Supplemental Table 1. CD4+ lineage-associated gene set

ProbeSetID	GeneSymbol	Description	CD4 (T_4SP24-_Th)	CD8 (T_8SP24-_Th)	Expression ratio (CD4/CD8)
10547894	Cd4	CD4 antigen	2132.7	40.7	52.405
10499612	Zbtb7b	zinc finger and BTB domain containing 7B	1524.3	85.9	17.750
10480238	St8sia6	ST8 alpha-N-acetyl-neuraminide alpha-28-sialyltransferase 6	368.3	34.6	10.647
10402268	Lgmn	legumain	394.7	49.7	7.936
10599802	Cd40lg	CD40 ligand	149.7	23.8	6.301
10381809	Itgb3	integrin beta 3	1242.8	228.5	5.438
10423293	Myo10	myosin X	272.1	57.9	4.701
10511282	Tnfrsf4	tumor necrosis factor receptor superfamily member 4	566.2	126.3	4.484
10425207	H1f0	H1 histone family member 0	393.1	87.9	4.472
10469278	Il2ra	interleukin 2 receptor alpha chain	141.6	34.2	4.145
10606369	Itm2a	integral membrane protein 2A	2853.0	692.6	4.119
10469151	Itih5	inter-alpha (globulin) inhibitor H5	145.9	37.6	3.878
10496438	Adh1	alcohol dehydrogenase 1 (class I)	198.8	51.7	3.844
10590365	Vipr1	vasoactive intestinal peptide receptor 1	751.3	199.2	3.772
10550394	Ptgir	prostaglandin I receptor (IP)	248.8	70.2	3.544
10503410	Tmem64	transmembrane protein 64	1067.0	307.6	3.469
10427035	Nr4a1	nuclear receptor subfamily 4 group A member 1	1434.2	415.0	3.456
10407435	Akr1c18	aldo-keto reductase family 1 member C18	50.7	15.6	3.258
10435907	Cd200r1	CD200 receptor 1	80.0	25.2	3.169
10363541	Ass1	argininosuccinate synthetase 1	1531.4	490.5	3.122
10511363	Penk	preproenkephalin	82.3	26.6	3.099
10471154	Ass1	argininosuccinate synthetase 1	1429.9	469.9	3.043
10605113	L1cam	L1 cell adhesion molecule	232.7	78.8	2.952
10585286	Arhgap20	Rho GTPase activating protein 20	107.5	36.5	2.948
10533345	Aldh2	aldehyde dehydrogenase 2 mitochondrial	230.2	78.1	2.946
10590242	Ccr8	chemokine (C-C motif) receptor 8	468.2	160.5	2.917
10402708	Ckb	creatine kinase brain	509.5	175.6	2.902
10500204	Ecm1	extracellular matrix protein 1	492.0	172.0	2.861
10576639	Nrp1	neuropilin 1	123.6	43.8	2.822
10555174	Lrrc32	leucine rich repeat containing 32	224.5	80.1	2.803
10429564	Ly6a	lymphocyte antigen 6 complex locus A	1414.2	509.0	2.778
10403821	Tcrg-V3	T-cell receptor gamma variable 3	206.3	74.3	2.777
10346783	Cd28	CD28 antigen	1345.7	486.3	2.767
10407940	Tcrg-V2	NLR family apoptosis inhibitory protein 3	227.9	82.9	2.750
10593225	Zbtb16	zinc finger and BTB domain containing 16	157.6	57.8	2.729
10554863	Sytl2	synaptotagmin-like 2	169.0	62.2	2.718
10422028	Tbc1d4	TBC1 domain family member 4	115.8	45.3	2.559
10575534	St3gal2	ST3 beta-galactoside alpha-23-sialyltransferase 2	199.6	78.4	2.546
10467110	Lipo1	expressed sequence AI747699	112.3	44.1	2.544
10502791	Ifi44	interferon-induced protein 44	230.5	91.7	2.514
10547100	Plxnd1	plexin D1	276.1	109.8	2.514
10414914	Trav14n-3	---	120.1	48.3	2.486
10492815	Tmem154	transmembrane protein 154	284.8	116.0	2.455
10353450	Gm4956	predicted gene 4956	66.4	27.2	2.442
10579347	Ifi30	interferon gamma inducible protein 30	589.9	241.7	2.441
10439955	Fam55c	family with sequence similarity 55 member C	1239.8	517.6	2.395
10479981	Gata3	GATA binding protein 3	1013.9	423.5	2.394
10556280	Swap70	SWA-70 protein	120.6	50.8	2.376
10598292	Foxp3	forkhead box P3	189.6	79.9	2.372
10517373	Rcan3	regulator of calcineurin 3	488.4	206.6	2.364
10559261	Cd81	CD81 antigen	597.2	254.3	2.348
10418341	Il17rb	interleukin 17 receptor B	118.1	50.7	2.331
10514255	Mllt3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog Drosophila); translocated to 3	980.7	425.0	2.308
10417264	Gm3002	predicted gene 544988	77.4	33.6	2.300
10379615	Slfn5	schlafen 5	735.1	321.7	2.285
10538356	Chn2	chimerin (chimaerin) 2	373.6	164.4	2.272

