Supplementary Information

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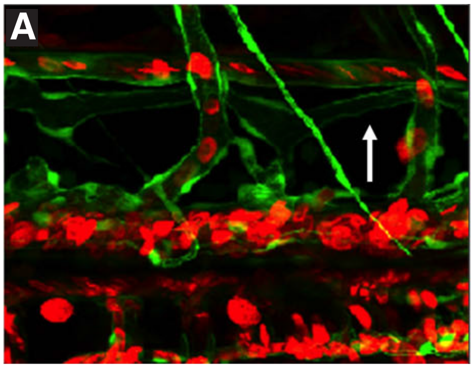
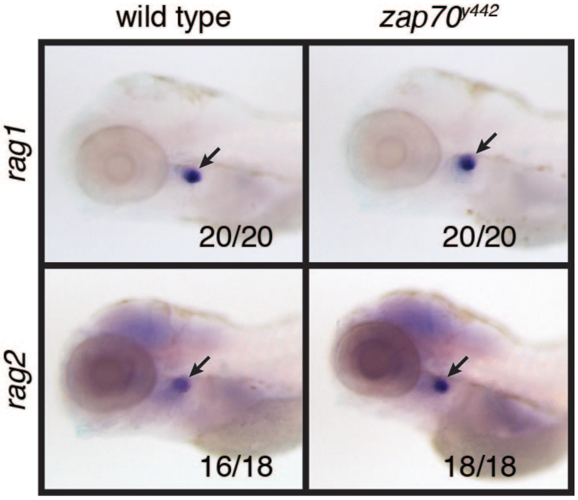
Supplementary Figure 1.



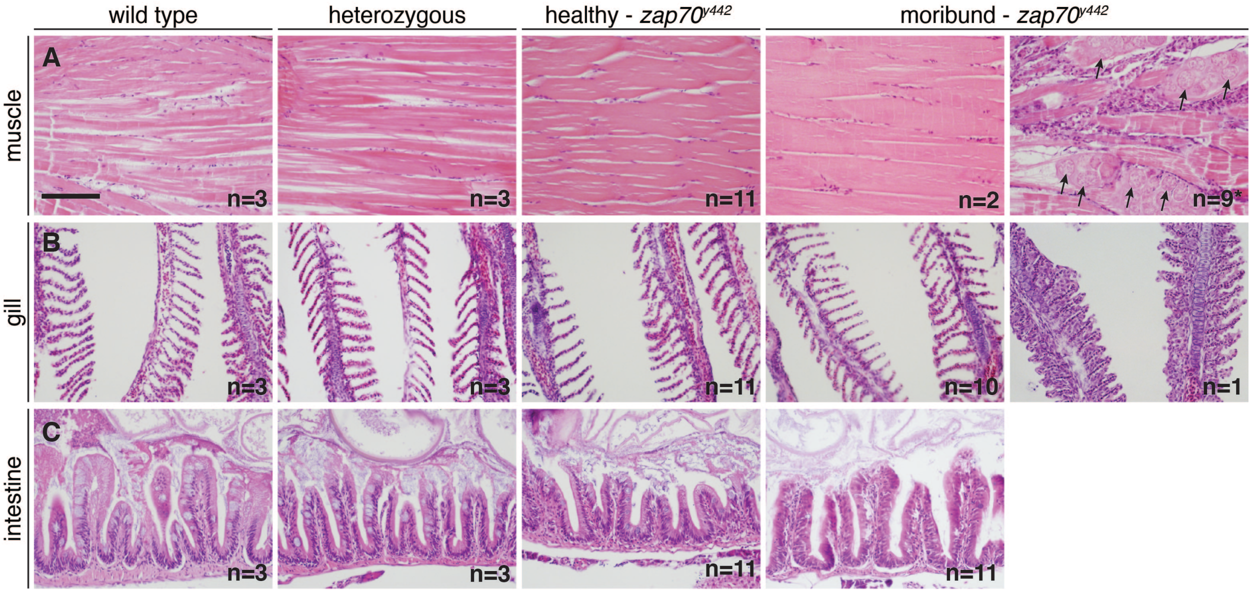
SUP. FIG. 1. *Tg(fli1a:egfp)*^{y1}, *Tg(gata1:dsred)*^{sd2} transgenic, *zap70*^{y442} homozygous mutant zebrafish have normal vascular and lymphatic development. A) Merged confocal image of representative animal shown at 5 dpf (n>6 fish analyzed). Thoracic duct denoted by arrow.

Supplementary Figure 2.



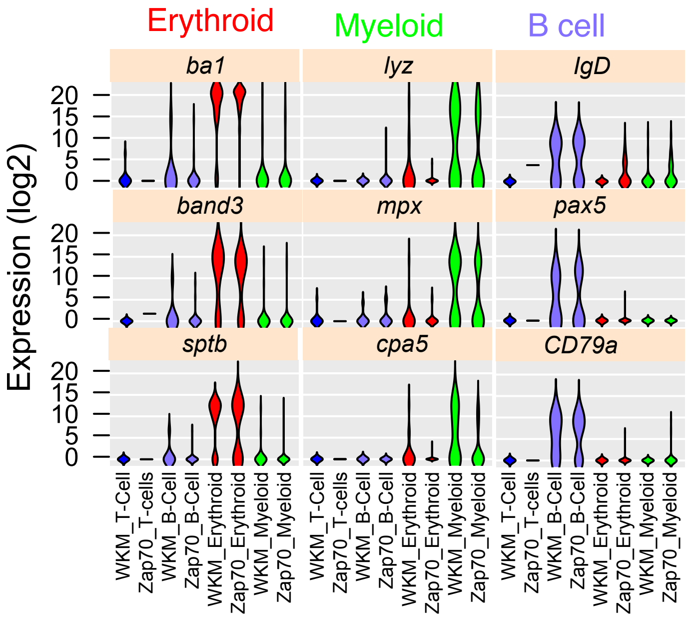
SUP. FIG. 2. - *rag1* and *rag2* are expressed in lymphocyte progenitors of *zap70*^{y442} mutants *at* 5 dpf. Images of whole mount *in situ* hybridization showing expression levels of *rag1* and *rag2* in the thymus (arrows) of wild type and *zap70*^{y442} mutant zebrafish at 5 dpf.

Supplementary Figure 3.



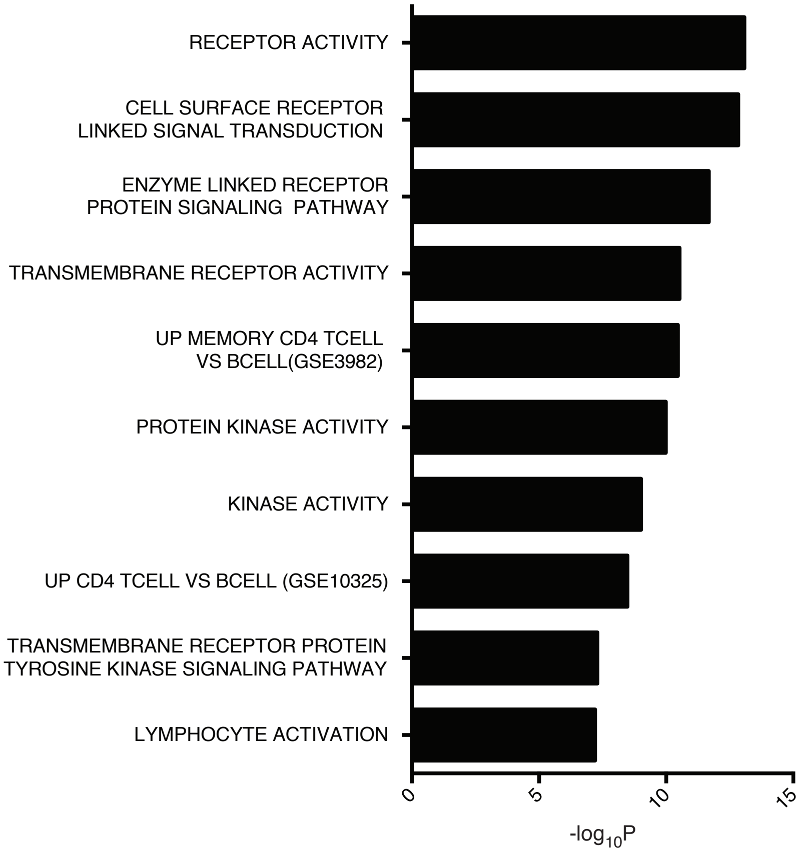
SUP. FIG. 3. Moribund homozygous *zap70*^{y442} mutants develop opportunistic infections. (A-C) Hematoxylin and eosin stained sections of 5-7 month old zebrafish, muscle (A), gills (B), and intestine (C). Genotypes and clinical health of animal at time of sacrifice are indicated. Arrows in right panel A show *Pseudoloma neurophilia* xenomas in moribund *zap70*^{y442} mutant muscle. Numbers embedded in each panel indicate the number of fish with the associated phenotype. A total of 11 healthy and 11 moribund homozygous *zap70*^{y442} mutant fish were analyzed. Asterisk denotes significant difference in number of healthy and moribund homozygous *zap70*^{y442} mutant fish that developed infection ($p < 0.002$, Fisher exact test).Scale bar equals 100 µm.

