

Supplementary Figures & Tables

Sjögren's syndrome minor salivary gland CD4⁺ memory T cells associate with glandular disease features and have a germinal center T follicular helper transcriptional profile

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Supplementary Figures: 3

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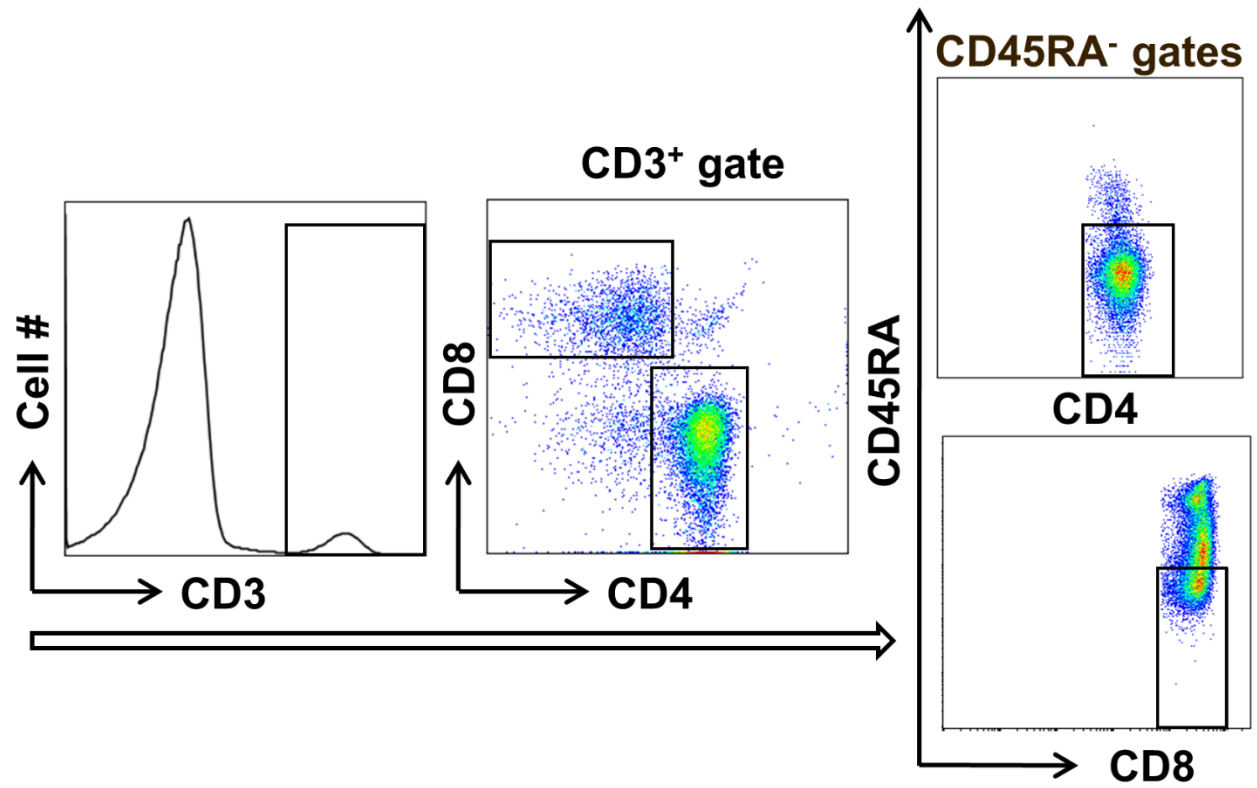


Figure S1. Gating strategy for CD3⁺CD4⁺CD45RA⁻ and CD3⁺CD8⁺CD45RA⁻ T cells.

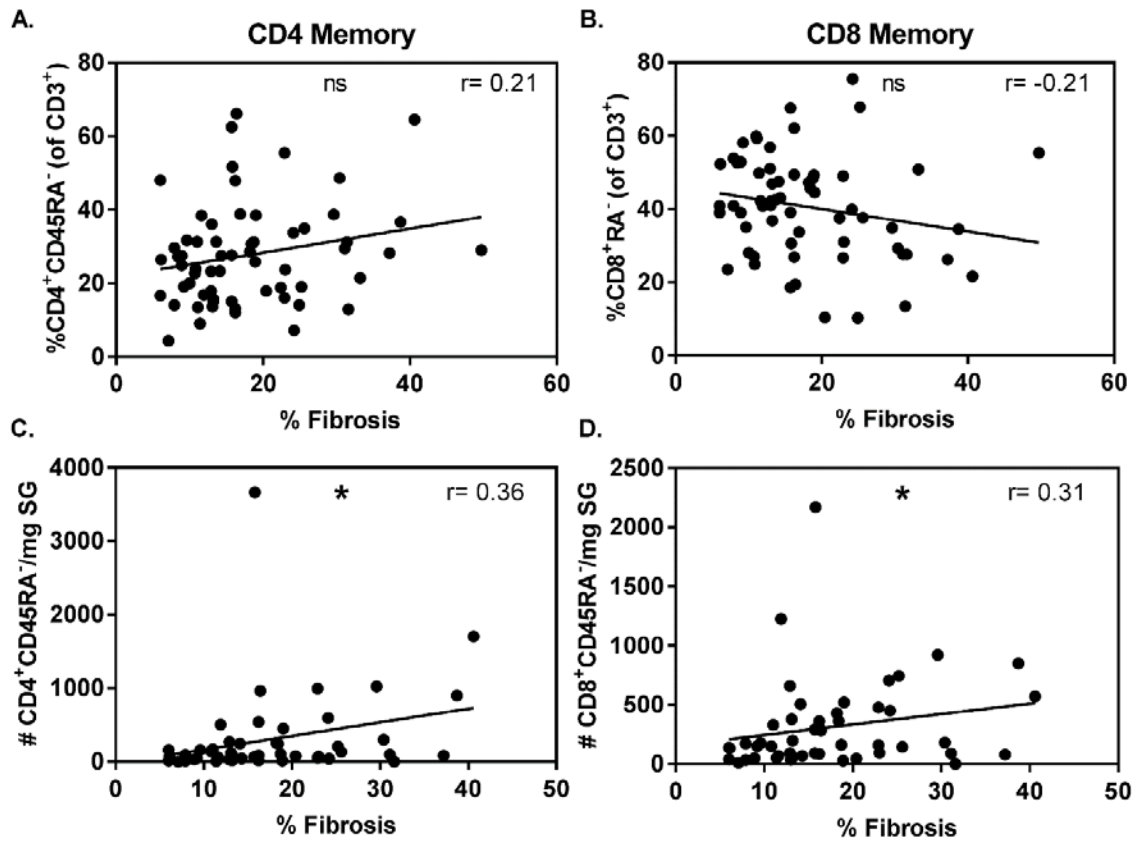


Figure S2. Salivary gland fibrosis is correlated with numbers, but not proportions of SG tissue resident T cells. Correlation of proportions of memory CD4 (A) and CD8 (B) salivary gland T cells with degree of salivary gland fibrosis (pSS, n=32 and nSS, n=30). Correlations of absolute numbers of memory CD4 (C) and CD8 (D) salivary gland T cells/mg biopsy tissue with degree of salivary gland fibrosis (pSS, n=22 and nSS, n=27). Spearman's two-tailed tests were used for all analyses. * $p < 0.05$, ns = $p \geq 0.5$.

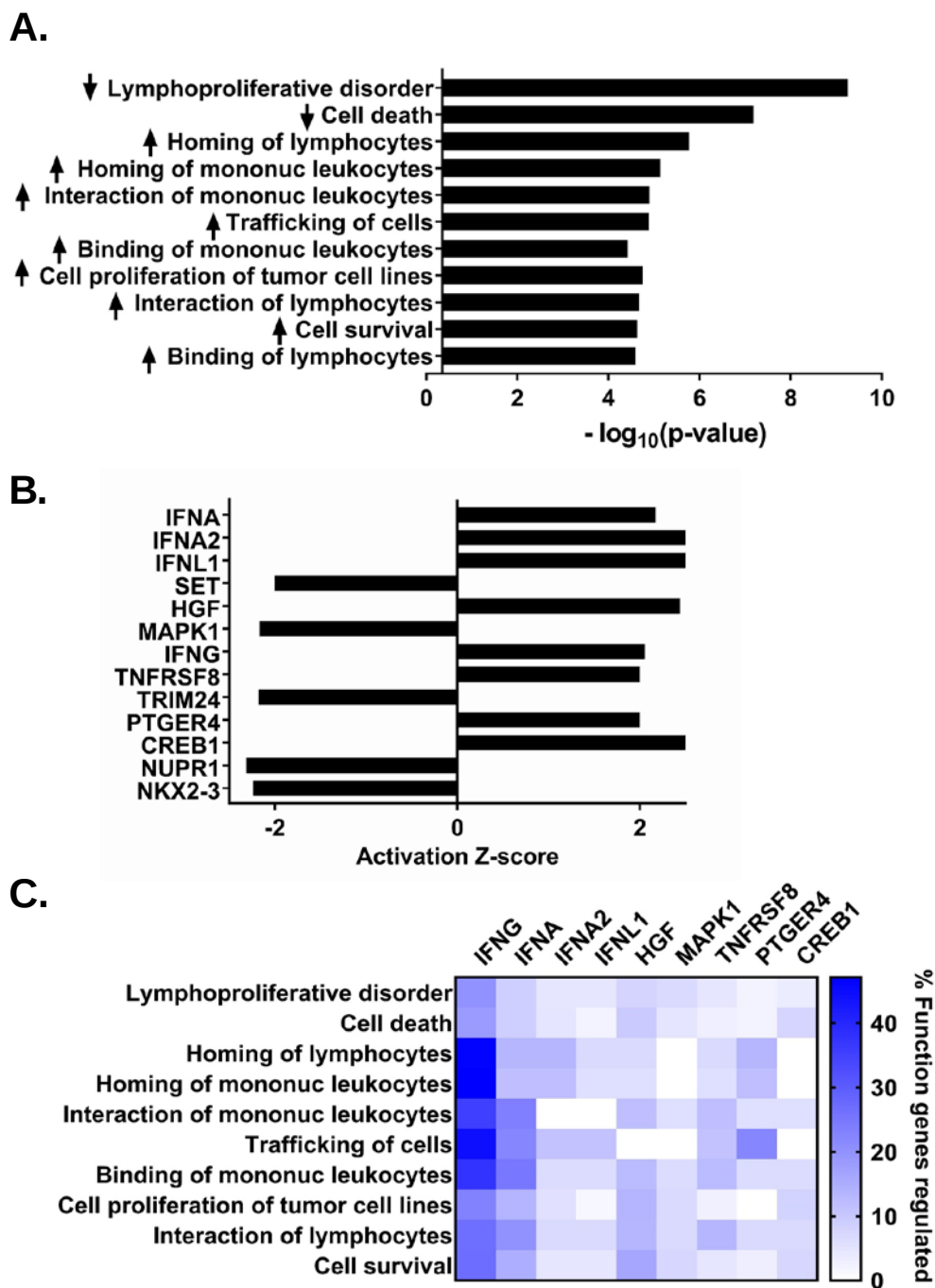


Figure S3. Functions and upstream drivers predicted by Ingenuity Pathways Analysis (IPA). (A) IPA predicted Diseases and Functions at $p < 0.0001$ significance. Up and down arrows denote activation Z scores > 2.0 or < -2.0 , indicating predicted up- or down-regulated activity, respectively. (B) Activation Z-scores of Ingenuity protein-encoding predicted upstream regulators in order of significance (top to bottom). (C) Heatmap showing the percentage of differentially expressed Ingenuity Diseases and Function genes known to be regulated by the predicted upstream regulators listed at the top of the panel. Regulators influencing at least 5% of genes in any pathway are shown.

Table S1. Clinical Exam Values

		FACS Study			Microarray Study		
Clinical Test		pSS (n=51)	nSS (n=69)	p-value ^a	pSS (n=17)	nSS (n=15)	p-value ^a
Focus	Score, Med ^b	1.8	0	<0.0001	2.8	0	<0.0001
Score	(Range)	(0-12)	(0-2)		(1.1-12)	(0-0)	
Anti-Ro ^c	Avg ± SEM	3.8 ± 0.52	0.39 ± 0.12	<0.0001	4.5 ± 0.87	0.2 ± 0	<0.0001
Anti-La ^c	Avg ± SEM	1.4 ± 0.32	0.28 ± 0.07	<0.0001	0.96 ± 0.49	0.2 ± 0	0.019
WUSF ^d	mL, Med	1.2	1.6	0.19	1.3	2.5	0.062
	(Range)	(0.001-11.8)	(0.005-16.9)		(0.01-11.7)	(0.74-7.1)	
Avg % ^e Fibrosis	% area, Med (Range)	22.6 (6.0-49.7)	13.2 (6.0-31.1)	0.0005^f	16.4 (6.0-40.6)	12.9 (6.0-18.9)	0.019
Schirmer's score	mm, Med (Range)	9 (0-35)	15 (0-35)	0.04	15 (2-35)	15 (0-35)	0.69^f
vBS ^g	Score, Med	6	2	<0.0001	5	2	0.011^f
	(Range)	(0-9)	(0-9)		(0-9)	(0-8)	

^a Mann Whitney U-test, 2-tailed unless otherwise indicated

^b Med = median

^c Bio-Rad Bioplex 2200 result

^d WUSF = whole unstimulated salivary flow (mL/15 min)

^e Fibrosis data available from n=32 pSS, n=30 nSS (FACS study) and n=15 pSS, n=14 nSS (microarray study)

^f Unpaired Student's t test

^g vBS = van Bijsterveld score, maximum value

Table S2. SG Memory T cell proportion associations with clinical features in pSS (n=51)

Clinical Feature	CD4 ⁺ CD45RA ⁺ (% of CD3 ⁺)			
	Pearson's correlation ^a		Gamma regression model	
	r	p-value	Model	Variable p-value
vBS ^b	0.3	0.034	x + age x	0.072 0.043
Schirmer's test ^c	0.056	0.7	x + age x	0.45 0.7
WUSF ^d	0.042	0.77	x + age x	0.37 0.76
Biopsy Focus Score	0.44	0.0013	x + age x	0.0054 0.0019
Ro Ab Status ^e	0.43	0.0017	x + age x	0.011 0.0055
Serum IgG	0.37	0.007	x + age x	0.004 0.0078

^a Pearson's two-tailed test

^b vBS = van Bijsterveld score, maximum value

^c Shirmer's test, minimal score

^d WUSF = whole unstimulated salivary flow (mL/15 min)

^e Bio-Rad Bioplex 2200 test outcome (positive/negative)

Table S3. Genes up-regulated in pSS salivary gland CD3⁺CD4⁺CD45RA⁺ T cells

Gene Symbol	Log Fc pSS/nSS	p-value	Adj p-value	Description
FCRL3	5.68	2.83E-09	1.25E-05	Fc receptor-like 3 (FCRL3)
CXCL13	7.18	6.86E-08	2.15E-04	chemokine (C-X-C motif) ligand 13 (CXCL13)
SMN2	3.67	1.29E-06	1.87E-03	survival of motor neuron 2, centromeric (SMN2)
SIRPG	3.44	1.36E-06	1.87E-03	signal-regulatory protein gamma (SIRPG)
C18orf25	3.53	2.13E-06	2.79E-03	chromosome 18 open reading frame 25 (C18orf25), transcript variant 1
FLIP1L	3.70	2.57E-06	3.23E-03	filamin A interacting protein 1-like (FLIP1L), transcript variant 1
C9orf156	4.45	2.66E-06	3.23E-03	chromosome 9 open reading frame 156 (C9orf156)
BRWD1	3.44	5.05E-06	5.68E-03	bromodomain and WD repeat domain containing 1 (BRWD1), transcript variant 3
BIRC2	4.22	5.27E-06	5.72E-03	baculoviral IAP repeat containing 2 (BIRC2)
CD200	4.87	5.51E-06	5.78E-03	CD200 molecule (CD200), transcript variant 2
LOC100129936	4.42	7.39E-06	7.50E-03	cDNA FLJ42830 fis, clone BRCAN2017905
PVT1	3.74	9.19E-06	8.82E-03	PVT1 oncogene (non-protein coding) (PVT1)
FLJ44715	4.15	9.45E-06	8.82E-03	cDNA FLJ44715 fis, clone BRACE3021430
COX16	3.67	9.52E-06	8.82E-03	COX16 cytochrome c oxidase assembly homolog (S. cerevisiae) (COX16), nuclear gene encoding mitochondrial protein, transcript variant 1
lincRNA:chr4:89637527-89646627_R	3.98	1.00E-05	9.03E-03	lincRNA:chr4:89637527-89646627 reverse strand
IFITM1	4.37	1.15E-05	1.00E-02	interferon induced transmembrane protein 1 (9-27) (IFITM1)
lincRNA:chr3:32508871-32518521_R	4.57	1.32E-05	1.10E-02	lincRNA:chr3:32508871-32518521 reverse strand
PDS5A	3.80	1.33E-05	1.10E-02	PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae) (PDS5A), transcript variant 1
PPP2CA	4.33	1.61E-05	1.27E-02	protein phosphatase 2, catalytic subunit, alpha isozyme (PPP2CA)
PLAC8	3.91	1.79E-05	1.28E-02	placenta-specific 8 (PLAC8), transcript variant 2
CSNK1G3	3.79	2.13E-05	1.40E-02	casein kinase 1, gamma 3 (CSNK1G3), transcript variant 4
MDN1	3.46	2.37E-05	1.52E-02	MDN1, midasin homolog (yeast) (MDN1)
ENST00000422938	3.32	2.54E-05	1.60E-02	TEST12 Homo sapiens cDNA clone TEST12044585 5'
PASK	4.92	2.96E-05	1.77E-02	PAS domain containing serine/threonine kinase (PASK), transcript variant 2
CXCR5	4.28	2.98E-05	1.77E-02	chemokine (C-X-C motif) receptor 5 (CXCR5), transcript variant 2
NR3C1	3.72	3.24E-05	1.77E-02	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), transcript variant 5
EPSTI1	4.70	3.24E-05	1.77E-02	epithelial stromal interaction 1 (breast) (EPSTI1), transcript variant 2
VOPPI1	4.41	3.26E-05	1.77E-02	vesicular, overexpressed in cancer, prosurvival protein 1 (VOPPI1)
HERC2P2	3.53	3.60E-05	1.89E-02	hect domain and RLD 2 pseudogene 2 (HERC2P2)
APH1A	4.10	3.71E-05	1.89E-02	anterior pharynx defective 1 homolog A (C. elegans) (APH1A), transcript variant 2
RNF19A	3.72	3.78E-05	1.89E-02	ring finger protein 19A (RNF19A), transcript variant 1
DAPP1	4.09	4.00E-05	1.93E-02	dual adaptor of phosphotyrosine and 3-phosphoinositides (DAPP1)
LOC100509498	3.06	4.04E-05	1.93E-02	hypothetical LOC100509498 (LOC100509498)
DHFR	3.66	4.06E-05	1.93E-02	dihydrofolate reductase (DHFR)
FEZ2	4.05	4.44E-05	2.00E-02	fasciculation and elongation protein zeta 2 (zygin II) (FEZ2), transcript variant 2
ARIH1	3.65	4.92E-05	2.13E-02	ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila) (ARIH1)
SKIV2L2	3.54	4.94E-05	2.13E-02	superkiller viralicidic activity 2-like 2 (S. cerevisiae) (SKIV2L2)
lincRNA:chr6:158658627-158666616_F	3.82	5.08E-05	2.16E-02	lincRNA:chr6:158658627-158666616 forward strand
TSTD1	3.57	5.28E-05	2.22E-02	thiosulfate sulfurtransferase (rhodanese)-like domain containing 1 (TSTD1), transcript variant 1
lincRNA:chr8:129108594-129113502_R	3.85	5.65E-05	2.23E-02	lincRNA:chr8:129108594-129113502 reverse strand
SATB1	4.18	5.68E-05	2.23E-02	SATB homeobox 1 (SATB1), transcript variant 1
TCF7	4.20	5.74E-05	2.23E-02	transcription factor 7 (T-cell specific, HMG-box) (TCF7), transcript variant 1
TIGIT	3.93	5.80E-05	2.23E-02	T cell immunoreceptor with Ig and ITIM domains (TIGIT)
ENST00000390622	3.30	6.04E-05	2.23E-02	immunoglobulin heavy variable 1-46
ZBTB24	4.39	6.19E-05	2.23E-02	zinc finger and BTB domain containing 24 (ZBTB24), transcript variant 1
SHPRH	3.52	7.19E-05	2.41E-02	SNF2 histone linker PHD RING helicase (SHPRH), transcript variant 2
GNL3	3.02	7.61E-05	2.50E-02	guanine nucleotide binding protein-like 3 (nucleolar) (GNL3), transcript variant 1
MKRN7P	3.63	7.96E-05	2.51E-02	makorin ring finger protein 7, pseudogene (MKRN7P)
lincRNA:chrX:73425071-73428011_R	4.38	8.43E-05	2.63E-02	lincRNA:chrX:73425071-73428011 reverse strand
DGKH	3.99	9.08E-05	2.70E-02	diacylglycerol kinase, eta (DGKH), transcript variant 1
LIMS3L	3.57	9.31E-05	2.74E-02	LIM and senescent cell antigen-like domains 3-like (LIMS3L)
LOC100133991	4.43	9.69E-05	2.75E-02	uncharacterized LOC100133991 (LOC100133991)
IL6ST	3.13	1.03E-04	2.86E-02	interleukin 6 signal transducer (gp130, oncostatin M receptor) (IL6ST), transcript variant 3

SETD1B	4.35	1.05E-04	2.88E-02	SET domain containing 1B (SETD1B)
SPRY1	3.94	1.06E-04	2.88E-02	sprouty homolog 1, antagonist of EGF signaling (Drosophila) (SPRY1), transcript variant 2
BABAM1	4.00	1.08E-04	2.89E-02	BRIS and BRCA1 A complex member 1 (BABAM1), transcript variant 1
lincRNA:chr11:130730240-130745336_R	2.63	1.16E-04	2.94E-02	lincRNA:chr11:130730240-130745336 reverse strand
MRP55	4.62	1.16E-04	2.94E-02	mitochondrial ribosomal protein S5 (MRP55), nuclear gene encoding mitochondrial protein
MIAT	3.97	1.16E-04	2.94E-02	myocardial infarction associated transcript (non-protein coding) (MIAT)
A_33_P3404759	2.76	1.23E-04	2.95E-02	Unknown
MAML2	3.06	1.23E-04	2.95E-02	mastermind-like 2 (Drosophila) (MAML2)
PDE4DIP	4.10	1.26E-04	2.95E-02	phosphodiesterase 4D interacting protein (PDE4DIP), transcript variant 9
PLEKHG2	3.31	1.26E-04	2.95E-02	pleckstrin homology domain containing, family G (with RhoGef domain) member 2 (PLEKHG2)
COX7B	4.24	1.27E-04	2.95E-02	cytochrome c oxidase subunit VIIb (COX7B), nuclear gene encoding mitochondrial protein
ZACN	3.87	1.28E-04	2.95E-02	zinc activated ligand-gated ion channel (ZACN)
KLHL12	2.96	1.37E-04	3.03E-02	kelch-like 12 (Drosophila) (KLHL12)
KLHL18	3.37	1.37E-04	3.03E-02	kelch-like 18 (Drosophila) (KLHL18)
UBA7	3.88	1.38E-04	3.03E-02	ubiquitin-like modifier activating enzyme 7 (UBA7)
VWA5A	3.73	1.42E-04	3.08E-02	von Willebrand factor A domain containing 5A (VWA5A), transcript variant 2
RASA4	3.57	1.46E-04	3.14E-02	RAS p21 protein activator 4 (RASA4)
RASSF2	4.58	1.47E-04	3.14E-02	Ras association (RalGDS/AF-6) domain family member 2 (RASSF2), transcript variant 1
TPP1	3.74	1.47E-04	3.14E-02	tripeptidyl peptidase I (TPP1)
NEDD9	3.97	1.51E-04	3.17E-02	neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), transcript variant 2
CUL4B	3.35	1.53E-04	3.18E-02	culin 4B (CUL4B), transcript variant 1
KIAA1671	3.40	1.54E-04	3.18E-02	KIAA1671 (KIAA1671)
UBAP2L	3.52	1.57E-04	3.22E-02	ubiquitin associated protein 2-like (UBAP2L), transcript variant 2
A_24_P32215	3.06	1.59E-04	3.23E-02	Unknown
PDE3B	3.32	1.67E-04	3.29E-02	phosphodiesterase 3B, cGMP-inhibited (PDE3B)
CCDC127	3.29	1.72E-04	3.36E-02	coiled-coil domain containing 127 (CCDC127)
GNL3L	3.83	1.76E-04	3.41E-02	guanine nucleotide binding protein-like 3 (nucleolar)-like (GNL3L), transcript variant 2
METTL23	3.78	1.88E-04	3.53E-02	methyltransferase like 23 (METTL23), transcript variant 6
X57723	3.26	1.98E-04	3.67E-02	rearranged TCR Vbeta 16a mRNA for T cell receptor
CRLS1	3.33	1.99E-04	3.67E-02	cardiolipin synthase 1 (CRLS1), transcript variant 1
GTFC3C	4.15	2.03E-04	3.69E-02	general transcription factor IIIC, polypeptide 2, beta 110kDa (GTF3C2), transcript variant 1
lincRNA:chr8:129108840-129113465_R	3.14	2.13E-04	3.76E-02	lincRNA:chr8:129108840-129113465 reverse strand
lincRNA:chr13:27831250-27836500_F	3.94	2.15E-04	3.78E-02	lincRNA:chr13:27831250-27836500 forward strand
DYNLL1	4.81	2.23E-04	3.85E-02	dynein, light chain, LC8-type 1 (DYNLL1), transcript variant 1
PRR14L	2.96	2.24E-04	3.85E-02	proline rich 14-like (PRR14L)
TAF7	3.73	2.29E-04	3.85E-02	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa (TAF7)
IRF9	3.94	2.30E-04	3.85E-02	interferon regulatory factor 9 (IRF9)
ATRN	3.15	2.43E-04	3.93E-02	attractin (ATRN), transcript variant 2
RAB12	4.11	2.45E-04	3.93E-02	RAB12, member RAS oncogene family (RAB12)
DCTD	4.00	2.49E-04	3.93E-02	dCMP deaminase (DCTD), transcript variant 1
LOC100133315	3.78	2.51E-04	3.93E-02	transient receptor potential cation channel, subfamily C, member 2-like (LOC100133315)
EIF3G	3.52	2.66E-04	4.09E-02	eukaryotic translation initiation factor 3, subunit G (EIF3G)
LDLRAP1	3.94	2.76E-04	4.18E-02	low density lipoprotein receptor adaptor protein 1 (LDLRAP1)
SELL	2.95	2.82E-04	4.22E-02	selectin L (SELL), transcript variant 1
SNIP1	3.07	2.85E-04	4.22E-02	Smad nuclear interacting protein 1 (SNIP1)
NAB1	3.67	2.85E-04	4.22E-02	NGFI-A binding protein 1 (EGRI binding protein 1) (NAB1)
FKBP3	3.72	2.86E-04	4.22E-02	FK506 binding protein 3, 25kDa (FKBP3)
GNA13	3.64	2.88E-04	4.24E-02	guanine nucleotide binding protein (G protein), alpha 13 (GNA13)
PGAP1	3.51	2.92E-04	4.28E-02	post-GPI attachment to proteins 1 (PGAP1)
PIK3CD	3.17	2.95E-04	4.29E-02	phosphoinositide-3-kinase, catalytic, delta polypeptide (PIK3CD)
OAS2	3.22	3.18E-04	4.51E-02	2'-5'-oligoadenylate synthetase 2, 69/71kDa (OAS2), transcript variant 1
VBP1	4.39	3.18E-04	4.51E-02	von Hippel-Lindau binding protein 1 (VBP1)
lincRNA:chr8:129021903-129113336_R	2.64	3.24E-04	4.56E-02	lincRNA:chr8:129021903-129113336 reverse strand
A_33_P3376781	3.40	3.24E-04	4.56E-02	Unknown
lincRNA:chr8:129108828-129113500_R	2.61	3.28E-04	4.57E-02	lincRNA:chr8:129108828-129113500 reverse strand

lincRNA:chr20:1646825-1667675_F	THC2727510	3.01	3.33E-04	4.60E-02	GLT8D3 protein (Fragment), partial (91%)
	UCLK1	2.89	3.43E-04	4.68E-02	lincRNA:chr20:1646825-1667675 forward strand
		4.27	3.43E-04	4.68E-02	uridine-cytidine kinase 1-like 1 (UCLK1), transcript variant 1
ENST00000390633	NF1P2	2.83	3.49E-04	4.71E-02	immunoglobulin heavy variable 1-69
	AB360850	2.69	3.60E-04	4.77E-02	neurofibromin 1 pseudogene 2 (NF1P2)
		3.87	3.70E-04	4.81E-02	mRNA for T cell receptor beta variable 7, partial cds, clone: non 379
PPP4R2	TERF1	3.24	3.75E-04	4.82E-02	telomeric repeat binding factor (NIMA-interacting) 1 (TERF1), transcript variant 1
	FOXO1	2.62	3.92E-04	4.98E-02	rotein phosphatase 4, regulatory subunit 2 (PPP4R2)
	CASK	3.12	3.94E-04	4.98E-02	forkhead box O1 (FOXO1)
FAM184B	FAM184B	3.40	3.98E-04	4.99E-02	alcium/calmodulin-dependent serine protein kinase (MAGUK family) (CASK), transcript variant 1
	RAPGEF2	2.79	4.07E-04	5.07E-02	family with sequence similarity 184, member B (FAM184B)
	NECAP2	3.81	4.14E-04	5.07E-02	Rap guanine nucleotide exchange factor (GEF) 2 (RAPGEF2)
COMMD3	COMMD3	2.83	4.17E-04	5.07E-02	NECAP endocytosis associated 2 (NECAP2), transcript variant 1
	PSMD12	3.33	4.20E-04	5.07E-02	COMM domain containing 3 (COMMD3)
	EIF4EBP2	2.91	4.39E-04	5.21E-02	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 (PSMD12), transcript variant 1
ZC3H8	ZC3H8	2.28	4.43E-04	5.21E-02	eukaryotic translation initiation factor 4E binding protein 2 (EIF4EBP2)
	MKI67IP	2.96	4.44E-04	5.21E-02	zinc finger CCCH-type containing 8 (ZC3H8)
	FAIM3	2.25	4.52E-04	5.25E-02	MKI67 (FHA domain) interacting nucleolar phosphoprotein (MKI67IP)
TRIM5	TRIM5	3.95	4.59E-04	5.28E-02	Fas apoptotic inhibitory molecule 3 (FAIM3), transcript variant 1
	TOMM6	2.89	4.62E-04	5.29E-02	tripartite motif containing 5 (TRIM5), transcript variant gamma
	ESD	4.44	4.67E-04	5.33E-02	translocase of outer mitochondrial membrane 6 homolog (yeast) (TOMM6)
GDE1	DKC1	2.93	4.69E-04	5.33E-02	esterase D (ESD)
	GDE1	3.31	4.73E-04	5.36E-02	dyskeratosis congenita 1, dyskerin (DKC1), transcript variant 1
	LOC441455	2.78	4.77E-04	5.36E-02	glycerophosphodiester phosphodiesterase 1 (GDE1)
A_33_P33357964	A_33_P33357964	2.70	4.77E-04	5.36E-02	makorin ring finger protein 1 pseudogene (LOC441455)
	PARP9	3.64	4.80E-04	5.36E-02	Unknown
	ARFIP1	2.92	4.80E-04	5.36E-02	poly (ADP-ribose) polymerase family, member 9 (PARP9)
RPA2	RBL1	3.41	4.84E-04	5.36E-02	ADP-ribosylation factor interacting protein 1 (ARFIP1), transcript variant 1
	RPA2	3.98	4.85E-04	5.36E-02	retinoblastoma-like 1 (p107) (RBL1), transcript variant 2
	DNAH17	3.28	4.91E-04	5.36E-02	replication protein A2, 32kDa (RPA2)
ENST00000390610	ENST00000390610	3.25	4.92E-04	5.36E-02	dynein, axonemal, heavy chain 17 (DNAH17)
	CKS1B	3.69	4.97E-04	5.39E-02	immunoglobulin heavy variable 1-24
	A_33_P3424108	2.65	5.10E-04	5.50E-02	CDC28 protein kinase regulatory subunit 1B (CKS1B)
ERP44	ERP44	3.08	5.13E-04	5.50E-02	Unknown
	DDX42	2.96	5.15E-04	5.50E-02	endoplasmic reticulum protein 44 (ERP44)
	LONP1	2.67	5.20E-04	5.50E-02	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42 (DDX42), transcript variant 1
MOC51	SNX27	3.99	5.39E-04	5.64E-02	lon peptidase 1, mitochondrial (LONP1), nuclear gene encoding mitochondrial protein
	MOC51	2.76	5.41E-04	5.64E-02	sorting nexin family member 27 (SNX27)
	OSBP	3.48	5.52E-04	5.74E-02	molybdenum cofactor synthesis 1 (MOC51)
lincRNA:chr15:69951596-69988646_F	UROS	2.91	5.60E-04	5.76E-02	oxysterol binding protein (OSBP)
	CSF1R	2.41	5.67E-04	5.81E-02	uroporphyrinogen III synthase (UROS)
	RABGAP1L	3.94	5.71E-04	5.82E-02	lincRNA:chr15:69951596-69988646 forward strand
GLS	SKP2	2.69	5.74E-04	5.83E-02	colony stimulating factor 1 receptor (CSF1R)
	GLS	4.51	5.86E-04	5.91E-02	RAB GTPase activating protein 1-like (RABGAP1L)
	LOC100506190	4.05	5.93E-04	5.94E-02	S-phase kinase-associated protein 2 (p45) (SKP2)
CHN1	CHN1	3.68	5.98E-04	5.94E-02	glutaminase (GLS), nuclear gene encoding mitochondrial protein
	GGCT	2.47	6.00E-04	5.94E-02	Alu subfamily SC sequence contamination warning entry
	NF1	2.88	6.34E-04	6.22E-02	chimerin (chimaerin) 1 (CHN1), transcript variant 1
RAB3GAP1	NONO	2.52	6.48E-04	6.26E-02	gamma-glutamylcyclotransferase (GGCT)
	RAB3GAP1	3.28	6.49E-04	6.26E-02	neurofibromin 1 (NF1), transcript variant 2
	GCC2	3.26	6.51E-04	6.26E-02	non-POU domain containing, octamer-binding (NONO)
lincRNA:chr5:43014835-43017310_F	GCC2	2.78	6.52E-04	6.26E-02	RAB3 GTPase activating protein subunit 1 (catalytic) (RAB3GAP1), transcript variant 2
	PHKB	3.97	6.54E-04	6.26E-02	GRIP and coiled-coil domain containing 2 (GCC2), transcript variant 1
					lincRNA:chr5:43014835-43017310 forward strand
					phosphorylase kinase, beta (PHKB), transcript variant 2

cytidine monophospho-N-acetylneuraminic acid hydroxylase, pseudogene (CMAHP), transcript variant 1

