Supplemental Table 1 Gene Symbol	p-value (CD8IL13+ vs. CD8IL13- and allo CD8)	Fold-Change (CD8IL13+ vs. CD8IL13- and allo CD8)	p-value (CD8IL13+ vs. CD8IL13-)	Fold-Change (CD8IL13+ vs. CD8IL13-)	p-value (CD8IL13+ vs. allo CD8)	Fold-Change (CD8IL13+ vs. allo CD8)	same direction	sig	>3	gene title
1810011H11Rik	1.52E-15	22.31	2.12E-15	24.85	8.19E-14	20.03	Y	1	1	RIKEN cDNA 1810011H11 gene (uncharacterized protein LOC69069 precursor)
Pecam1	1.08E-03	11.02	1.84E-03	10.74	5.66E-03	11.31	Y	1	1	platelet/endothelial cell adhesion molecule 1
Amelx	8.75E-12	10.68	1.57E-10	7.75	4.13E-11	14.71	Y	1	1	amelogenin X chromosome
Sulf2	1.84E-06	10.10	2.14E-04	4.84	1.12E-06	21.07	Y	1	1	sulfatase 2
Tnfrsf11b	1.34E-09	9.19	4.03E-06	3.54	2.42E-10	23.83	Y	1	1	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)
Ccr8	2.15E-08	8.90	4.58E-08	8.89	4.49E-07	8.91	Y	1	1	chemokine (C-C motif) receptor 8
Prl2c5	9.94E-05	8.88	2.06E-04	8.54	7.44E-04	9.24	Y	1	1	prolactin family 2, subfamily c, member 5
Ctss	1.68E-05	8.74	4.02E-04	5.33	2.32E-05	14.34	Y	1	1	cathepsin S
2810055G20Rik	2.58E-04	8.74	3.39E-03	5.36	3.45E-04	14.25	Y	1	1	RIKEN cDNA 2810055G20 gene
Hpgds	1.20E-04	8.11	4.49E-04	6.86	5.25E-04	9.60	Y	1	1	hematopoietic prostaglandin D synthase
Arntl	5.51E-07	6.84	3.00E-08	12.80	5.00E-04	3.65	Y	1	1	aryl hydrocarbon receptor nuclear translocator-like
Gm9766	7.67E-05	6.79	7.61E-04	4.88	1.63E-04	9.44	Y	1	1	predicted gene 9766
Eml1	1.45E-07	6.46	2.66E-06	4.77	4.21E-07	8.76	Y	1	1	echinoderm microtubule associated protein like 1
Cd4	3.17E-05	6.39	2.04E-04	5.12	1.11E-04	7.98	Y	1	1	CD4 antigen
Dclk3	8.80E-12	6.20	3.77E-11	5.73	1.37E-10	6.72	Y	1	1	doublecortin-like kinase 3
Sla	1.02E-04	5.94	1.20E-04	6.39	1.24E-03	5.52	Y	1	1	src-like adaptor
Epdr1	1.36E-04	5.59	2.33E-04	5.60	1.13E-03	5.59	Y	1	1	ependymin related protein 1 (zebrafish)
Mtmr7	8.29E-09	5.40	5.86E-09	6.24	5.72E-07	4.67	Y	1	1	myotubularin related protein 7
2810055G20Rik	1.19E-03	5.28	8.15E-03	3.84	1.91E-03	7.26	Y	1	1	RIKEN cDNA 2810055G20 gene
Gabra1	5.51E-04	4.90	5.97E-04	5.30	5.01E-03	4.54	Y	1	1	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 1
Impact	1.31E-08	4.44	3.21E-05	2.30	2.22E-09	8.56	Y	1	1	imprinted and ancient
Csf2	2.84E-04	4.30	5.20E-03	2.92	2.86E-04	6.33	Y	1	1	colony stimulating factor 2 (granulocyte-macrophage)
Abca5	9.72E-10	4.14	5.34E-11	6.35	2.23E-06	2.70	Y	1	1	ATP-binding cassette, sub-family A (ABC1), member 5
Yipf6	6.19E-15	4.02	3.13E-04	1.25	2.39E-17	12.91	Y	1	1	Yip1 domain family, member 6
Lrrc49	1.69E-11	3.99	2.44E-07	2.07	1.84E-12	7.70	Y	1	1	leucine rich repeat containing 49
4930506M07Rik	2.86E-07	3.98	4.04E-07	4.15	7.07E-06	3.82	Y	1	1	RIKEN cDNA 4930506M07 gene
Ptpre	4.77E-08	3.94	2.54E-04	1.99	4.92E-09	7.80	Y	1	1	protein tyrosine phosphatase, receptor type, E
Mirlet7c-1	1.63E-03	3.79	5.34E-03	3.31	4.49E-03	4.34	Y	1	1	microRNA let7c-1
Mir99a	1.07E-03	3.65	7.08E-03	2.88	1.81E-03	4.64	Y	1	1	microRNA 99a
Farp1	2.16E-06	3.57	3.64E-08	6.42	6.53E-03	1.98	Y	1	1	FERM, RhoGEF (Arhgef) and pleckstrin domain protein 1 (chondrocyt
LOC280487	2.27E-06	3.48	6.69E-05	2.65	3.52E-06	4.58	Y	1	1	pol polyprotein
LOC280487	2.27E-06	3.48	6.69E-05	2.65	3.52E-06	4.58	Y	1	1	pol polyprotein
Mir23b	2.60E-05	3.42	1.66E-03	2.30	1.62E-05	5.08	Y	1	1	microRNA 23b
Mir155	3.93E-06	3.41	6.98E-05	2.72	8.35E-06	4.28	Y	1	1	microRNA 155
Mapk8	1.91E-04	3.35	7.35E-04	3.01	7.43E-04	3.73	Y	1	1	mitogen-activated protein kinase 8
Pank1	6.87E-06	3.28	8.63E-05	2.70	1.77E-05	3.97	Y	1	1	pantothenate kinase 1
Bicd1	1.24E-09	3.23	3.79E-09	3.14	2.22E-08	3.32	Y	1	1	bicaudal D homolog 1 (Drosophila)
Spry2	2.29E-09	3.21	1.10E-07	2.52	4.34E-09	4.10	Y	1	1	sprouty homolog 2 (Drosophila)
Pbxip1	2.22E-08	3.20	5.00E-06	2.23	1.36E-08	4.61	Y	1	1	pre-B-cell leukemia transcription factor interacting protein 1 /
Mir18	4.02E-05	3.15	1.31E-03	2.31	3.80E-05	4.30	Y	1	1	microRNA 18
Agap1	5.97E-05	3.11	7.70E-04	2.50	1.08E-04	3.88	Y	1	1	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1
S1pr3	1.63E-04	3.09	1.81E-03	2.47	2.73E-04	3.85	Y	1	1	sphingosine-1-phosphate receptor 3
Gm5785	5.61E-05	3.08	2.75E-04	2.76	2.25E-04	3.45	Y	1	1	predicted gene 5785
Tnfsf13b	2.26E-09	3.00	1.95E-10	4.00	2.43E-06	2.25	Y	1	1	tumor necrosis factor (ligand) superfamily, member 13b
Mir19b-1	4.07E-04	2.98	3.44E-03	2.43	7.05E-04	3.66	Y	1	1	microRNA 19b-1
Akr1c12	5.34E-10	2.96	1.78E-12	5.54	3.06E-04	1.58	Y	1	1	aldo-keto reductase family 1, member C12
Fut8	1.96E-10	2.92	1.93E-03	1.33	2.11E-12	6.43	Y	1	1	fucosyltransferase 8
Lair1	1.11E-05	2.91	3.11E-05	2.80	9.31E-05	3.03	Y	1	1	leukocyte-associated Ig-like receptor 1
B930095G15Rik	4.77E-05	2.89	5.13E-06	3.95	6.75E-03	2.11	Y	1	1	RIKEN cDNA B930095G15 gene
Mir92-1	2.14E-04	2.83	3.45E-03	2.20	2.52E-04	3.64	Y	1	1	microRNA 92-1
Cd81	3.65E-04	2.79	3.17E-04	3.01	4.43E-03	2.58	Y	1	1	CD81 antigen
Mical2	6.18E-04	2.73	5.44E-03	2.23	9.43E-04	3.35	Y	1	1	microtubule associated monoxygenase, calponin and LIM domain
Rab4a	6.04E-05	2.67	3.80E-03	1.91	3.23E-05	3.74	Y	1	1	RAB4A, member RAS oncogene family
Tarbp1	3.30E-05	2.66	1.11E-05	3.14	1.63E-03	2.26	Y	1	1	TAR (HIV-1) RNA binding protein 1
Wsb2	4.62E-06	2.60	3.06E-03	1.67	8.03E-07	4.05	Y	1	1	WD repeat and SOCS box-containing 2
Xlr4c	6.02E-10	2.58	4.52E-08	2.08	8.94E-10	3.21	Y	1	1	X-linked lymphocyte-regulated 4C
Xlr4b	2.84E-10	2.51	2.83E-08	2.01	3.63E-10	3.14	Y	1	1	X-linked lymphocyte-regulated 4B
Auh	5.62E-05	2.40	4.31E-03	1.75	2.63E-05	3.28	Y	1	1	AU RNA binding protein/enoyl-coenzyme A hydratase
Nfkb1	2.55E-15	2.37	4.65E-12	1.73	8.18E-16	3.25	Y	1	1	nuclear factor of kappa light polypeptide gene enhancer in B-cell
Camk2b	4.86E-07	2.34	1.38E-04	1.72	1.95E-07	3.18	Y	1	1	calcium/calmodulin-dependent protein kinase II, beta
Setd7	7.02E-08	2.31	1.35E-04	1.59	1.17E-08	3.35	Y	1	1	SET domain containing (lysine methyltransferase) 7
Tmem140	7.37E-07	2.23	1.92E-03	1.48	7.75E-08	3.35	Y	1	1	transmembrane protein 140
Psmb10	1.28E-07	2.22	1.88E-03	1.41	7.13E-09	3.49	Y	1	1	proteasome (prosome, macropain) subunit, beta type 10
Rbak	3.24E-09	2.00	3.91E-04	1.31	1.14E-10	3.05	Y	1	1	RB-associated KRAB repressor
Ipmk	4.47E-12	-1.85	2.16E-03	-1.13	2.58E-14	-3.03	Y	1	1	inositol polyphosphate multikinase
Retsat	2.40E-08	-2.03	6.01E-04	-1.36	1.30E-09	-3.04	Y	1	1	retinol saturase (all trans retinol 13,14 reductase)
Maged2	5.07E-08	-2.04	7.90E-04	-1.37	3.12E-09	-3.03	Y	1	1	melanoma antigen, family D, 2
Haus8	2.18E-06	-2.17	6.76E-03	-1.41	1.73E-07	-3.32	Y	1	1	4HAUS augmin-like complex, subunit 8
Sqle	4.45E-06	-2.21	6.38E-03	-1.46	4.83E-07	-3.33	Y	1	1	squalene epoxidase
Lrrc42	4.13E-10	-2.29	2.59E-07	-1.72	1.75E-10	-3.05	Y	1	1	leucine rich repeat containing 42
Dci	8.31E-07	-2.30	1.40E-08	-3.35	3.36E-03	-1.58	Y	1	1	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A is
Sp140	1.91E-09	-2.31	4.12E-12	-3.91	2.08E-03	-1.36	Y	1	1	Sp140 nuclear body protein
Rhobtb3	9.03E-08	-2.32	4.24E-05	-1.70	3.19E-08	-3.17	Y	1	1	Rho-related BTB domain containing 3
Cep72	5.98E-05	-2.40	5.02E-03	-1.74	2.58E-05	-3.31	Y	1	1	centrosomal protein 72
Phf11	5.19E-10	-2.42	7.10E-06	-1.57	4.98E-11	-3.75	Y	1	1	PHD finger protein 11
