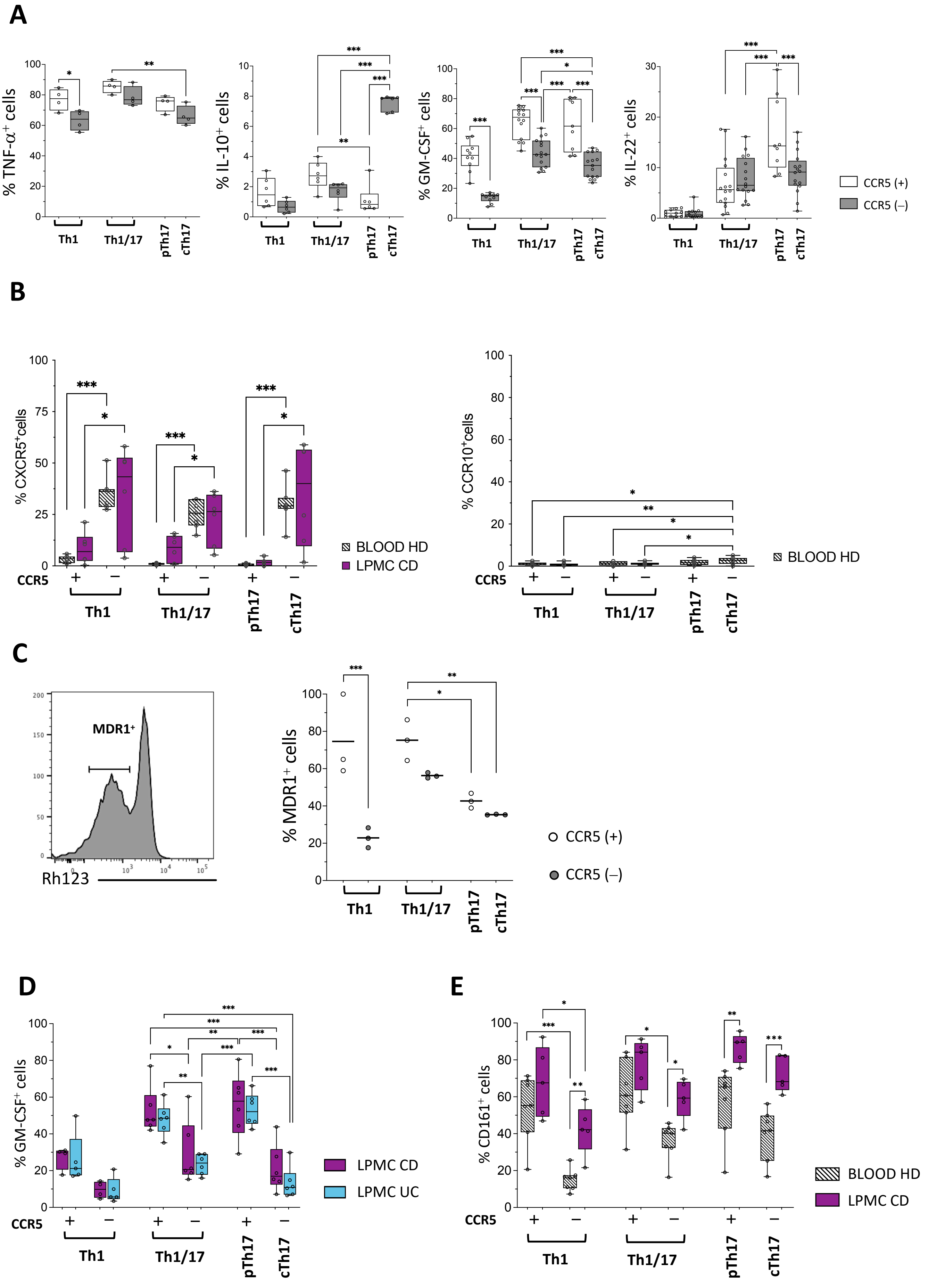
Supplementary Figure 1

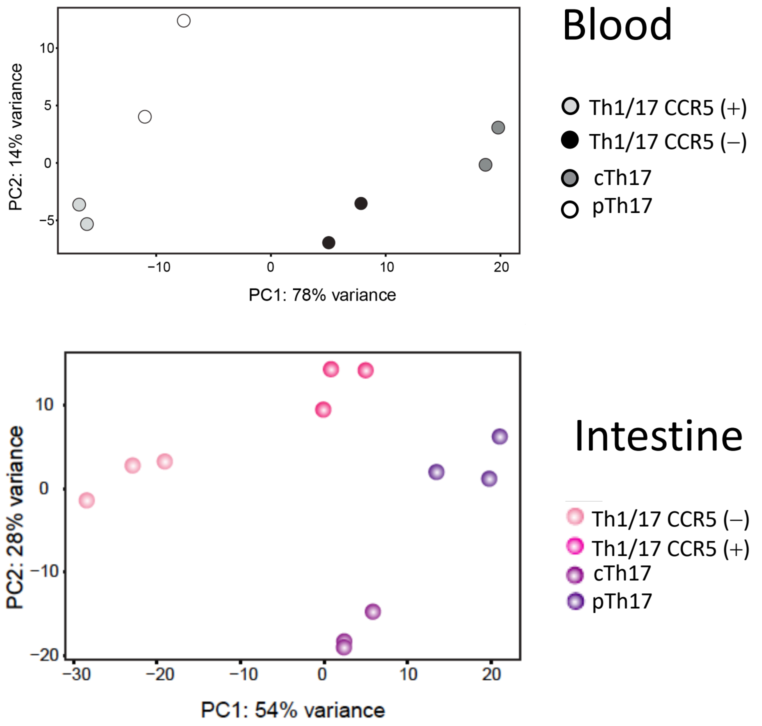


Supplementary Figure 2

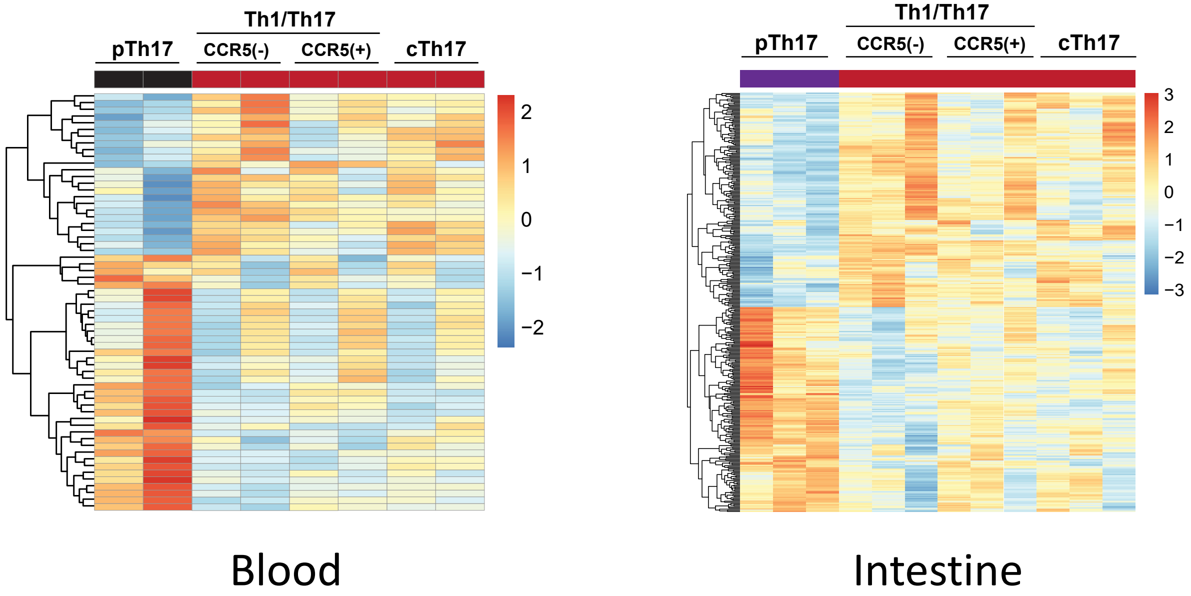


Supplementary Figure 3

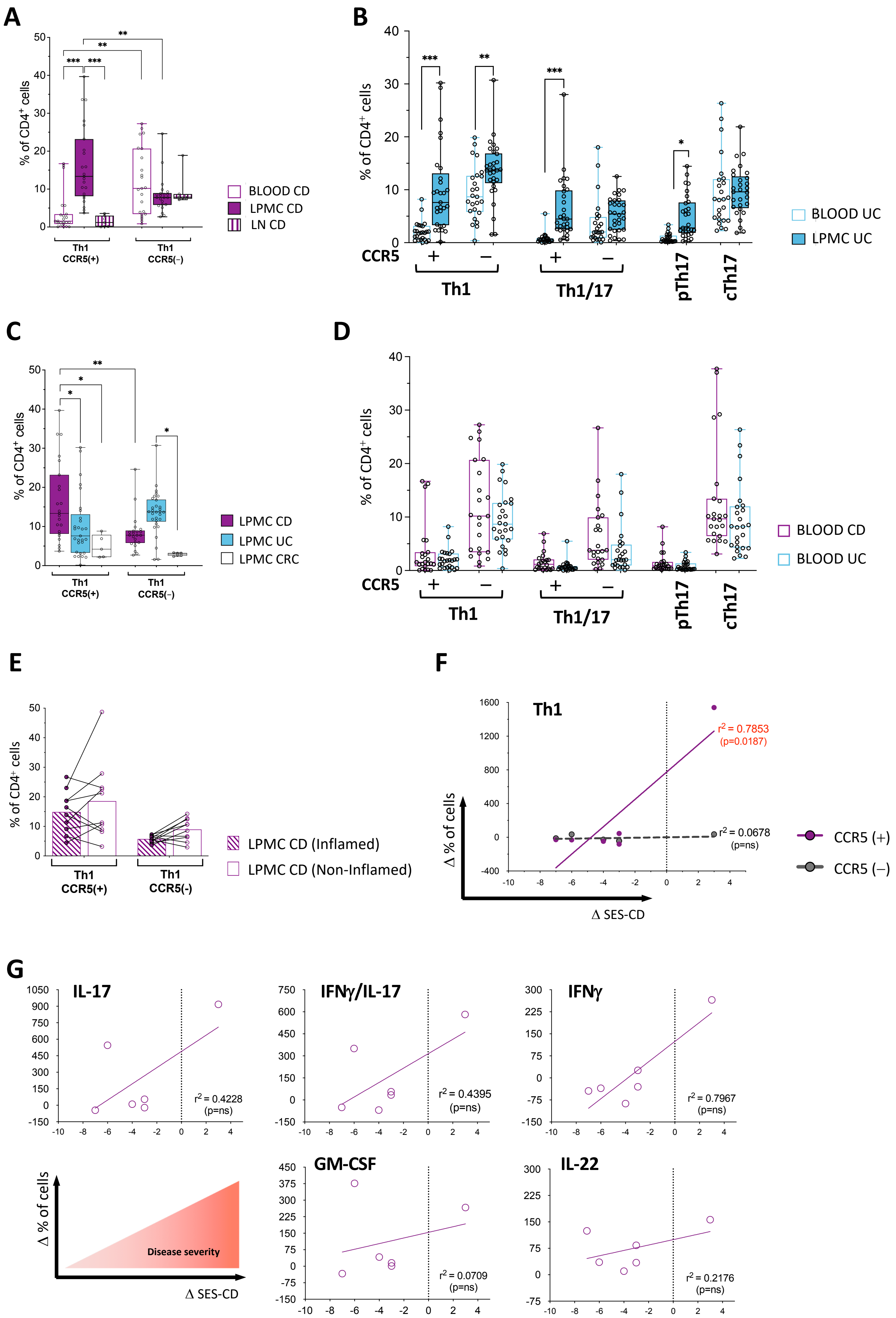
A



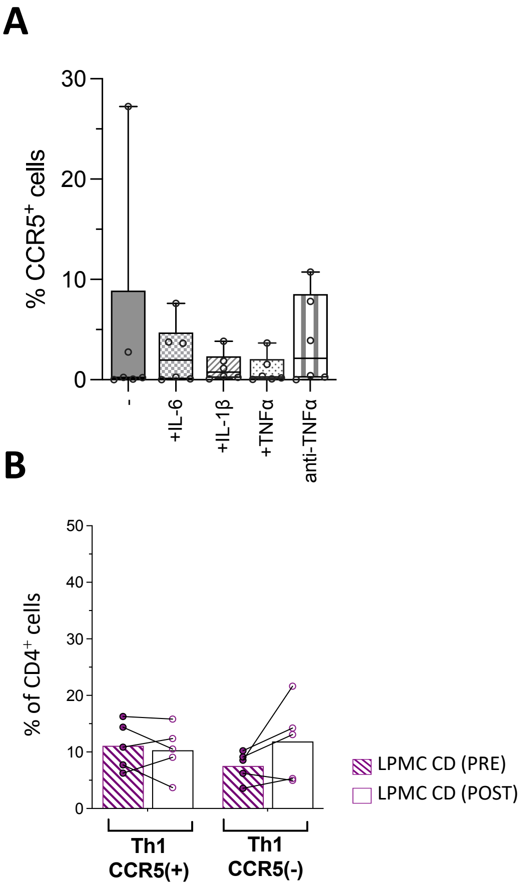
B



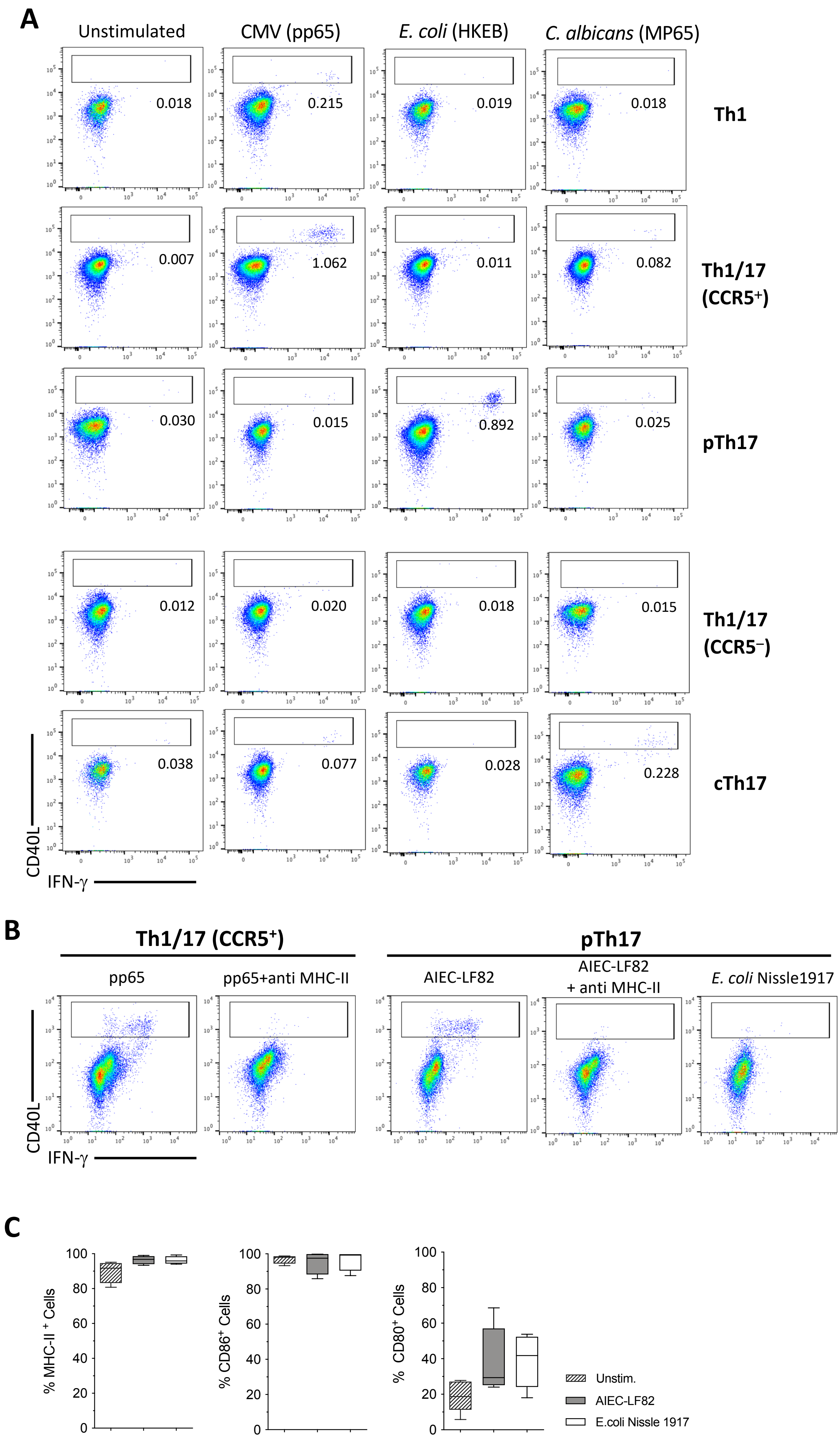
Supplementary Figure 4



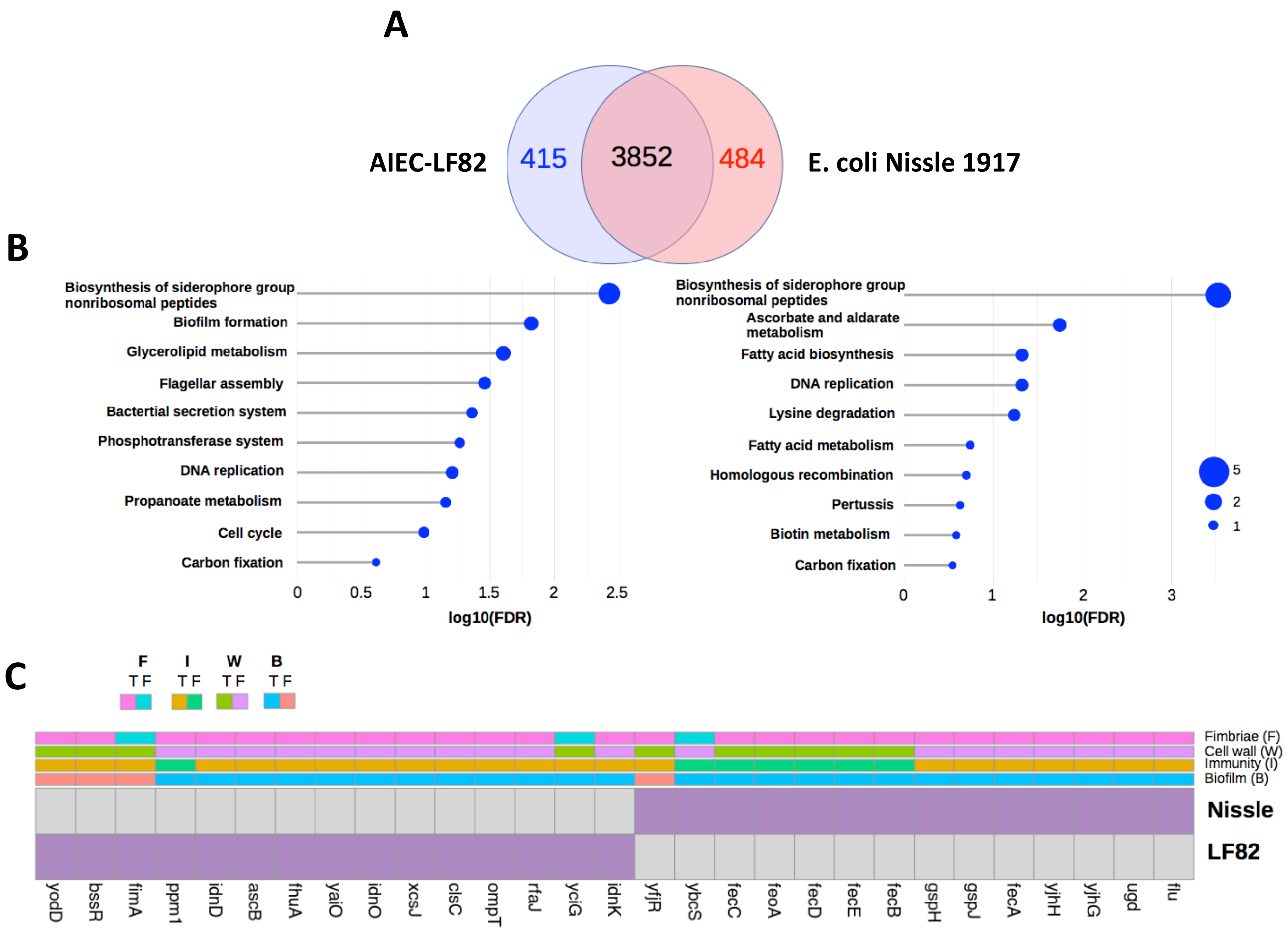
Supplementary Figure 5



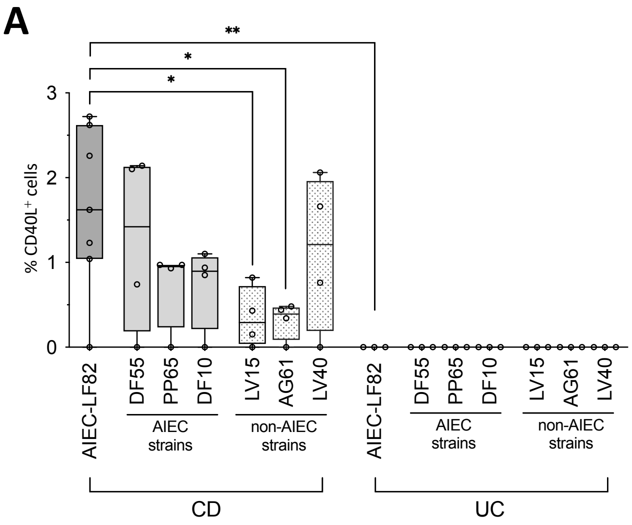
Supplementary Figure 6



Supplementary Figure 7



Supplementary Figure 8



Supplementary Figure 9

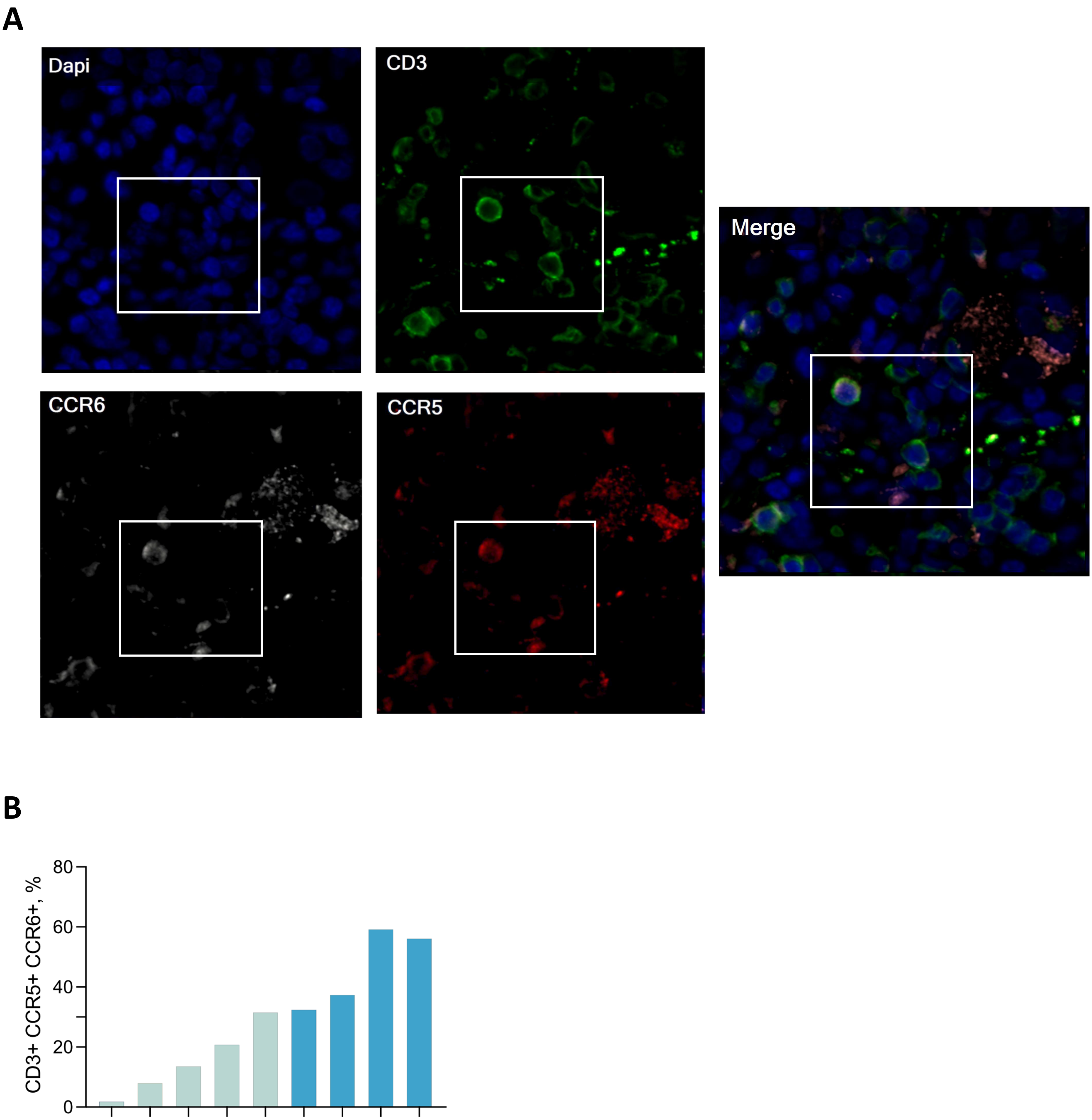


Table S1: Baseline clinical characteristics of Crohn's Disease (CD) patients treated with Infliximab or Risankizumab included in the study.

	Infliximab (n= 6)	**Risankizumab (n=5)**
Age, median (IQR)	30 (26 - 30)	34 (31 - 40)
Sex, female, n	1	3
Disease duration, median (IQR)	8 (3 - 13)	11 (11 - 12)
Smoking, active, n	2	2
Previous surgery, n	3	3
Localization		
- ileal	1	3
- colon	1	1
- ileocolonic	4	1
Behaviour		
- Non stricturing non penetrating	2	3
- Stricturing	1	1
- Penetrating	3	1
Extraintestinal manifestations, n	2	3
Previous immunomodulators, n	4	4
Baseline HBI score, median (IQR)	7,5 (6,25 - 8)	7 (6 - 11)
Baseline SES-CD	4,5 (3,25 - 6,5)	7 (7 - 8)
Baseline steroids, n	1	3
Baseline immunomodulators, n	2	1

HBI: Harvey Bradshaw Score
SES-CD: simplified endoscopic score for Crohn's disease

Table S2: Monoclonal antibodies and FACS reagents used in this study.

Antibodies	Clone	Company
Th-cell subsets:		
Anti-human CD4	RPA-T4	Biolegend
Anti-human CD25	BC96	Biolegend
Anti-human CD127 (IL-7R)	A019D5	Biolegend
Anti-human CXCR3	1C6	BD
Anti-human CCR6	G034E3	Biolegend
Anti-human CCR5	2D7	BD
Intracellular cytokines:		
Anti-human IL-17	BL168	Biolegend
Anti-human IFN-γ	B27	Biolegend
Anti-human GM-CSF	BVD2-21C11	BD Biosciences
Anti-human IL-22	2G12A41	Biolegend
Anti-human TNF-α	1D6	Biolegend
Anti-human IL-10	JES3-19F1	Biolegend
Anti-human CD154 (CD40L)	24-31	Biolegend
Transcription factors:		
Anti-human pSTAT3	pY705	BD Biosciences
Anti-human T-bet	O4-46	BD Biosciences
Anti-human RORγt	Q21-559	BD Biosciences
Surface markers:		
Anti-human CD161	DX12	BD
Anti-human PD1	EH12.2H7	Biolegend
Anti-human CD27	M-T271	Biolegend
Anti-human IL-1R1	FAB269P	R&D systems
Anti-human CCR7	G043H7	Biolegend
Anti-human CCR4	L291H4	Biolegend
Anti-human CXCR5	J252D4	Biolegend
Anti-human CCR10	6588-5	Biolegend
Rh123 (Rhodamine 123)	Cat#R8004	Sigma Aldrich
Anti-human HLA-DR	G46-6	BD
Anti-human CD80	BB1	BD
Anti-human CD86	BU63	Biolegend

Table S3: Microbial antigens used in this study.

Microbial antigens	Description	Final concentration
<u>Virus</u>		
Cytomegalovirus (CMV)	PepTivator® CMV pp65 (Milteny Biotec)	1µg peptide/ml (0.6 nmol/ml)
Epstein-Barr virus (EBV)	PepTivator® EBV Consensus pool (Milteny Biotec)	
JC Virus (JCV)	PepTivator® JCV VP1 (Milteny Biotec)	
Varicella-zoster virus (VZV)	PepMix VZV - IE63 (JPT Peptide Technologies GmbH)	
<u>Fungi</u>		
Candida albicans	PepTivator® *C. albicans* MP65 (Milteny Biotec)	1µg peptide/ml (0.6 nmol/ml)
<u>Bacteria</u>		
Staphylococcus aureus	heat-killed *S. aureus* - HKSA (InvivoGen)	10^7 CFU/ml
Salmonella enterica serovar typhimurium	bacterial lysates *of S. typhimurium SL1344 FB62 strain*	
Shigella flexneri	bacterial lysates *of S.* flexneri serotype 5a M90T strain	
Lactobacillus paracasei	bacterial lysates *of L. paracasei* CBA L74 strain	
Adherent-Invasive Escherichia coli (AIEC)	bacterial lysates *of AIEC* strain LF82	
	bacterial lysates *of AIEC* strain DF55	
	bacterial lysates *of AIEC* strain PP65	
	bacterial lysates *of AIEC* strain DF10	
Escherichia coli (non-AIEC)	Heat killed *E. coli* strain 0111:B4 (InvivoGen)	
	bacterial lysates *of E. coli* Nissle 1917 strain	
	bacterial lysates *of E. coli* strain LV15	
	bacterial lysates *of E. coli* strain AG61	
	bacterial lysates *of E. coli* strain LV40	

Table S4 A: up-regulated genes in circulating pTh17-cells as compared to cTh17-cells

gene_id	gene_name	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
ENSG00000163508.12	EOMES	626.4131388	6.682896762	0.458455649	14.57697551	3.94E-48	5.08E-45
ENSG00000271503.5	CCL5	3934.335083	6.031884636	0.263438912	22.896711	5.01E-116	8.40E-112
ENSG00000221869.4	CEBPD	1046.38127	5.545629598	0.528273274	10.49765315	8.86E-26	4.12E-23
ENSG00000131459.12	GFPT2	328.167101	5.449187761	0.373658019	14.5833556	3.58E-48	5.01E-45
ENSG00000160791.13	CCR5	1182.601033	5.327644167	0.310225925	17.17343311	4.20E-66	1.41E-62
ENSG00000065833.8	ME1	365.4458024	5.252924232	0.766830626	6.850175327	7.38E-12	8.19E-10
ENSG00000115607.9	IL18RAP	2210.959465	5.035872356	0.748679062	6.726343254	1.74E-11	1.85E-09
ENSG00000115523.16	GNLY	2333.623062	4.997749966	0.258267875	19.35103217	2.00E-83	1.12E-79
ENSG00000145649.7	GZMA	1694.964544	4.920242265	0.573775187	8.57520921	9.89E-18	2.22E-15
ENSG00000057704.11	TMCC3	402.2505951	4.902442463	0.417534231	11.74141448	7.82E-32	5.96E-29
ENSG00000172215.5	CXCR6	1274.979735	4.897053307	0.22229927	22.02910207	1.52E-107	1.27E-103
ENSG00000186810.7	CXCR3	1587.158809	4.815498643	0.256867382	18.74702272	2.05E-78	8.58E-75
ENSG00000105374.9	NKG7	447.8512636	4.581300095	0.405111685	11.30873354	1.19E-29	7.38E-27
ENSG00000196781.14	TLE1	350.5361691	4.334608853	0.396475008	10.9328678	8.03E-28	4.21E-25
ENSG00000080493.14	SLC4A4	91.20822057	4.150414645	0.575836477	7.207627188	5.69E-13	7.02E-11
ENSG00000050165.17	DKK3	102.282729	4.147486005	0.449233919	9.232352751	2.65E-20	7.52E-18
ENSG00000115956.9	PLEK	1296.519868	4.138845839	0.554589464	7.462900225	8.46E-14	1.21E-11
ENSG00000169252.5	ADRB2	484.8778165	3.913923107	0.247328134	15.82481964	2.10E-56	5.86E-53
ENSG00000144290.16	SLC4A10	1245.747324	3.545991938	0.289641201	12.24270553	1.84E-34	1.62E-31
ENSG00000124507.10	PACSIN1	110.4335766	3.516111476	0.55519734	6.333084149	2.40E-10	2.04E-08
ENSG00000112183.14	RBM24	35.63033633	3.458245063	0.65805393	5.255260863	1.48E-07	8.02E-06
ENSG00000180644.6	PRF1	1689.202896	3.402096325	0.221718837	15.34419163	3.87E-53	8.12E-50
ENSG00000169554.17	ZEB2	951.207903	3.368934262	0.265456778	12.69108399	6.63E-37	6.94E-34
ENSG00000168229.3	PTGDR	244.7469518	3.328428286	0.825852043	4.030296124	5.57E-05	0.001516468
ENSG00000127318.10	IL22	27.03548091	3.278079415	0.642788219	5.099781414	3.40E-07	1.67E-05
ENSG00000155629.14	PIK3AP1	154.4251183	3.254589434	0.360541867	9.02693899	1.77E-19	4.70E-17
ENSG00000062524.15	LTK	3896.235812	3.244058598	0.45454626	7.136916274	9.54E-13	1.14E-10
ENSG00000073861.2	TBX21	1245.773512	3.23994837	0.207266396	15.63180731	4.42E-55	1.06E-51
ENSG00000121807.5	CCR2	1339.875195	3.105956908	0.299560386	10.36838333	3.45E-25	1.52E-22
ENSG00000116667.12	C1orf21	115.9689331	3.097251697	0.479157212	6.463957174	1.02E-10	9.35E-09
ENSG00000162878.12	PKDCC	77.93766568	3.068517439	0.688174254	4.458925081	8.24E-06	0.000277368
ENSG00000159618.15	ADGRG5	238.5263018	3.008564398	0.333911324	9.010069993	2.06E-19	5.40E-17
ENSG00000254087.7	LYN	331.8245395	2.998633974	0.383485206	7.819425446	5.31E-15	8.47E-13
ENSG00000197057.8	DTHD1	80.74411365	2.978012936	0.563255324	5.287145652	1.24E-07	6.83E-06
ENSG00000156738.17	MS4A1	137.4939004	2.947966713	0.463506644	6.360139062	2.02E-10	1.73E-08
ENSG00000141934.9	PLPP2	87.07357058	2.899296525	0.451469212	6.421914156	1.35E-10	1.21E-08
ENSG00000130635.15	COL5A1	710.9179888	2.796800646	0.23110313	12.10195916	1.03E-33	8.23E-31
ENSG00000171476.21	HOPX	1257.653246	2.787559183	0.273549643	10.19032287	2.19E-24	8.75E-22
ENSG00000162543.5	UBXN10	109.8986595	2.761183576	0.362887673	7.608920844	2.76E-14	4.21E-12
ENSG00000136856.17	SLC2A8	162.6975923	2.749642718	0.379616479	7.243212213	4.38E-13	5.48E-11
ENSG00000120549.17	KIAA1217	99.30299201	2.715007967	0.530029199	5.122374334	3.02E-07	1.51E-05
ENSG00000164483.16	SAMD3	1141.002037	2.710378766	0.775093479	3.496841141	0.000470802	0.009343054
ENSG00000169896.16	ITGAM	310.5124155	2.70337456	0.286575298	9.433383051	3.97E-21	1.19E-18
ENSG00000104951.15	IL4I1	1335.459443	2.679313638	0.243665719	10.99585798	4.00E-28	2.24E-25
ENSG00000095397.13	WHRN	1510.363951	2.633582997	0.238988253	11.01971733	3.07E-28	1.78E-25