CMAHP	3.62	6.56E-04	6.26E-02	cytidine monophospho-N-acetylneuraminic acid hydroxylase, pseudogene (CMAHP), transcript variant 1
FAM86B2	3.39	6.63E-04	6.26E-02	family with sequence similarity 86, member B2 (FAM86B2)
PHF3	3.58	6.76E-04	6.30E-02	PHD finger protein 3 (PHF3)
BUB3	2.71	6.94E-04	6.37E-02	budding uninhibited by benzimidazoles 3 homolog (yeast) (BUB3)
lincRNA:chr8:129015583-129108805_F	2.46	7.01E-04	6.39E-02	lincRNA:chr8:129015583-129108805 forward strand
lincRNA:chr22:25588075-25594350_R	2.01	7.12E-04	6.46E-02	lincRNA:chr22:25588075-25594350 reverse strand
MCFD2	3.46	7.17E-04	6.47E-02	multiple coagulation factor deficiency 2 (MCFD2), transcript variant 1
SSRP1	4.29	7.28E-04	6.52E-02	structure specific recognition protein 1 (SSRP1)
CCDC75	3.81	7.32E-04	6.52E-02	coiled-coil domain containing 75 (CCDC75)
PDXDC1	3.05	7.32E-04	6.52E-02	pyridoxal-dependent decarboxylase domain containing 1 (PDXDC1)
PPP1CC	3.51	7.34E-04	6.52E-02	protein phosphatase 1, catalytic subunit, gamma isozyme (PPP1CC), transcript variant 1
COPB2	2.60	7.41E-04	6.53E-02	coatamer protein complex, subunit beta 2 (beta prime) (COPB2), transcript variant 1
APAF1	2.77	7.44E-04	6.53E-02	apoptotic peptidase activating factor 1 (APAF1), transcript variant 3
SNORA23	3.39	7.46E-04	6.53E-02	small nucleolar RNA, H/ACA box 23 (SNORA23), small nucleolar RNA [NR_002962]
SYNJ1	2.98	7.50E-04	6.54E-02	synaptotagmin 1 (SYNJ1), transcript variant 2
TAB2	2.54	7.53E-04	6.55E-02	TGF-beta activated kinase 1/MAP3K7 binding protein 2 (TAB2)
ZNF827	2.87	7.58E-04	6.56E-02	zinc finger protein 827 (ZNF827)
HSDL1	3.64	7.62E-04	6.57E-02	hydroxysteroid dehydrogenase like 1 (HSDL1), transcript variant 1
TARS2	4.45	7.65E-04	6.58E-02	threonyl-tRNA synthetase 2, mitochondrial (putative) (TARS2)
CCNL1	1.85	7.81E-04	6.67E-02	cyclin L1 (CCNL1)
DNMT3A	2.32	7.95E-04	6.74E-02	DNA (cytosine-5-)-methyltransferase 3 alpha (DNMT3A), transcript variant 1
lincRNA:chrX:73470227-73470871_R	2.05	7.96E-04	6.74E-02	lincRNA:chrX:73470227-73470871 reverse strand
S1PR1	3.89	8.01E-04	6.74E-02	sphingosine-1-phosphate receptor 1 (S1PR1)
ORF1	2.73	8.04E-04	6.74E-02	partial mRNA for hypothetical protein (ORF1), clone pT-Adv JuaX22
TPP2	2.54	8.06E-04	6.74E-02	tripeptidyl peptidase II (TPP2)
lincRNA:chr3:47207196-47217796_F	2.96	8.11E-04	6.74E-02	lincRNA:chr3:47207196-47217796 forward strand
DBF4	3.28	8.23E-04	6.82E-02	DBF4 homolog (S. cerevisiae) (DBF4)
DYNC1L12	3.12	8.52E-04	6.99E-02	dynein, cytoplasmic 1, light intermediate chain 2 (DYNC1L12)
CCR7	2.09	8.53E-04	6.99E-02	chemokine (C-C motif) receptor 7 (CCR7)
FANCD2	2.58	8.66E-04	6.99E-02	Fanconi anemia, complementation group D2 (FANCD2), transcript variant 2
MRPL33	3.37	8.69E-04	6.99E-02	mitochondrial ribosomal protein L33 (MRPL33), nuclear gene encoding mitochondrial protein, transcript variant 1
ENOSF1	3.08	8.69E-04	6.99E-02	enolase superfamily member 1 (ENOSF1), transcript variant 2
ARHGEF18	3.12	8.72E-04	6.99E-02	Rho/Rac guanine nucleotide exchange factor (GEF) 18 (ARHGEF18), transcript variant 1
NLRCS	3.15	8.73E-04	6.99E-02	NLR family, CARD domain containing 5 (NLRCS)
POLB	1.96	8.84E-04	6.99E-02	polymerase (DNA directed), beta (POLB)
GRAMD1B	3.01	8.86E-04	6.99E-02	GRAM domain containing 1B (GRAMD1B)
RASSF5	4.12	8.87E-04	6.99E-02	Ras association (RalGDS/AF-6) domain family member 5 (RASSF5), transcript variant 2
ENST00000540599	3.09	8.87E-04	6.99E-02	cDNA FLJ36021 fis, clone TEST12016568
lincRNA:chr8:129082331-129113343_F	2.70	8.91E-04	6.99E-02	lincRNA:chr8:129082331-129113343 forward strand
P2RY10	3.42	9.18E-04	7.09E-02	purinergic receptor P2Y, G-protein coupled, 10 (P2RY10), transcript variant 1
FAM115C	2.65	9.24E-04	7.10E-02	family with sequence similarity 115, member C (FAM115C), transcript variant 3
CTLA4	2.82	9.29E-04	7.11E-02	cytotoxic T-lymphocyte-associated protein 4 (CTLA4), transcript variant 1
GGCX	2.63	9.34E-04	7.11E-02	gamma-glutamyl carboxylase (GGCX), transcript variant 1
RBM8A	2.14	9.47E-04	7.16E-02	RNA binding motif protein 8A (RBM8A)
LRRC16A	2.46	9.51E-04	7.16E-02	leucine rich repeat containing 16A (LRRC16A), transcript variant 1
COG3	3.25	9.54E-04	7.16E-02	component of oligomeric golgi complex 3 (COG3)
PRKAR1A	3.81	9.55E-04	7.16E-02	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1) (PRKAR1A), transcript variant 3
lincRNA:chr5:74327969-74348269_F	3.35	9.62E-04	7.16E-02	lincRNA:chr5:74327969-74348269 forward strand
RPL19	3.36	9.70E-04	7.16E-02	ribosomal protein L19 (RPL19)
AKAP8	3.29	9.81E-04	7.16E-02	A kinase (PRKA) anchor protein 8 (AKAP8)
GALM	3.87	9.81E-04	7.16E-02	galactose mutarotase (aldose 1-epimerase) (GALM)
C4orf41	2.62	9.82E-04	7.16E-02	chromosome 4 open reading frame 41 (C4orf41), transcript variant 2
CD302	3.21	9.85E-04	7.16E-02	CD302 molecule (CD302), transcript variant 1
EEF2	4.07	9.93E-04	7.16E-02	eukaryotic translation elongation factor 2 (EEF2)
PSMC6	3.07	9.94E-04	7.16E-02	proteasome (prosome, macropain) 26S subunit, ATPase, 6 (PSMC6)

A_33_P3240966	2.71	9.95E-04	7.16E-02	Unknown
ENST00000391369	2.52	1.00E-03	7.18E-02	HCG2032337PRO1848 Uncharacterized protein
NDPIP2	2.66	1.01E-03	7.21E-02	Nedd4 family interacting protein 2 (NDPIP2), transcript variant 1
UBE3A	2.40	1.06E-03	7.41E-02	ubiquitin protein ligase E3A (UBE3A), transcript variant 3
RILP2	3.40	1.06E-03	7.41E-02	Rab interacting lysosomal protein-like 2 (RILP2)
lincRNA:chr2:67037871-67048646_F	2.17	1.06E-03	7.41E-02	lincRNA:chr2:67037871-67048646 forward strand
lincRNA:chr22:27062378-27064552_R	2.70	1.06E-03	7.41E-02	lincRNA:chr22:27062378-27064552 reverse strand
DDHD1	3.03	1.07E-03	7.41E-02	DDHD domain containing 1 (DDHD1), transcript variant 1
HIC2	2.50	1.08E-03	7.41E-02	hypermethylated in cancer 2 (HIC2)
PLAT	2.84	1.08E-03	7.41E-02	plasmalogen activator, tissue (PLAT), transcript variant 1
RICTOR	2.70	1.08E-03	7.41E-02	RPTOR independent companion of MTOR, complex 2 (RICTOR)
SNX3	3.38	1.09E-03	7.41E-02	sorting nexin 3 (SNX3), transcript variant 1
ENST00000390595	3.35	1.09E-03	7.41E-02	immunoglobulin heavy variable 1-3
OR1L4	2.16	1.09E-03	7.41E-02	olfactory receptor, family 1, subfamily L, member 4 (OR1L4)
LIMS1	2.98	1.10E-03	7.41E-02	LIM and senescent cell antigen-like domains 1 (LIMS1), transcript variant 2
CEP68	3.12	1.10E-03	7.41E-02	centrosomal protein 68kDa (CEP68)
SF3B3	3.91	1.10E-03	7.41E-02	splicing factor 3b, subunit 3, 130kDa (SF3B3)
ADI1	2.95	1.10E-03	7.41E-02	acireductone dioxygenase 1 (ADI1)
NOD2	3.42	1.10E-03	7.41E-02	nucleotide-binding oligomerization domain containing 2 (NOD2)
lincRNA:chr6:29701971-29740296_F	3.27	1.10E-03	7.41E-02	lincRNA:chr6:29701971-29740296 forward strand
ATF7IP	2.94	1.11E-03	7.41E-02	activating transcription factor 7 interacting protein (ATF7IP)
ZNFA10	2.56	1.12E-03	7.41E-02	zinc finger protein 410 (ZNFA10), transcript variant 2
AGPS	3.42	1.12E-03	7.41E-02	alkylglycerone phosphate synthase (AGPS)
CBX7	3.59	1.12E-03	7.41E-02	chromobox homolog 7 (CBX7)
PPFIA1	3.26	1.14E-03	7.50E-02	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 (PPFIA1), transcript variant 2
EDEM1	3.36	1.16E-03	7.54E-02	ER degradation enhancer, mannosidase alpha-like 1 (EDEM1)
MCM6	2.92	1.18E-03	7.60E-02	minichromosome maintenance complex component 6 (MCM6)
RBM18	3.37	1.18E-03	7.61E-02	RNA binding motif protein 18 (RBM18), transcript variant 1
ALG6	2.63	1.18E-03	7.61E-02	asparagine-linked glycosylation 6, alpha-1,3-glucosyltransferase homolog (S. cerevisiae) (ALG6)
ATP2C1	3.22	1.19E-03	7.62E-02	ATPase, Ca++ transporting, type 2C, member 1 (ATP2C1), transcript variant 3
SKIV2L	2.94	1.19E-03	7.62E-02	superkiller Viralidic activity 2-like (S. cerevisiae) (SKIV2L)
MRPS18A	2.57	1.20E-03	7.62E-02	mitochondrial ribosomal protein S18A (MRPS18A), nuclear gene encoding mitochondrial protein, transcript variant 1
NEK4	3.71	1.21E-03	7.67E-02	NIMA (never in mitosis gene a)-related kinase 4 (NEK4), transcript variant 1
A_33_P3376954	3.08	1.22E-03	7.70E-02	Unknown
RAB30	2.51	1.22E-03	7.70E-02	RAB30, member RAS oncogene family (RAB30)
AAK1	3.67	1.23E-03	7.70E-02	AP2 associated kinase 1 (AAK1)
RPL18	3.43	1.24E-03	7.73E-02	ribosomal protein L18 (RPL18)
ENST00000390639	1.79	1.24E-03	7.73E-02	immunoglobulin heavy variable 7-81 (non-functional)
DLEU1	2.77	1.24E-03	7.73E-02	deleted in lymphocytic leukemia 1 (non-protein coding) (DLEU1)
RBAK	2.90	1.24E-03	7.73E-02	RB-associated KRAB zinc finger (RBAK), transcript variant 1
LOC100507429	2.49	1.26E-03	7.78E-02	Homo sapiens hypothetical LOC100507429 (LOC100507429)
NAT10	2.94	1.26E-03	7.78E-02	N-acetyltransferase 10 (GCN5-related) (NAT10), transcript variant 1
lincRNA:chr8:129032934-129113447_R	2.60	1.27E-03	7.78E-02	lincRNA:chr8:129032934-129113447 reverse strand
ENST00000502284	2.40	1.27E-03	7.78E-02	cDNA FLJ44668 fis, clone BRACE3004981
JHDM1D	3.81	1.28E-03	7.78E-02	jumonji C domain containing histone demethylase 1 homolog D (S. cerevisiae) (JHDM1D)
NDUFS6	3.09	1.28E-03	7.78E-02	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase) (NDUFS6), nuclear gene encoding mitochondrial protein
C7orf42	3.09	1.29E-03	7.78E-02	chromosome 7 open reading frame 42 (C7orf42)
STT3A	3.32	1.29E-03	7.78E-02	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae) (STT3A)
CDYL2	2.81	1.29E-03	7.78E-02	chromodomain protein, Y-like 2 (CDYL2)
VAMP1	3.52	1.30E-03	7.83E-02	vesicle-associated membrane protein 1 (synaptobrevin 1) (VAMP1), transcript variant 3
UBN1	3.12	1.31E-03	7.86E-02	ubiquitin 1 (UBN1), transcript variant 1
XLOC_I2_014645	3.21	1.31E-03	7.86E-02	lincRNA (XLOC_I2_014645), lincRNA [TCONS_I2_00028399]
VNN2	1.86	1.32E-03	7.90E-02	vanin 2 (VNN2), transcript variant 1
ZZZ3	1.94	1.34E-03	7.94E-02	zinc finger, ZZ-type containing 3 (ZZZ3)
MRPL35	3.53	1.34E-03	7.94E-02	mitochondrial ribosomal protein L35 (MRPL35), nuclear gene encoding mitochondrial protein, transcript variant 2

IGFBP4	2.95	1.35E-03	7.95E-02	insulin-like growth factor binding protein 4 (IGFBP4)
TFRC	2.98	1.36E-03	7.99E-02	transferrin receptor (p90, CD71) (TFRC), transcript variant 1
TMEM194B	1.82	1.37E-03	8.01E-02	transmembrane protein 194B
TXK	2.75	1.38E-03	8.06E-02	TXK tyrosine kinase (TXK)
EVC	2.85	1.40E-03	8.15E-02	Ellis van Creveld syndrome (EVC)
OSBPL3	2.91	1.41E-03	8.15E-02	oxysterol binding protein-like 3 (OSBPL3), transcript variant 1
UOCHRH	3.30	1.41E-03	8.15E-02	ubiquinol-cytochrome c reductase hinge protein (UOCHRH), nuclear gene encoding mitochondrial protein
SEPN1	2.39	1.43E-03	8.20E-02	selenoprotein N, 1 (SEPN1), transcript variant 1
FBXL20	2.86	1.43E-03	8.20E-02	F-box and leucine-rich repeat protein 20 (FBXL20), transcript variant 1
lincRNA:chr14:22994620-23016487_F	3.03	1.44E-03	8.20E-02	lincRNA:chr14:22994620-23016487 forward strand
FAU	3.13	1.45E-03	8.20E-02	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (FAU)
DCTN6	4.26	1.48E-03	8.30E-02	dynactin 6 (DCTN6)
IPO7	3.55	1.48E-03	8.31E-02	importin 7 (IPO7)
ADSL	3.12	1.49E-03	8.33E-02	adenylosuccinate lyase (ADSL), transcript variant 1
FBXW2	3.28	1.50E-03	8.33E-02	F-box and WD repeat domain containing 2 (FBXW2)
lincRNA:chr8:141532461-141536259_R	2.87	1.50E-03	8.37E-02	lincRNA:chr8:141532461-141536259 reverse strand
WTAP	2.50	1.51E-03	8.37E-02	Wilms tumor 1 associated protein
AK096917	3.16	1.54E-03	8.46E-02	cDNA FLJ39598 fis, clone SKNSH2002866
RAB4A	3.42	1.58E-03	8.63E-02	RAB4A, member RAS oncogene family (RAB4A)
ENST00000445752	2.88	1.61E-03	8.65E-02	coiled-coil domain containing 144A
lincRNA:chr3:9387975-9397375_R	2.82	1.62E-03	8.67E-02	lincRNA:chr3:9387975-9397375 reverse strand
C12orf23	3.10	1.64E-03	8.71E-02	chromosome 12 open reading frame 23 (C12orf23)
SEC11A	3.66	1.68E-03	8.82E-02	SEC11 homolog A (S. cerevisiae) (SEC11A)
C2orf3	2.44	1.71E-03	8.89E-02	chromosome 2 open reading frame 3 (C2orf3), transcript variant 1
MLF1	2.87	1.74E-03	8.94E-02	myeloid leukemia factor 1 (MLF1), transcript variant 1
LOC100506774	3.07	1.75E-03	8.94E-02	Homo sapiens hypothetical LOC100506774 (LOC100506774)
EIF4A3	3.43	1.75E-03	8.94E-02	eukaryotic translation initiation factor 4A3 (EIF4A3)
STAT1	3.37	1.76E-03	8.94E-02	signal transducer and activator of transcription 1, 91kDa (STAT1), transcript variant beta
TRIM14	2.00	1.76E-03	8.94E-02	tripartite motif containing 14 (TRIM14), transcript variant 2
ELK1	3.06	1.77E-03	8.94E-02	ELK1, member of ETS oncogene family (ELK1), transcript variant 2
LYPLA1	2.37	1.77E-03	8.94E-02	lysophospholipase I (LYPLA1)
MBIP	3.45	1.77E-03	8.94E-02	MAP3K12 binding inhibitory protein 1 (MBIP), transcript variant 2
CKAP2	3.08	1.78E-03	8.94E-02	cytoskeleton associated protein 2 (CKAP2), transcript variant 1
TLE3	1.87	1.78E-03	8.94E-02	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), transcript variant 1
PRKCB	3.25	1.79E-03	8.94E-02	protein kinase C, beta (PRKCB), transcript variant 2
HSPA4	2.97	1.79E-03	8.94E-02	heat shock 70kDa protein 4 (HSPA4)
A_24_P255473	3.20	1.79E-03	8.94E-02	Unknown
SLC25A14	2.84	1.79E-03	8.94E-02	solute carrier family 25 (mitochondrial carrier, brain), member 14 (SLC25A14), nuclear gene encoding mitochondrial protein, transcript variant long
HDGF	2.69	1.79E-03	8.94E-02	hepatoma-derived growth factor (HDGF), transcript variant 1
RBCK1	2.50	1.80E-03	8.94E-02	RanBP-type and C3HC4-type zinc finger containing 1 (RBCK1), transcript variant 2,
USP3	3.35	1.81E-03	8.97E-02	ubiquitin specific peptidase 3 (USP3)
ENST00000390394	2.71	1.82E-03	8.97E-02	T cell receptor beta variable 20-1
A_33_P3385387	2.67	1.82E-03	8.97E-02	Unknown
PILRA	2.82	1.83E-03	8.99E-02	paired immunoglobulin-like type 2 receptor alpha (PILRA), transcript variant 3
C10orf46	2.20	1.84E-03	9.04E-02	chromosome 10 open reading frame 46 (C10orf46)
C17orf49	3.00	1.87E-03	9.05E-02	chromosome 17 open reading frame 49 (C17orf49)
LOC100127885	2.46	1.87E-03	9.05E-02	hypothetical protein LOC100127885 (LOC100127885)
MAN1C1	2.72	1.87E-03	9.05E-02	mannosidase, alpha, class 1C, member 1 (MAN1C1)
SYNC	2.71	1.87E-03	9.05E-02	syncollin, intermediate filament protein (SYNC), transcript variant 1
POLE	2.02	1.87E-03	9.05E-02	polymrase (DNA directed), epsilon (POLE)
IKBKE	3.43	1.88E-03	9.06E-02	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon (IKBKE), transcript variant 1
POLR3E	3.60	1.88E-03	9.06E-02	polymerase (RNA) III (DNA directed) polypeptide E (80kD) (POLR3E)
CDKAL1	2.99	1.89E-03	9.07E-02	CDK5 regulatory subunit associated protein 1-like 1 (CDKAL1)
lincRNA:chr8:129001411-129082607_R	3.10	1.91E-03	9.15E-02	lincRNA:chr8:129001411-129082607 reverse strand
BRMS1	2.86	1.92E-03	9.18E-02	breast cancer metastasis suppressor 1 (BRMS1), transcript variant 2

NECAP1	2.68	1.93E-03	9.20E-02	NECAP endocytosis associated 1 (NECAP1), transcript variant 1
ATP6V1A	2.84	1.94E-03	9.20E-02	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A (ATP6V1A)
ARHGAP35	2.78	1.94E-03	9.20E-02	Rho GTPase activating protein 35 (ARHGAP35)
GNAQ	2.41	1.96E-03	9.21E-02	guanine nucleotide binding protein (G protein), q polypeptide (GNAQ)
ENST00000435913	2.79	1.96E-03	9.21E-02	Unknown
TAB3	2.42	1.96E-03	9.21E-02	TGF-beta activated kinase 1/MAP3K7 binding protein 3 (TAB3)
FDPS	3.45	1.97E-03	9.21E-02	farnesyl diphosphate synthase (FDPS), transcript variant 1
CHD6	2.09	2.00E-03	9.27E-02	chromodomain helicase DNA binding protein 6 (CHD6)
A_33_P3362453	2.19	2.01E-03	9.30E-02	Unknown
lincRNA:chr12:68421607-68422081_forward_strand	2.43	2.01E-03	9.30E-02	lincRNA:chr12:68421607-68422081_forward_strand
MAT2B	3.45	2.03E-03	9.30E-02	methionine adenosyltransferase II, beta (MAT2B), transcript variant 2
lincRNA:chr1:40004013-40020238_forward_strand	2.86	2.03E-03	9.30E-02	lincRNA:chr1:40004013-40020238_forward_strand
C5orf56	3.06	2.03E-03	9.30E-02	cDNA: FLJ21568 fis, clone COL06492
CD2	3.07	2.03E-03	9.30E-02	cDNA, FLJ17718
DCAF13	3.45	2.03E-03	9.30E-02	DDB1 and CUL4 associated factor 13 (DCAF13)
PGAM1	2.94	2.04E-03	9.30E-02	phosphoglycerate mutase 1 (brain) (PGAM1)
GEM	3.86	2.04E-03	9.30E-02	GTP binding protein overexpressed in skeletal muscle (GEM), transcript variant 1
MGA	2.52	2.05E-03	9.31E-02	ref Homo sapiens MAX gene associated (MGA), transcript variant 1
MEAF6	2.48	2.06E-03	9.31E-02	MYST/Esa1-associated factor 6 (MEAF6)
RHBDD2	3.34	2.07E-03	9.31E-02	rhomboid domain containing 2 (RHBDD2), transcript variant 2
ZCCHC17	3.61	2.07E-03	9.31E-02	zinc finger, CCHC domain containing 17 (ZCCHC17)
ILKAP	3.34	2.08E-03	9.34E-02	integrin-linked kinase-associated serine/threonine phosphatase (ILKAP)
CLASP1	2.72	2.09E-03	9.37E-02	cytoplasmic linker associated protein 1 (CLASP1), transcript variant 1
ETFA	2.86	2.09E-03	9.37E-02	electron-transfer-flavoprotein, alpha polypeptide (ETFA), nuclear gene encoding mitochondrial protein, transcript variant 1
RAB43	2.91	2.12E-03	9.45E-02	RAB43, member RAS oncogene family (RAB43), transcript variant 1
PDPK1	2.17	2.13E-03	9.46E-02	3-phosphoinositide dependent protein kinase-1 (PDPK1), transcript variant 1
ENST00000399576	3.08	2.14E-03	9.48E-02	Uncharacterized protein
ST6GAL1	2.79	2.15E-03	9.48E-02	T6 beta-galactosamide alpha-2,6-sialyltransferase 1 (ST6GAL1), transcript variant 1
NFKBID	3.13	2.18E-03	9.53E-02	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, delta (NFKBID)
ELMO1	3.13	2.19E-03	9.53E-02	engulfment and cell motility 1 (ELMO1), transcript variant 1
AGFG1	3.13	2.19E-03	9.53E-02	ArfGAP with FG repeats 1 (AGFG1), transcript variant 1
VMP1	2.54	2.19E-03	9.53E-02	vacuole membrane protein 1 (VMP1)
C1orf124	2.51	2.23E-03	9.63E-02	chromosome 1 open reading frame 124 (C1orf124), transcript variant 1
FAM20B	2.42	2.24E-03	9.63E-02	family with sequence similarity 20, member B (FAM20B)
CREB3L2	2.45	2.24E-03	9.63E-02	cAMP responsive element binding protein 3-like 2 (CREB3L2)
MTRR	2.63	2.24E-03	9.63E-02	5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 2
ACTR3B	3.44	2.24E-03	9.63E-02	ARP3 actin-related protein 3 homolog B (yeast) (ACTR3B), transcript variant 2
HNRPLL	2.54	2.26E-03	9.67E-02	heterogeneous nuclear ribonucleoprotein L-like
TNFSF8	2.87	2.27E-03	9.69E-02	tumor necrosis factor (ligand) superfamily, member 8 (TNFSF8), transcript variant 1, mRNA
ATP2B1	3.16	2.30E-03	9.73E-02	ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1), transcript variant 1
ENST00000379435	2.40	2.30E-03	9.73E-02	T cell receptor beta variable 20/OR9-2 (non-functional)
PRMT10	2.71	2.31E-03	9.73E-02	protein arginine methyltransferase 10 (putative) (PRMT10)
THRAP3	2.93	2.31E-03	9.73E-02	thyroid hormone receptor associated protein 3 (THRAP3)
A_33_P3397473	2.53	2.31E-03	9.73E-02	Unknown
BET1	3.41	2.31E-03	9.73E-02	blocked early in transport 1 homolog (S. cerevisiae) (BET1)
TES	3.15	2.33E-03	9.74E-02	testis derived transcript (3 LIM domains) (TES), transcript variant 2, mRNA
LPXN	1.97	2.34E-03	9.74E-02	leupaxin (LPXN), transcript variant 2
TNRC6C	2.70	2.35E-03	9.75E-02	trinucleotide repeat containing 6C (TNRC6C)
MBD1	3.27	2.36E-03	9.75E-02	methyl-CpG binding domain protein 1 (MBD1)
TOMM5	3.00	2.37E-03	9.78E-02	translocase of outer mitochondrial membrane 5 homolog (yeast) (TOMM5), nuclear gene encoding mitochondrial protein, transcript variant 3
SIC11A2	2.34	2.37E-03	9.78E-02	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 (SLC11A2), transcript variant 4
SMARCA5	3.15	2.39E-03	9.78E-02	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 (SMARCA5)
RBM38	3.34	2.39E-03	9.78E-02	RNA binding motif protein 38 (RBM38), transcript variant 1
ZBTB46	2.88	2.39E-03	9.78E-02	zinc finger and BTB domain containing 46 (ZBTB46)
RCOR1	2.78	2.40E-03	9.79E-02	REST corepressor 1 (RCOR1)

STAG2	1.88	2.40E-03	9.79E-02	stromal antigen 2 (STAG2), transcript variant 1
PREB	3.19	2.42E-03	9.81E-02	prolactin regulatory element binding (PREB)
GNAS	4.05	2.43E-03	9.82E-02	GNAS complex locus
ENST00000419160	2.76	2.43E-03	9.83E-02	Alu subfamily J sequence contamination warning entry, partial (13%)
TRAP1	3.17	2.45E-03	9.88E-02	TNF receptor-associated protein 1 (TRAP1)
NFATC3	3.32	2.46E-03	9.90E-02	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 (NFATC3), transcript variant 1

Table S4. Genes down-regulated in pSS salivary gland CD3⁺CD4⁺CD45RA⁺ T cells

Gene Symbol	Log FC	pSS/non-SS	p-value	Adj p-value	Description
lincRNA:chr3:65012510-65037885_R	0.44	2.81E-05	1.74E-02		lincRNA:chr3:65012510-65037885 reverse strand
AIF1	0.40	6.24E-05	2.23E-02		allograft inflammatory factor 1 (AIF1), transcript variant 2
CRNN	0.52	1.51E-04	3.17E-02		cornulin (CRNN)
VAMP2	0.48	1.65E-04	3.28E-02		vesicle-associated membrane protein 2 (synaptobrevin 2) (VAMP2)
lincRNA:chr18:48545077-48556150_F	0.47	2.23E-04	3.85E-02		lincRNA:chr18:48545077-48556150 forward strand
ZBP1	0.35	2.29E-04	3.85E-02		Z-DNA binding protein 1 (ZBP1), transcript variant 1
SLC5A10	0.48	2.34E-04	3.85E-02		solute carrier family 5 (sodium/glucose cotransporter), member 10 (SLC5A10), transcript variant 1
ADRB2	0.51	2.46E-04	3.93E-02		adrenergic, beta-2-, receptor, surface (ADRB2)
IL15	0.58	2.71E-04	4.14E-02		interleukin 15 (IL15), transcript variant 2
LOC256880	0.51	2.80E-04	4.22E-02		uncharacterized LOC256880 (LOC256880)
ENST00000439423	0.44	3.61E-04	4.77E-02		hypothetical LOC554174, mRNA (cDNA clone MGC:16743 IMAGE:4130428)
A_33_P3212570	0.44	3.62E-04	4.77E-02		Unknown
ERCC-00104_60	0.54	3.71E-04	4.81E-02		
lincRNA:chr8:128181722-128182314_R	0.38	4.20E-04	5.07E-02		lincRNA:chr8:128181722-128182314 reverse strand
ENST00000457108	0.44	4.12E-04	5.07E-02		Zinc finger protein 21 (Zinc finger protein KOX14)
lincRNA:chr6:22020628-22111150_R	0.45	4.17E-04	5.07E-02		lincRNA:chr6:22020628-22111150 reverse strand
C21orf67	0.42	4.43E-04	5.21E-02		chromosome 21 open reading frame 67 (C21orf67), transcript variant 1
SLC22A2	0.57	4.35E-04	5.21E-02		solute carrier family 22 (organic cation transporter), member 2 (SLC22A2)
BRD1	0.49	4.90E-04	5.36E-02		bromodomain containing 1 (BRD1)
BEST1	0.55	4.98E-04	5.39E-02		bestrophin 1 (BEST1), transcript variant 1
lincRNA:chr7:32969114-32982514_R	0.40	5.17E-04	5.50E-02		lincRNA:chr7:32969114-32982514 reverse strand
FASLG	0.33	5.92E-04	5.94E-02		Fas ligand (TNF superfamily, member 6) (FASLG)
ADH7	0.61	5.96E-04	5.94E-02		alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide (ADH7), transcript variant 2
MKS1	0.44	6.20E-04	6.12E-02		Meckel syndrome, type 1 (MKS1), transcript variant 1
XAGE5	0.49	6.24E-04	6.14E-02		X antigen family, member 5 (XAGE5)
lincRNA:chr2:184032455-184084780_R	0.54	6.36E-04	6.22E-02		lincRNA:chr2:184032455-184084780 reverse strand
FKBP11	0.33	6.58E-04	6.26E-02		FK506 binding protein 11, 19 kDa (FKBP11), transcript variant 1
TPRN	0.49	6.75E-04	6.30E-02		taperin (TPRN)
PLD1	0.53	6.75E-04	6.30E-02		phosphatidylcholine-specific (PLD1), transcript variant 1
SLC4A10	0.42	6.96E-04	6.37E-02		solute carrier family 4, sodium bicarbonate transporter, member 10 (SLC4A10), transcript variant 2
lincRNA:chr10:50217119-50223094_F	0.49	7.15E-04	6.47E-02		lincRNA:chr10:50217119-50223094 forward strand
lincRNA:chr19:56791970-56826162_F	0.50	7.35E-04	6.52E-02		lincRNA:chr19:56791970-56826162 forward strand
C1orf88	0.58	7.34E-04	6.52E-02		chromosome 1 open reading frame 88 (C1orf88)
KLHL4	0.51	7.42E-04	6.53E-02		kelch-like 4 (Drosophila) (KLHL4), transcript variant 2
ATP13A2	0.42	7.81E-04	6.67E-02		ATPase type 13A2 (ATP13A2), transcript variant 1
C2orf53	0.50	7.80E-04	6.67E-02		chromosome 2 open reading frame 53 (C2orf53)
MMP1	0.48	7.99E-04	6.74E-02		matrix metalloproteinase 1 (interstitial collagenase) (MMP1), transcript variant 1
lincRNA:chr10:131848410-131919360_F	0.48	8.41E-04	6.93E-02		lincRNA:chr10:131848410-131919360 forward strand
LOC100652995	0.45	8.65E-04	6.99E-02		hypothetical LOC100652995 (LOC100652995)
ENST00000434150	0.47	8.75E-04	6.99E-02		Unknown
CLTB	0.55	8.75E-04	6.99E-02		clathrin, light chain B (CLTB), transcript variant 2
ENST00000414816	0.55	8.92E-04	6.99E-02		Homo sapiens hypothetical LOC400511 (FLJ45256)
ZFPM1	0.56	8.94E-04	6.99E-02		zinc finger protein, multitype 1 (ZFPM1)
CACNA1I	0.57	8.72E-04	6.99E-02		calcium channel, voltage-dependent, T type, alpha 1I subunit (CACNA1I), transcript variant 1
PHYHD1	0.56	9.05E-04	7.05E-02		phytanoyl-CoA dioxygenase domain containing 1 (PHYHD1), transcript variant 2
lincRNA:chr8:38616218-38630243_F	0.46	9.15E-04	7.09E-02		lincRNA:chr8:38616218-38630243 forward strand
GPC3	0.50	9.17E-04	7.09E-02		glypican 3 (GPC3), transcript variant 1