Supplementary Figure 4.



SUP. FIG. 4. Erythroid, myeloid and B cell lineage marker gene expression is normal in *zap70*^{y442} mutants. Violin plots show the distribution of gene expression within single whole kidney marrow cells. Cells types were assigned based on hierarchical clustering and assessed for transcript expression of well-known blood cell lineage genes.

Supplementary Figure 5.



SUP. FIG. 5. Selected GO terms and pathways from GSEAsig analysis of *zap70*^{y442} downregulated genes. FDR rate <0.0001 with $\log_{10}$ p-values noted.

Supplementary Table 1 - Genes downregulated in zap70^{y442} mutants

Zap70^{y442} vs wt downregulated genes						
ZFIN ID	ENSEMBL#	log$_2$FC	logCPM	PValue	FDR	Human ID
cebp1	ENSDARG00000045240	-11.10	2.86	1.34E-23	9.13E-21	CEBPB
mcm3	ENSDARG00000090802	-10.69	4.80	4.00E-37	7.63E-34	MCM3
zgc:158260	ENSDARG00000089020	-10.04	1.83	3.54E-10	4.41E-08	FAM47E
cox5aa	ENSDARG00000088383	-9.36	1.20	1.41E-12	2.88E-10	COX5A
si:ch211-283g2.3	ENSDARG00000046092	-9.02	0.89	3.10E-09	3.08E-07	ASGR2
larsa	ENSDARG00000089031	-8.94	0.81	2.54E-10	3.28E-08	lars
prpf4	ENSDARG00000076717	-8.66	0.57	5.06E-09	4.76E-07	PRPF4
ggact.2	ENSDARG00000038248	-8.64	2.81	1.09E-04	2.05E-03	GGACT
il34	ENSDARG00000091003	-8.60	0.51	1.03E-06	4.63E-05	IL20
narf	ENSDARG00000024184	-8.44	3.42	6.40E-26	5.31E-23	NARF
fasn	ENSDARG00000087657	-8.38	3.32	1.21E-16	4.73E-14	FASN
cbln9	ENSDARG00000030254	-8.34	2.43	1.05E-05	3.17E-04	cbln9
rtn3	ENSDARG00000058028	-8.26	3.81	1.77E-06	7.26E-05	RTN3
btr07	ENSDARG00000094877	-8.22	0.18	3.53E-05	8.51E-04	btr07
irgq2	ENSDARG00000068657	-7.87	-0.12	1.64E-06	6.84E-05	irgq2
ftr28l	ENSDARG00000088280	-7.86	-0.13	1.02E-06	4.60E-05	ftr28
tas1r3	ENSDARG00000006341	-7.75	-0.22	4.49E-05	1.04E-03	TAS1R3
rfesd	ENSDARG00000058725	-7.75	3.90	9.82E-20	5.21E-17	RFESD
chrm3a	ENSDARG00000071091	-7.50	-0.43	2.19E-05	5.77E-04	CHRM3
bfb	ENSDARG00000005616	-7.48	-0.45	6.68E-05	1.40E-03	CFB
rab14	ENSDARG00000045261	-7.38	4.27	9.37E-33	1.37E-29	RAB14
rrm2	ENSDARG00000020711	-7.37	4.89	1.70E-23	1.12E-20	RRM2
kcnh5a	ENSDARG00000043220	-7.34	1.52	8.91E-13	1.91E-10	KCNH5
syt9a	ENSDARG00000003994	-7.33	-0.56	3.11E-04	4.57E-03	SYT9
pparab	ENSDARG00000091024	-7.26	-0.62	1.14E-04	2.12E-03	PPARA
unc45b	ENSDARG00000008433	-6.97	1.27	7.05E-06	2.31E-04	UNC45B
ttc25	ENSDARG00000090531	-6.89	-0.91	1.44E-04	2.57E-03	TTC25
gzmk	ENSDARG00000090380	-6.87	1.09	3.36E-10	4.21E-08	GZMK
sarm1	ENSDARG00000010610	-6.86	4.43	1.98E-34	3.15E-31	SARM1
dnajb12b	ENSDARG00000008312	-6.82	-0.96	4.79E-04	6.36E-03	dnajb12
grid1b	ENSDARG00000044161	-6.75	-1.02	1.58E-03	1.55E-02	GRID1
CCDC57	ENSDARG00000089863	-6.71	1.72	8.47E-13	1.84E-10	CCDC57
cnp	ENSDARG00000091351	-6.70	5.76	6.27E-13	1.38E-10	CNP
ribc1	ENSDARG00000055739	-6.66	0.96	2.45E-08	1.90E-06	RIBC1
ankef1b	ENSDARG00000060211	-6.52	-1.20	4.71E-04	6.28E-03	ANKEF1
slc35b1	ENSDARG00000038213	-6.50	0.81	4.71E-09	4.50E-07	SLC35B1
foxp3a	ENSDARG00000055750	-6.36	0.66	6.80E-08	4.55E-06	FOXP3
si:ch211-161n3.3	ENSDARG00000092989	-6.35	0.61	1.87E-07	1.06E-05	DMBT1
TP53I3	ENSDARG00000078084	-6.27	0.54	9.70E-08	6.26E-06	TP53I3
pkhd1l1	ENSDARG00000091116	-5.90	3.62	3.39E-11	5.58E-09	PKHD1L1
cryba4	ENSDARG00000024548	-5.86	0.16	1.14E-04	2.12E-03	CRYBA4
chrnb1l	ENSDARG00000022532	-5.81	3.06	1.83E-06	7.46E-05	CHRNB1
tas1r2.1	ENSDARG00000053135	-5.70	0.04	1.35E-05	3.90E-04	TAS1R2
ccr7	ENSDARG00000044561	-5.63	2.74	2.85E-15	8.76E-13	CCR7