ENSG00000081985.10	IL12RB2	866.7042118	2.621604766	0.835419808	3.13806872	0.00170065	0.026067824
ENSG00000117560.7	FASLG	69.08769009	2.520474892	0.405079202	6.222177984	4.90E-10	3.88E-08
ENSG00000007264.14	MATK	693.4877003	2.519268039	0.217041013	11.60733634	3.78E-31	2.64E-28
ENSG00000186197.13	EDARADD	82.89464598	2.502303064	0.415022615	6.029317373	1.65E-09	1.21E-07
ENSG00000204475.9	NCR3	105.0162986	2.490202465	0.408867785	6.090483415	1.13E-09	8.43E-08
ENSG00000124019.9	FAM124B	67.36339937	2.482365412	0.504054751	4.924793206	8.44E-07	3.82E-05
ENSG00000109458.8	GAB1	32.63197812	2.479708917	0.772040935	3.211887874	0.001318658	0.021052166
ENSG00000176845.12	METRNL	103.5718582	2.470782448	0.382998794	6.451149427	1.11E-10	1.00E-08
ENSG00000171954.12	CYP4F22	35.85521499	2.46226809	0.576138245	4.273745252	1.92E-05	0.000599123
ENSG00000116016.13	EPAS1	112.0057537	2.456027429	0.58040489	4.231576043	2.32E-05	0.000715332
ENSG00000178860.8	MSC	347.6137529	2.441514466	0.657869872	3.711242256	0.000206245	0.004711874
ENSG00000150457.8	LATS2	699.4958333	2.412314054	0.19371213	12.45308722	1.35E-35	1.25E-32
ENSG00000204287.13	HLA-DRA	365.0714368	2.40749943	0.288752704	8.337582293	7.58E-17	1.50E-14
ENSG00000076706.15	MCAM	1068.806163	2.406421543	0.296508915	8.115848878	4.82E-16	8.70E-14
ENSG00000170522.9	ELOVL6	557.9001242	2.39356672	0.235625955	10.15833218	3.04E-24	1.16E-21
ENSG00000137501.17	SYTL2	5502.140276	2.368820411	0.188568911	12.56209414	3.41E-36	3.37E-33
ENSG00000173905.8	GOLIM4	81.21896665	2.342632413	0.409643444	5.718710858	1.07E-08	7.04E-07
ENSG00000107317.11	PTGDS	397.3234233	2.341324132	0.598382935	3.912752179	9.13E-05	0.002332582
ENSG00000113758.13	DBN1	47.99678249	2.333967892	0.514313987	4.538021423	5.68E-06	0.000199209
ENSG00000196189.12	SEMA4A	158.1232213	2.312943425	0.47662118	4.85279195	1.22E-06	5.22E-05
ENSG00000011422.11	PLAUR	299.8392024	2.310655609	0.254226534	9.08896318	1.00E-19	2.75E-17
ENSG00000181104.6	F2R	1873.874383	2.301325189	0.553678349	4.156429796	3.23E-05	0.000939469
ENSG00000075651.15	PLD1	361.2020519	2.298892802	0.343346692	6.695543759	2.15E-11	2.25E-09
ENSG00000077984.5	CST7	1040.516608	2.293016105	0.240004678	9.554047539	1.25E-21	3.80E-19
ENSG00000189350.12	FAM179A	288.3774294	2.279484336	0.358649505	6.355743708	2.07E-10	1.77E-08
ENSG00000178075.19	GRAMD1C	247.4536876	2.277051275	0.717470348	3.173721786	0.001504979	0.0234926
ENSG00000157404.15	KIT	602.536403	2.276476508	0.262386029	8.676058378	4.10E-18	9.82E-16
ENSG00000100298.15	APOBEC3H	192.3268472	2.245430904	0.309586339	7.253003831	4.08E-13	5.22E-11
ENSG00000204161.13	C10orf128	985.5708965	2.244233365	0.200531127	11.19144645	4.49E-29	2.69E-26
ENSG00000061337.15	LZTS1	206.9064306	2.230830597	0.268079784	8.321517424	8.68E-17	1.67E-14
ENSG00000143842.14	SOX13	509.0782905	2.222621012	0.33711544	6.593056103	4.31E-11	4.20E-09
ENSG00000196126.10	HLA-DRB1	112.1061146	2.203664123	0.379255739	5.810496443	6.23E-09	4.23E-07
ENSG00000148848.14	ADAM12	646.1796112	2.172977492	0.198139392	10.9669131	5.51E-28	2.98E-25
ENSG00000116574.5	RHOU	581.4045929	2.168855106	0.201812277	10.7468938	6.13E-27	3.11E-24
ENSG00000080573.6	COL5A3	4766.905869	2.143275941	0.655952624	3.267424904	0.001085307	0.018055065
ENSG00000108370.16	RGS9	66.50082315	2.137772612	0.423385402	5.049235529	4.44E-07	2.14E-05
ENSG00000088826.17	SMOX	58.87738331	2.137479049	0.438534604	4.874139992	1.09E-06	4.77E-05
ENSG00000169429.10	CXCL8	2034.189937	2.107522773	0.328759308	6.410534153	1.45E-10	1.29E-08
ENSG00000124145.6	SDC4	364.8476695	2.101395579	0.218368663	9.62315541	6.38E-22	2.02E-19
ENSG00000198400.11	NTRK1	32.15884998	2.101078889	0.568452413	3.696138573	0.000218904	0.004967244
ENSG00000205730.6	ITPRIPL2	93.66619281	2.08235497	0.376068789	5.537165086	3.07E-08	1.89E-06
ENSG00000085563.14	ABCB1	4112.828724	2.07585854	0.201651832	10.29427068	7.48E-25	3.22E-22
ENSG00000124772.11	CPNE5	72.88191991	2.071267565	0.415881599	4.980426086	6.34E-07	2.96E-05
ENSG00000157985.18	AGAP1	673.3080834	2.058637703	0.240316802	8.566349445	1.07E-17	2.30E-15
ENSG00000175048.16	ZDHHC14	328.9193457	2.045168482	0.324757367	6.297527601	3.02E-10	2.52E-08
ENSG00000198369.9	SPRED2	92.82463509	2.044955597	0.42528955	4.808384308	1.52E-06	6.30E-05
ENSG00000091436.16	AC013461.1	232.8907538	2.03731042	0.254787783	7.996107173	1.28E-15	2.22E-13
ENSG00000149573.8	MPZL2	84.62072926	2.028641042	0.458324429	4.426211898	9.59E-06	0.000319719

ENSG00000185340.15	GAS2L1	196.1576608	2.011360249	0.258146239	7.791553561	6.62E-15	1.05E-12
ENSG00000186648.14	CARMIL3	65.22597324	1.998121357	0.472590162	4.228021482	2.36E-05	0.000722357
ENSG00000181264.8	TMEM136	26.64253656	1.992800919	0.631142587	3.157449615	0.001591557	0.024666198
ENSG00000163393.12	SLC22A15	99.22650203	1.991965319	0.445068234	4.475640283	7.62E-06	0.000258605
ENSG00000125735.10	TNFSF14	930.4247659	1.988143136	0.27206209	7.307681634	2.72E-13	3.56E-11
ENSG00000182511.11	FES	234.3770834	1.98207549	0.349979382	5.663406455	1.48E-08	9.43E-07
ENSG00000120708.16	TGFBI	350.6744023	1.973456787	0.272419168	7.244192095	4.35E-13	5.48E-11
ENSG00000162438.11	CTRC	151.7578476	1.956953114	0.467725003	4.183982262	2.86E-05	0.000839759
ENSG00000163421.8	PROK2	107.102515	1.944996463	0.39564246	4.916045825	8.83E-07	3.97E-05
ENSG00000104321.10	TRPA1	31.11084982	1.944204713	0.557556902	3.487006809	0.000488459	0.009602541
ENSG00000147852.15	VLDLR	110.0168292	1.939496827	0.375046855	5.171345399	2.32E-07	1.18E-05
ENSG00000137801.10	THBS1	2085.591796	1.924444909	0.227463615	8.460451622	2.66E-17	5.38E-15
ENSG00000171860.4	C3AR1	364.3805197	1.913355894	0.253242121	7.55544095	4.17E-14	6.25E-12
ENSG00000179388.8	EGR3	81.78231338	1.899260524	0.437864027	4.337557798	1.44E-05	0.000460188
ENSG00000125810.9	CD93	117.0889493	1.893141437	0.54769701	3.456548792	0.00054714	0.010485706
ENSG00000116741.7	RGS2	3043.00767	1.891762074	0.162723978	11.6255889	3.05E-31	2.23E-28
ENSG00000115738.9	ID2	3282.999995	1.886645967	0.164132594	11.49464541	1.40E-30	9.41E-28
ENSG00000050438.16	SLC4A8	105.7364125	1.885770769	0.35223964	5.353658574	8.62E-08	4.90E-06
ENSG00000213949.8	ITGA1	1292.886476	1.878413769	0.253291629	7.416012036	1.21E-13	1.67E-11
ENSG00000213171.2	LINGO4	59.10202749	1.872647642	0.415137734	4.510906839	6.46E-06	0.000223187
ENSG00000115339.13	GALNT3	442.5717627	1.872303096	0.265113661	7.062265621	1.64E-12	1.91E-10
ENSG00000116991.10	SIPA1L2	447.5139719	1.870382869	0.239018396	7.825267431	5.07E-15	8.17E-13
ENSG00000196576.14	PLXNB2	341.489875	1.846558407	0.362043518	5.100376936	3.39E-07	1.67E-05
ENSG00000145220.13	LYAR	3725.35262	1.823479143	0.46052691	3.959549606	7.51E-05	0.001986128
ENSG00000188886.3	ASTL	339.2567595	1.82323614	0.367445972	4.96191625	6.98E-07	3.21E-05
ENSG00000172543.7	CTSW	1332.639353	1.822329693	0.225759706	8.07198826	6.92E-16	1.23E-13
ENSG00000035664.11	DAPK2	470.3955685	1.793613042	0.307917695	5.824975535	5.71E-09	3.89E-07
ENSG00000075426.11	FOSL2	7942.305838	1.791392784	0.265495569	6.747354723	1.51E-11	1.61E-09
ENSG00000152969.17	JAKMIP1	386.786226	1.786987097	0.294378452	6.070373302	1.28E-09	9.51E-08
ENSG00000134830.5	C5AR2	45.34408347	1.785527276	0.496082746	3.599252931	0.000319133	0.006782682
ENSG00000276231.4	PIK3R6	40.48388807	1.782420339	0.566824396	3.144572377	0.001663298	0.02563588
ENSG00000115009.11	CCL20	603.9510322	1.779740559	0.20760374	8.57277694	1.01E-17	2.23E-15
ENSG00000120875.8	DUSP4	1962.212506	1.756683476	0.493656285	3.55851537	0.000372957	0.007683184
ENSG00000197943.9	PLCG2	100.3678237	1.752348048	0.456125972	3.841807206	0.000122132	0.002994192
ENSG00000139629.15	GALNT6	310.2739142	1.750170549	0.273977985	6.387997006	1.68E-10	1.48E-08
ENSG00000111817.16	DSE	1663.8973	1.747938277	0.240543022	7.266634715	3.69E-13	4.75E-11
ENSG00000099194.5	SCD	203.4488968	1.747575638	0.319359612	5.472124749	4.45E-08	2.66E-06
ENSG00000008256.15	CYTH3	2930.45607	1.745655078	0.177074202	9.858325266	6.31E-23	2.20E-20
ENSG00000124564.17	SLC17A3	109.2682148	1.738052934	0.36169066	4.805357524	1.54E-06	6.38E-05
ENSG00000065989.15	PDE4A	498.3854542	1.731671112	0.280752903	6.167954425	6.92E-10	5.35E-08
ENSG00000070614.14	NDST1	55.69408694	1.726789113	0.475413727	3.632181856	0.000281035	0.006144296
ENSG00000121594.11	CD80	75.82923664	1.72238632	0.447894414	3.84551865	0.000120298	0.002957877
ENSG00000074657.13	ZNF532	678.64219	1.719957085	0.179242677	9.595689559	8.34E-22	2.59E-19
ENSG00000144843.11	ADPRH	191.5165268	1.713515937	0.283476919	6.044640037	1.50E-09	1.10E-07
ENSG00000235162.8	C12orf75	853.4504677	1.711678397	0.162842735	10.51123586	7.67E-26	3.67E-23
ENSG00000204131.8	NHSL2	2670.410034	1.697465435	0.197788192	8.582238508	9.30E-18	2.14E-15
ENSG00000131037.14	EPS8L1	47.38443252	1.696036913	0.485901244	3.490497164	0.000482123	0.009511431
ENSG00000135362.13	PRR5L	1147.946626	1.693127248	0.284743943	5.946139647	2.75E-09	1.93E-07

ENSG00000160318.6	CLDND2	36.92822285	1.690660963	0.541338353	3.123113214	0.001789489	0.027082979
ENSG00000115604.10	IL18R1	3153.079684	1.686096854	0.256848326	6.564562368	5.22E-11	4.97E-09
ENSG00000173930.8	SLCO4C1	43.52460483	1.677872912	0.553560286	3.031057241	0.00243699	0.034661487
ENSG00000092445.11	TYRO3	30.29960731	1.673924646	0.554942154	3.016394835	0.002557999	0.035834214
ENSG00000158470.5	B4GALT5	1729.675276	1.664851538	0.163867986	10.15971196	3.00E-24	1.16E-21
ENSG00000125726.10	CD70	108.592329	1.650440562	0.377936945	4.366973333	1.26E-05	0.000408619
ENSG00000139318.7	DUSP6	283.7876555	1.643598347	0.332728851	4.939753028	7.82E-07	3.55E-05
ENSG00000160293.16	VAV2	370.1346601	1.640320638	0.248902755	6.59020684	4.39E-11	4.21E-09
ENSG00000160593.17	JAML	14040.48103	1.639626321	0.191353732	8.568562021	1.05E-17	2.28E-15
ENSG00000181215.13	C4orf50	52.46561864	1.638582711	0.486571051	3.367612414	0.000758221	0.013569487
ENSG00000198756.10	COLGALT2	105.8462199	1.632877809	0.459488946	3.553682458	0.000379878	0.00778749
ENSG00000124762.13	CDKN1A	3228.018099	1.632505474	0.217586711	7.502781138	6.25E-14	9.19E-12
ENSG00000143365.16	RORC	2355.170725	1.621001881	0.178006832	9.106402644	8.52E-20	2.38E-17
ENSG00000146192.14	FGD2	53.75402396	1.617531796	0.468875241	3.449812773	0.000560975	0.01071412
ENSG00000134247.9	PTGFRN	63.31772684	1.613500071	0.388387377	4.154357646	3.26E-05	0.000944748
ENSG00000115902.10	SLC1A4	996.696211	1.612477585	0.231245122	6.973023145	3.10E-12	3.54E-10
ENSG00000179583.18	CIITA	329.6823355	1.600448364	0.343718688	4.656273928	3.22E-06	0.000122712
ENSG00000231389.7	HLA-DPA1	580.2583435	1.592023754	0.254828624	6.247429077	4.17E-10	3.32E-08
ENSG00000178773.14	CPNE7	861.92876	1.582641345	0.25095087	6.306578438	2.85E-10	2.39E-08
ENSG00000204396.10	VWA7	40.40188579	1.582531288	0.48114897	3.289067184	0.0010052	0.016975028
ENSG00000139187.9	KLRG1	668.3920327	1.57886222	0.298353373	5.291920127	1.21E-07	6.68E-06
ENSG00000164120.13	HPGD	485.811863	1.563339582	0.211375072	7.396045163	1.40E-13	1.91E-11
ENSG00000274286.1	ADRA2B	185.1144213	1.558908421	0.387981173	4.018000179	5.87E-05	0.001592625
ENSG00000106069.20	CHN2	121.6192648	1.549289972	0.311477419	4.974004146	6.56E-07	3.03E-05
ENSG00000112378.11	PERP	902.4905354	1.540525921	0.172947954	8.90745388	5.22E-19	1.32E-16
ENSG00000145246.13	ATP10D	299.2399407	1.534235182	0.24856119	6.172464742	6.72E-10	5.24E-08
ENSG00000163701.18	IL17RE	376.1687526	1.530135784	0.282093051	5.424223587	5.82E-08	3.42E-06
ENSG00000074527.11	NTN4	810.9690383	1.526301415	0.30455225	5.011624161	5.40E-07	2.56E-05
ENSG00000110446.10	SLC15A3	80.87294872	1.524776511	0.460563925	3.310672913	0.000930719	0.015893311
ENSG00000103257.8	SLC7A5	4870.892989	1.520308081	0.473955265	3.207703747	0.001337992	0.021252821
ENSG00000139289.13	PHLDA1	1440.29888	1.51295303	0.209433247	7.224034628	5.05E-13	6.27E-11
ENSG00000029153.14	ARNTL2	53.026605	1.512659872	0.425628946	3.553940318	0.000379505	0.00778749
ENSG00000101665.8	SMAD7	5776.034159	1.504110063	0.206298115	7.290953963	3.08E-13	4.00E-11
ENSG00000239713.7	APOBEC3G	2316.78349	1.498429494	0.152920429	9.798752877	1.14E-22	3.90E-20
ENSG00000163754.17	GYG1	1961.899605	1.497993901	0.149262079	10.03599785	1.06E-23	3.86E-21
ENSG00000006327.13	TNFRSF12A	114.2938452	1.496007132	0.357315372	4.186797569	2.83E-05	0.000830867
ENSG00000120318.15	ARAP3	1181.063633	1.493279457	0.29428197	5.074315145	3.89E-07	1.89E-05
ENSG00000162772.16	ATF3	983.1503259	1.482798456	0.20453495	7.249609215	4.18E-13	5.31E-11
ENSG00000196923.13	PDLIM7	176.2587602	1.464753243	0.28589018	5.123482181	3.00E-07	1.50E-05
ENSG00000159335.15	PTMS	118.702032	1.464070609	0.455735062	3.212547663	0.001315633	0.021051386
ENSG00000138764.13	CCNG2	1730.877731	1.459076098	0.142903237	10.21023825	1.78E-24	7.48E-22
ENSG00000088992.17	TESC	85.94575814	1.456216376	0.402862403	3.6146743	0.000300725	0.006481832
ENSG00000132561.13	MATN2	165.904713	1.446260666	0.291751524	4.957165761	7.15E-07	3.27E-05
ENSG00000105339.10	DENND3	3383.765631	1.446038415	0.1743512	8.293825443	1.10E-16	2.07E-14
ENSG00000169641.13	LUZP1	3649.920085	1.445836629	0.174166078	8.301482407	1.03E-16	1.96E-14
ENSG00000160588.9	MPZL3	4577.203621	1.431178551	0.146704188	9.755539828	1.75E-22	5.86E-20
ENSG00000054967.12	RELT	1630.184804	1.427913502	0.231359937	6.171826976	6.75E-10	5.24E-08
ENSG00000109906.13	ZBTB16	190.8471523	1.418236872	0.434003807	3.267798231	0.001083876	0.018049173

ENSG00000196814.14	MVB12B	926.1841875	1.415432063	0.180635472	7.835847803	4.66E-15	7.58E-13
ENSG00000073282.12	TP63	46.7169545	1.410843453	0.447688114	3.151398055	0.001624909	0.025080959
ENSG00000165424.6	ZCCHC24	127.7136297	1.398887763	0.304115813	4.599852104	4.23E-06	0.000154461
ENSG00000198910.12	L1CAM	86.23332104	1.396131725	0.458475045	3.04516405	0.002325534	0.033251313
ENSG00000182621.17	PLCB1	598.0527151	1.391693261	0.270484388	5.145188868	2.67E-07	1.35E-05
ENSG00000122877.14	EGR2	179.6517008	1.389726831	0.33883243	4.101516589	4.10E-05	0.001160684
ENSG00000121297.6	TSHZ3	54.4047254	1.387103534	0.462120486	3.001605805	0.002685597	0.037157405
ENSG00000147650.11	LRP12	354.9937131	1.386978088	0.193364173	7.172880411	7.34E-13	8.86E-11
ENSG00000136286.14	MYO1G	6125.858085	1.386508433	0.239309549	5.793786493	6.88E-09	4.63E-07
ENSG00000131981.15	LGALS3	2264.103993	1.384560776	0.177800408	7.787163119	6.85E-15	1.07E-12
ENSG00000185920.15	PTCH1	1136.199211	1.383402932	0.207663838	6.661742098	2.71E-11	2.72E-09
ENSG00000134107.4	BHLHE40	12182.11164	1.381563834	0.227748387	6.066184939	1.31E-09	9.72E-08
ENSG00000063438.16	AHRR	407.548823	1.380103599	0.358026111	3.854756834	0.000115845	0.002860972
ENSG00000186642.15	PDE2A	85.02923751	1.379534315	0.408229058	3.379314354	0.000726669	0.013130934
ENSG00000150045.11	KLRF1	134.8859921	1.377166585	0.381870137	3.606374134	0.000310505	0.006657223
ENSG00000138835.22	RGS3	937.7533357	1.375990884	0.296875052	4.634915844	3.57E-06	0.000133806
ENSG00000197629.5	MPEG1	168.9656631	1.374183674	0.363411012	3.781348474	0.000155981	0.003710139
ENSG00000158321.15	AUTS2	4806.540729	1.373698486	0.141733341	9.692133673	3.26E-22	1.07E-19
ENSG00000113070.7	HBEGF	176.4427429	1.371721672	0.401285941	3.4183148	0.000630102	0.011714166
ENSG00000180263.13	FGD6	71.34779108	1.362762501	0.423234251	3.219877643	0.001282453	0.020605604
ENSG00000141682.11	PMAIP1	2488.207868	1.356047783	0.22108557	6.133587923	8.59E-10	6.55E-08
ENSG00000175352.10	NRIP3	222.8483218	1.343624989	0.336346184	3.994768046	6.48E-05	0.001739465
ENSG00000176485.10	PLA2G16	209.8872222	1.343082383	0.281845868	4.765308048	1.89E-06	7.66E-05
ENSG00000112149.9	CD83	1289.664583	1.341743218	0.180059566	7.451663067	9.22E-14	1.30E-11
ENSG00000165548.10	TMEM63C	87.37137037	1.341095195	0.414504502	3.235417681	0.001214649	0.019733914
ENSG00000198933.9	TBKBP1	773.0276084	1.340034522	0.30193906	4.438095965	9.08E-06	0.000303672
ENSG00000151208.16	DLG5	777.4047235	1.339829198	0.213644829	6.271292435	3.58E-10	2.90E-08
ENSG00000141526.15	SLC16A3	850.9451911	1.338250552	0.24873903	5.380138991	7.44E-08	4.25E-06
ENSG00000196154.11	S100A4	7338.763482	1.334616845	0.174983434	7.627103963	2.40E-14	3.69E-12
ENSG00000156475.18	PPP2R2B	542.6151454	1.329632078	0.17999217	7.387166222	1.50E-13	2.01E-11
ENSG00000196169.14	KIF19	166.3664407	1.327962705	0.371477743	3.57481095	0.000350481	0.007309971
ENSG00000100097.11	LGALS1	1014.41496	1.323577743	0.264257349	5.008669579	5.48E-07	2.60E-05
ENSG00000232434.2	C9orf172	302.5561198	1.323162936	0.318096039	4.159633483	3.19E-05	0.000929611
ENSG00000189233.11	NUGGC	265.4880093	1.31838084	0.290175865	4.543385579	5.54E-06	0.000196257
ENSG00000223865.10	HLA-DPB1	291.4544012	1.317451223	0.280929241	4.689619417	2.74E-06	0.000106742
ENSG00000101400.5	SNTA1	747.2127709	1.313686661	0.211800247	6.202479357	5.56E-10	4.36E-08
ENSG00000204257.14	HLA-DMA	72.73832351	1.310809937	0.427205058	3.068338994	0.002152523	0.031442209
ENSG00000142634.12	EFHD2	5781.531439	1.310149927	0.225662258	5.805799941	6.41E-09	4.33E-07
ENSG00000135114.12	OASL	1743.328612	1.305326269	0.199591189	6.539999471	6.15E-11	5.80E-09
ENSG00000177191.2	B3GNT8	69.30722325	1.294859819	0.396045774	3.269470109	0.001077491	0.017978557
ENSG00000114541.14	FRMD4B	1597.190509	1.290217608	0.174777631	7.382052265	1.56E-13	2.07E-11
ENSG00000147889.17	CDKN2A	141.8124764	1.288566601	0.272323402	4.731751269	2.23E-06	8.87E-05
ENSG00000005379.15	TSPOAP1	3895.1056	1.281498308	0.178025428	7.19840038	6.09E-13	7.40E-11
ENSG00000127946.16	HIP1	593.2684236	1.277320411	0.23395104	5.459776599	4.77E-08	2.82E-06
ENSG00000155366.16	RHOC	238.0242713	1.276021572	0.244800342	5.212499141	1.86E-07	9.82E-06
ENSG00000160219.11	GAB3	2169.845911	1.275688297	0.185199726	6.888175949	5.65E-12	6.36E-10
ENSG00000140859.15	KIFC3	87.4258795	1.27184589	0.37909273	3.354973042	0.000793727	0.014069779
ENSG00000165030.3	NFIL3	433.927739	1.269872587	0.199131307	6.377061472	1.81E-10	1.57E-08

ENSG00000060558.3	GNA15	913.1756182	1.268040691	0.259528339	4.885943069	1.03E-06	4.52E-05
ENSG00000126838.9	PZP	167.6818489	1.267391635	0.410648754	3.086315547	0.002026536	0.030020308
ENSG00000099985.3	OSM	176.7240864	1.26660029	0.304564759	4.158722412	3.20E-05	0.000931706
ENSG00000065361.14	ERBB3	200.3652832	1.263992407	0.372843963	3.390137785	0.000698575	0.012746904
ENSG00000196358.10	NTNG2	381.0256162	1.258570867	0.202848171	6.204496997	5.49E-10	4.32E-08
ENSG00000196914.8	ARHGEF12	1948.037965	1.257739688	0.174601102	7.203503717	5.87E-13	7.18E-11
ENSG00000151014.5	NOCT	180.6791595	1.255071623	0.298969891	4.197986688	2.69E-05	0.00080673
ENSG00000106089.11	STX1A	597.2989354	1.254842691	0.31961969	3.92604939	8.64E-05	0.002217525
ENSG00000143036.16	SLC44A3	62.97434867	1.251584496	0.415048964	3.015510471	0.002565471	0.035850317
ENSG00000182718.16	ANXA2	5057.899698	1.247465386	0.14658692	8.510072987	1.74E-17	3.60E-15
ENSG00000145819.15	ARHGAP26	1382.818592	1.238203148	0.187225504	6.613432059	3.76E-11	3.68E-09
ENSG00000136193.16	SCRN1	470.9452042	1.236984298	0.185062033	6.684160307	2.32E-11	2.35E-09
ENSG00000232810.3	TNF	172.7790932	1.23519138	0.302933737	4.077430896	4.55E-05	0.001273133
ENSG00000007402.11	CACNA2D2	395.4725201	1.232978504	0.350026835	3.522525648	0.000427456	0.008667478
ENSG00000174871.10	CNIH2	132.3322314	1.23067798	0.308079335	3.994678773	6.48E-05	0.001739465
ENSG00000170837.2	GPR27	74.22170769	1.227207869	0.420809841	2.916300305	0.003542094	0.04604431
ENSG00000166483.10	WEE1	906.4537486	1.226014056	0.183353472	6.686614907	2.28E-11	2.34E-09
ENSG00000049759.17	NEDD4L	350.8915503	1.222778865	0.305734143	3.999484169	6.35E-05	0.001711427
ENSG00000064201.15	TSPAN32	574.6196989	1.220513811	0.298015306	4.095473578	4.21E-05	0.001189375
ENSG00000132334.16	PTPRE	3258.415593	1.215583371	0.234850202	5.17599458	2.27E-07	1.16E-05
ENSG00000115594.11	IL1R1	452.2356186	1.21382976	0.187536911	6.472484556	9.64E-11	8.93E-09
ENSG00000142945.12	KIF2C	82.94339083	1.209202688	0.370259931	3.265821076	0.001091472	0.018139636
ENSG00000105963.13	ADAP1	125.859947	1.206701748	0.311215889	3.877378339	0.000105588	0.002642697
ENSG00000143507.17	DUSP10	1932.100065	1.200800903	0.264293987	4.543428761	5.53E-06	0.000196257
ENSG00000121964.14	GTDC1	1248.552013	1.192635537	0.157484671	7.57302618	3.65E-14	5.51E-12
ENSG00000104490.17	NCALD	510.1413216	1.190568557	0.187562379	6.347587212	2.19E-10	1.86E-08
ENSG00000069702.10	TGFBR3	3689.743126	1.189892269	0.1503588	7.913685593	2.50E-15	4.15E-13
ENSG00000186891.13	TNFRSF18	935.4283405	1.188469804	0.291258271	4.080467141	4.49E-05	0.001262458
ENSG00000119900.7	OGFRL1	2407.775489	1.179788755	0.173607801	6.795712798	1.08E-11	1.17E-09
ENSG00000137166.14	FOXP4	980.5000829	1.179076489	0.257824463	4.573175383	4.80E-06	0.000172129
ENSG00000161921.14	CXCL16	380.4737524	1.173887029	0.289254709	4.058316057	4.94E-05	0.001361011
ENSG00000118503.14	TNFAIP3	91589.25973	1.173523282	0.172639843	6.797522872	1.06E-11	1.17E-09
ENSG00000118156.12	ZNF541	184.2072441	1.166120221	0.351910683	3.313682354	0.00092076	0.015787558
ENSG00000117411.16	B4GALT2	118.1880969	1.158190395	0.330013559	3.509523665	0.00044891	0.008983023
ENSG00000148175.12	STOM	6523.987964	1.157766865	0.193260068	5.990719535	2.09E-09	1.50E-07
ENSG00000160183.13	TMPRSS3	238.5381299	1.154827657	0.263182137	4.387940873	1.14E-05	0.000374046
ENSG00000188677.14	PARVB	134.9840981	1.15276103	0.30374747	3.795129656	0.000147566	0.003540114
ENSG00000076356.6	PLXNA2	189.2860539	1.151375001	0.26407553	4.360021547	1.30E-05	0.000419385
ENSG00000184730.10	APOBR	1904.863467	1.148435192	0.220488533	5.208593729	1.90E-07	9.97E-06
ENSG00000140564.10	FURIN	11861.24502	1.147095995	0.26056287	4.40237704	1.07E-05	0.000353441
ENSG00000144824.19	PHLDB2	436.4304423	1.147069357	0.272304663	4.212448454	2.53E-05	0.000764646
ENSG00000020633.18	RUNX3	17744.88264	1.146131006	0.231461109	4.951721751	7.36E-07	3.35E-05
ENSG00000166900.15	STX3	625.4704619	1.144563272	0.252483213	4.533225227	5.81E-06	0.000202517
ENSG00000105329.9	TGFB1	12773.56958	1.142508819	0.232048595	4.92357567	8.50E-07	3.83E-05
ENSG00000175274.18	TP53I11	249.801151	1.135814838	0.331244233	3.428934675	0.000605955	0.011366069
ENSG00000171368.11	TPPP	763.3763833	1.1284572	0.277119205	4.072100309	4.66E-05	0.001297818
ENSG00000213719.8	CLIC1	2609.687761	1.12766118	0.137901752	8.177279544	2.90E-16	5.29E-14
ENSG00000135842.16	FAM129A	7834.982179	1.127570793	0.176039059	6.405230743	1.50E-10	1.33E-08