10346790	Ctla4	cytotoxic T-lymphocyte-associated protein 4	159.9	70.8	2.258
10483381	Stk39	serine/threonine kinase 39 STE20/SPS1 homolog (yeast)	418.3	186.1	2.248
10373902	Gatsl3	GATS protein-like 3	302.3	135.0	2.239
10455961	Iigp1	interferon inducible GTPase 1	129.9	58.1	2.237
10417359	Gm3002	hematological and neurological expressed 1-like	75.3	33.7	2.236
10441003	Runx1	runt related transcription factor 1	562.7	252.3	2.230
10556598	Xylt1	xylosyltransferase 1	366.1	165.1	2.218
10532085	Tgfbr3	transforming growth factor beta receptor III	754.9	344.4	2.192
10587315	Gsta4	glutathione S-transferase alpha 4	103.3	47.2	2.190
10558001	Inpp5f	inositol polyphosphate-5-phosphatase F	170.9	78.3	2.182
10495405	Slc25a24	solute carrier family 25 (mitochondrial carrier phosphate carrier) member 24	155.6	71.3	2.182
10431410	Mapk11	mitogen-activated protein kinase 11	259.1	118.8	2.181
10439790	Trat1	T cell receptor associated transmembrane adaptor 1	161.6	74.1	2.181
10407792	Gpr137b-ps	G protein-coupled receptor 137B pseudogene	88.0	40.4	2.178
10412537	Gm3002	RIKEN cDNA B930046C15 gene	65.7	30.2	2.177
10560719	2210010C17Ri	RIKEN cDNA 2210010C17 gene	164.1	75.6	2.172
10559248	Tspan32	tetraspanin 32	885.6	409.0	2.165
10414784	Gm26	gene model 26 (NCBI)	968.4	447.8	2.162
10560709	Pvr	poliovirus receptor	411.5	190.6	2.159
10414738	LOC547323	similar to RIKEN cDNA A430107P09 gene	429.2	199.8	2.148
10414807	Trav14-3	T-cell receptor alpha chain	692.6	323.1	2.143
10445877	Gm16489	predicted gene 16489	299.9	140.0	2.142
10467068	Sgms1	sphingomyelin synthase 1	253.3	118.7	2.135
10405693	Dapk1	death associated protein kinase 1	190.8	89.6	2.129
10417258	Gm3002	predicted gene 544988	57.5	27.1	2.122
10504838	Nr4a3	nuclear receptor subfamily 4 group A member 3	250.8	118.5	2.116
10417235	Gm2897	predicted gene 3264	49.1	23.2	2.115
10508651	Sdc3	syndecan 3	209.1	99.0	2.112
10590974	Folr4	folate receptor 4 (delta)	847.0	401.3	2.110
10489051	5730471H19R	RIKEN cDNA 5730471H19 gene	296.3	140.5	2.109
10368947	Aim1	absent in melanoma 1	1157.9	549.2	2.108
10402063	Foxn3	forkhead box N3	639.8	303.8	2.106
10386951	Hs3st3b1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	577.9	274.7	2.104
10417226	Gm3002		56.0	26.6	2.101
10463836	Gsto1	glutathione S-transferase omega 1	131.9	63.0	2.094
10495685	Arhgap29	Rho GTPase activating protein 29	101.7	48.6	2.093
10412517	Gm3002	predicted gene 10021	202.1	96.7	2.090
10590381	Vipr1	vasoactive intestinal peptide receptor 1	200.1	95.9	2.086
10447294	Prkce	protein kinase C epsilon	175.6	84.6	2.076
10408450	Sox4	SRY-box containing gene 4	444.1	216.6	2.050
10484227	Sestd1	SEC14 and spectrin domains 1	75.3	36.7	2.049
10417302	Gm3002	predicted gene 544988	56.9	27.8	2.047
10570516	Kbtbd11	kelch repeat and BTB (POZ) domain containing 11	977.3	479.4	2.038
10422496	Gpr183	G protein-coupled receptor 183	542.7	266.3	2.038
10417286	Gm3002		58.6	28.8	2.036
10404913	Cap2	CAP adenylate cyclase-associated protein 2 (yeast)	105.3	51.8	2.031
10525419	P2rx7	purinergic receptor P2X ligand-gated ion channel 7	160.5	79.3	2.024
10548030	Cd9	CD9 antigen	496.0	245.2	2.023
10439651	Cd200	CD200 antigen	145.5	71.9	2.022
10417421	Gm3696	hematological and neurological expressed 1-like	61.3	30.4	2.016
10466040	Cd5	CD5 antigen	2925.2	1452.6	2.014
10356866	Pdcd1	programmed cell death 1	247.0	123.3	2.004