Bcat2	4.62E-10	-2.44	1.88E-06	-1.65	7.62E-11	-3.61	Y	1	1	branched chain aminotransferase 2, mitochondrial
Pgp	1.25E-05	-2.45	9.96E-04	-1.83	7.54E-06	-3.27	Y	1	1	phosphoglycolate phosphatase
Grhpr	2.23E-05	-2.46	6.26E-03	-1.65	5.01E-06	-3.67	Y	1	1	glyoxylate reductase/hydroxypyruvate reductase

Bard1	1.51E-04	-2.47	9.27E-03	-1.77	6.70E-05	-3.46	Y	1	1	BRCA1 associated RING domain 1
Cdc25b	3.22E-04	-2.53	2.97E-03	-2.12	5.47E-04	-3.03	Y	1	1	cell division cycle 25 homolog B (S. pombe)
Scp2	4.80E-06	-2.54	3.31E-03	-1.64	8.05E-07	-3.93	Y	1	1	sterol carrier protein 2, liver
Fam117b	6.08E-06	-2.55	2.35E-04	-2.01	6.81E-06	-3.23	Y	1	1	family with sequence similarity 117, member B
Hist1h4f	7.71E-04	-2.57	5.56E-03	-2.15	1.32E-03	-3.05	Y	1	1	histone cluster 1, H4f
Hist1h2ak	3.65E-04	-2.57	4.10E-03	-2.09	5.14E-04	-3.16	Y	1	1	histone cluster 1, H2ak
Abi3	1.64E-04	-2.58	1.25E-03	-2.22	3.74E-04	-3.00	Y	1	1	ABI gene family, member 3
Usp28	9.19E-08	-2.59	8.04E-09	-3.35	6.11E-05	-2.00	Y	1	1	ubiquitin specific peptidase 28
Hist1h3g	5.76E-04	-2.62	4.51E-03	-2.19	9.85E-04	-3.14	Y	1	1	histone cluster 1, H3g
Hist1h3a	5.15E-04	-2.63	4.11E-03	-2.19	8.87E-04	-3.15	Y	1	1	histone cluster 1, H3a
Hist1h3h	5.48E-04	-2.63	4.30E-03	-2.20	9.45E-04	-3.15	Y	1	1	histone cluster 1, H3h
Hist1h3i	5.82E-04	-2.67	4.44E-03	-2.22	1.01E-03	-3.20	Y	1	1	histone cluster 1, H3i
Hist1h3d	5.41E-04	-2.68	4.17E-03	-2.24	9.50E-04	-3.22	Y	1	1	histone cluster 1, H3d
Hist1h3b	5.15E-04	-2.69	4.05E-03	-2.24	9.01E-04	-3.24	Y	1	1	histone cluster 1, H3b
Gm13154	2.20E-04	-2.71	1.12E-03	-2.40	6.57E-04	-3.06	Y	1	1	predicted gene 13154
Hist1h3e	4.92E-04	-2.72	3.93E-03	-2.26	8.58E-04	-3.27	Y	1	1	histone cluster 1, H3e
Hist1h3c	5.43E-04	-2.72	4.15E-03	-2.27	9.60E-04	-3.27	Y	1	1	histone cluster 1, H3c
Dag1	3.15E-04	-2.73	5.31E-03	-2.11	3.30E-04	-3.54	Y	1	1	dystroglycan 1
Psrc1	1.01E-05	-2.75	6.88E-03	-1.67	1.48E-06	-4.50	Y	1	1	proline/serine-rich coiled-coil 1
Hibch	1.96E-11	-2.75	2.38E-09	-2.14	2.41E-11	-3.53	Y	1	1	3-hydroxyisobutyryl-Coenzyme A hydrolase
Hist3h2ba	2.81E-07	-2.75	7.22E-06	-2.27	6.01E-07	-3.34	Y	1	1	histone cluster 3, H2ba
Hist2h3c1	4.57E-04	-2.75	4.10E-03	-2.25	7.36E-04	-3.36	Y	1	1	histone cluster 2, H3c1
Hist2h3b	4.12E-04	-2.76	3.56E-03	-2.28	7.02E-04	-3.36	Y	1	1	histone cluster 2, H3b
Mettl7a1	1.64E-04	-2.81	6.77E-05	-3.31	4.66E-03	-2.39	Y	1	1	methyltransferase like 7A1
Mki67	1.01E-03	-2.81	8.00E-03	-2.28	1.49E-03	-3.48	Y	1	1	antigen identified by monoclonal antibody Ki 67
Akr1b10	7.95E-06	-2.82	2.06E-06	-3.43	6.85E-04	-2.32	Y	1	1	aldo-keto reductase family 1, member B10 (aldose reductase)
Cdc20	5.01E-04	-2.86	9.51E-03	-2.11	4.27E-04	-3.87	Y	1	1	cell division cycle 20 homolog (S. cerevisiae)
Eif4ebp1	3.75E-06	-2.90	3.00E-04	-2.10	2.68E-06	-4.00	Y	1	1	eukaryotic translation initiation factor 4E binding protein 1
Insl6	7.25E-04	-2.92	3.34E-03	-2.54	1.83E-03	-3.35	Y	1	1	insulin-like 6
Larp1b	8.15E-14	-2.93	9.42E-12	-2.27	1.14E-13	-3.77	Y	1	1	La ribonucleoprotein domain family, member 1B
Wdr54	1.67E-08	-2.93	8.70E-06	-1.99	6.39E-09	-4.31	Y	1	1	WD repeat domain 54
Kif15	1.01E-03	-2.94	3.15E-03	-2.68	3.26E-03	-3.23	Y	1	1	kinesin family member 15
Tmsb15l	2.06E-05	-2.96	7.75E-06	-3.50	1.01E-03	-2.50	Y	1	1	thymosin beta 15b like
Qser1	2.45E-03	-3.05	5.68E-03	-2.85	8.13E-03	-3.26	Y	1	1	glutamine and serine rich 1
Hvcn1	4.61E-08	-3.05	5.26E-04	-1.67	3.32E-09	-5.56	Y	1	1	hydrogen voltage-gated channel 1
D2Ertd750e	2.23E-04	-3.08	3.58E-03	-2.34	2.61E-04	-4.05	Y	1	1	DNA segment, Chr 2, ERATO Doi 750, expressed
Fam38a	1.38E-06	-3.08	5.20E-07	-3.63	1.07E-04	-2.62	Y	1	1	family with sequence similarity 38, member A
Tfpi	1.58E-03	-3.09	9.13E-03	-2.53	2.73E-03	-3.77	Y	1	1	tissue factor pathway inhibitor
E330013P04Rik	5.45E-07	-3.09	4.17E-05	-2.27	5.05E-07	-4.21	Y	1	1	RIKEN cDNA E330013P04 gene
Csnk1e	1.05E-06	-3.11	7.57E-06	-2.77	5.31E-06	-3.51	Y	1	1	casein kinase 1, epsilon
AF529169	8.72E-08	-3.12	1.27E-04	-1.90	1.64E-08	-5.13	Y	1	1	cDNA sequence AF529169
Stk38l	3.52E-09	-3.14	1.82E-05	-1.84	4.61E-10	-5.33	Y	1	1	serine/threonine kinase 38 like
Gpsm2	3.55E-04	-3.14	2.04E-03	-2.67	8.72E-04	-3.70	Y	1	1	G-protein signalling modulator 2 (AGS3-like, C. elegans)
Sema6d	5.33E-04	-3.20	2.93E-04	-3.72	8.74E-03	-2.75	Y	1	1	sema domain, transmembrane domain (TM), and cytoplasmic domain,
Tpmt	1.08E-11	-3.21	1.60E-10	-2.78	5.87E-11	-3.71	Y	1	1	thiopurine methyltransferase
Ikzf3	4.26E-04	-3.22	7.57E-04	-3.18	2.70E-03	-3.25	Y	1	1	IKAROS family zinc finger 3
Pde6d	3.21E-07	-3.25	6.35E-07	-3.26	5.69E-06	-3.24	Y	1	1	phosphodiesterase 6D, cGMP-specific, rod, delta
Il12rb2	1.33E-08	-3.26	3.58E-07	-2.64	3.48E-08	-4.02	Y	1	1	interleukin 12 receptor, beta 2
Cenpm	7.72E-05	-3.29	8.93E-04	-2.63	1.45E-04	-4.10	Y	1	1	centromere protein M
Dhcr7	7.05E-09	-3.31	1.55E-04	-1.73	4.57E-10	-6.33	Y	1	1	7-dehydrocholesterol reductase
Zfp781	3.59E-10	-3.40	3.95E-12	-5.90	1.62E-05	-1.96	Y	1	1	zinc finger protein 781
Gyk	3.16E-08	-3.44	6.06E-03	-1.50	6.95E-10	-7.91	Y	1	1	glycerol kinase
Racgap1	1.92E-04	-3.48	9.29E-04	-3.03	6.19E-04	-4.01	Y	1	1	Rac GTPase-activating protein 1
Cdkn3	9.75E-04	-3.49	4.68E-03	-2.93	2.21E-03	-4.16	Y	1	1	cyclin-dependent kinase inhibitor 3
1700008I05Rik	8.59E-09	-3.57	7.55E-09	-3.89	4.68E-07	-3.27	Y	1	1	RIKEN cDNA 1700008I05 gene
Tdpoz4	7.11E-08	-3.57	8.53E-07	-3.03	3.05E-07	-4.21	Y	1	1	TD and POZ domain containing 4
4933436C20Rik	1.74E-07	-3.59	1.28E-06	-3.17	1.03E-06	-4.07	Y	1	1	RIKEN cDNA 4933436C20 gene
Uhrf1	4.04E-04	-3.60	2.85E-03	-2.90	8.16E-04	-4.45	Y	1	1	ubiquitin-like, containing PHD and RING finger domains, 1
Pafah1b3	2.10E-07	-3.67	3.91E-07	-3.71	4.11E-06	-3.64	Y	1	1	platelet-activating factor acetylhydrolase, isoform 1b, subuni
Selm	1.34E-04	-3.68	9.73E-03	-2.23	5.41E-05	-6.06	Y	1	1	selenoprotein M
Rnpepl1	5.66E-05	-3.72	4.75E-04	-3.05	1.45E-04	-4.54	Y	1	1	arginyl aminopeptidase (aminopeptidase B)-like 1
Ncaph	1.38E-03	-3.73	5.86E-03	-3.13	3.18E-03	-4.44	Y	1	1	non-SMC condensin I complex, subunit H
Top2a	5.59E-04	-3.75	2.85E-03	-3.14	1.37E-03	-4.50	Y	1	1	topoisomerase (DNA) II alpha
Idh1	1.20E-06	-3.76	1.66E-03	-1.99	1.66E-07	-7.10	Y	1	1	isocitrate dehydrogenase 1 (NADP+), soluble
Aurkb	4.77E-04	-3.77	7.19E-03	-2.67	4.96E-04	-5.32	Y	1	1	aurora kinase B
Hsd11b1	1.94E-07	-3.81	2.90E-06	-3.12	6.45E-07	-4.66	Y	1	1	hydroxysteroid 11-beta dehydrogenase 1
Ckap2l	4.02E-04	-3.81	3.45E-03	-2.96	6.92E-04	-4.91	Y	1	1	cytoskeleton associated protein 2-like
Tmem180	3.81E-11	-3.82	2.38E-08	-2.44	1.76E-11	-5.98	Y	1	1	transmembrane protein 180
Pecr	4.22E-07	-3.82	6.04E-04	-2.06	6.70E-08	-7.07	Y	1	1	peroxisomal trans-2-enoyl-CoA reductase
2510002D24Rik	6.13E-07	-3.82	2.64E-05	-2.79	8.36E-07	-5.23	Y	1	1	RIKEN cDNA 2510002D24 gene
Sord	4.26E-07	-3.87	6.60E-06	-3.13	1.29E-06	-4.79	Y	1	1	sorbitol dehydrogenase
Oxr1	2.32E-03	-3.88	6.95E-03	-3.41	6.29E-03	-4.43	Y	1	1	oxidation resistance 1
Cyp4f39	1.03E-06	-3.90	1.12E-07	-5.58	3.48E-04	-2.73	Y	1	1	cytochrome P450, family 4, subfamily f, polypeptide 39
Arhgap19	1.35E-04	-3.92	1.65E-03	-2.97	2.20E-04	-5.17	Y	1	1	Rho GTPase activating protein 19