ENSG00000127561.14	SYNGR3	154.1767595	1.127302953	0.325616696	3.462055128	0.000536067	0.010308845
ENSG00000178607.15	ERN1	21471.68703	1.120960319	0.126759684	8.84319279	9.30E-19	2.26E-16
ENSG00000168268.10	NT5DC2	196.094145	1.118534783	0.298172604	3.751299645	0.00017592	0.004120122
ENSG00000165029.15	ABCA1	1448.143076	1.107632352	0.302822194	3.657698724	0.00025449	0.005644896
ENSG00000128309.16	MPST	225.3030117	1.106741779	0.26412678	4.190191463	2.79E-05	0.000828612
ENSG00000134684.10	YARS	4895.606311	1.102963278	0.160341519	6.878837641	6.03E-12	6.75E-10
ENSG00000110880.10	CORO1C	325.3066324	1.099434119	0.232427628	4.730221321	2.24E-06	8.91E-05
ENSG00000187583.10	PLEKHN1	219.7004265	1.096367996	0.327146298	3.35130797	0.000804308	0.014182377
ENSG00000146858.7	ZC3HAV1L	379.2069057	1.096146545	0.23078026	4.749741352	2.04E-06	8.17E-05
ENSG00000127951.6	FGL2	368.7028205	1.093771	0.277279885	3.944646047	7.99E-05	0.002090708
ENSG00000070182.18	SPTB	83.06840256	1.088198422	0.367952037	2.957446385	0.003101987	0.041647092
ENSG00000122694.15	GLIPR2	1731.63531	1.085485773	0.146511487	7.408878275	1.27E-13	1.75E-11
ENSG00000167094.15	TTC16	199.6171235	1.078479754	0.265077414	4.068546378	4.73E-05	0.001315584
ENSG00000133808.4	MICALCL	94.30373726	1.075741929	0.331104139	3.248953429	0.001158304	0.019005486
ENSG00000198113.2	TOR4A	203.4872027	1.072906277	0.281691245	3.808802359	0.000139642	0.003369279
ENSG00000143013.12	LMO4	1295.720676	1.072177554	0.204938453	5.231705131	1.68E-07	8.94E-06
ENSG00000106799.12	TGFBR1	1770.089239	1.071867779	0.204485789	5.241771488	1.59E-07	8.54E-06
ENSG00000118242.15	MREG	344.3872065	1.071361431	0.198623917	5.393919569	6.89E-08	3.95E-06
ENSG00000171867.16	PRNP	5979.978634	1.067448612	0.169803309	6.286382875	3.25E-10	2.66E-08
ENSG00000107331.16	ABCA2	11135.04909	1.067324956	0.230146149	4.637596419	3.52E-06	0.000132529
ENSG00000042493.15	CAPG	643.1260428	1.067135935	0.320125058	3.333497047	0.000857616	0.014964994
ENSG00000117016.9	RIMS3	355.2772064	1.066920053	0.204351269	5.221010165	1.78E-07	9.41E-06
ENSG00000162711.16	NLRP3	610.4974265	1.066689143	0.247980426	4.301505412	1.70E-05	0.000538773
ENSG00000104368.17	PLAT	146.2276173	1.060628265	0.326693219	3.246557335	0.001168099	0.019128765
ENSG00000130402.11	ACTN4	6605.427698	1.059414719	0.201877465	5.247810689	1.54E-07	8.30E-06
ENSG00000162676.11	GFI1	686.6863092	1.057924089	0.182817574	5.786774565	7.18E-09	4.81E-07
ENSG00000173482.16	PTPRM	2546.863206	1.057107089	0.228703053	4.622181801	3.80E-06	0.000140876
ENSG00000108798.8	ABI3	319.8542665	1.050903711	0.235941146	4.454092595	8.42E-06	0.000282553
ENSG00000188211.8	NCR3LG1	452.6161617	1.038230737	0.224514864	4.624329629	3.76E-06	0.000139734
ENSG00000213722.8	DDAH2	167.6877245	1.036446414	0.268029265	3.866915109	0.000110221	0.002746348
ENSG00000105656.12	ELL	2349.034514	1.032813779	0.240897965	4.287349541	1.81E-05	0.00056726
ENSG00000008516.16	MMP25	286.7041193	1.031455881	0.316426114	3.259705305	0.00111528	0.01844392
ENSG00000163171.7	CDC42EP3	3637.397919	1.024636885	0.184883166	5.542077764	2.99E-08	1.85E-06
ENSG00000135631.16	RAB11FIP5	1169.124402	1.023157448	0.291836227	3.505930222	0.000455014	0.009072697
ENSG00000163820.14	FYCO1	5430.519627	1.022685542	0.166899548	6.127551282	8.92E-10	6.77E-08
ENSG00000021762.19	OSBPL5	316.9415646	1.017576138	0.324422604	3.136575952	0.001709332	0.026176969
ENSG00000225556.1	C2CD4D	329.4827597	1.010619514	0.256307331	3.942998861	8.05E-05	0.002098577
ENSG00000121621.6	KIF18A	83.95724872	1.008569871	0.340053379	2.965916331	0.003017826	0.04068
ENSG00000179820.15	MYADM	7626.31446	1.007613463	0.240560321	4.188610408	2.81E-05	0.000828612
ENSG00000179588.8	ZFPM1	935.34211	1.006873659	0.278800067	3.611454143	0.000304485	0.006546036
ENSG00000186350.9	RXRA	704.9878395	1.006780078	0.241262805	4.172960176	3.01E-05	0.000879912
ENSG00000167851.13	CD300A	486.3964026	1.003236809	0.296469787	3.38394283	0.000714529	0.012995589
ENSG00000140030.5	GPR65	1627.573598	1.001183645	0.156142955	6.411968074	1.44E-10	1.28E-08
ENSG00000105281.12	SLC1A5	543.6033882	1.000952657	0.215101995	4.65338622	3.27E-06	0.000123881

Table S4 B: down-regulated genes in circulating pTh17-cells as compared to cTh17-cells

Gene_id	Gene_name	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
ENSG00000173597.8	SULT1B1	520.0399923	-4.465363078	0.33169823	-13.46212514	2.61E-41	2.92E-38
ENSG00000143167.11	GPA33	513.1665569	-4.391407372	0.29913207	-14.6804967	8.60E-49	1.31E-45
ENSG00000227051.6	C14orf132	374.9876431	-4.215826604	0.275947058	-15.27766464	1.08E-52	2.01E-49
ENSG00000151490.13	PTPRO	111.6849879	-4.163361996	0.526548365	-7.906893786	2.64E-15	4.34E-13
ENSG00000092096.15	SLC22A17	77.48656333	-3.293067522	0.414669711	-7.941422851	2.00E-15	3.39E-13
ENSG00000072110.13	ACTN1	1029.499259	-3.200674416	1.055526749	-3.03230062	0.002426974	0.034548321
ENSG00000204219.9	TCEA3	142.7670567	-3.182302703	0.342706414	-9.285798507	1.60E-20	4.64E-18
ENSG00000101230.5	ISM1	100.1487906	-3.02451016	0.429513311	-7.041714622	1.90E-12	2.20E-10
ENSG00000278195.1	SSTR3	279.5758432	-2.930346498	0.341743142	-8.574704614	9.93E-18	2.22E-15
ENSG00000151914.19	DST	456.5566125	-2.784869617	0.276458927	-10.07335754	7.25E-24	2.70E-21
ENSG00000174175.16	SELP	80.32344489	-2.708460688	0.368367951	-7.352595907	1.94E-13	2.57E-11
ENSG00000185272.13	RBM11	82.0700817	-2.664005368	0.423167768	-6.295388188	3.07E-10	2.53E-08
ENSG00000149970.14	CNKSR2	89.24630049	-2.6348036	0.413783503	-6.367589769	1.92E-10	1.66E-08
ENSG00000182463.15	TSHZ2	1481.937049	-2.571226772	0.490560056	-5.241410789	1.59E-07	8.54E-06
ENSG00000182983.14	ZNF662	35.97718716	-2.563947793	0.549170492	-4.668764678	3.03E-06	0.000116543
ENSG00000261115.5	TMEM178B	64.6247507	-2.563551796	0.46337082	-5.532397998	3.16E-08	1.93E-06
ENSG00000176928.5	GCNT4	1020.834855	-2.550136751	0.187463135	-13.60340392	3.82E-42	4.58E-39
ENSG00000182272.11	B4GALNT4	49.33080728	-2.523738435	0.522451075	-4.83057372	1.36E-06	5.74E-05
ENSG00000181847.11	TIGIT	1624.172626	-2.519945676	0.4905201	-5.137293408	2.79E-07	1.40E-05
ENSG00000111863.12	ADTRP	571.2675413	-2.50177418	0.237127954	-10.55031318	5.06E-26	2.50E-23
ENSG00000106624.9	AEBP1	100.5741292	-2.459452861	0.409342697	-6.008297886	1.87E-09	1.35E-07
ENSG00000181690.7	PLAG1	564.1155657	-2.445662598	0.201627818	-12.1295892	7.36E-34	6.17E-31
ENSG00000112874.9	NUDT12	85.47700414	-2.439760449	0.356481597	-6.84400111	7.70E-12	8.50E-10
ENSG00000047634.14	SCML1	1123.354197	-2.424419952	0.231494715	-10.47289549	1.15E-25	5.22E-23
ENSG00000188404.8	SELL	11285.69113	-2.423001621	0.161293074	-15.02235383	5.24E-51	8.79E-48
ENSG00000166681.13	BEX3	302.8058138	-2.370843025	0.366845064	-6.462791123	1.03E-10	9.37E-09
ENSG00000070018.8	LRP6	43.18907466	-2.36378255	0.483233436	-4.891595606	1.00E-06	4.40E-05
ENSG00000153291.15	SLC25A27	44.28083423	-2.318910248	0.48815954	-4.750312266	2.03E-06	8.17E-05
ENSG00000110777.11	POU2AF1	37.83157587	-2.316584669	0.539516702	-4.293814555	1.76E-05	0.000554383
ENSG00000262655.3	SPON1	2920.81319	-2.247034001	0.266849272	-8.420611326	3.75E-17	7.48E-15
ENSG00000135678.11	CPM	44.75821404	-2.214519026	0.509721846	-4.344563695	1.40E-05	0.000446595
ENSG00000277586.1	NEFL	295.238734	-2.21003859	0.27382547	-8.070975256	6.97E-16	1.23E-13
ENSG00000188266.13	HYKK	74.53812492	-2.207539326	0.387140565	-5.702164862	1.18E-08	7.66E-07
ENSG00000177425.10	PAWR	126.728969	-2.146310851	0.342912983	-6.259053923	3.87E-10	3.12E-08
ENSG00000116191.17	RALGPS2	573.6617119	-2.145971388	0.210509219	-10.19419194	2.10E-24	8.61E-22
ENSG00000143869.6	GDF7	160.7686076	-2.143924926	0.436769668	-4.908593896	9.17E-07	4.08E-05
ENSG00000116690.12	PRG4	85.50999847	-2.104528667	0.394817416	-5.330384589	9.80E-08	5.50E-06
ENSG00000133138.19	TBC1D8B	97.54184192	-2.103289742	0.525488433	-4.002542417	6.27E-05	0.001694898
ENSG00000119771.14	KLHL29	76.22523812	-2.080540325	0.389322921	-5.343996497	9.09E-08	5.12E-06
ENSG00000034053.14	APBA2	857.9366837	-2.074617649	0.244834557	-8.473549129	2.38E-17	4.87E-15
ENSG00000129422.14	MTUS1	131.803947	-2.018492121	0.301545641	-6.693819606	2.17E-11	2.26E-09
ENSG00000172915.18	NBEA	283.8993486	-2.008322198	0.387903232	-5.177379395	2.25E-07	1.15E-05
ENSG00000187554.11	TLR5	54.22839002	-1.94593005	0.453227093	-4.29349895	1.76E-05	0.000554383
ENSG00000100116.16	GCAT	37.05099803	-1.938180632	0.540262699	-3.587478157	0.000333892	0.007033957
ENSG00000113645.14	WWC1	82.85720452	-1.925630384	0.429662457	-4.481728282	7.40E-06	0.000252356
ENSG00000008441.16	NFIX	73.17212674	-1.924915392	0.392033323	-4.910081057	9.10E-07	4.06E-05
ENSG00000174837.14	ADGRE1	330.2810682	-1.892767428	0.22115189	-8.558676245	1.14E-17	2.42E-15

ENSG00000123454.10	DBH	180.67704	-1.865609415	0.385392475	-4.84080395	1.29E-06	5.49E-05
ENSG00000184557.4	SOCS3	4955.429035	-1.850844776	0.49592955	-3.732071981	0.000189911	0.004392581
ENSG00000163864.15	NMNAT3	61.99691478	-1.848085514	0.509877354	-3.624568732	0.000289444	0.00630349
ENSG00000139193.3	CD27	577.1332149	-1.809471399	0.20317414	-8.906012359	5.29E-19	1.32E-16
ENSG00000151715.7	TMEM45B	1222.392061	-1.791134468	0.179256607	-9.992013647	1.65E-23	5.89E-21
ENSG00000197880.8	MDS2	72.73903243	-1.768085553	0.389333279	-4.541316262	5.59E-06	0.000197749
ENSG00000106688.11	SLC1A1	93.14160605	-1.764918268	0.480318168	-3.674477433	0.000238337	0.005350292
ENSG00000160856.20	FCRL3	34.25045381	-1.756988236	0.543703013	-3.231521979	0.001231329	0.019930645
ENSG00000151320.10	AKAP6	35.84651078	-1.737173653	0.5260724	-3.302156991	0.000959444	0.016350517
ENSG00000164649.19	CDCA7L	102.3262082	-1.730270781	0.381565875	-4.534658091	5.77E-06	0.000201987
ENSG00000138795.9	LEF1	5361.693124	-1.719862044	0.178471784	-9.636604776	5.60E-22	1.81E-19
ENSG00000242866.9	STRC	33.63503683	-1.71372863	0.526411212	-3.255494164	0.001131952	0.018646078
ENSG00000173809.16	TDRD12	91.6927496	-1.678291395	0.364409921	-4.605504123	4.11E-06	0.000151314
ENSG00000215475.4	SIAH3	96.63536445	-1.677985358	0.369662809	-4.539232292	5.65E-06	0.000198901
ENSG00000003147.17	ICA1	54.12784079	-1.673916977	0.466733745	-3.586449433	0.000335211	0.007052891
ENSG00000114948.12	ADAM23	1773.927696	-1.670141216	0.233248198	-7.160360625	8.05E-13	9.64E-11
ENSG00000163359.15	COL6A3	103.4823918	-1.669579339	0.449252684	-3.716348054	0.000202123	0.004630331
ENSG00000123453.17	SARDH	332.5922936	-1.655586631	0.3690244	-4.486387973	7.24E-06	0.00024791
ENSG00000072163.19	LIMS2	60.99714385	-1.652179915	0.50936441	-3.243610824	0.001180249	0.019271269
ENSG00000117322.16	CR2	258.8376466	-1.647479591	0.377506635	-4.36410764	1.28E-05	0.000413213
ENSG00000105173.13	CCNE1	98.86872412	-1.643334635	0.340780547	-4.822266552	1.42E-06	5.92E-05
ENSG00000140470.13	ADAMTS17	124.7741135	-1.617319924	0.353130526	-4.579949354	4.65E-06	0.000167362
ENSG00000197093.10	GAL3ST4	169.8938412	-1.593725613	0.300466083	-5.304178087	1.13E-07	6.28E-06
ENSG00000174500.12	GCSAM	455.4838218	-1.574312621	0.190942875	-8.24494038	1.65E-16	3.05E-14
ENSG00000109321.10	AREG	133.286477	-1.570832632	0.369018416	-4.256786558	2.07E-05	0.000644011
ENSG00000149212.11	SESN3	6382.484112	-1.566442178	0.209141529	-7.489866739	6.89E-14	1.01E-11
ENSG00000154027.18	AK5	152.6344631	-1.565512187	0.3006621	-5.206882375	1.92E-07	1.00E-05
ENSG00000187079.15	TEAD1	39.69456449	-1.561813954	0.477184018	-3.272980434	0.001064198	0.017774446
ENSG00000156299.13	TIAM1	2279.19684	-1.555470776	0.471255231	-3.300697101	0.000964449	0.016402487
ENSG00000055732.12	MCOLN3	176.5494706	-1.545172342	0.309449586	-4.993292648	5.94E-07	2.78E-05
ENSG00000151491.12	EPS8	76.45906601	-1.525968504	0.412343913	-3.700717905	0.00021499	0.004898334
ENSG00000140443.13	IGF1R	969.1620825	-1.525822124	0.197393769	-7.729839346	1.08E-14	1.67E-12
ENSG00000138449.10	SLC40A1	910.6404529	-1.518764537	0.224527544	-6.764268258	1.34E-11	1.44E-09
ENSG00000223547.9	ZNF844	305.1312072	-1.517317148	0.280420543	-5.410863033	6.27E-08	3.65E-06
ENSG00000198520.10	C1orf228	701.3485108	-1.4764343	0.223102421	-6.617742183	3.65E-11	3.60E-09
ENSG00000120915.13	EPHX2	975.0901822	-1.476335867	0.185722409	-7.949153114	1.88E-15	3.21E-13
ENSG00000113231.13	PDE8B	54.9278645	-1.469566847	0.431490018	-3.405795696	0.000659715	0.012170259
ENSG00000082781.11	ITGB5	46.35325134	-1.468518312	0.503086757	-2.919016038	0.003511382	0.045751638
ENSG00000166105.15	GLB1L3	331.9827682	-1.465573199	0.248901594	-5.888163176	3.91E-09	2.68E-07
ENSG00000198939.7	ZFP2	73.09226834	-1.4602555	0.395195497	-3.695020597	0.000219869	0.004975685
ENSG00000120896.13	SORBS3	2460.743765	-1.457553298	0.221161222	-6.590455985	4.38E-11	4.21E-09
ENSG00000154227.13	CERS3	48.64563003	-1.445988865	0.484306861	-2.985687342	0.002829418	0.038480539
ENSG00000126353.3	CCR7	7259.365634	-1.434704783	0.214386678	-6.692135883	2.20E-11	2.27E-09
ENSG00000114529.12	C3orf52	116.3269258	-1.42736201	0.293845655	-4.857522948	1.19E-06	5.14E-05
ENSG00000112303.13	VNN2	177.1418773	-1.421048751	0.374708479	-3.792411515	0.000149191	0.003573987
ENSG00000166405.14	RIC3	1175.513417	-1.415524156	0.164449882	-8.60763253	7.46E-18	1.76E-15
ENSG00000113749.7	HRH2	101.828989	-1.415417379	0.480330624	-2.946756479	0.00321126	0.042805737
ENSG00000126217.20	MCF2L	640.9428502	-1.414790688	0.277127622	-5.1051955	3.30E-07	1.63E-05
ENSG00000172292.14	CERS6	325.965882	-1.414175871	0.213208576	-6.632828258	3.29E-11	3.27E-09

ENSG00000156510.12	HKDC1	165.2783966	-1.402629795	0.283728784	-4.943558328	7.67E-07	3.49E-05
ENSG00000186310.9	NAP1L3	297.3529222	-1.395809431	0.251344628	-5.55336886	2.80E-08	1.75E-06
ENSG00000165568.17	AKR1E2	87.90175089	-1.393689517	0.332722204	-4.18874815	2.80E-05	0.000828612
ENSG00000151846.8	PABPC3	304.6076233	-1.385987991	0.286821362	-4.832234193	1.35E-06	5.70E-05
ENSG00000155970.11	MICU3	283.7135984	-1.385058443	0.218886907	-6.327735466	2.49E-10	2.10E-08
ENSG00000117318.8	ID3	64.52657382	-1.380411215	0.470831485	-2.931858339	0.003369404	0.044349714
ENSG00000167889.12	MGAT5B	441.7757808	-1.380222291	0.243629702	-5.665246396	1.47E-08	9.36E-07
ENSG00000178732.5	GP5	117.7859836	-1.375423696	0.301365028	-4.563979119	5.02E-06	0.000179082
ENSG00000213420.7	GPC2	154.4285191	-1.37447208	0.29210669	-4.705376934	2.53E-06	9.97E-05
ENSG00000151376.16	ME3	65.17255135	-1.367707125	0.449390269	-3.043472944	0.002338645	0.033347562
ENSG00000274349.4	ZNF658	160.9252215	-1.365927865	0.345158513	-3.957392947	7.58E-05	0.001994701
ENSG00000171502.14	COL24A1	109.0789964	-1.354855677	0.451473838	-3.000961656	0.002691285	0.037174753
ENSG00000109654.14	TRIM2	286.6582625	-1.342732142	0.366199336	-3.666670066	0.00024573	0.005489074
ENSG00000165591.6	FAAH2	773.0899176	-1.332946892	0.178766856	-7.456342404	8.90E-14	1.26E-11
ENSG00000102098.17	SCML2	52.72400677	-1.320741451	0.431994617	-3.057309976	0.002233332	0.032285123
ENSG00000164904.16	ALDH7A1	59.96371203	-1.315532945	0.42201855	-3.117239621	0.001825531	0.027504343
ENSG00000055118.14	KCNH2	100.4563048	-1.314168911	0.375936229	-3.495722973	0.000472779	0.0093712
ENSG00000171291.8	ZNF439	630.7150077	-1.31025404	0.242006929	-5.414117885	6.16E-08	3.60E-06
ENSG00000107104.18	KANK1	761.1191201	-1.30588239	0.216005936	-6.045585664	1.49E-09	1.10E-07
ENSG00000196381.10	ZNF781	130.6805967	-1.302816631	0.327658557	-3.976141025	7.00E-05	0.00186732
ENSG00000073331.17	ALPK1	1435.742555	-1.297619866	0.182495575	-7.11041823	1.16E-12	1.37E-10
ENSG00000143502.14	SUSD4	122.592248	-1.287307481	0.31449912	-4.093198998	4.25E-05	0.001199089
ENSG00000136153.19	LMO7	713.3367079	-1.287189329	0.189423691	-6.795292206	1.08E-11	1.17E-09
ENSG00000179088.14	C12orf42	116.4427075	-1.277462909	0.406526988	-3.142381554	0.001675795	0.025781107
ENSG00000189060.5	H1F0	131.94254	-1.276029805	0.371283667	-3.43680565	0.000588618	0.011131624
ENSG00000164684.13	ZNF704	309.3018519	-1.268861599	0.361898982	-3.506120942	0.000454689	0.009072697
ENSG00000102678.6	FGF9	274.6431829	-1.256429497	0.325529405	-3.859649787	0.00011355	0.002816737
ENSG00000136111.12	TBC1D4	8105.325607	-1.239642362	0.18808171	-6.590977725	4.37E-11	4.21E-09
ENSG00000171105.13	INSR	59.95328719	-1.236314492	0.410440671	-3.012163704	0.002593927	0.036187651
ENSG00000090975.12	PITPNM2	767.7213439	-1.234633699	0.25464638	-4.848424305	1.24E-06	5.32E-05
ENSG00000196724.12	ZNF418	92.98164661	-1.225388166	0.402611333	-3.043600776	0.002337651	0.033347562
ENSG00000173198.5	CYSLTR1	851.2026939	-1.224796699	0.263513736	-4.647942523	3.35E-06	0.000126337
ENSG00000164251.4	F2RL1	201.063307	-1.224207759	0.278654005	-4.393289659	1.12E-05	0.000367104
ENSG00000148429.14	USP6NL	216.6855335	-1.215230217	0.265266633	-4.581165006	4.62E-06	0.000167127
ENSG00000182871.14	COL18A1	261.8092963	-1.214529136	0.308780921	-3.933303692	8.38E-05	0.002168228
ENSG00000186265.9	BTLA	534.0054288	-1.214476132	0.181319146	-6.69800272	2.11E-11	2.23E-09
ENSG00000184867.13	ARMCX2	93.33002126	-1.21407966	0.373611084	-3.249581486	0.00115575	0.018993755
ENSG00000123191.14	ATP7B	66.96659992	-1.188332275	0.37452947	-3.172867211	0.001509415	0.023523594
ENSG00000173762.7	CD7	2396.811807	-1.185693602	0.286369081	-4.140438619	3.47E-05	0.00099535
ENSG00000167642.12	SPINT2	473.922448	-1.185677038	0.236810648	-5.006856944	5.53E-07	2.61E-05
ENSG00000038382.17	TRIO	474.7017294	-1.177547316	0.339627563	-3.467172413	0.000525964	0.010172892
ENSG00000142192.20	APP	2043.310496	-1.175982281	0.188135039	-6.250735047	4.09E-10	3.28E-08
ENSG00000176160.9	HSF5	76.88086881	-1.166973105	0.398438808	-2.928864057	0.003402032	0.044660737
ENSG00000165821.11	SALL2	154.8024583	-1.164067211	0.280510581	-4.149815688	3.33E-05	0.000957079
ENSG00000041515.15	MYO16	194.3773456	-1.150374163	0.314917055	-3.652943349	0.000259251	0.00573534
ENSG00000122378.13	FAM213A	89.11567374	-1.138032507	0.333385582	-3.413562456	0.000641195	0.011880875
ENSG00000170074.19	FAM153A	1657.418744	-1.129165003	0.168923801	-6.684463609	2.32E-11	2.35E-09
ENSG00000184635.13	ZNF93	152.429942	-1.121555092	0.26177306	-4.284455745	1.83E-05	0.000573109
ENSG00000135925.8	WNT10A	215.0617397	-1.118060318	0.370145068	-3.020600337	0.002522741	0.03554945

ENSG00000074966.10	TXK	1371.033421	-1.113624923	0.202887101	-5.488889727	4.04E-08	2.43E-06
ENSG00000137266.14	SLC22A23	439.4436524	-1.111121709	0.240218296	-4.62546661	3.74E-06	0.000139588
ENSG00000165028.11	NIPSNAP3B	77.02110825	-1.089293046	0.360230255	-3.023879952	0.002495554	0.035366983
ENSG00000132122.11	SPATA6	91.09216636	-1.086634523	0.369020014	-2.944649296	0.003233209	0.043035474
ENSG00000110002.15	VWA5A	590.8549852	-1.086029909	0.197372298	-5.502443446	3.75E-08	2.27E-06
ENSG00000163545.8	NUAK2	456.8428468	-1.082763727	0.190759735	-5.676060144	1.38E-08	8.82E-07
ENSG00000172005.10	MAL	1795.556158	-1.077037209	0.237580007	-4.533366357	5.81E-06	0.000202517
ENSG00000196411.9	EPHB4	497.2592154	-1.075776944	0.285933848	-3.762328079	0.000168339	0.003970291
ENSG00000049192.14	ADAMTS6	132.282345	-1.073463985	0.318744877	-3.36778428	0.000757749	0.013569487
ENSG00000124613.8	ZNF391	140.5077345	-1.069242106	0.324983221	-3.290145575	0.001001356	0.01692715
ENSG00000170293.8	CMTM8	370.8620754	-1.063525106	0.227441225	-4.676043691	2.92E-06	0.000113263
ENSG00000169047.5	IRS1	632.1033033	-1.061452224	0.238002036	-4.459845146	8.20E-06	0.000276735
ENSG00000164398.12	ACSL6	1316.834025	-1.06046329	0.185444487	-5.718494559	1.07E-08	7.04E-07
ENSG00000204677.10	FAM153C	350.6226054	-1.055916122	0.224081668	-4.712193247	2.45E-06	9.67E-05
ENSG00000131067.16	GGT7	1537.315204	-1.051775764	0.164874498	-6.379250744	1.78E-10	1.55E-08
ENSG00000176533.12	GNG7	211.6078581	-1.043166624	0.265803276	-3.924581517	8.69E-05	0.002227678
ENSG00000198734.10	F5	1868.035158	-1.039676544	0.269969853	-3.85108387	0.000117596	0.002895699
ENSG00000116983.12	HPCAL4	2285.418369	-1.035626331	0.154762884	-6.691697017	2.21E-11	2.27E-09
ENSG00000170209.4	ANKK1	208.468426	-1.028053063	0.243215348	-4.226925123	2.37E-05	0.000722357
ENSG00000166503.8	RP11-382A20.3	257.5082798	-1.027387183	0.331203298	-3.101983554	0.001922286	0.028729786
ENSG00000124243.17	BCAS4	440.9134889	-1.026783539	0.203448346	-5.046900401	4.49E-07	2.16E-05
ENSG00000203710.10	CR1	1583.36894	-1.02321081	0.188381322	-5.431593741	5.59E-08	3.30E-06
ENSG00000183087.14	GAS6	659.5276889	-1.020036091	0.196558501	-5.189478385	2.11E-07	1.09E-05
ENSG00000070756.14	PABPC1	118951.6104	-1.009835832	0.125932024	-8.018896251	1.07E-15	1.86E-13
ENSG00000187601.4	MAGEH1	503.7120779	-1.006536589	0.20230138	-4.975431148	6.51E-07	3.02E-05

Table S5 A: up-regulated genes in circulating pTh17-cells as compared to CCR5$^+$Th1/17-cells

Gene_id	Gene_name	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
ENSG00000063438.16	AHRR	407.548823	3.835433804	0.385916559	9.93850539	2.83E-23	2.48E-19
ENSG00000186522.14	SEPT10	156.9090299	3.544291811	0.530415952	6.682098826	2.36E-11	2.75E-08
ENSG00000010319.6	SEMA3G	47.96423605	3.329257529	0.779734579	4.269731802	1.96E-05	0.003535054
ENSG00000137474.19	MYO7A	154.3417016	3.191617094	0.924627223	3.451787936	0.000556885	0.044150163
ENSG00000134489.6	HRH4	337.2891653	3.14886706	0.671105784	4.692057697	2.70E-06	0.0006969
ENSG00000198910.12	L1CAM	86.23332104	2.907139039	0.500351384	5.810194854	6.24E-09	4.05E-06
ENSG00000182463.15	TSHZ2	1481.937049	2.832045178	0.507127752	5.584480764	2.34E-08	1.28E-05
ENSG00000115594.11	IL1R1	452.2356186	2.768990149	0.209738567	13.20210296	8.53E-40	1.49E-35
ENSG00000005102.12	MEOX1	94.19577069	2.593927852	0.587155074	4.417790065	9.97E-06	0.001941233
ENSG00000183813.6	CCR4	4545.900849	2.543463277	0.478348696	5.317174061	1.05E-07	4.20E-05
ENSG00000167693.16	NXN	57.4217863	2.440699607	0.522942416	4.667243531	3.05E-06	0.000753323
ENSG00000154165.4	GPR15	2338.208748	2.415995186	0.491140317	4.919154678	8.69E-07	0.000267176
ENSG00000072163.19	LIMS2	60.99714385	2.311659139	0.66279649	3.487735941	0.000487129	0.039883111
ENSG00000129521.13	EGLN3	357.1939043	2.307331324	0.267390307	8.62907616	6.18E-18	1.81E-14
ENSG00000127318.10	IL22	27.03548091	2.295380809	0.614469487	3.735548888	0.000187306	0.020640199
ENSG00000277586.1	NEFL	295.238734	2.256402665	0.346564312	6.510776177	7.48E-11	6.55E-08
ENSG00000163492.14	CCDC141	54.75146551	2.217572271	0.629668886	3.521806969	0.000428616	0.036812662
ENSG00000281106.2	RP11-327P2.7	62.25525272	2.203095245	0.523237969	4.210503399	2.55E-05	0.004376854
ENSG00000164530.13	PI16	494.802236	2.200560576	0.642498035	3.425007483	0.000614782	0.047129153
ENSG00000049759.17	NEDD4L	350.8915503	2.129575616	0.31626499	6.733516772	1.66E-11	2.23E-08
ENSG00000104432.12	IL7	102.9088109	2.109771117	0.39036002	5.404680318	6.49E-08	2.84E-05
ENSG00000137942.16	FNBP1L	137.6717349	2.076982026	0.368684128	5.633499968	1.77E-08	1.03E-05
ENSG00000198846.5	TOX	379.7074889	2.020405743	0.3526037	5.729961835	1.00E-08	6.07E-06
ENSG00000106688.11	SLC1A1	93.14160605	1.998098679	0.576165489	3.467924956	0.000524494	0.042348639
ENSG00000156011.16	PSD3	146.5566086	1.926551224	0.326931126	5.892835132	3.80E-09	2.68E-06
ENSG00000198752.10	CDC42BPB	797.2263541	1.920764709	0.521842182	3.680738692	0.000232559	0.024399224
ENSG00000104427.11	ZC2HC1A	438.4235252	1.865635417	0.23754167	7.853929023	4.03E-15	1.01E-11
ENSG00000197646.7	PDCD1LG2	108.0004515	1.85197232	0.405295309	4.569439316	4.89E-06	0.001084596
ENSG00000156535.13	CD109	63.42313459	1.849886172	0.521779963	3.545337698	0.00039211	0.03523162
ENSG00000029153.14	ARNTL2	53.026605	1.789545727	0.447390837	3.999960615	6.34E-05	0.009823083
ENSG00000042493.15	CAPG	643.1260428	1.761227901	0.323939121	5.43691017	5.42E-08	2.57E-05
ENSG00000179388.8	EGR3	81.78231338	1.749340372	0.446808091	3.91519403	9.03E-05	0.012561102
ENSG00000076706.15	MCAM	1068.806163	1.746076142	0.296352016	5.891898977	3.82E-09	2.68E-06
ENSG00000198734.10	F5	1868.035158	1.726739872	0.274429608	6.292104864	3.13E-10	2.61E-07
ENSG00000144354.13	CDCA7	652.1629881	1.697345504	0.313099507	5.421105641	5.92E-08	2.66E-05
ENSG00000056736.9	IL17RB	205.9077277	1.677124156	0.375720838	4.463750701	8.05E-06	0.001640806
ENSG00000121594.11	CD80	75.82923664	1.664676419	0.461140393	3.609912393	0.0003063	0.02931806
ENSG00000181409.11	AATK	139.6894047	1.655895962	0.322972668	5.127046727	2.94E-07	0.000101114
ENSG00000070526.14	ST6GALNAC1	345.0292808	1.598235077	0.291585427	5.48118982	4.22E-08	2.18E-05
ENSG00000141447.16	OSBPL1A	374.6036709	1.569193237	0.299249374	5.243764472	1.57E-07	5.87E-05
ENSG00000170128.4	GPR25	238.0086622	1.562143751	0.416844081	3.747549319	0.000178571	0.020056012
ENSG00000176273.14	SLC35G1	325.8388812	1.549761439	0.233331299	6.641892641	3.10E-11	3.39E-08
ENSG00000108797.11	CNTNAP1	382.5857475	1.535007295	0.327684804	4.68440183	2.81E-06	0.000712974
ENSG00000227051.6	C14orf132	374.9876431	1.505234674	0.419773558	3.585825371	0.000336014	0.031000759
ENSG00000186827.10	TNFRSF4	1070.600623	1.489066304	0.255841832	5.820261255	5.88E-09	3.96E-06