SRRM4	ENSDARG00000096920	-5.57	0.03	1.03E-04	1.96E-03	SRRM4
stc2b	ENSDARG00000089134	-5.51	-0.12	2.88E-05	7.20E-04	stc2
lrp2b	ENSDARG00000007906	-5.49	1.19	4.98E-06	1.76E-04	lrp2
sc:d217	ENSDARG00000079645	-5.48	3.20	6.54E-05	1.38E-03	sc:d217
pacsin1a	ENSDARG00000032865	-5.45	-0.17	7.18E-05	1.48E-03	pacsin1
si:ch211-152c2.3	ENSDARG00000045898	-5.45	1.18	1.23E-06	5.34E-05	ncRNA
rbm22	ENSDARG00000087678	-5.44	1.73	3.83E-11	6.09E-09	RBM22
nsmfa	ENSDARG00000060025	-5.44	-0.14	5.53E-06	1.91E-04	NSMF
fam169aa	ENSDARG00000059719	-5.40	-0.21	1.10E-05	3.28E-04	FAM169A
myo5b	ENSDARG00000093553	-5.33	0.59	1.21E-05	3.57E-04	MYO5B
si:dkey-147f3.4	ENSDARG00000071029	-5.25	2.90	9.25E-17	3.76E-14	FBXO6
ptprua	ENSDARG00000092638	-5.21	4.07	1.83E-12	3.64E-10	PTPRU
si:ch211-197g15.6	ENSDARG00000094747	-5.15	0.43	5.03E-06	1.77E-04	IFI44
xylb	ENSDARG00000043260	-5.12	1.35	6.11E-09	5.58E-07	XYLB
tfr1b	ENSDARG00000077372	-5.11	6.32	2.45E-29	2.60E-26	TFRC
ntrk3a	ENSDARG00000077228	-5.11	0.26	2.91E-06	1.11E-04	NTRK3
col5a2b	ENSDARG00000024847	-5.05	0.23	4.25E-03	3.18E-02	COL5A2
eomesb	ENSDARG00000019428	-5.05	-0.50	1.16E-04	2.15E-03	EOMES
ccdc80l1	ENSDARG00000030975	-5.03	2.64	2.28E-08	1.78E-06	CCDC80
GP5	ENSDARG00000062303	-4.99	0.74	2.13E-06	8.52E-05	GP5
emp1	ENSDARG00000069632	-4.97	2.36	1.67E-09	1.75E-07	EMP1
cd8a	ENSDARG00000044797	-4.86	0.50	1.17E-06	5.15E-05	CD8A
myo3a	ENSDARG00000010186	-4.85	3.36	4.48E-10	5.44E-08	MYO3A
cx27.5	ENSDARG00000035553	-4.80	-0.01	5.27E-05	1.16E-03	GJB1
pcloa	ENSDARG00000063299	-4.78	-0.71	2.09E-04	3.39E-03	PCLO
slc1a5	ENSDARG00000090706	-4.77	1.12	1.65E-05	4.57E-04	SLC1A4
men1	ENSDARG00000058021	-4.76	2.93	1.51E-05	4.27E-04	MEN1
ugt5a4	ENSDARG00000097397	-4.69	-0.78	8.95E-04	1.01E-02	ugt5a4
mapre3b	ENSDARG00000012330	-4.68	-0.74	2.91E-04	4.34E-03	MAPRE3
prf1.1	ENSDARG00000030394	-4.62	0.41	9.55E-06	2.96E-04	PRF1
b4galt5	ENSDARG00000037815	-4.57	1.97	5.53E-11	8.30E-09	B4GALT5
zbtb20	ENSDARG00000005586	-4.52	3.80	7.35E-19	3.69E-16	ZBTB20
serpind1	ENSDARG00000021208	-4.49	5.02	3.10E-18	1.41E-15	SERPIND1
kcnq3	ENSDARG00000060085	-4.47	-0.90	7.18E-04	8.63E-03	KCNQ3
nradd	ENSDARG00000057143	-4.46	0.16	1.28E-05	3.76E-04	NGFR
pdia2	ENSDARG00000018263	-4.45	5.99	7.58E-14	1.81E-11	pdia2
gfra3	ENSDARG00000087704	-4.41	-0.92	1.26E-03	1.32E-02	gfra3
gabbr2	ENSDARG00000061042	-4.40	0.17	2.45E-05	6.32E-04	GABBR2
themis	ENSDARG00000010619	-4.33	2.03	3.65E-09	3.57E-07	THEMIS
si:ch211-197g15.6	ENSDARG00000009673	-4.31	0.72	1.18E-06	5.17E-05	IFI44
abhd8a	ENSDARG00000079719	-4.26	-0.41	1.61E-04	2.79E-03	ABHD8
zbtb16a	ENSDARG00000007184	-4.24	4.71	1.03E-14	2.64E-12	ZBTB16
zap70	ENSDARG00000015752	-4.16	2.68	1.11E-08	9.34E-07	ZAP70
scn4bb	ENSDARG00000060319	-4.14	-0.54	3.13E-04	4.59E-03	SCN4B
prg4a	ENSDARG00000010482	-4.12	3.15	9.74E-10	1.08E-07	PRG4
rgs8	ENSDARG00000070037	-4.08	-0.06	1.94E-03	1.80E-02	RGS8
elfn1b	ENSDARG00000074372	-4.07	-0.62	6.64E-03	4.38E-02	ELFN1
itga10	ENSDARG00000002507	-4.06	0.31	1.26E-04	2.29E-03	ITGA10
galnt18a	ENSDARG00000030292	-4.06	0.20	7.36E-05	1.51E-03	GALNT18

SPOCK1	ENSDARG00000074644	-4.04	-0.62	5.25E-04	6.78E-03	SPOCK1
gbgt1l3	ENSDARG00000035555	-3.99	1.57	2.47E-04	3.88E-03	GBGT1
cfhl5	ENSDARG00000092786	-3.98	-0.59	8.96E-04	1.01E-02	cfhl5
mlnl	ENSDARG00000092916	-3.91	0.99	1.14E-04	2.11E-03	mlnl
b4galnt4a	ENSDARG00000046150	-3.91	0.72	7.07E-06	2.32E-04	B4GALNT4
crispld1a	ENSDARG00000077275	-3.87	1.05	1.46E-06	6.15E-05	CRISPLD1
ctrl	ENSDARG00000068680	-3.84	1.75	1.71E-04	2.92E-03	CTRL
lingo4a	ENSDARG00000094908	-3.82	-0.75	1.28E-03	1.32E-02	lingo4
ttna	ENSDARG00000028213	-3.81	3.82	1.18E-03	1.25E-02	TTN
kif17	ENSDARG00000055238	-3.81	1.08	5.43E-06	1.89E-04	KIF17
crb2b	ENSDARG00000060081	-3.79	2.45	7.50E-09	6.65E-07	CRB2
ntng2a	ENSDARG00000077367	-3.79	0.70	1.48E-05	4.20E-04	NTNG2
pde8b	ENSDARG00000063706	-3.78	4.65	9.25E-08	6.09E-06	PDE8B
RAB27B	ENSDARG00000087762	-3.76	-0.30	5.09E-04	6.63E-03	RAB27B
adam11	ENSDARG00000079204	-3.69	1.41	4.20E-07	2.15E-05	ADAM11
abi1b	ENSDARG00000062991	-3.69	2.51	4.84E-08	3.42E-06	ABI1
si:dkey-147f3.4	ENSDARG00000092077	-3.67	1.85	5.05E-08	3.53E-06	FBXO6
neb	ENSDARG00000032630	-3.66	3.00	4.78E-03	3.45E-02	NEB
gdpd4a	ENSDARG00000078196	-3.65	-0.52	1.47E-03	1.48E-02	GDPD5
csde1	ENSDARG00000062157	-3.64	5.89	1.19E-05	3.52E-04	CSDE1
abhd2a	ENSDARG00000025797	-3.64	4.20	3.27E-15	9.86E-13	ABHD2
sult2st3	ENSDARG00000028367	-3.63	4.50	1.16E-10	1.64E-08	SULT2B1
RAI1	ENSDARG00000076679	-3.63	-0.94	4.63E-03	3.37E-02	rai1
pabpc4	ENSDARG00000059259	-3.62	2.03	3.19E-05	7.86E-04	PABPC4
tcf7	ENSDARG00000038672	-3.61	2.09	2.68E-08	2.06E-06	TCF7
adpgk2	ENSDARG00000062785	-3.60	4.05	3.89E-10	4.82E-08	ADPGK
apoeb	ENSDARG00000040295	-3.58	3.94	5.63E-09	5.24E-07	APOE
myhz1.1	ENSDARG00000067990	-3.57	0.49	1.18E-03	1.25E-02	MYH1
eps8l1	ENSDARG00000057984	-3.56	1.41	2.20E-07	1.21E-05	eps8l1
ctnnd2a	ENSDARG00000062415	-3.55	1.15	1.19E-03	1.25E-02	CTNND2
cyp2aa6	ENSDARG00000088744	-3.52	3.96	5.93E-13	1.33E-10	cyp2aa6
upk1a	ENSDARG00000021866	-3.51	-0.52	7.84E-04	9.16E-03	UPK1A
gucy2f	ENSDARG00000025504	-3.50	0.02	1.60E-04	2.78E-03	GUCY2F
snx6	ENSDARG00000058444	-3.48	4.56	5.31E-15	1.49E-12	SNX6
npc1l1	ENSDARG00000077891	-3.47	-0.06	3.02E-04	4.46E-03	NPC1L1
wnt9b	ENSDARG00000037889	-3.44	1.59	1.23E-06	5.34E-05	WNT9B
neu3.2	ENSDARG00000010047	-3.43	0.38	2.68E-04	4.13E-03	NEU3
SDSL	ENSDARG00000074698	-3.42	5.03	1.34E-11	2.33E-09	SDSL
slc27a2b	ENSDARG00000013177	-3.41	9.28	9.01E-06	2.81E-04	SLC27A2
tmtopsb	ENSDARG00000032246	-3.40	3.05	2.15E-08	1.68E-06	tmtops
slc18a3a	ENSDARG00000006356	-3.40	1.51	1.08E-05	3.26E-04	SLC18A3
ptrfa	ENSDARG00000076411	-3.40	-0.70	2.62E-03	2.25E-02	PTRF
nos1	ENSDARG00000068910	-3.38	1.42	2.71E-06	1.05E-04	NOS1
gpx3	ENSDARG00000043342	-3.37	1.32	1.06E-06	4.76E-05	GPX3
dvl1b	ENSDARG00000055552	-3.36	0.15	7.32E-04	8.71E-03	DVL1
ccdc125	ENSDARG00000056477	-3.36	2.47	1.61E-06	6.73E-05	CCDC125
igfn1.1	ENSDARG00000005526	-3.35	2.69	4.31E-04	5.88E-03	IGFN1
ppm1f	ENSDARG00000005786	-3.34	0.28	1.79E-04	3.02E-03	PPM1F
ASCC1	ENSDARG00000037617	-3.33	1.37	2.03E-06	8.16E-05	ASCC1