Ube2c	1.46E-04	-3.92	1.77E-03	-2.97	2.34E-04	-5.18	Y	1	1	ubiquitin-conjugating enzyme E2C
Fbxo5	7.10E-04	-3.92	2.84E-03	-3.37	2.02E-03	-4.57	Y	1	1	F-box protein 5
Zdhhc23	4.83E-09	-3.94	3.14E-03	-1.53	8.65E-11	-10.10	Y	1	1	zinc finger, DHHC domain containing 23
Casc5	1.76E-03	-3.94	9.91E-03	-3.09	3.02E-03	-5.02	Y	1	1	cancer susceptibility candidate 5
Slc5a8	4.74E-16	-3.94	3.97E-03	-1.15	1.10E-18	-13.57	Y	1	1	solute carrier family 5 (iodide transporter), member 8
Sord	4.75E-07	-3.95	7.01E-06	-3.20	1.47E-06	-4.88	Y	1	1	sorbitol dehydrogenase
Fancd2	6.48E-04	-3.97	8.88E-03	-2.78	6.78E-04	-5.67	Y	1	1	Fanconi anemia, complementation group D2
Fam38a	1.82E-07	-3.99	7.67E-08	-4.78	1.65E-05	-3.32	Y	1	1	family with sequence similarity 38, member A
Lpin1	7.41E-08	-4.04	1.45E-05	-2.61	4.50E-08	-6.26	Y	1	1	lipin 1
Syt1	1.56E-10	-4.05	1.65E-09	-3.49	1.03E-09	-4.70	Y	1	1	synaptotagmin I

Ndc80	7.20E-04	-4.06	2.90E-03	-3.47	2.03E-03	-4.76	Y	1	1	NDC80 homolog, kinetochore complex component (S. cerevisiae)
Tmbim4	2.77E-04	-4.08	1.25E-04	-5.04	6.36E-03	-3.30	Y	1	1	transmembrane BAX inhibitor motif containing 4
Ccnb1	2.48E-04	-4.08	4.22E-03	-2.86	2.72E-04	-5.82	Y	1	1	cyclin B1
Ccnb1	2.58E-04	-4.12	4.02E-03	-2.92	3.01E-04	-5.83	Y	1	1	cyclin B1
Sorcs1	7.93E-04	-4.14	8.07E-04	-4.48	6.95E-03	-3.82	Y	1	1	VPS10 domain receptor protein SORCS 1
Hist1h1b	5.14E-04	-4.16	2.99E-03	-3.36	1.15E-03	-5.15	Y	1	1	histone cluster 1, H1b
Depdc1a	1.09E-03	-4.18	7.55E-03	-3.18	1.76E-03	-5.48	Y	1	1	DEP domain containing 1a
Bard1	8.67E-05	-4.23	3.65E-03	-2.69	5.83E-05	-6.67	Y	1	1	BRCA1 associated RING domain 1
Ccnb1	2.19E-04	-4.23	3.44E-03	-2.99	2.63E-04	-5.99	Y	1	1	cyclin B1
Melk	6.86E-04	-4.24	3.14E-03	-3.53	1.76E-03	-5.09	Y	1	1	maternal embryonic leucine zipper kinase
Rgs2	1.77E-06	-4.26	1.06E-06	-4.95	8.24E-05	-3.66	Y	1	1	regulator of G-protein signaling 2
Casp12	3.49E-09	-4.29	1.05E-07	-3.30	9.03E-09	-5.57	Y	1	1	caspase 12
Birc5	8.51E-04	-4.30	3.37E-03	-3.64	2.34E-03	-5.07	Y	1	1	baculoviral IAP repeat-containing 5
Tpx2	3.50E-04	-4.30	7.67E-03	-2.81	2.89E-04	-6.58	Y	1	1	TPX2, microtubule-associated protein homolog (Xenopus laevis) /
Kif18b	2.71E-04	-4.36	2.81E-03	-3.24	4.34E-04	-5.87	Y	1	1	kinesin family member 18B
Mt2	1.73E-09	-4.37	1.21E-06	-2.58	6.42E-10	-7.40	Y	1	1	metallothionein 2
Cd1d1	7.46E-14	-4.40	1.62E-11	-2.95	7.11E-14	-6.56	Y	1	1	CD1d1 antigen
1700025G04Rik	1.27E-04	-4.44	1.60E-04	-4.67	1.39E-03	-4.23	Y	1	1	RIKEN cDNA 1700025G04 gene
Trim16	2.15E-06	-4.45	3.54E-05	-3.43	5.20E-06	-5.77	Y	1	1	tripartite motif-containing 16
Nrm	6.24E-06	-4.46	1.62E-05	-4.28	6.06E-05	-4.64	Y	1	1	nurim (nuclear envelope membrane protein)
Depdc1a	9.40E-04	-4.46	6.43E-03	-3.39	1.60E-03	-5.87	Y	1	1	DEP domain containing 1a
Spag5	2.93E-04	-4.49	5.54E-03	-3.00	2.84E-04	-6.72	Y	1	1	sperm associated antigen 5
Airn	6.43E-04	-4.51	4.32E-04	-5.31	8.47E-03	-3.84	Y	1	1	antisense Igf2r RNA
Cdca3	1.58E-04	-4.52	1.85E-03	-3.33	2.56E-04	-6.13	Y	1	1	cell division cycle associated 3
Kif14	7.44E-04	-4.53	5.37E-03	-3.43	1.28E-03	-5.98	Y	1	1	kinesin family member 14
Creb5	1.87E-14	-4.62	3.61E-13	-3.76	9.21E-14	-5.68	Y	1	1	cAMP responsive element binding protein 5
Tmem195	6.18E-04	-4.72	1.99E-03	-4.15	2.18E-03	-5.37	Y	1	1	transmembrane protein 195
Cstb	9.36E-04	-4.78	8.25E-04	-5.37	8.89E-03	-4.25	Y	1	1	cystatin B
Stmn1	1.92E-04	-4.78	5.85E-04	-4.33	9.08E-04	-5.28	Y	1	1	stathmin 1
Mastl	4.68E-04	-4.81	6.85E-03	-3.22	5.02E-04	-7.17	Y	1	1	microtubule associated serine/threonine kinase-like
Stmn1	2.06E-04	-4.81	6.41E-04	-4.34	9.47E-04	-5.34	Y	1	1	stathmin 1
Prr11	1.83E-04	-4.93	4.56E-03	-3.13	1.57E-04	-7.77	Y	1	1	proline rich 11
Aldh1a1	3.28E-05	-4.95	1.44E-03	-3.09	2.58E-05	-7.92	Y	1	1	aldehyde dehydrogenase family 1, subfamily A1
Chpt1	6.19E-10	-4.99	6.65E-09	-4.18	3.81E-09	-5.94	Y	1	1	choline phosphotransferase 1
Kif2c	4.09E-04	-5.02	2.79E-03	-3.85	8.47E-04	-6.53	Y	1	1	kinesin family member 2C
Neil3	2.34E-04	-5.20	2.37E-03	-3.77	3.96E-04	-7.18	Y	1	1	nei like 3 (E. coli)
Sgol1	7.33E-04	-5.23	9.50E-03	-3.42	7.79E-04	-7.98	Y	1	1	shugoshin-like 1 (S. pombe)
Kif11	3.99E-04	-5.23	3.21E-03	-3.87	7.26E-04	-7.07	Y	1	1	kinesin family member 11
Gas2l3	1.31E-04	-5.24	2.17E-03	-3.56	1.68E-04	-7.71	Y	1	1	growth arrest-specific 2 like 3
Cenpf	2.47E-04	-5.24	1.51E-03	-4.15	6.23E-04	-6.63	Y	1	1	centromere protein F
Smpdl3b	1.02E-11	-5.27	2.74E-12	-6.86	3.26E-09	-4.04	Y	1	1	sphingomyelin phosphodiesterase, acid-like 3B
Kif4	2.58E-04	-5.27	2.30E-03	-3.89	4.73E-04	-7.16	Y	1	1	kinesin family member 4
Kif23	1.81E-04	-5.30	1.90E-03	-3.84	3.12E-04	-7.31	Y	1	1	kinesin family member 23
Kif20a	4.72E-04	-5.40	5.67E-03	-3.65	5.95E-04	-7.99	Y	1	1	kinesin family member 20A
Cep55	1.19E-04	-5.43	1.64E-03	-3.79	1.80E-04	-7.77	Y	1	1	centrosomal protein 55
Esco2	8.76E-04	-5.47	3.91E-03	-4.39	2.17E-03	-6.81	Y	1	1	establishment of cohesion 1 homolog 2 (S. cerevisiae)
2810417H13Rik	8.21E-04	-5.48	5.79E-03	-4.01	1.41E-03	-7.51	Y	1	1	RIKEN cDNA 2810417H13 gene
Nek2	1.40E-04	-5.51	1.89E-03	-3.82	2.08E-04	-7.95	Y	1	1	NIMA (never in mitosis gene a)-related expressed kinase 2
Nap1l3	2.21E-13	-5.60	2.19E-11	-3.78	3.38E-13	-8.31	Y	1	1	nucleosome assembly protein 1-like 3
Atp2b4	6.42E-07	-5.62	2.80E-07	-7.04	4.78E-05	-4.49	Y	1	1	ATPase, Ca++ transporting, plasma membrane 4
Ccnb2	1.69E-04	-5.83	1.96E-03	-4.08	2.73E-04	-8.33	Y	1	1	cyclin B2
Aspm	5.49E-05	-5.85	2.84E-04	-4.87	2.11E-04	-7.04	Y	1	1	asp (abnormal spindle)-like, microcephaly associated (Drosophila)
Lrmp	1.86E-08	-5.89	5.17E-08	-5.68	3.05E-07	-6.10	Y	1	1	lymphoid-restricted membrane protein
Hist1h2ab	1.24E-03	-6.00	8.87E-03	-4.20	1.90E-03	-8.55	Y	1	1	histone cluster 1, H2ab
Nusap1	1.60E-04	-6.06	1.21E-03	-4.56	3.70E-04	-8.04	Y	1	1	nucleolar and spindle associated protein 1
Clec2i	1.26E-08	-6.11	1.02E-10	-15.05	5.23E-04	-2.48	Y	1	1	C-type lectin domain family 2, member i
Pdlim1	8.38E-06	-6.15	1.48E-04	-4.33	1.61E-05	-8.74	Y	1	1	PDZ and LIM domain 1 (elfin)
Gm8736	6.83E-13	-6.41	1.05E-07	-2.31	3.47E-14	-17.80	Y	1	1	predicted gene 8736
Gm8800	7.44E-13	-6.60	8.08E-08	-2.39	4.24E-14	-18.24	Y	1	1	predicted gene 8800
Fam38a	5.69E-08	-6.90	3.51E-08	-8.34	3.87E-06	-5.71	Y	1	1	family with sequence similarity 38, member A
Inpp5d	1.41E-08	-6.91	8.30E-08	-5.98	1.21E-07	-7.98	Y	1	1	inositol polyphosphate-5-phosphatase D
Bub1	3.95E-04	-7.01	8.59E-03	-3.95	3.20E-04	-12.45	Y	1	1	budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae)
Nuf2	3.01E-04	-7.05	4.22E-03	-4.44	3.70E-04	-11.20	Y	1	1	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)
Hmmr	1.01E-04	-7.48	7.48E-04	-5.56	2.59E-04	-10.07	Y	1	1	hyaluronan mediated motility receptor (RHAMM)
Ccna2	2.69E-04	-7.63	2.19E-03	-5.35	5.26E-04	-10.88	Y	1	1	cyclin A2
Pdlim1	2.26E-05	-7.70	3.24E-04	-5.24	4.42E-05	-11.29	Y	1	1	PDZ and LIM domain 1 (elfin)
Cpa6	5.06E-15	-7.72	3.25E-14	-6.74	6.23E-14	-8.86	Y	1	1	carboxypeptidase A6
D17H6S56E-5	8.54E-06	-7.74	2.29E-04	-4.86	1.20E-05	-12.33	Y	1	1	DNA segment, Chr 17, human D6S56E 5
Gem	2.27E-05	-7.98	1.17E-04	-6.54	1.01E-04	-9.74	Y	1	1	GTP binding protein (gene overexpressed in skeletal muscle)