GZMB	0.52	9.22E-04	7.10E-02	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB)
B3GALT6	0.55	9.34E-04	7.11E-02	UDP-Gal:betaGal beta 1,3-galactosyltransferase polypeptide 6 (B3GALT6)
ZNF202	0.39	9.77E-04	7.16E-02	zinc finger protein 202 (ZNF202)
TMEM104	0.48	9.64E-04	7.16E-02	transmembrane protein 104 (TMEM104)
lincRNA:chr5:93988844-94003469_F	0.52	9.83E-04	7.16E-02	lincRNA:chr5:93988844-94003469 forward strand
lincRNA:chr19:52195738-52206988_R	0.49	1.14E-03	7.50E-02	lincRNA:chr19:52195738-52206988 reverse strand
INTS5	0.54	1.15E-03	7.53E-02	integrator complex subunit 5 (INTS5),
ABCB1	0.30	1.19E-03	7.62E-02	ATP-binding cassette, sub-family B (MDR/TAP), member 1 (ABCB1)
lincRNA:chr16:88805249-88810399_F	0.57	1.20E-03	7.62E-02	lincRNA:chr16:88805249-88810399 forward strand
CCDC57	0.50	1.22E-03	7.70E-02	coiled-coil domain containing 57 (CCDC57)
FLAP	0.47	1.28E-03	7.78E-02	HSFLAP five-lipoxygenase activating protein (FLAP) (Homo sapiens) (exp=-1; wgp=0; cg=0), partial (66%)
KIR3DL1	0.50	1.35E-03	7.97E-02	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1 (KIR3DL1)
SLC27A1	0.46	1.36E-03	7.99E-02	solute carrier family 27 (fatty acid transporter), member 1 (SLC27A1)
AY203961	0.54	1.40E-03	8.15E-02	LP8151 mRNA, complete cds
ENST00000531225	0.50	1.41E-03	8.15E-02	Putative transmembrane protein C8orfK29
GGTLC2	0.51	1.41E-03	8.15E-02	gamma-glutamyltransferase light chain 2 (GGTLC2), transcript variant 1
ZNF285	0.45	1.42E-03	8.20E-02	zinc finger protein 285 (ZNF285)
MATK	0.47	1.45E-03	8.20E-02	megakaryocyte-associated tyrosine kinase (MATK), transcript variant 1
ZNF692	0.53	1.45E-03	8.20E-02	zinc finger protein 692
EDA	0.56	1.44E-03	8.20E-02	ectodysplasin A (EDA), transcript variant 3
A_33_P3260021	0.54	1.51E-03	8.38E-02	Unknown
PHOSPHO1	0.59	1.52E-03	8.40E-02	phosphatase, orphan 1 (PHOSPHO1), transcript variant 1
CU691877	0.59	1.58E-03	8.63E-02	Synthetic construct Homo sapiens gateway clone IMAGE:100021124 3' read C1QTNF9
PLEKHG3	0.48	1.59E-03	8.63E-02	pleckstrin homology domain containing, family G (with RhoGef domain) member 3 (PLEKHG3)
ADAM8	0.50	1.59E-03	8.63E-02	ADAM metalloproteinase domain 8 (ADAM8), transcript variant 1
ARX	0.58	1.60E-03	8.64E-02	aristaeless related homeobox (ARX)
ENST00000381261	0.40	1.60E-03	8.64E-02	A kinase (PRKA) anchor protein 17A
lincRNA:chr4:93175777-93192627_F	0.56	1.61E-03	8.64E-02	lincRNA:chr4:93175777-93192627 forward strand
GOSR1	0.41	1.63E-03	8.67E-02	golgi SNAP receptor complex member 1 (GOSR1), transcript variant 3
MUC3A	0.47	1.63E-03	8.67E-02	mucin 3A, cell surface associated (MUC3A)
FFAR3	0.53	1.62E-03	8.67E-02	free fatty acid receptor 3 (FFAR3)
lincRNA:chr6:113682343-113682601_F	0.57	1.63E-03	8.67E-02	lincRNA:chr6:113682343-113682601 forward strand
ERCC-00108_60	0.61	1.66E-03	8.74E-02	
SLC2A11	0.66	1.69E-03	8.85E-02	solute carrier family 2 (facilitated glucose transporter), member 11
lincRNA:chr8:49499922-49506997_F	0.52	1.70E-03	8.86E-02	lincRNA:chr8:49499922-49506997 forward strand
LOC100132356	0.46	1.71E-03	8.88E-02	uncharacterized LOC100132356 (LOC100132356)
lincRNA:chr15:25322012-25328606_F	0.62	1.71E-03	8.89E-02	lincRNA:chr15:25322012-25328606 forward strand
LOC440297	0.49	1.74E-03	8.94E-02	chondroitin sulfate proteoglycan 4 pseudogene (LOC440297)
A_33_P3385671	0.61	1.77E-03	8.94E-02	Unknown
C14orf93	0.49	1.80E-03	8.95E-02	chromosome 14 open reading frame 93 (C14orf93), transcript variant 1
HMG2	0.55	1.81E-03	8.96E-02	high mobility group AT-hook 2 (HMG2), transcript variant 2
AK123110	0.58	1.90E-03	9.12E-02	cDNA FLJ41115 fis, clone BRACE1000533
RRM1	0.51	1.95E-03	9.21E-02	ribonucleotide reductase M1 (RRM1)
A_33_P3247068	0.52	1.96E-03	9.21E-02	Unknown
A_33_P3232637	0.55	1.97E-03	9.21E-02	Unknown
MSMB	0.56	1.99E-03	9.25E-02	microseminoprotein, beta- (MSMB)
CSF1	0.56	1.99E-03	9.26E-02	colony stimulating factor 1 (macrophage) (CSF1), transcript variant 1
A_33_P3268395	0.55	2.03E-03	9.30E-02	Unknown
SSTR3	0.58	2.03E-03	9.30E-02	somatostatin receptor 3 (SSTR3)

DMPK	0.47	2.06E-03	9.31E-02	dystrophia myotonica-protein kinase (DMPK)
GTPBP5	0.57	2.05E-03	9.31E-02	GTP binding protein 5 (putative) (GTPBP5)
ENST00000401851	0.64	2.06E-03	9.31E-02	hypothetical protein MGC10955
MUC7	0.43	2.12E-03	9.45E-02	mucin 7, secreted (MUC7), transcript variant 3
lincRNA:chr18:77398927-77439745_R	0.60	2.13E-03	9.46E-02	lincRNA:chr18:77398927-77439745 reverse strand
NEK6	0.54	2.15E-03	9.48E-02	NIMA (never in mitosis gene a)-related kinase 6 (NEK6), transcript variant 2
SUN5	0.56	2.15E-03	9.48E-02	Sad1 and UNC84 domain containing 5 (SUN5)
PNPO	0.49	2.19E-03	9.53E-02	pyridoxamine 5'-phosphate oxidase (PNPO)
CK906254	0.68	2.19E-03	9.53E-02	ie98c03.y5 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens cDNA clone IMAGE:5674757 5'
CNTN1	0.55	2.21E-03	9.57E-02	contactin 1 (CNTN1), transcript variant 1
A_33_P3240652	0.44	2.24E-03	9.63E-02	Unknown
PNKD	0.61	2.26E-03	9.67E-02	paroxysmal nonkinesigenic dyskinesia (PNKD), nuclear gene encoding mitochondrial protein, transcript variant 1
PLCG2	0.65	2.34E-03	9.74E-02	phospholipase C, gamma 2 (phosphatidylinositol-specific) (PLCG2)
NAT8B	0.52	2.38E-03	9.78E-02	N-acetyltransferase 8B (GCN5-related, putative, gene/pseudogene) (NAT8B)
PLEKHF1	0.60	2.39E-03	9.78E-02	pleckstrin homology domain containing, family F (with FYVE domain) member 1 (PLEKHF1)
GJA4	0.60	2.39E-03	9.78E-02	gap junction protein, alpha 4, 37kDa (GJA4)
MCC	0.59	2.40E-03	9.79E-02	mutated in colorectal cancers (MCC), transcript variant 1
DSCAML1	0.65	2.41E-03	9.79E-02	Down syndrome cell adhesion molecule like 1 (DSCAML1)
LOC728684	0.50	2.42E-03	9.81E-02	cDNA FLJ44019 fis, clone TEST14026192
ACOT11	0.52	2.46E-03	9.90E-02	acyl-CoA thioesterase 11 (ACOT11), transcript variant 2
ENST00000525262	0.62	2.48E-03	9.96E-02	Unknown

Table S5. Ingenuity Diseases and Functions enriched among DEGs in SG CD4+CD45RA- T cells of pSS cases versus nSS controls

Disease or Function	p-value	Z-score ^a	# DEGs in Category	Disease and Function Molecules Present in DEG Dataset
Lymphohematopoietic cancer	1.21E-09	-0.894	126	ABCB1, ACOT11, ADRB2, ADL, AKAP17A, AKAP8, APAF1, APH1A, ARHGAP35, ARIH1, ATP6V1A, ATRN, BEST1, CBX7, CCR7, CD2, CD200, CEP68, CHD6, CLTB, C RNN, CSF1R, CTLA4, CXCL13, CXCR5, DHFR, DLEU1, DNMT3A, ELK1, ELMO1, EPSTI1, ETFA, EVC, FAM86B2, FAM86KP, FANCD2, FASLG, FCMR, FDPs, FLIP1L, F KBP3, FOXO1, GCC2, GJA4, GLS, GNA13, GNAQ, GNAS, GZMB, HMGA2, IFITM1, IGFBP4, IKBKE, IL15, ILKAP, IPO7, KIR3DL1, KLHL4, LIMS3, LIMS4, LONP1, LYPL A1, MAML2, MBD1, MCM6, MGA, MLF1, MMP1, MOCs1, MRPS5, NEDD9, NEK4, NEK6, NF1, NONO, NR3C1, OAS2, OSBP, PDE3B, PDE4DIP, PDPK1, PHF3, PHK B, PHYHD1, PIK3CD, PLAC8, PLCG2, PLEKHG3, PNKD, POLB, POLE, PPP2CA, PPP4R2, PRKCB, PRR14L, RAB4A, RASA4, RASSF5, RBCK1, RBM38, RICT OR, RRM1, S1PR1, SATB1, SELL, SETD1B, SIRPG, SKIV2L2, SKP2, SLC4A10, SSTR3, STAG2, STAT1, TCF7, TERC, THRAP3, TIGIT, TLE3, TNFSF8, TNRC6C, UBE3A, UC KL1, UROS, USP3, VMP1, ZBTB24, ZNF827
Lymphoproliferative disorder	1.27E-09	↓ -2.183	89	ACOT11, ADRB2, ADL, AKAP8, APAF1, APH1A, ARIH1, ATRN, CCR7, CD2, CD200, CEP68, CHD6, CRNN, CSF1R, CTLA4, CXCL13, CXCR5, DHFR, DLEU1, DNMT3A, ELK1, ELMO1, EPSTI1, ETFA, EVC, FAM86B2, FAM86KP, FANCD2, FASLG, FCMR, FDPs, FLIP1L, F KBP3, FOXO1, GCC2, GJA4, GLS, GNA13, GNAQ, GNAS, GZMB, HMGA2, IFITM1, IGFBP4, IKBKE, IL15, ILKAP, IPO7, KIR3DL1, KLHL4, LIMS3, LIMS4, LONP1, LYPL A1, MAML2, MBD1, MCM6, MGA, MLF1, MMP1, MOCs1, MRPS5, NEDD9, NEK4, NEK6, NF1, NONO, NR3C1, OAS2, OSBP, PDE3B, PLEKHG3, PNKD, POLB, POLE, PPP2CA, PRKCB, RAB4A, RASSF5, RBCK1, RBM38, RICTOR, RRM1, S1PR1, SATB1, SELL, SKIV2L2, SKP2, SLC4A10, STAG2, STAT1, TCF7, TERC, THRAP3, TIGIT, TLE3, TNFSF8, TNRC6C, UBE3A, UCKL1, UROS, VMP1, ZBTB24
Hematologic cancer	1.55E-09	-0.894	125	ABCB1, ACOT11, ADRB2, ADL, AKAP17A, AKAP8, APAF1, APH1A, ARHGAP35, ARIH1, ATP6V1A, ATRN, BEST1, CBX7, CCR7, CD2, CD200, CEP68, CHD6, CLTB, C RNN, CSF1R, CTLA4, CXCL13, CXCR5, DHFR, DLEU1, DNMT3A, ELK1, ELMO1, EPSTI1, ETFA, EVC, FAM86B2, FAM86KP, FANCD2, FASLG, FCMR, FDPs, FLIP1L, F KBP3, FOXO1, GCC2, GJA4, GLS, GNA13, GNAQ, GNAS, GZMB, HMGA2, IFITM1, IGFBP4, IKBKE, IL15, ILKAP, IPO7, KIR3DL1, KLHL4, LIMS3, LIMS4, LONP1, LYPL A1, MAML2, MBD1, MCM6, MGA, MLF1, MMP1, MOCs1, MRPS5, NEDD9, NEK4, NEK6, NF1, NONO, NR3C1, OAS2, OSBP, PDE3B, PDE4DIP, PDPK1, PHF3, PHK B, PHYHD1, PIK3CD, PLAC8, PLCG2, PLEKHG3, PNKD, POLB, POLE, PPP2CA, PPP4R2, PRKCB, PRR14L, RAB4A, RASA4, RASSF5, RBCK1, RBM38, RICT OR, RRM1, S1PR1, SATB1, SELL, SETD1B, SIRPG, SKIV2L2, SKP2, SLC4A10, STAG2, STAT1, TCF7, TERC, THRAP3, TIGIT, TLE3, TNFSF8, TNRC6C, UBE3A, UCKL1, U ROS, USP3, VMP1, ZBTB24, ZNF827
Lymphoid cancer	4.24E-09	-0.902	122	ABCB1, ACOT11, ADRB2, ADL, AKAP17A, AKAP8, APAF1, APH1A, ARHGAP35, ARIH1, ATP6V1A, ATRN, BEST1, CCR7, CD2, CD200, CEP68, CHD6, CLTB, CRNN, CSF1R, CTLA4, CXCL13, CXCR5, DHFR, DLEU1, DNMT3A, ELK1, ELMO1, ETFA, EVC, FAM86B2, FAM86KP, FANCD2, FASLG, FCMR, FDPs, FLIP1L, FKBP3, FOXO1 ,GCC2, GJA4, GLS, GNA13, GNAQ, GNAS, GZMB, HMGA2, IFITM1, IGFBP4, IKBKE, IL15, ILKAP, IPO7, KIR3DL1, KLHL4, LIMS3, LIMS4, LONP1, LYPLA1, MAML2, MBD1, MCM6, MGA, MLF1, MMP1, MOCs1, MRPS5, NEDD9, NEK4, NEK6, NF1, NONO, NR3C1, OAS2, OSBP, PDE3B, PDE4DIP, PDPK1, PHK8, PHYHD1, PIK3CD ,PLAC8, PLCG2, PLEKHG2, PLEKHG3, PNKD, POLB, POLE, PPP2CA, PRKCB, PRR14L, RAB4A, RASA4, RASSF5, RBCK1, RBM38, RICTOR, RRM1, S1PR1, SATB1, SEL L, SETD1B, SIRPG, SKIV2L2, SKP2, SLC4A10, SSTR3, STAG2, STAT1, TCF7, TERC, THRAP3, TIGIT, TLE3, TNFSF8, TNRC6C, UBE3A, UCKL1, UROS, USP3, VMP1, ZBT B24, ZNF827
Necrosis	1.42E-08	-1.691	124	AAK1, ABCB1, ADAM8, ADI1, ADRB2, APAF1, ATP13A2, ATP2B1, ATP2C1, BIRC2, BRMS1, BUB3, CCR7, CD2, CD200, CKAP2, CLASP1, COPB2, CREB3L2, CSF1, CS F1R, CTLA4, CUL4B, DCTD, DHFR, DMPK, DNMT3A, DYNLL1, EEF2, EIF3G, ELK1, FANCD2, FASLG, FAU, FCMR, FCRL3, FDPs, FOXO1, GEM, GLS, GNA13, GNAQ, G NAS, GNL3, GPC3, GZMB, HDGF, HMGA2, HSPA4, IGFBP4, IGHG1, IKBKE, IL15, IL6ST, ILKAP, IRF9, KIR3DL1, LIMS1, LONP1, LYPLA1, MAML2, MBD1, MDN1, M MPI, MTG2, NAT10, NEDD9, NEK4, NEK6, NF1, NFKBID, NR3C1, PDE3B, PDPK1, PIK3CD, PLAC8, PLAT, PLCG2, PLD1, PLEKHF1, POLB, POLR3E, PPP1CC, PPP2C A, PRKAR1A, PRKCB, PSMC6, PSMMD12, RAPGEF2, RASA4, RASSF5, RBCK1, RB1L1, RBM8A, RICTOR, RNF19A, RPA2, RPL19, RRM1, S1PR1, SATB1, SELL, SF3B3, SK P2, SLC11A2, SLC22A2, SMN1, SMN2, SSRP1, SSTR3, ST6GAL1, STAT1, TCF7, TERF1, TERC, TNFSF8, TPP1, TPP2, TRAP1, UBA7, UBE3A, VOPP1, WTAP, YME1L1, ZC3H8
Lymphoproliferative malignancy	2.46E-08	-1.459	83	ACOT11, ADRB2, ADL, AKAP8, ATRN, CCR7, CD2, CD200, CEP68, CHD6, CRNN, CSF1R, CTLA4, CXCL13, CXCR5, DHFR, DLEU1, DNMT3A, ELK1, ELMO1, FASLG, F CMR, FDPs, FLIP1L, FKBP3, FOXO1, GJA4, GNA13, GZMB, HMGA2, IFITM1, IGFBP4, IKBKE, IL15, IPO7, KIR3DL1, KLHL4, LONP1, LYPLA1, MAML2, MBD1, MGA, MMP1, NEDD9, NEK4, NEK6, NF1, NONO, NR3C1, OAS2, OSBP, PDE3B, PIK3CD, PLAC8, PLCG2, PLEKHG3, PNKD, POLB, POLE, PPP2CA, PRKCB, RAB4A, RASSF5, RBCK1, RBM38, RICTOR, RRM1, S1PR1, SATB1, SELL, SKIV2L2, SKP2, SLC4A10, STAT1, TCF7, TIGIT, TNFSF8, TNRC6C, UBE3A, UCK1, UROS, VMP1, ZBTB24
Lymphoma	3.30E-08	-1.179	67	ADRB2, ADL, AKAP8, ATRN, CCR7, CD2, CD200, CHD6, CRNN, CSF1R, CTLA4, CXCL13, CXCR5, DHFR, DNMT3A, ELK1, FASLG, FDPs, FLIP1L, FKBP3, FOXO1, GJA 4, GNA13, GZMB, HMGA2, IFITM1, IGFBP4, IKBKE, IL15, IPO7, KIR3DL1, LONP1, MBD1, MGA, MMP1, NEK4, NEK6, NF1, NONO, NR3C1, OAS2, OSBP, PIK3CD, P LAC8, PLCG2, PLEKHG3, POLB, POLE, PPP2CA, PRKCB, RAB4A, RASSF5, RBCK1, RBM38, RICTOR, RRM1, SATB1, SELL, SKIV2L2, SKP2, SLC4A10, STAT1, TNFSF8, TNRC6C, UBE3A, UROS, ZBTB24
Lymphocytic neoplasm	3.81E-08	-1.459	84	ACOT11, ADRB2, ADL, AKAP8, ATRN, CCR7, CD2, CD200, CEP68, CHD6, CRNN, CSF1R, CTLA4, CXCL13, CXCR5, DHFR, DLEU1, DNMT3A, ELK1, ELMO1, FASLG, F CMR, FDPs, FLIP1L, FKBP3, FOXO1, GJA4, GNA13, GZMB, HMGA2, IFITM1, IGFBP4, IKBKE, IL15, IPO7, KIR3DL1, KLHL4, LONP1, LYPLA1, MAML2, MBD1, MGA, MMP1, NEDD9, NEK4, NEK6, NF1, NONO, NR3C1, OAS2, OSBP, PDE3B, PIK3CD, PLAC8, PLCG2, PLEKHG3, PNKD, POLB, POLE, PPP2CA, PRKCB, RAB4A, RASSF5, RBCK1, RBM38, RICTOR, RRM1, S1PR1, SATB1, SELL, SKIV2L2, SKP2, SLC4A10, STAT1, TCF7, TERC, TIGIT, TNFSF8, TNRC6C, UBE3A, UCKL1, UROS, VMP1, ZBTB

Non-Hodgkin disease	58	8.60E-08		ADSL,AKAP8,ATRN,CCR7,CD2,CD200,CHD6,CRNN,CSF1R,CXCL13,CXCR5,DHFR,DNMT3A,ELK1,FASLG,FDPS,FILIP1L,FOXO1,GJAA4,GNA13,GZMB,IFITM1,IGFBP4,IKBKE,IL15,KIR3DL1,LONP1,MBD1,MGA,MMP1,NEK4,NEK6,NF1,NONO,NR3C1,OAS2,OSBP,PIK3CD,PLCG2,PLEKHG3,POLB,POLE,PPP2C A,PRKCB,RAB4A,RBCK1,RICTOR,RRM1,SATB1,SELL,SKIV2L2,SKP2,SLC4A10,STAT1,TNRC6C,UBE3A,UROS,ZBTB24
				AAK1,ABCB1,ADAM8,ADI1,ADRB2,AGO2,AIF1,AKAP8,APAF1,APH1A,ARHGAP35,ARX,ATP13A2,ATP2B1,ATP2C1,BIRC2,BRD1,BRMS1,BUB3,CBX7,CCR7,CD2,CD200,CKAP2,CLASP1,CO PB2,CREB3L2,CSF1,CSF1R,CTLA4,CUL4B,DCTD,DDX42,DHFR,DMPK,DNMT3A,DYNLL1,EDA,EEF2,EIF3G,ELK1,ELMO1,FANCD2,FASLG,FAU,FCMR,FCRL3,FDPS,FFAR3,GNA13,GNAQ,GNAS,GNP3,GPC3,GZMB,HDFG,HMGA2,HSPA4,IGFBP4,IGHG1,IKBKE,IL15,IL6ST,ILKAP,IRF9,KIR3DL1,LIMS1,LONP1,LYP1A1,MAMLI2,MBD1,MCFD2,MDN1,MMP1,MTG2,NAT10,NAT8B,NEDD9,NEK4,NEK6,NF1,NFKB1,D,NOD2,NR3C1,PDE3B,PDPK1,PIK3CD,PLAC8,PLAT,PLCG2,PLD1,PLEKHF1,POLB,POLR3E,PP1CC,PPP2CA,PRKAR1A,PRKCB,PSMCG,PSMD12,RAPGEF2,RASA4,RASSF2,RASSF5,RBCK1,RBL1,RBM8A,RICTOR,RNF19A,RP2A,RPL19,RRM1,S1PR1,SATB1,SELENON,SELL,SF3B3,SKP2,SLC11A2,SLC22A2,SMARCA5,SMN1/SMN2,SSRP1,SSTR3,ST6GAL1,STAT1,TAB2,TCF7,TERF1,TERC,TNFSF8,TPP1,TPP2,TRAP1,TKX,UBA7,UBE3A,VAMP2,VOPP1,WTAP,YME1L1,ZC3H8
Cell death	145	1.47E-07	↓ -2.118	ABCB1,ADAM8,BIRC2,BRD1,CCR7,CD200,CD302,CSF1,CSF1R,CTLA4,CXCL13,CXCR5,DAPP1,DKC1,DNMT3A,ELMO1,FANCD2,FASLG,FCMR,FOXO1,GLS,GNA13,GNAS,GPC3,HMGA2,IL15,IL6ST,MATK,NEDD9,NF1,NFATC3,NLRCS,NOD2,NR3C1,PIK3CD,PILRA,PLAC8,PLAT,PLCG2,POLR3E,PPP2CA,PRKCB,RAPGEF2,RASSF2,RASSF5,RBM38,RCOR1,RICTOR,S1PR1,SATB1,SELL,SLC11A2,ST6GAL1,STAT1,TFCR,TIGIT,TPP2,TKX,ZBTB46
				ABCB1,APAF1,APH1A,ARIH1,CSF1R,DHFR,DNMT3A,FANCD2,NF1,NR3C1,POLB,RRM1,STAG2 CCR7,CXCL13,FOXO1,IL15,NEDD9,PDPK1,S1PR1,SELL
Quantity of blood cells	59	1.57E-07	0.537	ABCB1,AGFG1,CTLA4,DHFR,FASLG,FOXO1,GNAQ,GZMB,IL6ST,NR3C1,PPP2CA,S1PR1,SELL,SKIV2L,ST6GAL1,STAT1,TCF7,TLE3,ZBP1
				APAF1,APH1A,ARIH1,CSF1R,DHFR,DNMT3A,FANCD2,NF1,NR3C1,POLB,RRM1,STAG2
Chronic myelomonocytic leukemia	12	1.67E-06		ABCB1,ADAM8,ADI1,ADRB2,AGO2,AIF1,AKAP8,APAF1,APH1A,ARHGAP35,ATP2C1,BIRC2,BRD1,BRMS1,BUB3,CCR7,CD2,CD200,CKAP2,CLASP1,CREB3L2,CSF1,CSF1R,CTLA4,CUL4B,DDX42,DHFR,DMPK,DNMT3A,DYNLL1,EDA,ELK1,ELMO1,FASLG,FAU,FCMR,FFAR3,FOXO1,GEM,GLS,GNA13,GNAQ,GNAS,GNL3,GPC3,GZMB,HDFG,HMGA2,HSPA4,IGFBP4,IGHG1,IKBKE,IL15,IL6ST,ILKAP,KIR3DL1,LIMS1,LYP1A1,MDN1,MMP1,NAT10,NAT8B,NEDD9,NEK6,NF1,NFKBID,NOD2,NR3C1,PDPK1,PIK3CD,PLAC8,PLAT,PLCG2,PLD1,PLEKHF1,POLB,POLR3E,PP1CC,PPP2CA,PRKAR1A,PRKCB,RAPGEF2,RASA4,RASSF2,RASSF5,RBCK1,RBL1,RICTOR,RP2A,RRM1,S1PR1,SATB1,SELENON,SELL,SKP2,SLC22A2,SMARCA5,SMN1/SMN2,SSRP1,SSTR3,ST6GAL1,STAT1,TAB2,TERF1,TFCR,TNFSF8,TPP2,TRAP1,TKX,UBA7,VOPP1,WTAP,YME1L1,ZC3H8
				AT1,TAB2,TERF1,TFCR,TNFSF8,TPP2,TRAP1,TKX,UBA7,VOPP1,WTAP,YME1L1,ZC3H8
Apoptosis	114	2.64E-06	-1.357	ABCB1,ADAM8,ADI1,ADRB2,AGO2,AIF1,AKAP8,APAF1,APH1A,ARHGAP35,ATP2C1,BIRC2,BRD1,BRMS1,BUB3,CCR7,CD2,CD200,CKAP2,CLASP1,CREB3L2,CSF1,CSF1R,CTLA4,CUL4B,DDX42,DHFR,DMPK,DNMT3A,DYNLL1,EDA,ELK1,ELMO1,FASLG,FAU,FCMR,FFAR3,FOXO1,GEM,GLS,GNA13,GNAQ,GNAS,GNL3,GPC3,GZMB,HDFG,HMGA2,HSPA4,IGFBP4,IGHG1,IKBKE,IL15,IL6ST,ILKAP,KIR3DL1,LIMS1,LYP1A1,MDN1,MMP1,NAT10,NAT8B,NEDD9,NEK6,NF1,NFKBID,NOD2,NR3C1,PDPK1,PIK3CD,PLAC8,PLAT,PLCG2,PLD1,PLEKHF1,POLB,POLR3E,PP1CC,PPP2CA,PRKAR1A,PRKCB,RAPGEF2,RASA4,RASSF2,RASSF5,RBCK1,RBL1,RICTOR,RP2A,RRM1,S1PR1,SATB1,SELENON,SELL,SKP2,SLC22A2,SMARCA5,SMN1/SMN2,SSRP1,SSTR3,ST6GAL1,STAT1,TAB2,TERF1,TFCR,TNFSF8,TPP2,TRAP1,TKX,UBA7,VOPP1,WTAP,YME1L1,ZC3H8
				AT1,TAB2,TERF1,TFCR,TNFSF8,TPP2,TRAP1,TKX,UBA7,VOPP1,WTAP,YME1L1,ZC3H8
Homing of lymphocytes	15	3.81E-06	↑ 2.252	ADAM8,CCR7,CXCL13,CXCR5,ELMO1,FOXO1,GNA13,GNAS,IGHG1,IL15,NEDD9,NR3C1,PIK3CD,S1PR1,SELL
				ABCB1,APAF1,APH1A,ARIH1,CSF1R,DHFR,DNMT3A,FANCD2,NF1,NR3C1,POLB,RRM1,STAG2
Myelodysplastic-myeloproliferative disease	13	6.83E-06		ABCB1,APAF1,APH1A,ARIH1,CSF1R,DHFR,DNMT3A,FANCD2,NF1,NR3C1,POLB,RRM1,STAG2
				AKAP8,APAF1,APH1A,ARIH1,CD200,CEP68,CSF1R,DHFR,DLEU1,DNMT3A,FANCD2,FASLG,FCMR,FOXO1,GNAQ,LONP1,LYP1A1,NEDD9,NF1,NR3C1,P
Chronic leukemia	33	8.63E-06		DE3B,PIK3CD,PLCG2,PNKD,POLB,POLE,PRKCB,RASSF5,RRM1,S1PR1,STAG2,TIGIT,UCKL1
				IL6ST,PLAT,STAT1
Chronic inflammation of joint	3	9.14E-06		CCR7,CSF1,CSF1R,CTLA4,FASLG,FCMR,FCRL3,FOXO1,IL15,IL6ST,NF1,PDPK1,PIK3CD,PLAT,PLCG2,PRKCB,RICTOR,STAT1,TCF7,TNFSF8
				ABCB1,ADAM8,BIRC2,CCR7,CD200,CD302,CSF1,CSF1R,CTLA4,CXCL13,CXCR5,DAPP1,DKC1,DNMT3A,ELMO1,FASLG,FCMR,FOXO1,GLS,GNA13,GNA S,IL15,IL6ST,NEDD9,NF1,NFATC3,NLRCS,NOD2,NR3C1,PIK3CD,PILRA,PLAC8,PLAT,PLCG2,POLR3E,PPP2CA,PRKCB,RASSF2,RASSF5,RICTOR,S1PR1,SA
Quantity of leukocytes	49	1.18E-05	0.296	TB1,SELL,ST6GAL1,STAT1,TIGIT,TPP2,TKX,ZBTB46
				ADSL,CHD6,CRNN,CSF1R,DHFR,ELK1,FILIP1L,GNA13,KBKE,LONP1,MBD1,MGA,NEK4,NR3C1,OSBP,PIK3CD,PLCG2,PLEKHG3,POLB,POLE,RBCK1,RRM1,SKIV2L2,SLC4A10,UBE3A,UROS
Diffuse small-cell lymphoma	26	1.32E-05		CCR7,CD200,CTLA4,CXCR5,FASLG,IGHG1,IL15,NFATC3,NOD2,PIK3CD,RASSF5,SATB1,SELL,TPP2,ZBTB46
				M1,SKIV2L2,SLC4A10,UBE3A,UROS
Morphology of lymph node	15	1.35E-05		CCR7,CXCR5,DAPP1,FCRL3,IGHG1,IL15,NOD2,PIK3CD,PLCG2,PRKCB,ST6GAL1,TAB2,TAB3
				APAF1,APH1A,ARIH1,CSF1R,DHFR,DNMT3A,FANCD2,FASLG,FOXO1,GNAQ,NF1,NR3C1,POLB,RRM1,STAG2
Chronic myeloid leukemia	15	1.44E-05		ADAM8,AIF1,CCR7,CXCL13,CXCR5,ELMO1,FOXO1,GNA13,GNAS,IGHG1,IL15,NEDD9,NR3C1,PIK3CD,PRKCB,S1PR1,SELL
				ABCB1,CSF1R,DHFR,NR3C1,POLB,RRM1
Homing of mononuclear leukocytes	17	1.65E-05	↑ 2.396	ABCB1,CSF1R,DHFR,NR3C1,POLB,RRM1
				ABCB1,CSF1R,DHFR,NR3C1,POLB,RRM1
Type M4 acute myeloid leukemia	6	1.66E-05		ABCB1,CSF1R,DHFR,NR3C1,POLB,RRM1
				ABCB1,CSF1R,DHFR,NR3C1,POLB,RRM1
Immune response of cells	34	1.78E-05	0.656	ABCB1,CSF1R,DHFR,NR3C1,POLB,RRM1
				LD1,PRKCB,RAB43,RASA4,RICTOR,SLC22A2,SNX3,SPRY1,STAT1,TIGIT,TNFSF8,TRIM14,TRIM5
Psoriatic arthritis	10	1.88E-05		APAF1,DHFR,FOXO1,IGHG1,NOD2,NR3C1,POLB,PPF1A1,PRKCB,TCF7
				CCR7,CD200,CTLA4,CXCR5,FASLG,IL15,NFATC3,NOD2,PIK3CD,RASSF5,SATB1,SELL,TPP2,ZBTB46
Abnormal morphology of lymph node	14	2.13E-05		CCR7,CD200,CTLA4,CXCR5,FASLG,IL15,NFATC3,NOD2,PIK3CD,RASSF5,SATB1,SELL,TPP2,ZBTB46
				CCR7,CD200,CTLA4,CXCR5,FASLG,IL15,NFATC3,NOD2,PIK3CD,RASSF5,SATB1,SELL,TPP2,ZBTB46
Leukemia	78	2.19E-05	-0.588	ABCB1,ACOT11,ADRB2,AKAP17A,AKAP8,APAF1,APH1A,ARHGAP35,ARIH1,ATP6V1A,BEST1,CCR7,CD2,CD200,CEP68,CLTB,CSF1R,CXCL13,DHFR,DLEU1,DNMT3A,ELMO1,ETFA,EVC,FAM86B2/FAM86KP,FANCD2,FASLG,FCMR,FOXO1,GCC2,GLS,GNAQ,GNAS,GZMB,IL15,ILKAP,IPOT,KLHL4,LIMS3/LIMS4,LONP1,LYP1A1,MAMLI2,MCM16,MLF1,MOC51,MRP5,NEDD9,NF1,NR3C1,PDE3B,PDE4DIP,PDPK1,PHF3,PHKB,PHYHD1,PIK3CD,PLCG2,PNKD,POLB,POLE,PRKCB,PRR14L,RASA4,RASSF5,RRM1,S1PR1,SELL,SETD1B,SIRPG,SKP2,STAG2,TCF7,THRAP3,TIGIT,UCKL1,USP3,VMP1,ZNF827
				ABCB1,ACOT11,ADRB2,AKAP17A,AKAP8,APAF1,APH1A,ARHGAP35,ARIH1,ATP6V1A,BEST1,CCR7,CD2,CD200,CEP68,CLTB,CSF1R,CXCL13,DHFR,DLEU1,DNMT3A,ELMO1,ETFA,EVC,FAM86B2/FAM86KP,FANCD2,FASLG,FCMR,FOXO1,GCC2,GLS,GNAQ,GNAS,GZMB,IL15,ILKAP,IPOT,KLHL4,LIMS3/LIMS4,LONP1,LYP1A1,MAMLI2,MCM16,MLF1,MOC51,MRP5,NEDD9,NF1,NR3C1,PDE3B,PDE4DIP,PDPK1,PHF3,PHKB,PHYHD1,PIK3CD,PLCG2,PNKD,POLB,POLE,PRKCB,PRR14L,RASA4,RASSF5,RRM1,S1PR1,SELL,SETD1B,SIRPG,SKP2,STAG2,TCF7,THRAP3,TIGIT,UCKL1,USP3,VMP1,ZNF827