cthrc1b	ENSDARG00000001971	-3.32	0.27	2.16E-04	3.49E-03	CTHRC1
qkia	ENSDARG00000044462	-3.32	1.02	2.56E-04	3.98E-03	QKI
ddx6	ENSDARG00000061338	-3.32	4.41	7.22E-12	1.30E-09	DDX6
ndst2a	ENSDARG00000060678	-3.29	5.45	6.61E-10	7.69E-08	NDST2
pigt	ENSDARG00000075842	-3.27	2.23	6.58E-08	4.44E-06	PIGT
pdlim7	ENSDARG00000030638	-3.27	0.86	6.53E-04	8.01E-03	PDLIM7
ocstamp	ENSDARG00000022139	-3.27	0.36	2.02E-04	3.29E-03	OCSTAMP
mboat2a	ENSDARG00000031845	-3.23	3.15	2.41E-09	2.46E-07	MBOAT2
rbm45	ENSDARG00000063731	-3.21	2.13	1.71E-07	9.76E-06	RBM45
cyp1b1	ENSDARG00000068934	-3.21	4.11	1.72E-10	2.23E-08	CYP1B1
atp8a1	ENSDARG00000063001	-3.19	1.21	2.07E-05	5.57E-04	atp8a1
fat3a	ENSDARG00000033840	-3.19	2.25	2.25E-07	1.23E-05	fat3
osmr	ENSDARG00000042903	-3.16	4.53	6.71E-10	7.76E-08	OSMR
p2rx1	ENSDARG00000016695	-3.16	2.13	5.38E-07	2.65E-05	P2RX1
LIN28B	ENSDARG00000052511	-3.16	-0.52	1.97E-03	1.82E-02	LIN28B
ppp1r32	ENSDARG00000089183	-3.16	2.20	2.49E-04	3.90E-03	PPP1R32
PKD1	ENSDARG00000030417	-3.15	3.36	6.11E-09	5.58E-07	PKD1
zgc:101810	ENSDARG00000004658	-3.13	-0.27	1.66E-03	1.60E-02	ACTR2
cel.2	ENSDARG00000029822	-3.10	1.01	4.04E-04	5.57E-03	CEL
jarid2b	ENSDARG00000062268	-3.10	4.06	1.69E-10	2.21E-08	JARID2
ptprdb	ENSDARG00000019945	-3.10	2.09	6.52E-06	2.19E-04	PTPRD
znf536	ENSDARG00000022251	-3.08	1.02	4.10E-04	5.63E-03	ZNF536
cacng6b	ENSDARG00000046079	-3.07	0.43	3.91E-04	5.41E-03	CACNG6
mitfb	ENSDARG00000037833	-3.07	1.33	1.59E-04	2.77E-03	MITF
cd40lg	ENSDARG00000079333	-3.07	-0.06	1.23E-03	1.29E-02	cd40lg
itk	ENSDARG00000017565	-3.05	2.55	1.53E-07	9.00E-06	ITK
nefma	ENSDARG00000021351	-3.05	0.15	1.27E-03	1.32E-02	NEFM
crebrf	ENSDARG00000078581	-3.05	3.01	1.67E-07	9.61E-06	CREBRF
trim35-36	ENSDARG00000032169	-3.04	1.53	5.76E-04	7.31E-03	trim35
greb1l	ENSDARG00000039196	-3.02	5.24	1.61E-07	9.39E-06	GREB1L
kdr	ENSDARG00000017321	-3.02	6.50	1.72E-13	4.01E-11	KDR
hdac5	ENSDARG00000075139	-3.02	4.67	3.81E-08	2.80E-06	HDAC5
abca12	ENSDARG00000074749	-3.01	1.61	1.02E-04	1.94E-03	ABCA12
ATXN1L	ENSDARG00000086977	-2.98	1.79	5.09E-06	1.79E-04	ATXN1L
mst1rb	ENSDARG00000004871	-2.98	4.93	9.18E-07	4.16E-05	MST1R
osbpl6	ENSDARG00000063730	-2.97	2.04	1.80E-06	7.34E-05	OSBPL6
gfra1b	ENSDARG00000013975	-2.96	0.61	9.52E-04	1.06E-02	GFRA1
hspb6	ENSDARG00000077236	-2.94	3.93	5.98E-05	1.28E-03	HSPB6
GPR52	ENSDARG00000093460	-2.93	2.24	8.20E-07	3.79E-05	GPR52
hmbox1a	ENSDARG00000027082	-2.89	0.63	1.02E-03	1.12E-02	HMBOX1
phkg1a	ENSDARG00000030604	-2.89	2.55	8.53E-06	2.69E-04	PHKG1
cpa1	ENSDARG00000030915	-2.88	-0.22	4.41E-03	3.27E-02	CPA1
tnnt1	ENSDARG00000037954	-2.88	1.27	4.65E-03	3.38E-02	TNNT2
klf7a	ENSDARG00000073857	-2.87	-0.09	2.16E-03	1.93E-02	KLF7
dennd1b	ENSDARG00000029374	-2.86	2.27	3.55E-06	1.32E-04	DENND1B
slc6a6a	ENSDARG00000012534	-2.85	9.45	6.42E-06	2.16E-04	SLC6A6
opa1	ENSDARG00000044329	-2.84	2.96	2.45E-04	3.85E-03	OPA1
dlgap3	ENSDARG00000055459	-2.83	0.25	7.00E-04	8.50E-03	DLGAP3
cel.1	ENSDARG00000017490	-2.82	1.63	1.75E-04	2.97E-03	CEL

fam101a	ENSDARG00000023484	-2.81	4.36	1.80E-09	1.85E-07	FAM101A
FBLN7	ENSDARG00000089519	-2.81	0.43	5.53E-03	3.81E-02	FBLN7
dnah9	ENSDARG00000097705	-2.79	1.63	1.77E-04	3.00E-03	DNAH9
grb10b	ENSDARG00000035308	-2.76	4.08	1.13E-08	9.43E-07	GRB10
grm6b	ENSDARG00000025671	-2.74	1.27	2.42E-03	2.12E-02	GRM6
celsr1b	ENSDARG00000058259	-2.74	2.82	5.71E-05	1.24E-03	CELSR1
si:dkeyp-75b4.10	ENSDARG00000079043	-2.72	8.16	1.26E-08	1.03E-06	REG1B
ptges3b	ENSDARG00000089626	-2.71	1.97	2.74E-04	4.18E-03	PTGES3
mkl2a	ENSDARG00000088307	-2.70	2.15	5.15E-05	1.15E-03	MKL2
mical2a	ENSDARG00000075608	-2.70	3.06	3.06E-07	1.61E-05	MICAL2
map2	ENSDARG00000055052	-2.69	3.04	1.47E-05	4.18E-04	MAP2
cacna1aa	ENSDARG00000037905	-2.68	1.45	4.68E-04	6.25E-03	CACNA1A
try	ENSDARG00000042993	-2.67	2.91	1.22E-03	1.28E-02	PRSS1
roraa	ENSDARG00000031768	-2.67	2.96	8.81E-07	4.01E-05	RORA
cdr2a	ENSDARG00000035952	-2.67	1.63	3.30E-04	4.77E-03	CDR2
fgfr3	ENSDARG00000004782	-2.66	0.42	1.68E-03	1.62E-02	FGFR3
ptprq	ENSDARG00000008849	-2.66	3.53	1.72E-08	1.37E-06	PTPRQ
nav3	ENSDARG00000005476	-2.66	6.77	1.29E-09	1.38E-07	NAV3
rab44	ENSDARG00000028389	-2.66	6.71	1.03E-10	1.47E-08	rab44
phlda1	ENSDARG00000039714	-2.65	3.11	2.36E-06	9.36E-05	PHLDA1
bend5	ENSDARG00000075624	-2.63	2.09	6.97E-06	2.30E-04	BEND5
lcor	ENSDARG00000070907	-2.63	0.81	3.13E-04	4.58E-03	LCOR
xylt1	ENSDARG00000061248	-2.62	3.81	4.64E-07	2.34E-05	XYLT1
colq	ENSDARG00000019692	-2.62	4.10	3.14E-07	1.64E-05	colq
prkceb	ENSDARG00000069928	-2.62	0.99	5.68E-04	7.25E-03	PRKCE
dscamb	ENSDARG00000028118	-2.60	3.61	5.17E-05	1.15E-03	DSCAM
AGO1	ENSDARG00000092644	-2.59	2.03	1.22E-04	2.23E-03	AGO1
sla2	ENSDARG00000020788	-2.59	2.28	1.92E-05	5.21E-04	SLA2
tenm1	ENSDARG00000003403	-2.59	0.28	1.51E-03	1.50E-02	TENM1
slc23a2	ENSDARG00000017365	-2.58	2.32	1.01E-05	3.09E-04	SLC23A2
sh3gl3a	ENSDARG00000013360	-2.58	1.38	9.71E-05	1.88E-03	SH3GL3
si:dkey-71b5.7	ENSDARG00000080675	-2.56	2.25	2.11E-05	5.63E-04	OTOA
il2rb	ENSDARG00000075720	-2.55	4.35	4.52E-07	2.28E-05	IL2RB
dgkh	ENSDARG00000018716	-2.54	4.69	7.88E-06	2.52E-04	DGKH
nkiras2	ENSDARG00000089585	-2.53	2.33	4.88E-03	3.51E-02	NKIRAS2
lrrc58a	ENSDARG00000076773	-2.52	2.95	7.25E-04	8.65E-03	LRRC58
TPPP2	ENSDARG00000035338	-2.52	0.46	5.54E-03	3.82E-02	TPPP3
mia2	ENSDARG00000078023	-2.51	1.56	3.87E-04	5.38E-03	MIA2
zbtb34	ENSDARG00000013492	-2.50	2.07	1.61E-05	4.51E-04	ZBTB34
cd4	ENSDARG00000070668	-2.50	1.90	8.03E-04	9.30E-03	cd4
LRP3	ENSDARG00000008485	-2.50	2.63	1.26E-03	1.32E-02	LRP3
col4a3	ENSDARG00000003395	-2.49	3.71	1.53E-07	9.00E-06	COL4A5
atf2	ENSDARG00000023903	-2.49	0.74	8.72E-04	9.93E-03	ATF2
atp10a	ENSDARG00000061039	-2.49	2.81	2.17E-05	5.73E-04	ATP10A
notch1b	ENSDARG00000052094	-2.48	5.93	6.40E-10	7.54E-08	NOTCH1
scamp5a	ENSDARG00000018743	-2.48	1.12	7.80E-04	9.15E-03	SCAMP5
aatka	ENSDARG00000078222	-2.48	6.26	2.36E-07	1.28E-05	AATK
slc6a8	ENSDARG00000043646	-2.47	4.42	8.91E-06	2.79E-04	SLC6A8
si:ch211-207d6.2	ENSDARG00000031658	-2.47	1.68	1.33E-04	2.41E-03	KIAA1217