Ermn	6.73E-10	-8.12	3.39E-07	-4.02	3.15E-10	-16.40	Y	1	1	ermin, ERM-like protein
Rgs18	3.06E-04	-8.14	3.53E-03	-5.17	4.37E-04	-12.79	Y	1	1	regulator of G-protein signaling 18
Peci	1.42E-05	-9.11	2.45E-05	-9.24	1.74E-04	-8.98	Y	1	1	peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase
S1pr1	1.87E-13	-9.98	1.29E-14	-18.55	5.04E-10	-5.36	Y	1	1	sphingosine-1-phosphate receptor 1
Gpr128	1.59E-14	-11.47	5.76E-06	-1.85	1.31E-16	-71.24	Y	1	1	G protein-coupled receptor 128
Tmem159	2.49E-12	-12.48	9.50E-13	-17.36	5.30E-10	-8.96	Y	1	1	transmembrane protein 159
A930038C07Rik	3.48E-10	-14.70	2.40E-10	-18.56	3.01E-08	-11.65	Y	1	1	RIKEN cDNA A930038C07 gene
Atp2a3	2.53E-10	-14.95	5.69E-09	-9.84	9.07E-10	-22.71	Y	1	1	ATPase, Ca++ transporting, ubiquitous
Sccpdh	1.51E-06	-15.03	1.65E-05	-10.31	5.23E-06	-21.91	Y	1	1	saccharopine dehydrogenase (putative)
Wls	1.85E-07	-15.38	7.90E-07	-13.15	1.72E-06	-17.97	Y	1	1	wntless homolog (Drosophila)
Slc27a6	6.19E-14	-16.05	1.64E-12	-10.46	2.37E-13	-24.62	Y	1	1	solute carrier family 27 (fatty acid transporter), member 6
Phyh	2.60E-15	-17.08	1.38E-14	-14.62	3.80E-14	-19.96	Y	1	1	phytanoyl-CoA hydroxylase
Mr1	2.37E-13	-17.81	7.15E-13	-16.87	5.51E-12	-18.80	Y	1	1	major histocompatibility complex, class I-related
Hadh	1.45E-11	-18.48	2.01E-09	-8.82	1.65E-11	-38.75	Y	1	1	hydroxyacyl-Coenzyme A dehydrogenase
Lxn	9.05E-08	-24.69	4.33E-07	-20.13	8.14E-07	-30.29	Y	1	1	latexin

Macc1	1.28E-14	-25.02	3.37E-13	-15.30	5.05E-14	-40.90	Y	1	1	metastasis associated in colon cancer 1
Rny1	9.90E-10	-28.06	6.78E-09	-21.51	8.69E-09	-36.62	Y	1	1	RNA, Y1 small cytoplasmic, Ro-associated
Aldoc	1.48E-08	-41.38	6.85E-07	-18.72	2.58E-08	-91.49	Y	1	1	aldolase C, fructose-bisphosphate

	CD8IL13+ vs CD8IL13-			**CD8IL13+ vs CD8IL13- & alloCD8**			**CD8IL13+ vs alloCD8**							
Supplemental Table 1 Gene Symbol	p-value (sAg1 and sAg3 vs. 8uvmo-2 and 8uvmo-3)	FDR (sAg1 and sAg3 vs. 8uvmo-2 and 8uvmo-3)	Fold-Change (sAg1 and sAg3 vs. 8uvmo-2 and 8uvmo-3)	p-value (sAg1 and sAg3 vs. 8uvmo-2 and 8uvmo-3 and CD8bm1)	FDR (sAg1 and sAg3 vs. 8uvmo-2 and 8uvmo-3 and CD8bm1)	Fold-Change (sAg1 and sAg3 vs. 8uvmo-2 and 8uvmo-3 and CD8bm1)	p-value (sAg1 and sAg3 vs. CD8bm1)	FDR (sAg1 and sAg3 vs. CD8bm1)	Fold-Change (sAg1 and sAg3 vs. CD8bm1)	all p < 0.01	any fold > 3	all fold > 3	same direction	gene description
	8.37E-21	3.61E-17	46.63	2.23E-21	1.93E-17	46.16	1.95E-19	3.31E-16	45.23	1	1	1	Y	
Amelx	2.20E-15	6.32E-13	32.10	4.07E-16	1.97E-13	34.78	1.64E-14	2.48E-12	40.81	1	1	1	Y	amelogenin X chromosome
Il5	1.32E-13	1.71E-11	30.03	2.74E-14	5.40E-12	31.69	1.30E-12	7.97E-11	35.28	1	1	1	Y	interleukin 5
Tm4sf19	2.96E-17	2.55E-14	25.57	4.13E-17	3.30E-14	18.06	1.86E-13	1.76E-11	9.01	1	1	1	Y	transmembrane 4 L six family member 19
Il13	3.00E-12	2.11E-10	15.71	4.01E-13	4.54E-11	17.95	7.98E-12	3.42E-10	23.41	1	1	1	Y	interleukin 13
Gabra1	4.49E-17	3.52E-14	14.21	1.09E-17	1.26E-14	14.35	7.74E-16	1.97E-13	14.64	1	1	1	Y	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 1
I830127L07Rik	4.32E-12	2.85E-10	6.55	2.96E-14	5.64E-12	11.16	1.02E-14	1.62E-12	32.42	1	1	1	Y	RIKEN cDNA I830127L07 gene
Clgn	1.92E-13	2.36E-11	5.70	4.49E-16	1.97E-13	10.97	5.42E-17	2.44E-14	40.66	1	1	1	Y	calmegin
Mest	6.91E-21	3.61E-17	10.98	2.05E-21	1.93E-17	10.72	2.26E-19	3.31E-16	10.22	1	1	1	Y	mesoderm specific transcript
Ccr8	4.73E-15	1.12E-12	9.75	1.77E-15	5.90E-13	9.23	2.86E-13	2.41E-11	8.25	1	1	1	Y	chemokine (C-C motif) receptor 8
Prl2c5	6.01E-11	2.42E-09	7.83	1.27E-11	7.46E-10	8.11	5.16E-10	1.09E-08	8.71	1	1	1	Y	prolactin family 2, subfamily c, member 5
Ctsg	2.45E-15	6.71E-13	7.44	7.28E-16	2.93E-13	7.30	7.39E-14	8.50E-12	7.03	1	1	1	Y	cathepsin G
Tubb6	6.12E-15	1.38E-12	3.95	6.63E-18	8.43E-15	7.28	4.11E-19	4.98E-16	24.75	1	1	1	Y	tubulin, beta 6
Gm9766	5.05E-12	3.29E-10	5.19	3.20E-13	3.70E-11	6.15	1.90E-12	1.06E-10	8.65	1	1	1	Y	predicted gene 9766
Penk	1.80E-11	9.18E-10	8.90	1.76E-10	6.63E-09	5.47	2.26E-04	7.37E-04	2.07	1	1	0	Y	preproenkephalin
B4galnt2	1.50E-07	1.61E-06	1.83	2.13E-14	4.56E-12	5.45	7.91E-18	5.93E-15	48.11	1	1	0	Y	beta-1,4-N-acetyl-galactosaminyl transferase 2
Epdr1	1.24E-14	2.55E-12	5.46	3.72E-15	1.06E-12	5.37	3.73E-13	2.94E-11	5.20	1	1	1	Y	ependymin related protein 1 (zebrafish)
Hcn1	9.65E-18	1.04E-14	5.16	3.01E-18	5.22E-15	5.05	3.54E-16	1.07E-13	4.84	1	1	1	Y	hyperpolarization-activated, cyclic nucleotide-gated K+ 1
Edil3	1.03E-16	6.58E-14	6.51	3.05E-16	1.71E-13	4.90	1.50E-11	5.71E-10	2.78	1	1	0	Y	EGF-like repeats and discoidin I-like domains 3
Arntl	2.19E-17	2.10E-14	5.68	2.54E-17	2.20E-14	4.81	6.76E-14	8.04E-12	3.44	1	1	1	Y	aryl hydrocarbon receptor nuclear translocator-like
Ctla2a	3.07E-13	3.42E-11	8.76	9.78E-12	6.32E-10	4.76	8.52E-03	1.66E-02	1.41	1	1	0	Y	cytotoxic T lymphocyte-associated protein 2 alpha
Olfm3	8.82E-14	1.27E-11	4.79	2.59E-14	5.24E-12	4.73	2.41E-12	1.28E-10	4.62	1	1	1	Y	olfactomedin 3
Cd4	2.34E-14	4.25E-12	4.09	1.46E-15	4.96E-13	4.72	9.28E-15	1.54E-12	6.28	1	1	1	Y	CD4 antigen
Gja5	3.23E-09	6.27E-08	3.57	5.75E-11	2.60E-09	4.70	4.89E-11	1.51E-09	8.17	1	1	1	Y	gap junction protein, alpha 5
Ctss	6.55E-09	1.13E-07	4.16	6.57E-10	1.94E-08	4.66	5.80E-09	8.35E-08	5.83	1	1	1	Y	cathepsin S
Dusp4	7.44E-14	1.10E-11	4.78	2.91E-14	5.60E-12	4.58	4.92E-12	2.24E-10	4.21	1	1	1	Y	dual specificity phosphatase 4
Mcc	1.67E-18	2.45E-15	4.28	2.48E-19	6.14E-16	4.52	7.06E-18	5.56E-15	5.03	1	1	1	Y	mutated in colorectal cancers
Ly6g5b	9.95E-12	5.74E-10	7.21	1.35E-10	5.39E-09	4.49	6.94E-04	1.94E-03	1.75	1	1	0	Y	lymphocyte antigen 6 complex, locus G5B
Serpinb9g	1.38E-04	5.29E-04	3.34	4.98E-06	3.24E-05	4.48	3.23E-06	1.81E-05	8.06	1	1	1	Y	serine (or cysteine) peptidase inhibitor, clade B, member 9g
Tcrg-C	2.29E-16	1.23E-13	6.83	2.65E-15	8.51E-13	4.42	4.73E-08	4.89E-07	1.86	1	1	0	Y	T-cell receptor gamma, constant region
Tm4sf1	2.01E-16	1.16E-13	4.31	4.19E-17	3.30E-14	4.40	2.17E-15	4.50E-13	4.59	1	1	1	Y	transmembrane 4 superfamily member 1
	8.23E-10	1.97E-08	3.33	1.50E-11	8.44E-10	4.30	1.38E-11	5.30E-10	7.15	1	1	1	Y	
Il3	2.08E-04	7.59E-04	1.70	2.99E-10	1.02E-08	4.28	1.55E-13	1.56E-11	27.10	1	1	0	Y	interleukin 3
Pecam1	2.02E-05	1.01E-04	3.14	4.18E-07	3.97E-06	4.28	1.98E-07	1.65E-06	7.91	1	1	1	Y	platelet/endothelial cell adhesion molecule 1
Spats2	2.07E-13	2.51E-11	3.02	9.84E-16	3.79E-13	4.27	2.39E-16	8.37E-14	8.51	1	1	1	Y	spermatogenesis associated, serine-rich 2
1810011H11Rik	7.04E-15	1.56E-12	4.81	7.49E-15	1.85E-12	4.17	1.43E-11	5.47E-10	3.13	1	1	1	Y	RIKEN cDNA 1810011H11 gene
Fam169b	1.73E-12	1.37E-10	3.27	4.03E-14	6.85E-12	4.05	6.02E-14	7.35E-12	6.21	1	1	1	Y	family with sequence similarity 169, member B
	1.91E-12	1.50E-10	5.40	7.73E-12	5.34E-10	4.05	6.11E-07	4.33E-06	2.27	1	1	0	Y	
Lepr	1.41E-14	2.77E-12	4.26	8.09E-15	1.97E-12	3.95	3.29E-12	1.65E-10	3.40	1	1	1	Y	leptin receptor
Gmfg	4.47E-08	5.80E-07	1.50	3.22E-16	1.74E-13	3.95	5.23E-20	1.55E-16	27.30	1	1	0	Y	glia maturation factor, gamma
Cd2ap	2.03E-10	6.46E-09	3.27	9.16E-12	6.08E-10	3.84	2.95E-11	1.00E-09	5.28	1	1	1	Y	CD2-associated protein
Tnfsf4	9.09E-08	1.04E-06	3.01	2.32E-09	5.41E-08	3.76	2.53E-09	4.14E-08	5.84	1	1	1	Y	tumor necrosis factor (ligand) superfamily, member 4