Transcription	90	1.075	2.28E-05	ADRB2,AGO2,AIF1,ARHGAP35,ARX,ATF7IP,ATP2C1,BIRC2,BRMS1,BRWD1,CASK,CBX7,CKAP2,CKS1B,CNTN1,CREB3L2,CSF1,DNMT3A,EIF4A3,ELK1,E LMO1,FASLG,FOXO1,GCFC2,GEM,GNA13,GNAQ,GNAS,GTF3C2,HDGF,HMGA2,HSPA4,IKBKE,IL6ST,IRF9,KDM7A,LIMS1,MAML2,MBD1,METTL23,M GA,MILF1,NAB1,NAT88,NDPIP2,NEK4,NEK6,NFATC3,NFKBID,NLRCS,NOD2,NONO,NR3C1,PARP9,PIK3CD,PLAC8,PLEKHG2,PPP1CC,PPP2CA,PREB,PR KAR1A,PRKCB,PVT1,RAB3GAP1,RBAK,RBCK1,RBL1,RCOR1,RPAIN,S1PR1,SATB1,SMARCA5,SNIP1,SSRP1,STAT1,TAB2,TAF7,TCF7,THRAP3,TLE3,TNFS F8,TXK,UBE3A,UBN1,USP3,ZBP1,ZC3H8,ZFPM1,ZNF202,ZNF692
Mycosis fungoides	9		2.36E-05	CCR7,CD2,CXCL13,DHFR,IL15,NR3C1,POLB,RRM1,SELL
Quantity of lymphoid tissue	25	1.863	2.55E-05	ABCB1,CCR7,CD200,CTLA4,CXCL13,CXCR5,FCMR,FOXO1,GNA13,IL6ST,NEDD9,NFATC3,NOD2,NR3C1,PIK3CD,PLCG2,POLR3E,RASSF5,RBM38,RICTO R,SATB1,ST6GAL1,STAT1,TPP2,TXK
Cell death of tumor cell lines	73	-1.165	2.59E-05	ABCB1,ADIL,APAF1,ATP13A2,ATP2B1,BIRC2,BUB3,CKAP2,CLASP1,CREB3L2,CSF1R,DCTD,DHFR,DNMT3A,DYNLL1,EEF2,EIF3G,ELK1,FASLG,FAU,FCM R,FOXO1,GEM,GLS,GNA13,GNAS,GPC3,GZMB,HSPA4,IGFBP4,IGHG1,IKBKE,IL15,IL6ST,ILKAP,KIR3DL1,LIMS1,LONP1,LYPLA1,MAML2,MBD1,MTG2, NAT10,NEDD9,NEK6,NF1,NR3C1,PDPK1,PIK3CD,PLAT,PLCG2,PPP2CA,PRKAR1A,PRKCB,RAPGEF2,RASSF5,RICTOR,RPA2,RRM1,SATB1,SF3B3,SKP2,SL C11A2,SSRP1,ST6GAL1,STAT1,TERF1,TFRC,TPP2,TRAP1,UBA7,UBE3A,VOPP1
Morphology of blood cells	27		2.71E-05	ABCB1,CD200,CSF1,CSF1R,CTLA4,CXCR5,FANCD2,FASLG,FCMR,GNA13,GNAQ,IGHG1,IL15,NOD2,PDPK1,PIK3CD,PLCG2,RAPGEF2,RASSF2,RBL1,RB M38,SLC11A2,STAT1,TFRC,TPP2,ZBTB46,ZFPM1
Quantity of lymphatic system cells	42	1.636	2.82E-05	ABCB1,BIRC2,CCR7,CSF1,CSF1R,CTLA4,CXCL13,CXCR5,DAPP1,DKC1,DNMT3A,FASLG,FCMR,FOXO1,GLS,GNA13,IL15,IL6ST,NEDD9,NF1,NFATC3,NLR C5,NOD2,NR3C1,PIK3CD,PLCG2,POLR3E,PRKCB,RAPGEF2,RASSF2,RASSF5,RBL1,RBM38,RICTOR,S1PR1,SATB1,SELL,ST6GAL1,STAT1,TIGIT,TPP2,TXK
Interaction of mononuclear leukocytes	17	↑ 2.541	2.90E-05	ATRN,CCR7,CD2,CTLA4,CXCL13,FASLG,FOXO1,IL15,IL6ST,NEDD9,NFATC3,NR3C1,RASSF5,RICTOR,SELL,TFRC,TXK
Trafficking of cells	9	↑ 2.153	2.94E-05	CCR7,CXCL13,CXCR5,FOXO1,IL15,NEDD9,PDPK1,S1PR1,SELL
Adult leukemia	13		3.14E-05	ABCB1,CCR7,CD2,CSF1R,DHFR,DNMT3A,NR3C1,POLB,POLB,PRKCB,RRM1,S1PR1,VMP1
Liquid tumor	82	-0.636	3.53E-05	ABCB1,ACOT11,ADRB2,AKAP17A,AKAP8,APAF1,APH1A,ARHGAP35,ARIH1,ATP6V1A,BEST1,CCR7,CD2,CD200,CEP68,CLTB,CSF1R,CXCL13,DHFR,DLE U1,DNMT3A,ELMO1,ETFA,EVC,FAM86B2/FAM86KP,FANCD2,FASLG,FCMR,FOXO1,GCC2,GLS,GNAQ,GNAS,GZMB,HMGA2,IL15,ILKAP,IPO7,KLHL4,LI MS3/LIMS4,LONP1,LYPLA1,MAML2,MCM6,MGA,MIF1,MMP1,MOC51,MRP55,NEDD9,NF1,NR3C1,PDE3B,PDE4DIP,PDPK1,PHF3,PHKB,PHYHD1,PIK 3CD,PLCG2,PNKD,POLB,POLB,PRKCB,PRR14L,RASA4,RASSF5,RRM1,S1PR1,SELL,SETD1B,SIRPG,SKP2,STAG2,TCF7,THRAP3,TIGIT,TLE3,UCLK1,USP3,V MPI,ZNF827
Migration of marginal-zone B lymphocytes	4	0.849	3.61E-05	CXCL13,CXCR5,GNA13,S1PR1
Deletion of cells	6		3.85E-05	CD2,CTLA4,FASLG,IL15,IL6ST,TCF7
Rheumatic Disease	58	-1.242	3.92E-05	ABCB1,ADAM8,ADRB2,AGFG1,AIF1,APAF1,ARIH1,ATP2B1,ATP2C1,BRMS1,CCR7,CD200,CSF1,CSF1R,CTLA4,CXCL13,CXCR5,DHFR,DYNLL1,EEF2,EVC, FASLG,FAU,FCRL3,FDPS,FOXO1,GNAQ,GZMB,IGFBP4,IGHG1,IL15,IL6ST,KIR3DL1,MBD1,MMP1,NOD2,NONO,NR3C1,PDE3B,PIK3CD,PILRA,PLAT,PLC G2,POLB,PPFIA1,PPP2CA,PRKCB,RBM38,RPL19,S1PR1,SELL,SKIV2L,ST6GAL1,STAT1,TCF7,TFRC,TLE3,ZBP1
Binding of mononuclear leukocytes	16	↑ 2.335	4.06E-05	CCR7,CD2,CTLA4,CXCL13,FASLG,FOXO1,IL15,IL6ST,NEDD9,NFATC3,NR3C1,RASSF5,RICTOR,SELL,TFRC,TXK
Cell proliferation of tumor cell lines	74	↑ 2.075	4.39E-05	ABCB1,ADSL,APAF1,ARIH1,BIRC2,BUB3,CBX7,CKS1B,COPB2,CSF1,CSNK1G3,CTLA4,ELK1,FASLG,FOXO1,GIA4,GLS,GNAQ,GNAS,GNL3,GPC3,GZMB,H DGF,HMGA2,IGFBP4,IKBKE,IL15,IL6ST,ILKAP,IPO7,MAT2B,MATK,MMP1,MSMB,NAT10,NEDD9,NF1,NR3C1,PDPK1,PIK3CD,PLAC8,PLAT,PLCG2,PLD1 ,PPP1CC,PPP2CA,PRKAR1A,PRKCB,RAB30,RAPGEF2,RASSF5,RBCK1,RBL1,RBM38,RICTOR,RRM1,SATB1,SKP2,SMN1/SMN2,SNIP1,STAG2,STAT1,TAB 2,TAB3,TAF7,TERF1,TES,TFRC,TNFSF8,TPP2,VAMP2,VBP1,VMP1,WTAP
Adult T cell leukemia	12		4.56E-05	CCR7,CD2,CSF1R,DHFR,DNMT3A,NR3C1,POLB,POLB,PRKCB,RRM1,S1PR1,VMP1
Quantity of lymphocytes	39	1.739	4.57E-05	ABCB1,BIRC2,CCR7,CSF1,CSF1R,CTLA4,CXCL13,CXCR5,DAPP1,DKC1,DNMT3A,FASLG,FCMR,FOXO1,GLS,GNA13,IL15,IL6ST,NEDD9,NF1,NFATC3,NLR C5,NOD2,NR3C1,PIK3CD,PLCG2,POLR3E,PRKCB,RASSF2,RASSF5,RICTOR,S1PR1,SATB1,SELL,ST6GAL1,STAT1,TIGIT,TPP2,TXK
Leukemia of lymphocytes	18		4.57E-05	CCR7,CD2,CSF1R,CXCL13,DHFR,DNMT3A,GZMB,IL15,NF1,NR3C1,POLB,POLB,PRKCB,RRM1,S1PR1,SELL,TCF7,VMP1
Cell death of immune cells	36	0.062	4.66E-05	ADAM8,APAF1,BIRC2,CCR7,CD2,CSF1,CSF1R,CTLA4,FASLG,FCMR,FCRL3,FOXO1,GLS,GNAS,GZMB,IKBKE,IL15,IL6ST,NF1,NFKBID,NR3C1,PDPK1,PIK3 CD,PLAT,PLCG2,POLR3E,PRKCB,RICTOR,S1PR1,SATB1,ST6GAL1,STAT1,TCF7,TNFSF8,TPP2,ZC3H8
Chronic myeloproliferative neoplasm	18		4.78E-05	APAF1,APH1A,ARIH1,CSF1R,DHFR,DNMT3A,FANCD2,FASLG,FOXO1,GNAQ,HMGA2,IL15,NF1,NR3C1,POLB,POLB,RRM1,STAG2
Interaction of lymphocytes	15	↑ 2.888	4.81E-05	ATRN,CCR7,CD2,CTLA4,CXCL13,FASLG,IL6ST,NEDD9,NFATC3,NR3C1,RASSF5,RICTOR,SELL,TFRC,TXK
Lymphocytic leukemia	38		4.92E-05	ACOT11,AKAP8,CCR7,CD2,CD200,CEP68,CSF1R,CXCL13,DHFR,DLEU1,DNMT3A,ELMO1,FASLG,FCMR,GZMB,IL15,KLHL4,LONP1,LYPLA1,MAML2,NE DD9,NF1,NR3C1,PDE3B,PIK3CD,PLCG2,PNKD,POLB,POLB,PRKCB,RASSF5,RRM1,S1PR1,SELL,TCF7,TIGIT,UCLK1,VMP1
Quantity of mononuclear leukocytes	40	1.333	5.06E-05	ABCB1,BIRC2,CCR7,CSF1,CSF1R,CTLA4,CXCL13,CXCR5,DAPP1,DKC1,DNMT3A,FASLG,FCMR,FOXO1,GLS,GNA13,GNAS,IL15,IL6ST,NEDD9,NF1,NFATC 3,NLRCS,NOD2,NR3C1,PIK3CD,PLCG2,POLR3E,PRKCB,RASSF2,RASSF5,RICTOR,S1PR1,SATB1,SELL,ST6GAL1,STAT1,TIGIT,TPP2,TXK

Quantity of B lymphocytes	5.19E-05	0.868	23	CCR7,CSF1,CXCL13,CXCR5,DAPP1,DKC1,FASLG,FCMR,FOXO1,GLS,GNA13,IL6ST,NEDD9,NFATC3,PIK3CD,PLCG2,PRKCB,RASSF2,RASSF5,S1PR1,ST6GAL1,STAT1,TPP2
Function of blood cells	5.20E-05	-1.076	31	ABCB1,ADRB2,CCR7,CD200,CSF1,CSF1R,CTLA4,FCMR,GNAQ,GPC3,IL15,NEDD9,NF1,NFKBID,NLRCS,NOD2,PIK3CD,PLAT,PLCG2,PLD1,RAPGEF2,RASSF5,S1PR1,SELL,SKP2,ST6GAL1,STAT1,TCF7,TIGIT,TPP2,TKX
Cell survival	5.21E-05	↑ 3.290	67	ABCB1,AGO2,AGPS,APAF1,ATP13A2,ATP2C1,BIRC2,CASK,CCR7,CD200,CKS1B,COPB2,CSF1,CSF1R,CTLA4,EDA,EEF2,EIF4A3,ELK1,FANCD2,FASLG,FCMR,FCRL3,FOXO1,GNA13,GPC3,GZMB,HDGF,HMGA2,HSPA4,IKBKE,IL15,IL6ST,IRF9,LIMS1,MCFD2,MMP1,NEDD9,NEK4,NF1,NR3C1,PDPK1,PIK3CD,PLAC8,PLAT,PLCG2,PLEKHG2,POLB,PPP1CC,PPP2CA,PRKAR1A,PRKCB,RICTOR,RRM1,S1PR1,SELL,SHPRH,SLC11A2,SLC22A2,SMN1/SMN2,SPRY1,STAT1,TCF7,TERF1,TNFSF8,VBPI1,WTAP
Differentiation of hematopoietic progenitor cells	5.46E-05	0.408	22	APAF1,BRD1,CD2,CSF1,CSF1R,EEF2,ELK1,HMGA2,IL15,IL6ST,LONP1,MLF1,PIK3CD,PLCG2,PPP4R2,RCOR1,SATB1,SMARCA5,TCAF2,TFRC,ZBTB24,ZFP M1
Binding of lymphocytes	5.90E-05	↑ 2.697	14	CCR7,CD2,CTLA4,CXCL13,FASLG,IL6ST,NEDD9,NFATC3,NR3C1,RASSF5,RICTOR,SELL,TFRC,TKX
Apoptosis of mononuclear leukocytes	5.96E-05	0.085	23	ADAM8,CD2,CSF1,CTLA4,FASLG,FCMR,GNAS,GZMB,IKBKE,IL15,IL6ST,NFKBID,NR3C1,PDPK1,PIK3CD,PLCG2,POLR3E,PRKCB,S1PR1,SATB1,STAT1,TPP2,ZC3H8
Apoptosis of fibroblast cell lines	6.30E-05	-0.686	22	ABCB1,APAF1,BIRC2,CD2,CSF1R,FASLG,GLS,GNA13,GNAQ,GZMB,MDN1,NR3C1,PLAC8,PLEKHF1,PRKAR1A,PRKCB,RASA4,RASSF5,RBL1,SKP2,STAT1,YME1L1
FLT3 activating mutation positive acute myeloid leukemia	6.67E-05		6	CSF1R,DNMT3A,NR3C1,POLB,POLE,RRM1
Apoptosis of leukocytes	6.86E-05	-0.658	27	ADAM8,BIRC2,CCR7,CD2,CSF1,CTLA4,FASLG,FCMR,GNAS,GZMB,IKBKE,IL15,IL6ST,NFKBID,NR3C1,PDPK1,PIK3CD,PLAT,PLCG2,POLR3E,PRKCB,S1PR1,SATB1,ST6GAL1,STAT1,TPP2,ZC3H8
Activation of mononuclear leukocytes	6.94E-05	-0.412	28	CCR7,CD2,CD200,CSF1,CTLA4,CXCR5,DAPP1,FASLG,FCRL3,FOXO1,GJA4,HSPA4,IGHG1,IL15,KIR3DL1,NFATC3,NFKBID,NOD2,PIK3CD,PLCG2,PRKCB,SATB1,SIRPG,ST6GAL1,STAT1,TAB2,TAB3,TIGIT
Activation of lymphocytes	7.07E-05	-0.159	27	CCR7,CD2,CD200,CTLA4,CXCR5,DAPP1,FASLG,FCRL3,FOXO1,GJA4,HSPA4,IGHG1,IL15,KIR3DL1,NFATC3,NFKBID,NOD2,PIK3CD,PLCG2,PRKCB,SATB1,SIRPG,ST6GAL1,STAT1,TAB2,TAB3,TIGIT
B-cell lymphoproliferative disorder	7.16E-05		39	AKAP8,ATRN,CCR7,CHD6,CRNN,CSF1R,CXCL13,CXCR5,DHFR,ELK1,FASLG,FILIP1L,FOXO1,GNA13,LONP1,LYPLA1,MBD1,MGA,NEK4,NF1,NONO,NR3C1,OSBP,PIK3CD,PLCG2,PLEKHG3,POLB,POLE,PPP2CA,PRKCB,RAB4A,RBCK1,RICTOR,RRM1,S1PR1,SATB1,SKIV2L2,SLC4A10,TNRC6C
Expression of RNA	7.46E-05	0.638	92	ADRB2,AGO2,AIF1,ARHGAP35,ARX,ATF7IP,ATP2C1,BIRC2,BRMS1,BRWD1,CASK,CBX7,CKAP2,CKS1B,CNTN1,CREB3L2,CSF1,DHFR,DNMT3A,EIF3G,EI F4A3,EIF4EBP2,ELK1,FASLG,FOXO1,GCFC2,GEM,GNA13,GNAQ,GNAS,GTFC2,HDGF,HMGA2,HSPA4,IKBKE,IL6ST,IRF9,KDM7A,LIMS1,MAML2,MAML2,MBD1,METTL23,MGA,MLF1,NAB1,NAB1,NEK4,NEK6,NFATC3,NFKBID,NLRCS,NOD2,NONO,NR3C1,PARP9,PIK3CD,PLAC8,PLEKHG2,PPP1CC,PPP2CA,PRED,PRKAR1A,PRKCB,RAB3GAP1,RBAK,RBCK1,RBL1,RCOR1,RPAIN,RPL19,S1PR1,SATB1,SMARCA5,SNIP1,USP3,ZBP1,TAB2,TAF7,TCF7,THRA P3,TLE3,TNFSF8,TKX,UBE3A,UBN1,USP3,ZBP1,ZC3H8,ZFPM1,ZNF202,ZNF692
Transcription of RNA	7.81E-05	1.285	81	ADRB2,AGO2,ARHGAP35,ARX,ATF7IP,ATP2C1,BIRC2,BRMS1,BRWD1,CASK,CBX7,CKAP2,CKS1B,CREB3L2,CSF1,DNMT3A,EIF4A3,ELK1,FASLG,FOXO1,GCFC2,GEM,GNA13,GNAQ,GNAS,GTFC2,HDGF,HMGA2,IKBKE,IL6ST,IRF9,KDM7A,LIMS1,MAML2,MBD1,METTL23,MGA,MLF1,NAB1,NEK4,NEK6,NFATC3,NFKBID,NLRCS,NOD2,NONO,NR3C1,PARP9,PLAC8,PLEKHG2,PPP1CC,PPP2CA,PRED,PRKAR1A,PRKCB,RAB3GAP1,RBAK,RBCK1,RBL1,RCOR1,RPAIN,RPL19,S1PR1,SATB1,SMARCA5,SNIP1,USP3,ZBP1,ZC3H8,ZFPM1,ZNF202,ZNF692
Cell death of blood cells	8.00E-05	0.206	37	ABCB1,ADAM8,APAF1,BIRC2,CCR7,CD2,CSF1,CSF1R,CTLA4,FASLG,FCMR,FCRL3,FOXO1,GLS,GNAS,GZMB,IKBKE,IL15,IL6ST,NF1,NFKBID,NR3C1,PDP K1,PIK3CD,PLAT,PLCG2,POLR3E,PRKCB,RICTOR,S1PR1,SATB1,ST6GAL1,STAT1,TCF7,TNFSF8,TPP2,ZC3H8
Arrest in proliferation of tumor cell lines	8.09E-05		11	CBX7,GLS,IL6ST,IPO7,NR3C1,PPP1CC,RASSF5,RBL1,SKP2,STAT1,TAF7
Cell death of tumor cells	8.18E-05	-1.057	27	APAF1,BIRC2,BRMS1,COPB2,CSF1,CTLA4,EIF3G,FASLG,FAU,FOXO1,GZMB,HMGA2,IGHG1,IL15,IL6ST,LYPLA1,NEK4,NR3C1,PIK3CD,PPP2CA,PSM C6,PSMD12,RBM8A,RPA2,RPL19,SELL,SF3B3
Cytogenetically abnormal acute myeloid leukemia	8.63E-05		9	ABCB1,CD2,CSF1R,DHFR,DNMT3A,NR3C1,POLB,POLE,RRM1
Sezary syndrome	8.63E-05		9	CD2,CXCL13,DHFR,IGFBP4,IL15,KIR3DL1,POLE,RRM1,SATB1
Quantity of antigen presenting cells	8.71E-05	-0.811	19	ADAM8,CCR7,CD200,CD302,CSF1,CSF1R,CTLA4,CXCL13,ELMO1,GNAS,IL15,IL6ST,PILRA,PLAT,RICTOR,SELL,ST6GAL1,TIGIT,ZBTB46
Cellular homeostasis	9.06E-05	1.721	73	ACOT11,ADRB2,APAF1,ARHGAP35,ATP13A2,ATP2C1,ATP6V1A,BIRC2,CCR7,CD2,CTLA4,CXCL13,CXCR5,DMPK,EEF2,ELK1,FASLG,FBXL20,FFAR3,FOX O1,GJA4,GNA13,GNAQ,GNAS,GZMB,HSPA4,IGFBP4,IGHG1,IL15,IL6ST,LONP1,MIMP1,NAB1,NF1,NFATC3,NFKBID,NOD2,NR3C1,PD E3B,PDPK1,PIK3 CD,PLCG2,PLD1,PLEKHF1,POLB,PPP2CA,PRKCB,RAB12,RAPGEF2,RBL1,RICTOR,S1PR1,SATB1,SELENON,SKP2,SLC11A2,SLC25A14,SLC27A1,SLC4A10,STAT1,TAB2,TAB3,TCF7,TFRC,TNFSF8,TPP2,TRIM5,TKX,VMP1,ZACN,ZBTB24,ZC3H8,ZFPM1
Function of mononuclear leukocytes	9.19E-05	-1.076	20	ABCB1,ADRB2,CCR7,CSF1,CTLA4,IL15,NEDD9,NFKBID,NLRCS,NOD2,PIK3CD,PLCG2,RASSF5,S1PR1,SELL,SKP2,STAT1,TCF7,TPP2,TKX

Apoptosis of lymphocytes	9.26E-05	-0.140	22	ADAM8,CD2,CSF1,CTLA4,FASLG,FCMR,GNAS,GZMB,KBKE,IL15,NFKBID,NR3C1,PDPK1,PIK3CD,PLCG2,POLR3E,PRKCB,S1PR1,SATB1,STAT1,TPP2,ZC3H8
Quantity of cells	9.33E-05	0.277	79	ABCB1,ADAM8,ADRB2,APAF1,ARX,ATP2C1,BIRC2,BRD1,CCR7,CD200,CD302,CREB3L2,CSF1,CSF1R,CTLA4,CXCL13,CXCR5,DAPP1,DHFR,DKC1,DNMT3A,DYNLL1,EDA,EIF4EBP2,ELMO1,FANCD2,FASLG,FCMR,FFAR3,FOXO1,GLS,GNA13,GNAQ,GNAS,GPC3,HDFG,HMGA2,IGHG1,IL15,IL6ST,MATK,NAT10,NEDD9,NF1,NFATC3,NLRCS,NOD2,NR3C1,PIK3CD,PILRA,PLAC8,PLAT,PLCG2,POLR3E,PPP2CA,PRKCB,RAPGEF2,RASSF2,RASSF5,RBL1,RBM38,RCOR1,RICTOR,S1PR1,SATB1,SELENON,SELL,SKP2,SLC11A2,SMN1/SMN2,SNX27,ST6GAL1,STAT1,TFRCT,TTG1T,TPP2,TKX,UBE3A,ZBTB46
M1 childhood acute myeloid leukemia	9.72E-05		5	ABCB1,DHFR,NR3C1,POLB,RRM1
M2 childhood acute myeloid leukemia	9.72E-05		5	ABCB1,DHFR,NR3C1,POLB,RRM1
M4 childhood acute myeloid leukemia	9.72E-05		5	ABCB1,DHFR,NR3C1,POLB,RRM1
M5a childhood acute myeloid leukemia	9.72E-05		5	ABCB1,DHFR,NR3C1,POLB,RRM1
M5b childhood acute monocytic leukemia	9.72E-05		5	ABCB1,DHFR,NR3C1,POLB,RRM1
M6 childhood acute erythroid leukemia	9.72E-05		5	ABCB1,DHFR,NR3C1,POLB,RRM1
M7 childhood acute myeloid leukemia	9.72E-05		5	ABCB1,DHFR,NR3C1,POLB,RRM1
Fibrosis	1.05E-04	-1.027	30	ADRB2,AGO2,CSF1,CSF1R,CXCL13,DHFR,DNMT3A,ELK1,FASLG,GNAS,HDFG,HMGA2,IGHG1,IKBKE,IL6ST,LIMS1,MMP1,NDUFS6,NF1,NR3C1,PILRA,PLAC8,PLAT,PNKD,POLB,PRKCB,RASSF2,SELL,SKP2,STAT1
Inflammation of joint	1.07E-04	-1.662	52	ABCB1,ADAM8,ADRB2,AIF1,APAF1,ARIH1,ATP2B1,ATP2C1,BRM51,CCR7,CD200,CSF1,CSF1R,CTLA4,CXCL13,CXCR5,DHFR,DYNLL1,EEF2,EVC,FASLG,FAU,FCRL3,FDP5,FOXO1,GZMB,IGFBP4,IGHG1,IL15,IL6ST,KIR3DL1,MBD1,MMP1,NOD2,NONO,NR3C1,PDE3B,PIK3CD,PILRA,PLAT,PLCG2,POLB,PPFIA1,PRKCB,RBM38,RPL19,S1PR1,SKIV2L,STAT1,TCF7,TFRCT,TLF3
Abnormal morphology of lymphoid organ	1.32E-04		23	CCR7,CD200,CSF1,CSF1R,CTLA4,CXCR5,FASLG,GPC3,IL15,IL6ST,NFATC3,NLRCS,NOD2,PIK3CD,RASSF2,RASSF5,RBL1,RBM38,SATB1,SELL,SNX27,TPP2,ZBTB46
Apoptosis of lymphatic system cells	1.32E-04	0.047	23	ADAM8,CD2,CSF1,CTLA4,FASLG,FCMR,GNAS,GZMB,KBKE,IL15,IL6ST,NFKBID,NR3C1,PDPK1,PIK3CD,PLCG2,POLR3E,PRKCB,S1PR1,SATB1,STAT1,TPP2,ZC3H8
Cell death of mononuclear leukocytes	1.32E-04	0.561	24	ADAM8,APAF1,CD2,CSF1,CTLA4,FASLG,FCMR,GNAS,GZMB,KBKE,IL15,IL6ST,NFKBID,NR3C1,PDPK1,PIK3CD,PLCG2,POLR3E,PRKCB,S1PR1,SATB1,STAT1,TPP2,ZC3H8
Cell viability of mononuclear leukocytes	1.38E-04	1.288	15	CSF1,CSF1R,CTLA4,FASLG,FCMR,FCRL3,IL15,IL6ST,PDPK1,PIK3CD,PLCG2,PRKCB,RICTOR,STAT1,TCF7
T-cell leukemia	1.42E-04		17	CCR7,CD2,CSF1R,CXCL13,DHFR,DNMT3A,GZMB,NF1,NR3C1,POLB,POLE,PRKCB,RRM1,S1PR1,SELL,TCF7,VMP1
Cell viability	1.49E-04	↑ 2.969	62	ABCB1,AGO2,AGPS,APAF1,ATP13A2,ATP2C1,BIRC2,CASK,CCR7,CD200,CKS1B,COPB2,CSF1,CSF1R,CTLA4,EDA,EEF2,EIF4A3,ELK1,FANCD2,FASLG,FCMR,FCRL3,FOXO1,GNA13,HDFG,HMGA2,KBKE,IL15,IL6ST,IRF9,MCFD2,MMP1,NEK4,NF1,NR3C1,PDPK1,PIK3CD,PLAC8,PLAT,PLCG2,PLEKHG2,POLB,PPP1CC,PPP2CA,PRKAR1A,PRKCB,RICTOR,RRM1,S1PR1,SELL,SHPRH,SLC11A2,SLC22A2,SMN1/SMN2,SPRY1,STAT1,TCF7,TERF1,TNFSF8,VBP1,WTAP
Cell death of connective tissue cells	1.51E-04	-0.871	33	ABCB1,APAF1,BIRC2,CD2,CREB3L2,CSF1,CSF1R,ELK1,FANCD2,FASLG,FOXO1,GLS,GNA13,GNAQ,GNL3,GZMB,MDN1,NFKBID,NR3C1,PLAC8,PLEKHF1,POLB,PRKAR1A,PRKCB,RAS44,RASSF5,RBL1,S1PR1,SKP2,STAT1,TPP1,TPP2,YME1L1
Chemotaxis of lymphocytes	1.59E-04	↑ 2.279	11	ADAM8,CCR7,CXCL13,ELMO1,GNA13,GNAS,IL15,NEDD9,NR3C1,PIK3CD,S1PR1
Hematopoiesis of mononuclear leukocytes	1.65E-04	1.831	37	APAF1,CCR7,CD2,CSF1,CSF1R,CTLA4,CXCR5,ELK1,FASLG,FOXO1,IGHG1,IL15,IL6ST,IONP1,NAB1,NF1,NFATC3,NFKBID,PDPK1,PIK3CD,PLCG2,POLB,RASSF5,RBL1,RICTOR,S1PR1,SATB1,SKP2,STAT1,TAB2,TAB3,TCF7,TNFSF8,TPP2,TKX,ZBTB46,ZFPM1
Neoplasia of leukocytes	1.71E-04		30	CCR7,CD2,CD200,CSF1R,CXCL13,DHFR,DNMT3A,FASLG,GIA4,GZMB,IFITM1,IGFBP4,IL15,KIR3DL1,MMMP1,NF1,NR3C1,OAS2,POLB,POLE,PRKCB,RRM1,S1PR1,SATB1,SELL,SKP2,STAT1,TCF7,VMP1,ZBTB24
Graft-vs-host disease	1.72E-04		8	CD2,DHFR,FASLG,KIR3DL1,NR3C1,POLB,RRM1,TNFSF8
Abnormal morphology of spleen	1.72E-04		18	CCR7,CSF1,CSF1R,CTLA4,FASLG,GPC3,IL6ST,NFATC3,NLRCS,PIK3CD,RASSF2,RASSF5,RBL1,RBM38,SATB1,SELL,SNX27,TPP2
Organization of lymphoid tissue	1.74E-04		3	CCR7,CXCL13,CXCR5
Quantity of hematopoietic progenitor cells	1.85E-04	↑ 2.291	26	ABCB1,BRD1,CCR7,CSF1,CTLA4,FANCD2,FOXO1,GPC3,IL15,IL6ST,MATK,NOD2,NR3C1,PIK3CD,PLCG2,POLR3E,RAPGEF2,RASSF2,RASSF5,RBM38,RCOR1,SATB1,ST6GAL1,TFRCT,TPP2,TKX
B-cell lymphoma	1.86E-04		38	AKAP8,ATRN,CCR7,CHD6,CRNN,CSF1R,CXCL13,CXCR5,DHFR,ELK1,FILIP1L,FOXO1,GNA13,LONP1,MBD1,MGA,NEK4,NF1,NONO,NR3C1,OSBP,PIK3CD,PLCG2,PLEKHG3,POLB,POLE,PPP2CA,PRKCB,RAB4A,RASSF5,RBCK1,RICTOR,RRM1,SATB1,SKIV2L2,SLC4A10,TNFSF8,TNRC6C
Quantity of dendritic cells	1.92E-04	-0.489	11	CCR7,CD200,CD302,CSF1,CSF1R,CTLA4,CXCL13,IL15,RICTOR,SELL,ZBTB46