ENSG00000196169.14	KIF19	166.3664407	1.449485511	0.377664028	3.838029054	0.000124026	0.01561969
ENSG00000173198.5	CYSLTR1	851.2026939	1.408556078	0.273357479	5.152798762	2.57E-07	8.99E-05
ENSG00000100097.11	LGALS1	1014.41496	1.400529639	0.266236157	5.260478714	1.44E-07	5.47E-05
ENSG00000075618.17	FSCN1	215.9963815	1.358891677	0.357039046	3.806002989	0.000141231	0.016833352
ENSG00000111961.17	SASH1	264.0254696	1.357324741	0.254530987	5.332650285	9.68E-08	3.94E-05
ENSG00000178732.5	GP5	117.7859836	1.355574806	0.361454205	3.75033624	0.000176598	0.020056012
ENSG00000189350.12	FAM179A	288.3774294	1.348128429	0.355755462	3.789480619	0.000150963	0.017516659
ENSG00000166002.6	SMCO4	131.7291127	1.341254272	0.351621464	3.814483502	0.000136468	0.016377101
ENSG00000182511.11	FES	234.3770834	1.284095044	0.348687463	3.682653325	0.000230819	0.024362524
ENSG00000132694.18	ARHGEF11	1206.621609	1.282059107	0.232714192	5.509157367	3.61E-08	1.91E-05
ENSG00000173040.12	EVC2	272.9043705	1.276069801	0.372539863	3.425324181	0.000614066	0.047129153
ENSG00000163629.12	PTPN13	4806.598336	1.259953371	0.175027812	7.198589501	6.08E-13	1.07E-09
ENSG00000147408.14	CSGALNACT1	4272.518491	1.255383687	0.163302694	7.687464637	1.50E-14	2.92E-11
ENSG00000041515.15	MYO16	194.3773456	1.253787752	0.35770666	3.505072428	0.000456483	0.038452116
ENSG00000163599.14	CTLA4	1900.413407	1.25236861	0.241742587	5.180587446	2.21E-07	8.01E-05
ENSG00000160712.12	IL6R	5562.244178	1.236839665	0.221461935	5.584886031	2.34E-08	1.28E-05
ENSG00000053524.11	MCF2L2	1048.344212	1.230537093	0.230476789	5.339093349	9.34E-08	3.90E-05
ENSG00000182809.10	CRIP2	455.9640259	1.229955638	0.358159343	3.434101785	0.000594521	0.046296004
ENSG00000029534.19	ANK1	1944.840944	1.218992141	0.181700576	6.708796248	1.96E-11	2.46E-08
ENSG00000131747.14	TOP2A	157.1100885	1.208736637	0.354284461	3.411768706	0.000645429	0.048743764
ENSG00000163701.18	IL17RE	376.1687526	1.203036845	0.283147481	4.248799386	2.15E-05	0.003787058
ENSG00000137265.14	IRF4	889.9146947	1.193782146	0.295349622	4.041928809	5.30E-05	0.00866298
ENSG00000118263.14	KLF7	1805.235081	1.172706628	0.238123604	4.924781107	8.45E-07	0.000264238
ENSG00000174136.11	RGMB	257.4178432	1.146134658	0.316611478	3.620003492	0.000294599	0.028675943
ENSG00000155970.11	MICU3	283.7135984	1.122577173	0.249445041	4.500298613	6.79E-06	0.001415406
ENSG00000115902.10	SLC1A4	996.696211	1.107330179	0.231326343	4.786874531	1.69E-06	0.000471819
ENSG00000203485.12	INF2	2601.73643	1.099896418	0.240466864	4.574004092	4.78E-06	0.001074825
ENSG00000151914.19	DST	456.5566125	1.086923741	0.319492177	3.402035541	0.000668859	0.049471881
ENSG00000073910.19	FRY	2121.409907	1.086405364	0.164632998	6.598952687	4.14E-11	3.82E-08
ENSG00000060558.3	GNA15	913.1756182	1.068511516	0.261104624	4.092273434	4.27E-05	0.007060707
ENSG00000128536.15	CDHR3	352.0146703	1.057146025	0.294259708	3.592561254	0.000327444	0.030679894
ENSG00000144843.11	ADPRH	191.5165268	1.048729859	0.282138978	3.717068329	0.000201548	0.02166455
ENSG00000137804.12	NUSAP1	237.1530294	1.044055039	0.262475659	3.977721373	6.96E-05	0.010600789
ENSG00000136111.12	TBC1D4	8105.325607	1.033888877	0.189099663	5.467428464	4.57E-08	2.29E-05
ENSG00000143110.11	C1orf162	692.6752064	1.022167232	0.264737202	3.861063813	0.000112894	0.014652022
ENSG00000080854.14	IGSF9B	1532.803158	1.012702164	0.217450069	4.657171045	3.21E-06	0.000780132
ENSG00000139679.15	LPAR6	3886.299659	1.011626708	0.209361561	4.831960096	1.35E-06	0.000401484
ENSG00000059377.15	TBXAS1	519.2976547	1.008054867	0.218317961	4.617370286	3.89E-06	0.000895954

Table S5 B: down-regulated genes in circulating pTh17-cells as compared to CCR5^{+}Th1/17-cells

Gene_id	Gene_name	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
ENSG00000124507.10	PACSIN1	110.4335766	-2.233813642	0.367976181	-6.070538691	1.27E-09	9.71E-07
ENSG00000213949.8	ITGA1	1292.886476	-2.229673609	0.243658155	-9.150826924	5.65E-20	1.98E-16
ENSG00000271503.5	CCL5	3934.335083	-2.026195302	0.208459312	-9.71985985	2.48E-22	1.45E-18
ENSG00000215475.4	SIAH3	96.63536445	-2.010137518	0.372504068	-5.396283393	6.80E-08	2.91E-05
ENSG00000186810.7	CXCR3	1587.158809	-1.887771767	0.195976926	-9.632622616	5.82E-22	2.55E-18
ENSG00000146904.8	EPHA1	694.1666901	-1.740868298	0.255496967	-6.813655444	9.51E-12	1.39E-08
ENSG00000171502.14	COL24A1	109.0789964	-1.629133764	0.454342003	-3.585699217	0.000336176	0.031000759
ENSG00000166833.19	NAV2	106.7732559	-1.575585017	0.391810717	-4.021291276	5.79E-05	0.009219229
ENSG00000114948.12	ADAM23	1773.927696	-1.55229076	0.234025054	-6.633011002	3.29E-11	3.39E-08
ENSG00000126838.9	PZP	167.6818489	-1.502823741	0.391718903	-3.83648512	0.000124808	0.01561969
ENSG00000198756.10	COLGALT2	105.8462199	-1.479116748	0.426817797	-3.465452376	0.00052934	0.042543903
ENSG00000162415.6	ZSWIM5	405.5187365	-1.460983332	0.303880086	-4.807762663	1.53E-06	0.000445702
ENSG00000146674.14	IGFBP3	715.7329892	-1.408908455	0.265195965	-5.312706987	1.08E-07	4.21E-05
ENSG00000110811.19	P3H3	110.1774473	-1.402326803	0.380281976	-3.687597339	0.000226382	0.024038972
ENSG00000163508.12	EOMES	626.4131388	-1.39670364	0.227375706	-6.142712723	8.11E-10	6.46E-07
ENSG00000157657.14	ZNF618	97.37125346	-1.395790649	0.367900909	-3.793930962	0.000148281	0.0173202
ENSG00000139187.9	KLRG1	668.3920327	-1.317720844	0.291032381	-4.527746505	5.96E-06	0.001289546
ENSG00000164684.13	ZNF704	309.3018519	-1.284906182	0.364063663	-3.529344759	0.00041659	0.03649537
ENSG00000100311.16	PDGFB	299.850589	-1.207038923	0.274581583	-4.395920909	1.10E-05	0.002123778
ENSG00000198915.11	RASGEF1A	582.1107883	-1.194414194	0.281214454	-4.247342823	2.16E-05	0.003787058
ENSG00000176533.12	GNG7	211.6078581	-1.178515598	0.268296408	-4.392588053	1.12E-05	0.002133167
ENSG00000071242.11	RPS6KA2	1682.396625	-1.177724799	0.270010285	-4.361777554	1.29E-05	0.002430521
ENSG00000236609.3	ZNF853	244.6565154	-1.17620971	0.253181662	-4.645714458	3.39E-06	0.000802418
ENSG00000088538.12	DOCK3	379.653524	-1.160048447	0.29615034	-3.91709308	8.96E-05	0.012561102
ENSG00000144290.16	SLC4A10	1245.747324	-1.130737046	0.275119263	-4.109988644	3.96E-05	0.006602556
ENSG00000184613.10	NELL2	7117.647444	-1.118407264	0.206166562	-5.424775254	5.80E-08	2.66E-05
ENSG00000034053.14	APBA2	857.9366837	-1.111247547	0.247694107	-4.486370552	7.24E-06	0.00149334
ENSG00000166707.10	ZCCHC18	415.9260376	-1.110608687	0.299932436	-3.702862889	0.00021318	0.022775175
ENSG00000100298.15	APOBEC3H	192.3268472	-1.077198876	0.274512058	-3.924049394	8.71E-05	0.012504949
ENSG00000147180.16	ZNF711	187.903474	-1.0771918	0.28188813	-3.821345009	0.000132726	0.016262161
ENSG00000008311.14	AASS	422.4976677	-1.042295854	0.269202755	-3.871787472	0.00010804	0.0143153
ENSG00000123612.15	ACVR1C	488.9183263	-1.024151168	0.293187972	-3.493155474	0.000477349	0.039265836
ENSG00000187118.12	CMC1	597.5769109	-1.023498542	0.294414682	-3.476384181	0.000508224	0.041224941
ENSG00000168824.14	NSG1	2134.81068	-1.011686086	0.254896291	-3.96901062	7.22E-05	0.010807861
ENSG00000214193.9	SH3D21	121.4844516	-1.004667067	0.28714516	-3.498812475	0.000467335	0.038991328

Table S6 A: up-regulated genes in circulating pTh17-cells as compared to all other CCR6^{+}Th subsets

Gene_id	Gene_name	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
ENSG00000178860.8	MSC	347.6137529	2.345445676	0.373219622	6.284357893	3.29E-10	1.05E-06
ENSG00000198910.12	L1CAM	86.23332104	2.265056629	0.544619133	4.158973656	3.20E-05	0.007429462
ENSG00000076706.15	MCAM	1068.806163	2.203103043	0.321527196	6.851995944	7.28E-12	1.11E-07
ENSG00000080573.6	COL5A3	4766.905869	1.907517932	0.495360815	3.850764685	0.00011775	0.016952609
ENSG00000124019.9	FAM124B	67.36339937	1.90067851	0.418636115	4.540168513	5.62E-06	0.002199513
ENSG00000189350.12	FAM179A	288.3774294	1.834552211	0.360900171	5.083267777	3.71E-07	0.000246164
ENSG00000179388.8	EGR3	81.78231338	1.819008497	0.319911312	5.685977419	1.30E-08	1.80E-05
ENSG00000182511.11	FES	234.3770834	1.767507764	0.294988342	5.991788532	2.08E-09	4.14E-06
ENSG00000121594.11	CD80	75.82923664	1.718452407	0.321153839	5.350869887	8.75E-08	7.42E-05
ENSG00000029153.14	ARNTL2	53.026605	1.711921056	0.301952588	5.669502847	1.43E-08	1.82E-05
ENSG00000163701.18	IL17RE	376.1687526	1.562407813	0.305588284	5.112787016	3.17E-07	0.000220202
ENSG00000049759.17	NEDD4L	350.8915503	1.490171596	0.330772571	4.505124451	6.63E-06	0.002410295
ENSG00000144843.11	ADPRH	191.5165268	1.478452857	0.288313019	5.127943445	2.93E-07	0.000212872
ENSG00000042493.15	CAPG	643.1260428	1.446990639	0.313994633	4.608329213	4.06E-06	0.001720752
ENSG00000073282.12	TP63	46.7169545	1.398713101	0.348954054	4.00830162	6.12E-05	0.011244779
ENSG00000056736.9	IL17RB	205.9077277	1.389131737	0.33453526	4.15242249	3.29E-05	0.007429462
ENSG00000196169.14	KIF19	166.3664407	1.382853676	0.287790216	4.80507536	1.55E-06	0.000694345
ENSG00000100097.11	LGALS1	1014.41496	1.35864655	0.216430411	6.277521449	3.44E-10	1.05E-06
ENSG00000122877.14	EGR2	179.6517008	1.344904631	0.269596169	4.988589551	6.08E-07	0.000357
ENSG00000115902.10	SLC1A4	996.696211	1.333130711	0.225691063	5.906883026	3.49E-09	5.91E-06
ENSG00000138764.13	CCNG2	1730.877731	1.320098913	0.204392386	6.458650155	1.06E-10	8.06E-07
ENSG00000115009.11	CCL20	603.9510322	1.305635741	0.339800452	3.842360228	0.000121857	0.017061072
ENSG00000144354.13	CDCA7	652.1629881	1.282919307	0.339070948	3.783630869	0.000154557	0.020510386
ENSG00000180549.7	FUT7	340.1415854	1.267458454	0.346803531	3.654687284	0.000257496	0.028894419
ENSG00000060558.3	GNA15	913.1756182	1.250783148	0.230117674	5.435406706	5.47E-08	5.21E-05
ENSG00000120875.8	DUSP4	1962.212506	1.231892823	0.320359866	3.845340679	0.000120385	0.017038157
ENSG00000072832.14	CRMP1	70.70737402	1.207746407	0.348456357	3.465990457	0.000528282	0.04915922
ENSG00000188389.10	PDCD1	98.85163297	1.185689575	0.309014626	3.837001469	0.000124546	0.017149264
ENSG00000139289.13	PHLDA1	1440.29888	1.165811671	0.267773622	4.353721103	1.34E-05	0.004168619
ENSG00000143013.12	LMO4	1295.720676	1.131273755	0.213580954	5.296697723	1.18E-07	9.47E-05
ENSG00000163629.12	PTPN13	4806.598336	1.12141378	0.203505281	5.51048983	3.58E-08	3.64E-05
ENSG00000164120.13	HPGD	485.811863	1.091590953	0.269781295	4.046206959	5.21E-05	0.010316875
ENSG00000137804.12	NUSAP1	237.1530294	1.050915821	0.203569261	5.16244848	2.44E-07	0.000185986
ENSG00000059377.15	TBXAS1	519.2976547	1.046368971	0.193507866	5.407371769	6.40E-08	5.74E-05
ENSG00000136286.14	MYO1G	6125.858085	1.043978537	0.271519359	3.844950657	0.000120577	0.017038157
ENSG00000135631.16	RAB11FIP5	1169.124402	1.015601768	0.247527862	4.102979603	4.08E-05	0.008645001
ENSG00000196154.11	S100A4	7338.763482	1.009591537	0.270911473	3.726647402	0.000194044	0.02447355
ENSG00000106089.11	STX1A	597.2989354	1.005029559	0.278029793	3.61482685	0.000300548	0.031415545

Table S6 B: down-regulated genes in circulating pTh17-cells as compared to all other CCR6$^+$Th subsets

Gene_id	Gene_name	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
ENSG00000261115.5	TMEM178B	64.6247507	-2.471817498	0.623325633	-3.965531609	7.32E-05	0.012038275
ENSG00000215475.4	SIAH3	96.63536445	-2.431159818	0.494416728	-4.917228084	8.78E-07	0.000449213
ENSG00000114948.12	ADAM23	1773.927696	-2.244796029	0.621896947	-3.609594871	0.000306676	0.031837934
ENSG00000185272.13	RBM11	82.0700817	-2.127744972	0.612855482	-3.471854349	0.000516877	0.048392976
ENSG00000133138.19	TBC1D8B	97.54184192	-1.907151438	0.518573225	-3.677689755	0.000235356	0.027227206
ENSG00000034053.14	APBA2	857.9366837	-1.813285336	0.325380581	-5.572813636	2.51E-08	2.94E-05
ENSG00000164684.13	ZNF704	309.3018519	-1.72372396	0.422377379	-4.081004441	4.48E-05	0.00924765
ENSG00000151491.12	EPS8	76.45906601	-1.705552117	0.442045807	-3.858315342	0.000114171	0.016794028
ENSG00000139193.3	CD27	577.1332149	-1.502231274	0.351284362	-4.276396668	1.90E-05	0.005367991
ENSG00000151376.16	ME3	65.17255135	-1.336334491	0.342411307	-3.902717185	9.51E-05	0.014925425
ENSG00000146904.8	EPHA1	694.1666901	-1.318062119	0.296605612	-4.443820563	8.84E-06	0.002931947
ENSG00000184613.10	NELL2	7117.647444	-1.258134558	0.259003824	-4.857590664	1.19E-06	0.000549501
ENSG00000198939.7	ZFP2	73.09226834	-1.253524732	0.326725467	-3.836630011	0.000124734	0.017149264
ENSG00000147180.16	ZNF711	187.903474	-1.215734423	0.260004495	-4.675820796	2.93E-06	0.001276605
ENSG00000140443.13	IGF1R	969.1620825	-1.204758928	0.326971794	-3.684595895	0.000229066	0.027227206
ENSG00000176533.12	GNG7	211.6078581	-1.187914705	0.213978902	-5.551550627	2.83E-08	3.09E-05
ENSG00000223547.9	ZNF844	305.1312072	-1.158836796	0.330361822	-3.507780617	0.000451862	0.043370179
ENSG00000120915.13	EPHX2	975.0901822	-1.135989662	0.313709198	-3.621155095	0.000293291	0.031174442
ENSG00000126217.20	MCF2L	640.9428502	-1.130123317	0.305148764	-3.703515955	0.000212632	0.026169145
ENSG00000148429.14	USP6NL	216.6855335	-1.101191631	0.298802709	-3.685346876	0.000228391	0.027227206
ENSG00000124613.8	ZNF391	140.5077345	-1.090679214	0.275068805	-3.965114158	7.34E-05	0.012038275
ENSG00000171291.8	ZNF439	630.7150077	-1.073139481	0.256929942	-4.176778586	2.96E-05	0.007289231
ENSG00000067445.20	TRO	60.92680308	-1.020984674	0.279109085	-3.658013045	0.000254178	0.028733424
ENSG00000136854.18	STXBP1	383.9461426	-1.001718352	0.242905793	-4.123896509	3.73E-05	0.008104473

Table S7 A: up-regulated genes in intestinal pTh17-cells as compared to cTh17-cells

Gene_id	Gene_name	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
ENSG00000131459.12	GFPT2	1068.588703	5.147887666	0.369450201	13.9339149	3.94E-44	1.89E-40
ENSG00000160791.13	CCR5	1581.789269	4.644365221	0.339451206	13.6819818	1.30E-42	4.67E-39
ENSG00000221869.4	CEBPD	1000.596222	4.445327483	0.357904651	12.42042389	2.02E-35	2.42E-32
ENSG00000104267.9	CA2	391.4859723	4.080368668	0.324710428	12.56617686	3.24E-36	4.23E-33
ENSG00000196781.14	TLE1	212.3593734	3.745420675	0.315692217	11.86415272	1.82E-32	1.74E-29
ENSG00000062524.15	LTK	2387.549681	3.642639601	0.316213325	11.51956388	1.05E-30	8.88E-28
ENSG00000172215.5	CXCR6	3070.169847	3.588901622	0.65436387	5.484565674	4.14E-08	2.01E-06
ENSG00000155629.14	PIK3AP1	473.2938346	3.579618218	0.418101667	8.561597569	1.11E-17	2.58E-15
ENSG00000144290.16	SLC4A10	814.4208956	3.553477257	0.530674222	6.696155783	2.14E-11	1.91E-09
ENSG00000178860.8	MSC	579.5898228	3.483458799	0.289022474	12.05255341	1.88E-33	1.93E-30
ENSG00000157404.15	KIT	2195.429181	3.421497108	0.492871826	6.941961238	3.87E-12	4.08E-10
ENSG00000153563.15	CD8A	412.3038889	3.4146575	0.75795356	4.505101212	6.63E-06	0.000189264
ENSG00000271503.5	CCL5	11501.23145	3.321664186	0.298516732	11.12722948	9.25E-29	5.53E-26
ENSG00000050165.17	DKK3	352.1518506	3.15717251	0.293128804	10.77059799	4.74E-27	2.62E-24
ENSG00000026751.16	SLAMF7	1472.645612	3.109401312	0.703473869	4.420066542	9.87E-06	0.000266652
ENSG00000134256.12	CD101	723.351847	3.034003322	0.367918197	8.246407357	1.63E-16	3.17E-14
ENSG00000157985.18	AGAP1	111.1083272	3.02529974	0.386907924	7.819172341	5.32E-15	8.87E-13
ENSG00000137825.10	ITPKA	32.7003107	2.881197957	0.45311826	6.358600415	2.04E-10	1.55E-08
ENSG00000270379.5	HEATR9	47.39379751	2.819809808	0.531896676	5.301424008	1.15E-07	5.14E-06
ENSG00000171476.21	HOPX	1541.568841	2.816638736	0.167151912	16.85077187	1.04E-63	1.49E-59
ENSG00000187479.5	C11orf96	108.402774	2.791561555	0.433194977	6.444122627	1.16E-10	9.22E-09
ENSG00000213949.8	ITGA1	6324.408364	2.78926338	0.298190329	9.353969967	8.44E-21	2.69E-18
ENSG00000196914.8	ARHGEF12	2527.702269	2.749103898	0.187379286	14.671333	9.84E-49	7.06E-45
ENSG00000117560.7	FASLG	51.60353846	2.676380685	0.740210947	3.615699949	0.000299537	0.005024138
ENSG00000136856.17	SLC2A8	185.5756913	2.656449967	0.457089132	5.811667308	6.19E-09	3.54E-07
ENSG00000149573.8	MPZL2	456.076042	2.606649526	0.233500697	11.16334793	6.16E-29	3.84E-26
ENSG00000075651.15	PLD1	195.9355963	2.569770444	0.27734745	9.265527563	1.94E-20	5.93E-18
ENSG00000125726.10	CD70	216.937412	2.539441327	0.22405076	11.33422324	8.88E-30	5.79E-27
ENSG00000162594.15	IL23R	114.7690542	2.530893436	0.463895483	5.455740628	4.88E-08	2.32E-06
ENSG00000007350.16	TKTL1	79.30990276	2.469265186	0.366418177	6.738926568	1.60E-11	1.47E-09
ENSG00000159335.15	PTMS	742.8548316	2.453455778	0.295838287	8.293232776	1.10E-16	2.20E-14
ENSG00000181264.8	TMEM136	92.81799674	2.376471721	0.362170216	6.561753609	5.32E-11	4.46E-09
ENSG00000092445.11	TYRO3	65.40373641	2.373752901	0.366179882	6.482477652	9.02E-11	7.23E-09
ENSG00000109906.13	ZBTB16	110.4745926	2.351376063	0.459716103	5.114843803	3.14E-07	1.28E-05
ENSG00000159307.18	SCUBE1	181.525952	2.328096623	0.476514096	4.885682586	1.03E-06	3.71E-05
ENSG00000158292.6	GPR153	111.909364	2.313309032	0.512753603	4.511541252	6.44E-06	0.000183972
ENSG00000175048.16	ZDHHC14	607.214429	2.311958863	0.190753673	12.12012763	8.26E-34	9.12E-31
ENSG00000116016.13	EPAS1	340.8723779	2.295264009	0.334015977	6.871719226	6.34E-12	6.50E-10
ENSG00000163421.8	PROK2	311.4232022	2.269175889	0.331764906	6.839710435	7.94E-12	8.02E-10
ENSG00000177191.2	B3GNT8	80.18055274	2.267945865	0.338153886	6.706845492	1.99E-11	1.78E-09
ENSG00000150457.8	LATS2	229.1361132	2.257382044	0.23423263	9.63735088	5.56E-22	2.05E-19
ENSG00000154917.10	RAB6B	408.956532	2.243561063	0.330700953	6.784259445	1.17E-11	1.12E-09
ENSG00000158806.13	NPM2	61.28502265	2.233606486	0.341239168	6.545574768	5.93E-11	4.94E-09
ENSG00000198483.12	ANKRD35	60.34885828	2.220789661	0.450621535	4.928281249	8.30E-07	3.04E-05
ENSG00000169252.5	ADRB2	164.1725368	2.214782806	0.325173416	6.811082026	9.69E-12	9.65E-10
ENSG00000134253.9	TRIM45	139.5286997	2.184347503	0.292750183	7.461472705	8.56E-14	1.24E-11

ENSG00000162772.16	ATF3	2146.841961	2.140849138	0.564683933	3.791234376	0.0001499	0.002837268
ENSG00000177602.5	GSG2	538.087807	2.137570179	0.367183447	5.82153198	5.83E-09	3.38E-07
ENSG00000005020.12	SKAP2	1186.518067	2.080901781	0.203542883	10.22340723	1.56E-24	7.21E-22
ENSG00000139629.15	GALNT6	344.9822019	2.073691807	0.208631448	9.939497741	2.80E-23	1.18E-20
ENSG00000125657.4	TNFSF9	36.46502554	2.071937965	0.389109962	5.324813458	1.01E-07	4.56E-06
ENSG00000089692.8	LAG3	659.8636874	2.070593465	0.278519001	7.43429876	1.05E-13	1.48E-11
ENSG00000121297.6	TSHZ3	43.39832752	2.0463735	0.401914913	5.091559015	3.55E-07	1.42E-05
ENSG00000130635.15	COL5A1	2128.890246	2.043131855	0.249793709	8.179276666	2.86E-16	5.46E-14
ENSG00000140470.13	ADAMTS17	118.2575966	2.029383889	0.384747274	5.274589388	1.33E-07	5.86E-06
ENSG00000135898.9	GPR55	730.9814874	2.010285337	0.315827444	6.365138223	1.95E-10	1.49E-08
ENSG00000083457.11	ITGAE	4213.774947	1.996746142	0.278919369	7.158865113	8.13E-13	9.98E-11
ENSG00000165030.3	NFIL3	424.442677	1.965372214	0.292140577	6.727487963	1.73E-11	1.56E-09
ENSG00000065833.8	ME1	286.7951642	1.949082183	0.326382633	5.971770507	2.35E-09	1.46E-07
ENSG00000146250.6	PRSS35	138.0950663	1.94857893	0.462835647	4.210088275	2.55E-05	0.000613091
ENSG00000137501.17	SYTL2	2512.004337	1.927212634	0.195052434	9.880484907	5.06E-23	2.02E-20
ENSG00000120549.17	KIAA1217	283.8505954	1.921919533	0.229456152	8.375977349	5.48E-17	1.12E-14
ENSG00000189420.8	ZFP92	450.1593034	1.921305855	0.271307132	7.081663662	1.42E-12	1.65E-10
ENSG00000134317.17	GRHL1	34.8634498	1.908129545	0.543427274	3.511287777	0.000445941	0.006933108
ENSG00000073861.2	TBX21	1264.301842	1.899503036	0.14563072	13.04328538	6.94E-39	1.24E-35
ENSG00000109471.4	IL2	272.8474718	1.892677809	0.37803268	5.006651305	5.54E-07	2.14E-05
ENSG00000075426.11	FOSL2	2004.774737	1.879077786	0.35104658	5.352787607	8.66E-08	3.98E-06
ENSG00000115607.9	IL18RAP	1868.927744	1.877383132	0.164070229	11.44255813	2.56E-30	2.04E-27
ENSG00000112290.12	WASF1	93.83298764	1.866886409	0.496556596	3.759664909	0.000170141	0.003158488
ENSG00000076706.15	MCAM	351.4856969	1.851970143	0.277498131	6.67381124	2.49E-11	2.21E-09
ENSG00000104951.15	IL4I1	1656.752857	1.851328905	0.281555332	6.575364391	4.85E-11	4.15E-09
ENSG00000181104.6	F2R	2527.862899	1.834708366	0.200481006	9.151532131	5.61E-20	1.64E-17
ENSG00000105374.9	NKG7	170.884424	1.82485804	0.304035217	6.002127185	1.95E-09	1.24E-07
ENSG00000129521.13	EGLN3	470.0464236	1.818321795	0.626149035	2.903976039	0.003684564	0.037445812
ENSG00000152684.10	PELO	1691.493521	1.795294079	0.26066748	6.887295947	5.69E-12	5.91E-10
ENSG00000169583.12	CLIC3	303.644538	1.78827143	0.381275275	4.690237072	2.73E-06	8.74E-05
ENSG00000065361.14	ERBB3	416.9463476	1.763671485	0.291443399	6.051506032	1.43E-09	9.44E-08
ENSG00000135253.13	KCP	43.84691768	1.755421472	0.42555401	4.125026273	3.71E-05	0.000852474
ENSG00000113758.13	DBN1	167.5359191	1.753193124	0.45721721	3.834486289	0.000125827	0.002436731
ENSG00000143507.17	DUSP10	1266.576516	1.747892959	0.284730659	6.138759221	8.32E-10	5.77E-08
ENSG00000167664.8	TMIGD2	1793.038091	1.747630011	0.186338098	9.378812113	6.67E-21	2.23E-18
ENSG00000228278.3	ORM2	198.3236865	1.744040018	0.383229706	4.550899871	5.34E-06	0.000154887
ENSG00000125966.9	MMP24	768.1319808	1.719654802	0.186010583	9.244929921	2.35E-20	7.04E-18
ENSG00000107130.9	NCS1	76.07587974	1.715790957	0.494617428	3.468925394	0.000522545	0.007960206
ENSG00000074416.13	MGLL	134.0809392	1.700366996	0.45284958	3.754816327	0.000173469	0.00319715
ENSG00000117461.14	PIK3R3	77.29439521	1.694434417	0.494616997	3.425750485	0.000613103	0.009031312
ENSG00000150681.9	RGS18	220.8576355	1.693024977	0.479522306	3.530649058	0.000414541	0.006536998
ENSG00000187796.13	CARD9	127.2857791	1.691194781	0.37885365	4.463979111	8.05E-06	0.000223303
ENSG00000160183.13	TMPRSS3	404.014634	1.688474281	0.286484281	5.893776349	3.77E-09	2.28E-07
ENSG00000121797.9	CCRL2	89.76861059	1.683351368	0.289173399	5.821252482	5.84E-09	3.38E-07
ENSG00000164056.10	SPRY1	910.7642979	1.668420591	0.255203287	6.537614048	6.25E-11	5.18E-09
ENSG00000125384.6	PTGER2	686.2512533	1.661001837	0.234769515	7.075032013	1.49E-12	1.72E-10
ENSG00000010278.12	CD9	373.4205709	1.654053908	0.303756365	5.445330864	5.17E-08	2.45E-06
ENSG00000095397.13	WHRN	1065.724677	1.653500566	0.244133144	6.772945853	1.26E-11	1.18E-09