Serpinb9f	2.52E-04	8.99E-04	2.75	7.33E-06	4.52E-05	3.65	3.25E-06	1.82E-05	6.45	1	1	0	Y	serine (or cysteine) peptidase inhibitor, clade B, member 9f
Areg	1.64E-12	1.33E-10	4.04	1.32E-12	1.18E-10	3.64	1.04E-09	1.94E-08	2.97	1	1	0	Y	amphiregulin
Ebi3	6.81E-10	1.68E-08	3.09	2.90E-11	1.47E-09	3.63	8.24E-11	2.32E-09	4.98	1	1	1	Y	Epstein-Barr virus induced gene 3
Kif3a	6.57E-17	4.53E-14	5.20	8.87E-16	3.49E-13	3.54	4.18E-08	4.41E-07	1.64	1	1	0	Y	kinesin family member 3A
Serpinb9g	7.68E-04	2.36E-03	2.78	4.84E-05	2.23E-04	3.49	4.10E-05	1.66E-04	5.50	1	1	0	Y	serine (or cysteine) peptidase inhibitor, clade B, member 9g
Farp1	1.98E-14	3.63E-12	4.89	1.94E-13	2.45E-11	3.46	9.26E-07	6.19E-06	1.73	1	1	0	Y	FERM, RhoGEF (Arhgef) and pleckstrin domain protein 1 (chondrocyt
	3.83E-11	1.72E-09	2.69	4.08E-13	4.57E-11	3.45	2.20E-13	2.01E-11	5.65	1	1	0	Y	
Rtn1	7.85E-15	1.69E-12	3.58	3.15E-15	9.58E-13	3.45	5.85E-13	4.15E-11	3.20	1	1	1	Y	reticulon 1
Tnfsf11	2.48E-13	2.89E-11	3.03	1.39E-14	3.17E-12	3.42	7.29E-14	8.50E-12	4.37	1	1	1	Y	tumor necrosis factor (ligand) superfamily, member 11
Kynu	3.43E-11	1.56E-09	3.02	2.15E-12	1.80E-10	3.40	1.19E-11	4.70E-10	4.30	1	1	1	Y	kynureninase (L-kynurenine hydrolase)
Akr1c12	4.44E-13	4.56E-11	4.82	5.04E-12	3.70E-10	3.37	2.81E-05	1.19E-04	1.65	1	1	0	Y	aldo-keto reductase family 1, member C12
Serpinb9e	2.59E-03	6.74E-03	2.39	6.51E-05	2.87E-04	3.35	1.34E-05	6.23E-05	6.54	1	1	0	Y	serine (or cysteine) peptidase inhibitor, clade B, member 9e
Cyp11a1	3.98E-13	4.16E-11	3.57	2.25E-13	2.68E-11	3.34	8.05E-11	2.28E-09	2.94	1	1	0	Y	cytochrome P450, family 11, subfamily a, polypeptide 1
Pam	1.59E-11	8.26E-10	3.33	4.11E-12	3.14E-10	3.34	2.56E-10	6.04E-09	3.36	1	1	1	Y	peptidylglycine alpha-amidating monooxygenase
Cdkn2a	1.01E-07	1.14E-06	2.26	2.57E-10	9.05E-09	3.17	2.34E-11	8.23E-10	6.25	1	1	0	Y	cyclin-dependent kinase inhibitor 2A
Amtn	1.73E-14	3.28E-12	3.13	3.87E-15	1.08E-12	3.16	2.18E-13	2.01E-11	3.24	1	1	1	Y	amelotin
Ptpre	3.55E-11	1.60E-09	2.08	1.32E-14	3.09E-12	3.15	3.16E-16	1.04E-13	7.24	1	1	0	Y	protein tyrosine phosphatase, receptor type, E
Gpr97	1.77E-18	2.45E-15	4.98	7.04E-17	5.08E-14	3.14	2.40E-05	1.03E-04	1.25	1	1	0	Y	G protein-coupled receptor 97
Igf2bp2	1.93E-13	2.36E-11	3.03	3.26E-14	6.04E-12	3.13	1.04E-12	6.63E-11	3.35	1	1	1	Y	insulin-like growth factor 2 mRNA binding protein 2
Rcsd1	6.17E-15	1.38E-12	3.95	2.48E-14	5.12E-12	3.13	3.10E-09	4.92E-08	1.96	1	1	0	Y	RCSD domain containing 1
Syt11	7.41E-08	8.83E-07	1.72	7.15E-13	7.18E-11	3.08	1.50E-15	3.38E-13	9.95	1	1	0	Y	synaptotagmin XI
Pyhin1	2.21E-03	5.89E-03	1.53	2.49E-08	3.72E-07	3.03	2.08E-11	7.41E-10	11.89	1	1	0	Y	pyrin and HIN domain family, member 1
Kcnk10	6.57E-11	2.61E-09	3.44	9.11E-11	3.89E-09	3.01	2.14E-07	1.75E-06	2.31	1	1	0	Y	potassium channel, subfamily K, member 10
	1.94E-04	7.14E-04	1.53	5.97E-10	1.78E-08	3.01	4.21E-13	3.27E-11	11.63	1	1	0	Y	
Rnf213	4.45E-11	1.93E-09	2.96	9.89E-12	6.37E-10	3.00	4.43E-10	9.56E-09	3.09	1	1	0	Y	ring finger protein 213
H1f0	1.57E-12	1.28E-10	2.70	1.19E-13	1.59E-11	2.95	9.62E-13	6.31E-11	3.52	1	1	0	Y	H1 histone family, member 0
Hpcal1	1.24E-08	1.95E-07	2.53	4.64E-10	1.45E-08	2.94	9.47E-10	1.82E-08	3.95	1	1	0	Y	hippocalcin-like 1
	1.24E-08	1.95E-07	2.53	4.64E-10	1.45E-08	2.94	9.47E-10	1.82E-08	3.95	1	1	0	Y	
Dusp1	5.36E-08	6.77E-07	2.21	2.37E-10	8.50E-09	2.93	3.78E-11	1.23E-09	5.16	1	1	0	Y	dual specificity phosphatase 1
Mtmr7	6.73E-11	2.64E-09	2.82	1.11E-11	6.82E-10	2.93	2.86E-10	6.60E-09	3.15	1	1	0	Y	myotubularin related protein 7
Cd226	1.99E-05	9.96E-05	1.83	5.24E-09	1.05E-07	2.92	5.13E-11	1.57E-09	7.40	1	1	0	Y	CD226 antigen
Ndst1	6.62E-12	4.08E-10	2.14	1.29E-14	3.06E-12	2.89	1.26E-15	2.92E-13	5.30	1	1	0	Y	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1
Acpp	4.79E-07	4.27E-06	1.98	3.95E-10	1.29E-08	2.88	1.24E-11	4.88E-10	6.12	1	1	0	Y	acid phosphatase, prostate
Klk1b11	1.79E-04	6.67E-04	1.86	1.75E-07	1.92E-06	2.84	3.30E-09	5.19E-08	6.61	1	1	0	Y	kallikrein 1-related peptidase b11
Rnf213	3.02E-12	2.12E-10	2.75	5.01E-13	5.43E-11	2.84	1.45E-11	5.53E-10	3.04	1	1	0	Y	ring finger protein 213
Igsf9b	5.07E-10	1.31E-08	2.19	2.46E-12	2.03E-10	2.82	5.26E-13	3.84E-11	4.71	1	1	0	Y	immunoglobulin superfamily, member 9B
	2.45E-06	1.65E-05	2.63	3.88E-07	3.74E-06	2.79	3.71E-06	2.04E-05	3.14	1	1	0	Y	
1810009J06Rik	9.19E-06	5.13E-05	2.11	6.30E-08	8.14E-07	2.78	1.01E-08	1.32E-07	4.83	1	1	0	Y	RIKEN cDNA 1810009J06 gene
Rnf213	1.33E-10	4.59E-09	2.60	1.43E-11	8.15E-10	2.77	1.74E-10	4.37E-09	3.15	1	1	0	Y	ring finger protein 213
Gm1527	6.87E-07	5.76E-06	2.40	3.11E-08	4.48E-07	2.77	5.90E-08	5.93E-07	3.67	1	1	0	Y	predicted gene 1527
Gatm	6.44E-11	2.57E-09	2.49	3.92E-12	3.05E-10	2.75	2.04E-11	7.29E-10	3.35	1	1	0	Y	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
Hpgds	1.28E-06	9.63E-06	2.53	1.45E-07	1.65E-06	2.74	9.11E-07	6.13E-06	3.22	1	1	0	Y	hematopoietic prostaglandin D synthase
Rasgrp1	7.71E-08	9.14E-07	2.52	1.01E-08	1.76E-07	2.67	1.12E-07	1.02E-06	3.00	1	1	0	Y	RAS guanyl releasing protein 1
Endod1	1.54E-10	5.17E-09	3.17	4.71E-10	1.46E-08	2.65	8.62E-06	4.25E-05	1.84	1	1	0	Y	endonuclease domain containing 1
1810009J06Rik	1.78E-05	9.08E-05	2.00	9.88E-08	1.19E-06	2.64	1.18E-08	1.51E-07	4.62	1	1	0	Y	RIKEN cDNA 1810009J06 gene
Tarm1	2.15E-10	6.71E-09	2.40	1.44E-11	8.18E-10	2.63	8.13E-11	2.29E-09	3.15	1	1	0	Y	T cell-interacting, activating receptor on myeloid cells 1
Crim1	3.67E-04	1.25E-03	1.40	3.42E-10	1.14E-08	2.62	1.41E-13	1.46E-11	9.24	1	1	0	Y	cysteine rich transmembrane BMP regulator 1 (chordin like)
Eml1	2.03E-07	2.08E-06	2.03	1.00E-09	2.73E-08	2.62	1.65E-10	4.20E-09	4.35	1	1	0	Y	echinoderm microtubule associated protein like 1
Lrrc49	2.80E-10	8.25E-09	2.12	3.20E-12	2.54E-10	2.55	1.77E-12	9.99E-11	3.71	1	1	0	Y	leucine rich repeat containing 49
Tnip3	8.70E-09	1.44E-07	1.69	9.37E-13	8.73E-11	2.49	8.29E-15	1.40E-12	5.42	1	1	0	Y	TNFAIP3 interacting protein 3
Fut8	1.26E-07	1.39E-06	2.06	1.72E-09	4.25E-08	2.48	8.72E-10	1.70E-08	3.61	1	1	0	Y	fucosyltransferase 8
Tmem229b	1.21E-06	9.22E-06	1.72	4.25E-10	1.36E-08	2.47	6.52E-12	2.85E-10	5.08	1	1	0	Y	transmembrane protein 229B
Elovl4	1.76E-08	2.62E-07	2.12	3.96E-10	1.29E-08	2.47	4.12E-10	9.03E-09	3.35	1	1	0	Y	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3,

BC094916	3.12E-05	1.46E-04	2.10	1.21E-06	9.81E-06	2.45	1.14E-06	7.41E-06	3.35	1	1	0	Y	cDNA sequence BC094916
Gng12	7.72E-10	1.87E-08	1.97	4.31E-12	3.26E-10	2.44	1.05E-12	6.67E-11	3.75	1	1	0	Y	guanine nucleotide binding protein (G protein), gamma 12
4930486L24Rik	2.20E-12	1.68E-10	3.01	1.21E-11	7.16E-10	2.44	2.75E-06	1.57E-05	1.61	1	1	0	Y	RIKEN cDNA 4930486L24 gene
Dip2c	3.29E-09	6.36E-08	1.79	2.39E-12	1.98E-10	2.43	8.60E-14	9.74E-12	4.46	1	1	0	Y	DIP2 disco-interacting protein 2 homolog C (Drosophila)
Ncam2	1.59E-09	3.43E-08	1.98	1.14E-11	6.91E-10	2.43	3.54E-12	1.72E-10	3.63	1	1	0	Y	neural cell adhesion molecule 2
St3gal6	6.20E-08	7.62E-07	1.61	3.17E-12	2.53E-10	2.41	1.65E-14	2.48E-12	5.42	1	1	0	Y	ST3 beta-galactoside alpha-2,3-sialyltransferase 6
Prdx4	7.19E-06	4.17E-05	2.07	2.73E-07	2.77E-06	2.39	3.12E-07	2.39E-06	3.19	1	1	0	Y	peroxiredoxin 4