SIPA1	ENSDARG00000076697	-2.46	3.85	2.74E-08	2.10E-06	SIPA1L2
rorca	ENSDARG00000057231	-2.45	4.80	7.86E-09	6.91E-07	rorc
slc12a2	ENSDARG00000086870	-2.45	3.13	1.06E-05	3.20E-04	SLC12A2
epha4b	ENSDARG00000011600	-2.45	2.98	3.12E-05	7.73E-04	EPHA4
scube3	ENSDARG00000011490	-2.45	1.88	7.71E-05	1.56E-03	SCUBE3
hspa4a	ENSDARG00000004754	-2.44	7.15	9.43E-04	1.05E-02	HSPA4
kif1aa	ENSDARG00000061817	-2.44	2.63	2.64E-05	6.72E-04	KIF1A
PLEKHA6	ENSDARG00000020328	-2.41	6.47	5.68E-07	2.78E-05	PLEKHA6
rab3ab	ENSDARG00000043835	-2.41	1.54	2.00E-04	3.27E-03	RAB3A
camkvl	ENSDARG00000057000	-2.41	1.37	1.62E-03	1.58E-02	ADNP
sall3b	ENSDARG00000057586	-2.40	0.76	1.18E-03	1.25E-02	sall3
rhobtb2a	ENSDARG00000016868	-2.40	3.81	2.22E-05	5.81E-04	RHOBTB1
mtf1	ENSDARG00000090180	-2.39	2.11	4.10E-05	9.61E-04	MTF1
map1ab	ENSDARG00000022045	-2.37	1.83	8.91E-04	1.01E-02	MAP1A
TNFSF14	ENSDARG00000076274	-2.37	0.49	3.27E-03	2.62E-02	tnfsf14
pcnxl3	ENSDARG00000019501	-2.37	4.95	2.21E-09	2.27E-07	pcnxl3
ATP8B4	ENSDARG00000079453	-2.37	4.03	1.37E-07	8.24E-06	ATP8B4
crhr1	ENSDARG00000003989	-2.37	1.01	3.77E-03	2.92E-02	CRHR1
crtac1a	ENSDARG00000059826	-2.37	0.57	5.61E-03	3.86E-02	CRTAC1
slco1f1	ENSDARG00000037605	-2.36	7.80	7.42E-04	8.79E-03	slco1f1
vdrb	ENSDARG00000070721	-2.36	2.18	2.51E-04	3.92E-03	VDR
MAP3K2	ENSDARG00000062884	-2.36	2.99	4.87E-06	1.73E-04	MAP3K2
pnoca	ENSDARG00000025024	-2.35	1.40	6.42E-03	4.27E-02	PNOC
KIF21B	ENSDARG00000009733	-2.35	3.24	2.48E-06	9.74E-05	KIF21B
stim2b	ENSDARG00000001776	-2.33	2.31	3.24E-05	7.92E-04	STIM2
il11ra	ENSDARG00000026736	-2.33	3.17	7.04E-06	2.31E-04	IL11RA
nbeal2	ENSDARG00000057508	-2.33	5.59	5.34E-09	5.00E-07	NBEAL2
MCF2L2	ENSDARG00000079742	-2.32	2.32	4.04E-05	9.51E-04	MCF2L2
tnc	ENSDARG00000021948	-2.32	2.97	2.84E-06	1.09E-04	TNC
sptbn2	ENSDARG00000053956	-2.32	6.56	1.24E-07	7.56E-06	SPTBN2
irx3b	ENSDARG00000031138	-2.32	5.61	5.01E-05	1.13E-03	IRX3
ascc1	ENSDARG00000077760	-2.32	4.32	3.07E-06	1.16E-04	ASCC1
eef2a.2	ENSDARG00000042065	-2.31	2.15	8.63E-05	1.71E-03	EEF2
ar	ENSDARG00000067976	-2.31	6.77	6.79E-08	4.55E-06	AR
DNAH9	ENSDARG00000087112	-2.30	1.68	6.44E-04	7.93E-03	DNAH9
itga9	ENSDARG00000032435	-2.30	0.58	3.10E-03	2.53E-02	ITGA9
ppp1r9a	ENSDARG00000061304	-2.29	2.97	7.79E-06	2.50E-04	PPP1R9A
ctsbb	ENSDARG00000067570	-2.29	5.38	1.12E-08	9.40E-07	CTSB
col4a4	ENSDARG00000002831	-2.28	2.85	2.70E-05	6.83E-04	COL4A4
hydin	ENSDARG00000056764	-2.28	5.06	1.50E-07	8.87E-06	HYDIN
col27a1b	ENSDARG00000028236	-2.27	1.52	2.98E-04	4.42E-03	COL27A1
gatad2b	ENSDARG00000005834	-2.27	4.16	1.29E-08	1.05E-06	GATAD2B
msh4	ENSDARG00000075826	-2.27	1.14	3.99E-03	3.05E-02	MSH4
scn4ab	ENSDARG00000034588	-2.27	4.11	1.09E-07	6.89E-06	SCN4A
lamb2	ENSDARG00000002084	-2.27	4.46	4.73E-08	3.38E-06	LAMB2
zmiz2	ENSDARG00000079812	-2.26	4.85	1.61E-07	9.39E-06	ZMIZ2
JADE2	ENSDARG00000053389	-2.25	3.28	3.22E-05	7.88E-04	JADE2
gnao1a	ENSDARG00000016676	-2.23	4.47	1.63E-07	9.49E-06	GNAO1
atp1b1b	ENSDARG00000076833	-2.23	1.59	2.60E-03	2.23E-02	ATP1B1