ENSG00000075702.16	WDR62	348.2990919	1.647095371	0.221154426	7.447716046	9.50E-14	1.36E-11
ENSG00000180644.6	PRF1	1193.808003	1.641068954	0.36018547	4.556177558	5.21E-06	0.000151938
ENSG00000035664.11	DAPK2	2867.684206	1.639527288	0.285394485	5.744775643	9.20E-09	5.14E-07
ENSG00000204161.13	C10orf128	818.7964231	1.634737319	0.303895751	5.379270072	7.48E-08	3.46E-06
ENSG00000196872.11	KIAA1211L	107.3875195	1.619446128	0.246701017	6.564407983	5.22E-11	4.44E-09
ENSG00000037280.15	FLT4	214.9027435	1.613060155	0.420743214	3.833835224	0.000126161	0.0024399
ENSG00000134242.15	PTPN22	3713.581509	1.596208311	0.152817588	10.44518716	1.54E-25	7.90E-23
ENSG00000160593.17	JAML	22517.40932	1.590956666	0.228017073	6.977357647	3.01E-12	3.29E-10
ENSG00000127946.16	HIP1	671.1305637	1.579699768	0.239777502	6.588190118	4.45E-11	3.87E-09
ENSG00000143434.15	SEMA6C	701.3887952	1.578103668	0.160134618	9.854856414	6.53E-23	2.47E-20
ENSG00000061337.15	LZTS1	643.5700579	1.576036265	0.305722221	5.155124998	2.53E-07	1.05E-05
ENSG00000171954.12	CYP4F22	216.9120156	1.56287614	0.202054694	7.734916251	1.03E-14	1.69E-12
ENSG00000151117.8	TMEM86A	85.9939	1.552978247	0.313177856	4.958774113	7.09E-07	2.66E-05
ENSG00000101000.5	PROCR	55.30853354	1.552798108	0.368745756	4.211026389	2.54E-05	0.000613091
ENSG00000171860.4	C3AR1	590.6581125	1.54198356	0.228426947	6.750445078	1.47E-11	1.36E-09
ENSG00000120318.15	ARAP3	1231.999615	1.537502448	0.301238089	5.103944365	3.33E-07	1.34E-05
ENSG00000198756.10	COLGALT2	383.7967943	1.528916121	0.237651968	6.433425048	1.25E-10	9.78E-09
ENSG00000072682.18	P4HA2	102.5810578	1.520259956	0.460814699	3.299070017	0.000970057	0.01312
ENSG00000063438.16	AHRR	1698.216035	1.518308778	0.284150224	5.343331271	9.13E-08	4.16E-06
ENSG00000134802.17	SLC43A3	421.994912	1.506607895	0.242473289	6.21350048	5.18E-10	3.72E-08
ENSG00000197635.9	DPP4	4274.807367	1.50159241	0.304037481	4.938839789	7.86E-07	2.91E-05
ENSG00000185340.15	GAS2L1	208.1421959	1.492331419	0.208507312	7.15721385	8.23E-13	1.00E-10
ENSG00000129654.7	FOXJ1	110.5753211	1.488217122	0.431241901	3.451003064	0.000558507	0.008445288
ENSG00000120833.13	SOCS2	124.9446246	1.477300091	0.429851941	3.436764966	0.000588706	0.00873623
ENSG00000164120.13	HPGD	166.9358189	1.470363961	0.485919876	3.025939121	0.002478622	0.027615082
ENSG00000237693.4	IRGM	68.37622708	1.466454229	0.283268395	5.176907326	2.26E-07	9.47E-06
ENSG00000138741.10	TRPC3	51.3037523	1.465006918	0.481329736	3.043665928	0.002337145	0.026324987
ENSG00000155093.17	PTPRN2	211.1496877	1.462035808	0.258353786	5.65904541	1.52E-08	8.12E-07
ENSG00000188001.9	TPRG1	242.5993994	1.450738559	0.314865902	4.607480676	4.08E-06	0.000124706
ENSG00000117016.9	RIMS3	765.908729	1.44146125	0.167477872	8.606875812	7.51E-18	1.77E-15
ENSG00000167123.18	CERCAM	86.98595395	1.429426369	0.384288874	3.719666282	0.000199486	0.003614428
ENSG00000145246.13	ATP10D	286.3144298	1.425917378	0.254445319	5.604022841	2.09E-08	1.09E-06
ENSG00000091436.16	AC013461.1	146.005475	1.420784024	0.342191171	4.152018364	3.30E-05	0.000767715
ENSG00000135318.11	NT5E	184.5958089	1.418629087	0.376829397	3.764645486	0.000166786	0.003102017
ENSG00000138670.17	RASGEF1B	1090.09913	1.413879988	0.340210904	4.155892632	3.24E-05	0.000759753
ENSG00000134247.9	PTGFRN	205.7951709	1.413594279	0.219601304	6.437094186	1.22E-10	9.60E-09
ENSG00000142949.16	PTPRF	128.907957	1.403940116	0.264593222	5.306032056	1.12E-07	5.02E-06
ENSG00000068489.12	PRR11	59.76286092	1.395661801	0.413099148	3.378515325	0.000728784	0.010323836
ENSG00000145220.13	LYAR	1260.90703	1.388858551	0.213591784	6.502396875	7.91E-11	6.41E-09
ENSG00000247595.4	SPTY2D1-AS1	28.58222479	1.380571008	0.409842365	3.368541483	0.00075567	0.010646884
ENSG00000147889.17	CDKN2A	281.7188874	1.380311497	0.272809053	5.059624964	4.20E-07	1.66E-05
ENSG00000158321.15	AUTS2	3411.165005	1.379085224	0.221891402	6.215135931	5.13E-10	3.70E-08
ENSG00000101773.17	RBBP8	175.0933682	1.365979501	0.402843744	3.390842039	0.000696782	0.01001634
ENSG00000198796.6	ALPK2	224.006633	1.363740821	0.363210444	3.754685037	0.00017356	0.00319715
ENSG00000160588.9	MPZL3	3343.070318	1.361340785	0.196357864	6.932957788	4.12E-12	4.32E-10
ENSG00000112378.11	PERP	1660.636601	1.35758301	0.160358893	8.465904103	2.54E-17	5.61E-15
ENSG00000100298.15	APOBEC3H	323.3438752	1.3561595	0.299746441	4.524355635	6.06E-06	0.000174913
ENSG00000170522.9	ELOVL6	355.7195377	1.354279223	0.225806151	5.997530256	2.00E-09	1.27E-07

ENSG00000118503.14	TNFAIP3	62877.5039	1.351669951	0.305061017	4.430818341	9.39E-06	0.000255621
ENSG00000185920.15	PTCH1	301.7230488	1.351335799	0.316518661	4.269371652	1.96E-05	0.000489209
ENSG00000138336.8	TET1	77.54695211	1.334154382	0.320833858	4.158396461	3.20E-05	0.000753938
ENSG00000174307.6	PHLDA3	555.283	1.332423484	0.226862442	5.873266065	4.27E-09	2.55E-07
ENSG00000154229.11	PRKCA	2355.338672	1.330566215	0.153616044	8.661635748	4.65E-18	1.11E-15
ENSG00000123685.8	BATF3	65.43292885	1.327896307	0.465776452	2.850930532	0.004359149	0.042524671
ENSG00000184730.10	APOBR	1923.189322	1.325699184	0.167569582	7.911335523	2.55E-15	4.46E-13
ENSG00000120129.5	DUSP1	10048.01166	1.32091203	0.299821557	4.405660634	1.05E-05	0.000282347
ENSG00000092853.13	CLSPN	53.74465946	1.31686618	0.409045219	3.219365777	0.001284745	0.016519793
ENSG00000143036.16	SLC44A3	133.3318833	1.315306587	0.357606959	3.678078834	0.000234997	0.004142766
ENSG00000160469.16	BRSK1	124.5371291	1.309932226	0.2618904	5.001833695	5.68E-07	2.18E-05
ENSG00000168917.8	SLC35G2	25.37015265	1.309547071	0.421030132	3.110340503	0.001868718	0.022016504
ENSG00000105255.10	FSD1	412.988232	1.293650219	0.262059798	4.936469576	7.95E-07	2.94E-05
ENSG00000168487.17	BMP1	835.1426568	1.292136585	0.235027112	5.497819258	3.85E-08	1.88E-06
ENSG00000196814.14	MVB12B	2203.594363	1.290827086	0.196282298	6.576380543	4.82E-11	4.14E-09
ENSG00000169554.17	ZEB2	492.4885255	1.290790131	0.328211894	3.932795108	8.40E-05	0.00172372
ENSG00000065989.15	PDE4A	1029.052271	1.290669128	0.164090658	7.865585659	3.67E-15	6.28E-13
ENSG00000115594.11	IL1R1	941.8105023	1.283640119	0.201923535	6.357060438	2.06E-10	1.55E-08
ENSG00000163040.14	CCDC74A	99.40012398	1.282964915	0.2225536	5.764745736	8.18E-09	4.62E-07
ENSG00000104490.17	NCALD	417.964228	1.278072331	0.3434822	3.720927401	0.000198492	0.00360097
ENSG00000104368.17	PLAT	430.0475301	1.277677832	0.303370485	4.211608897	2.54E-05	0.000613091
ENSG00000130202.9	NECTIN2	128.8341785	1.27767197	0.45807911	2.789195015	0.005283924	0.049013772
ENSG00000158747.13	NBL1	123.6023715	1.268091085	0.25637826	4.946172443	7.57E-07	2.81E-05
ENSG00000256235.1	SMIM3	918.6427636	1.266385914	0.170696907	7.418915409	1.18E-13	1.65E-11
ENSG00000182621.17	PLCB1	425.8716652	1.265569174	0.286272091	4.42086118	9.83E-06	0.000266174
ENSG00000173114.12	LRRN3	1483.275348	1.265442174	0.264372713	4.786583912	1.70E-06	5.71E-05
ENSG00000115009.11	CCL20	1051.81954	1.260013346	0.272130198	4.630185678	3.65E-06	0.000113476
ENSG00000088826.17	SMOX	920.5811335	1.259417756	0.185820669	6.77759779	1.22E-11	1.15E-09
ENSG00000206013.2	IFITM5	175.5237576	1.256189306	0.430854402	2.915577278	0.003550312	0.036496717
ENSG00000085563.14	ABCB1	3625.846948	1.255800033	0.18047705	6.958225602	3.45E-12	3.69E-10
ENSG00000205730.6	ITPRIPL2	325.553302	1.252426953	0.344404776	3.636497048	0.000276371	0.004726962
ENSG00000215045.8	GRID2IP	73.59028093	1.251602555	0.307706104	4.06752592	4.75E-05	0.001057115
ENSG00000124813.20	RUNX2	1712.232959	1.249099727	0.147038956	8.495025813	1.98E-17	4.44E-15
ENSG00000177606.6	JUN	42237.56453	1.246611462	0.294105324	4.238656559	2.25E-05	0.000547837
ENSG00000163754.17	GYG1	3154.365924	1.245388789	0.207203367	6.010465982	1.85E-09	1.19E-07
ENSG00000169679.14	BUB1	105.7443694	1.240897505	0.352706594	3.518214642	0.000434461	0.006798814
ENSG00000124145.6	SDC4	512.1492203	1.240031651	0.173125754	7.162606495	7.92E-13	9.79E-11
ENSG00000105767.2	CADM4	119.4982642	1.237884973	0.193267442	6.405036248	1.50E-10	1.17E-08
ENSG00000167613.15	LAIR1	505.5703063	1.214803511	0.315631226	3.848806487	0.000118695	0.002312684
ENSG00000235162.8	C12orf75	308.5874216	1.207847637	0.202706566	5.958601451	2.54E-09	1.57E-07
ENSG00000111817.16	DSE	1598.554781	1.203786634	0.189710212	6.345397135	2.22E-10	1.67E-08
ENSG00000123080.10	CDKN2C	178.9333286	1.200299301	0.204462633	5.870506908	4.34E-09	2.57E-07
ENSG00000178075.19	GRAMD1C	532.9610523	1.196059323	0.33597301	3.559986325	0.000370874	0.005966416
ENSG00000141682.11	PMAIP1	959.8103203	1.195842005	0.314048871	3.807821378	0.000140196	0.002682426
ENSG00000162073.13	PAQR4	106.8928948	1.187283001	0.422940734	2.807208919	0.004997282	0.046962015
ENSG00000050438.16	SLC4A8	75.59784485	1.180660782	0.399534039	2.955094353	0.003125734	0.033054008
ENSG00000185010.13	F8	315.2126882	1.176395476	0.238969273	4.922789706	8.53E-07	3.12E-05
ENSG00000138764.13	CCNG2	1295.200637	1.172627617	0.275130901	4.262071662	2.03E-05	0.000503718

ENSG00000008256.15	CYTH3	3674.335653	1.170344286	0.139892141	8.366047432	5.96E-17	1.20E-14
ENSG00000125462.16	C1orf61	69.88396531	1.170095512	0.286005192	4.091168782	4.29E-05	0.000968833
ENSG00000163923.9	RPL39L	139.6938207	1.170011302	0.262647973	4.454674784	8.40E-06	0.000232311
ENSG00000177374.12	HIC1	2340.244673	1.16734593	0.240225469	4.85937622	1.18E-06	4.16E-05
ENSG00000122877.14	EGR2	171.8061143	1.163654791	0.403845942	2.881432425	0.003958721	0.039642462
ENSG00000185697.16	MYBL1	1287.844298	1.162894211	0.152956952	7.60275488	2.90E-14	4.57E-12
ENSG00000145990.10	GFOD1	164.6112713	1.159560999	0.344777521	3.363215196	0.000770403	0.010806726
ENSG00000153885.14	KCTD15	127.8426321	1.159139306	0.385242781	3.008854057	0.002622351	0.028835808
ENSG00000175556.16	LONRF3	407.1900852	1.151177666	0.246413686	4.671727805	2.99E-06	9.48E-05
ENSG00000152229.18	PSTPIP2	242.0901655	1.145598807	0.321387988	3.564535236	0.000364501	0.005903608
ENSG00000119326.14	CTNNAL1	329.5579897	1.141163324	0.200726534	5.685164304	1.31E-08	7.00E-07
ENSG00000151062.14	CACNA2D4	660.0142938	1.14069219	0.150209978	7.593984144	3.10E-14	4.84E-12
ENSG00000236320.3	SLFN14	119.0442216	1.139769338	0.294992404	3.863724362	0.000111671	0.002195181
ENSG00000172602.9	RND1	74.89466369	1.139451988	0.299901861	3.799416197	0.000145037	0.002767667
ENSG00000077984.5	CST7	2701.183998	1.138175679	0.227815858	4.996033599	5.85E-07	2.24E-05
ENSG00000183963.18	SMTN	123.0637085	1.132423167	0.404962179	2.796367726	0.005168056	0.048240464
ENSG00000127951.6	FGL2	135.4970759	1.126784859	0.404389182	2.786387246	0.005329916	0.049344703
ENSG00000142046.14	TMEM91	213.8320349	1.124494686	0.186018865	6.045057233	1.49E-09	9.74E-08
ENSG00000161031.12	PGLYRP2	149.3603902	1.112301333	0.311797057	3.567388811	0.000360556	0.00585955
ENSG00000215529.12	EFCAB8	107.557233	1.111329856	0.371919535	2.988092184	0.002807249	0.030495094
ENSG00000185924.6	RTN4RL1	50.02892345	1.109621879	0.372362397	2.979951486	0.00288294	0.031203908
ENSG00000103269.13	RHBDL1	124.6365183	1.107364519	0.371868278	2.977840765	0.002902868	0.03134398
ENSG00000137804.12	NUSAP1	300.0283106	1.106542863	0.276440338	4.002827051	6.26E-05	0.00133855
ENSG00000196141.13	SPATS2L	578.5994144	1.103618247	0.239277861	4.612287335	3.98E-06	0.000122378
ENSG00000142945.12	KIF2C	89.91184596	1.101886918	0.276348397	3.987310691	6.68E-05	0.001409424
ENSG00000137801.10	THBS1	1142.627852	1.10126412	0.297380246	3.703218814	0.000212881	0.003818555
ENSG00000272899.3	RP11-309L24.4	72.68376883	1.097061937	0.23567433	4.654991223	3.24E-06	0.000102408
ENSG00000160293.16	VAV2	1307.473753	1.092489751	0.295987677	3.690997414	0.000223376	0.003972059
ENSG00000187642.9	PERM1	73.12014506	1.090431538	0.287212041	3.796608014	0.000146689	0.002783369
ENSG00000135916.15	ITM2C	3272.204145	1.088896764	0.253953032	4.287788	1.80E-05	0.000455793
ENSG00000090104.11	RGS1	8178.659776	1.086991679	0.307193906	3.538454568	0.000402477	0.006395945
ENSG00000187240.13	DYNC2H1	232.6475089	1.086344462	0.296967311	3.658128085	0.000254064	0.004413825
ENSG00000182534.13	MXRA7	1671.741691	1.086020842	0.151889186	7.150086667	8.67E-13	1.04E-10
ENSG00000020426.10	MNAT1	151.7979786	1.083020195	0.204982638	5.283472812	1.27E-07	5.61E-06
ENSG00000187583.10	PLEKHN1	582.6215848	1.080280755	0.228511769	4.727462226	2.27E-06	7.53E-05
ENSG00000124767.6	GLO1	3449.897612	1.078218035	0.163445881	6.596789267	4.20E-11	3.68E-09
ENSG00000196576.14	PLXNB2	635.025451	1.076476163	0.369225635	2.915496813	0.003551227	0.036496717
ENSG00000197852.9	FAM212B	351.3698221	1.0755027	0.350508931	3.068403126	0.002152061	0.02484252
ENSG00000176170.13	SPHK1	99.69070075	1.074385901	0.259752231	4.136195086	3.53E-05	0.000816388
ENSG00000182742.5	HOXB4	296.696961	1.072410275	0.242653241	4.419517624	9.89E-06	0.000266828
ENSG00000162783.10	IER5	5999.381823	1.071717557	0.192216157	5.575585193	2.47E-08	1.26E-06
ENSG00000170819.4	BFSP2	59.98389095	1.071205527	0.26300025	4.073020945	4.64E-05	0.001037296
ENSG00000134897.13	BIVM	264.1089987	1.067096583	0.314714814	3.390677961	0.0006972	0.01001634
ENSG00000107331.16	ABCA2	4519.645659	1.066164343	0.23735856	4.491788041	7.06E-06	0.000199903
ENSG00000151725.11	CENPU	144.3535361	1.062372642	0.252351389	4.209894168	2.55E-05	0.000613091
ENSG00000100599.15	RIN3	1075.408983	1.06205882	0.239380829	4.4366912	9.14E-06	0.000249221
ENSG00000151116.16	UEVLD	482.3941101	1.054358182	0.140545641	7.501891722	6.29E-14	9.40E-12
ENSG00000140465.13	CYP1A1	99.0770446	1.050705275	0.304975706	3.445209751	0.000570616	0.008538421

ENSG00000178053.17	MLF1	158.5858301	1.047371481	0.33389467	3.136831984	0.00170784	0.020559982
ENSG00000116741.7	RGS2	2209.761316	1.046040381	0.220901952	4.735315254	2.19E-06	7.27E-05
ENSG00000105339.10	DENND3	1529.482935	1.045896976	0.143557299	7.285571557	3.20E-13	4.28E-11
ENSG00000136193.16	SCRN1	716.847532	1.039996039	0.202227028	5.142715337	2.71E-07	1.12E-05
ENSG00000105963.13	ADAP1	273.0736729	1.039153277	0.230840901	4.50159947	6.74E-06	0.000191648
ENSG00000166483.10	WEE1	1569.931093	1.038479256	0.167755517	6.190432788	6.00E-10	4.28E-08
ENSG00000186654.20	PRR5	1003.978371	1.036723196	0.16246284	6.38129432	1.76E-10	1.35E-08
ENSG00000155265.10	GOLGA7B	420.875357	1.034990848	0.187309594	5.525562392	3.28E-08	1.62E-06
ENSG00000179820.15	MYADM	12807.3972	1.025483806	0.281351843	3.644844818	0.000267553	0.00459257
ENSG00000099282.9	TSPAN15	154.3542954	1.020112096	0.310975137	3.280365458	0.001036727	0.013826238
ENSG00000100365.14	NCF4	1766.522383	1.017622317	0.149920429	6.787749497	1.14E-11	1.11E-09
ENSG00000083444.16	PLOD1	282.8408409	1.016790975	0.280477723	3.625211168	0.000288725	0.004885861
ENSG00000155366.16	RHOC	705.6099362	1.008297871	0.182480449	5.525511791	3.29E-08	1.62E-06
ENSG00000183688.4	FAM101B	1950.079909	1.005888558	0.169678653	5.92819745	3.06E-09	1.88E-07
ENSG00000125735.10	TNFSF14	997.4799037	1.005337769	0.254655286	3.947837826	7.89E-05	0.001632964
ENSG00000232434.2	C9orf172	456.3728532	1.004721846	0.287369191	3.496275445	0.000471801	0.007264324

Table S7 B: down-regulated genes in intestinal pTh17-cells as compared to cTh17-cells

Gene_id	Gene_name	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
ENSG00000182463.15	TSHZ2	222.8105	-5.52067	0.844559	-6.53674	6.29E-11	5.19E-09
ENSG00000188404.8	SELL	1880.019	-5.13659	0.516281	-9.94923	2.54E-23	1.11E-20
ENSG00000137474.19	MYO7A	587.0363	-4.32216	1.070156	-4.03882	5.37E-05	0.001175
ENSG00000138795.9	LEF1	3288.263	-4.18867	0.309699	-13.525	1.11E-41	3.20E-38
ENSG00000156299.13	TIAM1	651.0679	-4.17785	0.316414	-13.2037	8.35E-40	2.00E-36
ENSG00000124191.17	TOX2	464.7712	-3.92137	0.767166	-5.11151	3.20E-07	1.30E-05
ENSG00000126353.3	CCR7	3444.087	-3.59887	0.277949	-12.948	2.41E-38	3.46E-35
ENSG00000183813.6	CCR4	2444.444	-3.35073	0.796769	-4.20539	2.61E-05	0.000624
ENSG00000182230.11	FAM153B	142.0927	-3.2529	0.347433	-9.36269	7.77E-21	2.54E-18
ENSG00000186310.9	NAP1L3	111.2208	-3.23471	0.299692	-10.7934	3.70E-27	2.12E-24
ENSG00000118263.14	KLF7	279.9951	-3.18771	0.457999	-6.96007	3.40E-12	3.67E-10
ENSG00000008441.16	NFIX	134.2891	-3.18391	0.521714	-6.10279	1.04E-09	7.12E-08
ENSG00000263264.1	CTB-133G6.1	417.8211	-3.17024	0.270435	-11.7227	9.75E-32	8.74E-29
ENSG00000135925.8	WNT10A	109.0592	-3.12856	0.598457	-5.22771	1.72E-07	7.42E-06
ENSG00000204219.9	TCEA3	113.1282	-3.07699	0.331143	-9.29203	1.51E-20	4.72E-18
ENSG00000141753.6	IGFBP4	2116.633	-3.07484	0.489598	-6.28033	3.38E-10	2.49E-08
ENSG00000182272.11	B4GALNT4	168.0748	-3.05532	0.267664	-11.4148	3.53E-30	2.66E-27
ENSG00000132694.18	ARHGEF11	161.6979	-3.04135	0.534799	-5.68691	1.29E-08	7.00E-07
ENSG00000160712.12	IL6R	2497.946	-3.03144	0.294124	-10.3067	6.57E-25	3.14E-22
ENSG00000104361.9	NIPAL2	69.64933	-3.00369	0.561371	-5.35064	8.76E-08	4.02E-06
ENSG00000107281.9	NPDC1	388.1337	-2.9866	0.760222	-3.9286	8.54E-05	0.001749
ENSG00000166405.14	RIC3	256.8894	-2.95868	0.286641	-10.3219	5.61E-25	2.78E-22
ENSG00000186854.10	TRABD2A	599.6396	-2.86326	0.28954	-9.88898	4.65E-23	1.91E-20
ENSG00000170989.8	S1PR1	2606.257	-2.78647	0.309678	-8.99794	2.30E-19	6.11E-17
ENSG00000092096.15	SLC22A17	71.74946	-2.77195	0.292135	-9.48861	2.34E-21	8.40E-19
ENSG00000173198.5	CYSLTR1	299.2795	-2.76435	0.646718	-4.27443	1.92E-05	0.000481
ENSG00000131398.13	KCNC3	263.9192	-2.73718	0.423702	-6.46015	1.05E-10	8.34E-09
ENSG00000072110.13	ACTN1	245.9607	-2.71376	0.424606	-6.39123	1.65E-10	1.28E-08
ENSG00000185989.10	RASA3	2434.46	-2.6948	0.237086	-11.3663	6.15E-30	4.41E-27
ENSG00000172292.14	CERS6	178.5897	-2.68294	0.392668	-6.83258	8.34E-12	8.37E-10
ENSG00000080854.14	IGSF9B	378.4805	-2.65659	0.372326	-7.13513	9.67E-13	1.13E-10
ENSG00000143869.6	GDF7	123.0776	-2.64106	0.578709	-4.56371	5.03E-06	0.000148
ENSG00000135678.11	CPM	93.11924	-2.62571	0.635661	-4.13068	3.62E-05	0.000833
ENSG00000103522.15	IL21R	728.9845	-2.55953	0.225397	-11.3557	6.95E-30	4.75E-27
ENSG00000116690.12	PRG4	77.33469	-2.49402	0.593313	-4.20355	2.63E-05	0.000627
ENSG00000165591.6	FAAH2	336.0419	-2.47446	0.278487	-8.88539	6.37E-19	1.66E-16
ENSG00000116106.11	EPHA4	735.8713	-2.44084	0.409981	-5.95354	2.62E-09	1.62E-07
ENSG00000166105.15	GLB1L3	271.9393	-2.4367	0.308797	-7.89095	3.00E-15	5.18E-13
ENSG00000181847.11	TIGIT	1477.529	-2.42331	0.266553	-9.09129	9.79E-20	2.75E-17
ENSG00000163545.8	NUAK2	488.2554	-2.40287	0.276652	-8.68552	3.77E-18	9.17E-16
ENSG00000128536.15	CDHR3	74.12517	-2.38709	0.427249	-5.58712	2.31E-08	1.19E-06
ENSG00000160856.20	FCRL3	83.05903	-2.3653	0.555152	-4.26064	2.04E-05	0.000506
ENSG00000072163.19	LIMS2	98.64089	-2.34716	0.301526	-7.78429	7.01E-15	1.16E-12
ENSG00000147408.14	CSGALNACT1	178.8126	-2.33336	0.255712	-9.12493	7.18E-20	2.06E-17
ENSG00000196422.10	PPP1R26	61.21193	-2.26499	0.584898	-3.87245	0.000108	0.002133
ENSG00000104903.4	LYL1	106.2509	-2.24988	0.309053	-7.27993	3.34E-13	4.40E-11

ENSG00000126217.20	MCF2L	135.4752	-2.204	0.417542	-5.27852	1.30E-07	5.75E-06
ENSG00000180543.4	TSPYL5	63.37924	-2.20012	0.475957	-4.62251	3.79E-06	0.000117
ENSG00000050327.14	ARHGEF5	84.13948	-2.16437	0.319014	-6.78457	1.16E-11	1.12E-09
ENSG00000132359.14	RAP1GAP2	398.1428	-2.15762	0.366304	-5.89025	3.86E-09	2.32E-07
ENSG00000102349.16	KLF8	107.8081	-2.14795	0.470692	-4.56338	5.03E-06	0.000148
ENSG00000104689.9	TNFRSF10A	593.5665	-2.12337	0.16194	-13.1121	2.81E-39	5.75E-36
ENSG00000006704.10	GTF2IRD1	107.5658	-2.09425	0.396127	-5.28681	1.24E-07	5.53E-06
ENSG00000116191.17	RALGPS2	270.7878	-2.07725	0.746185	-2.78382	0.005372	0.049513
ENSG00000139193.3	CD27	610.3281	-2.03345	0.271623	-7.4863	7.08E-14	1.04E-11
ENSG00000100600.14	LGMN	222.7363	-2.01703	0.496657	-4.06121	4.88E-05	0.001081
ENSG00000177469.12	PTRF	66.08229	-2.00702	0.585639	-3.42706	0.00061	0.009008
ENSG00000140545.14	MFGE8	364.878	-2.00208	0.295592	-6.77312	1.26E-11	1.18E-09
ENSG00000110777.11	POU2AF1	180.8359	-1.98018	0.493376	-4.01353	5.98E-05	0.001291
ENSG00000136111.12	TBC1D4	3019.28	-1.97252	0.260374	-7.57573	3.57E-14	5.51E-12
ENSG00000163082.9	SGPP2	638.2869	-1.9719	0.361166	-5.45982	4.77E-08	2.29E-06
ENSG00000138449.10	SLC40A1	190.647	-1.94724	0.309795	-6.28558	3.27E-10	2.42E-08
ENSG00000113645.14	WWC1	75.06796	-1.94237	0.499434	-3.88913	0.000101	0.002011
ENSG00000174500.12	GCSAM	183.4009	-1.93556	0.306575	-6.31351	2.73E-10	2.04E-08
ENSG00000160255.17	ITGB2	7547.879	-1.933	0.213708	-9.04505	1.50E-19	4.05E-17
ENSG00000184557.4	SOCS3	1530.297	-1.93066	0.493528	-3.91196	9.15E-05	0.001861
ENSG00000149212.11	SESN3	2247.122	-1.90943	0.341459	-5.59198	2.24E-08	1.16E-06
ENSG00000134198.9	TSPAN2	130.1179	-1.90606	0.456003	-4.17994	2.92E-05	0.000693
ENSG00000148429.14	USP6NL	138.5034	-1.89345	0.489313	-3.86962	0.000109	0.002155
ENSG00000182809.10	CRIP2	77.62271	-1.86075	0.551123	-3.3763	0.000735	0.010397
ENSG00000174837.14	ADGRE1	191.6099	-1.85322	0.377038	-4.9152	8.87E-07	3.22E-05
ENSG00000146216.11	TTBK1	104.8959	-1.85235	0.614151	-3.01612	0.00256	0.028292
ENSG00000160284.14	SPATC1L	44.75997	-1.84663	0.432282	-4.27181	1.94E-05	0.000486
ENSG00000204271.11	SPIN3	252.2056	-1.84129	0.196316	-9.37921	6.65E-21	2.23E-18
ENSG00000186265.9	BTLA	285.344	-1.84125	0.39053	-4.71476	2.42E-06	7.94E-05
ENSG00000047634.14	SCML1	404.9966	-1.83805	0.62299	-2.95037	0.003174	0.033465
ENSG00000070526.14	ST6GALNAC1	213.4245	-1.82581	0.321103	-5.68607	1.30E-08	7.00E-07
ENSG00000168824.14	NSG1	934.3938	-1.80735	0.248104	-7.28466	3.22E-13	4.28E-11
ENSG00000198780.11	FAM169A	141.8927	-1.80188	0.288112	-6.25409	4.00E-10	2.91E-08
ENSG00000181804.14	SLC9A9	575.2593	-1.80149	0.318943	-5.64831	1.62E-08	8.55E-07
ENSG00000183087.14	GAS6	193.2021	-1.78852	0.34657	-5.16063	2.46E-07	1.02E-05
ENSG00000034053.14	APBA2	1300.977	-1.75081	0.220951	-7.92395	2.30E-15	4.08E-13
ENSG00000101842.13	VSIG1	244.2266	-1.73778	0.307355	-5.65397	1.57E-08	8.33E-07
ENSG00000137507.11	LRRC32	141.6769	-1.73583	0.51779	-3.35238	0.000801	0.011163
ENSG00000155970.11	MICU3	114.1202	-1.71868	0.253252	-6.78645	1.15E-11	1.11E-09
ENSG00000100311.16	PDGFB	105.6094	-1.71534	0.407432	-4.21013	2.55E-05	0.000613
ENSG00000101004.14	NINL	243.1686	-1.70996	0.22842	-7.48605	7.10E-14	1.04E-11
ENSG00000065717.14	TLE2	105.1692	-1.70692	0.298366	-5.72088	1.06E-08	5.83E-07
ENSG00000035862.12	TIMP2	161.7639	-1.70292	0.250107	-6.80875	9.85E-12	9.74E-10
ENSG00000177383.4	MAGEF1	260.1802	-1.68051	0.2497	-6.73011	1.70E-11	1.54E-09
ENSG00000155099.7	TMEM55A	119.7184	-1.65693	0.351701	-4.71119	2.46E-06	8.02E-05
ENSG00000157570.11	TSPAN18	329.5201	-1.65169	0.332866	-4.96203	6.98E-07	2.63E-05
ENSG00000188266.13	HYKK	29.42185	-1.64998	0.462872	-3.56466	0.000364	0.005904
ENSG00000116771.5	AGMAT	120.8627	-1.63861	0.432965	-3.78463	0.000154	0.002899

ENSG00000186827.10	TNFRSF4	734.1317	-1.63009	0.522185	-3.12166	0.001798	0.021483
ENSG00000184613.10	NELL2	3117.828	-1.60464	0.345021	-4.65085	3.31E-06	0.000104
ENSG00000067840.12	PDZD4	109.1711	-1.59826	0.496512	-3.21898	0.001286	0.016527
ENSG00000110987.8	BCL7A	29.04993	-1.59574	0.470398	-3.39232	0.000693	0.009985
ENSG00000114948.12	ADAM23	1107.028	-1.59471	0.339432	-4.69818	2.62E-06	8.46E-05
ENSG00000198814.12	GK	412.2895	-1.58958	0.419308	-3.79096	0.00015	0.002837
ENSG00000172794.19	RAB37	2650.108	-1.58408	0.226418	-6.99626	2.63E-12	2.90E-10
ENSG00000135821.17	GLUL	2763.942	-1.58108	0.302394	-5.22853	1.71E-07	7.41E-06
ENSG00000196218.12	RYR1	1591.154	-1.56879	0.291474	-5.38225	7.36E-08	3.43E-06
ENSG00000203710.10	CR1	157.6703	-1.5634	0.428908	-3.64508	0.000267	0.004593
ENSG00000104427.11	ZC2HC1A	135.4937	-1.56239	0.443158	-3.52559	0.000423	0.006641
ENSG00000150347.14	ARID5B	2242.036	-1.53791	0.24541	-6.2667	3.69E-10	2.70E-08
ENSG00000170677.5	SOCS6	69.13637	-1.52374	0.355345	-4.28806	1.80E-05	0.000456
ENSG00000146776.14	ATXN7L1	880.8262	-1.51987	0.190079	-7.99597	1.29E-15	2.34E-13
ENSG00000116983.12	HPCAL4	1056.309	-1.51466	0.258026	-5.8702	4.35E-09	2.57E-07
ENSG00000143502.14	SUSD4	75.50415	-1.51366	0.243211	-6.22367	4.86E-10	3.52E-08
ENSG00000088256.8	GNA11	75.44225	-1.51347	0.45841	-3.30158	0.000961	0.013053
ENSG00000223547.9	ZNF844	148.7124	-1.5045	0.32067	-4.69174	2.71E-06	8.72E-05
ENSG00000152782.16	PANK1	149.4055	-1.50396	0.281236	-5.34767	8.91E-08	4.07E-06
ENSG00000125430.8	HS3ST3B1	308.1363	-1.50178	0.406794	-3.69174	0.000223	0.003965
ENSG00000186462.8	NAP1L2	237.3913	-1.49897	0.18732	-8.00222	1.22E-15	2.25E-13
ENSG00000154589.6	LY96	249.2703	-1.49234	0.392147	-3.80558	0.000141	0.002703
ENSG00000172824.14	CES4A	167.7661	-1.48631	0.200395	-7.41689	1.20E-13	1.65E-11
ENSG00000148053.15	NTRK2	276.1923	-1.48323	0.447985	-3.31089	0.00093	0.012674
ENSG00000152969.17	JAKMIP1	274.5123	-1.47667	0.38897	-3.79637	0.000147	0.002783
ENSG00000077782.19	FGFR1	123.9127	-1.46229	0.460389	-3.1762	0.001492	0.018553
ENSG00000164684.13	ZNF704	85.42108	-1.45831	0.428535	-3.40302	0.000666	0.00966
ENSG00000081059.19	TCF7	18321.76	-1.45038	0.188665	-7.68756	1.50E-14	2.42E-12
ENSG00000105699.16	LSR	1125.748	-1.45031	0.288805	-5.02177	5.12E-07	1.99E-05
ENSG00000221890.2	NPTXR	749.4114	-1.44795	0.273442	-5.29528	1.19E-07	5.30E-06
ENSG00000151715.7	TMEM45B	365.7654	-1.43903	0.233235	-6.16985	6.84E-10	4.86E-08
ENSG00000089159.16	PXN	2184.12	-1.42528	0.150726	-9.45607	3.20E-21	1.12E-18
ENSG00000070087.13	PFN2	101.5347	-1.41952	0.380698	-3.72872	0.000192	0.0035
ENSG00000104177.17	MYEF2	627.8424	-1.4148	0.23717	-5.96532	2.44E-09	1.52E-07
ENSG00000142303.13	ADAMTS10	425.8086	-1.41324	0.400938	-3.52484	0.000424	0.006653
ENSG00000182010.10	RTKN2	284.3838	-1.39616	0.305987	-4.56282	5.05E-06	0.000148
ENSG00000173218.14	VANGL1	108.235	-1.39583	0.440207	-3.17085	0.00152	0.018739
ENSG00000140511.11	HAPLN3	877.291	-1.36495	0.24677	-5.53127	3.18E-08	1.59E-06
ENSG00000117318.8	ID3	57.66296	-1.36245	0.320837	-4.24656	2.17E-05	0.000533
ENSG00000167371.17	PRRT2	63.36068	-1.35741	0.270534	-5.01752	5.23E-07	2.03E-05
ENSG00000181754.6	AMIGO1	532.645	-1.33517	0.261035	-5.11491	3.14E-07	1.28E-05
ENSG00000038382.17	TRIO	345.9137	-1.32236	0.28838	-4.58546	4.53E-06	0.000137
ENSG00000163864.15	NMNAT3	91.80017	-1.32185	0.471583	-2.80301	0.005063	0.047361
ENSG00000083290.19	ULK2	355.4047	-1.31923	0.300531	-4.38968	1.14E-05	0.000301
ENSG00000030419.16	IKZF2	228.9082	-1.31306	0.356966	-3.67841	0.000235	0.004143
ENSG00000167037.18	SGSM1	113.9675	-1.31274	0.229234	-5.72662	1.02E-08	5.68E-07
ENSG00000136379.11	ABHD17C	72.35161	-1.30912	0.364422	-3.59232	0.000328	0.005431
ENSG00000179242.15	CDH4	87.58347	-1.30911	0.443814	-2.94968	0.003181	0.033516