Gbp2	9.50E-04	2.84E-03	1.80	8.52E-06	5.14E-05	2.38	7.93E-07	5.42E-06	4.14	1	1	0	Y	guanylate binding protein 2
Arhgap6	8.32E-08	9.72E-07	1.90	3.96E-10	1.29E-08	2.38	6.66E-11	1.95E-09	3.74	1	1	0	Y	Rho GTPase activating protein 6
Dip2c	5.70E-08	7.11E-07	1.77	5.65E-11	2.58E-09	2.37	2.33E-12	1.25E-10	4.25	1	1	0	Y	DIP2 disco-interacting protein 2 homolog C (Drosophila)
Fam46c	1.18E-03	3.41E-03	1.30	3.73E-10	1.22E-08	2.34	9.11E-14	1.02E-11	7.66	1	1	0	Y	family with sequence similarity 46, member C
Hgfac	9.81E-08	1.12E-06	1.96	1.21E-09	3.19E-08	2.34	5.50E-10	1.14E-08	3.35	1	1	0	Y	hepatocyte growth factor activator
Hbegf	2.10E-04	7.66E-04	1.39	8.40E-10	2.39E-08	2.32	6.55E-13	4.63E-11	6.46	1	1	0	Y	heparin-binding EGF-like growth factor
Slc24a3	3.01E-05	1.42E-04	1.48	6.63E-10	1.95E-08	2.30	1.42E-12	8.54E-11	5.57	1	1	0	Y	solute carrier family 24 (sodium/potassium/calcium exchanger),
Hcst	2.82E-08	3.93E-07	1.80	6.47E-11	2.88E-09	2.29	5.73E-12	2.55E-10	3.74	1	1	0	Y	hematopoietic cell signal transducer
Adam22	8.64E-08	1.01E-06	1.87	7.09E-10	2.06E-08	2.26	2.08E-10	5.05E-09	3.30	1	1	0	Y	a disintegrin and metallopeptidase domain 22
Slc41a2	1.05E-05	5.76E-05	1.78	5.53E-08	7.29E-07	2.24	6.73E-09	9.47E-08	3.55	1	1	0	Y	solute carrier family 41, member 2
2810055G20Rik	6.63E-03	1.50E-02	1.43	1.22E-06	9.86E-06	2.24	3.26E-09	5.14E-08	5.47	1	1	0	Y	RIKEN cDNA 2810055G20 gene
Dennd5a	3.81E-03	9.37E-03	1.23	3.88E-10	1.27E-08	2.22	5.62E-14	6.92E-12	7.22	1	1	0	Y	DENN/MADD domain containing 5A
Rab4a	8.59E-12	5.07E-10	1.85	5.50E-14	8.59E-12	2.21	1.74E-14	2.59E-12	3.16	1	1	0	Y	RAB4A, member RAS oncogene family
Sdr42e1	6.07E-16	2.41E-13	3.03	2.60E-14	5.24E-12	2.19	2.50E-03	5.81E-03	1.15	1	1	0	Y	short chain dehydrogenase/reductase family 42E, member 1
Impact	1.46E-07	1.58E-06	1.55	1.70E-11	9.38E-10	2.18	1.40E-13	1.46E-11	4.28	1	1	0	Y	imprinted and ancient
Irf1	2.05E-05	1.02E-04	1.68	4.64E-08	6.25E-07	2.18	2.38E-09	3.94E-08	3.67	1	1	0	Y	interferon regulatory factor 1
Pmepa1	6.88E-03	1.54E-02	1.22	1.60E-09	4.02E-08	2.13	2.61E-13	2.27E-11	6.49	1	1	0	Y	prostate transmembrane protein, androgen induced 1
Ly96	4.42E-04	1.46E-03	1.30	8.53E-10	2.42E-08	2.06	4.49E-13	3.42E-11	5.17	1	1	0	Y	lymphocyte antigen 96
Il10ra	8.89E-05	3.61E-04	1.44	1.36E-08	2.24E-07	2.00	7.74E-11	2.20E-09	3.86	1	1	0	Y	interleukin 10 receptor, alpha
Edaradd	4.71E-03	1.12E-02	1.23	3.42E-09	7.42E-08	1.98	8.53E-13	5.77E-11	5.20	1	1	0	Y	EDAR (ectodysplasin-A receptor)-associated death domain
Dip2c	1.51E-04	5.72E-04	1.51	2.14E-07	2.28E-06	1.96	5.53E-09	8.04E-08	3.30	1	1	0	Y	DIP2 disco-interacting protein 2 homolog C (Drosophila)
Zbtb7b	4.62E-09	8.35E-08	1.57	4.37E-12	3.29E-10	1.96	1.93E-13	1.82E-11	3.06	1	1	0	Y	zinc finger and BTB domain containing 7B
Unc119	6.25E-06	3.68E-05	1.31	1.00E-11	6.42E-10	1.95	7.50E-15	1.31E-12	4.36	1	1	0	Y	unc-119 homolog (C. elegans)
Stox2	6.06E-09	1.06E-07	1.47	7.84E-13	7.59E-11	1.94	7.91E-15	1.37E-12	3.37	1	1	0	Y	storkhead box 2
Tmem229b	3.75E-07	3.48E-06	1.52	2.80E-10	9.70E-09	1.93	8.23E-12	3.51E-10	3.09	1	1	0	Y	transmembrane protein 229B
Atp10b	7.29E-07	6.05E-06	1.41	3.83E-11	1.84E-09	1.91	1.78E-13	1.72E-11	3.52	1	1	0	Y	ATPase, class V, type 10B
AI607873	4.21E-04	1.40E-03	1.50	1.16E-06	9.44E-06	1.91	4.34E-08	4.57E-07	3.07	1	1	0	Y	expressed sequence AI607873
Tgtp1	3.22E-03	8.12E-03	1.40	3.64E-06	2.49E-05	1.88	4.08E-08	4.32E-07	3.34	1	1	0	Y	T-cell specific GTPase 1
Gmfg	4.72E-04	1.55E-03	1.39	1.70E-07	1.89E-06	1.84	1.30E-09	2.34E-08	3.24	1	1	0	Y	glia maturation factor, gamma
Lsp1	3.53E-03	8.79E-03	1.39	4.61E-06	3.04E-05	1.82	5.63E-08	5.69E-07	3.15	1	1	0	Y	lymphocyte specific 1
Tgtp1	2.38E-03	6.28E-03	1.42	5.07E-06	3.29E-05	1.82	1.02E-07	9.46E-07	3.02	1	1	0	Y	T-cell specific GTPase 1
Sfmbt1	2.44E-04	8.75E-04	1.29	4.71E-09	9.59E-08	1.80	7.37E-12	3.19E-10	3.47	1	1	0	Y	Scm-like with four mbt domains 1
Gtpbp10	5.50E-03	1.28E-02	1.24	1.68E-07	1.87E-06	1.75	1.81E-10	4.50E-09	3.45	1	1	0	Y	GTP-binding protein 10 (putative)
Rap2a	6.98E-04	2.17E-03	1.17	4.67E-10	1.45E-08	1.60	1.57E-13	1.58E-11	3.00	1	1	0	Y	RAS related protein 2a
P2rx4	7.62E-03	1.68E-02	-1.18	6.83E-08	8.72E-07	-1.63	3.87E-11	1.25E-09	-3.09	1	1	0	Y	purinergic receptor P2X, ligand-gated ion channel 4
Creb3l2	4.97E-03	1.17E-02	-1.22	1.14E-07	1.35E-06	-1.67	1.09E-10	2.95E-09	-3.12	1	1	0	Y	cAMP responsive element binding protein 3-like 2
Pgap1	2.97E-03	7.57E-03	-1.38	3.49E-06	2.40E-05	-1.80	4.12E-08	4.36E-07	-3.06	1	1	0	Y	post-GPI attachment to proteins 1
Arhgdig	2.32E-06	1.58E-05	-1.38	1.66E-10	6.30E-09	-1.83	8.61E-13	5.77E-11	-3.21	1	1	0	Y	Rho GDP dissociation inhibitor (GDI) gamma
Tmem48	1.88E-04	6.96E-04	-1.35	1.42E-08	2.33E-07	-1.83	4.79E-11	1.48E-09	-3.40	1	1	0	Y	transmembrane protein 48
Nr2c1	5.66E-08	7.07E-07	-1.46	1.55E-11	8.64E-10	-1.86	2.40E-13	2.12E-11	-3.04	1	1	0	Y	nuclear receptor subfamily 2, group C, member 1
Idh1	1.03E-03	3.04E-03	-1.46	2.39E-06	1.75E-05	-1.87	6.37E-08	6.32E-07	-3.06	1	1	0	Y	isocitrate dehydrogenase 1 (NADP+), soluble
Flrt3	3.45E-07	3.25E-06	-1.39	1.04E-11	6.51E-10	-1.91	3.65E-14	4.96E-12	-3.58	1	1	0	Y	fibronectin leucine rich transmembrane protein 3
Zdhhc23	3.24E-03	8.16E-03	-1.29	5.08E-08	6.77E-07	-1.94	4.52E-11	1.42E-09	-4.38	1	1	0	Y	zinc finger, DHHC domain containing 23
Cdyl2	1.20E-06	9.16E-06	-1.53	1.15E-09	3.08E-08	-1.94	3.78E-11	1.23E-09	-3.10	1	1	0	Y	chromodomain protein, Y chromosome-like 2
Tjp2	5.11E-05	2.25E-04	-1.32	2.41E-10	8.61E-09	-1.94	2.36E-13	2.10E-11	-4.22	1	1	0	Y	tight junction protein 2
Magi3	9.12E-03	1.96E-02	-1.26	1.11E-07	1.32E-06	-1.94	6.81E-11	1.98E-09	-4.63	1	1	0	Y	membrane associated guanylate kinase, WW and PDZ domain containin
Prss16	2.26E-04	8.16E-04	-1.40	3.08E-08	4.44E-07	-1.95	1.43E-10	3.74E-09	-3.74	1	1	0	Y	protease, serine, 16 (thymus)
Pak1	5.34E-06	3.21E-05	-1.44	2.78E-10	9.68E-09	-2.02	1.12E-12	7.03E-11	-3.99	1	1	0	Y	p21 protein (Cdc42/Rac)-activated kinase 1
Cd1d1	2.03E-06	1.41E-05	-1.63	2.76E-09	6.17E-08	-2.11	1.16E-10	3.12E-09	-3.51	1	1	0	Y	CD1d1 antigen
Trove2	4.51E-07	4.06E-06	-1.64	4.85E-10	1.49E-08	-2.13	1.89E-11	6.91E-10	-3.59	1	1	0	Y	TROVE domain family, member 2
Fam117b	1.52E-13	1.93E-11	-1.78	6.24E-16	2.58E-13	-2.15	1.31E-16	5.03E-14	-3.14	1	1	0	Y	family with sequence similarity 117, member B
Bcat2	5.91E-12	3.72E-10	-1.85	4.56E-14	7.32E-12	-2.19	1.78E-14	2.62E-12	-3.07	1	1	0	Y	branched chain aminotransferase 2, mitochondrial
Taf1a	3.76E-06	2.38E-05	-1.38	5.65E-12	4.10E-10	-2.22	4.23E-15	7.75E-13	-5.75	1	1	0	Y	TATA box binding protein (Tbp)-associated factor, RNA polymerase
Nap1l3	1.41E-08	2.17E-07	-1.70	1.16E-11	6.96E-10	-2.25	4.36E-13	3.37E-11	-3.90	1	1	0	Y	nucleosome assembly protein 1-like 3
Atp2b4	5.24E-10	1.35E-08	-1.70	1.97E-13	2.47E-11	-2.31	4.52E-15	8.18E-13	-4.26	1	1	0	Y	ATPase, Ca++ transporting, plasma membrane 4
Arhgap42	2.11E-03	5.65E-03	-1.73	1.43E-05	8.01E-05	-2.34	8.26E-07	5.62E-06	-4.29	1	1	0	Y	Rho GTPase activating protein 42
2510002D24Rik	1.01E-06	7.92E-06	-1.69	4.06E-10	1.31E-08	-2.37	6.96E-12	3.03E-10	-4.67	1	1	0	Y	RIKEN cDNA 2510002D24 gene