TMEM132E	ENSDARG00000090830	-2.23	1.78	6.71E-04	8.21E-03	TMEM132E
fmnl2a	ENSDARG00000012586	-2.22	3.01	1.62E-05	4.54E-04	FMNL2
setbp1	ENSDARG00000093799	-2.22	3.96	6.93E-07	3.31E-05	SETBP1
map2k7	ENSDARG00000008279	-2.22	2.00	1.94E-04	3.21E-03	MAP2K7
plekhf1	ENSDARG00000027852	-2.20	5.69	8.67E-04	9.88E-03	PLEKHF1
igf2bp1	ENSDARG00000061478	-2.20	3.06	2.88E-05	7.20E-04	IGF2BP1
dab1a	ENSDARG00000059939	-2.20	2.54	1.37E-04	2.47E-03	DAB1
slc6a2	ENSDARG00000016141	-2.19	7.26	5.17E-04	6.71E-03	SLC6A2
csad	ENSDARG00000026348	-2.19	5.99	2.35E-04	3.72E-03	CSAD
itgb3b	ENSDARG00000045070	-2.18	3.15	5.29E-05	1.17E-03	ITGB3
trioa	ENSDARG00000019426	-2.18	4.88	9.37E-08	6.15E-06	TRIO
sema3bl	ENSDARG00000007560	-2.18	2.51	1.40E-04	2.52E-03	SEMA3G
vcana	ENSDARG00000078680	-2.17	0.66	6.82E-03	4.47E-02	VCAN
nadl1.2	ENSDARG00000007149	-2.16	3.86	6.44E-04	7.93E-03	L1CAM
MAP1B	ENSDARG00000060434	-2.16	1.38	3.64E-03	2.84E-02	MAP1B
hdac4	ENSDARG00000041204	-2.16	3.61	1.17E-06	5.15E-05	HDAC4
pparab	ENSDARG00000054323	-2.16	0.53	6.75E-03	4.43E-02	PPARA
grin2ab	ENSDARG00000070543	-2.16	3.31	1.23E-03	1.29E-02	GRIN2A
hipk2	ENSDARG00000042518	-2.15	6.41	1.11E-06	4.92E-05	HIPK2
agrn	ENSDARG00000096339	-2.14	1.44	1.32E-03	1.36E-02	AGRN
zgc:101640	ENSDARG00000022807	-2.14	7.08	9.89E-08	6.36E-06	PITPNC1
fn1b	ENSDARG00000006526	-2.14	6.23	2.87E-04	4.32E-03	FN1
PHKA2	ENSDARG00000030687	-2.14	3.76	5.38E-06	1.87E-04	PHKA2
ryr1b	ENSDARG00000023797	-2.14	1.86	4.52E-03	3.33E-02	RYR2
kalrna	ENSDARG00000078117	-2.12	2.26	7.23E-04	8.65E-03	KALRN
igf1ra	ENSDARG00000027423	-2.12	3.66	1.36E-06	5.79E-05	IGF1R
tpbgb	ENSDARG00000037186	-2.12	2.60	3.38E-04	4.85E-03	TPBG
prss12	ENSDARG00000061830	-2.12	1.41	3.32E-03	2.66E-02	PRSS12
hmcn2	ENSDARG00000079327	-2.12	1.88	2.59E-03	2.23E-02	HMCN2
slc8a1b	ENSDARG00000043406	-2.12	4.36	1.95E-06	7.89E-05	SLC8A1
crim1	ENSDARG00000029668	-2.11	4.44	2.16E-07	1.20E-05	CRIM1
palm2	ENSDARG00000069608	-2.11	4.47	2.44E-07	1.31E-05	PALM2
rasgrp3	ENSDARG00000077864	-2.11	4.37	4.04E-05	9.51E-04	RASGRP3
cnnm4	ENSDARG00000074309	-2.11	4.49	1.02E-07	6.52E-06	CNNM4
gnb1b	ENSDARG00000005944	-2.11	4.79	1.34E-05	3.90E-04	GNB1
atp2b2	ENSDARG00000063433	-2.11	0.78	2.73E-03	2.31E-02	ATP2B2
cspg4	ENSDARG00000078227	-2.10	1.20	2.60E-03	2.24E-02	CSPG4
dnmt3aa	ENSDARG00000005394	-2.09	4.12	2.08E-07	1.16E-05	DNMT3A
cfh	ENSDARG00000075761	-2.09	6.04	2.33E-07	1.27E-05	CFH
col4a1	ENSDARG00000055009	-2.09	6.56	6.09E-07	2.96E-05	COL4A1
spen	ENSDARG00000074245	-2.08	5.32	1.38E-07	8.31E-06	SPEN
nfic	ENSDARG00000043210	-2.08	6.81	6.52E-08	4.41E-06	NFIC
MAP3K15	ENSDARG00000013310	-2.08	3.26	1.15E-05	3.41E-04	MAP3K15
cpeb3	ENSDARG00000060103	-2.08	2.63	4.94E-04	6.48E-03	CPEB3
smap2	ENSDARG00000061446	-2.07	2.43	1.35E-04	2.44E-03	SMAP2
itga3a	ENSDARG00000037917	-2.07	5.81	6.76E-06	2.25E-04	ITGA3
zbtb43	ENSDARG00000045983	-2.07	1.21	1.61E-03	1.57E-02	ZBTB43
fat1a	ENSDARG00000017591	-2.07	6.35	2.18E-07	1.20E-05	FAT1
aip	ENSDARG00000069699	-2.06	4.45	2.31E-04	3.67E-03	AIP

BBX	ENSDARG00000012699	-2.05	2.38	4.76E-04	6.33E-03	BBX
flncb	ENSDARG00000018820	-2.05	4.66	1.23E-07	7.51E-06	FLNC
b3gat2	ENSDARG00000030733	-2.04	2.13	2.24E-04	3.59E-03	B3GAT2
pdgfrb	ENSDARG00000057345	-2.04	4.25	3.90E-06	1.43E-04	PDGFRB
si:dkey-11f4.16	ENSDARG00000076224	-2.04	2.97	1.06E-04	2.02E-03	CD58
ankrd52a	ENSDARG00000036826	-2.03	3.98	8.73E-07	4.00E-05	ANKRD52
slco5a1	ENSDARG00000071685	-2.03	4.84	9.05E-06	2.82E-04	SLCO5A1
znf106a	ENSDARG00000016651	-2.03	7.82	4.49E-08	3.22E-06	ZNF106
zgc:112334	ENSDARG00000005879	-2.02	2.08	2.81E-04	4.27E-03	GDI1
dmd	ENSDARG00000008487	-2.02	3.37	4.95E-05	1.12E-03	DMD
kif5bb	ENSDARG00000075251	-2.02	3.46	1.31E-05	3.80E-04	KIF5B
SLC39A14	ENSDARG00000090174	-2.02	2.33	2.54E-04	3.97E-03	SLC39A14
zzef1	ENSDARG00000094380	-2.01	5.01	6.32E-08	4.29E-06	ZZEF1
ahnak	ENSDARG00000061764	-2.00	8.28	2.23E-07	1.22E-05	AHNAK
si:dkey-32e23.4	ENSDARG00000063159	-2.00	2.83	7.19E-05	1.48E-03	DNM1L
nphs1	ENSDARG00000060758	-2.00	4.52	1.07E-06	4.77E-05	NPHS1
tet3	ENSDARG00000062646	-2.00	5.38	2.60E-07	1.38E-05	TET3
PLA2R1	ENSDARG00000077474	-1.99	3.05	6.16E-05	1.31E-03	PLA2R1
epas1b	ENSDARG00000057671	-1.98	5.09	1.93E-06	7.83E-05	EPAS1
dgcr2	ENSDARG00000042962	-1.98	3.60	3.30E-05	8.03E-04	DGCR2
gch1	ENSDARG00000070453	-1.98	1.64	1.11E-03	1.19E-02	GCH1
FAT4	ENSDARG00000045665	-1.98	2.50	3.06E-04	4.50E-03	FAT4
sst3	ENSDARG00000031649	-1.98	2.21	1.41E-03	1.43E-02	sst3
pdk3a	ENSDARG00000014527	-1.98	4.23	3.45E-05	8.36E-04	PDK3
lck	ENSDARG00000059282	-1.97	2.01	1.06E-03	1.15E-02	LCK
enpp1	ENSDARG00000005789	-1.97	6.60	6.33E-06	2.15E-04	ENPP1
dnah9	ENSDARG00000004221	-1.97	2.93	8.37E-05	1.67E-03	DNAH9
sypa	ENSDARG00000042974	-1.96	1.26	3.67E-03	2.86E-02	SYP
ftr50	ENSDARG00000054153	-1.96	1.54	1.47E-03	1.48E-02	ftr50
cdhr1a	ENSDARG00000004643	-1.95	3.85	4.86E-06	1.73E-04	CDHR1
cyp2aa7	ENSDARG00000091601	-1.95	2.17	8.77E-04	9.96E-03	cyp2aa7
sema4ga	ENSDARG00000076595	-1.95	1.30	2.11E-03	1.90E-02	SEMA4G
atp1a3a	ENSDARG00000018259	-1.95	6.26	1.35E-05	3.92E-04	ATP1A3
gpa33	ENSDARG00000040898	-1.95	3.66	7.17E-05	1.48E-03	GPA33
ccdc85ca	ENSDARG00000005232	-1.95	2.74	2.89E-04	4.34E-03	CCDC85C
si:ch211-133n4.7	ENSDARG00000095424	-1.94	3.97	1.64E-03	1.59E-02	CLEC4E
ehd3	ENSDARG00000007869	-1.94	4.36	1.53E-06	6.45E-05	EHD3
CACUL1	ENSDARG00000021885	-1.93	2.26	7.17E-04	8.63E-03	CACUL1
FAM107A	ENSDARG00000086300	-1.93	2.22	7.16E-04	8.63E-03	FAM107A
pitpnb	ENSDARG00000036005	-1.93	5.20	4.25E-07	2.17E-05	PITPNB
slc41a1	ENSDARG00000070214	-1.93	1.63	2.97E-03	2.46E-02	SLC41A1
golgb1	ENSDARG00000061951	-1.93	6.19	8.23E-07	3.79E-05	GOLGB1
kank2	ENSDARG00000018393	-1.93	2.93	1.91E-04	3.16E-03	KANK2
COL13A1	ENSDARG00000091398	-1.93	2.19	1.44E-03	1.45E-02	COL13A1
SEMA4C	ENSDARG00000079611	-1.92	3.69	8.32E-06	2.65E-04	SEMA4C
pcdh1b	ENSDARG00000036175	-1.92	5.53	4.73E-06	1.70E-04	PCDH1
WWC1	ENSDARG00000076041	-1.92	3.25	7.05E-04	8.54E-03	WWC1
SPTBN5	ENSDARG00000097683	-1.92	6.84	6.42E-07	3.12E-05	SPTBN5
ches1	ENSDARG00000043553	-1.92	1.23	3.19E-03	2.58E-02	ches1