Progression of tumor	1.93E-04	0.239	18	BRMS1,CKS1B,CSF1,CSF1R,CTLA4,DHFR,FOXO1,GZMB,IGFBP4,MMP1,NEDD9,NR3C1,PIK3CD,POLB,POLE,RRM1,SKP2,STAT1
Apoptosis of T lymphocytes	2.00E-04	0.228	18	ADAM8,CD2,CTLA4,FASLG,FCMR,GNAS,GZMB,IKBKE,IL15,NFKBID,NR3C1,PDPK1,PIK3CD,POLR3E,SATB1,STAT1,TPP2,ZC3H8
Cell death of lymphocytes	2.03E-04	0.355	23	ADAM8,APAF1,CD2,CSF1,CTLA4,FASLG,FCMR,GNAS,GZMB,IKBKE,IL15,NFKBID,NR3C1,PDPK1,PIK3CD,PLCG2,POLR3E,PRKCB,S1PR1,SATB1,STAT1,TPP2,ZC3H8
Leukytosis	2.04E-04	0.896	11	BIRC2,CSF1,CSF1R,FASLG,IL15,IL6ST,PIK3CD,POLB,POLE,RRM1,SELL
Mammary tumor	2.05E-04	0.054	77	ABCB1,ADRB2,AGO2,AGPS,APH1A,ARHGAP35,ATP2C1,BRWD1,C17orf49,CASK,CCNL1,CCR7,CMAHP,CNTN1,CSF1,CSF1R,CTLA4,DBF4,DHFR,DKC1,DNMT3A,ETFA,FANCD2,FDP5,GGCT,GLS,GNA13,GNAS,GOSR1,GPC3,HMGAA2,IKBKE,ILKAP,KLHL12,LONP1,LYP1A1,MBD1,MCM6,MGA,MILF1,MMP1,MUC7,NEDD9,NEK4,NEK6,NF1,NR3C1,PDPK1,PIK3CD,PLAT,PNPO,POLB,POLE,PPPIA1,PPP1CC,PRKCB,PSMD12,RPL19,RRM1,SELL,SETD1B,SF3B3,SKP2,SLC25A14,SLC27A1,SLC5A10,SSTR3,STAG2,STAT1,TES,TLE3,UBAP2L,UBE3A,VBP1,VWA5A,ZFPM1,ZNF692
B-cell non-Hodgkin disease	2.08E-04		36	AKAP8,ATRN,CCR7,CHD6,CRNN,CSF1R,CXCL13,CXCR5,DHFR,ELK1,FILIP1L,FOXO1,GNA13,LONP1,MBD1,MGA,NEK4,NF1,NONO,NR3C1,OSBP,PIK3CD,PLCG2,PIEKHG3,POLB,POLE,PPP2CA,PRKCB,RAB4A,RBCK1,RICTOR,RRM1,SATB1,SKIV2L2,SLC4A10,TNRC6C
Systemic autoimmune syndrome	2.13E-04	0.351	53	ABCB1,ADAM8,ADRB2,AGFG1,AIF1,ARIH1,ATP2B1,ATP2C1,BRMS1,CCR7,CMAHP,CSF1,CTLA4,CXCL13,CXCR5,DHFR,DYNLL1,EEF2,EVC,FASLG,FAU,FCMR,FCRL3,FDP5,FOXO1,GNAQ,GZMB,IGFBP4,IGHG1,IL15,IL6ST,MBD1,MMP1,NOD2,NONO,NR3C1,P2RY10,POLB,PPP2CA,PRKCB,RBM38,RPL19,S1PR1,SELL,SKIV2L,ST6GAL1,STAT1,TCF7,TFRC,TLE3,TNFSF8,TPP2,ZBP1
Quantity of phagocytes	2.14E-04	-1.881	25	ABCB1,ADAM8,CCR7,CD200,CD302,CSF1,CSF1R,CTLA4,CXCL13,ELMO1,FASLG,GNAS,IL15,IL6ST,NF1,NOD2,PILRA,PLAC8,PLAT,PPP2CA,RICTOR,SELL,ST6GAL1,TIGIT,ZBTB46
Abnormal morphology of dendritic cells	2.18E-04		5	CSF1R,CXCR5,PDPK1,PLCG2,ZBTB46
Trafficking of T lymphocytes	2.18E-04	1.342	5	CCR7,FOXO1,PDPK1,S1PR1,SELL
Homing of leukocytes	2.22E-04	↑ 2.010	23	ADAM8,AIF1,CCR7,CSF1,CSF1R,CXCL13,CXCR5,ELMO1,FASLG,FOXO1,GNA13,GNAS,IGHG1,IL15,NEDD9,NOD2,NR3C1,PIK3CD,PLCG2,PRKCB,RICTOR,S1PR1,SELL
Function of leukocytes	2.27E-04	-1.076	27	ABCB1,ADRB2,CCR7,CD200,CSF1,CSF1R,CTLA4,FCMR,IL15,NEDD9,NF1,NFKBID,NLRCS,NOD2,PIK3CD,PLAT,PLCG2,RASSF5,S1PR1,SELL,SKP2,ST6GAL1,STAT1,TCF7,TIGIT,TPP2,TKX
Diffuse lymphoma	2.35E-04		31	ADSL,AKAP8,CD2,CHD6,CRNN,CSF1R,DHFR,ELK1,FILIP1L,FOXO1,GNA13,IKBKE,LONP1,MBD1,MGA,NEK4,NF1,NR3C1,OSBP,PIK3CD,PLCG2,PIEKHG3,POLB,POLE,RBCK1,RRM1,SKIV2L2,SLC4A10,TNRC6C,UBE3A,UROS
Function of lymphocytes	2.37E-04	-0.813	19	ABCB1,ADRB2,CCR7,CTLA4,IL15,NEDD9,NFKBID,NLRCS,NOD2,PIK3CD,PLCG2,RASSF5,S1PR1,SELL,SKP2,STAT1,TCF7,TPP2,TKX
T cell homeostasis	2.40E-04	↑ 2.001	30	APAF1,CCR7,CD2,CTLA4,CXCR5,ELK1,FOXO1,IGHG1,IL15,IL6ST,LONP1,NAB1,NF1,NFATC3,NFKBID,PDPK1,PIK3CD,POLB,RBL1,RICTOR,S1PR1,SATB1,SKP2,STAT1,TCF7,TNFSF8,TPP2,TKX,ZC3H8,ZFPM1
Hematologic cancer of cells	2.43E-04		29	CCR7,CD2,CD200,CSF1R,CXCL13,DHFR,DNMT3A,GJA4,GZMB,IFITM1,IGFBP4,IL15,KIR3DL1,MMP1,NF1,NR3C1,OAS2,POLB,POLE,PRKCB,RRM1,S1PR1,SATB1,SELL,SKP2,STAT1,TCF7,VMP1,ZBTB24
T-cell lymphoproliferative disorder	2.49E-04		29	CCR7,CD2,CD200,CXCL13,DHFR,DNMT3A,GJA4,GZMB,IFITM1,IGFBP4,IL15,KIR3DL1,MMP1,NF1,NR3C1,OAS2,POLB,POLE,PRKCB,RRM1,S1PR1,SATB1,SELL,SKP2,STAT1,TCF7,VMP1,ZBTB24
Function of regulatory T lymphocytes	2.58E-04	-0.832	6	ADRB2,CTLA4,PIK3CD,S1PR1,SELL,SKP2
Cell death of fibroblast cell lines	2.67E-04	-1.027	25	ABCB1,APAF1,BIRC2,CD2,CSF1R,ELK1,FANCD2,FASLG,GLS,GNA13,GNAQ,GZMB,MDN1,NR3C1,PLAC8,PLEKHF1,POLB,PRKAR1A,PRKCB,RASA4,RASSF5,RBL1,SKP2,STAT1,YME1L1
Cutaneous T-cell lymphoma	2.69E-04		8	CCR7,DHFR,IFITM1,IL15,NR3C1,OAS2,PRKCB,STAT1
Cell movement of lymphatic system cells	2.74E-04	↑ 2.192	25	ADAM8,CCR7,CD2,CTLA4,CXCL13,CXCR5,ELMO1,FASLG,FOXO1,GNA13,GNAS,IGHG1,IL15,IL6ST,NEDD9,NR3C1,PDPK1,PIK3CD,PLCG2,RASSF5,RICTOR,S1PR1,SELL,STAT1,TKX
T-cell non-Hodgkin disease	2.75E-04		24	CCR7,CD2,CD200,CXCL13,DHFR,DNMT3A,GJA4,GZMB,IFITM1,IGFBP4,IL15,KIR3DL1,MMP1,NR3C1,OAS2,POLB,POLE,PRKCB,RRM1,SATB1,SELL,SKP2,STAT1,ZBTB24
Binding of blood cells	2.89E-04	1.878	25	ADRB2,ATRN,CCR7,CD2,CD200,CSF1,CTLA4,CXCL13,FASLG,FOXO1,GZMB,IL15,IL6ST,NEDD9,NFATC3,NR3C1,PIK3CD,PILRA,PLCG2,RASSF5,RICTOR,S1PR1,SELL,STAT1,TFRC,TKX
Apoptosis of cervical cancer cell lines	2.92E-04	-1.442	19	ABCB1,BIRC2,CLASP1,CSF1R,FASLG,GZMB,IKBKE,LIMS1,LYP1A1,NEDD9,NEK6,NR3C1,PDPK1,RICTOR,STAT1,TERF1,TRAP1,UBA7,VOPP1
Stage I-IV B-cell non-Hodgkin lymphoma	2.94E-04		6	DHFR,NR3C1,PIK3CD,POLB,POLE,RRM1
Cell movement of leukemia cell lines	2.98E-04	0.909	12	AIF1,CSF1,CXCL13,FASLG,GNA13,MATK,NEDD9,PLD1,PRKCB,RICTOR,S1PR1,SELL
Cell movement of lymphocytes	2.99E-04	↑ 2.453	24	ADAM8,CCR7,CD2,CTLA4,CXCL13,CXCR5,ELMO1,FASLG,FOXO1,GNA13,GNAS,IGHG1,IL15,IL6ST,NEDD9,NR3C1,PDPK1,PIK3CD,RASSF5,RICTOR,S1PR1,SELL,STAT1,TKX
Small cell lymphocytic lymphoma/chronic lymphocytic leukemia	3.03E-04		33	AKAP8,CD200,CEP68,CHD6,CRNN,CSF1R,DLEU1,ELK1,FASLG,FCMR,FILIP1L,LONP1,LYP1A1,MBD1,MGA,NEDD9,NR3C1,OSBP,PIK3CD,PLCG2,PNKD,POLB,POLE,PRKCB,RASSF5,RBCK1,RRM1,S1PR1,SKIV2L2,SLC4A10,TIGIT,UCLL1

Cell death of lymphatic system cells	3.07E-04	0.527	24	ADAM8,APAF1,CD2,CSF1,CTLA4,FASLG,FCMR,GNAS,GZMB,IKBKE,IL15,IL6ST,NFKBID,NR3C1,PDPK1,PIK3CD,PLCG2,POLR3E,PRKCB,S1PR1,SATB1,STAT1,TPP2,ZC3H8
Acute myeloid leukemia with inv(16)	3.09E-04		5	ABCB1,CD2,DHFR,POLB,RRM1
Deletion of T lymphocytes	3.09E-04		5	CD2,CTLA4,FASLG,IL15,TCF7
FLT3 internal tandem duplication positive acute myeloid leukemia	3.09E-04		5	CSF1R,NR3C1,POLB,POLE,RRM1
Relapsed diffuse large B-cell lymphoma	3.09E-04		5	NR3C1,PIK3CD,POLB,POLE,RRM1
Cell movement of mononuclear leukocytes	3.33E-04	↑ 2.512	27	ADAM8,AIF1,ATRN,CCR7,CD2,CTLA4,CXCL13,CXCR5,ELMO1,FASLG,FOXO1,GNA13,GNAS,IGHG1,IL15,IL6ST,NEDD9,NR3C1,PDPK1,PIK3CD,PRKCB,RASSF5,RICTOR,S1PR1,SELL,STAT1,TXK
Philadelphia chromosome positive leukemia	3.39E-04		7	CSF1R,DHFR,GNAQ,NR3C1,POLB,POLE,RRM1
Survival of organism	3.64E-04	1.990	37	ABCB1,ADRB2,ATP2C1,BABAM1,CD2,CNTN1,CSF1,CTLA4,DNMT3A,EPN1,FANCD2,FASLG,FCMR,FOXO1,GNA13,GNAS,HMGA2,IKBKE,IL15,IL6ST,NFATC3,NLRCS,NOD2,NR3C1,PDPK1,PIK3CD,PLAT,PLD1,PRKAR1A,PRKCB,RBL1,SKP2,SLC22A2,SMN1/SMN2,SNX27,STAT1,TKK
17p deletion positive TP53 mutation positive chronic lymphocytic leukemia	3.64E-04		4	NR3C1,PIK3CD,POLB,RRM1
Binding of interferon-stimulated response element	3.64E-04	1.982	4	IKBKE,IRF9,RICTOR,STAT1
Cell movement of naive lymphocytes	3.64E-04	1.941	4	CCR7,CXCL13,CXCR5,SELL
T cell development	3.65E-04	↑ 2.016	29	APAF1,CCR7,CD2,CTLA4,CXCR5,ELK1,FOXO1,IGHG1,IL15,IL6ST,LONP1,NAB1,NF1,NFATC3,NFKBID,PDPK1,PIK3CD,POLB,RBL1,RICTOR,S1PR1,SATB1,SKP2,STAT1,TCF7,TNFSF8,TPP2,TKK,ZFPM1
Cell death of T lymphocytes	3.82E-04	0.578	19	ADAM8,APAF1,CD2,CTLA4,FASLG,FCMR,GNAS,GZMB,IKBKE,IL15,NFKBID,NR3C1,PDPK1,PIK3CD,POLR3E,SATB1,STAT1,TPP2,ZC3H8
B-cell malignant tumor	4.00E-04		39	AKAP8,ATRN,CCR7,CHD6,CRNN,CSF1R,CXCL13,CXCR5,DHFR,ELK1,FLIP1L,FOXO1,GNA13,LONP1,MBD1,MGA,NEK4,NF1,NONO,NR3C1,OSBP,PIK3CD,PLCG2,PLEKHG3,POLB,POLE,PPP2CA,PRKCB,RAB4A,RASSF5,RBCK1,RICTOR,RRM1,SATB1,SKIV2L2,SLC4A10,TFRC,TNFSF8,TNRC6C
Cortical T cell acute lymphoblastic leukemia	4.12E-04		7	CD2,CSF1R,DHFR,NR3C1,POLB,POLE,RRM1
Histiocytosis	4.12E-04		7	CSF1R,DHFR,MMP1,NR3C1,POLB,POLE,RRM1
Burkitt's lymphoma	4.17E-04		10	ADSL,DHFR,GNA13,IKBKE,NR3C1,POLB,POLE,RRM1,UBE3A,UROS
Quantity of follicular B lymphocytes	4.17E-04	0.997	10	FCMR,FOXO1,GNA13,IL6ST,NEDD9,NFATC3,PIK3CD,PLCG2,STG6AL1,STAT1
Differentiation of osteoclasts	4.23E-04	-0.733	14	ADAM8,ADRB2,CSF1,CSF1R,DYNLL1,GNAS,GPC3,IGHG1,IL6ST,NF1,PLCG2,RASSF2,STAT1,TFRC
Childhood myelodysplastic syndrome	4.27E-04		5	ABCB1,DHFR,NR3C1,POLB,RRM1
De novo myelodysplastic syndrome	4.27E-04		5	ABCB1,DHFR,NR3C1,POLB,RRM1
Acquired microcephaly	4.38E-04		2	ARX,PLEKHG2
Development of B-cell follicle	4.38E-04		2	CCR7,CXCR5
Entry into cell cycle progression of fibroblasts	4.38E-04		2	RBL1,SKP2
Formation of kinetochore microtubule	4.38E-04		2	NEK6,UBAP2L
Low grade malignant urothelial neoplasm	4.38E-04		2	FOXO1,STAG2
Moderate grade chronic obstructive pulmonary disease	4.38E-04		2	ADRB2,NR3C1
Retropitoneal fibrosis	4.38E-04		2	DHFR,NR3C1
Trafficking by naive T lymphocytes	4.38E-04		2	CCR7,SELL
11q deletion positive 17p deletion negative TP53 mutation negative chronic lymphocytic leukemia	4.61E-04		4	NR3C1,PIK3CD,POLB,RRM1

Rheumatoid arthritis	39	4.72E-04		ABCB1,ADAM8,ADRB2,AIF1,ARIH1,ATP2B1,ATP2C1,BRMS1,CCR7,CSF1,CTLA4,CXCL13,CXCR5,DHFR,DYNLL1,EEF2,EVC,FASLG,FAU,FCRL3,FDPs,FOX O1,GZMB,IGFBP4,IGHG1,IL15,IL6ST,MBD1,MMP1,NONO,NR3C1,POLB,RBM38,RPL19,S1PR1,SKIV2L,STAT1,TFRC,TLE3
Morphology of spleen	22	4.81E-04		CCR7,CSF1,CSF1R,CTLA4,CXCR5,FASLG,GPC3,IGHG1,IL15,IL6ST,NFATC3,NLRCS5,PDPK1,PIK3CD,RASSF2,RASSF5,RBL1,RBM38,SATB1,SELL,SNX27,TPP 2
Quantity of lymphoid organ	18	4.85E-04	1.776	ABCB1,CCR7,CD200,CTLA4,CXCL13,CXCR5,FOXO1,NOD2,NR3C1,PIK3CD,POLR3E,RASSF5,RBM38,RICTOR,SATB1,STAT1,TPP2,TKX
Lymphopoesis	34	4.89E-04	↑ 2.201	APAF1,CCR7,CD2,CTLA4,CXCR5,ELK1,FASLG,FOXO1,IGHG1,IL15,IL6ST,LONP1,NAB1,NF1,NFATC3,NFKBID,PDPK1,PIK3CD,PLCG2,POLB,RASSF5,RBL1, RICTOR,S1PR1,SATB1,SKP2,STAT1,TAB2,TAB3,TCF7,TNFSF8,TPP2,TKX,ZFPM1
Refractory Philadelphia chromosome-negative acute lymphoblastic leukemia	5	4.98E-04		DHFR,NR3C1,POLB,POLE,RRM1
Relapsed Philadelphia chromosome-negative acute lymphoblastic leukemia	5	4.98E-04		DHFR,NR3C1,POLB,POLE,RRM1
Viral Infection	69	5.00E-04	↑ 3.445	ABCB1,ADRB2,AGFG1,AGO2,APAF1,ATP2C1,ATP6V1A,CCR7,CD200,CEP68,CLTB,COG3,COPB2,CSF1,CTLA4,DCAF13,DHFR,DMPK,DNMT3A,EDEM1,E IF3G,EIF4A3,EIF4EBP2,EPN1,FASLG,FAU,FDPs,HSPA4,IFITM1,IKBKE,IL15,IRF9,KDM7A,LONP1,MDN1,NDUFS6,NLRCS,NR3C1,OAS2,OSBP,OSBPIL3,P2 RY10,PARP9,PDE3B,PHF3,PLAT,PLCG2,PLD1,POLB,PRKCB,PSMD12,PVT1,RPL18,RRM1,SELL,SETD1B,SMN1/SMN2,SSRP1,ST6GAL1,STAT1,STT3A,SY NJ1,TFRC,TRIM14,TRIM5,UBA7,VNN2,ZBP1,ZCCHC17
Invasion of cells	43	5.13E-04	1.645	ADAM8,ADI1,ADRB2,AGO2,ARHGEF18,CCR7,COPB2,CSF1,CUL4B,ELK1,ELMO1,FASLG,FOXO1,GEM1,GNA13,GNAQ,GNAS,GZMB,HDGF,HMGA2,IFIT M1,IGHG1,IPO7,LDLRAP1,LYPLA1,MATK,MMP1,NEDD9,NF1,NFKBID,NOD2,PDPK1,PIK3CD,PLAT,PLD1,PRKCB,RICTOR,RRM1,SATB1,SKP2,ST6GAL1, STAT1,UBE3A
Activation of blood cells	36	5.24E-04	0.415	CCR7,CD2,CD200,CSF1,CSF1R,CTLA4,CXCR5,DAPP1,FASLG,FCRL3,FOXO1,GJ44,GNA13,GNAQ,HSPA4,IGHG1,IL15,KIR3DL1,MMP1,NFATC3,NFKBID, NOD2,PIK3CD,PLAT,PLCG2,PRKCB,RAB4A,SATB1,SELL,SIRPG,ST6GAL1,STAT1,TAB2,TAB3,TIGIT,ZBTB46
Cell cycle progression	49	5.30E-04	0.148	AIF1,AKAP8,APAF1,ARX,BIRC2,BUB3,CACUL1,CBX7,CKAP2,CLASP1,CSF1,CSF1R,CTLA4,DBF4,DHFR,DYNC1L12,ELK1,FANCD2,FOXO1,GEM,GNA13,GN L3,IGHG1,IRF9,MATK,MLF1,NEDD9,NEK4,NEK6,NF1,NR3C1,PDPK1,PD55A,PLAC8,PPP2CA,PRKAR1A,PRKCB,RASSF2,RASSF5,RBL1,RRM1,S1PR1,SKP 2,SSRP1,STAT1,TERF1,TPP2,UBA7,USP3
Chemotaxis of mononuclear leukocytes	13	5.32E-04	↑ 2.440	ADAM8,AIF1,CCR7,CXCL13,ELMO1,GNA13,GNAS,IL15,NEDD9,NR3C1,PIK3CD,PRKCB,S1PR1
Refractory acute lymphocytic leukemia	6	5.33E-04		CSF1R,DHFR,NR3C1,POLB,POLE,RRM1
Apoptosis of lung cancer cell lines	15	5.41E-04	-1.075	APAF1,FASLG,GNAS,IKBKE,IL6ST,ILKAP,NR3C1,PPP2CA,PRKCB,RICTOR,RPA2,RRM1,SKP2,SSRP1,TRAP1
Development of hematopoietic progenitor cells	16	5.44E-04	1.077	AGO2,BRD1,CSF1,FOXO1,HMGA2,IL15,IL6ST,NAB1,PLCG2,RCOR1,RICTOR,SATB1,SMARCA5,STAT1,TCF7,ZFPM1
Urothelial bladder carcinoma	11	5.69E-04		ARHGAP35,CHD6,CTLA4,DHFR,FOXO1,NF1,NLRCS5,POLE,PRKCB,RRM1,STAG2
Stage I-IV diffuse large B-cell lymphoma	5	5.77E-04		DHFR,NR3C1,POLB,POLE,RRM1
Cell viability of antigen presenting cells	7	5.94E-04	0.904	CCR7,CSF1,CSF1R,FOXO1,IL15,PIK3CD,PLAT
Cell death of thymocytes	11	5.99E-04	0.510	ADAM8,APAF1,FASLG,GNAS,GZMB,NFKBID,NR3C1,PIK3CD,POLR3E,SATB1,ZC3H8
Cell death of lymphoid organ	12	6.02E-04	0.734	ADAM8,APAF1,FASLG,GNAS,GZMB,IL6ST,NFKBID,NR3C1,PIK3CD,POLR3E,SATB1,ZC3H8
Chemotaxis of leukocytes	21	6.37E-04	1.947	ADAM8,AIF1,CCR7,CSF1,CSF1R,CXCL13,CXCR5,ELMO1,FASLG,GNA13,GNAS,IL15,NEDD9,NOD2,NR3C1,PIK3CD,PLCG2,PRKCB,RICTOR,S1PR1,SELL
Relapsed childhood acute lymphoblastic leukemia	6	6.62E-04		CSF1R,DHFR,NR3C1,POLB,POLE,RRM1
Apoptosis of tumor cell lines	55	6.93E-04	-1.436	ABCB1,ADI1,APAF1,BIRC2,BUB3,CKAP2,CLASP1,CSF1R,DYNLL1,FASLG,FAU,FCMR,FOXO1,GEM,GLS,GNA13,GNAS,GZMB,HSPA4,IGFBP4,IGHG1,IKBK E,IL15,IL6ST,ILKAP,KIR3DL1,LIMS1,LYP1A1,NAT10,NEDD9,NEK6,NF1,NR3C1,PDPK1,PIK3CD,PLAT,PLCG2,PPP2CA,PRKAR1A,PRKCB,RAPGEF2,RASSF5 ,RICTOR,RPA2,RRM1,SATB1,SKP2,SSRP1,ST6GAL1,STAT1,TERF1,TFRC,TRAP1,UBA7,VOPPP1
Apoptosis of cytotoxic T cells	3	6.99E-04		FASLG,GZMB,IL15
Paternal imprinting	3	6.99E-04		GNAS,GPC3,UBE3A
Refractory childhood acute lymphoblastic leukemia	3	6.99E-04		POLB,POLE,RRM1
Granulomatosis	4	7.06E-04		DHFR,FDPs,NOD2,NR3C1
Binding of leukocytes	22	7.08E-04	↑ 2.119	ATRN,CCR7,CD2,CD200,CSF1,CTLA4,CXCL13,FASLG,FOXO1,IL15,IL6ST,NEDD9,NFATC3,NR3C1,PIK3CD,PILRA,RASSF5,RICTOR,SELL,STAT1,TFRC,TKX

Activation of cells	45	7.23E-04	0.175	ADAM8,CCR7,CD2,CD200,CSF1,CSF1R,CTLA4,CXCR5,DAPP1,FASLG,FCRL3,FFAR3,FOXO1,GJA4,GNA13,GNAS,GZMB,HSPA4,IGHG1,IL15,IL6ST,KIR3DL1,MMP1,NFATC3,NFKBID,NOD2,PDPK1,PIK3CD,PLAT,PLCG2,PPP2CA,PRKCB,RAB4A,RICTOR,SATB1,SELL,SIRPG,ST6GAL1,STAT1,TAB2,TAB3,TIGIT,ZBP1,ZBTB46
Thymic carcinoma	6	7.36E-04		CSF1R,DHFR,NR3C1,POLE,RRM1,SSTR3
Cell death of epithelial cell lines	18	7.64E-04	-1.143	AAK1,ATP13A2,BIRC2,CSF1R,CUL4B,DYNLL1,ELK1,FASLG,FOXO1,NEK6,PDPK1,PPP2CA,PRKCB,RASSF5,SLC22A2,SSRP1,TFR,VOPIP1
Non-M3 acute myeloid leukemia	7	7.69E-04		ABCB1,CSF1R,DHFR,DNMT3A,NR3C1,POLB,RRM1
Apoptosis of lymphoid organ	11	7.73E-04	0.425	ADAM8,FASLG,GNAS,GZMB,IL6ST,NFKBID,NR3C1,PIK3CD,POLR3E,SATB1,ZC3H8
Cell movement of cervical cancer cell lines	9	8.03E-04	0.853	ARHGAP35,CSF1R,DBF4,HDGF,NF1,PLD1,RICTOR,SNX27,ST6GAL1
Metabolism of DNA	22	8.08E-04	-1.342	ABCB1,APAF1,CD2,CSF1,CUL4B,DBF4,FASLG,FFAR3,GZMB,HMGA2,IGFBP4,NR3C1,PDSSA,POLB,POLE,PPP1CC,RPA2,RPAIN,SSRP1,STAT1,TERF1,VM P1
Advanced non-Hodgkin lymphoma	6	8.15E-04		DHFR,IL15,NR3C1,POLB,POLE,RRM1
Philadelphia-positive acute lymphoblastic leukemia	6	8.15E-04		CSF1R,DHFR,NR3C1,POLB,POLE,RRM1
Recurrent metastatic solid tumor	6	8.15E-04		CSF1R,CTLA4,DHFR,PIK3CD,POLE,RRM1
Myelodysplastic syndrome	18	8.38E-04		ABCB1,APAF1,APH1A,ARIH1,CSF1R,DHFR,DNMT3A,FANCD2,FASLG,GNAS,MGA,NF1,NR3C1,POLB,POLE,RRM1,STAG2,TLE3
Sjögren syndrome	9	8.53E-04		CCR7,CSF1,CXCL13,CXCR5,FASLG,IFITM1,MATK,NR3C1,STAT1
Inv(3) positive acute myeloid leukemia	4	8.57E-04		NR3C1,POLB,POLE,RRM1
Macular edema	4	8.57E-04		ADR82,DHFR,NR3C1,PRKCB
Anemia	23	8.76E-04	-1.491	ADR82,AGO2,BRD1,CTLA4,DHFR,DNMT3A,FANCD2,IL6ST,MTRR,NFATC3,NR3C1,PLCG2,POLB,RBM38,RRM1,SEC11A,SELL,SLC11A2,TFR,TPP1,TPP2,ZFPM1
Apoptosis of thymocytes	10	8.80E-04	0.170	ADAM8,FASLG,GNAS,GZMB,NFKBID,NR3C1,PIK3CD,POLR3E,SATB1,ZC3H8
Apoptosis of gonadal cell lines	6	9.01E-04		FASLG,GNAS,PLD1,POLB,SSTR3,TFR
Pallor	9	9.06E-04		BRD1,CUL4B,GNA13,NF1,POLB,SLC11A2,TAB2,TFR,ZFPM1
Cell movement of natural killer cells	7	9.07E-04	1.422	CCR7,GNA13,GNAS,IL15,PIK3CD,S1PR1,SELL
Quantity of memory T lymphocytes	7	9.07E-04	-1.681	CTLA4,DNMT3A,IL15,RASSF5,STAT1,TPP2,TKK
Grade 1 lymphocytic cancer	18	9.48E-04		CCR7,CHD6,CRNN,CSF1R,CXCL13,CXCR5,ELK1,FILIP1L,MBD1,MGA,NR3C1,OSBP,PIK3CD,POLE,RBCK1,RRM1,SKIV2L2,SLC4A10
Cell death of cancer cells	21	9.62E-04	-1.516	APAF1,COPB2,CSF1,CTLA4,EIF3G,FASLG,FAU,FOXO1,IL15,IL6ST,LYPLA1,NEK4,NR3C1,PIK3CD,PSMC6,PSMD12,RBM8A,RPA2,RPL19,SELL,SF3B3
Cell viability of lymphocytes	13	9.66E-04	1.497	CTLA4,FASLG,FCMR,FCRL3,IL15,IL6ST,PDPK1,PIK3CD,PLCG2,PRKCB,RICTOR,STAT1,TCF7
Cytosis	20	9.70E-04	0.342	AGPS,ATP13A2,BIRC2,CSF1,CSF1R,DHFR,DNMT3A,FASLG,IL15,IL6ST,MMP1,NF1,NFATC3,NLR5,NOD2,NR3C1,PDPK1,PIK3CD,POLB,POLE,RRM1,S1PR1,SELL,SLC11A2
Adaptive immune response	7	9.82E-04	0.655	CCR7,CTLA4,FFAR3,FOXO1,IL15,PIK3CD,TKK
Response of embryonic cell lines	7	9.82E-04	1.195	BIRC2,EIF4EBP2,NOD2,RICTOR,SPRY1,TRIM14,TRIM5
Eradication of tumor	3	9.83E-04		CD200,CTLA4,IL15
Memory T cell response	3	9.83E-04		CTLA4,FOXO1,IL15
Morphology of lymphoid tissue	28	9.83E-04		CCR7,CD200,CSF1,CSF1R,CTLA4,CXCR5,FASLG,GNAS13,GPC3,IGHG1,IL15,IL6ST,NF1,NFATC3,NLR5,NOD2,NR3C1,PDPK1,PIK3CD,RASSF2,RASSF5,RB L1,RBM38,SATB1,SELL,SNX27,TPP2,ZBTB46
Cell death of lung cancer cell lines	16	9.87E-04	-1.257	APAF1,BIRC2,FASLG,GNAS,IKBKE,IL6ST,ILKAP,NR3C1,PPP2CA,PRKCB,RICTOR,RPA2,RRM1,SKP2,SSRP1,TRAP1
Activation of regulatory T lymphocytes	5	9.89E-04	0.555	CD2,CTLA4,IL15,NFATC3,PIK3CD
Refractory anemia with ringed sideroblasts	5	9.89E-04		DHFR,DNMT3A,NR3C1,POLB,RRM1
Immunosuppression	4	1.03E-03	0	ADR82,CTLA4,NR3C1,S1PR1
Breast cancer	70	1.03E-03	-0.068	ABCB1,ADR82,AGO2,APH1A,ARHGAP35,ATP2C1,BRWD1,C17orf49,CASK,CCNL1,CCR7,CMAHP,CNTN1,CSF1R,CTLA4,DHFR,DKC1,DNMT3A,ETFA,FANCD2,FDPS,GGCT,GLS,GNAS13,GNAS,GOSR1,GPC3,HMGA2,IKBKE,ILKAP,KLHL12,LONP1,LYPLA1,MBD1,MCM6,MGA,MFL1,MMP1,MUC7,NEK6,NF1,NR3C1,PIK3CD,PLAT,PNO,POLB,POLE,PPFIA1,PRKCB,PSMD12,RPL19,RRM1,SELL,SETD1B,SF3B3,SKP2,SLC25A14,SLC27A1,SLC5A10,SSSTR3,STAG2,STAT1,TES,TLE3,UBAP2L,UBE3A,VBP1,VWA5A,ZFPM1,ZNF692
Organization of cytoplasm	67	1.04E-03	1.559	AGFG1,ARHGAP35,ARHGEF18,ATP13A2,ATP2B1,ATP2C1,ATRN,BRWD1,CARMIL1,CCR7,CD2,CHN1,CKAP2,CLASP1,CNTN1,COG3,COPB2,CSF1,CSF1R,CTLA4,CUL4B,DCTN6,DYNLL1,EIF4EBP2,ELK1,ELMO1,GCC2,GEM,GNAS13,GNAS,GZMB,HDGF,LONP1,MATK,MKS1,NEDD9,NEK6,NF1,PD EADIP,PDPK1,PIK3CD,PLAT,PLCG2,PLD1,PLEKHF1,PPP2CA,PRKCB,RAB30,RAB43,RAPGEF2,RASSF5,RICTOR,RNF19A,S1PR1,SELENON,SLC11A2,SMAR CA5,SMN1/SMN2,SSRP1,SSTR3,TERF1,TPP1,TRAPPC11,UBAP2L,UBE3A,YME1L1

Growth of organism	1.07E-03	1.815	39	ABCB1,AGO2,AIF1,APH1A,ARX,CSF1,EPN1,FANCD2,FOXO1,GNA13,GNAS,GPC3,GZMB,IGFBP4,IL15,IL6ST,IJMS1,NDUFS6,NF1,NR3C1,PDPK1,PGAP1,PLAT,POLB,PPP1CC,PRKCB,RAPGEF2,RBL1,S1PR1,SLC25A14,SLC4A10,SMARCA5,SMN1/SMN2,SNX27,ST6GAL1,STAT1,SYNJ1,TERF1,TFRC
Transitional-cell carcinoma	1.09E-03		13	ARHGAP35,CHD6,CTLA4,DHFR,FOXO1,GNA13,NF1,NLRCS,NR3C1,POLE,PRKCB,RRM1,STAG2
Activation of leukocytes	1.10E-03	0.172	33	CCR7,CD2,CD200,CSF1,CSF1R,CTLA4,CXCR5,DAPP1,FASLG,FCRL3,FOXO1,GIA4,HSPA4,IGHG1,IL15,KIR3DL1,NFATC3,NFKBID,NOD2,PIK3CD,PLAT,PLCG2,PRKCB,RAB4A,SATB1,SELL,SIRPG,ST6GAL1,STAT1,TAB2,TAB3,TIGIT,ZBTB46
Morphology of lymphoid organ	1.10E-03		26	CCR7,CD200,CSF1,CSF1R,CTLA4,CXCR5,FASLG,GPC3,IGHG1,IL15,IL6ST,NFATC3,NLRCS,NOD2,NR3C1,PDPK1,PIK3CD,RASSF2,RASSF5,RBL1,RBM38,SATB1,SELL,SNX27,TPP2,ZBTB46
Chronic inflammation	1.12E-03		5	IL6ST,NR3C1,PIK3CD,PLAT,STAT1
Cell death of cervical cancer cell lines	1.13E-03	-1.306	21	ABCB1,ATP2B1,BIRC2,BUB3,CLASP1,CSF1R,CTLA4,GZMB,IKBKE,IJMS1,LYPLA1,NEDD9,NEK6,NR3C1,PDPK1,RICTOR,STAT1,TERF1,TRAP1,UBA7,VOP1
Central nervous system cancer	1.17E-03		30	ARHGAP35,CD200,CLTB,CSF1,CSF1R,CTLA4,DHFR,DLEU1,ELK1,ELMO1,FOXO1,GIA4,GNAQ,IL15,MMMP1,NEK6,NF1,NR3C1,PLAC8,POLB,POLE,PRKCB,PVT1,RAPGEF2,RRM1,SEC11A,STAG2,SYNJ1,TERF1,TLE3
Fibrosis of bone marrow	1.20E-03		6	CSF1R,DNMT3A,HMG2A,IGHG1,NF1,NR3C1
Formation of microtubules	1.20E-03	0.896	8	CLASP1,DYNLL1,GNA13,GZMB,NEK6,PDPK1,TERF1,UBAP2L
Cell death of osteosarcoma cells	1.21E-03	↓ -3.000	9	COPB2,EIF3G,FAU,PSMC6,PSMD12,RBM8A,RPA2,RPL19,SF3B3
Migration of lymphatic system cells	1.22E-03	1.678	21	CCR7,CD2,CTLA4,CXCL13,CXCR5,ELMO1,FASLG,FOXO1,GNA13,IL15,IL6ST,NR3C1,PDPK1,PIK3CD,PLCG2,RASSF5,RICTOR,S1PR1,SELL,STAT1,TKK
Abnormal morphology of red pulp	1.23E-03		4	CCR7,RASSF2,RASSF5,RBL1
NPM1 mutation positive acute myeloid leukemia	1.23E-03		4	NR3C1,POLB,POLE,RRM1
Quantity of effector T lymphocytes	1.23E-03		4	CTLA4,DNMT3A,IL15,STAT1
Hemorrhagic disease	1.24E-03	-0.440	16	ATP2C1,CXCL13,FASLG,GGCX,IL15,MCFD2,NR3C1,OAS2,PDPK1,PLAT,POLB,RBM8A,RPL18,S1PR1,TPP2,ZFPM1
Abnormal morphology of immune system	1.25E-03		17	ABCB1,CD200,CSF1,CSF1R,CTLA4,CXCR5,FASLG,FCMR,IGHG1,IL15,NOD2,PDPK1,PIK3CD,PLCG2,RASSF2,TPP2,ZBTB46
Development of lymph follicle	1.26E-03		5	CCR7,CTLA4,CXCR5,FASLG,RICTOR
Function of heart ventricle	1.26E-03	-1.131	5	ADRB2,CSF1,GNAQ,GNAS,NDUFS6
Osteoclastogenesis of macrophages	1.26E-03	-1.474	5	CSF1,FASLG,FOXO1,PLCG2,STAT1
Urothelial cancer	1.29E-03		12	ARHGAP35,CHD6,CTLA4,DHFR,FOXO1,NF1,NLRCS,POLE,PRKCB,RRM1,SEC11A,STAG2
Activation-induced cell death of lymphoma cell lines	1.30E-03		2	FASLG,SATB1
Acute otitis media	1.30E-03		2	DHFR,NR3C1
Cytokinesis of lung cancer cell lines	1.30E-03		2	PPP1CC,SSRP1
Development of bone marrow precursor cells	1.30E-03		2	CSF1,IL15
Egression of follicular B lymphocytes	1.30E-03		2	GNA13,S1PR1
Enlargement of embryonic tissue	1.30E-03		2	APAF1,EDA
Focal dystonia	1.30E-03		2	VAMP1,VAMP2
Hyperplasia of tunica intima	1.30E-03		2	AIF1,NF1
Migration of adenocarcinoma cells	1.30E-03		2	CSF1,CSF1R
Moderate asthma	1.30E-03		2	ADRB2,NR3C1
Myxoma	1.30E-03		2	GNAS,PRKAR1A
Polarization of CD4+ T-lymphocytes	1.30E-03		2	CCR7,ELMO1
Production of macrophages	1.30E-03		2	CSF1,CSF1R
Production of osteoclasts	1.30E-03		2	CSF1,CSF1R
Quantity of epithelial precursor cells	1.30E-03		2	CSF1,CSF1R
Quantity of neuroepithelial tumor	1.30E-03		2	FOXO1,RBL1
Quantity of peripheral lymph node	1.30E-03		2	CCR7,CXCR5
Recruitment of tumor-associated macrophages	1.30E-03		2	CSF1,CSF1R
Size of centrosome	1.30E-03		2	LDLRAP1,TPP2
Size of medullary cavity	1.30E-03		2	CSF1,GNAS
Hematopoiesis in embryo	1.32E-03		6	BRD1,RAPGEF2,RCOR1,TFRC,TNRC6C,ZFPM1