Microarray data comparing CD4+ and CD8+ single positive mature thymocytes were downloaded from the Immunological Genome project. Genes shown ≥2 fold higher expression in CD4+ T cells than that in CD8+ T cells were identified.

Supplemental Table 2. Primers used in quantitative PCR.

a. Primers for cDNA detection

Gene symbol	5’ primer	3’ primer
Cd40lg	5'- GGCAATTTGAAGACCTTGTCA	5'- CTGCATTACTGTTGGCTTCG
St8sia6	5'- GCTACGAGGTGGAAAGCAAG	5'- TGAGAATTCCCCCATTACCA
Lgmn	5'- ACACCGGAGAGGATGTGACT	5'- CCGTGGTCGGTGAAGTAAAT
Runx3d	5'- CCAACCAAGTGGGTCTGAAC	5'- GTGCTCGGGTCTCGTATGAA
Itgae	5'- ATTTGGGGACCCTCTCAATC	5'- GGTCTGAGGCAATCAGCTTC
Nkg7	5'- TCCTCACTTCTCTGCCCACT	5'- GCAAGACAGAACCAGGAAGC
Prdm1	5'- TGGTATTGTCGGGACTTTGC	5'- ATTGCTTTGGGTTGCTTTCC
Prf1	5'- GATGTGAACCCTAGGCCAGA	5'- GGTTTTTGTACCAGGCGAAA
Fasl	5'- GCAGAAGGAACTGGCAGAAC	5'- TTAAATGGGCCACACTCCTC
Itgb3	5'- TGTCGTCAGCCTTTACCAGA	5'- GGATTTTCCCGTAAGCATCA
Thpok	5'- CCCTGCTCGAGTTTGCTTAC	5'- CTCGCTCACAGTCATCCTCA
Gata3	5'- CTTATCAAGCCCAAGCGAAG	5'- CATTAGCGTTCCTCCTCCAG

b. Primers for genomic region detection

Gene symbol	5’ primer	3’ primer
Cd4-TSS	5'- CAGAACATTCCGGCACATTA	5'- CATCTGTGAAGGCAAAGCAA
Cd4-silencer	5'- GAACCACAAGGGTCGCTTAG	5'- CACAGTGACAGCCTGTGGTC
St8sia6-TSS	5'- CAGAGCATACGCAGGAGGAG	5'- GTGGCTCAGGATGAGATCG
Cd40lg-upstream	5'- GGGATCTTGGTCATAAAGCAG	5'- CAATGCTGAGTCGGAAATGA
Itgb3-TSS	5'- CCGGAGCTAGGACTGAGAAG	5'- TCCATCTTTCCTCTGCTTCC
Thpok-TSS	5'- GGAATGCGACTGGTTGAAAT	5'- CCTTGGCTCGGGATACACTA
Prdm1-TSS	5'- TGACGGTCTGATTCACTCCT	5'- CCCAGTCCTTGTTGAAATCC
Fasl-TSS	5'- TCCTAATCCCATTCCAACCA	5'- CATCACAACCACTCCCACTG