Rreb1	1.17E-07	1.30E-06	-1.56	3.52E-12	2.79E-10	-2.38	1.32E-14	2.08E-12	-5.49	1	1	0	Y	ras responsive element binding protein 1
Tmem180	1.07E-10	3.85E-09	-2.11	2.78E-12	2.28E-10	-2.40	4.36E-12	2.06E-10	-3.13	1	1	0	Y	transmembrane protein 180
D17H6S56E-5	3.15E-04	1.09E-03	-1.71	4.36E-07	4.11E-06	-2.44	9.75E-09	1.28E-07	-4.96	1	1	0	Y	DNA segment, Chr 17, human D6S56E 5
Mcee	3.15E-12	2.16E-10	-3.18	3.20E-11	1.57E-09	-2.46	7.16E-05	2.72E-04	-1.47	1	1	0	Y	methylmalonyl CoA epimerase
Mt2	2.06E-07	2.11E-06	-2.10	4.60E-09	9.43E-08	-2.47	3.99E-09	6.12E-08	-3.41	1	1	0	Y	metallothionein 2
Vcl	8.22E-08	9.63E-07	-2.18	3.15E-09	6.96E-08	-2.47	5.84E-09	8.38E-08	-3.20	1	1	0	Y	vinculin
Gipc2	2.76E-04	9.72E-04	-1.30	1.93E-11	1.05E-09	-2.48	3.62E-15	6.95E-13	-8.93	1	1	0	Y	GIPC PDZ domain containing family, member 2
Rnpepl1	2.82E-13	3.20E-11	-1.90	4.09E-16	1.97E-13	-2.49	3.17E-17	1.78E-14	-4.27	1	1	0	Y	arginyl aminopeptidase (aminopeptidase B)-like 1
Egr1	2.88E-15	7.55E-13	-3.13	1.45E-14	3.26E-12	-2.55	4.49E-09	6.74E-08	-1.68	1	1	0	Y	early growth response 1
Vcan	8.99E-04	2.70E-03	-1.12	4.33E-16	1.97E-13	-2.56	9.54E-21	7.51E-17	-13.30	1	1	0	Y	versican
Cdh17	8.49E-10	2.02E-08	-2.13	1.06E-11	6.56E-10	-2.57	6.23E-12	2.75E-10	-3.71	1	1	0	Y	cadherin 17
1700008I05Rik	2.93E-12	2.10E-10	-3.13	1.13E-11	6.90E-10	-2.58	7.36E-07	5.09E-06	-1.76	1	1	0	Y	RIKEN cDNA 1700008I05 gene
Ica1	1.14E-05	6.18E-05	-1.36	8.45E-13	8.05E-11	-2.60	2.09E-16	7.52E-14	-9.52	1	1	0	Y	islet cell autoantigen 1
Nr4a2	5.14E-11	2.14E-09	-3.28	3.08E-10	1.04E-08	-2.60	5.48E-05	2.14E-04	-1.63	1	1	0	Y	nuclear receptor subfamily 4, group A, member 2
Hhipl1	9.74E-04	2.90E-03	-1.24	3.99E-12	3.09E-10	-2.60	3.26E-16	1.05E-13	-11.43	1	1	0	Y	hedgehog interacting protein-like 1
Kdm5b	2.29E-09	4.72E-08	-2.42	1.99E-10	7.32E-09	-2.62	1.50E-09	2.66E-08	-3.06	1	1	0	Y	lysine (K)-specific demethylase 5B
Ttc39c	1.61E-06	1.17E-05	-1.96	4.62E-09	9.44E-08	-2.62	3.83E-10	8.51E-09	-4.70	1	1	0	Y	tetratricopeptide repeat domain 39C
Tspyl2	8.18E-13	7.39E-11	-2.53	8.19E-14	1.16E-11	-2.69	1.03E-12	6.59E-11	-3.06	1	1	0	Y	TSPY-like 2
Zfp781	1.05E-11	6.02E-10	-3.17	2.25E-11	1.18E-09	-2.72	2.03E-07	1.68E-06	-1.99	1	1	0	Y	zinc finger protein 781
Gm8800	4.21E-03	1.02E-02	-1.25	4.83E-11	2.26E-09	-2.73	4.05E-15	7.50E-13	-13.04	1	1	0	Y	predicted gene 8800
Eif4ebp1	3.96E-11	1.76E-09	-2.19	2.76E-13	3.21E-11	-2.74	9.28E-14	1.04E-11	-4.29	1	1	0	Y	eukaryotic translation initiation factor 4E binding protein 1
Ly6c1	4.72E-10	1.23E-08	-3.05	5.20E-10	1.58E-08	-2.75	5.67E-07	4.05E-06	-2.23	1	1	0	Y	lymphocyte antigen 6 complex, locus C1
Gyk	1.56E-09	3.38E-08	-2.32	3.19E-11	1.57E-09	-2.75	3.34E-11	1.12E-09	-3.86	1	1	0	Y	glycerol kinase
Gm8736	2.94E-03	7.51E-03	-1.26	3.73E-11	1.80E-09	-2.75	3.39E-15	6.59E-13	-13.06	1	1	0	Y	predicted gene 8736
Slc17a9	2.88E-09	5.71E-08	-2.17	1.33E-11	7.79E-10	-2.81	2.54E-12	1.33E-10	-4.73	1	1	0	Y	solute carrier family 17, member 9
Nfe2l2	3.80E-12	2.55E-10	-3.15	4.03E-12	3.10E-10	-2.84	5.89E-09	8.45E-08	-2.30	1	1	0	Y	nuclear factor, erythroid derived 2, like 2
Ahr	3.88E-14	6.43E-12	-4.10	7.55E-13	7.39E-11	-2.86	1.04E-04	3.75E-04	-1.40	1	1	0	Y	aryl-hydrocarbon receptor
A430084P05Rik	6.71E-10	1.66E-08	-3.82	5.21E-09	1.04E-07	-2.87	1.06E-03	2.78E-03	-1.62	1	1	0	Y	RIKEN cDNA A430084P05 gene
Pdlim1	4.00E-07	3.68E-06	-2.25	3.50E-09	7.56E-08	-2.88	9.86E-10	1.86E-08	-4.75	1	1	0	Y	PDZ and LIM domain 1 (elfin)
Pdlim1	8.79E-12	5.17E-10	-2.28	5.85E-14	8.89E-12	-2.89	1.93E-14	2.81E-12	-4.65	1	1	0	Y	PDZ and LIM domain 1 (elfin)
Smox	1.06E-10	3.84E-09	-2.59	5.30E-12	3.88E-10	-2.92	2.02E-11	7.23E-10	-3.71	1	1	0	Y	spermine oxidase
Pdgfc	4.37E-11	1.91E-09	-3.90	3.41E-10	1.14E-08	-2.93	1.54E-04	5.28E-04	-1.65	1	1	0	Y	platelet-derived growth factor, C polypeptide
Plek	5.48E-14	8.59E-12	-3.89	3.55E-13	4.07E-11	-2.98	2.40E-07	1.92E-06	-1.75	1	1	0	Y	pleckstrin
Ocrl	1.10E-11	6.24E-10	-2.84	1.32E-12	1.18E-10	-3.01	2.10E-11	7.47E-10	-3.39	1	1	0	Y	oculocerebrorenal syndrome of Lowe
Hn1l	8.68E-11	3.26E-09	-3.02	2.13E-11	1.12E-09	-3.04	1.10E-09	2.04E-08	-3.09	1	1	1	Y	hematological and neurological expressed 1-like
Inhba	2.78E-07	2.73E-06	-3.56	4.17E-07	3.96E-06	-3.08	3.07E-04	9.61E-04	-2.29	1	1	0	Y	inhibin beta-A
Rassf3	5.39E-13	5.28E-11	-3.49	5.43E-13	5.82E-11	-3.13	7.71E-10	1.53E-08	-2.52	1	1	0	Y	Ras association (RalGDS/AF-6) domain family member 3
Mospd1	2.28E-09	4.71E-08	-3.22	6.40E-10	1.89E-08	-3.22	3.49E-08	3.78E-07	-3.22	1	1	1	Y	motile sperm domain containing 1
Hmgcll1	9.83E-13	8.48E-11	-4.72	1.49E-11	8.41E-10	-3.24	2.44E-04	7.90E-04	-1.52	1	1	0	Y	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1
Muc16	3.56E-08	4.82E-07	-2.49	3.05E-10	1.03E-08	-3.25	9.93E-11	2.73E-09	-5.53	1	1	0	Y	mucin 16
Gm13154	2.83E-12	2.04E-10	-2.97	2.07E-13	2.54E-11	-3.28	1.54E-12	9.02E-11	-4.01	1	1	0	Y	predicted gene 13154

Plin2	9.81E-12	5.68E-10	-2.74	2.10E-13	2.55E-11	-3.31	2.72E-13	2.33E-11	-4.84	1	1	0	Y	perilipin 2
Ermn	5.09E-08	6.49E-07	-2.00	6.89E-12	4.85E-10	-3.31	6.60E-14	7.94E-12	-9.10	1	1	0	Y	ermin, ERM-like protein
Neurl3	2.21E-06	1.51E-05	-1.94	2.37E-10	8.50E-09	-3.34	1.58E-12	9.15E-11	-9.92	1	1	0	Y	neuralized homolog 3 homolog (Drosophila)
Tmem5	4.00E-15	9.88E-13	-3.03	2.54E-16	1.52E-13	-3.38	1.69E-15	3.60E-13	-4.22	1	1	1	Y	transmembrane protein 5
Ccr5	6.34E-12	3.92E-10	-3.38	1.41E-12	1.23E-10	-3.43	6.78E-11	1.97E-09	-3.54	1	1	1	Y	chemokine (C-C motif) receptor 5
Ccr5	6.34E-12	3.92E-10	-3.38	1.41E-12	1.23E-10	-3.43	6.78E-11	1.97E-09	-3.54	1	1	1	Y	chemokine (C-C motif) receptor 5
Isyna1	8.27E-13	7.43E-11	-3.91	8.45E-13	8.05E-11	-3.46	1.22E-09	2.22E-08	-2.72	1	1	0	Y	myo-inositol 1-phosphate synthase A1
4930523C07Rik	2.45E-12	1.81E-10	-4.28	6.13E-12	4.38E-10	-3.47	1.00E-07	9.28E-07	-2.29	1	1	0	Y	RIKEN cDNA 4930523C07 gene
Airn	1.94E-10	6.23E-09	-3.06	1.04E-11	6.51E-10	-3.50	4.25E-11	1.36E-09	-4.59	1	1	1	Y	antisense Igf2r RNA
Klrg1	2.14E-05	1.06E-04	-2.44	1.17E-07	1.38E-06	-3.50	1.35E-08	1.69E-07	-7.25	1	1	0	Y	killer cell lectin-like receptor subfamily G, member 1
Fgl2	4.88E-11	2.08E-09	-2.78	5.69E-13	6.01E-11	-3.56	3.38E-13	2.72E-11	-5.85	1	1	0	Y	fibrinogen-like protein 2
Nefh	8.11E-11	3.09E-09	-2.42	1.08E-13	1.45E-11	-3.57	7.09E-15	1.25E-12	-7.80	1	1	0	Y	neurofilament, heavy polypeptide
H2-M10.1	1.63E-03	4.52E-03	-1.33	7.19E-12	5.01E-10	-3.59	5.63E-16	1.50E-13	-26.19	1	1	0	Y	histocompatibility 2, M region locus 10.1
Inpp5d	4.14E-13	4.28E-11	-2.81	4.56E-15	1.25E-12	-3.60	2.77E-15	5.45E-13	-5.92	1	1	0	Y	inositol polyphosphate-5-phosphatase D
Lrmp	9.81E-15	2.04E-12	-4.62	3.28E-14	6.04E-12	-3.62	2.05E-09	3.46E-08	-2.23	1	1	0	Y	lymphoid-restricted membrane protein
Pecr	1.20E-11	6.63E-10	-3.07	4.09E-13	4.57E-11	-3.64	9.75E-13	6.37E-11	-5.12	1	1	1	Y	peroxisomal trans-2-enoyl-CoA reductase
Gpr128	7.18E-04	2.23E-03	-1.14	2.25E-17	2.05E-14	-3.65	3.93E-22	6.19E-18	-37.30	1	1	0	Y	G protein-coupled receptor 128
Itm2a	2.13E-08	3.10E-07	-1.87	1.47E-13	1.90E-11	-3.75	2.72E-16	9.28E-14	-15.09	1	1	0	Y	integral membrane protein 2A
Ceacam1	1.90E-09	4.02E-08	-3.17	7.70E-11	3.37E-09	-3.76	1.94E-10	4.77E-09	-5.28	1	1	1	Y	carcinoembryonic antigen-related cell adhesion molecule 1 //