Ectopic ACTH secreting tumor	1.33E-03	3	GNAS,NR3C1,SSTR3
Giant cell arteritis	1.33E-03	3	DHFR,FDPs,NR3C1
Morphology of sebaceous glands	1.33E-03	3	CBX7,EDA,RBL1
Stimulation of cytotoxic T cells	1.33E-03	3	CTLA4,FASLG,IL15
Size of muscle	1.33E-03	10	ADRB2,DMPK,FOXO1,GNAQ,GNAS,IL6ST,LIMS1,PDPK1,SELENON,SMN1,SMN2
Relapsed lymphocytic leukemia	1.34E-03	7	CSF1R,DHFR,NR3C1,PIK3CD,POLB,POLE,RRM1
Metastatic breast cancer	1.36E-03	9	ABCB1,CCR7,DHFR,FDPs,NR3C1,PIK3CD,POLE,RRM1,STAT1
Brain metastasis	1.42E-03	5	CTLA4,DHFR,MMP1,NR3C1,POLB
Morphology of leukocytes	1.43E-03	18	ABCB1,CD200,CSF1,CSF1R,CTLA4,CXCR5,FASLG,FCMR,GNA13,IGHG1,IL15,NOD2,PDPK1,PIK3CD,PLCG2,RASSF2,TPP2,ZBTB46
Homing of T lymphocytes	1.44E-03	9	CCR7,CXCL13,CXCR5,ELMO1,FOXO1,IL15,NR3C1,S1PR1,SELL
Recurrent acute myeloid leukemia	1.44E-03	6	ABCB1,CSF1R,DHFR,POLB,POLE,RRM1
Colony formation of cervical cancer cell lines	1.45E-03	4	HMGA2,NEK6,NF1,TES
Migration of carcinoma cells	1.45E-03	4	CSF1,CSF1R,NEDD9,STG6AL1
Colony formation	1.46E-03	28	CCR7,CKS1B,CSF1,CSF1R,DHFR,GPC3,GZMB,HDGF,HMGA2,IGFBP4,IL6ST,MAML2,NEK6,NF1,NR3C1,PDPK1,PPP2CA,PRKAR1A,PRKCB,RASSF2,RASSF5,RICTOR,RRM1,SATB1,SPRY1,ST6GAL1,TES,UBE3A
Aggregation of blood cells	1.48E-03	15	ADRB2,ATRNLK1,GJA4,GNA13,GNAQ,GNAS,IL15,MMP1,PDPK1,PIK3CD,PLAT,PLCG2,SELL,ZFPM1
Lymphocyte migration	1.49E-03	20	CCR7,CD2,CTLA4,CXCL13,CXCR5,ELMO1,FASLG,FOXO1,GNA13,IL15,IL6ST,NR3C1,PDPK1,PIK3CD,RASSF5,RICTOR,S1PR1,SELL,STAT1,TXK
Adhesion of blood cells	1.49E-03	21	ADRB2,ATRNLK1,CD2,CD200,CSF1,CXCL13,FASLG,FOXO1,GZMB,IL15,IL6ST,NEDD9,NR3C1,PIK3CD,PILRA,PLCG2,RASSF5,RICTOR,SELL,STAT1
Cell death of epithelial cells	1.53E-03	26	AAK1,APAF1,ATP13A2,BIRC2,CSF1R,CUL4B,DYNLL1,ELK1,FASLG,FOXO1,IL15,NEK6,NR3C1,PDPK1,PLAT,PPP2CA,PRKCB,RASSF5,RBCK1,RBL1,S1PR1,SLC22A2,SSRP1,STAT1,TFRG,VOPP1
High bone mass disease	1.55E-03	7	CSF1,CSF1R,DHFR,FDPs,IGHG1,PLCG2,RRM1
Adult Philadelphia chromosome negative cortical T acute lymphoblastic leukemia	1.57E-03	6	CSF1R,DHFR,NR3C1,POLB,POLE,RRM1
Adult Philadelphia chromosome negative precursor T-cell acute lymphoblastic leukemia	1.57E-03	6	CSF1R,DHFR,NR3C1,POLB,POLE,RRM1
Adult Philadelphia chromosome negative pro-B-cell acute lymphoblastic leukemia	1.57E-03	6	CSF1R,DHFR,NR3C1,POLB,POLE,RRM1
ALK fusion negative large cell lymphoma	1.59E-03	5	DHFR,NR3C1,POLB,POLE,RRM1
Acute myeloid leukemia associated with myelodysplastic syndrome	1.59E-03	5	CSF1R,DHFR,DNMT3A,POLB,RRM1
Binding of B lymphocytes	1.59E-03	5	CXCL13,NFATC3,RASSF5,SELL,TFRG
Inflammation of peritoneum	1.59E-03	5	ADRB2,BIRC2,FASLG,SELL,ST6GAL1
Cytopenia	1.60E-03	19	ABCB1,ADRB2,ATP2C1,CXCL13,DHFR,FASLG,IGHG1,IL15,NR3C1,OAS2,PDPK1,PIK3CD,PLAT,POLB,RBM8A,RRM1,S1PR1,TPP2,ZFPM1
Function of T lymphocytes	1.64E-03	15	ABCB1,ADRB2,CCR7,CTLA4,IL15,NEDD9,NLRCS,NOD2,PIK3CD,S1PR1,SELL,SKP2,TCF7,TPP2,TKX
Immunodeficiency	1.64E-03	15	CSF1R,CTLA4,DHFR,DNMT3A,FASLG,PIK3CD,PLCG2,POLB,POLE,RBCK1,RRM1,SKIV2L,STAT1,TFRG,ZBTB24
Uptake of monosaccharide	1.65E-03	16	ADRB2,CSF1,CSF1R,ELK1,GNAQ,GNAS,NOD2,PDPK1,PLAT,PLD1,PRKCB,RAB4A,SKP2,SLC27A1,SLC5A10,SNX27
Necrosis of muscle	1.69E-03	19	ADRB2,APAF1,CSF1R,DMPK,FASLG,FOXO1,GNAQ,GNAS,IKBKE,IL6ST,LIMS1,PDPK1,PLAT,PLD1,PPP1CC,PRKCB,SMN1/SMN2,STAT1,WTAP
Differentiation of effector T lymphocytes	1.70E-03	4	CTLA4,FOXO1,IL15,RICTOR
Refractory anemia with excess blasts in transformation	1.70E-03	4	DHFR,NR3C1,POLB,RRM1
Quantity of T lymphocytes	1.73E-03	27	ABCB1,CCR7,CSF1,CTLA4,DKC1,DNMT3A,FASLG,FCMR,FOXO1,IL15,IL6ST,NF1,NFATC3,NLRCS,NOD2,NR3C1,PIK3CD,POLR3E,RASSF2,RASSF5,RICTOR,SATB1,SELL,STAT1,TIGIT,TPP2,TKX
Abnormal morphology of antigen presenting cells	1.75E-03	3	CSF1R,CXCR5,PDPK1

CD274 negative urothelial carcinoma	1.75E-03	3	CTLA4,POL,RRM1
CD274 positive urothelial carcinoma	1.75E-03	3	CTLA4,POL,RRM1
Distribution of leukocytes	1.75E-03	3	CCR7,PIK3CD,S1PR1
Pancreatic intraductal papillary mucinous tumor	1.75E-03	3	GNAS,POL,RRM1
Quantity of enteroendocrine cells	1.75E-03	3	ARX,CSF1,CSF1R
Stage IV non-Sezary/visceral disease	1.75E-03	3	DHFR,POL,RRM1
Stage IV recurrent squamous cell lung cancer	1.75E-03	3	CTLA4,POL,RRM1
Stage IV urethral cancer	1.75E-03	3	CTLA4,POL,RRM1
Transitional cell carcinoma of the renal pelvis	1.75E-03	3	CTLA4,POL,RRM1
Transcription of DNA	1.75E-03	1.476	64
Colony formation of cells	1.77E-03	1.615	26
Philadelphia positive B-cell precursor acute lymphoblastic leukemia	1.77E-03	5	DHFR,NR3C1,POLB,POL,RRM1
T-cell lymphoblastic lymphoma	1.77E-03	5	CD2,DHFR,NR3C1,POLB,POL
Progression of malignant tumor	1.78E-03	12	CKS1B,CSF1R,CTLA4,DHFR,FOXO1,MMP1,NR3C1,PIK3CD,POLB,POL,RRM1,SKP2
Aggregation of blood platelets	1.79E-03	0.788	13
Dysplasia	1.83E-03	-1.446	27
Langerhans cell histiocytosis	1.86E-03	6	DHFR,MMP1,NR3C1,POLB,POL,RRM1
Size of cardiac muscle	1.86E-03	6	ADRB2,FOXO1,GNAQ,IL6ST,LIMS1,PDPK1
Quantity of thymus gland	1.88E-03	↑ 2.020	14
Lymphoblastic lymphoma	1.91E-03	7	CD2,CSF1R,DHFR,NR3C1,POLB,POL,RRM1
Benign oral disorder	1.97E-03	22	AKAP8,APAF1,CCR7,COX7B,CSF1,CXCL13,CXCR5,DHFR,EVC,FASLG,FDPS,IFITM1,IGHG1,LONP1,MATK,MMP1,NR3C1,PLAC8,POL,STAT1,VAMP1,VA MP2
Philadelphia positive T-cell precursor acute lymphoblastic leukemia	1.97E-03	5	DHFR,NR3C1,POLB,POL,RRM1
Recurrent leukemia	1.97E-03	8	ABCB1,CSF1R,DHFR,NR3C1,PIK3CD,POLB,POL,RRM1
Size of muscle cells	1.98E-03	9	ADRB2,DMPK,FOXO1,GNAQ,GNAS,LIMS1,PDPK1,SELENON,SMN1/SMN2
Gastrointestinal stromal tumor	2.03E-03	6	ABCB1,CSF1R,DHFR,GLS,MTRR,NF1
Abnormal morphology of leukocytes	2.07E-03	13	ABCB1,CSF1,CSF1R,CTLA4,CXCR5,FASLG,FCMR,IGHG1,IL15,PDPK1,PIK3CD,RASSF2,TPP2
Acute leukemia	2.11E-03	0.152	56
Arrest in proliferation of cells	2.15E-03	13	CBX7,GLS,IL6ST,IPO7,NR3C1,PPP1CC,PRKCB,RASSF5,RBL1,SKP2,SMARCA5,STAT1,TAF7
Interphase	2.16E-03	0.101	32
Congenital anomaly of skin	2.16E-03	12	ADRB2,ATP6V1A,B3GALT6,COX7B,DKC1,EDA,EVC,GNAQ,MMP1,NF1,NR3C1,RRM1
Vasculitis	2.19E-03	-1.964	7
Antiviral response of cells	2.19E-03	1.000	5
Progression of squamous-cell carcinoma	2.19E-03	5	CKS1B,CTLA4,POL,RRM1,SKP2
Hereditary bleeding disorder	2.20E-03	6	GGCX,MCFD2,NR3C1,PLAT,POLB,RRM8A

Shape change of tumor cell lines	2.20E-03	0.860	11	CHN1,CSF1,FASLG,GEM,GNA13,GNAQ,MATK,PLD1,PPF1A1,PRKCB,RBL1
Incidence of digestive organ tumor	2.21E-03	-1.970	8	CBX7,NF1,PRKAR1A,PRKCB,RASSF5,RBM38,STAT1,TES
Metastatic head and neck tumor	2.21E-03		8	CSF1R,CTLA4,DHFR,MMP1,NR3C1,POLB,POLE,RRM1
Cell death of lymphoma cell lines	2.23E-03	-1.080	13	FASLG,FOXO1,GLS,GNA13,IGFBP4,IGHG1,LONP1,PLCG2,PRKCB,SATB1,ST6GAL1,STAT1,TPP2
Activation-induced cell death of tumor cell lines	2.24E-03		3	FASLG,KIR3DL1,SATB1
Cell movement of naive T lymphocytes	2.24E-03		3	CCR7,CXCR5,SELL
Hemophilia A	2.24E-03		3	MCFD2,NR3C1,POLB
Large cell transformed mycosis fungoides	2.24E-03		3	DHFR,POLE,RRM1
Recurrent CD274 positive malignant solid tumor	2.24E-03		3	CTLA4,POLE,RRM1
Refractory Philadelphia-negative B-cell acute lymphoblastic leukemia	2.24E-03		3	POLB,POLE,RRM1
Relapsed Philadelphia-negative B-cell acute lymphoblastic leukemia	2.24E-03		3	POLB,POLE,RRM1
Stimulation of leukemia cell lines	2.24E-03		3	CD2,CSF1,FASLG
Angioimmunoblastic T-cell lymphoma	2.25E-03		10	CD200,CXCL13,DHFR,DNMT3A,GJA4,MMP1,NR3C1,POLB,POLE,RRM1
Adult acute myeloid leukemia with del(5q)	2.28E-03		4	ABCB1,DHFR,POLB,RRM1
Hepatosplenic T-cell lymphoma	2.28E-03		4	DHFR,NR3C1,POLE,RRM1
Refractory peripheral T-cell lymphoma	2.28E-03		4	DHFR,NR3C1,POLE,RRM1
Relapsed peripheral T-cell lymphoma	2.28E-03		4	DHFR,NR3C1,POLE,RRM1
T(15;17) mutation negative acute myeloid leukemia	2.28E-03		4	CSF1R,POLB,POLE,RRM1
Cell death of embryonic cell lines	2.29E-03	-1.004	20	AAK1,APAF1,ATP13A2,BIRC2,CUL4B,FASLG,FOXO1,GZMB,PDPK1,POLB,PRKCB,RASSF5,RBL1,SKP2,SLC22A2,SSRP1,STAT1,TFRC,VOPPP1,YME1L1
Quantity of marginal-zone B lymphocytes	2.34E-03	1.746	7	FCMR,FOXO1,GNA13,NEDD9,NFATC3,PIK3CD,ST6GAL1
Recurrent acute leukemia	2.34E-03		7	ABCB1,CSF1R,DHFR,NR3C1,POLB,POLE,RRM1
Diffuse B-cell lymphoma	2.35E-03		26	AKAP8,CHD6,CRNN,CSF1R,DHFR,ELK1,FILIP1L,FOXO1,GNA13,LONP1,MBD1,MGA,NEK4,NF1,NR3C1,OSBP,PIK3CD,PLCG2,PLEKHG3,POLB,POLE,RBK1,RRM1,SKIV2L2,SLC4A10,TNRC6C
Systemic CD30 positive anaplastic large cell lymphoma	2.38E-03		6	DHFR,NR3C1,POLB,POLE,RRM1,STAT1
Development of hematopoietic system	2.42E-03	0.097	18	AGO2,BRD1,CSF1,FASLG,FOXO1,HMGA2,IL15,IL6ST,NAB1,PLCG2,RBM38,RCOR1,RICTOR,SATB1,SMARCA5,STAT1,TCF7,ZFPM1
Classic Hodgkin disease	2.42E-03		5	FOXO1,NR3C1,POLB,POLE,RRM1
Extranodal marginal zone cell lymphoma	2.42E-03		5	CCR7,CXCL13,CXCR5,NR3C1,PIK3CD
Stage IV non-Hodgkin lymphoma	2.42E-03		5	DHFR,NR3C1,POLB,POLE,RRM1
Plasma cell dyscrasia	2.45E-03		23	ABCB1,ADRB2,ATRN,CBX7,CSF1R,DHFR,EPSTI1,FDP5,IL15,NONO,NR3C1,PIK3CD,PLCG2,PLEKHG2,POLE,PPP2CA,PPP4R2,PRKCB,RAB4A,RICTOR,RRM1,SATB1,TFRC
AIDS dementia complex	2.56E-03		2	GLS,POLB
Binding of glucocorticoid response element	2.56E-03		2	ADRB2,NR3C1
Cell division of myeloid cells	2.56E-03		2	CSF1,RBL1
Cervical dystonia	2.56E-03		2	VAMP1,VAMP2
Childhood asthma	2.56E-03		2	ADRB2,NR3C1
Diffuse giant cell tumor of tendon sheath	2.56E-03		2	CSF1,CSF1R

Elongation of cervical cancer cell lines	2.56E-03	2	ELMO1,PLD1
Exercise induced asthma	2.56E-03	2	ADRB2,NR3C1
Experimental polyglutamine disease	2.56E-03	2	VAMP1,VAMP2
Inflammatory hepatocellular adenoma	2.56E-03	2	GNAS,IL6ST
Measles	2.56E-03	2	DHFR,FASLG
Refractory Philadelphia chromosome negative precursor T-cell acute lymphoblastic leukemia	2.56E-03	2	POLB,POLE
Relapsed Philadelphia chromosome negative precursor T-cell acute lymphoblastic leukemia	2.56E-03	2	POLB,POLE
Relapsed T-cell lymphoblastic lymphoma	2.56E-03	2	POLB,POLE
Ruffling of macrophage cancer cell lines	2.56E-03	2	CHN1,CSF1
Size of sebaceous glands	2.56E-03	2	CBX7,EDA
Status asthmaticus	2.56E-03	2	ADRB2,NR3C1
Cell movement of blood cells	2.56E-03	41	ADAM8,ADRB2,AIF1,ATRN,CCR7,CD2,CD200,CD302,CSF1,CSF1R,CTLA4,CXCL13,CXCR5,ELMO1,FASLG,FOXO1,GNA13,GNAS,GPC3,GZMB,IGHG1,IKBKE,IL15,IL6ST,MMP1,NEDD9,NOD2,NR3C1,PDPK1,PIK3CD,PLAT,PLCG2,PRKCB,RASSF5,RICTOR,S1PR1,SELL,STAT1,TNFSF8,TXK,VNN2
Replication of influenza virus	2.59E-03	16	ATP2C1,ATP6V1A,COPB2,EIF3G,EIF4A3,FASLG,FAU,FDPs,JFITM1,IKBKE,LONP1,NLRCS,STAT1,TRIM14,UBA7,VNN2
Metabolism of protein	2.61E-03	42	AAK1,AGO2,APAF1,APH1A,ARIH1,ATP13A2,COG3,CSF1,CTLA4,CUL4B,DHFR,DKC1,EDEM1,EEF2,EIF3G,EIF4A3,EIF4EBP2,ERP44,FBXW2,FOXO1,GNAQ,GNL3L,GPC3,GZMB,LONP1,MMP1,NR3C1,PASK,PDPK1,PLAT,PPP2CA,RASSF2,RBL1,RPL19,SF3B3,SKP2,SMN1/SMN2,SNX3,TPP1,TPP2,UBE3A,USP3
Adult acute myeloid leukemia with 11q23 abnormalities	2.61E-03	4	ABCB1,DHFR,POLB,RRM1
Adult acute myeloid leukemia with inv(16)(p13.1;q22)	2.61E-03	4	ABCB1,DHFR,POLB,RRM1
Adult t(16;16)(p13;q22) acute myeloid leukemia	2.61E-03	4	ABCB1,DHFR,POLB,RRM1
Cell movement of memory T lymphocytes	2.61E-03	4	CCR7,CXCL13,IL15,S1PR1
Osteoclastogenesis of bone marrow-derived macrophages	2.61E-03	4	CSF1,FASLG,FOXO1,PLCG2
Response of CD4+ T-lymphocytes	2.61E-03	4	CTLA4,GNAS,IL15,TIGIT
Cell viability of phagocytes	2.62E-03	8	CCR7,CSF1,CSF1R,FOXO1,IL15,NF1,PIK3CD,PLAT
Function of antigen presenting cells	2.62E-03	14	CCR7,CD200,CSF1,CSF1R,IL15,NOD2,PIK3CD,PLAT,PLCG2,RASSF5,SELL,ST6GAL1,STAT1,TIGIT
Uveitis	2.66E-03	7	ADRB2,CD200,CTLA4,DHFR,IL15,NR3C1,STAT1
Hereditary connective tissue disorder	2.72E-03	21	ADRB2,AGPS,ATP6V1A,B3GALT6,CREB3L2,CSF1,CSF1R,DHFR,DMPK,FDPS,GGCX,GNAS,IGHG1,MMP1,NF1,NR3C1,PLCG2,PRKAR1A,RRM1,SKIV2L,TLE3
Abnormal bone density	2.74E-03	13	ATP2C1,CSF1,CSF1R,CTLA4,DHFR,FDPS,GNAQ,IGHG1,NR3C1,PDE3B,PLCG2,RASSF2,RRM1
Inflammatory response	2.75E-03	36	ABCB1,ACOT11,ADAM8,ADRB2,AIF1,BIRC2,CCR7,CD200,CSF1,CSF1R,CXCL13,CXCR5,ELMO1,FANCD2,FASLG,GNA13,GNAS,IGHG1,IL15,IL6ST,MMP1,NEDD9,NFATC3,NOD2,NR3C1,PIK3CD,PLAT,PLCG2,POLB,PRKCB,RBL1,RICTOR,S1PR1,SELL,STAT1,ZBP1
Osteopetrosis	2.77E-03	6	CSF1,CSF1R,DHFR,IGHG1,PLCG2,RRM1
Apoptosis of muscle cells	2.79E-03	15	ADRB2,APAF1,CSF1R,DMPK,FASLG,FOXO1,GNAQ,GNAS,IKBKE,IL6ST,LIMS1,PLD1,PPP1CC,STAT1,WTAP
Cell movement of T lymphocytes	2.79E-03	14	CCR7,CTLA4,CXCL13,CXCR5,ELMO1,FASLG,FOXO1,IL15,IL6ST,NR3C1,PIK3CD,S1PR1,SELL,STAT1
Pediatric neoplasm	2.80E-03	9	ABCB1,ADRB2,CSF1R,CTLA4,DHFR,NR3C1,POLB,POLE,RRM1
Benign salivary gland disease	2.80E-03	3	CXCL13,VAMP1,VAMP2
Cell flattening of tumor cell lines	2.80E-03	3	GEM,PLD1,RBL1
Egression of lymphocytes	2.80E-03	3	CCR7,GNA13,S1PR1
Hypertrophy of mesangial cells	2.80E-03	3	FOXO1,NFATC3,PDPK1
Morphology of adrenal gland cells	2.80E-03	3	NR3C1,PDPK1,VAMP2

Oncogene-induced senescence of cells	2.80E-03	3	FANCD2,HMGA2,PDPK1
Recurrent prostatic carcinoma	2.80E-03	3	NR3C1,POLE,RRM1
Stage IV ALK translocation negative CD274 positive non-small cell lung cancer	2.80E-03	3	DHFR,POLE,RRM1
Adhesion of mononuclear leukocytes	2.80E-03	10	CCR7,CD2,FOXO1,IL15,IL6ST,NEDD9,NR3C1,RASSF5,RICTOR,SELL
Hodgkin disease	2.83E-03	7	DHFR,FOXO1,NR3C1,POLB,POLE,RRM1,TNFSF8
Estrogen receptor negative breast tumor	2.91E-03	11	ABCB1,AGPS,CSF1R,DHFR,FDP5,GNAS,PLAT,POLE,RRM1,STAT1,UBE3A
Embolus	2.93E-03	5	GGCX,GNAQ,PLAT,POLE,RRM1
Recurrent primary neoplasia	2.93E-03	5	DHFR,NR3C1,POLB,POLE,RRM1
Demyelination of spinal cord	2.98E-03	4	FASLG,NR3C1,PLAT,S1PR1
Shortening of telomeres	2.98E-03	4	GNL3L,HMGA2,NAT10,TERF1
Progesterone receptor negative breast tumor	3.03E-03	11	ABCB1,AGPS,CSF1R,DHFR,FDP5,GNAS,PLAT,POLE,RRM1,STAT1,UBE3A
Resorption of bone	3.03E-03	11	ADAM8,ADRB2,AGO2,CSF1,CSF1R,DYNLL1,NF1,S1PR1,STAT1,TFRCT,TPP1
Interaction of T lymphocytes	3.18E-03	10	ATRN,CCR7,CD2,CTLA4,FASLG,NR3C1,RASSF5,RICTOR,SELL,TXK
EZA-PBX1 positive B-cell acute lymphoblastic leukemia	3.22E-03	5	DHFR,NR3C1,POLB,POLE,RRM1
Meningeal neoplasm	3.22E-03	5	CSF1R,DHFR,GNAQ,NR3C1,POLB
Cardiac lesion	3.24E-03	12	ADRB2,CSF1,GNAS,IKBKE,ILMS1,NDUFS6,NF1,PLAT,PNKD,PRKAR1A,PRKCB,STAT1
Accumulation of T lymphocytes	3.25E-03	8	CCR7,CTLA4,FASLG,IL15,IL6ST,NR3C1,S1PR1,SELL
Cell death of carcinoma cell lines	3.29E-03	17	ADI1,APAF1,BIRC2,FASLG,GPC3,IKBKE,IL6ST,ILKAP,NR3C1,PPP2CA,PRKAR1A,RICTOR,RPA2,RRM1,SKP2,STAT1,TRAP1
Chronic lymphocytic leukemia	3.37E-03	22	AKAP8,CD200,CEP68,DLEU1,FASLG,FCMR,LONP1,LVPLA1,NEDD9,NR3C1,PDE3B,PIK3CD,PLCG2,PNKD,POLB,POLE,PRKCB,RASSF5,RRM1,S1PR1,TIGI T,UCKL1
Immune response of T lymphocytes	3.38E-03	9	CCR7,CTLA4,FASLG,FOXO1,GNAS,HSDL1,IL15,TIGIT,TNFSF8
Mantle cell lymphoma	3.38E-03	9	DHFR,LONP1,NEK4,NR3C1,PLCG2,PLEKHG3,POLB,POLE,RRM1
Weakness	3.38E-03	9	CNTN1,DMPK,GNAS,NAB1,NFATC3,NR3C1,SMN1/SMN2,SYNJ1,TRAPPC11
Differentiation of osteoclast precursor cells	3.38E-03	4	CD200,CSF1,CSF1R,DYNLL1
Hypoplasia of lymph node	3.38E-03	4	CTLA4,NEDD9,NFATC3,SELL
Stage IV ALK fusion negative CD274 negative non-small cell lung cancer	3.38E-03	4	CTLA4,DHFR,POLE,RRM1
Stage IV ALK fusion negative CD274 positive non-small cell lung cancer	3.38E-03	4	CTLA4,DHFR,POLE,RRM1
Stage IV EGFR mutation negative CD274 positive non-small cell lung cancer	3.38E-03	4	CTLA4,DHFR,POLE,RRM1
I-kappaB kinase/NF-kappaB cascade	3.40E-03	11	ATP2C1,NDFIP2,NEK6,NFKBID,NOD2,PDPK1,PRKCB,RBCK1,SNIP1,STAT1,TRIM5
T cell migration	3.43E-03	15	CCR7,CTLA4,CXCL13,CXCR5,ELMO1,FASLG,FOXO1,IL15,IL6ST,NR3C1,PIK3CD,S1PR1,SELL,STAT1,TXK
Chronic inflammatory disorder	3.44E-03	48	ABCB1,ADAM8,ADRB2,AIF1,ARIH1,ATP2B1,ATP2C1,BRMS1,BRWD1,CSorf56,CCR7,CDKAL1,CSF1,CTLA4,CXCL13,CXCR5,DHFR,DYNLL1,EEF2,EVC,FAS LG,FAU,FCRL3,FDP5,FOXO1,GZMB,IGFBP4,IGHG1,IL15,IL6ST,MBD1,MMP1,NOD2,NONO,NR3C1,PDE3B,PIK3CD,PLD1,POLB,RBM38,RPL19,S1PR1,S KIV2L,STAT1,TFRCT,TLF3,TNFSF8,VNN2
Dermatitis	3.44E-03	22	ARIH1,CCR7,CD2,CXCL13,DHFR,FASLG,GZMB,IGHG1,IL15,IRF9,MMP1,NR3C1,PIK3CD,PLCG2,POLE,PRKCB,RBCK1,RRM1,SELL,STAT1,TNFSF8,TXK
Cell viability of monocyte-derived dendritic cells	3.45E-03	3	CCR7,FOXO1,PIK3CD
Erythropoiesis of hematopoietic cells	3.45E-03	3	BRD1,SMARCA5,ZFPM1
Length of plasma membrane projections	3.45E-03	3	ARHGAP35,ARX,VAMP2
Mass of interscapular fat pad	3.45E-03	3	ADRB2,GNAS,RBL1

Migration of memory T lymphocytes	3.45E-03	3	CCR7,CXCL13,S1PR1
Progressive primary central nervous system lymphoma	3.45E-03	3	DHFR,NR3C1,POLB
Recurrent primary central nervous system lymphoma	3.45E-03	3	DHFR,NR3C1,POLB
Childhood solid tumor	3.46E-03	6	ADRB2,CTLA4,DHFR,NR3C1,POLB,RRM1
High risk acute lymphocytic leukemia	3.46E-03	6	CSF1R,DHFR,NR3C1,POLB,POLE,RRM1
Methylation of DNA	3.46E-03	6	ATF7IP,DNMT3A,GNAS,MTRR,PPP2CA,RBL1
Refractory non-Hodgkin lymphoma	3.46E-03	6	DHFR,NR3C1,PIK3CD,POLB,POLE,RRM1
Selection of lymphocytes	3.46E-03	6	CCR7,ELK1,IL6ST,NF1,TNFSF8,TKK
Stage I-IV nonsquamous non-small cell lung carcinoma	3.46E-03	6	AGO2,CTLA4,DHFR,NR3C1,POLE,RRM1
Uptake of D-hexose	3.46E-03	13	ADRB2,CSF1,CSF1R,ELK1,GNAS,NOD2,PDPK1,PLAT,PLD1,SKP2,SLC27A1,SLC5A10,SNX27
Depletion of lymphatic system cells	3.53E-03	5	CSF1,CTLA4,FASLG,IL15,SELL
Recurrent central nervous system tumor	3.53E-03	5	CSF1R,CTLA4,DHFR,NR3C1,POLB
Cell death of kidney cell lines	3.56E-03	17	AAK1,ATP13A2,BIRC2,CD2,CUL4B,FASLG,FOXO1,GLS,GNAI13,GNAQ,PDPK1,PRKCB,RASSF5,SLC22A2,SSRP1,TFRC,VOPP1
Mitosis	3.66E-03	25	AKAP8,APAF1,BUB3,CKAP2,CLASP1,CSF1,CSF1R,DBF4,DYNCL1L2,GEM,GNAI13,GNL3,IGHG1,MATK,NEK4,NEK6,PDS5A,PPP2CA,PRKCB,S1PR1,SKP2,S TAT1,TERF1,UBA7,USP3
Leukocyte migration	3.68E-03	40	ADAM8,ADRB2,AIF1,ATRNL,CCR7,CD2,CD200,CD302,CSF1,CSF1R,CTLA4,CXCL13,CXCR5,ELMO1,FASLG,FOXO1,GNA13,GNAS,GPC3,IGHG1,IKBKE,IL15,IL6ST,MMP1,NEDD9,NOD2,NR3C1,PDPK1,PIK3CD,PLAT,PLCG2,PRKCB,RASSF5,RICTOR,S1PR1,SELL,STAT1,TNFSF8,TKK,VNN2
Thoracic neoplasm	3.70E-03	66	ABCB1,ADAM8,AGO2,APH1A,ARHGAP35,ATF7IP,CBX7,CHD6,CKS1B,COPB2,CSF1,CSF1R,CTLA4,CUL4B,CXCL13,DHFR,DNMT3A,DSCAML1,FANCD2,FASLG,FDP5,GEM,GLS,GNAQ,GNAS,HMGA2,IGHG1,IKBKE,IL15,IL6ST,KIR3DL1,KLHL4,MGA,MMP1,NAB1,NEDD9,NEK6,NF1,NR3C1,PASK,PDPK1,PHF3,P1FO,PLAT,POLB,POLE,PRKAR1A,PRKCB,PRR14L,RABGAP1L,RASSF5,RBL1,RP9,RRM1,S1PR1,SEC24C,SKP2,SSTR3,STAG2,STAT1,TARS2,TERF1,TLE3,U BAP2L,UBN1,ZZZZ
Apoptosis of B lymphocytes	3.70E-03	9	CSF1,FASLG,FCMR,GZMB,IKBKE,PIK3CD,PLCG2,PRKCB,S1PR1
Interstitial lung disease	3.70E-03	9	AGO2,CSF1R,DHFR,ELK1,FASLG,HMGA2,NFATC3,NR3C1,PLAT
Mobilization of Ca2+	3.73E-03	18	ADRB2,ATP2B1,BRMS1,CCR7,CD2,CXCL13,CXCR5,GNAI13,GNAQ,GNAS,IGHG1,NFATC3,PIK3CD,PILRA,PLCG2,RICTOR,SELL,TKK
Remodeling of bone	3.73E-03	12	ADAM8,ADRB2,AGO2,CSF1,CSF1R,DYNLL1,NF1,RASSF2,S1PR1,STAT1,TFRC,TPP1
Pituitary lesion	3.76E-03	10	CTLA4,DHFR,DIC1,GNAS,HMGA2,NF1,NR3C1,RBL1,SKP2,SSTR3
Cell viability of macrophages	3.82E-03	4	CSF1,CSF1R,IL15,PLAT
Chemotaxis of natural killer cells	3.82E-03	4	GNA13,GNAS,PIK3CD,S1PR1
Proliferation of mast cells	3.82E-03	4	IL15,IL6ST,NF1,PIK3CD
Refractory acute lymphocytic leukemia, type L3	3.82E-03	4	DHFR,POLB,POLE,RRM1
Relapsed classical Hodgkin lymphoma	3.82E-03	4	NR3C1,POLB,POLE,RRM1
Secondary myelodysplastic syndrome	3.82E-03	4	DHFR,NR3C1,POLB,RRM1
Stage IV bladder cancer	3.82E-03	4	CTLA4,DHFR,POLE,RRM1
Swelling of joint	3.82E-03	4	CCR7,CXCR5,IL6ST,PLAT
Accumulation of antigen presenting cells	3.83E-03	7	CCR7,CD200,CSF1,FASLG,IGHG1,PLAT,STAT1
Polycystic ovary syndrome	3.83E-03	7	BUB3,DHFR,IGFBP4,NEK4,NR3C1,PRKAR1A,TLE3
Progression of carcinoma	3.87E-03	9	CKS1B,CSF1R,CTLA4,DHFR,FOXO1,NR3C1,POLE,RRM1,SKP2
Replication of virus	3.95E-03	26	AGFG1,AGO2,ATP2C1,ATP6V1A,CD200,COPB2,E1F3G,E1F4A3,E1F4EBP2,FASLG,FAU,FDPS,FAU,FDPS,IFITM1,IKBKE,IL15,IRF9,LONP1,NLRCS,PLD1,SSRP1,STAT1,TRIM14,TRIM5,UBA7,VNN2,ZBP1
Development of macrophages	3.98E-03	6	CSF1,CSF1R,FASLG,FOXO1,PLCG2,STAT1
Shape change of blood cells	3.99E-03	8	ATRNL,CCR7,CSF1,GNAI13,GZMB,PDPK1,PLCG2,SELL
Relapsed acute leukemia	4.06E-03	7	ABCB1,CSF1R,DHFR,NR3C1,POLB,POLE,RRM1
Apoptosis of thymoma cell lines	4.18E-03	3	FASLG,FAU,NR3C1
Bullous pemphigoid	4.18E-03	3	DHFR,NR3C1,PLAT

Cellular infiltration by CD8+ T lymphocyte	4.18E-03	3	CTLA4,IL15,STAT1
Development of invariant natural killer T cells	4.18E-03	3	CCR7,RICTOR,TXK
Response of CD8+ T lymphocyte	4.18E-03	3	FOXO1,HSDL1,IL15
Cell movement of leukocytes	4.20E-03	36	ADAM8,ADRB2,AIF1,ATRN,CCR7,CD2,CD302,CSF1,CSF1R,CTLA4,CXCL13,CXCR5,ELMO1,FASLG,FOXO1,GNA13,GNAS,IGHG1,IKBK1,IL15,IL6ST,NEDD9,NOD2,NR3C1,PDPK1,PIK3CD,PLAT,PLCG2,PRKCB,RASSF5,RICTOR,S1PR1,SELL,STAT1,TNFSF8,TKK
Apoptosis of neural tube cells	4.20E-03	2	ATP2C1,FOXO1
Arrest in development of B lymphocytes	4.20E-03	2	FOXO1,PLCG2
Cell death of peripheral blood monocytes	4.20E-03	2	CSF1,FASLG
Colony formation of liver cells	4.20E-03	2	CSF1,CSF1R
Cytotoxic reaction of kidney cell lines	4.20E-03	2	ABCB1,SLC22A2
Fibrous dysplasia	4.20E-03	2	FDPS,GNAS
Formation of mesenteric lymph node	4.20E-03	2	CCR7,CXCR5
Humoral hypercalcemia of malignancy	4.20E-03	2	FDPS,NR3C1
Invasion of neuroglia	4.20E-03	2	CSF1,NF1
Lack of Langerhans cells	4.20E-03	2	CSF1R,PDPK1
Localization of green fluorescent protein	4.20E-03	2	SATB1,TFRC
Migration of osteoclast precursor cells	4.20E-03	2	CSF1,FOXO1
Movement of lymphoma cells	4.20E-03	2	CXCL13,PARP9
Phosphorylation of phosphatidylinositol-3,4,5-triphosphate	4.20E-03	2	PIK3CD,SYNJ1
Relaxation of ventricular myocytes	4.20E-03	2	ADRB2,SLC27A1
Size of lung carcinoma	4.20E-03	2	IL6ST,MMP1
Steroidogenesis of Leydig cells	4.20E-03	2	CSF1,IGFBP4
Transformation of gonadal cell lines	4.20E-03	2	DHFR,NR3C1
ALK fusion negative T-cell lymphoma	4.30E-03	4	DHFR,NR3C1,POLE,RRM1
Pemphigus	4.30E-03	4	CTLA4,DHFR,NR3C1,PLAT

^a Absence of a Z-score entry indicates that Z-score cannot be calculated by IPA.