ENSG00000159640.15	ACE	769.2801	-1.30817	0.128845	-10.1531	3.21E-24	1.44E-21
ENSG00000105173.13	CCNE1	72.08675	-1.29637	0.432987	-2.99402	0.002753	0.030022
ENSG00000111879.18	FAM184A	154.7897	-1.2929	0.309126	-4.18243	2.88E-05	0.000686
ENSG00000129422.14	MTUS1	144.0066	-1.27941	0.292496	-4.37411	1.22E-05	0.00032
ENSG00000059915.16	PSD	387.3031	-1.27324	0.26341	-4.8337	1.34E-06	4.66E-05
ENSG00000054219.10	LY75	382.1652	-1.2715	0.281332	-4.51958	6.20E-06	0.000178
ENSG00000114812.12	VIPR1	414.2806	-1.2586	0.232298	-5.41804	6.03E-08	2.83E-06
ENSG00000132122.11	SPATA6	38.75707	-1.25562	0.326117	-3.85022	0.000118	0.002304
ENSG00000187231.13	SESTD1	212.8932	-1.25394	0.31279	-4.00889	6.10E-05	0.00131
ENSG00000188868.13	ZNF563	69.40821	-1.24091	0.255068	-4.865	1.14E-06	4.09E-05
ENSG00000196329.11	GIMAP5	834.2817	-1.23912	0.224048	-5.53062	3.19E-08	1.59E-06
ENSG00000196381.10	ZNF781	39.84237	-1.23675	0.399211	-3.098	0.001948	0.022823
ENSG00000174255.6	ZNF80	70.66222	-1.23303	0.312901	-3.94065	8.13E-05	0.001678
ENSG00000073849.14	ST6GAL1	4344.256	-1.22975	0.094765	-12.9769	1.65E-38	2.64E-35
ENSG00000275793.1	RIMBP3	78.9871	-1.22769	0.432235	-2.84033	0.004507	0.043668
ENSG00000101224.17	CDC25B	8090.983	-1.21867	0.180968	-6.73418	1.65E-11	1.51E-09
ENSG00000123454.10	DBH	222.3375	-1.21276	0.367531	-3.29974	0.000968	0.013114
ENSG00000266338.6	NBPF15	1690.454	-1.20557	0.167399	-7.20181	5.94E-13	7.41E-11
ENSG00000144115.16	THNSL2	40.32142	-1.19745	0.333819	-3.58712	0.000334	0.005528
ENSG00000197457.9	STMN3	1552.451	-1.19346	0.196682	-6.06797	1.30E-09	8.69E-08
ENSG00000008311.14	AASS	147.4298	-1.19069	0.277493	-4.29089	1.78E-05	0.000451
ENSG00000123453.17	SARDH	540.0202	-1.1809	0.247841	-4.76473	1.89E-06	6.33E-05
ENSG00000163235.15	TGFA	260.4263	-1.16509	0.260056	-4.48016	7.46E-06	0.000209
ENSG00000121989.14	ACVR2A	157.9084	-1.15246	0.268503	-4.29215	1.77E-05	0.000451
ENSG00000119771.14	KLHL29	85.80779	-1.15026	0.358894	-3.205	0.001351	0.017182
ENSG00000136026.13	CKAP4	397.6188	-1.13493	0.267064	-4.24967	2.14E-05	0.000528
ENSG00000109452.12	INPP4B	1811.665	-1.12944	0.148005	-7.6311	2.33E-14	3.71E-12
ENSG00000198520.10	C1orf228	378.4097	-1.12901	0.245304	-4.60251	4.17E-06	0.000127
ENSG00000104880.17	ARHGEF18	231.4287	-1.1253	0.278178	-4.04524	5.23E-05	0.001149
ENSG00000141540.10	TTYH2	641.3589	-1.12398	0.360668	-3.11637	0.001831	0.021718
ENSG00000147799.11	ARHGAP39	50.07748	-1.10762	0.352831	-3.13924	0.001694	0.020426
ENSG00000135541.20	AHI1	300.9706	-1.10421	0.184157	-5.99605	2.02E-09	1.28E-07
ENSG00000147457.13	CHMP7	4495.071	-1.10238	0.19907	-5.53766	3.07E-08	1.54E-06
ENSG00000228594.3	FNDC10	69.306	-1.09898	0.285551	-3.84864	0.000119	0.002313
ENSG00000188322.4	SBK1	419.9797	-1.09872	0.272675	-4.0294	5.59E-05	0.001216
ENSG00000104783.11	KCNN4	969.466	-1.09587	0.160184	-6.84131	7.85E-12	7.99E-10
ENSG00000133069.15	TMCC2	111.4865	-1.09075	0.365591	-2.98353	0.002849	0.03093
ENSG00000184602.5	SNN	529.6724	-1.08911	0.177245	-6.14468	8.01E-10	5.61E-08
ENSG00000145916.18	RMND5B	1002.632	-1.08776	0.128606	-8.45804	2.72E-17	5.91E-15
ENSG00000171621.13	SPSB1	656.2905	-1.07846	0.232539	-4.63777	3.52E-06	0.00011
ENSG00000101493.10	ZNF516	136.201	-1.07479	0.326325	-3.29362	0.000989	0.013327
ENSG00000066294.14	CD84	2662.887	-1.06264	0.221362	-4.80046	1.58E-06	5.40E-05
ENSG00000173258.12	ZNF483	150.0094	-1.05499	0.216234	-4.87892	1.07E-06	3.83E-05
ENSG00000125089.16	SH3TC1	2883.478	-1.05294	0.14537	-7.24322	4.38E-13	5.56E-11
ENSG00000164251.4	F2RL1	184.7892	-1.04991	0.333464	-3.1485	0.001641	0.019957
ENSG00000179144.4	GIMAP7	2495.298	-1.04706	0.341102	-3.06963	0.002143	0.024783
ENSG00000148700.14	ADD3	4972.308	-1.04679	0.124849	-8.38445	5.10E-17	1.06E-14
ENSG00000157978.11	LDLRAP1	2474.947	-1.04658	0.187879	-5.57051	2.54E-08	1.29E-06

ENSG00000171291.8	ZNF439	255.945	-1.04201	0.199087	-5.23396	1.66E-07	7.21E-06
ENSG00000140092.14	FBLN5	236.4508	-1.04201	0.228066	-4.56891	4.90E-06	0.000146
ENSG00000165821.11	SALL2	229.6505	-1.04089	0.208939	-4.98179	6.30E-07	2.40E-05
ENSG00000168646.12	AXIN2	243.0691	-1.04021	0.227683	-4.56869	4.91E-06	0.000146
ENSG00000197077.13	KIAA1671	2062.306	-1.03964	0.21203	-4.90325	9.43E-07	3.42E-05
ENSG00000091409.14	ITGA6	771.2774	-1.03356	0.23775	-4.34727	1.38E-05	0.000358
ENSG00000097096.8	SYDE2	69.17397	-1.02889	0.326126	-3.15488	0.001606	0.019569
ENSG00000197321.14	SVIL	233.0175	-1.02777	0.321268	-3.19911	0.001379	0.017414
ENSG00000183386.9	FHL3	102.1926	-1.02738	0.319454	-3.21604	0.0013	0.016643
ENSG00000116299.16	KIAA1324	787.1845	-1.02627	0.21157	-4.85075	1.23E-06	4.30E-05
ENSG00000181690.7	PLAG1	477.8552	-1.02573	0.221633	-4.62807	3.69E-06	0.000114
ENSG00000175643.8	RMI2	77.68171	-1.0224	0.360419	-2.83669	0.004558	0.043913
ENSG00000134352.19	IL6ST	3178.975	-1.0193	0.223745	-4.55563	5.22E-06	0.000152
ENSG00000167861.15	HID1	245.8288	-1.0174	0.301884	-3.37017	0.000751	0.01061
ENSG00000123600.18	METTL8	729.1607	-1.01135	0.195736	-5.16689	2.38E-07	9.96E-06
ENSG00000110665.11	C11orf21	205.1023	-1.00956	0.299689	-3.36869	0.000755	0.010647
ENSG00000134146.11	DPH6	101.551	-1.00947	0.271832	-3.71359	0.000204	0.003679
ENSG00000102109.8	PCSK1N	46.79572	-1.00858	0.360901	-2.79462	0.005196	0.048387
ENSG00000142192.20	APP	1038.177	-1.00554	0.201589	-4.98807	6.10E-07	2.33E-05

Table S8 A: up-regulated genes in intestinal pTh17-cells as compared to CCR5$^+$Th1/17-cells

Gene_id	Gene_name	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
ENSG00000181409.11	AATK	383.4450957	2.975189799	0.354441202	8.39402921	4.70E-17	2.13E-14
ENSG00000092068.19	SLC7A8	244.0343169	2.779564924	0.384184846	7.234967635	4.66E-13	1.17E-10
ENSG00000115594.11	IL1R1	941.8105023	2.682483342	0.206484049	12.99123762	1.37E-38	2.76E-35
ENSG00000129521.13	EGLN3	470.0464236	2.359275877	0.627523628	3.759660626	0.000170144	0.004904192
ENSG00000181264.8	TMEM136	92.81799674	2.337038176	0.362962349	6.438789534	1.20E-10	1.95E-08
ENSG00000131459.12	GFPT2	1068.588703	2.181049129	0.356993069	6.109499925	9.99E-10	1.36E-07
ENSG00000104267.9	CA2	391.4859723	2.150718436	0.311534703	6.903623955	5.07E-12	1.08E-09
ENSG00000130202.9	NECTIN2	128.8341785	2.000480004	0.463575703	4.315325395	1.59E-05	0.000746587
ENSG00000187796.13	CARD9	127.2857791	1.975217172	0.381998039	5.170752129	2.33E-07	1.85E-05
ENSG00000173114.12	LRRN3	1483.275348	1.923123691	0.265832465	7.234344727	4.68E-13	1.17E-10
ENSG00000104951.15	IL4I1	1656.752857	1.890693352	0.281680007	6.712202877	1.92E-11	3.75E-09
ENSG00000164056.10	SPRY1	910.7642979	1.880638409	0.255788627	7.352314406	1.95E-13	5.50E-11
ENSG00000155629.14	PIK3AP1	473.2938346	1.852788674	0.412089848	4.496079393	6.92E-06	0.0003606
ENSG00000154917.10	RAB6B	408.956532	1.836007836	0.329324359	5.5750745	2.47E-08	2.49E-06
ENSG00000140470.13	ADAMTS17	118.2575966	1.833209231	0.383681104	4.777950265	1.77E-06	0.000108776
ENSG00000120549.17	KIAA1217	283.8505954	1.816266964	0.229371426	7.918453462	2.40E-15	9.14E-13
ENSG00000130635.15	COL5A1	2128.890246	1.779929184	0.249649503	7.129712499	1.01E-12	2.44E-10
ENSG00000143502.14	SUSD4	75.50415335	1.777899278	0.30198897	5.887298735	3.93E-09	4.80E-07
ENSG00000062524.15	LTK	2387.549681	1.776961066	0.314470049	5.650652809	1.60E-08	1.67E-06
ENSG00000109906.13	ZBTB16	110.4745926	1.76831676	0.455604868	3.881250806	0.000103921	0.003284825
ENSG00000173926.5	MARCH3	172.2802721	1.725486263	0.303033777	5.694039381	1.24E-08	1.35E-06
ENSG00000178053.17	MLF1	158.5858301	1.722939464	0.341500254	5.04520698	4.53E-07	3.32E-05
ENSG00000157404.15	KIT	2195.429181	1.700315942	0.489965435	3.470277329	0.000519921	0.011589877
ENSG00000129654.7	FOXJ1	110.5753211	1.693670249	0.433679152	3.905353168	9.41E-05	0.003035413
ENSG00000134317.17	GRHL1	34.8634498	1.692861747	0.540989884	3.129192976	0.001752871	0.02928253
ENSG00000196914.8	ARHGEF12	2527.702269	1.687583167	0.185509091	9.097037544	9.28E-20	5.44E-17
ENSG00000162772.16	ATF3	2146.841961	1.679510874	0.564438555	2.975542437	0.002924709	0.042324027
ENSG00000137462.6	TLR2	215.921105	1.665623476	0.236950834	7.029405415	2.07E-12	4.78E-10
ENSG00000080573.6	COL5A3	7483.060162	1.655555147	0.48811199	3.391752673	0.000694471	0.01466731
ENSG00000134253.9	TRIM45	139.5286997	1.646244154	0.288358678	5.709015461	1.14E-08	1.26E-06
ENSG00000063438.16	AHRR	1698.216035	1.615493632	0.284298707	5.682381221	1.33E-08	1.42E-06
ENSG00000134256.12	CD101	723.351847	1.572144488	0.364362741	4.314778412	1.60E-05	0.000746587
ENSG00000187479.5	C11orf96	108.402774	1.567753037	0.422030251	3.714788295	0.000203374	0.005599329
ENSG00000071539.13	TRIP13	44.72352397	1.566317297	0.523772558	2.990453154	0.002785639	0.041034256
ENSG00000121297.6	TSHZ3	43.39832752	1.553622104	0.3934315	3.948901155	7.85E-05	0.002641943
ENSG00000215045.8	GRID2IP	73.59028093	1.51152356	0.312883432	4.830947906	1.36E-06	8.61E-05
ENSG00000140465.13	CYP1A1	99.0770446	1.493798119	0.310571464	4.809837001	1.51E-06	9.49E-05
ENSG00000029534.19	ANK1	3723.584082	1.470849826	0.138407748	10.6269327	2.23E-26	2.42E-23
ENSG00000167291.15	TBC1D16	329.0257259	1.467635414	0.236230805	6.212718178	5.21E-10	7.32E-08
ENSG00000177875.4	CCDC184	369.4784195	1.447439105	0.317701254	4.555975422	5.21E-06	0.000283183
ENSG00000186654.20	PRR5	1003.978371	1.446432824	0.1635054	8.846391791	9.04E-19	4.71E-16
ENSG00000135144.7	DTX1	867.1525706	1.439874262	0.255305458	5.63980994	1.70E-08	1.75E-06
ENSG00000275395.4	FCGBP	166.1817375	1.408864673	0.396980846	3.548948738	0.000386772	0.009315651
ENSG00000139200.13	PIANP	299.3338836	1.399399514	0.32858597	4.258853517	2.05E-05	0.000906036
ENSG00000145990.10	GFOD1	164.6112713	1.3799319	0.346966241	3.977135914	6.98E-05	0.002392946
ENSG00000100906.10	NFKBIA	21709.8045	1.366980167	0.344704492	3.965658118	7.32E-05	0.002480826

ENSG00000204161.13	C10orf128	818.7964231	1.362827194	0.303628038	4.48847611	7.17E-06	0.000372331
ENSG00000157985.18	AGAP1	111.1083272	1.350469682	0.367226716	3.677482115	0.000235548	0.006272578
ENSG00000111817.16	DSE	1598.554781	1.345742587	0.190117389	7.078482386	1.46E-12	3.47E-10
ENSG00000125266.6	EFNB2	33.14653777	1.34357353	0.453439127	2.963073654	0.003045837	0.043660893
ENSG00000196872.11	KIAA1211L	107.3875195	1.335637245	0.244415825	5.464610338	4.64E-08	4.41E-06
ENSG00000206013.2	IFITM5	175.5237576	1.31939425	0.432262278	3.052300231	0.002270948	0.03525735
ENSG00000142949.16	PTPRF	128.907957	1.315599479	0.264761293	4.969002316	6.73E-07	4.64E-05
ENSG00000182511.11	FES	583.2106114	1.311129512	0.362103379	3.620870691	0.000293613	0.007509025
ENSG00000174871.10	CNIH2	176.0716696	1.305104242	0.35853101	3.640143268	0.000272486	0.007071575
ENSG00000143845.14	ETNK2	83.50787458	1.294816317	0.26486304	4.888625895	1.02E-06	6.63E-05
ENSG00000215529.12	EFCAB8	107.557233	1.29410888	0.374322598	3.457202124	0.000545815	0.012033602
ENSG00000125726.10	CD70	216.937412	1.291461935	0.21359033	6.046443837	1.48E-09	1.95E-07
ENSG00000090104.11	RGS1	8178.659776	1.284051488	0.307261896	4.179013102	2.93E-05	0.001222017
ENSG00000119917.13	IFIT3	355.5429442	1.274417747	0.365617674	3.485656845	0.00049093	0.011155569
ENSG00000076706.15	MCAM	351.4856969	1.272828605	0.275600644	4.618380366	3.87E-06	0.000216732
ENSG00000143036.16	SLC44A3	133.3318833	1.271870096	0.357911487	3.553588364	0.000380014	0.009168559
ENSG00000137959.15	IFI44L	1291.937595	1.262920089	0.283988469	4.447082286	8.70E-06	0.000438842
ENSG00000143434.15	SEMA6C	701.3887952	1.254106922	0.159472247	7.864107653	3.72E-15	1.34E-12
ENSG00000148426.12	PROSER2	158.5767043	1.253552261	0.344197856	3.641952557	0.000270578	0.007035027
ENSG00000135898.9	GPR55	730.9814874	1.248906155	0.314647287	3.969225882	7.21E-05	0.002455811
ENSG00000050165.17	DKK3	352.1518506	1.238901247	0.283592176	4.368601654	1.25E-05	0.000608608
ENSG00000154240.16	CEP112	100.3950281	1.232301885	0.33050334	3.728561058	0.000192576	0.005406742
ENSG00000115896.15	PLCL1	1030.621067	1.226113969	0.159515504	7.686487781	1.51E-14	4.83E-12
ENSG00000170819.4	BFSP2	59.98389095	1.222705214	0.268444705	4.554774939	5.24E-06	0.00028371
ENSG00000102870.5	ZNF629	238.1443119	1.216489033	0.362524713	3.355603053	0.000791921	0.016285648
ENSG00000186603.5	HPDL	39.48564889	1.207568018	0.388551567	3.107870667	0.001884405	0.030928871
ENSG00000189420.8	ZFP92	450.1593034	1.207026535	0.269129927	4.484921276	7.29E-06	0.000377201
ENSG00000183570.16	PCBP3	160.2666008	1.198613916	0.271579225	4.413496347	1.02E-05	0.000502005
ENSG00000005020.12	SKAP2	1186.518067	1.190588728	0.200972845	5.924127354	3.14E-09	3.91E-07
ENSG00000177191.2	B3GNT8	80.18055274	1.188499883	0.323216742	3.677098761	0.000235902	0.006272578
ENSG00000102109.8	PCSK1N	46.79571924	1.181623199	0.40400298	2.924788326	0.003446906	0.047767665
ENSG00000144802.11	NFKBIZ	5872.263938	1.181051221	0.275906981	4.280613764	1.86E-05	0.000843443
ENSG00000169026.12	MFSD7	80.59086347	1.179626478	0.338080603	3.489187097	0.000484492	0.011045159
ENSG00000095397.13	WHRN	1065.724677	1.177924401	0.243605209	4.835382659	1.33E-06	8.49E-05
ENSG00000115009.11	CCL20	1051.81954	1.175672372	0.272076003	4.321117474	1.55E-05	0.000732758
ENSG00000083457.11	ITGAE	4213.774947	1.168396352	0.278680568	4.192600733	2.76E-05	0.001164878
ENSG00000155265.10	GOLGA7B	420.875357	1.166098464	0.188217713	6.19547674	5.81E-10	8.09E-08
ENSG00000041515.15	MYO16	493.7847694	1.150980691	0.349799832	3.290398063	0.001000457	0.019461089
ENSG00000165030.3	NFIL3	424.442677	1.148537465	0.288908169	3.975441299	7.02E-05	0.002404186
ENSG00000177602.5	GSG2	538.087807	1.137758967	0.365350146	3.114160426	0.001844692	0.030490519
ENSG00000198816.6	ZNF358	128.1982335	1.136460278	0.240496583	4.725473695	2.30E-06	0.000136256
ENSG00000167613.15	LAIR1	505.5703063	1.131412909	0.315672402	3.584136283	0.000338195	0.008321005
ENSG00000174885.12	NLRP6	2216.949326	1.127625316	0.219995085	5.12568412	2.96E-07	2.30E-05
ENSG00000184545.10	DUSP8	517.8817338	1.127050765	0.339009295	3.324542372	0.000885638	0.017770871
ENSG00000221869.4	CEBPD	1000.596222	1.124977469	0.349569281	3.218181719	0.001290061	0.023293956
ENSG00000076604.14	TRAF4	1981.345944	1.122626532	0.165018181	6.803047556	1.02E-11	2.09E-09
ENSG00000198846.5	TOX	645.3171028	1.119776942	0.259788536	4.310340084	1.63E-05	0.000756703
ENSG00000114631.10	PODXL2	187.3264063	1.119270236	0.260969339	4.288895542	1.80E-05	0.000822718

ENSG00000137965.10	IFI44	2138.318469	1.116977022	0.165546693	6.747202264	1.51E-11	2.99E-09
ENSG00000092445.11	TYRO3	65.40373641	1.115739104	0.34570656	3.227416638	0.001249134	0.022759486
ENSG00000224383.7	PRR29	140.9010225	1.099473326	0.272102828	4.040653809	5.33E-05	0.001947406
ENSG00000115828.15	QPCT	202.2823274	1.092917475	0.28845134	3.788914542	0.000151307	0.004480597
ENSG00000166963.12	MAP1A	202.9152374	1.092793341	0.352392549	3.101068234	0.001928239	0.031464737
ENSG00000178860.8	MSC	579.5898228	1.09121058	0.278468256	3.91861749	8.91E-05	0.002899755
ENSG00000162783.10	IER5	5999.381823	1.086731974	0.192249467	5.652717752	1.58E-08	1.66E-06
ENSG00000080823.21	MOK	93.09216748	1.084427993	0.302017235	3.59061625	0.000329897	0.008179968
ENSG00000104856.13	RELB	2239.78101	1.083883629	0.189206755	5.728567302	1.01E-08	1.15E-06
ENSG00000157077.14	ZFYVE9	261.5064717	1.08148924	0.227981556	4.743757612	2.10E-06	0.000126107
ENSG00000280649.1	AC245100.1	272.8714576	1.078213228	0.266694218	4.042881899	5.28E-05	0.001947406
ENSG00000136193.16	SCRN1	716.847532	1.077105834	0.202508148	5.318827154	1.04E-07	9.12E-06
ENSG00000079819.17	EPB41L2	416.8071596	1.076652249	0.235452018	4.57270343	4.81E-06	0.000267683
ENSG00000120129.5	DUSP1	10048.01166	1.074853487	0.299804182	3.585185102	0.000336839	0.008312246
ENSG00000111012.9	CYP27B1	144.1493606	1.068011506	0.357421897	2.98809758	0.002807199	0.041260254
ENSG00000180530.10	NRIP1	2277.277508	1.063802489	0.168049078	6.330308396	2.45E-10	3.66E-08
ENSG00000140859.15	KIFC3	392.8760988	1.058399063	0.355108001	2.980499059	0.002877791	0.041826552
ENSG00000160469.16	BRSK1	124.5371291	1.057465982	0.2604776	4.059719458	4.91E-05	0.001837996
ENSG00000138670.17	RASGEF1B	1090.09913	1.054143716	0.339627993	3.1038187	0.001910404	0.031209915
ENSG00000138185.17	ENTPD1	249.8661569	1.053571594	0.354406789	2.972774867	0.002951208	0.042488942
ENSG00000028277.21	POU2F2	2631.592039	1.051892528	0.173302366	6.069695152	1.28E-09	1.72E-07
ENSG00000007038.10	PRSS21	81.10051205	1.043840584	0.338267107	3.085847136	0.002029731	0.032666135
ENSG00000131080.14	EDA2R	69.47381668	1.040038601	0.273876527	3.797472572	0.000146179	0.004356256
ENSG00000158806.13	NPM2	61.28502265	1.039471092	0.321217552	3.236034535	0.001212027	0.022461627
ENSG00000182621.17	PLCB1	425.8716652	1.036996674	0.285612277	3.630784659	0.000282561	0.007292663
ENSG00000120278.15	PLEKHG1	971.3104204	1.032690303	0.242374043	4.260729781	2.04E-05	0.000901288
ENSG00000175866.15	BAIAP2	299.9268836	1.029565369	0.22678412	4.539847718	5.63E-06	0.000299941
ENSG00000160183.13	TMPRSS3	404.014634	1.028619411	0.284051804	3.621238785	0.000293196	0.007509025
ENSG00000122644.12	ARL4A	1377.006956	1.024817947	0.254946587	4.019735895	5.83E-05	0.002090646
ENSG00000256235.1	SMIM3	918.6427636	1.023554189	0.170412097	6.006347003	1.90E-09	2.45E-07
ENSG00000233276.3	GPX1	4436.952322	1.022534539	0.173641364	5.88877278	3.89E-09	4.80E-07
ENSG00000206560.11	ANKRD28	2762.349288	1.021768571	0.120073191	8.509547925	1.75E-17	8.47E-15
ENSG00000125384.6	PTGER2	686.2512533	1.021185445	0.233246555	4.378137301	1.20E-05	0.000584608
ENSG00000087074.7	PPP1R15A	39259.60792	1.020402754	0.328196962	3.109117004	0.001876474	0.030834675
ENSG00000130522.5	JUND	18200.86017	1.019601807	0.266533758	3.825413392	0.000130553	0.003940678
ENSG00000137269.14	LRRC1	171.3676335	1.01917779	0.321967766	3.165465293	0.001548351	0.026921026
ENSG00000176834.13	VSIG10	114.6993511	1.018001675	0.24995354	4.072763584	4.65E-05	0.001752468
ENSG00000231672.6	DIRC3	209.250281	1.016053008	0.199116768	5.102799834	3.35E-07	2.54E-05
ENSG00000187017.15	ESPN	754.6384761	1.007888108	0.240494744	4.190894538	2.78E-05	0.00117016
ENSG00000112667.12	DNPH1	1338.357514	1.004107591	0.144735312	6.937543958	3.99E-12	8.81E-10
ENSG00000137501.17	SYTL2	2512.004337	1.00296389	0.193620798	5.18004212	2.22E-07	1.78E-05
ENSG00000149573.8	MPZL2	456.076042	1.001792522	0.226330311	4.426241095	9.59E-06	0.000478291
ENSG00000159335.15	PTMS	742.8548316	1.00121279	0.293233163	3.414391398	0.000639247	0.013706775

Table S8 B: down-regulated genes in intestinal pTh17-cells as compared to CCR5^{+}Th1/17-cells

Gene_id	Gene_name	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
ENSG00000186810.7	CXCR3	3506.145553	-5.016918705	0.24545557	-20.43921314	7.49E-93	1.05E-88
ENSG00000152969.17	JAKMIP1	274.5123134	-4.508481848	0.375178923	-12.01688466	2.90E-33	4.53E-30
ENSG00000137474.19	MYO7A	587.0363055	-4.450845987	1.070161698	-4.159040633	3.20E-05	0.001303819
ENSG00000138795.9	LEF1	3288.262823	-4.155384431	0.309740712	-13.41568698	4.89E-41	1.15E-37
ENSG00000141753.6	IGFBP4	2116.632654	-3.859020323	0.489362195	-7.885816194	3.12E-15	1.16E-12
ENSG00000116574.5	RHOU	388.8021531	-3.802126941	0.215035281	-17.6814099	5.83E-70	4.10E-66
ENSG00000196126.10	HLA-DRB1	241.3433864	-3.583711837	0.71828315	-4.989274543	6.06E-07	4.28E-05
ENSG00000166105.15	GLB1L3	271.9393087	-3.475727143	0.304929114	-11.39847585	4.26E-30	5.99E-27
ENSG00000169413.2	RNASE6	367.1705435	-3.406598874	1.039306316	-3.277762121	0.001046335	0.020106219
ENSG00000136250.11	AOAH	446.567238	-3.35057819	0.670391937	-4.997939273	5.79E-07	4.14E-05
ENSG00000116106.11	EPHA4	735.8712913	-3.297736814	0.408863925	-8.065609634	7.29E-16	3.01E-13
ENSG00000109956.12	B3GAT1	137.9765636	-3.173512282	0.407175758	-7.793961739	6.49E-15	2.17E-12
ENSG00000205336.11	ADGRG1	210.4771515	-3.152702352	0.754698335	-4.177433824	2.95E-05	0.00122689
ENSG00000156299.13	TIAM1	651.0678922	-3.133925446	0.317893905	-9.858400549	6.30E-23	4.93E-20
ENSG00000158714.10	SLAMF8	244.7066899	-3.116383259	0.850757774	-3.663067627	0.000249213	0.006539974
ENSG00000131398.13	KCNC3	263.9191631	-3.082461637	0.423197765	-7.283737978	3.25E-13	8.62E-11
ENSG00000261371.5	PECAM1	183.8964229	-3.051276649	0.479210214	-6.367303027	1.92E-10	3.04E-08
ENSG00000135821.17	GLUL	2763.941929	-3.046510874	0.301821953	-10.09373519	5.89E-24	5.92E-21
ENSG00000149328.14	GLB1L2	823.2495193	-2.984487486	0.327704903	-9.10724087	8.45E-20	5.17E-17
ENSG00000166833.19	NAV2	96.4929618	-2.983146121	0.423563223	-7.042977198	1.88E-12	4.41E-10
ENSG00000204287.13	HLA-DRA	383.494382	-2.964503474	0.974890096	-3.040859155	0.002359042	0.036139901
ENSG00000137936.16	BCAR3	115.1486374	-2.947188633	0.898274686	-3.280943655	0.001034604	0.019935262
ENSG00000179583.18	CIITA	401.2020559	-2.888595937	0.658728055	-4.385111452	1.16E-05	0.000568161
ENSG00000134198.9	TSPAN2	130.1179239	-2.848120844	0.450873887	-6.316890209	2.67E-10	3.91E-08
ENSG00000124191.17	TOX2	464.7711582	-2.800585403	0.768230674	-3.645500628	0.000266872	0.006964412
ENSG00000173905.8	GOLIM4	247.3231924	-2.800157572	0.377701625	-7.413676254	1.23E-13	3.60E-11
ENSG00000135114.12	OASL	953.7065508	-2.799723216	0.586595188	-4.772836999	1.82E-06	0.00011109
ENSG00000103522.15	IL21R	728.9844763	-2.765652079	0.22521958	-12.27980304	1.16E-34	2.04E-31
ENSG00000172236.16	TPSAB1	514.6752259	-2.748354547	0.903657453	-3.041367652	0.002355061	0.036136634
ENSG00000120885.20	CLU	1543.245803	-2.727955467	0.278274436	-9.803112006	1.09E-22	8.08E-20
ENSG00000148053.15	NTRK2	276.1923049	-2.722437409	0.445047331	-6.117186236	9.52E-10	1.31E-07
ENSG00000172292.14	CERS6	178.5896585	-2.717651953	0.392928373	-6.916405475	4.63E-12	1.00E-09
ENSG00000223865.10	HLA-DPB1	461.6839124	-2.681578961	0.412031828	-6.508184021	7.61E-11	1.32E-08
ENSG00000196218.12	RYR1	1591.154078	-2.630572226	0.290744347	-9.047715823	1.46E-19	7.90E-17
ENSG00000118263.14	KLF7	279.9951417	-2.595324516	0.459631301	-5.646535623	1.64E-08	1.69E-06
ENSG00000144354.13	CDCA7	1083.082527	-2.559776941	0.328286608	-7.797384606	6.32E-15	2.17E-12
ENSG00000107281.9	NPDC1	388.1337076	-2.546572864	0.760754316	-3.347431371	0.000815642	0.016651404
ENSG00000166503.8	RP11-382A20.3	363.8139886	-2.492150852	0.382305438	-6.518742879	7.09E-11	1.26E-08
ENSG00000146216.11	TTBK1	104.8958679	-2.466818531	0.61043658	-4.04107259	5.32E-05	0.001947406
ENSG00000128656.13	CHN1	969.5033405	-2.418306647	0.266758912	-9.065513995	1.24E-19	6.98E-17
ENSG00000160255.17	ITGB2	7547.878738	-2.387118458	0.213651459	-11.17295652	5.53E-29	6.48E-26
ENSG00000173482.16	PTPRM	2122.60124	-2.376196951	0.210688308	-11.27825733	1.68E-29	2.15E-26
ENSG00000100292.16	HMOX1	336.0806204	-2.33528172	0.763813862	-3.05739636	0.002232688	0.034894438
ENSG00000088992.17	TESC	204.5903518	-2.268270574	0.359815989	-6.303973818	2.90E-10	4.21E-08
ENSG00000173218.14	VANGL1	108.2349708	-2.2638974	0.435728939	-5.195655367	2.04E-07	1.65E-05