Fam78b	8.95E-10	2.12E-08	-2.10	5.70E-14	8.74E-12	-3.78	3.88E-16	1.13E-13	-12.19	1	1	0	Y	family with sequence similarity 78, member B
Igf2r	5.18E-18	6.38E-15	-4.22	4.24E-18	6.68E-15	-3.79	4.60E-15	8.23E-13	-3.06	1	1	1	Y	insulin-like growth factor 2 receptor
Ptprcap	1.77E-16	1.05E-13	-4.85	4.22E-16	1.97E-13	-3.90	9.61E-12	3.92E-10	-2.51	1	1	0	Y	protein tyrosine phosphatase, receptor type, C polypeptide-asso
Insl6	2.56E-12	1.88E-10	-5.34	1.36E-11	7.86E-10	-3.91	2.67E-06	1.53E-05	-2.09	1	1	0	Y	insulin-like 6
Syce2	3.42E-08	4.66E-07	-2.80	1.82E-10	6.78E-09	-3.96	3.60E-11	1.18E-09	-7.92	1	1	0	Y	synaptonemal complex central element protein 2
Ccdc104	2.86E-13	3.22E-11	-4.20	1.06E-13	1.45E-11	-4.06	1.56E-11	5.89E-10	-3.80	1	1	1	Y	coiled-coil domain containing 104
Atp2a3	1.24E-13	1.63E-11	-3.10	1.32E-15	4.77E-13	-4.08	7.74E-16	1.97E-13	-7.07	1	1	1	Y	ATPase, Ca++ transporting, ubiquitous
Me1	9.04E-07	7.21E-06	-1.46	2.05E-15	6.70E-13	-4.20	2.31E-19	3.31E-16	-34.76	1	1	0	Y	malic enzyme 1, NADP(+)-dependent, cytosolic
Aldoc	1.93E-07	2.00E-06	-3.13	2.52E-09	5.75E-08	-4.24	1.18E-09	2.16E-08	-7.74	1	1	1	Y	aldolase C, fructose-bisphosphate
Cstb	7.01E-14	1.05E-11	-4.97	7.03E-14	1.03E-11	-4.32	1.07E-10	2.92E-09	-3.27	1	1	1	Y	cystatin B
Me1	2.35E-06	1.59E-05	-1.46	3.58E-15	1.05E-12	-4.43	3.56E-19	4.67E-16	-40.91	1	1	0	Y	malic enzyme 1, NADP(+)-dependent, cytosolic
Casd1	2.91E-11	1.36E-09	-2.44	3.70E-15	1.06E-12	-4.49	4.17E-17	2.05E-14	-15.29	1	1	0	Y	CAS1 domain containing 1
Tmbim4	5.42E-13	5.28E-11	-5.36	6.50E-13	6.59E-11	-4.54	1.45E-09	2.57E-08	-3.26	1	1	1	Y	transmembrane BAX inhibitor motif containing 4
Lass6	1.81E-10	5.92E-09	-2.08	1.14E-15	4.24E-13	-4.60	2.27E-18	2.31E-15	-22.40	1	1	0	Y	LAG1 homolog, ceramide synthase 6
Sema6d	2.70E-07	2.66E-06	-3.86	1.45E-08	2.37E-07	-4.68	3.80E-08	4.06E-07	-6.86	1	1	1	Y	sema domain, transmembrane domain (TM), and cytoplasmic domain,
Wls	3.83E-13	4.08E-11	-4.62	7.77E-14	1.12E-11	-4.74	3.42E-12	1.68E-10	-5.01	1	1	1	Y	wntless homolog (Drosophila)
Phyh	5.23E-12	3.35E-10	-4.49	7.95E-13	7.65E-11	-4.76	1.95E-11	7.06E-10	-5.36	1	1	1	Y	phytanoyl-CoA hydroxylase
Fam38a	6.94E-17	4.60E-14	-4.97	2.19E-17	2.05E-14	-4.87	2.62E-15	5.29E-13	-4.66	1	1	1	Y	family with sequence similarity 38, member A
Rgs2	4.84E-08	6.19E-07	-3.33	2.30E-10	8.34E-09	-5.07	3.99E-11	1.28E-09	-11.75	1	1	1	Y	regulator of G-protein signaling 2
Fam5c	4.19E-15	1.00E-12	-9.18	6.46E-14	9.65E-12	-5.37	3.92E-06	2.13E-05	-1.84	1	1	0	Y	family with sequence similarity 5, member C
A930038C07Rik	2.77E-10	8.24E-09	-4.35	9.30E-12	6.11E-10	-5.50	1.97E-11	7.10E-10	-8.75	1	1	1	Y	RIKEN cDNA A930038C07 gene
Peci	1.79E-18	2.45E-15	-6.33	1.30E-18	2.50E-15	-5.59	1.07E-15	2.55E-13	-4.36	1	1	1	Y	peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase
Tmem159	1.20E-15	4.06E-13	-9.49	6.81E-15	1.71E-12	-6.22	3.58E-09	5.54E-08	-2.67	1	1	0	Y	transmembrane protein 159
Fam38a	1.19E-15	4.06E-13	-6.52	3.90E-16	1.97E-13	-6.33	4.87E-14	6.14E-12	-5.97	1	1	1	Y	family with sequence similarity 38, member A
Mr1	3.94E-16	1.74E-13	-5.29	1.85E-17	1.89E-14	-6.47	7.93E-17	3.29E-14	-9.70	1	1	1	Y	major histocompatibility complex, class I-related
Slc2a3	2.79E-16	1.34E-13	-8.67	4.67E-16	1.97E-13	-6.72	3.45E-12	1.69E-10	-4.03	1	1	1	Y	solute carrier family 2 (facilitated glucose transporter), membe
Serpine2	2.61E-19	6.19E-16	-8.68	3.28E-19	7.11E-16	-6.98	1.16E-15	2.73E-13	-4.51	1	1	1	Y	serine (or cysteine) peptidase inhibitor, clade E, member 2 //
Hadh	5.08E-14	8.04E-12	-4.51	3.04E-16	1.71E-13	-6.99	9.61E-17	3.78E-14	-16.77	1	1	1	Y	hydroxyacyl-Coenzyme A dehydrogenase
Slc27a6	1.48E-09	3.24E-08	-4.74	1.71E-11	9.41E-10	-7.02	9.00E-12	3.74E-10	-15.39	1	1	1	Y	solute carrier family 27 (fatty acid transporter), member 6
Macc1	5.86E-12	3.70E-10	-4.00	5.45E-15	1.43E-12	-7.67	2.77E-16	9.28E-14	-28.26	1	1	1	Y	metastasis associated in colon cancer 1
Rgs18	2.11E-11	1.05E-09	-5.14	1.78E-13	2.29E-11	-7.98	7.49E-14	8.55E-12	-19.24	1	1	1	Y	regulator of G-protein signaling 18
Sema3d	1.29E-12	1.07E-10	-4.35	1.39E-15	4.82E-13	-8.45	8.22E-17	3.32E-14	-31.97	1	1	1	Y	sema domain, immunoglobulin domain (Ig), short basic domain, sec
Rny1	5.86E-06	3.48E-05	-5.92	6.95E-08	8.86E-07	-10.22	2.09E-08	2.45E-07	-30.43	1	1	1	Y	RNA, Y1 small cytoplasmic, Ro-associated
Klra9	4.01E-15	9.88E-13	-5.88	1.73E-17	1.87E-14	-10.31	3.93E-18	3.44E-15	-31.74	1	1	1	Y	killer cell lectin-like receptor subfamily A, member 9
Fam38a	1.01E-19	2.90E-16	-11.99	2.69E-20	1.17E-16	-11.91	2.35E-18	2.31E-15	-11.76	1	1	1	Y	family with sequence similarity 38, member A
Sccpdh	2.43E-15	6.71E-13	-18.11	1.15E-15	4.24E-13	-16.13	3.16E-13	2.59E-11	-12.79	1	1	1	Y	saccharopine dehydrogenase (putative)
Lxn	5.13E-16	2.11E-13	-13.31	4.44E-17	3.35E-14	-16.21	4.89E-16	1.33E-13	-24.05	1	1	1	Y	latexin
Gem	1.52E-18	2.45E-15	-36.01	5.37E-18	7.76E-15	-20.21	5.40E-13	3.90E-11	-6.37	1	1	1	Y	GTP binding protein (gene overexpressed in skeletal muscle)
Nrn1	2.87E-19	6.19E-16	-30.35	1.52E-20	8.78E-17	-44.31	8.12E-20	1.83E-16	-94.44	1	1	1	Y	neuritin 1
Klra5	7.62E-15	1.66E-12	-39.08	1.90E-16	1.22E-13	-73.16	3.32E-16	1.05E-13	-256.40	1	1	1	Y	killer cell lectin-like receptor, subfamily A, member 5

Supplemental Table 3		CD8γ13 T cell clones		Score	
Lineage		mRNA signal			
		Mean 8sAg1	**Mean 8sAg3**		**gene title**
	CD4 T cells	230*	1398*	+/++	CD4 antigen
	CD8 T cells	5256	4938	+++/+++	CD8 antigen, beta chain 1
	NK/NKT cells	27	16	0/0	killer cell lectin-like receptor subfamily B member 1c
	B cells	20	16	0/0	CD79A antigen (immunoglobulin associated alpha)
Cytokine	Th1	1675	1031	++/++	T-box 21 (T-bet)
	Th2	1052	1217	++/++	GATA binding protein 3 (Gata3)
	Th17	90	62	0/0	RAR-related orphan receptor (RORγT)
	Th22	77	38	0/0	aryl-hydrocarbon receptor (Ahr)
	CD4γ13	69	75	0/0	four and a half LIM domains 2 (Fhl2)
	?	43	604	0/+	eomesodermin (Eomes)
Trm	Klrg1	56	1128	0/++	killer cell lectin-like receptor subfamilyG, member 1
	Klf2	188	195	+/+	Kruppel-like factor 2 (lung)
	Hnf1a	744	760	+/+	HNF1 homeobox A
	S1pr1	93	61	0/0	sphingosine-1-phosphate receptor 1
	Ccr7	218	122	+/0	chemokine (C-C motif) receptor 7
	Prdm1	1024	1052	++/++	PR domain containing 1, with ZNF domain (Blimp-1)
	Rgs1	385	1332	+/++	regulator of G-protein signaling 1
	Rgs2	104	54	0/0	regulator of G-protein signaling 2
	Cd69	442	1629	+/++	CD69 antigen
	Cd44	803	63	+/0	CD44 antigen
	Itgal	8659	6472	++++/+++	integrin alpha L
	Itgb7	2134	95	++/0	integrin beta 7
	Itga1	4837	5752	+++/+++	integrin alpha 1
	Itgae	46	46	0/0	integrin alpha E, epithelial-associated
Treg	Cd27	57	45	0/0	CD27 antigen
	IL2ra	6936	8841	+++/++++	interleukin 2 receptor, alpha chain
	Foxp3	67	71	0/0	forkhead box P3
	Ctla4	491	455	+/+	cytotoxic T-lymphocyte-associated protein 4
Th22	Ahr	77	95	0/0	aryl-hydrocarbon receptor (Ahr)
	Foxo4	196	119	+/0	forkhead box O4
	Bnc2	30	32	0/0	basonudin2
Cm Effector	Casd1	25	17	0/0	CAS1 domain containing 1
	Plac8	29	23	0/0	placenta-specific 8

[a] Scores are defined as follows: <150 arbitrary units (AU) = 0, 150 to 999 AU +, 1,000 to 2,499 AU ++, 2,500 to 7,499 AU +++ and 7,500 to 10,000 AU ++++.

* no cell surface expression