Table S6. Ingenuity Canonical Pathways enriched among DEGs in SG CD4+CD45RA- T cells of pSS cases versus nSS controls

Canonical Pathway	Pathway Molecules Present in DEG Dataset	
	p-value	Z-score ^a
B Cell Receptor Signaling	1.32E-04	1.732
PI3K Signaling in B Lymphocytes	1.35E-03	↑ 2.333
Molecular Mechanisms of Cancer	1.48E-03	
Role of PKR in Interferon Induction and Antiviral Response	1.58E-03	
Prolactin Signaling	1.78E-03	1.633
Gαq Signaling	1.95E-03	1.667
G-Protein Coupled Receptor Signaling	2.00E-03	
Small Cell Lung Cancer Signaling	2.04E-03	
G Beta Gamma Signaling	2.51E-03	1.890
Lymphotoxin β Receptor Signaling	2.75E-03	↑ 2.000
IL-1 Signaling	3.24E-03	↑ 2.646
PI3K/AKT Signaling	4.17E-03	0.816
Relaxin Signaling	5.25E-03	1.342
Oncostatin M Signaling	5.37E-03	1.000
TWEAK Signaling	5.37E-03	0
p70S6K Signaling	6.46E-03	0.707
Erythropoietin Signaling	7.08E-03	
Activation of IRF by Cytosolic Pattern Recognition Receptors	7.24E-03	0.447
Tec Kinase Signaling	7.59E-03	1.633
Corticotropin Releasing Hormone Signaling	7.76E-03	1.633
Insulin Receptor Signaling	7.94E-03	0
Induction of Apoptosis by HIV1	8.32E-03	-0.447
Growth Hormone Signaling	8.32E-03	1.633
April Mediated Signaling	8.71E-03	1.000
α-Adrenergic Signaling	8.91E-03	0.816
GPCR-Mediated Nutrient Sensing in Enteroendocrine Cells	8.91E-03	FFAR3,GNAS,PLCG2,GNAQ,PRKAR1A,PRKCB
Cardiac β-adrenergic Signaling	9.12E-03	0.816
IL-7 Signaling Pathway	9.33E-03	↑ 2.000
PDF Signaling	1.00E-02	1.342
B Cell Activating Factor Signaling	1.05E-02	
Apoptosis Signaling	1.10E-02	0
PDGF Signaling	1.15E-02	1.633
Role of NFAT in Regulation of the Immune Response	1.17E-02	1.890
Death Receptor Signaling	1.29E-02	0
Tumoricidal Function of Hepatic Natural Killer Cells	1.35E-02	
Renin-Angiotensin Signaling	1.38E-02	1.633
Regulation of eIF4 and p70S6K Signaling	1.45E-02	EIF3G,EIF4EBP2,PPP2CA,EIF4A3,AGO2,PDPK1,PIK3CD,FAU
Protein Kinase A Signaling	1.55E-02	↑ 2.309
ErbB4 Signaling	1.58E-02	1.000
ErbB Signaling	1.62E-02	
Cytotoxic T Lymphocyte-mediated Apoptosis of Target Cells	1.66E-02	
IL-15 Production	1.66E-02	
GPCR-Mediated Integration of Enteroendocrine Signaling Exemplified by an L Cell	1.74E-02	
Calcium Transport I	1.78E-02	
TNFR1 Signaling	1.78E-02	1.000
RANK Signaling in Osteoclasts	1.86E-02	↑ 2.236
Dopamine-DARPP32 Feedback in cAMP Signaling	2.00E-02	1.414
cAMP-mediated signaling	2.00E-02	0
Type I Diabetes Mellitus Signaling	2.04E-02	0.816
Methylthiopropionate Biosynthesis	2.09E-02	ADI1
mTOR Signaling	2.14E-02	0.816
TNFR2 Signaling	2.24E-02	
Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis	2.24E-02	
Regulation of IL-2 Expression in Activated and Anergic T Lymphocytes	2.29E-02	
IGF-1 Signaling	2.34E-02	↑ 2.000
eNOS Signaling	2.34E-02	1.414

Docosahexaenoic Acid (DHA) Signaling	2.34E-02	FOXO1,APAF1,PDPK1,PIK3CD
T Cell Receptor Signaling	2.40E-02	TXK,NFATC3,IKBKE,PIK3CD,ELK1,CTLA4
Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis	2.51E-02	IL6ST,NFKBID,CSF1,NFATC3,PLCG2,IL15,GNAQ,IKBKE,PIK3CD,IGHG1,MMP1,PRKCB
Hematopoiesis from Multipotent Stem Cells	2.51E-02	CSF1,IL15
BER pathway	2.51E-02	POLE,POLB
PPARα/RXRα Activation	2.57E-02	0.447 NFKBID,GNAS,PLCG2,GNAQ,IKBKE,SLC27A1,PRKAR1A,PRKCB
Telomerase Signaling	2.63E-02	1.000 PPP2CA,DKC1,TPP1,PDPK1,PIK3CD,TERF1
G Protein Signaling Mediated by Tubby	2.69E-02	GNAS,PLCG2,GNAQ
Androgen Signaling	2.75E-02	HSPA4,GNAS,GNAQ,GNA13,PRKAR1A,PRKCB
Macropinocytosis Signaling	2.75E-02	CSF1,PLCG2,PIK3CD,CSF1R,PRKCB
Breast Cancer Regulation by Stathmin1	2.75E-02	PPP1CC,GNAS,PPP2CA,GNAQ,ARHGEF18,PIK3CD,GNA13,PRKAR1A,PRKCB
Cell Cycle Control of Chromosomal Replication	2.95E-02	MCM6,POLE,DBF4,RPA2
IL-3 Signaling	3.02E-02	1.342 FOXO1,PIK3CD,ELK1,STAT1,PRKCB
Dendritic Cell Maturation	3.24E-02	1.414 NFKBID,PLCG2,IL15,IKBKE,PIK3CD,IGHG1,STAT1,CCR7
EIF2 Signaling	3.24E-02	↑ 2.236 EIF3G,PPP1CC,EIF4A3,RP L19,AGO2,PDPK1,PIK3CD,RP L18,FAU
Neuregulin Signaling	3.31E-02	1.342 PLCG2,PDPK1,ELK1,MATK,PRKCB
Leptin Signaling in Obesity	3.31E-02	FOXO1,PDE3B,PLCG2,PIK3CD,PRKAR1A
Interferon Signaling	3.39E-02	IRF9,STAT1,IFITM1
Huntington's Disease Signaling	3.63E-02	1.342 HSPA4,GLS,CLTB,APAF1,GNAQ,RCOR1,PDPK1,PIK3CD,GOSR1,PRKCB
LPS-stimulated MAPK Signaling	3.63E-02	↑ 2.236 NFKBID,IKBKE,PIK3CD,ELK1,PRKCB
NF-κB Activation by Viruses	3.63E-02	↑ 2.236 NFKBID,IKBKE,PIK3CD,CXCR5,PRKCB
Autoimmune Thyroid Disease Signaling	3.63E-02	GZMB,IGHG1,FASLG
IL-17A Signaling in Fibroblasts	3.63E-02	NFKBID,IKBKE,MMP1
AMPK Signaling	3.80E-02	0 GNAS,FOXO1,PPP2CA,EEF2,PDPK1,ILKAP,PIK3CD,PRKAR1A,ADRB2
PTEN Signaling	3.80E-02	-1.633 FOXO1,SYN1,PDPK1,IKBKE,PIK3CD,FASLG
PXR/RXR Activation	3.89E-02	ABCB1,FOXO1,NR3C1,PRKAR1A
CCR5 Signaling in Macrophages	3.89E-02	GNAS,PLCG2,FASLG,PRKCB
CREB Signaling in Neurons	4.07E-02	1.633 GNAS,PLCG2,GNAQ,PIK3CD,GNA13,ELK1,PRKAR1A,PRKCB
Formaldehyde Oxidation II (Glutathione-dependent)	4.17E-02	ESD
Glutamine Degradation I	4.17E-02	GLS
Notch Signaling	4.17E-02	CNTN1,APH1A,MAML2
Granzyme B Signaling	4.37E-02	GZMB,APAF1
fMLP Signaling in Neutrophils	4.37E-02	1.633 NFKBID,GNAS,NFATC3,PIK3CD,ELK1,PRKCB
CD28 Signaling in T Helper Cells	4.37E-02	1.342 NFKBID,NFATC3,PDPK1,IKBKE,PIK3CD,CTLA4
Gap Junction Signaling	4.79E-02	GNAS,PLCG2,CSNK1G3,GNAQ,PIK3CD,PRKAR1A,PRKCB,GJA4
Neuroinflammation Signaling Pathway	4.79E-02	0.905 CD200,NFATC3,PLCG2,GLS,APH1A,IKBKE,PIK3CD,STAT1,CSF1R,FASLG,BIRC2
Thrombopoietin Signaling	4.79E-02	1.000 PLCG2,PIK3CD,STAT1,PRKCB
Cell Cycle: G1/S Checkpoint Regulation	4.79E-02	FOXO1,GNL3,RBL1,SKP2
Phospholipase C Signaling	4.90E-02	1.890 GNAS,NFATC3,PLCG2,GNAQ,ARHGEF18,IGHG1,GNA13,PLD1,PRKCB

^a Absence of a Z-score entry indicates that Z-score cannot be calculated by IPA.

Table S7. Ingenuity Predicted Upstream Regulators of DEGs in S6 CD4-CD45RA- T cells of pSS cases versus nSS controls

Upstream Regulator		Regulator Type	p-value	Z-score ^a	Downstream Target Molecules Present in DEG Dataset	
Interferon alpha	FAS	transmembrane receptor	6.28E-05	↑2.172	CCR7, EPSTI1, FASLG, GLS, GZMB, IFITM1, IGFBP4, IK8KE, IL15, IL6ST, IRF9, OAS2, PARP9, PLAT, RABGAP1L, RBCK1, SPRY1, STAT1, TRIM5, UBA7, ZBP1	CCR7, EPSTI1, FASLG, GLS, GZMB, IFITM1, IGFBP4, IK8KE, IL15, IL6ST, IRF9, OAS2, PARP9, PLAT, RABGAP1L, RBCK1, SPRY1, STAT1, TRIM5, UBA7, ZBP1
			1.57E-04	-1.695	AKAP8, BIRC2, CD200, CLASP1, CLTB, CSF1, DNAH17, FASLG, FOXO1, GDE1, MMP1, NR3C1, P2RY10, PIK3CD, PLD1, PPF1A1, PPP1CC, PRKCB, T	AKAP8, BIRC2, CD200, CLASP1, CLTB, CSF1, DNAH17, FASLG, FOXO1, GDE1, MMP1, NR3C1, P2RY10, PIK3CD, PLD1, PPF1A1, PPP1CC, PRKCB, T
miR-6740-3p (miRNAs w/seed GUCUUUCU)	IL10	cytokine	1.80E-04	1.884	CCR7, CD2, CSF1, CSF1R, CTLA4, CXCL13, FASLG, GZMB, IGFBP4, IL6ST, MMP1, NEDD9, NFKBID, NOD2, SELL, STAT1, TFR	CCR7, CD2, CSF1, CSF1R, CTLA4, CXCL13, FASLG, GZMB, IGFBP4, IL6ST, MMP1, NEDD9, NFKBID, NOD2, SELL, STAT1, TFR
			2.58E-04	0.199	CSF1R, DDX42, DYNCL1U2, EIF4EBP2, GNAS, MMP1, NDFIP2, NEDD9, NF1, NR3C1, OSBP13, PDE3B, PLAT, POLE, PPP2CA, ZBP1	CSF1R, DDX42, DYNCL1U2, EIF4EBP2, GNAS, MMP1, NDFIP2, NEDD9, NF1, NR3C1, OSBP13, PDE3B, PLAT, POLE, PPP2CA, ZBP1
miR-589-5p (and other miRNAs w/seed GAGAAC)	IFNA2	cytokine	2.73E-04	↑2.921	CXCL13, GEM, GNAS, GPATCH11, IFITM1, IRF9, OAS2, PARP9, PLAT, RBL1, STAT1, TRIM14, UBA7, ZBP1	CXCL13, GEM, GNAS, GPATCH11, IFITM1, IRF9, OAS2, PARP9, PLAT, RBL1, STAT1, TRIM14, UBA7, ZBP1
			4.00E-04	0.965	CCR7, CD200, CTLA4, CXCL13, CXCR5, DKC1, FASLG, GZMB, KIR3DL1, NR3C1, PASK, PDE3B, PGAM1, PIK3CD, SELL, STAT1, TLE3, TXK	CCR7, CD200, CTLA4, CXCL13, CXCR5, DKC1, FASLG, GZMB, KIR3DL1, NR3C1, PASK, PDE3B, PGAM1, PIK3CD, SELL, STAT1, TLE3, TXK
miR-6740-3p (miRNAs w/seed GUCUUUCU)	MID1	other	4.47E-04	PPK3, PPP2CA		PPK3, PPP2CA
			5.07E-04	-1.265	ADP1, AIF1, C18orf25, CHD6, CRNN, EIF3G, FASLG, GCFC2, NDFIP2, RILP2	ADP1, AIF1, C18orf25, CHD6, CRNN, EIF3G, FASLG, GCFC2, NDFIP2, RILP2
miR-589-5p (and other miRNAs w/seed GAGAAC)	mature microRNA	mature microRNA	5.50E-04	↓-2.121	BABAM1, DHFR, FAM86B2, FAM86KP, PGAM1, PHK8, PNPO, SIRPG, SLC25A14	BABAM1, DHFR, FAM86B2, FAM86KP, PGAM1, PHK8, PNPO, SIRPG, SLC25A14
			6.27E-04	0.775	CCR7, IFITM1, IL15, IRF9, OAS2, SPRY1, STAT1, TRIM14, ZBP1	CCR7, IFITM1, IL15, IRF9, OAS2, SPRY1, STAT1, TRIM14, ZBP1
IFN Beta	IFNL1	cytokine	6.29E-04	↑2.646	CCR7, GPATCH11, IFITM1, IRF9, OAS2, STAT1, TRIM14	CCR7, GPATCH11, IFITM1, IRF9, OAS2, STAT1, TRIM14
			7.18E-04	CXCR5, MMP1, NFATC3		CXCR5, MMP1, NFATC3
CXCL13	cytokine	cytokine	8.06E-04	-0.487	CD2, CKS1B, COPB2, CSF1, FASLG, GALM, GNAS, GZMB, IFITM1, KIR3DL1, LYPLA1, PLCG2, PLD1, S1PR1, SELL, TCF7, TFR, TRIM5, VBP1	CD2, CKS1B, COPB2, CSF1, FASLG, GALM, GNAS, GZMB, IFITM1, KIR3DL1, LYPLA1, PLCG2, PLD1, S1PR1, SELL, TCF7, TFR, TRIM5, VBP1
			8.97E-04	1.709	CTLA4, IFITM1, IL15, IRF9, OAS2, PLAC8, STAT1, TRIM5, UBA7, ZBP1	CTLA4, IFITM1, IL15, IRF9, OAS2, PLAC8, STAT1, TRIM5, UBA7, ZBP1
IL15	transcriptional	transcriptional	1.01E-03	-1.095	AIF1, FASLG, HMG2, IGHG1, NIFK, NLRCS, OAS2, PGAM1, PLAT, PPP4R2, SPRY1, STAT1, UBA7	AIF1, FASLG, HMG2, IGHG1, NIFK, NLRCS, OAS2, PGAM1, PLAT, PPP4R2, SPRY1, STAT1, UBA7
			1.16E-03	0.412	APH1A, CCR7, CD2, CD200, CSF1, CSF1R, CXCR5, DDHD1, DDX42, EIF3G, FASLG, IGFBP4, IGHG1, IL15, IL6ST, IRF9, MATK, MMP1, NEDD9, NR3C	APH1A, CCR7, CD2, CD200, CSF1, CSF1R, CXCR5, DDHD1, DDX42, EIF3G, FASLG, IGFBP4, IGHG1, IL15, IL6ST, IRF9, MATK, MMP1, NEDD9, NR3C
mir-21	microRNA	microRNA	1.16E-03	1.928	ADAM8, ATP6V1A, CHD6, CKS1B, CSF1R, DHFR, ELK1, EPSTI1, FEZ2, FOXO1, GLS, HMG2, IGFBP4, IL6ST, MCM6, MMP1, MSMB, NEDD9, PDP	ADAM8, ATP6V1A, CHD6, CKS1B, CSF1R, DHFR, ELK1, EPSTI1, FEZ2, FOXO1, GLS, HMG2, IGFBP4, IL6ST, MCM6, MMP1, MSMB, NEDD9, PDP
			1.27E-03	K1, PIK3CD, PLAC8, PLAT, POLB, POLE, POLR3E, RPA2, RRM1, SKP2		K1, PIK3CD, PLAC8, PLAT, POLB, POLE, POLR3E, RPA2, RRM1, SKP2
ERBB2	kinase	kinase	1.32E-03	SLC11A2, TFR		SLC11A2, TFR
			1.45E-03	APAF1, DBF4, DHFR, FOXO1, MCM6, RBL1, RPA2, RPL19		APAF1, DBF4, DHFR, FOXO1, MCM6, RBL1, RPA2, RPL19
FBXL5	enzyme	enzyme	1.51E-03	-0.816	DNMT3A, GOSR1, NLRCS, PDPK1, PLEKHG3, POLR3E	DNMT3A, GOSR1, NLRCS, PDPK1, PLEKHG3, POLR3E
			1.68E-03	0.926	AAK1, ABCB1, ADAM8, ADRB2, BIRC2, CCR7, COMMD3, FASLG, HDGF, NECAP2, SELL	AAK1, ABCB1, ADAM8, ADRB2, BIRC2, CCR7, COMMD3, FASLG, HDGF, NECAP2, SELL
CD44	other	other	1.79E-03	0.503	APAF1, CCR7, CXCL13, CXCR5, DHFR, GNA13, GNAS, GNL3, IL15, MMP1, NR3C1, RRM1, SKP2, TPP1	APAF1, CCR7, CXCL13, CXCR5, DHFR, GNA13, GNAS, GNL3, IL15, MMP1, NR3C1, RRM1, SKP2, TPP1
			1.86E-03	-1.026	AGO2, DHFR, DNMT3A, ELK1, FASLG, FKBP11, GNA13, GPC3, JF1TM1, IRF9, MTRR, NAB1, NR3C1, PLAT, PLD1, PSMC6, SKP2, STAT1, TLE3, VMP	AGO2, DHFR, DNMT3A, ELK1, FASLG, FKBP11, GNA13, GPC3, JF1TM1, IRF9, MTRR, NAB1, NR3C1, PLAT, PLD1, PSMC6, SKP2, STAT1, TLE3, VMP
KRAS	enzyme	enzyme	2.28E-03	-1.342	ADH7, BIRC2, EEF2, GGCT, SMARCA5	ADH7, BIRC2, EEF2, GGCT, SMARCA5
			2.35E-03	0.901	CCR7, CXCR5, FCMR, GZMB, IGHG1, S1PR1, SELL, TNFSF8	CCR7, CXCR5, FCMR, GZMB, IGHG1, S1PR1, SELL, TNFSF8
miR-6513-3p (miRNAs w/seed CAAGUGU)	mature microRNA	mature microRNA	2.39E-03	0.687	CSF1, CSF1R, CTLA4, EIF3G, FKBP3, GNA13, GNAS, HDGF, MMP1, NEDD9, NFATC3, NIFK, SELL, STT3A, TNFSF8	CSF1, CSF1R, CTLA4, EIF3G, FKBP3, GNA13, GNAS, HDGF, MMP1, NEDD9, NFATC3, NIFK, SELL, STT3A, TNFSF8
			2.57E-03	1.943	BET1, COG3, COPB2, EDEM1, ERP44, FKBP11, GGCK, MCFD2, S1PR1, SEC11A, VAMP2	BET1, COG3, COPB2, EDEM1, ERP44, FKBP11, GGCK, MCFD2, S1PR1, SEC11A, VAMP2
XBP1	transcriptional	transcriptional	2.88E-03	ABCB1, FASLG, RICTOR		ABCB1, FASLG, RICTOR
			3.06E-03	1.480	GEM, IFITM1, OAS2, STAT1, ZBP1	GEM, IFITM1, OAS2, STAT1, ZBP1
IFNA1/IFNA13	cytokine	cytokine	3.13E-03	0.618	CCR7, CD2, CXCL13, CXCR5, FASLG, GZMB, IGHG1, OAS2, SELL	CCR7, CD2, CXCL13, CXCR5, FASLG, GZMB, IGHG1, OAS2, SELL
			3.13E-03	-0.308	CCR7, CSF1, FASLG, GZMB, IL15, PLAC8, RPA2, SELL, TFR, TXK	CCR7, CSF1, FASLG, GZMB, IL15, PLAC8, RPA2, SELL, TFR, TXK
IL12 (complex)	complex	complex	3.18E-03	-1.000	CTLA4, CXCL13, FASLG, PDE3B, SATB1, SELL, SKP2	CTLA4, CXCL13, FASLG, PDE3B, SATB1, SELL, SKP2
			3.28E-03	0.490	ADAM8, EIF4A3, FASLG, IFITM1, IL15, IRF9, OAS2, SELL, STAT1	ADAM8, EIF4A3, FASLG, IFITM1, IL15, IRF9, OAS2, SELL, STAT1
FOXP3	transcriptional	transcriptional	3.54E-03	IL15, PLAT, RBL1		IL15, PLAT, RBL1
			3.63E-03	1.342	CNTN1, CREB3L2, EDEM1, FKBP11, IFITM1, OAS2, OSBP, SEC11A	CNTN1, CREB3L2, EDEM1, FKBP11, IFITM1, OAS2, OSBP, SEC11A
ZC3H14	other	other	3.67E-03	-1.342	CD200, GCFC2, MLF1, MRPL35, PLD1	CD200, GCFC2, MLF1, MRPL35, PLD1
			4.12E-03	-1.265	CCR7, CKS1B, DBF4, FANCD2, HMG2, MCM6, RRM1, SKP2, TAB2	CCR7, CKS1B, DBF4, FANCD2, HMG2, MCM6, RRM1, SKP2, TAB2
ERN1	kinase	kinase	4.13E-03	-1.309	ATP2B1, CCR7, DHFR, ETFA, FDPs, PPP2CA, PRKAR1A, RAB4A, S1PR1, SELL, SKP2, ST6GAL1, STAT1	ATP2B1, CCR7, DHFR, ETFA, FDPs, PPP2CA, PRKAR1A, RAB4A, S1PR1, SELL, SKP2, ST6GAL1, STAT1
			4.19E-03	1.207	BIRC2, CCR7, CSF1, DAPP1, DDX42, FASLG, GZMB, IFITM1, IGHG1, IL15, RASSF2, SELL, STAT1, TFR, TNFSF8, ZZZ3	BIRC2, CCR7, CSF1, DAPP1, DDX42, FASLG, GZMB, IFITM1, IGHG1, IL15, RASSF2, SELL, STAT1, TFR, TNFSF8, ZZZ3
let-7	microRNA	microRNA	4.28E-03	ELK1, GZMB		ELK1, GZMB
			4.29E-03	FOXO1, IL15, PRKCB		FOXO1, IL15, PRKCB
MTOR	enzyme	enzyme	4.29E-03	-1.414	APAF1, CASTOR2, COX7B, HDGF, MUC7, STAG2, TPP1, VAMP1	APAF1, CASTOR2, COX7B, HDGF, MUC7, STAG2, TPP1, VAMP1
			4.44E-03	-1.000	ABCB1, CCR7, SELL, TAF7	ABCB1, CCR7, SELL, TAF7
CD40LG	cytokine	cytokine	4.47E-03	-1.544	1, TCF7, TFR, TRIM5, VBP1	1, TCF7, TFR, TRIM5, VBP1
			4.67E-03	1.949	CCR7, CXCL13, FCMR, IFITM1, IRF9, OAS2, PLAT, STAT1	CCR7, CXCL13, FCMR, IFITM1, IRF9, OAS2, PLAT, STAT1
OPRD1	g-protein coupled receptor	g-protein coupled receptor	4.75E-03	0.461	GNL3, GTTF3C2, IGFBP4, IPO7, IRF9, LYPLA1, MCM6, MMP1, NAB1, PD55A, POLB, POLR3E, PPP2CA, PPP4R2, PRKCB, PSM12, STAT	GNL3, GTTF3C2, IGFBP4, IPO7, IRF9, LYPLA1, MCM6, MMP1, NAB1, PD55A, POLB, POLR3E, PPP2CA, PPP4R2, PRKCB, PSM12, STAT
			4.77E-03	↓-2.449	GCFC2, MCFD2, RBM18, SNX3, THRAP3, TSTD1	GCFC2, MCFD2, RBM18, SNX3, THRAP3, TSTD1
PHLPP1	enzyme	enzyme	4.93E-03	-1.745	ASSF2, RBL1, S1PR1, SATB1, SLC11A2, SSRP1, ST6GAL1, SUN5, TPP1, VAMP2	ASSF2, RBL1, S1PR1, SATB1, SLC11A2, SSRP1, ST6GAL1, SUN5, TPP1, VAMP2
			4.93E-03	-1.745	ASSF2, RBL1, S1PR1, SATB1, SLC11A2, SSRP1, ST6GAL1, SUN5, TPP1, VAMP2	ASSF2, RBL1, S1PR1, SATB1, SLC11A2, SSRP1, ST6GAL1, SUN5, TPP1, VAMP2
miR-6823-5p (miRNAs w/seed CAGGGUU)	mature microRNA	mature microRNA	4.93E-03	-1.745	ASSF2, RBL1, S1PR1, SATB1, SLC11A2, SSRP1, ST6GAL1, SUN5, TPP1, VAMP2	ASSF2, RBL1, S1PR1, SATB1, SLC11A2, SSRP1, ST6GAL1, SUN5, TPP1, VAMP2
			4.93E-03	-1.745	ASSF2, RBL1, S1PR1, SATB1, SLC11A2, SSRP1, ST6GAL1, SUN5, TPP1, VAMP2	ASSF2, RBL1, S1PR1, SATB1, SLC11A2, SSRP1, ST6GAL1, SUN5, TPP1, VAMP2
miR-3140-3p (miRNAs w/seed GCUUUUG)	mature microRNA	mature microRNA	4.93E-03	-1.745	ASSF2, RBL1, S1PR1, SATB1, SLC11A2, SSRP1, ST6GAL1, SUN5, TPP1, VAMP2	ASSF2, RBL1, S1PR1, SATB1, SLC11A2, SSRP1, ST6GAL1, SUN5, TPP1, VAMP2
			4.93E-03	-1.745	ASSF2, RBL1, S1PR1, SATB1, SLC11A2, SSRP1, ST6GAL1, SUN5, TPP1, VAMP2	ASSF2, RBL1, S1PR1, SATB1, SLC11A2, SSRP1, ST6GAL1, SUN5, TPP1, VAMP2
APP	other	other	4.93E-03	-1.745	ASSF2, RBL1, S1PR1, SATB1, SLC11A2, SSRP1, ST6GAL1, SUN5, TPP1, VAMP2	ASSF2, RBL1, S1PR1, SATB1, SLC11A2, SSRP1, ST6GAL1, SUN5, TPP1, VAMP2
			4.93E-03	-1.745	ASSF2, RBL1, S1PR1, SATB1, SLC11A2, SSRP1, ST6GAL1, SUN5, TPP1, VAMP2	ASSF2, RBL1, S1PR1, SATB1, SLC11A2, SSRP1, ST6GAL1, SUN5, TPP1, VAMP2