ENSG00000100311.16	PDGFB	105.6093737	-2.233695782	0.404916934	-5.516429648	3.46E-08	3.36E-06
ENSG00000119408.16	NEK6	134.1551548	-2.224047958	0.345420279	-6.438672225	1.21E-10	1.95E-08
ENSG00000067840.12	PDZD4	109.1711369	-2.192460082	0.493942339	-4.438696402	9.05E-06	0.000453042
ENSG00000003096.13	KLHL13	39.30566191	-2.176481272	0.488962543	-4.451222907	8.54E-06	0.000433571
ENSG00000184613.10	NELL2	3117.827838	-2.155645462	0.344875227	-6.250508284	4.09E-10	5.81E-08
ENSG00000079308.16	TNS1	108.783084	-2.155054838	0.537070617	-4.012609832	6.01E-05	0.002143856
ENSG00000050327.14	ARHGEF5	84.1394807	-2.143155029	0.320259909	-6.691924189	2.20E-11	4.24E-09
ENSG00000186854.10	TRABD2A	599.6395865	-2.138468051	0.290871705	-7.351928754	1.95E-13	5.50E-11
ENSG00000197943.9	PLCG2	375.5659257	-2.114479825	0.304509716	-6.943882948	3.81E-12	8.65E-10
ENSG00000178773.14	CPNE7	2766.038802	-2.073402952	0.20585602	-10.0721026	7.34E-24	6.45E-21
ENSG00000160856.20	FCRL3	83.05903278	-2.058712952	0.55750838	-3.692703153	0.000221883	0.005967506
ENSG00000159307.18	SCUBE1	181.525952	-2.046757618	0.444550591	-4.604105045	4.14E-06	0.00023122
ENSG00000102349.16	KLF8	107.8081117	-2.01992773	0.471892154	-4.280485942	1.86E-05	0.000843443
ENSG00000110777.11	POU2AF1	180.8358715	-1.992797273	0.493730686	-4.036202996	5.43E-05	0.001979561
ENSG00000013619.13	MAMLD1	215.4930986	-1.980771587	0.421551934	-4.698760525	2.62E-06	0.000153404
ENSG00000135925.8	WNT10A	109.0591507	-1.946515992	0.603786039	-3.223850614	0.001264794	0.022955596
ENSG00000198915.11	RASGEF1A	175.4470248	-1.934009785	0.269670732	-7.17174523	7.40E-13	1.83E-10
ENSG00000168994.13	PXDC1	93.91150066	-1.924367591	0.426889243	-4.507884946	6.55E-06	0.000342379
ENSG00000118402.5	ELOVL4	199.2896925	-1.921178607	0.383273551	-5.012552009	5.37E-07	3.87E-05
ENSG00000131746.12	TNS4	72.08035919	-1.905507395	0.484288165	-3.934656126	8.33E-05	0.002777065
ENSG00000187808.4	SOWAHD	104.834542	-1.898930548	0.574251317	-3.306793546	0.000943704	0.018801902
ENSG00000164687.10	FABP5	162.6796161	-1.887369955	0.340155843	-5.548544866	2.88E-08	2.85E-06
ENSG00000159640.15	ACE	769.2800904	-1.882441295	0.127383634	-14.77773276	2.04E-49	9.56E-46
ENSG00000115956.9	PLEK	519.6499175	-1.869089491	0.386604335	-4.834631488	1.33E-06	8.49E-05
ENSG00000186265.9	BTLA	285.3439909	-1.86082337	0.390696135	-4.762840491	1.91E-06	0.000116234
ENSG00000184524.5	CEND1	100.9928291	-1.842308286	0.512460467	-3.59502519	0.00032436	0.008089451
ENSG00000198794.11	SCAMP5	52.36204821	-1.84124327	0.434878266	-4.23392801	2.30E-05	0.001003161
ENSG00000087589.16	CASS4	433.5445652	-1.836138391	0.276688047	-6.636131955	3.22E-11	6.11E-09
ENSG00000172794.19	RAB37	2650.108297	-1.818544005	0.226357155	-8.033958566	9.44E-16	3.79E-13
ENSG00000177301.13	KCNA2	212.1829439	-1.811997032	0.345880591	-5.238793609	1.62E-07	1.35E-05
ENSG00000185989.10	RASA3	2434.460044	-1.794234691	0.237590056	-7.551808864	4.29E-14	1.34E-11
ENSG00000182230.11	FAM153B	142.0926762	-1.776324329	0.357763227	-4.965083601	6.87E-07	4.71E-05
ENSG00000128578.9	STRIP2	81.73256111	-1.76883365	0.493536726	-3.583995994	0.000338377	0.008321005
ENSG00000231389.7	HLA-DPA1	1415.130707	-1.756878202	0.350438028	-5.013377721	5.35E-07	3.87E-05
ENSG00000189233.11	NUGGC	410.5858975	-1.750570651	0.313597359	-5.582223828	2.37E-08	2.40E-06
ENSG00000124496.12	TRERF1	5279.964623	-1.743607534	0.175148226	-9.955039637	2.40E-23	1.98E-20
ENSG00000169715.14	MT1E	151.4242208	-1.732834712	0.482645362	-3.590285637	0.000330316	0.008179968
ENSG00000168734.13	PKIG	288.0858068	-1.714649209	0.442706621	-3.873104959	0.000107458	0.003373878
ENSG00000184916.8	JAG2	234.6186293	-1.70805441	0.321838108	-5.307185092	1.11E-07	9.67E-06
ENSG00000181804.14	SLC9A9	575.2592584	-1.702955123	0.319198584	-5.335096116	9.55E-08	8.50E-06
ENSG00000125430.8	HS3ST3B1	308.1363347	-1.673009013	0.406662328	-4.114000482	3.89E-05	0.001527853
ENSG00000018408.14	WWTR1	170.6909749	-1.662592467	0.37288365	-4.458743272	8.24E-06	0.000420153
ENSG00000105707.13	HPN	63.32121681	-1.656231479	0.395459417	-4.188119959	2.81E-05	0.001181018
ENSG00000180543.4	TSPYL5	63.37923821	-1.645517895	0.481108283	-3.420265151	0.000625601	0.013517216
ENSG00000170989.8	S1PR1	2606.256623	-1.63371688	0.310190969	-5.266809942	1.39E-07	1.18E-05
ENSG00000105369.9	CD79A	136.8942599	-1.607617233	0.497503444	-3.231369051	0.001231988	0.022652467
ENSG00000163545.8	NUAK2	488.2553937	-1.59215504	0.279227322	-5.702003046	1.18E-08	1.30E-06
ENSG00000188322.4	SBK1	419.9796616	-1.589177484	0.271573539	-5.851739056	4.86E-09	5.90E-07

ENSG00000128268.11	MGAT3	149.5431002	-1.574498257	0.497203214	-3.166709731	0.001541741	0.026839273
ENSG00000165959.11	CLMN	63.1609524	-1.571186436	0.42149555	-3.727646562	0.000193276	0.005412039
ENSG00000101004.14	NINL	243.1685648	-1.564706809	0.229401363	-6.820826116	9.05E-12	1.87E-09
ENSG00000131370.15	SH3BP5	288.5203935	-1.561029212	0.274545373	-5.68586967	1.30E-08	1.40E-06
ENSG00000188404.8	SELL	1880.019099	-1.541249272	0.519059792	-2.969309691	0.002984696	0.042927135
ENSG00000204257.14	HLA-DMA	139.1572244	-1.537771126	0.384415949	-4.000279208	6.33E-05	0.002219264
ENSG00000126353.3	CCR7	3444.087397	-1.529230475	0.278792891	-5.485184609	4.13E-08	3.98E-06
ENSG00000179388.8	EGR3	39.17160089	-1.525980701	0.498911571	-3.058619583	0.002223593	0.034790947
ENSG00000133069.15	TMCC2	111.486512	-1.513629476	0.362905274	-4.170866574	3.03E-05	0.001251682
ENSG00000080854.14	IGSF9B	378.4804582	-1.513607671	0.375432778	-4.031634316	5.54E-05	0.002013231
ENSG00000204475.9	NCR3	157.3098228	-1.511015621	0.420392087	-3.594300815	0.000325264	0.008097631
ENSG00000188886.3	ASTL	92.22831065	-1.510670329	0.361052765	-4.184070792	2.86E-05	0.001198686
ENSG00000081985.10	IL12RB2	1298.149315	-1.497941183	0.234052604	-6.400019308	1.55E-10	2.48E-08
ENSG00000127124.14	HIVEP3	756.8238305	-1.485186525	0.199000764	-7.463220234	8.44E-14	2.58E-11
ENSG00000186310.9	NAP1L3	111.2207774	-1.470645746	0.31357552	-4.689925244	2.73E-06	0.000159515
ENSG00000176438.12	SYNE3	2013.110323	-1.469814654	0.103709762	-14.17238481	1.36E-45	4.78E-42
ENSG00000212916.4	MAP10	94.7686769	-1.461359419	0.353562177	-4.133245903	3.58E-05	0.001436194
ENSG00000064666.14	CNN2	7672.338531	-1.457949959	0.17784823	-8.197719808	2.45E-16	1.04E-13
ENSG00000100027.14	YPEL1	228.5210828	-1.448721225	0.241273622	-6.004474147	1.92E-09	2.45E-07
ENSG00000142512.14	SIGLEC10	26.45546591	-1.443429006	0.46375855	-3.112457996	0.001855364	0.030611812
ENSG00000020129.15	NCDN	6240.305513	-1.44175013	0.23954946	-6.018590614	1.76E-09	2.29E-07
ENSG00000152782.16	PANK1	149.4054625	-1.431769996	0.282560167	-5.067133184	4.04E-07	2.99E-05
ENSG00000104689.9	TNFRSF10A	593.5665061	-1.387741542	0.164030049	-8.460288528	2.67E-17	1.25E-14
ENSG00000184792.15	OSBP2	137.0952099	-1.347245206	0.310869294	-4.33379955	1.47E-05	0.000698627
ENSG00000197077.13	KIAA1671	2062.305551	-1.343875039	0.21191424	-6.341598544	2.27E-10	3.48E-08
ENSG00000141161.11	UNC45B	30.77584911	-1.34128397	0.410381009	-3.268387035	0.001081623	0.020509565
ENSG00000143153.12	ATP1B1	66.33906783	-1.337393775	0.443644721	-3.014560329	0.00257352	0.03867429
ENSG00000175471.19	MCTP1	120.1444568	-1.334463814	0.302077074	-4.417626914	9.98E-06	0.00049599
ENSG00000149212.11	SESN3	2247.121847	-1.33306805	0.341741116	-3.900812601	9.59E-05	0.003074716
ENSG00000263264.1	CTB-133G6.1	417.8211195	-1.319106435	0.275757164	-4.783579931	1.72E-06	0.000106236
ENSG00000034053.14	APBA2	1300.977216	-1.315517095	0.221376902	-5.942431591	2.81E-09	3.53E-07
ENSG00000178075.19	GRAMD1C	532.9610523	-1.315280993	0.328683457	-4.001664712	6.29E-05	0.002211822
ENSG00000158050.4	DUSP2	1094.539162	-1.311764645	0.290310628	-4.518486469	6.23E-06	0.000330595
ENSG00000139193.3	CD27	610.3281062	-1.298394911	0.27326233	-4.75145957	2.02E-06	0.000121918
ENSG00000122547.10	EEPD1	318.4625072	-1.295319423	0.377584018	-3.430546216	0.000602367	0.013095671
ENSG00000035664.11	DAPK2	2867.684206	-1.291985793	0.283532208	-4.556751418	5.20E-06	0.000283183
ENSG00000073849.14	ST6GAL1	4344.255685	-1.281621587	0.094796036	-13.51978039	1.20E-41	3.36E-38
ENSG00000204396.10	VWA7	46.2672434	-1.281410532	0.379236469	-3.37892222	0.000727706	0.015186813
ENSG00000229474.6	PATL2	1210.382454	-1.275352442	0.192720784	-6.617617543	3.65E-11	6.76E-09
ENSG00000132718.8	SYT11	2840.871743	-1.272844057	0.278495458	-4.570430216	4.87E-06	0.000268481
ENSG00000180644.6	PRF1	1193.808003	-1.264542415	0.357479947	-3.537379999	0.000404118	0.009537451
ENSG00000104447.11	TRPS1	1143.233701	-1.261044727	0.371687363	-3.392756531	0.000691931	0.014657685
ENSG00000126822.16	PLEKHG3	974.1328732	-1.260663971	0.234009451	-5.387235294	7.15E-08	6.41E-06
ENSG00000105963.13	ADAP1	273.0736729	-1.260547079	0.217018574	-5.808475546	6.30E-09	7.33E-07
ENSG00000129116.17	PALLD	117.5409399	-1.258626331	0.428566867	-2.936826034	0.003315901	0.046363278
ENSG00000078900.14	TP73	76.31631325	-1.254184292	0.397180765	-3.15771659	0.001590101	0.027443381
ENSG00000173208.3	ABCD2	923.4670176	-1.25100413	0.239563972	-5.222004459	1.77E-07	1.46E-05
ENSG00000083290.19	ULK2	355.4047356	-1.243456872	0.301008653	-4.130967196	3.61E-05	0.001443524

ENSG00000100298.15	APOBEC3H	323.3438752	-1.241533067	0.289751067	-4.284826553	1.83E-05	0.000832497
ENSG00000112303.13	VNN2	178.7672811	-1.227047669	0.284125682	-4.318679189	1.57E-05	0.000738421
ENSG00000186350.9	RXRA	487.6140809	-1.221028773	0.262370683	-4.653830838	3.26E-06	0.000185548
ENSG00000168824.14	NSG1	934.3937716	-1.220636715	0.248893436	-4.904254352	9.38E-07	6.25E-05
ENSG00000120738.7	EGR1	211.0466596	-1.220423489	0.373071164	-3.271288713	0.001070586	0.020377342
ENSG00000127311.9	HELB	1941.066956	-1.213781564	0.301328905	-4.028095362	5.62E-05	0.002038502
ENSG00000136379.11	ABHD17C	72.3516146	-1.20765018	0.366279323	-3.297074404	0.000976976	0.019241358
ENSG00000116133.11	DHCR24	1341.550541	-1.206735713	0.32811283	-3.677807156	0.000235248	0.006272578
ENSG00000066294.14	CD84	2662.886891	-1.199149561	0.22132791	-5.417977156	6.03E-08	5.53E-06
ENSG00000140939.14	NOL3	126.4690277	-1.182283463	0.285606399	-4.139555228	3.48E-05	0.001406518
ENSG00000069702.10	TGFBR3	1066.622625	-1.173527676	0.157573118	-7.447511951	9.51E-14	2.85E-11
ENSG00000140545.14	MFGE8	364.8779521	-1.171917417	0.298252014	-3.929285844	8.52E-05	0.00281977
ENSG00000187231.13	SESTD1	212.8931636	-1.161435774	0.313630651	-3.703196001	0.0002129	0.00579237
ENSG00000127824.13	TUBA4A	8158.383115	-1.151056807	0.221140267	-5.205098198	1.94E-07	1.58E-05
ENSG00000139679.15	LPAR6	960.5100264	-1.148466657	0.302739607	-3.793579135	0.000148491	0.00441581
ENSG00000122188.12	LAX1	1257.471509	-1.120644789	0.276961196	-4.046215879	5.21E-05	0.001926755
ENSG00000116991.10	SIPA1L2	316.5242009	-1.116322091	0.361940361	-3.084270811	0.002040518	0.032679443
ENSG00000198743.6	SLC5A3	2551.916505	-1.113174294	0.227737866	-4.887963139	1.02E-06	6.63E-05
ENSG00000091831.21	ESR1	193.4932578	-1.102028031	0.235398847	-4.681535388	2.85E-06	0.000164818
ENSG00000172716.16	SLFN11	1334.854795	-1.091667383	0.273531196	-3.991016013	6.58E-05	0.002273526
ENSG00000105409.16	ATP1A3	653.2979906	-1.089162189	0.212943603	-5.11479177	3.14E-07	2.41E-05
ENSG00000146904.8	EPHA1	792.9075898	-1.079517153	0.281413242	-3.836056707	0.000125026	0.003814771
ENSG00000006756.15	ARSD	131.2600096	-1.079360777	0.275862834	-3.912671966	9.13E-05	0.002958413
ENSG00000142687.17	KIAA0319L	8287.960973	-1.06649822	0.271859862	-3.922970499	8.75E-05	0.002855103
ENSG00000266338.6	NBPF15	1690.45372	-1.063700398	0.167607753	-6.34636752	2.20E-10	3.41E-08
ENSG00000153094.21	BCL2L11	2611.840785	-1.061997567	0.184408304	-5.758946563	8.46E-09	9.76E-07
ENSG00000114948.12	ADAM23	1107.027954	-1.057289567	0.339898762	-3.110601403	0.001867068	0.030715995
ENSG00000239713.7	APOBEC3G	1819.766815	-1.047874778	0.135836898	-7.714213105	1.22E-14	3.98E-12
ENSG00000092964.17	DPYSL2	360.7518462	-1.044109735	0.278540941	-3.748496472	0.000177898	0.005075682
ENSG00000159216.18	RUNX1	5640.64563	-1.043394098	0.112316223	-9.28978978	1.55E-20	1.04E-17
ENSG00000243811.7	APOBEC3D	711.3594969	-1.025286722	0.224275386	-4.571552596	4.84E-06	0.000268098
ENSG00000271503.5	CCL5	11501.23145	-1.01612484	0.297279876	-3.418074752	0.000630658	0.013584737
ENSG00000146776.14	ATXN7L1	880.8261701	-1.015935897	0.190973279	-5.319780354	1.04E-07	9.12E-06
ENSG00000204219.9	TCEA3	113.1281689	-1.013888528	0.347189185	-2.920276816	0.003497206	0.048164365
ENSG00000099219.13	ERMP1	929.3988984	-1.002129005	0.276838471	-3.619905145	0.000294711	0.007523422

Table S9 A: up-regulated genes in intestinal pTh17-cells as compared to all other CCR6^{+}Th subsets

Gene_id	Gene_name	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
ENSG00000062524.15	LTK	2387.549681	2.855007227	0.763174711	3.740961521	0.000183318	0.004780923
ENSG00000155629.14	PIK3AP1	473.2938346	2.779360279	0.688519658	4.036718846	5.42E-05	0.001907593
ENSG00000157404.15	KIT	2195.429181	2.596393133	0.630425009	4.118480544	3.81E-05	0.00148195
ENSG00000181264.8	TMEM136	92.81799674	2.53048514	0.314282463	8.051626929	8.17E-16	8.85E-13
ENSG00000134256.12	CD101	723.351847	2.477524006	0.666869704	3.715154534	0.00020308	0.005192465
ENSG00000187479.5	C11orf96	108.402774	2.445649363	0.530450838	4.610510885	4.02E-06	0.000260711
ENSG00000109906.13	ZBTB16	110.4745926	2.364988263	0.494064172	4.786803811	1.69E-06	0.00013468
ENSG00000196914.8	ARHGEF12	2527.702269	2.355657297	0.35889694	6.563603731	5.25E-11	2.28E-08
ENSG00000154917.10	RAB6B	408.956532	2.301526036	0.379564579	6.063595409	1.33E-09	3.47E-07
ENSG00000129521.13	EGLN3	470.0464236	2.297259742	0.467449388	4.914456625	8.90E-07	8.24E-05
ENSG00000157985.18	AGAP1	111.1083272	2.266898659	0.519592309	4.362841061	1.28E-05	0.000648431
ENSG00000140470.13	ADAMTS17	118.2575966	2.230566607	0.410765341	5.430269747	5.63E-08	8.07E-06
ENSG00000130635.15	COL5A1	2128.890246	2.210127276	0.372053698	5.94034487	2.84E-09	6.69E-07
ENSG00000120549.17	KIAA1217	283.8505954	2.196767305	0.365808405	6.005240102	1.91E-09	4.64E-07
ENSG00000050165.17	DKK3	352.1518506	2.170552553	0.631743149	3.435814945	0.000590774	0.011789337
ENSG00000134253.9	TRIM45	139.5286997	2.16577432	0.354524245	6.10895968	1.00E-09	2.77E-07
ENSG00000115594.11	IL1R1	941.8105023	2.148925145	0.565296683	3.801411207	0.000143874	0.004007248
ENSG00000137825.10	ITPKA	32.7003107	2.126268736	0.618936308	3.435359515	0.000591768	0.011789337
ENSG00000104951.15	IL4I1	1656.752857	2.118571073	0.328659968	6.446087987	1.15E-10	4.33E-08
ENSG00000162772.16	ATF3	2146.841961	2.115274458	0.425167273	4.975158227	6.52E-07	6.49E-05
ENSG00000164056.10	SPRY1	910.7642979	2.013605967	0.318562697	6.320909462	2.60E-10	9.10E-08
ENSG00000187796.13	CARD9	127.2857791	1.991374028	0.332095724	5.996385635	2.02E-09	4.82E-07
ENSG00000134317.17	GRHL1	34.8634498	1.981022805	0.442789504	4.473960623	7.68E-06	0.000435331
ENSG00000149573.8	MPZL2	456.076042	1.980203676	0.689178066	2.873283079	0.004062299	0.043517269
ENSG00000121297.6	TSHZ3	43.39832752	1.97961083	0.354464633	5.584790827	2.34E-08	3.90E-06
ENSG00000135898.9	GPR55	730.9814874	1.930068859	0.569576733	3.388602003	0.000702499	0.013311288
ENSG00000130202.9	NECTIN2	128.8341785	1.927313095	0.508028404	3.793711299	0.000148412	0.004068179
ENSG00000117399.13	CDC20	41.47237108	1.911462136	0.630137452	3.033405059	0.002418108	0.030886322
ENSG00000204161.13	C10orf128	818.7964231	1.891276112	0.642643965	2.942960979	0.003250894	0.037788349
ENSG00000173114.12	LRRN3	1483.275348	1.871316518	0.417155391	4.485897962	7.26E-06	0.000414933
ENSG00000125726.10	CD70	216.937412	1.857881801	0.336602169	5.519518206	3.40E-08	5.24E-06
ENSG00000177191.2	B3GNT8	80.18055274	1.852260324	0.392103786	4.723903186	2.31E-06	0.000171198
ENSG00000141756.18	FKBP10	42.47909145	1.843938416	0.620244436	2.972922139	0.002949793	0.03525622
ENSG00000092445.11	TYRO3	65.40373641	1.824769217	0.42280554	4.315859288	1.59E-05	0.000752626
ENSG00000162594.15	IL23R	114.7690542	1.803483903	0.472512766	3.816794026	0.000135197	0.003840129
ENSG00000005020.12	SKAP2	1186.518067	1.777384119	0.320356117	5.548151017	2.89E-08	4.60E-06
ENSG00000159335.15	PTMS	742.8548316	1.776260676	0.44712348	3.972640121	7.11E-05	0.002343856
ENSG00000063438.16	AHRR	1698.216035	1.766642276	0.300625988	5.876545431	4.19E-09	9.39E-07
ENSG00000137501.17	SYTL2	2512.004337	1.748044206	0.545544765	3.204217727	0.0013543	0.021046676
ENSG00000175048.16	ZDHHC14	607.214429	1.739003713	0.426330436	4.079004374	4.52E-05	0.001682828
ENSG00000165030.3	NFIL3	424.442677	1.736762393	0.36295062	4.785120338	1.71E-06	0.00013468
ENSG00000089692.8	LAG3	659.8636874	1.720514147	0.598874037	2.872914903	0.004067036	0.043535501
ENSG00000129654.7	FOXJ1	110.5753211	1.709234082	0.348367496	4.906410899	9.28E-07	8.42E-05
ENSG00000177602.5	GSG2	538.087807	1.687230954	0.387785833	4.350935002	1.36E-05	0.000677508
ENSG00000095397.13	WHRN	1065.724677	1.677990241	0.355699418	4.717438817	2.39E-06	0.000175259

ENSG00000158806.13	NPM2	61.28502265	1.657425341	0.372099938	4.454247831	8.42E-06	0.000471715
ENSG00000112290.12	WASF1	93.83298764	1.640443596	0.430399153	3.811447085	0.000138156	0.003900993
ENSG00000142949.16	PTPRF	128.907957	1.635838802	0.320339236	5.106582702	3.28E-07	3.71E-05
ENSG00000094804.9	CDC6	88.92393706	1.635528866	0.512116096	3.193668151	0.001404775	0.021620271
ENSG00000083457.11	ITGAE	4213.774947	1.628897959	0.309697921	5.259634791	1.44E-07	1.83E-05
ENSG00000125384.6	PTGER2	686.2512533	1.619110253	0.390612769	4.145052035	3.40E-05	0.001346183
ENSG00000189420.8	ZFP92	450.1593034	1.618408454	0.28685161	5.641970958	1.68E-08	2.98E-06
ENSG00000143036.16	SLC44A3	133.3318833	1.612307657	0.429810088	3.751209431	0.000175984	0.004623277
ENSG00000143434.15	SEMA6C	701.3887952	1.595691607	0.234144581	6.814984156	9.43E-12	4.66E-09
ENSG00000111817.16	DSE	1598.554781	1.582824787	0.342883919	4.61621178	3.91E-06	0.000257145
ENSG00000137462.6	TLR2	215.921105	1.573782655	0.432038104	3.64269411	0.000269799	0.006450004
ENSG00000166165.12	CKB	208.8722849	1.571080944	0.502115022	3.128926393	0.001754463	0.024991073
ENSG00000215045.8	GRID2IP	73.59028093	1.568175446	0.293926356	5.335266525	9.54E-08	1.28E-05
ENSG00000171860.4	C3AR1	590.6581125	1.563435716	0.439356875	3.558464213	0.00037303	0.008308597
ENSG00000076706.15	MCAM	351.4856969	1.561073674	0.257679155	6.058207043	1.38E-09	3.53E-07
ENSG00000140465.13	CYP1A1	99.0770446	1.559038534	0.388484098	4.013133462	5.99E-05	0.002066019
ENSG00000113758.13	DBN1	167.5359191	1.555338924	0.393149217	3.956103324	7.62E-05	0.00248354
ENSG00000143878.9	RHOB	6736.268127	1.550643433	0.360523279	4.301091004	1.70E-05	0.000794103
ENSG00000196872.11	KIAA1211L	107.3875195	1.546920825	0.195741838	7.902862472	2.73E-15	2.61E-12
ENSG00000150457.8	LATS2	229.1361132	1.546225807	0.449927831	3.436608497	0.000589046	0.011789337
ENSG00000146250.6	PRSS35	138.0950663	1.53119047	0.536586747	2.853574895	0.004323034	0.045395018
ENSG00000107130.9	NCS1	76.07587974	1.525991037	0.477120932	3.198331772	0.001382252	0.021365319
ENSG00000080573.6	COL5A3	7483.060162	1.505875953	0.528507231	2.849300565	0.004381547	0.045774876
ENSG00000145990.10	GFOD1	164.6112713	1.502614239	0.341821879	4.395898364	1.10E-05	0.000575406
ENSG00000167613.15	LAIR1	505.5703063	1.487835258	0.417753722	3.56151287	0.000368724	0.008251135
ENSG00000090104.11	RGS1	8178.659776	1.469056165	0.391501636	3.752362777	0.000175176	0.004610496
ENSG00000115009.11	CCL20	1051.81954	1.468489268	0.329959218	4.450517475	8.57E-06	0.000475866
ENSG00000071539.13	TRIP13	44.72352397	1.466182911	0.406939399	3.602951484	0.000314624	0.007269647
ENSG00000139200.13	PIANP	299.3338836	1.446088185	0.389402456	3.713608281	0.000204325	0.00519652
ENSG00000173585.15	CCR9	2922.461	1.443770973	0.409101458	3.529126929	0.000416933	0.009088888
ENSG00000206013.2	IFITM5	175.5237576	1.44223757	0.362236591	3.981479528	6.85E-05	0.002271145
ENSG00000134802.17	SLC43A3	421.994912	1.438242801	0.311930114	4.610785347	4.01E-06	0.000260711
ENSG00000182621.17	PLCB1	425.8716652	1.437045402	0.368339264	3.901417916	9.56E-05	0.002982021
ENSG00000138670.17	RASGEF1B	1090.09913	1.406956528	0.33354679	4.218168398	2.46E-05	0.001060917
ENSG00000178053.17	MLF1	158.5858301	1.401235738	0.303498127	4.616950202	3.89E-06	0.000257145
ENSG00000075651.15	PLD1	195.9355963	1.399524793	0.4908523	2.851213681	0.004355269	0.045533512
ENSG00000088826.17	SMOX	920.5811335	1.394796864	0.333298669	4.184825782	2.85E-05	0.001193458
ENSG00000160183.13	TMPRSS3	404.014634	1.380398254	0.275091301	5.017964035	5.22E-07	5.39E-05
ENSG00000186654.20	PRR5	1003.978371	1.364027287	0.209959728	6.496613888	8.21E-11	3.37E-08
ENSG00000173868.11	PHOSPHO1	80.56729881	1.360007661	0.407306786	3.339025295	0.000840729	0.014980643
ENSG00000256235.1	SMIM3	918.6427636	1.357047986	0.261281293	5.193819929	2.06E-07	2.44E-05
ENSG00000167291.15	TBC1D16	329.0257259	1.35314332	0.30053936	4.502383056	6.72E-06	0.000392248
ENSG00000037280.15	FLT4	214.9027435	1.352689057	0.39734019	3.404360016	0.000663193	0.012837838
ENSG00000215529.12	EFCAB8	107.557233	1.342419259	0.307622473	4.363853024	1.28E-05	0.000647718
ENSG00000120129.5	DUSP1	10048.01166	1.342374808	0.287073044	4.676074032	2.92E-06	0.000203012
ENSG00000120318.15	ARAP3	1231.999615	1.341564116	0.385922219	3.476255192	0.000508468	0.010479121
ENSG00000170819.4	BFSP2	59.98389095	1.329907242	0.242472799	5.484768791	4.14E-08	6.32E-06
ENSG00000160469.16	BRSK1	124.5371291	1.325415225	0.237462086	5.581586716	2.38E-08	3.92E-06