trak1	ENSDARG00000041304	-1.92	5.76	1.74E-06	7.14E-05	TRAK1
CCDC178	ENSDARG00000090429	-1.91	1.83	7.58E-03	4.82E-02	CCDC178
unc5b	ENSDARG00000033327	-1.91	4.74	8.91E-05	1.75E-03	UNC5B
zbtb44	ENSDARG00000061110	-1.91	2.10	3.55E-03	2.79E-02	ZBTB44
ZNF462	ENSDARG00000063381	-1.91	4.29	1.80E-06	7.34E-05	ZNF462
NACC1	ENSDARG00000078238	-1.89	1.35	3.62E-03	2.83E-02	NACC1
ahcyl2	ENSDARG00000039343	-1.89	7.65	1.26E-04	2.29E-03	AHCYL2
mark2b	ENSDARG00000032458	-1.89	7.01	6.79E-07	3.26E-05	MARK2
dhh	ENSDARG00000037062	-1.88	5.56	2.75E-06	1.06E-04	DHH
histh1l	ENSDARG00000035519	-1.88	7.21	2.29E-05	5.97E-04	HIST1H1E
ptch2	ENSDARG00000055026	-1.88	3.08	4.79E-04	6.36E-03	PTCH2
naalad2	ENSDARG00000021383	-1.88	6.57	5.37E-06	1.87E-04	NAALAD2
lyst	ENSDARG00000008575	-1.87	5.05	1.32E-06	5.65E-05	LYST
gpd2	ENSDARG00000062430	-1.87	4.88	1.40E-06	5.93E-05	GPD2
glsa	ENSDARG00000062812	-1.86	3.24	1.83E-04	3.07E-03	GLS
sema4f	ENSDARG00000079014	-1.86	1.09	4.23E-03	3.18E-02	SEMA4F
slc26a2	ENSDARG00000011618	-1.85	4.42	1.76E-03	1.67E-02	SLC26A2
lrp2a	ENSDARG00000060649	-1.85	9.00	2.31E-06	9.20E-05	LRP2
mxd1	ENSDARG00000032039	-1.83	3.05	3.43E-04	4.92E-03	MXD1
FOXJ3	ENSDARG00000075774	-1.83	2.97	3.72E-04	5.21E-03	FOXJ3
anks1ab	ENSDARG00000078901	-1.83	1.21	6.87E-03	4.49E-02	ANKS1a
slc25a37	ENSDARG00000073743	-1.83	5.67	5.98E-05	1.28E-03	SLC25A37
pygo1	ENSDARG00000044963	-1.83	1.50	2.72E-03	2.31E-02	PYGO1
ankrd11	ENSDARG00000051886	-1.83	6.62	1.63E-06	6.80E-05	ANKRD11
prkcz	ENSDARG00000043332	-1.83	2.96	3.57E-04	5.06E-03	PRKCZ
chst12a	ENSDARG00000028786	-1.83	2.13	1.49E-03	1.49E-02	CHST12
atm	ENSDARG00000063465	-1.83	2.29	2.06E-03	1.87E-02	ATM
slc27a4	ENSDARG00000017047	-1.82	3.41	7.76E-05	1.57E-03	SLC27A4
usp34	ENSDARG00000037734	-1.82	2.78	1.88E-04	3.14E-03	USP34
egln2	ENSDARG00000062562	-1.82	3.95	4.60E-06	1.66E-04	EGLN2
frem3	ENSDARG00000074677	-1.82	1.32	6.89E-03	4.50E-02	FREM2
flrt2	ENSDARG00000079355	-1.82	3.55	7.40E-05	1.51E-03	FLRT2
numb	ENSDARG00000027279	-1.81	5.82	1.37E-05	3.97E-04	NUMB
lama1	ENSDARG00000056043	-1.81	1.86	3.28E-03	2.63E-02	LAMA1
SBNO1	ENSDARG00000087600	-1.81	2.18	1.27E-03	1.32E-02	SBNO1
scinlb	ENSDARG00000058348	-1.81	8.75	1.93E-06	7.83E-05	scinl
si:dkeyp-87a6.1	ENSDARG00000056888	-1.81	5.75	1.21E-04	2.22E-03	DNAH5
lamb1b	ENSDARG00000045524	-1.80	5.61	3.59E-04	5.08E-03	lamb1
DST	ENSDARG00000024748	-1.80	6.70	2.62E-06	1.02E-04	DST
azi2	ENSDARG00000042997	-1.80	3.97	1.05E-04	2.00E-03	AZI2
RPS6KA5	ENSDARG00000060551	-1.80	3.85	4.81E-04	6.38E-03	RPS6KA5
cept1a	ENSDARG00000058716	-1.79	3.04	3.13E-03	2.55E-02	CHPT1
MXD4	ENSDARG00000054031	-1.79	3.07	4.43E-04	6.01E-03	MXD4
CTIF	ENSDARG00000090617	-1.79	2.25	1.35E-03	1.39E-02	CTIF
TBC1D10C	ENSDARG00000037408	-1.79	5.25	4.44E-06	1.60E-04	TBC1D10C
kmt2a	ENSDARG00000004537	-1.78	6.67	1.63E-05	4.54E-04	KMT2A
prune2	ENSDARG00000059423	-1.78	4.30	3.62E-05	8.68E-04	PRUNE2
nudt3b	ENSDARG00000042123	-1.77	2.46	7.87E-04	9.17E-03	NUDT3
hcn2b	ENSDARG00000061665	-1.77	2.30	2.89E-03	2.41E-02	HCN2

slc7a1	ENSDARG00000016439	-1.77	2.65	1.14E-03	1.22E-02	SLC7A1
prlrb	ENSDARG00000045955	-1.77	5.64	1.22E-05	3.60E-04	PRLR
appa	ENSDARG00000059036	-1.76	5.91	3.33E-06	1.25E-04	APP
pho	ENSDARG00000035133	-1.76	3.23	1.59E-04	2.77E-03	pho
alox5a	ENSDARG00000057273	-1.76	5.18	7.49E-06	2.43E-04	ALOX5
arhgap31	ENSDARG00000059472	-1.76	4.25	1.99E-05	5.37E-04	arhgap31
UGT8	ENSDARG00000037455	-1.75	5.21	2.15E-05	5.72E-04	UGT8