CD4	transmembrane receptor	4.97E-03	-1.941	CXCL13,CXCR5,FASLG,IL15	
GAPDH	enzyme	4.97E-03	-1.964	GEM,JFITM1,OAS2,STAT1	
miR-4533 (miRNAs w/seed GGAAGGA)	mature microRNA	5.09E-03	↓-2.887	ARFIP1,CEP68,EIF4EBP2,HDGF,IGFBP4,MGA,OAS2,SELL,SIRPG,ST6GAL1,TPP1,VAMP2	
TCF4	transcriptional	5.10E-03		ARHGEF18,CD2,CREB3L2,EDEM1,FASLG,FKBP11,MMP1,PLAC8,SELL,ZBP1	
BNIP3L	other	5.16E-03	-1.387	CKAP2,FANCD2,PIK3CD,RBL1,TFRC	
IL2	cytokine	5.22E-03	-0.233	ADAM8,CCR7,CD2,CSF1,CTLA4,CXCR5,DKC1,FASLG,FCMR,FOXO1,GNAAQ,GNL3,GZMB,KIR3DL1,NIFK,PDE3B,PLAC8,SATB1,SELL	
SET	phosphatase	5.55E-03	↓-2.000	BET1,FDP5,GZMB,ZCCHC17	
EGR3	transcriptional	6.16E-03	-0.330	B3GALT6,ESD,FASLG,NF1	
E2F1	transcriptional	6.29E-03	1.377	ABCB1,APAF1,BUB3,CBX7,DBF4,DHFR,DLEU1,FANCD2,FKBP3,FOXO1,MCM6,MMP1,RBL1,RCOR1,RP42,RRM1,SMARCA5,TRAP1	
TNFSF13B	cytokine	6.52E-03		CCR7,CXCR5,FOXO1,IL15,SELL	
miR-155-5p (miRNAs w/seed UAAUGCU)	mature microRNA	6.78E-03	↓-3.375	APAF1,ARFIP1,BET1,CSF1R,CTLA4,CUL4B,GN413,HSDL1,IKBKE,RCOR1,SATB1,TAB2	
FSH	complex	6.80E-03	0.721	ARHGAP35,ATP2B1,FLIP1L,FOXO1,GDE1,GEM,GNAS,GZMB,IGFBP4,PIK3CD,PLAT,PRKAR1A,RAB4A,RASSF2,STAT1,TFRC	
miR-145-5p (and other miRNAs w/seed UCCAGUU)	mature microRNA	6.84E-03	↓-2.155	AGFG1,BIRC2,COX16,EIF4EBP2,FKBP3,MMP1,PPP4R2,TARS2,TFRC	
miR-3607-3p (miRNAs w/seed CUGUAAA)	mature microRNA	7.03E-03	↓-2.236	CHN1,DBF4,DCTN6,IL6ST,P2RY10	
TGFB1	growth factor	7.10E-03		ADI1,ARHGAP35,CCR7,CKS1B,CSF1,CTLA4,CXCL13,CXCR5,DKC1,DNM1T3A,DYNLL1,EIF4A3,ELMO1,FASLG,FLIP1L,FOXO1,GAL	
IRF3	transcriptional	7.12E-03	1.688	M,GEM,GN413,GNAS,GZMB,HDGF,HMGA2,IGFBP4,IL15,LIMS1,MBD1,MMP1,MSMB,MTRR,NAB1,NEDD9,PIK3CD,PILRA,PLAT,PPP2C	
miR-6746-5p (miRNAs w/seed CGGGAGA)	mature microRNA	7.12E-03	0.317	BIRC2,IL15,NLRCS,NR3C1,OAS2,PLAC8,PLCG2,STAT1,ZBP1	
STAT6	transcriptional	7.43E-03	-0.333	ADAM8,ADI1,ARX,CDC127,COX7B,GNAS,GNL3L,PHOSPHO1,PYCARD-AS1	
ARHGAP21	other	7.51E-03	-0.728	CCR7,CD2,DDHD1,IGHG1,IL15,IL6ST,IRF9,NEDD9,PLD1,ST6GAL1,TCF7,TKX	
miR-634 (miRNAs w/seed ACCAGCA)	mature microRNA	7.70E-03	1.000	IL15,PLAT,RBL1,TNFSF8	
NFKB1	transcriptional	7.88E-03	-1.000	ADRB2,CKS1B,GNAAQ,GNL3L,HSDL1,MBIP,PLD1,PNPO,TFRC	
PLK4	kinase	8.20E-03	1.302	ABCB1,AGO2,CSF1,CXCR5,FANCD2,FASLG,IGHG1,IKBKE,NOD2,POLB,STAT1	
CD2	transmembrane receptor	8.26E-03	1.067	CCR7,FASLG,SELL,STAT1	
miR-4272 (miRNAs w/seed AUUCAAAC)	mature microRNA	8.26E-03	-1.000	IL15,P2RY10,PSMC6,TFRC	
RARB and-dependent nuclear recep	transcriptional	8.31E-03		BIRC2,JFITM1,MMP1,SATB1,STAT1,UBA7	
miR-329-3p (and other miRNAs w/seed ACACACC)	mature microRNA	8.48E-03	-1.134	CDC127,EPT1L,FASLG,GZMB,HSPA4,PLAT,VOPP1	
miR-6967-5p (and other miRNAs w/seed AGGGAGG)	mature microRNA	8.56E-03	-0.894	COX7B,CREB3L2,EIF4EBP2,ELK1,ELMO1,FFAR3,GOSR1,IGFBP4,PGAM1,PHYHD1,PLD1,PNPO,RAB30,RASSF5,RHBDD2,SIRPG,SLC27A1	
DOCK8	other	8.71E-03	1.342	IL15,PLAT,RBL1,STAT1,TNFSF8	
SENP7	peptidase	8.74E-03		BIRC2,DHFR	
IL21R	transmembrane receptor	8.74E-03		CCR7,IGHG1	
Rb	group	9.33E-03	-1.941	APAF1,ARX,DHFR,RBL1,RP42	
PLK2	kinase	9.42E-03		IL15,PLAT,RBL1	
RC3H1	enzyme	9.42E-03		CCR7,CXCL13,IL6ST	
HGF	growth factor	9.90E-03	↑2.440	APAF1,BIRC2,CKS1B,CSF1,DBF4,DKC1,DYNLL1,EDA,FASLG,GEM,GN413,HDGF,IGFBP4,IL6ST,MMP1,NEK4,PGAM1,SKP2	
ADORA2A	g-protein coupled receptor	1.02E-02	1.195	ATP2B1,CSF1R,EEF2,PGAM1,PPP2CA,PRKAR1A,SSRP1	
TNFSF10	cytokine	1.04E-02	-0.436	BIRC2,FASLG,JFITM1,IRF9,STAT1,TFRC	
miR-4268 (miRNAs w/seed GCUCCUC)	mature microRNA	1.07E-02	-1.134	CLTB,IL6ST,MAML2,OSBP,RASSF5,SLC22A2,ZC3H8	
BAK1	other	1.07E-02		APAF1,EDEM1,IL15	
MAPK1	kinase	1.10E-02	↓-2.168	FASLG,FCMR,GLS,GRAMD1B,HIC2,JFITM1,IRF9,MMP1,OAS2,OSBPL3,PLD1,STAT1,TRIM14,TRIMS	
TNFSF11	cytokine	1.11E-02	0.053	AIF1,CSF1R,DMPK,FOXO1,IKBKE,IL15,MMP1,NFATC3,PLD1,SLC11A2,STAT1	
SASH1	other	1.14E-02	1.342	IL15,PLAT,RBL1,STAT1,TNFSF8	
miR-3923 (miRNAs w/seed ACUAGUA)	mature microRNA	1.14E-02	↓-2.236	AGPS,CKS1B,IL6ST,MLF1,UCLK1	
TCIRG1	enzyme	1.15E-02		CTLA4,SELL	
ZNF382	transcriptional	1.15E-02		HMGA2,IKBKE	
miR-153-3p (miRNAs w/seed UGCAUAG)	mature microRNA	1.21E-02	↓-2.121	FOXO1,LIMS1,NFATC3,SATB1,TAF7,TES,UCLK1,VAMP2	
LCK	kinase	1.22E-02		CD2,ELK1,FASLG	
BAX	transporter	1.27E-02		APAF1,BIRC2,EDEM1,IL15	
miR-421-3p (and other miRNAs w/seed UCAACAG)	mature microRNA	1.28E-02	↓-2.646	ADI1,CBX7,CD200,PPP1CC,RAB30,SPRY1,TFRC	
miR-361-5p (miRNAs w/seed UAUACAGA)	mature microRNA	1.29E-02	↓-2.236	CKS1B,DCTN6,RAB30,SPRTN,VBP1	
RBL1	transcriptional	1.37E-02	-1.467	DHFR,MCM6,RBL1,RRM1,SKP2	
HNF4A	transcriptional	1.37E-02		ADRB2,APH1A,BET1,CDKAL1,COPB2,DCAF13,EIF4EBP2,ELMO1,FBXW2,FDP5,FKBP3,FOXO1,GALM,GGCX,GNL3,IL15,IL6ST,LIMS1,MR	
			0	PL33,MSMB,NAT10,NECAP1,NEK4,NOD2,NONO,OSBP,PARP9,PDE4DIP,PHKB,PNPO,POLB,POLR3E,RAB30,RASSF5,RBAK,RBL1,RBM1	
				8,RP42,RPAIN,RPL18,RRM1,SEC11A,SKP2,SMARCA5,SNX3,STAT1,STT3A,TCF7,TFRC,THRAP3,TLE3,TPP2,UROS,VAMP1,VMP1,WTAP,	
				ZNF410	
TLR4	transmembrane receptor	1.45E-02	0.225	CCR7,CD200,DNM1T3A,FASLG,IL15,MMP1,NFKBID,NOD2,PLAT,RBL1,STAT1,TFRC,TNFSF8	
miR-4715-5p (miRNAs w/seed AGUUGGC)	mature microRNA	1.45E-02	-1.890	FAM184B,FAU,INTS5,MLF1,MOC51,PHKB,TFRC	

FBXO42	other	1.46E-02	CSF1,STAT1
IFNL4	cytokine	1.46E-02	OAS2,STAT1
KNK3	ion channel	1.46E-02	CTLA4,FOXO1
miR-19b-3p (and other miRNAs w/seed GUGCAAA)	mature microRNA	1.48E-02	↓-3.317 AGFG1,ARFP1,C5orf56,CACUL1,CCN1L,MRPL35,NDHIP2,S1PR1,SNX3,TKX,VMP1
miR-520d-5p (and other miRNAs w/seed UACAAG)	mature microRNA	1.49E-02	-1.000 DCTN6,HMGA2,RAB12,TFRC
miR-627-3p (miRNAs w/seed CUUUUCU)	mature microRNA	1.51E-02	-1.890 DGKH,GLS,LOC107985899,PDS5A,PRKCB,RAB30,VBP1
miR-554 (miRNAs w/seed CUAGUUC)	mature microRNA	1.60E-02	0 DCAF13,GZMB,HMGA2,MAN1C1
IFNG	cytokine	1.62E-02	↑2.052 ABCB1,AIF1,BIRC2,CD2,CD200,CSF1,CSF1R,ELK1,FASLG,FOXO1,GLS,GNA13,GNAS,GZMB,IFITM1,IGFBP4,IGHG1,IKBKE,IL15,IRF9,MM
CD28	transmembrane receptor	1.64E-02	-0.352 CTLA4,CXCL13,FASLG,FDPs,GZMB,IFITM1,MBD1,NDHIP2,PGAM1,PSMD12,TCF7,TFRC,VBP1
miR-4316 (miRNAs w/seed GUGAGGC)	mature microRNA	1.70E-02	-1.633 DGKH,EPSTI1,EVC,FAM86B2/FAM86KP,SNX3,TPRN
BRAF	kinase	1.72E-02	BIRC2,CSF1,CSF1R,MMP1
miR-1252-5p (miRNAs w/seed GAAGGAA)	mature microRNA	1.72E-02	↓-3.000 AAK1,DGKH,EIF4EBP2,IGFBP4,LPXN,SELL,SNX27,SPRY1,TFRC
miR-4288 (and other miRNAs w/seed UGUCUGC)	mature microRNA	1.78E-02	↓-2.646 CDC127,GCFC2,GGCT,METTL23,PLAC8,TFRC,TOMM6
miR-4778-5p (miRNAs w/seed AUUCUGU)	mature microRNA	1.78E-02	-1.633 ABCB1,DBF4,DCTN6,GGCT,IL6ST,TAB2
miR-662 (miRNAs w/seed CCCACGU)	mature microRNA	1.78E-02	↓-2.449 ARFP1,CBX7,HSDL1,MCFD2,NLRCS,SIRPG
miR-320b (and other miRNAs w/seed AAAGCUG)	mature microRNA	1.78E-02	↓-2.449 AGFG1,ARFP1,ETFA,MBIP,MUF1,TFRC
lfn	group	1.78E-02	IFITM1,IL15,OAS2,STAT1,TFRC,ZBP1
miR-93-3p (miRNAs w/seed GUCGUGA)	mature microRNA	1.89E-02	↓-3.000 IL6ST,MCFD2,NFATC3,PLAC8,RASSF2,SNX27,TFRC,TOMM6,ZCCHC17
SATB1	transcriptional	1.94E-02	-1.450 DNMT3A,ENOSF1,EPSTI1,FASLG,FEZ2,PRKCB,S1PR1,SELL
BTk	kinase	1.95E-02	-1.633 CCR7,CD2,IFITM1,IRF9,OAS2,STAT1
TGM2	enzyme	1.96E-02	1.320 CXCR5,DLEU1,FFAR3,IRF9,MDN1,OAS2,PARP9,SELL,STAT1,UBA7
BCl6	transcriptional	2.01E-02	0.152 CCR7,CD2,CSF1,CTLA4,CXCR5,HNRNPLL,IRF9,UBA7,VWASA
miR-609 (miRNAs w/seed GGGUGUU)	mature microRNA	2.08E-02	0 GEM,GOSR1,HGDF,PLEKHF1,PNPO,PRKCB,SLC22A2,TMEM263
MGEA5	enzyme	2.08E-02	-0.832 CD302,CDKAL1,CREB3L2,CSF1R,ELK1,FDPs,HSDL1,IGFBP4,IL6ST,LIMS4,LPXN,PHKB,SLC27A1,STAT1
IRF9	transcriptional	2.08E-02	IFITM1,OAS2,STAT1
ARRDC3	other	2.12E-02	ADRB2
TFILF	complex	2.12E-02	POLB
tubulin (complex)	complex	2.12E-02	GNAQ
ALG2	enzyme	2.12E-02	CREB3L2
RHOBTB2	enzyme	2.12E-02	BRMS1
FCRL4	other	2.12E-02	ELK1
FOXD2	transcriptional	2.12E-02	PRKAR1A
Integrin alpha V beta 3	complex	2.12E-02	MMP1
GRSF1	other	2.12E-02	AGO2
H2BFM	other	2.12E-02	DNMT3A
DNAJC24	other	2.12E-02	EEF2
HDLBP	transporter	2.12E-02	CSF1R
GGN	other	2.12E-02	ADRB2
RDH11	enzyme	2.12E-02	NR3C1
GGT7	enzyme	2.12E-02	ADRB2
FAF2	other	2.12E-02	NF1
TCFL5	transcriptional	2.12E-02	CD2
DNAJC15	other	2.12E-02	ABCB1
LCMT1	enzyme	2.12E-02	PPP2CA
RIC8A	other	2.12E-02	GNAQ
DPH2	enzyme	2.12E-02	EEF2
PCGF5	other	2.12E-02	MCC
ACBD3	other	2.12E-02	SLC11A2
TRPC5	ion channel	2.12E-02	ABCB1
MED25	other	2.12E-02	MMP1
SRSF9	enzyme	2.12E-02	NR3C1
SNAPC5	transcriptional	2.12E-02	ADRB2
SYP	transporter	2.12E-02	VAMP2
PCAT6	other	2.12E-02	KLHL12
CCNB1	kinase	2.12E-02	FASLG
miR-184	microRNA	2.12E-02	AGO2
SOS2	other	2.12E-02	SELL
GBP1	enzyme	2.12E-02	MMP1

DPF2	other	2.12E-02	CXCL13
FDP5	enzyme	2.12E-02	ADRB2
PTGES2	transcriptional	2.12E-02	IRF9
ELP2	other	2.12E-02	HSPA4
NPIPA7 (includes others)	other	2.12E-02	ADRB2
	other	2.12E-02	NR3C1
	peptidase	2.12E-02	STAT1
	transcriptional	2.12E-02	MMP1
P4HA1	enzyme	2.12E-02	AGO2
PAQR3	other	2.12E-02	ELK1
PIM1	kinase	2.12E-02	1.000 ABCB1,CTLA4,GNL3,SKP2
miR-3074-5p (miRNAs w/seed UUUUCG)	mature microRNA	2.12E-02	0 LOC107985899,PREB,RILP12,RP9
	transcriptional	2.12E-02	CXCR5,GZMB,IL6ST,SELL
TBX21	transcriptional	2.12E-02	0.563 FOXO1,HMGA2,IFITM1,NEDD9,NR3C1,POLR3E,RBL1,STAT1
BRCA1	transcriptional	2.15E-02	DHFR,RBL1
CDC47L	other	2.17E-02	
MDK	growth factor	2.17E-02	GZMB,PLAT
mir-137	microRNA	2.17E-02	CKS1B,NECAP1
LTB	cytokine	2.17E-02	CXCL13,SELL
miR-1287-5p (miRNAs w/seed GCGUGAU)	mature microRNA	2.23E-02	-1.912 AAK1,CHD6,CHN1,LIMS3/LIMS4,MBIP,MCC,TNRC6C
	transcriptional	2.25E-02	1.342 CCNL1,CKAP2,CKS1B,MCM6,RBL1
	group	2.29E-02	FASLG,SELL,SKP2
Focal adhesion kinase	transcriptional	2.34E-02	-1.664 BIRC2,CKS1B,CSF1,FASLG,GZMB,IL15,MATK,MMP1,NOD2,PLAT,POLB,RNF19A,RRM1,TIRC,UBE3A
	mature microRNA	2.36E-02	↓-2.219 CDKAL1,LIMS3/LIMS4,MBIP,SPRTN,TIRC
IL18	cytokine	2.40E-02	-1.127 CCR7,CSF1,FASLG,GZMB,MMP1,SELL,TXK
TNFRSF8	transmembrane receptor	2.41E-02	↑2.000 CCR7,FASLG,GZMB,KIR3DL1
TFDP1	transcriptional	2.50E-02	APAF1,DHFR,RBL1
PDPK1	kinase	2.50E-02	CCR7,S1PR1,SELL
miR-3136 (and other miRNAs w/seed UGACUGA)	mature microRNA	2.52E-02	-1.633 ABCB1,COX7B,FAU,GPATCH11,IL6ST,NEDD9
	mature microRNA	2.52E-02	↓-2.449 BABAM1,GCFC2,IGFBP4,SELENON,SHPRH,TIRC
ORMDL3	other	2.56E-02	ADAM8,OAS2
RG51	other	2.56E-02	IL15,RBL1
NFATC2	transcriptional	2.58E-02	-0.218 CTLA4,FASLG,IL15,PLAT,PLD1,STAT1,TNFSF8
miR-143-3p (and other miRNAs w/seed GAGAUGA)	mature microRNA	2.58E-02	↓-2.611 ATP6V1A,DNMT3A,GNL3,NECAP1,RHBDD2,SELL,TPP1
	other	2.60E-02	1.342 IL15,PLAT,RBL1,STAT1,TNFSF8
CREBBP	transcriptional	2.61E-02	-0.152 CCR7,CSF1,DHFR,EPN1,EPSTI1,FASLG,FDP5,GNAS,KLHL4,MGA,NR3C1,PDE3B,PLEKHF1,ST6GAL1
miR-140-3p (and other miRNAs w/seed ACCACAG)	mature microRNA	2.62E-02	↓-2.449 AGP5,COX7B,FBXL20,STAG2,TIRC,UBAP2L
	mature microRNA	2.73E-02	BET1,RABGAP1L,VBP1
miR-5583-5p (and other miRNAs w/seed AACUAU)	transcriptional	2.73E-02	IFITM1,OAS2,STAT1
CN07	enzyme	2.73E-02	ATP2B1,CTLA4,IL15
CYP27B1	transmembrane receptor	2.73E-02	-1.929 ABCB1,CCR7,CTLA4,DDHD1,FASLG,IKBKE,NLRG5,S1PR1,SELL,STAT1,ZBP1
IL10RA	complex	2.76E-02	-1.914 APAF1,BIRC2,FOXO1,MLF1,PPP2CA,S1PR1,STAT1
26S Proteasome	transcriptional	2.98E-02	0.670 ABCB1,DBF4,DHFR,DNMT3A,EDA,FASLG,GNAS,IGFBP4,IL15,MAT28,MMP1,NF1,POLB,PRKCB,RBL1,SELL,SLC11A2,STAT1
	other	2.99E-02	APAF1,MMP1
YWHAQ	other	2.99E-02	CSF1,CTLA4
LAT	other	2.99E-02	
TNFAIP2	other	2.99E-02	PLAT,RBL1
miR-4709-5p (miRNAs w/seed CAACAGU)	mature microRNA	3.00E-02	↓-2.236 BET1,HSDL1,PPP1CC,SPRY1,TIRC
	mature microRNA	3.03E-02	↓-2.121 CD2,CLASP1,GDE1,GIA4,TAB3,TIRC,TOMM5,VOPP1
miR-5008-3p (and other miRNAs w/seed CUGUGCU)	peptidase	3.14E-02	APH1A,CSF1,GNL3,GNL3,IL6ST
ADAM10			AAK1,ADAM8,ADRB2,APAF1A,TP2B1,BIRC2,CCR7,CLASP1,CSF1,CSF1R,CTLA4,CXCL13,CXCR5,DLEU1,ELK1,FASLG,FDP5,GEM,GLS,HSP
TNF	cytokine	3.16E-02	1.668 A4,IFITM1,IGFBP4,IKBKE,IL15,KIAA1671,MAN1C1,MMP1,NEDD9,NOD2,NR3C1,OAS2,PIK3CD,PLAT,RRM1,SELL,SLC11A2,SLC27A1,ST
miR-3551-5p (and other miRNAs w/seed CUUACAC)	mature microRNA	3.18E-02	6GAL1,STAT1,TIRC,TNFSF8,TPP2,VMP1,WTAP
	transcriptional	3.21E-02	-0.816 AKAP8,FANCD2,GALM,GZMB,RBM8A,SLC22A2
ID3	other	3.21E-02	-0.651 APAF1,CCR7,CSF1,CXCR5,FOXO1,GNL3,SELL,TNFSF8
TSC1	other	3.21E-02	ATP6V1A,FOXO1,STAT1
CRP	other	3.21E-02	PRKCB,PSMCG,SELL
miR-4698 (miRNAs w/seed CAAAAUG)	mature microRNA	3.24E-02	↓-2.000 AGFG1,DGKH,GGCT,PGAP1
	transcriptional	3.24E-02	CCR7,CXCL13,CXCR5,SELL
NFKB2	group	3.30E-02	1.951 DBF4,DHFR,DLEU1,FANCD2,MCM6,RBL1
E2f	transmembrane receptor	3.40E-02	1.947 CCR7,CSF1,FCMR,IFITM1,IRF9,OAS2,SPRY1,STAT1
TLR9			

HOXD10	transcriptional	3.42E-02	0	DAPP1,ERP44,SELENON,TNFSF8
E2F6	transcriptional	3.42E-02		APAF1,DHFR,PRKARIA,RPA2
TRIM24	transcriptional	3.43E-02	↓-2.177	EPSTI1,RF9,PLAC8,STAT1,UBA7
SP2	transcriptional	3.44E-02		DHFR,MAT2B
Hsp70	group	3.47E-02		GZMB,IL15,NOD2
CD40	transmembrane receptor	3.50E-02	0.068	CSF1,CTLA4,DAPP1,EDEM1,FASLG,IGHG1,IL15,SELL
IFNAR1	transmembrane receptor	3.55E-02	1.131	CSF1,IFITM1,IL15,OAS2,PLAT,STAT1
miR-1284 (and other miRNAs w/seed CUUAUCA)	mature microRNA	3.58E-02	-1.342	ADRB2,CARMIL1,TES,TFRC,VAMP1
miR-155	microRNA	3.58E-02	-1.964	APAF1,KBKE,RICTOR,S1PR1,TAB2
miR-3714 (miRNAs w/seed AAGGCAG)	mature microRNA	3.61E-02	↓-2.000	ADI1,DLEU1,GCFC2,RAB43
miR-6838-3p (miRNAs w/seed AGUCCUG)	mature microRNA	3.73E-02	-0.447	ATP6V1A,CRNN,HMGA2,MRPL35,NECAP1
ABL1	kinase	3.73E-02		CSF1,DHFR,MMP1
CD3E	transmembrane receptor	3.81E-02		CTLA4,FASLG,NFATC3,PIK3CD
miR-148a-3p (and other miRNAs w/seed CAGUGCA)	mature microRNA	3.89E-02	↓-3.162	AGFG1,ARFIP1,C18orf25,FEZ2,S1PR1,SNX27,SNX3,TNRC6C,UBAP2L,VMP1
miR-1233-5p (and other miRNAs w/seed GUGGGAG)	mature microRNA	3.90E-02	-0.775	BRMS1,CSF1R,FFAR3,HDGF,INTS5,MCFD2,MRPL35,PYCARD-AS1,RBCK1,RP9,SELENON,TCAF2,TMEM104,VAMP1,VAMP2
Cyclin E	group	3.91E-02		DHFR,RBL1
ITGB3	transmembrane receptor	4.01E-02	-0.378	FASLG,GNAQ,PHYHD1,RABGAP1L,TRMO,TXK,ZNF692
miR-6856-3p (miRNAs w/seed ACAGCCC)	mature microRNA	4.01E-02	1.698	BIRC2,CSF1,LIMS1,MMP1
miR-1306-3p (miRNAs w/seed CGUUGGC)	mature microRNA	4.01E-02	-1.000	MAT2B,STAT1,VP1,ZNF285
miR-513c-5p (and other miRNAs w/seed UCUCAAG)	mature microRNA	4.01E-02	↓-2.000	CKS1B,GGCT,TFRC,UBE3A
miR-3929 (and other miRNAs w/seed AGGCUGA)	mature microRNA	4.01E-02		CKS1B,COX7B,DYNLL1
BACH2	transcriptional	4.01E-02		FOXO1,PDE3B,SATB1
miR-4474-3p (miRNAs w/seed UUGUGGU)	mature microRNA	4.02E-02	↓-2.121	DCTN6,GOSR1,HDGF,MCFD2,NAB1,PRR14L,RAB30,RASSF2
miR-219b-5p (and other miRNAs w/seed GAUGUCC)	mature microRNA	4.09E-02	-1.633	CCR7,CRNN,GNAS,PDE3B,UCKL1,USP3
Rab5	group	4.19E-02		ADRB2
ZFAT	transcriptional	4.19E-02		FOXO1
ADGRL2	g-protein coupled receptor	4.19E-02		ADRB2
FBXO44	enzyme	4.19E-02		ADRB2
2-Mar	enzyme	4.19E-02		TFRC
SENP5	peptidase	4.19E-02		BIRC2
GLRX3	enzyme	4.19E-02		TFRC
FZD1	g-protein coupled receptor	4.19E-02		ABCB1
LGALS8	other	4.19E-02		FASLG
RPL13A	other	4.19E-02		CXCL13
LAMA3	other	4.19E-02		MMP1
TPP3	other	4.19E-02		ADRB2
NUBP1	other	4.19E-02		TFRC
RPL15	other	4.19E-02		HMGA2
GLUL	enzyme	4.19E-02		GLS
DR1	transcriptional	4.19E-02		DHFR
VAMP3	other	4.19E-02		VAMP2
ARHGEF28	other	4.19E-02		GNAQ
ZNF410	other	4.19E-02		MMP1
SOS1	other	4.19E-02		SELL
FBXO4	enzyme	4.19E-02		TERF1
RBMX	other	4.19E-02		SMN1/SMN2
GEMIN2	other	4.19E-02		SMN1/SMIN2
KHDRB52	other	4.19E-02		STAT1
MLF1	other	4.19E-02		SKP2
TFPI2	other	4.19E-02		ABCB1
DUSP2	phosphatase	4.19E-02		MMP1
APPL1	other	4.19E-02		VAMP2
DPH1	other	4.19E-02		EEF2
USP1	peptidase	4.19E-02		FANCD2
ANGPTL4	other	4.19E-02		STAT1
CRABP2	transporter	4.19E-02		APAF1
APH1B	peptidase	4.19E-02		APH1A
SNRPA	other	4.19E-02		SMN1/SMIN2
RELB	transcriptional	4.22E-02	1.154	ABCB1,CXCL13,FANCD2,IGHG1

miR-2052 (miRNAs w/seed GUUUUUGA)	mature microRNA	4.22E-02	0	DGKH,HMGA2,IL15,IL6ST
miR-4301 (miRNAs w/seed CCCACUA)	mature microRNA	4.22E-02	↓-2.000	BET1,CACU1,KLHL12,MRPL35
MAP2K3	kinase	4.22E-02		FASLG,IRF9,MMP1,STAT1
miR-5009-3p (miRNAs w/seed CCUAAAU)	mature microRNA	4.30E-02		NDP1P2,PPP4R2,VBP1
ZEB2	transcriptional	4.30E-02		CXCR5,PLCG2,SELL
miR-3605-5p (and other miRNAs w/seed GAGGAUG)	mature microRNA	4.31E-02	-1.134	C18orf25,FFAR3,FKBP11,RAB30,SNX27,TIGIT,UCKL1
VHL	transcriptional	4.38E-02		AIF1,FILIP1L,NEDD9,PRES,SKP2,TFRC
miR-924 (miRNAs w/seed GAGUCUU)	mature microRNA	4.39E-02	↓-2.236	CXCL13,ELK1,MRPL35,ZCCHC17,ZNF410
E2F4	transcriptional	4.40E-02		BUB3,CKS1B,DBF4,DHFR,FANCD2,MCM6,RBL1,RRM1,SMARCA5
CBX4	transcriptional	4.41E-02		DHFR,RBL1
DAXX	transcriptional	4.41E-02		FASLG,MMP1
miR-4703-3p (miRNAs w/seed GUAGUUG)	mature microRNA	4.43E-02	0	ADH7,KLHL12,MCFD2,MUC7
miR-6835-3p (miRNAs w/seed AAAGCAC)	mature microRNA	4.43E-02	↓-2.000	BIRC2,PARP9,TFRC,TMEM248
miR-4638-3p (and other miRNAs w/seed CUGGACA)	mature microRNA	4.44E-02	-1.134	GALM,IL6ST,NDP1P2,SLC22A2,SLCSA10,TFRC,WTAP
EPO	cytokine	4.45E-02	1.524	DCTN6,FASLG,GCC2,NR3C1,PRKCB,RAB4A,SKP2,SLC11A2,SSRP1,TFRC
SPI1	transcriptional	4.47E-02	0.955	CCR7,CSF1,CSF1R,FOXO1,IRF9,MMP1,P2RY10,RPL18
miR-6786-3p (miRNAs w/seed GAGCCCC)	mature microRNA	4.57E-02	-0.447	ARX,BEST1,FANCD2,GNAS,PDPK1
miR-6814-5p (miRNAs w/seed CCCAAGG)	mature microRNA	4.57E-02	↓-2.236	BABAM1,ELK1,FEZ2,IGFBP4,PARP9
IFN type 1	group	4.60E-02		CXCL13,STAT1,UBA7
IFNAR2	transmembrane receptor	4.60E-02		IFITM1,OAS2,UBA7
miR-8066 (miRNAs w/seed AAUGUGA)	mature microRNA	4.65E-02	↓-2.000	BET1,IL6ST,TFRC,TRIM5
ZBTB16	transcriptional	4.68E-02	-1.000	CD2,FASLG,IL6ST,SATB1,SELL,TNFSF8
miR-4771 (miRNAs w/seed GCAGACU)	mature microRNA	4.68E-02	-1.633	FILIP1L,GCFC2,KIR3DL1,LDLRAP1,ZCCHC17,ZZZ3
miR-6864-5p (miRNAs w/seed UGAAAGGG)	mature microRNA	4.70E-02	-1.890	CEP68,DHFR,ENOSF1,MEAF6,RILP2,RPL18,VAMP2
IFNB1	cytokine	4.72E-02	1.871	IFITM1,IRF9,MCM6,NOD2,OAS2,SPRY1,STAT1,UBA7,ZBP1
WT1	transcriptional	4.72E-02	0.270	CSF1,CSF1R,CUL4B,ETFA,FDP5,RPL19,SPRY1,ST6GAL1,TRAP1
miR-760-3p (and other miRNAs w/seed GGCUCUG)	mature microRNA	4.82E-02	-0.302	CLASP1,CSF1,GIA4,HDGF,HMGA2,MCC,PDPK1,PLD1,RAB43,SELENON,TCF7
IL7	cytokine	4.83E-02	0.271	CD2,CSF1,FOXO1,S1PR1,SELL,TNFSF8
TNFRSF1B	transmembrane receptor	4.88E-02		BIRC2,CXCL13,MMP1,SELL
ZBTB20	transcriptional	4.91E-02		GPC3,NEDD9,NR3C1
miR-6506-3p (miRNAs w/seed CGUAUCA)	mature microRNA	4.91E-02		GNA13,TERF1,TMEM248
SST	other	4.91E-02		ABCB1,NR3C1,SSTR3
KLRC4-KLRK1/KLRK1	transmembrane receptor	4.93E-02		FASLG,TCF7
HELLS	enzyme	4.93E-02		PDSSA,RBL1
miR-616-3p (miRNAs w/seed GUCAUUG)	mature microRNA	4.93E-02	-0.447	BRD1,FFAR3,TFRC,TOMM5,TKX
miR-4774-5p (miRNAs w/seed CUGGUAU)	mature microRNA	4.93E-02	↓-2.236	ATP6V1A,DHFR,DYNLL1,TRIM5,USP3
miR-1184 (miRNAs w/seed CUGGAGC)	mature microRNA	4.95E-02	-1.414	ADH7,FAM86B2/FAM86KP,KIR3DL1,NFKBID,PGAM1,RILP2,STAT1,TFRC
PTGER4	g-protein coupled receptor	1.23E-01	↑2.000	CCR7,FBXL20,RASSF2,S1PR1,ST6GAL1
CREB1	transcriptional	3.18E-01	↑3.124	ARHGAP35,ESD,GEM,GLS,HSPA4,MCM6,MMP1,NF1,NFKBID,PDE3B,PLAT,SMN1/SMN2,TFRC
NUPR1	transcriptional	3.72E-01	↓-2.309	ACTR3B,ADRB2,CARMIL1,CASTOR2,FANCD2,GTFC3C2,LOC100133315,PARP9,RILP2,SKP2,SPRTN,TCAF2
NKX2-3	transcriptional	4.54E-01	↓-2.236	PARP9,PLD1,STAT1,TRIM5,UBA7

^a Absence of a Z-score entry indicates that Z-score cannot be calculated by IPA.

Table S8. Gene Set Enrichment Analyses

Gene Set ^a		Reference	Size ^d	ES ^e	NES ^f	Nom p-value	FDR q-value
Up in CXCR5 ⁺ CD57 ⁺ germinal center Tfh (vs. Th1, Th2, Tcm, Tem)	Down in Th17 (vs. Th0) ^b Up in Tcm (vs. Tem)	Chtanova, J Immunol 173 (1): 68-78	314	0.51	1.86	0.000	0.003
		Kim, Blood 104 (7): 1952-60	55	0.56	1.64	0.020	0.020
Up in activated Treg (vs. CD45RA ⁺ memory T)	Up in CD69 ⁺ Trm (vs. CD69 ⁺ non-Trm)	Tuomela, Oncotarget 7(12):13416-28	61	0.52	1.58	0.012	0.121
		Chtanova, J Immunol 173 (1): 68-78	10	0.65	1.51	0.053	0.148
Up in Th1 (vs. Th2) ^c	Up in Tcm (vs. Tem and naive)	Miyara, Immunity 30(6): 899-911	139	0.36	1.43	0.034	0.192
		Kumar, Cell Rep 20(12): 2921-34	12	0.53	1.25	0.235	0.351
Down in activated Treg (vs. CD45RA ⁺ memory T)	Up in Tem (vs. Tcm and naive)	Rogge, Nat Genet 25(1): 96-101	112	0.29	1.17	0.244	0.437
		Novershtern, Cell 144(2): 296-309	13	0.41	1.10	0.351	0.500
Up in Th17 (vs. non-Th17)	Up in Th1 (vs. Th2)	Miyara, Immunity 30(6): 899-911	110	0.21	1.05	0.330	0.541
		Novershtern, Cell 144(2): 296-309	16	-0.44	-1.36	0.111	0.640
Down in CD69 ⁺ Trm (vs. CD69 ⁺ Trm)	Up in Th17 (vs. Th0) ^b	Zhang, PLoS One 7(6): e38510	124	-0.20	-0.83	0.753	0.714
		Chtanova, J Immunol 173 (1): 68-78	16	0.27	0.82	0.721	0.739
Up in Tem (vs. Tcm)	Up in Th2 (vs. Th1) ^c	Kumar, Cell Rep 20(12): 2921-34	13	0.30	0.84	0.667	0.759
		Tuomela, Oncotarget 7(12):13416-28	184	0.18	0.88	0.798	0.766
Up in Th2 (vs. Th1) ^c	Up in Th2 (vs. Th1)	Chtanova, J Immunol 173 (1): 68-78	14	-0.33	-0.94	0.533	0.771
		Rogge, Nat Genet 25(1): 96-101	37	-0.24	-0.86	0.677	0.783
Up in Th2 (vs. Th1)		Chtanova, J Immunol 173 (1): 68-78	20	0.32	0.89	0.589	0.823

^aTfh= T follicular helper, Tcm = T central memory, Tem = T effector memory, Trm = T resident memory;

^bInclusion required reads per kilobase of transcript (RPKM)>10, RPKM>mean, logFC≥1.0;

^cInclusion required FC ≥2.0;

^dNumber of genes in gene set;

^eEnrichment Score;

^fNormalized Enrichment Score