ENSG00000129244.8	ATP1B2	22.57469159	1.322440007	0.421574796	3.136904811	0.001707416	0.024589526
ENSG00000125657.4	TNFSF9	36.46502554	1.318461785	0.423070097	3.116414503	0.001830648	0.025643368
ENSG00000169583.12	CLIC3	303.644538	1.315065701	0.413188611	3.182724946	0.001458961	0.022215862
ENSG00000182511.11	FES	583.2106114	1.310727045	0.339962719	3.8555023	0.000115492	0.003401685
ENSG00000185924.6	RTN4RL1	50.02892345	1.305534771	0.338139036	3.860940709	0.000112951	0.003340564
ENSG00000125462.16	C1orf61	69.88396531	1.279433923	0.379219164	3.373864099	0.00074121	0.013807674
ENSG00000143507.17	DUSP10	1266.576516	1.279069977	0.318859978	4.011384508	6.04E-05	0.002076396
ENSG00000135253.13	KCP	43.84691768	1.278305617	0.373722961	3.420463155	0.000625146	0.012300541
ENSG00000136193.16	SCRN1	716.847532	1.27795689	0.264983286	4.822783006	1.42E-06	0.000117379
ENSG00000167513.8	CDT1	58.71626844	1.271504733	0.429510667	2.96035659	0.003072831	0.036217498
ENSG00000143061.17	IGSF3	31.9623738	1.258003205	0.367771588	3.420610092	0.000624808	0.012300541
ENSG00000099282.9	TSPAN15	154.3542954	1.256595715	0.374523589	3.355184437	0.000793121	0.014418917
ENSG00000115828.15	QPCT	202.2823274	1.24998114	0.335299615	3.727952808	0.000193042	0.004962343
ENSG00000184730.10	APOBR	1923.189322	1.246896153	0.21684894	5.750068012	8.92E-09	1.71E-06
ENSG00000174307.6	PHLDA3	555.283	1.246189971	0.26017347	4.789842597	1.67E-06	0.000134505
ENSG00000154229.11	PRKCA	2355.338672	1.245619193	0.232190183	5.364650559	8.11E-08	1.12E-05
ENSG00000151117.8	TMEM86A	85.9939	1.243547129	0.367244751	3.386153579	0.000708797	0.013360033
ENSG00000100906.10	NFKBIA	21709.8045	1.240518228	0.323458324	3.83517175	0.000125477	0.003605457
ENSG00000237693.4	IRGM	68.37622708	1.23213877	0.337610149	3.649590437	0.000262659	0.006342723
ENSG00000131080.14	EDA2R	69.47381668	1.226455092	0.340520601	3.601706001	0.000316136	0.007290436
ENSG00000121797.9	CCRL2	89.76861059	1.220792742	0.364167443	3.352284137	0.000801477	0.014497337
ENSG00000109471.4	IL2	272.8474718	1.215636849	0.384698111	3.159976132	0.001577821	0.02342884
ENSG00000177875.4	CCDC184	369.4784195	1.21521918	0.328893252	3.694874162	0.000219996	0.005516816
ENSG00000154240.16	CEP112	100.3950281	1.213186468	0.322743348	3.758982097	0.000170606	0.004523425
ENSG00000125266.6	EFNB2	33.14653777	1.212659015	0.379758343	3.193238645	0.001406866	0.021629249
ENSG00000228278.3	ORM2	198.3236865	1.210013388	0.41454929	2.918864937	0.003513084	0.039772436
ENSG00000162783.10	IER5	5999.381823	1.207465849	0.194628652	6.20394703	5.51E-10	1.68E-07
ENSG00000125740.13	FOSB	14716.86405	1.195526712	0.342956006	3.485947734	0.000490397	0.010239086
ENSG00000177374.12	HIC1	2340.244673	1.193994604	0.252538063	4.727978778	2.27E-06	0.000169413
ENSG00000048052.21	HDAC9	201.6375647	1.189561773	0.384410986	3.094505145	0.001971415	0.027086187
ENSG00000188483.7	IER5L	136.7039893	1.176752359	0.385554153	3.052106563	0.002272414	0.029760205
ENSG00000152684.10	PELO	1691.493521	1.175961498	0.366903451	3.205097948	0.001350165	0.021027981
ENSG00000141682.11	PMAIP1	959.8103203	1.175513228	0.335994878	3.498604605	0.0004677	0.009928392
ENSG00000147889.17	CDKN2A	281.7188874	1.174918015	0.261464203	4.493609457	7.00E-06	0.000403404
ENSG00000140859.15	KIFC3	392.8760988	1.171463966	0.387097212	3.026278488	0.002475842	0.031400063
ENSG00000155265.10	GOLGA7B	420.875357	1.169325576	0.159802127	7.317334227	2.53E-13	1.81E-10
ENSG00000146670.9	CDCA5	58.92777261	1.168274766	0.372283106	3.138135321	0.001700264	0.024585263
ENSG00000151062.14	CACNA2D4	660.0142938	1.159838668	0.166527643	6.964841666	3.29E-12	1.89E-09
ENSG00000075702.16	WDR62	348.2990919	1.14601192	0.296370227	3.866825395	0.000110261	0.003281303
ENSG00000122877.14	EGR2	171.8061143	1.145480087	0.379911441	3.015123953	0.002568743	0.032095856
ENSG00000111012.9	CYP27B1	144.1493606	1.139314865	0.339278882	3.358048276	0.000784949	0.014361363
ENSG00000124762.13	CDKN1A	2893.986012	1.128842857	0.357411428	3.158384895	0.001586459	0.023462759
ENSG00000174871.10	CNIH2	176.0716696	1.127179647	0.317702486	3.547909438	0.000388302	0.008582126
ENSG00000206561.12	COLQ	274.8771051	1.123814378	0.300620532	3.738315442	0.000185257	0.004819883
ENSG00000079819.17	EPB41L2	416.8071596	1.110723195	0.333527842	3.330226308	0.000867754	0.015291237
ENSG00000206560.11	ANKRD28	2762.349288	1.109923943	0.203162783	5.463224732	4.68E-08	7.06E-06
ENSG00000080823.21	MOK	93.09216748	1.107003534	0.273274532	4.050884386	5.10E-05	0.001834321
ENSG00000187240.13	DYNC2H1	232.6475089	1.105458983	0.278376888	3.97108751	7.15E-05	0.002353774

ENSG00000144802.11	NFKBIZ	5872.263938	1.104203401	0.315892585	3.495502754	0.00047317	0.009967368
ENSG00000061337.15	LZTS1	643.5700579	1.101097063	0.356311349	3.090266602	0.001999769	0.027266813
ENSG00000105767.2	CADM4	119.4982642	1.093087298	0.185252297	5.900533036	3.62E-09	8.26E-07
ENSG00000123685.8	BATF3	65.43292885	1.092301581	0.366931177	2.976856835	0.0029122	0.035032704
ENSG00000163818.16	LZTFL1	1425.387497	1.087916247	0.256095719	4.248084472	2.16E-05	0.000952119
ENSG00000087074.7	PPP1R15A	39259.60792	1.087251721	0.28501016	3.81478232	0.000136303	0.003856273
ENSG00000140836.14	ZFHX3	150.5180244	1.087154574	0.268219	4.05323476	5.05E-05	0.00182513
ENSG00000008256.15	CYTH3	3674.335653	1.082410831	0.265380329	4.078715381	4.53E-05	0.001682828
ENSG00000172602.9	RND1	74.89466369	1.077998532	0.30557234	3.527801414	0.000419026	0.00911023
ENSG00000184545.10	DUSP8	517.8817338	1.070629702	0.293264195	3.650734454	0.000261491	0.006325184
ENSG00000104368.17	PLAT	430.0475301	1.065366568	0.336510664	3.165922164	0.001545922	0.023122731
ENSG00000255274.9	TMPRSS4-AS1	267.0034751	1.062044679	0.328161984	3.236342814	0.001210719	0.019534928
ENSG00000176834.13	VSIG10	114.6993511	1.057655528	0.241491342	4.379683013	1.19E-05	0.000611044
ENSG00000179057.13	IGSF22	30.10796333	1.053954336	0.35418445	2.975721647	0.002923	0.035056453
ENSG00000120278.15	PLEKHG1	971.3104204	1.049539918	0.336763591	3.116548068	0.001829818	0.025643368
ENSG00000085563.14	ABCB1	3625.846948	1.048512153	0.261217845	4.01393769	5.97E-05	0.00206395
ENSG00000166963.12	MAP1A	202.9152374	1.038558403	0.281299197	3.692006287	0.000222492	0.005559973
ENSG00000171444.17	MCC	406.5878095	1.036859247	0.287633552	3.604792411	0.000312403	0.007250974
ENSG00000100599.15	RIN3	1075.408983	1.035798121	0.286475387	3.615661829	0.000299581	0.00703305
ENSG00000101000.5	PROCR	55.30853354	1.034413545	0.332573226	3.110333194	0.001868764	0.026052633
ENSG00000115902.10	SLC1A4	2361.935181	1.031880282	0.324028002	3.184540461	0.00144984	0.022123948
ENSG00000108798.8	ABI3	1271.454714	1.029090556	0.273714455	3.759723082	0.000170102	0.004518401
ENSG00000185010.13	F8	315.2126882	1.027220848	0.210378258	4.882732934	1.05E-06	9.26E-05
ENSG00000088727.12	KIF9	88.9052331	1.026559756	0.278866042	3.681193118	0.000232145	0.005751104
ENSG00000169026.12	MFSD7	80.59086347	1.026224677	0.281256517	3.648714305	0.000263556	0.006353693
ENSG00000151014.5	NOCT	120.343456	1.025252194	0.310513814	3.301792538	0.000960691	0.016542799
ENSG00000188211.8	NCR3LG1	209.7365377	1.02364619	0.340643592	3.005035805	0.002655496	0.032950201
ENSG00000137965.10	IFI44	2138.318469	1.023096013	0.301299212	3.395614632	0.000684747	0.01306252
ENSG00000106665.15	CLIP2	775.1053609	1.021434277	0.247951787	4.11948746	3.80E-05	0.001480067
ENSG00000174791.10	RIN1	154.9948677	1.020488754	0.344425412	2.962873003	0.003047823	0.035981869
ENSG00000167664.8	TMIGD2	1793.038091	1.017180197	0.310452195	3.276447105	0.00105122	0.017656557
ENSG00000151689.12	INPP1	345.8981906	1.016366146	0.201322582	5.048445812	4.45E-07	4.80E-05
ENSG00000167083.6	GNGT2	109.7404432	1.014733775	0.305584583	3.320631447	0.000898141	0.015648407
ENSG00000175556.16	LONRF3	407.1900852	1.010422335	0.219848795	4.595987595	4.31E-06	0.00027216
ENSG00000145391.13	SETD7	2009.85126	1.010265485	0.285058128	3.544068338	0.000394003	0.008668068
ENSG00000165914.14	TTC7B	103.199839	1.007612669	0.339477014	2.968132234	0.002996154	0.035665422
ENSG00000163923.9	RPL39L	139.6938207	1.004974062	0.242057593	4.151797307	3.30E-05	0.001325206
ENSG00000180530.10	NRIP1	2277.277508	1.001017956	0.221848383	4.512171521	6.42E-06	0.000378772

Table S9 B: down-regulated genes in intestinal pTh17-cells as compared to all other CCR6$^+$Th subsets

Gene_id	Gene_name	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
ENSG00000138795.9	LEF1	3288.262823	-4.743993821	0.436312125	-10.87293601	1.55E-27	2.23E-23
ENSG00000182463.15	TSHZ2	222.8104845	-4.734235411	0.986754977	-4.797782144	1.60E-06	0.000130752
ENSG00000137474.19	MYO7A	587.0363055	-4.716188469	0.841658551	-5.603446272	2.10E-08	3.55E-06
ENSG00000186810.7	CXCR3	3506.145553	-4.576333521	1.190790835	-3.84310442	0.000121488	0.003541911
ENSG00000188404.8	SELL	1880.019099	-4.341545266	0.921353774	-4.712137065	2.45E-06	0.000177585
ENSG00000141753.6	IGFBP4	2116.632654	-4.258165333	0.661800228	-6.43421557	1.24E-10	4.56E-08
ENSG00000152969.17	JAKMIP1	274.5123134	-4.086081887	0.87355332	-4.677541479	2.90E-06	0.000203012
ENSG00000156299.13	TIAM1	651.0678922	-4.014682042	0.403491749	-9.949849174	2.53E-23	1.81E-19
ENSG00000166105.15	GLB1L3	271.9393087	-3.748648463	0.642980689	-5.830110499	5.54E-09	1.18E-06
ENSG00000124191.17	TOX2	464.7711582	-3.622721113	0.641347431	-5.648609378	1.62E-08	2.94E-06
ENSG00000156234.7	CXCL13	409.3276446	-3.455246377	1.033567851	-3.343028109	0.000828695	0.014821449
ENSG00000116106.11	EPHA4	735.8712913	-3.360850264	0.580638851	-5.788193918	7.11E-09	1.44E-06
ENSG00000116574.5	RHOU	388.8021531	-3.298900727	1.0115153	-3.261345358	0.001108849	0.018324112
ENSG00000172292.14	CERS6	178.5896585	-3.283610001	0.501208773	-6.551381736	5.70E-11	2.41E-08
ENSG00000107281.9	NPDC1	388.1337076	-3.261606082	0.672850693	-4.847444044	1.25E-06	0.00010608
ENSG00000134198.9	TSPAN2	130.1179239	-3.205158639	0.602729029	-5.317743933	1.05E-07	1.36E-05
ENSG00000103522.15	IL21R	728.9844763	-3.18407944	0.392437765	-8.113590798	4.91E-16	5.87E-13
ENSG00000182230.11	FAM153B	142.0926762	-3.178085218	0.514902883	-6.172203187	6.73E-10	1.97E-07
ENSG00000118263.14	KLF7	279.9951417	-3.172813346	0.435707934	-7.281972849	3.29E-13	2.25E-10
ENSG00000126353.3	CCR7	3444.087397	-3.151584957	0.632693758	-4.981217086	6.32E-07	6.34E-05
ENSG00000131398.13	KCNC3	263.9191631	-3.150023083	0.391561031	-8.044781873	8.64E-16	8.85E-13
ENSG00000186854.10	TRABD2A	599.6395865	-2.999275836	0.409777968	-7.319270602	2.49E-13	1.81E-10
ENSG00000135821.17	GLUL	2763.941929	-2.924882038	0.593257008	-4.930210679	8.21E-07	7.65E-05
ENSG00000109956.12	B3GAT1	137.9765636	-2.880766855	0.744530027	-3.869242004	0.000109174	0.003276141
ENSG00000196126.10	HLA-DRB1	241.3433864	-2.88075861	0.942419497	-3.0567689	0.002237367	0.029497052
ENSG00000146216.11	TTBK1	104.8958679	-2.823112389	0.652869314	-4.324161556	1.53E-05	0.000734533
ENSG00000080854.14	IGSF9B	378.4804582	-2.808664343	0.648621616	-4.330204657	1.49E-05	0.000719474
ENSG00000170989.8	S1PR1	2606.256623	-2.790620414	0.553546974	-5.041343457	4.62E-07	4.90E-05
ENSG00000263264.1	CTB-133G6.1	417.8211195	-2.785909895	0.494394535	-5.634993304	1.75E-08	3.03E-06
ENSG00000261371.5	PECAM1	183.8964229	-2.758486049	0.891644257	-3.093706965	0.001976726	0.027103255
ENSG00000183813.6	CCR4	2444.443604	-2.745334471	0.76248873	-3.600491866	0.000317616	0.007301091
ENSG00000136250.11	AOAH	446.567238	-2.729012407	0.682863402	-3.996425053	6.43E-05	0.002185802
ENSG00000185989.10	RASA3	2434.460044	-2.712791432	0.385623177	-7.034824658	2.00E-12	1.24E-09
ENSG00000186310.9	NAP1L3	111.2207774	-2.694586673	0.478216687	-5.634656314	1.75E-08	3.03E-06
ENSG00000149328.14	GLB1L2	823.2495193	-2.650702145	0.866460941	-3.059228663	0.002219077	0.029422342
ENSG00000137936.16	BCAR3	115.1486374	-2.633334561	0.897021474	-2.935642721	0.003328575	0.038411161
ENSG00000148053.15	NTRK2	276.1923049	-2.622792394	0.52435604	-5.00193036	5.68E-07	5.82E-05
ENSG00000008441.16	NFIX	134.289097	-2.536426497	0.608227193	-4.170195818	3.04E-05	0.00124095
ENSG00000160255.17	ITGB2	7547.878738	-2.485772787	0.301829803	-8.235677074	1.79E-16	2.85E-13
ENSG00000196218.12	RYR1	1591.154078	-2.475162075	0.392788168	-6.301518933	2.95E-10	9.83E-08
ENSG00000166503.8	RP11-382A20.3	363.8139886	-2.47082947	0.657649205	-3.757062964	0.000171919	0.004549833
ENSG00000184613.10	NELL2	3117.827838	-2.469655435	0.554024692	-4.457663116	8.29E-06	0.000466084
ENSG00000132694.18	ARHGEF11	161.6979046	-2.465845907	0.760463042	-3.242558511	0.001184616	0.019227077
ENSG00000182272.11	B4GALNT4	168.0747506	-2.465026302	0.525214595	-4.693369772	2.69E-06	0.000190164
ENSG00000135925.8	WNT10A	109.0591507	-2.461045855	0.556223554	-4.42456246	9.66E-06	0.000521118

ENSG00000204219.9	TCEA3	113.1281689	-2.456563971	0.533722911	-4.602695371	4.17E-06	0.000265879
ENSG00000179583.18	CIITA	401.2020559	-2.453517657	0.827495646	-2.964991623	0.003026912	0.035878897
ENSG00000104361.9	NIPAL2	69.64933281	-2.441209911	0.582733089	-4.189241968	2.80E-05	0.001173892
ENSG00000102349.16	KLF8	107.8081117	-2.436605306	0.446766295	-5.453870025	4.93E-08	7.36E-06
ENSG00000135678.11	CPM	93.11924287	-2.407140477	0.594446176	-4.049383403	5.14E-05	0.00184151
ENSG00000067840.12	PDZD4	109.1711369	-2.394491698	0.527223244	-4.541703586	5.58E-06	0.000342908
ENSG00000163545.8	NUAK2	488.2553937	-2.340062169	0.361185957	-6.478829326	9.24E-11	3.68E-08
ENSG00000120885.20	CLU	1543.245803	-2.317499137	0.728451312	-3.181405676	0.001465622	0.022270008
ENSG00000050327.14	ARHGEF5	84.1394807	-2.314676008	0.284571714	-8.133893473	4.16E-16	5.42E-13
ENSG00000166833.19	NAV2	96.4929618	-2.307034107	0.523810507	-4.404329575	1.06E-05	0.000562626
ENSG00000144354.13	CDCA7	1083.082527	-2.289772534	0.73741003	-3.105155124	0.001901793	0.026407853
ENSG00000135114.12	OASL	953.7065508	-2.284936916	0.736374182	-3.102956312	0.001915979	0.026527805
ENSG00000128656.13	CHN1	969.5033405	-2.283347063	0.679452923	-3.360566987	0.000777827	0.014249228
ENSG00000166405.14	RIC3	256.889355	-2.281072234	0.495335182	-4.605108451	4.12E-06	0.000265172
ENSG00000160712.12	IL6R	2497.945713	-2.263240139	0.625155398	-3.620284086	0.00029428	0.006954116
ENSG00000116690.12	PRG4	77.33469307	-2.203382095	0.648892182	-3.395605861	0.000684769	0.01306252
ENSG00000132359.14	RAP1GAP2	398.1428457	-2.183024649	0.639814535	-3.411964761	0.000644965	0.012586899
ENSG00000159640.15	ACE	769.2800904	-2.172347815	0.387596997	-5.60465595	2.09E-08	3.55E-06
ENSG00000186265.9	BTLA	285.3439909	-2.161319155	0.381177128	-5.670117629	1.43E-08	2.66E-06
ENSG00000118402.5	ELOVL4	199.2896925	-2.160754142	0.555342226	-3.890851517	9.99E-05	0.00307482
ENSG00000152782.16	PANK1	149.4054625	-2.15829981	0.469255079	-4.599417045	4.24E-06	0.000268902
ENSG00000172794.19	RAB37	2650.108297	-2.136878977	0.343947763	-6.212800906	5.20E-10	1.62E-07
ENSG00000140545.14	MFGE8	364.8779521	-2.116260443	0.431754011	-4.901542055	9.51E-07	8.47E-05
ENSG00000092096.15	SLC22A17	71.74946349	-2.115221133	0.524533418	-4.032576499	5.52E-05	0.001930095
ENSG00000070526.14	ST6GALNAC1	213.4244585	-2.109916822	0.529185732	-3.987100734	6.69E-05	0.00225213
ENSG00000173218.14	VANGL1	108.2349708	-2.099823829	0.431691582	-4.864175992	1.15E-06	0.000100526
ENSG00000160856.20	FCRL3	83.05903278	-2.080952437	0.4637212	-4.487507662	7.21E-06	0.000413458
ENSG00000180543.4	TSPYL5	63.37923821	-2.070596053	0.414228579	-4.998679852	5.77E-07	5.87E-05
ENSG00000173198.5	CYSLTR1	299.2795305	-2.058856176	0.688551971	-2.990124584	0.002788637	0.033956033
ENSG00000119408.16	NEK6	134.1551548	-2.020004314	0.499683966	-4.042563802	5.29E-05	0.001874977
ENSG00000100311.16	PDGFB	105.6093737	-1.983007674	0.343687965	-5.76979085	7.94E-09	1.56E-06
ENSG00000188322.4	SBK1	419.9796616	-1.97022242	0.444709248	-4.430360805	9.41E-06	0.000509215
ENSG00000104689.9	TNFRSF10A	593.5665061	-1.969190018	0.259332847	-7.593291947	3.12E-14	2.63E-11
ENSG00000131746.12	TNS4	72.08035919	-1.95896982	0.495077436	-3.956895782	7.59E-05	0.00248354
ENSG00000173482.16	PTPRM	2122.60124	-1.945641641	0.441458878	-4.407299838	1.05E-05	0.000558122
ENSG00000133069.15	TMCC2	111.486512	-1.941772324	0.503883435	-3.853614131	0.000116387	0.003414018
ENSG00000110987.8	BCL7A	29.04992593	-1.933466945	0.568241399	-3.402545026	0.000667614	0.012905995
ENSG00000088992.17	TESC	204.5903518	-1.9320111	0.544039987	-3.551229959	0.000383435	0.008500765
ENSG00000128536.15	CDHR3	74.12517198	-1.926051167	0.460680488	-4.180882882	2.90E-05	0.001207305
ENSG00000181804.14	SLC9A9	575.2592584	-1.912386208	0.286184724	-6.682349011	2.35E-11	1.09E-08
ENSG00000168824.14	NSG1	934.3937716	-1.852767483	0.326677405	-5.671550751	1.42E-08	2.66E-06
ENSG00000149212.11	SESN3	2247.121847	-1.852381165	0.341284861	-5.427668727	5.71E-08	8.11E-06
ENSG00000110777.11	POU2AF1	180.8358715	-1.830411425	0.423660494	-4.32046757	1.56E-05	0.000741975
ENSG00000147408.14	CSGALNACT1	178.8125783	-1.802466518	0.409334693	-4.403405206	1.07E-05	0.000562626
ENSG00000131370.15	SH3BP5	288.5203935	-1.79589248	0.42400675	-4.235528044	2.28E-05	0.000994119
ENSG00000072163.19	LIMS2	98.64088962	-1.78667576	0.477546726	-3.741363226	0.000183025	0.004780923
ENSG00000139193.3	CD27	610.3281062	-1.781593301	0.287649739	-6.193620426	5.88E-10	1.76E-07
ENSG00000044459.14	CNTLN	41.60686571	-1.780479505	0.612896326	-2.905025581	0.003672231	0.041023738

ENSG00000163082.9	SGPP2	638.2869215	-1.77476355	0.393851911	-4.506169709	6.60E-06	0.000388042
ENSG00000105173.13	CCNE1	72.0867536	-1.750775424	0.492498302	-3.554886213	0.000378143	0.008396407
ENSG00000101842.13	VSIG1	244.226599	-1.729506208	0.373412922	-4.631618533	3.63E-06	0.000244332
ENSG00000104903.4	LYL1	106.2509317	-1.725197531	0.397732178	-4.337586008	1.44E-05	0.000710083
ENSG00000124496.12	TRERF1	5279.964623	-1.721443688	0.409257076	-4.206264933	2.60E-05	0.001105066
ENSG00000128578.9	STRIP2	81.73256111	-1.713981758	0.566582598	-3.02512249	0.002485325	0.031415848
ENSG00000013619.13	MAMLD1	215.4930986	-1.709834879	0.524965401	-3.257042991	0.001125794	0.018476415
ENSG00000087589.16	CASS4	433.5445652	-1.684473042	0.396998555	-4.243020582	2.21E-05	0.000970337
ENSG00000198915.11	RASGEF1A	175.4470248	-1.677048974	0.448702325	-3.737553565	0.00018582	0.004819883
ENSG00000176533.12	GNG7	389.2352459	-1.667304762	0.428729064	-3.88894736	0.00010068	0.003092405
ENSG00000101004.14	NINL	243.1685648	-1.641044849	0.181239805	-9.054549866	1.37E-19	6.56E-16
ENSG00000184524.5	CEND1	100.9928291	-1.639610706	0.581843265	-2.817959416	0.004832992	0.048751361
ENSG00000187231.13	SESTD1	212.8931636	-1.635958662	0.392311151	-4.170053942	3.05E-05	0.00124095
ENSG00000198794.11	SCAMP5	52.36204821	-1.627747744	0.469255075	-3.468790919	0.000522806	0.010728371
ENSG00000006704.10	GTF2IRD1	107.5658289	-1.606536981	0.43973383	-3.653430485	0.00025876	0.006302919
ENSG00000034053.14	APBA2	1300.977216	-1.581412878	0.208899955	-7.570192515	3.73E-14	2.97E-11
ENSG00000122547.10	EEPD1	318.4625072	-1.575671734	0.428443217	-3.677667592	0.000235376	0.005821102
ENSG00000157570.11	TSPAN18	329.5200869	-1.571535555	0.438399736	-3.584709174	0.000337454	0.007671063
ENSG00000083290.19	ULK2	355.4047356	-1.56123371	0.310722192	-5.024532359	5.05E-07	5.25E-05
ENSG00000212916.4	MAP10	94.7686769	-1.550417918	0.425886199	-3.640451186	0.000272161	0.006495629
ENSG00000125430.8	HS3ST3B1	308.1363347	-1.538900968	0.333620142	-4.612733993	3.97E-06	0.000260292
ENSG00000126822.16	PLEKHG3	974.1328732	-1.511206298	0.352642909	-4.285372705	1.82E-05	0.000841421
ENSG00000160284.14	SPATC1L	44.75996867	-1.506269374	0.400613898	-3.759902943	0.000169979	0.004518401
ENSG00000176438.12	SYNE3	2013.110323	-1.491857623	0.277600472	-5.37411774	7.70E-08	1.07E-05
ENSG00000197077.13	KIAA1671	2062.305551	-1.490057717	0.280169195	-5.318420962	1.05E-07	1.36E-05
ENSG00000146776.14	ATXN7L1	880.8261701	-1.465947617	0.240254594	-6.101642402	1.05E-09	2.79E-07
ENSG00000174500.12	GCSAM	183.4009087	-1.461025193	0.407703087	-3.583551952	0.000338953	0.007692953
ENSG00000089159.16	PXN	2184.119543	-1.460492339	0.287956259	-5.071924268	3.94E-07	4.31E-05
ENSG00000179242.15	CDH4	87.58347215	-1.44831311	0.375340021	-3.85866955	0.000114006	0.003364818
ENSG00000114948.12	ADAM23	1107.027954	-1.436495854	0.310888165	-4.620619298	3.83E-06	0.000254072
ENSG00000073849.14	ST6GAL1	4344.255685	-1.430225931	0.16710657	-8.558765399	1.14E-17	3.27E-14
ENSG00000154589.6	LY96	249.2703133	-1.42039737	0.351587148	-4.039958162	5.35E-05	0.00188877
ENSG00000116771.5	AGMAT	120.8626659	-1.41559554	0.373822381	-3.786813235	0.000152592	0.00416117
ENSG00000136379.11	ABHD17C	72.3516146	-1.409442265	0.298807588	-4.716889127	2.39E-06	0.000175259
ENSG00000104427.11	ZC2HC1A	135.4936669	-1.384210329	0.392937696	-3.52272216	0.000427139	0.009255106
ENSG00000170677.5	SOCS6	69.13637197	-1.382988956	0.318511856	-4.342032896	1.41E-05	0.000698258
ENSG00000184916.8	JAG2	234.6186293	-1.371459134	0.451995755	-3.034230118	0.002411504	0.030856927
ENSG00000066294.14	CD84	2662.886891	-1.367563192	0.251572289	-5.436064518	5.45E-08	7.89E-06
ENSG00000064666.14	CNN2	7672.338531	-1.363742573	0.281336267	-4.84737566	1.25E-06	0.00010608
ENSG00000112303.13	VNN2	178.7672811	-1.361783824	0.368959268	-3.690878485	0.000223481	0.005574974
ENSG00000164687.10	FABP5	162.6796161	-1.35013235	0.465444633	-2.900736747	0.003722865	0.041319388
ENSG00000143110.11	C1orf162	486.1120038	-1.350091047	0.446341697	-3.024792563	0.002488037	0.031415848
ENSG00000186827.10	TNFRSF4	734.1316698	-1.335307863	0.39889607	-3.347508193	0.000815416	0.014657047
ENSG00000197457.9	STMN3	1552.450527	-1.324970822	0.276748021	-4.787643346	1.69E-06	0.00013468
ENSG00000172824.14	CES4A	167.7660578	-1.323786726	0.2243573	-5.900350574	3.63E-09	8.26E-07
ENSG00000127124.14	HIVEP3	756.8238305	-1.312046401	0.388810738	-3.374511741	0.000739468	0.013793138
ENSG00000198814.12	GK	412.2895437	-1.304383604	0.365656791	-3.567234729	0.000360768	0.008098373
ENSG00000204271.11	SPIN3	252.2056165	-1.295827781	0.378676098	-3.421995179	0.000621634	0.012281984

ENSG00000174837.14	ADGRE1	191.6098713	-1.293316274	0.423185763	-3.05614316	0.002242042	0.029504447
ENSG00000184557.4	SOCS3	1530.29733	-1.28762274	0.447866214	-2.875016465	0.004040064	0.043376259
ENSG00000158050.4	DUSP2	1094.539162	-1.287252584	0.273307626	-4.709903647	2.48E-06	0.00017864
ENSG00000101224.17	CDC25B	8090.983161	-1.268659346	0.283101375	-4.481289952	7.42E-06	0.000422313
ENSG00000184792.15	OSBP2	137.0952099	-1.257390502	0.309300753	-4.065268153	4.80E-05	0.001754309
ENSG00000221890.2	NPTXR	749.4113828	-1.257007981	0.25983224	-4.83776756	1.31E-06	0.000110143
ENSG00000104177.17	MYEF2	627.8424251	-1.251582016	0.252281971	-4.961044227	7.01E-07	6.85E-05
ENSG00000177383.4	MAGEF1	260.1801503	-1.250768401	0.373901139	-3.345184785	0.000822278	0.014743439
ENSG00000114405.10	C3orf14	48.29325117	-1.246174974	0.437684712	-2.847197855	0.004410594	0.045877854
ENSG00000223547.9	ZNF844	148.7123507	-1.223557652	0.321747847	-3.802846435	0.000143043	0.00400051
ENSG00000188886.3	ASTL	92.22831065	-1.221522654	0.362346348	-3.371146582	0.00074856	0.013890488
ENSG00000116133.11	DHCR24	1341.550541	-1.212029404	0.324776432	-3.731888419	0.00019005	0.004903008
ENSG00000181754.6	AMIGO1	532.6450431	-1.208745773	0.27115773	-4.457721976	8.28E-06	0.000466084
ENSG00000054219.10	LY75	382.1651977	-1.204451534	0.243814812	-4.940026092	7.81E-07	7.37E-05
ENSG00000132718.8	SYT11	2840.871743	-1.202952855	0.344866073	-3.488173958	0.000486332	0.010169008
ENSG00000167371.17	PRRT2	63.36067822	-1.192034779	0.263734478	-4.519829144	6.19E-06	0.000369893
ENSG00000266338.6	NBPF15	1690.45372	-1.179558908	0.140474406	-8.396966667	4.58E-17	1.06E-13
ENSG00000173208.3	ABCD2	923.4670176	-1.175683278	0.388982488	-3.022458115	0.002507308	0.031520441
ENSG00000203710.10	CR1	157.6703345	-1.174196357	0.386714761	-3.03633705	0.002394715	0.030751829
ENSG00000148700.14	ADD3	4972.308395	-1.164266077	0.214869595	-5.418477549	6.01E-08	8.45E-06
ENSG00000012779.10	ALOX5	100.5708256	-1.161196754	0.388149103	-2.991625499	0.002774965	0.033818259
ENSG00000140939.14	NOL3	126.4690277	-1.156321174	0.307383888	-3.761814524	0.000168685	0.004506802
ENSG00000104783.11	KCNN4	969.4660391	-1.140117165	0.219388865	-5.196786831	2.03E-07	2.42E-05
ENSG00000025423.11	HSD17B6	19.98309756	-1.137728674	0.368367849	-3.088566704	0.002011245	0.027345312
ENSG00000104447.11	TRPS1	1143.233701	-1.126685836	0.36779507	-3.0633522	0.002188723	0.02921005
ENSG00000171621.13	SPSB1	656.2905204	-1.105437473	0.219222004	-5.042547984	4.59E-07	4.90E-05
ENSG00000241945.7	PWP2	173.1656834	-1.097424808	0.342230966	-3.206678872	0.001342768	0.020975368
ENSG00000081059.19	TCF7	18321.75569	-1.090701654	0.334829548	-3.257483276	0.001124049	0.018475777
ENSG00000127311.9	HELB	1941.066956	-1.084838382	0.295152277	-3.675520964	0.000237365	0.005860167
ENSG00000150347.14	ARID5B	2242.036263	-1.079750716	0.318398273	-3.391195268	0.000695885	0.013203406
ENSG00000091409.14	ITGA6	771.2773768	-1.078578768	0.239898593	-4.495977886	6.93E-06	0.00040216
ENSG00000104880.17	ARHGEF18	231.4286703	-1.076842538	0.320052307	-3.364582961	0.000766594	0.01411557
ENSG00000178209.14	PLEC	55053.61639	-1.068502096	0.222571365	-4.800716833	1.58E-06	0.000129835
ENSG00000182010.10	RTKN2	284.3837908	-1.045790122	0.289001865	-3.618627592	0.000296169	0.006975788
ENSG00000110665.11	C11orf21	205.1022806	-1.043394758	0.248885788	-4.192263313	2.76E-05	0.00116176
ENSG00000121989.14	ACVR2A	157.9083971	-1.040421274	0.243639219	-4.270335788	1.95E-05	0.000885964
ENSG00000166387.11	PPFIBP2	139.9997477	-1.032737655	0.308042598	-3.352580652	0.000800619	0.014497337
ENSG00000157193.15	LRP8	1075.450592	-1.020918743	0.14777789	-6.908467462	4.90E-12	2.51E-09
ENSG00000167207.11	NOD2	614.4566732	-1.019303119	0.162476286	-6.273550092	3.53E-10	1.15E-07
ENSG00000213658.10	LAT	589.5856081	-1.017838492	0.234877243	-4.333491316	1.47E-05	0.000713135
ENSG00000186174.12	BCL9L	7037.126189	-1.017152774	0.207153761	-4.910134237	9.10E-07	8.32E-05
ENSG00000110881.11	ASIC1	214.9440607	-1.016184653	0.355184649	-2.861003864	0.004223019	0.044870359
ENSG00000181690.7	PLAG1	477.8551748	-1.006929611	0.19633022	-5.128755056	2.92E-07	3.35E-05
ENSG00000139679.15	LPAR6	960.5100264	-1.00644404	0.255107991	-3.945168623	7.97E-05	0.002577544
ENSG00000196381.10	ZNF781	39.84236765	-1.005242528	0.313266747	-3.208902758	0.001332425	0.020864968
ENSG00000164466.12	SFXN1	3486.620444	-1.000816264	0.291904331	-3.428576271	0.000606756	0.012037771