Supplementary Table 2 - GSEA signatures for zap70y442 downregulated genes

Zap70^{y442} vs wt downregulated genes GSEA gene signatures					
Gene Set Name	# Genes in Gene Set (K)	# Genes in Overlap (k)	k/K	p-value	FDR q-value
BLALOCK_ALZHEIMERS_DISEASE_UP	1691	66	0.039	2.00E-24	1.93E-20
YOSHIMURA_MAPK8_TARGETS_UP	1305	56	0.0429	1.09E-22	5.24E-19
GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN	1781	62	0.0348	1.91E-20	6.13E-17
BENPORATH_ES_WITH_H3K27ME3	1118	48	0.0429	1.52E-19	3.66E-16
BENPORATH_SUZ12_TARGETS	1038	46	0.0443	2.68E-19	5.17E-16
BRUINS_UVC_RESPONSE_VIA_TP53_GROUP_A	898	42	0.0468	1.55E-18	2.50E-15
MEISSNER_BRAIN_HCP_WITH_H3K4ME3_AND_H3K27ME3	1069	45	0.0421	4.73E-18	6.52E-15
NABA_MATRISOME	1028	43	0.0418	3.44E-17	4.15E-14
DACOSTA_UV_RESPONSE_VIA_ERCC3_DN	855	39	0.0456	6.43E-17	6.89E-14
GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_DN	1080	43	0.0398	2.00E-16	1.93E-13
NABA_CORE_MATRISOME	275	23	0.0836	6.29E-16	5.52E-13
GOZGIT_ESR1_TARGETS_DN	781	36	0.0461	7.73E-16	6.22E-13
WONG_ADULT_TISSUE_STEM_MODULE	721	34	0.0472	2.62E-15	1.95E-12
BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP	425	26	0.0612	1.42E-14	9.80E-12
PID_INTEGRIN1_PATHWAY	66	13	0.197	1.95E-14	1.25E-11
KEGG_ECM_RECEPTOR_INTERACTION	84	14	0.1667	2.23E-14	1.35E-11
SCHAEFFER_PROSTATE_DEVELOPMENT_6HR_DN	514	28	0.0545	2.43E-14	1.38E-11
MILI_PSEUDOPODIA_CHEMOTAXIS_DN	457	26	0.0569	7.70E-14	4.13E-11
RIGGI_EWING_SARCOMA_PROGENITOR_UP	430	25	0.0581	1.45E-13	7.34E-11
KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN	329	22	0.0669	2.66E-13	1.18E-10
GSE14699_NAIVE_VS_DELETIONAL_TOLERANCE_CD8_TCELL_DN	200	18	0.09	2.69E-13	1.18E-10
GSE7460_TCONV_VS_TREG_LN_UP	200	18	0.09	2.69E-13	1.18E-10
BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP	811	33	0.0407	4.11E-13	1.72E-10
FEVR_CTNNB1_TARGETS_UP	682	30	0.044	7.09E-13	2.79E-10
BROWNE_HCMV_INFECTION_48HR_DN	504	26	0.0516	7.24E-13	2.79E-10
REACTOME_AXON_GUIDANCE	251	19	0.0757	1.30E-12	4.82E-10
DELYS_THYROID_CANCER_UP	443	24	0.0542	2.01E-12	7.19E-10
SANSOM_APC_TARGETS_DN	366	22	0.0601	2.23E-12	7.68E-10
GSE33374_CD8_ALPHAALPHA_VS_ALPHABETA_CD161_HIGH_TCELL_UP	200	17	0.085	3.13E-12	9.75E-10
GSE7460_FOXP3_MUT_VS_WT_ACT_TCONV_DN	200	17	0.085	3.13E-12	9.75E-10
GSE7852_TREG_VS_TCONV_LN_DN	200	17	0.085	3.13E-12	9.75E-10
PID_INTEGRIN3_PATHWAY	43	10	0.2326	3.48E-12	1.05E-09
MIKKELSEN_MEF_HCP_WITH_H3K27ME3	590	27	0.0458	4.19E-12	1.22E-09
REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS	79	12	0.1519	5.15E-12	1.46E-09
ZWANG_TRANSIENTLY_UP_BY_1ST_EGF_PULSE_ONLY	1839	49	0.0266	5.81E-12	1.60E-09
BENPORATH_EED_TARGETS	1062	36	0.0339	6.71E-12	1.80E-09
BENPORATH_PRC2_TARGETS	652	28	0.0429	7.44E-12	1.94E-09
DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN	483	24	0.0497	1.23E-11	3.12E-09
MILI_PSEUDOPODIA_HAPTOTAXIS_DN	668	28	0.0419	1.31E-11	3.24E-09
LIM_MAMMARY_STEM_CELL_UP	489	24	0.0491	1.59E-11	3.83E-09
ONDER_CDH1_TARGETS_2_UP	256	18	0.0703	1.75E-11	4.11E-09
GAVIN_FOXP3_TARGETS_CLUSTER_P7	90	12	0.1333	2.53E-11	5.81E-09
PEREZ_TP53_TARGETS	1174	37	0.0315	2.72E-11	6.10E-09
CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN	460	23	0.05	2.93E-11	6.42E-09
GSE3982_BCELL_VS_CENT_MEMORY_CD4_TCELL_DN	200	16	0.08	3.42E-11	7.18E-09
GSE3982_MEMORY_CD4_TCELL_VS_BCELL_UP	200	16	0.08	3.42E-11	7.18E-09
KEGG_FOCAL_ADHESION	201	16	0.0796	3.69E-11	7.57E-09
DODD_NASOPHARYNGEAL_CARCINOMA_UP	1821	47	0.0258	4.77E-11	9.58E-09
SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP	351	20	0.057	5.86E-11	1.14E-08
NABA_BASEMENT_MEMBRANES	40	9	0.225	5.90E-11	1.14E-08
SWEET_LUNG_CANCER_KRAS_DN	435	22	0.0506	6.38E-11	1.21E-08
MARTINEZ_RB1_TARGETS_UP	673	27	0.0401	8.16E-11	1.51E-08
KEGG_PATHWAYS_IN_CANCER	328	19	0.0579	1.34E-10	2.45E-08
IVANOVA_HEMATOPOIESIS_STEM_CELL	254	17	0.0669	1.38E-10	2.47E-08
SENESE_HDAC3_TARGETS_UP	501	23	0.0459	1.58E-10	2.77E-08
SMID_BREAST_CANCER_BASAL_DN	701	27	0.0385	2.01E-10	3.46E-08
REACTOME_L1CAM_INTERACTIONS	86	11	0.1279	2.72E-10	4.61E-08
GSE11057_EFF_MEM_VS_CENT_MEM_CD4_TCELL_UP	200	15	0.075	3.49E-10	5.62E-08
GSE13522_CTRL_VS_T_CRUZI_Y_STRAIN_INF_SKIN_IFNAR_KO_UP	200	15	0.075	3.49E-10	5.62E-08
HALLMARK_MYOGENESIS	200	15	0.075	3.49E-10	5.62E-08
MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3	349	19	0.0544	3.82E-10	6.04E-08
BAELDE_DIABETIC_NEPHROPATHY_DN	434	21	0.0484	3.89E-10	6.05E-08
CUI_TCF21_TARGETS_2_DN	830	29	0.0349	4.05E-10	6.20E-08
LIU_PROSTATE_CANCER_DN	481	22	0.0457	4.26E-10	6.42E-08
BLALOCK_ALZHEIMERS_DISEASE_DN	1237	36	0.0291	4.44E-10	6.60E-08
REACTOME_DEVELOPMENTAL_BIOLOGY	396	20	0.0505	4.88E-10	7.13E-08
LIAO_METASTASIS	539	23	0.0427	6.50E-10	9.36E-08
PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_7	403	20	0.0496	6.60E-10	9.37E-08
ONDER_CDH1_TARGETS_2_DN	464	21	0.0453	1.29E-09	1.80E-07
JAATINEN_HEMATOPOIETIC_STEM_CELL_DN	226	15	0.0664	1.90E-09	2.61E-07
LINDGREN_BLADDER_CANCER_CLUSTER_3_DN	229	15	0.0655	2.27E-09	3.09E-07
CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_4	307	17	0.0554	2.50E-09	3.36E-07
NABA_ECM_GLYCOPROTEINS	196	14	0.0714	2.56E-09	3.38E-07

MCBRYAN_PUBERTAL_BREAST_6_7WK_UP	197	14	0.0711	2.73E-09	3.56E-07
NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN	634	24	0.0379	2.91E-09	3.75E-07
GSE10325_CD4_TCELL_VS_BCELL_UP	200	14	0.07	3.32E-09	3.96E-07
GSE20366_TREG_VS_NAIVE_CD4_TCELL_DN	200	14	0.07	3.32E-09	3.96E-07
GSE22886_NAIVE_CD8_TCELL_VS_NKCELL_DN	200	14	0.07	3.32E-09	3.96E-07
GSE23568_CTRL_TRANSDUCED_VS_WT_CD8_TCELL_DN	200	14	0.07	3.32E-09	3.96E-07
GSE35685_CD34POS_CD38NEG_VS_CD34POS_CD10NEG_CD62LPOS_BONE_MARROW_DN	200	14	0.07	3.32E-09	3.96E-07
HALLMARK_ESTROGEN_RESPONSE_EARLY	200	14	0.07	3.32E-09	3.96E-07
MARTINEZ_TP53_TARGETS_DN	593	23	0.0388	3.97E-09	4.67E-07
NUYTTEN_EZH2_TARGETS_UP	1037	31	0.0299	4.09E-09	4.71E-07
KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM	85	10	0.1176	4.10E-09	4.71E-07
DAZARD_RESPONSE_TO_UV_NHEK_DN	318	17	0.0535	4.24E-09	4.82E-07
BRUECKNER_TARGETS_OF_MIRLET7A3_UP	111	11	0.0991	4.33E-09	4.86E-07
PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP	205	14	0.0683	4.56E-09	5.06E-07
WANG_SMARCE1_TARGETS_UP	280	16	0.0571	4.73E-09	5.19E-07
REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH	64	9	0.1406	4.94E-09	5.36E-07
MARTINEZ_RB1_AND_TP53_TARGETS_UP	601	23	0.0383	5.10E-09	5.47E-07
FOSTER_TOLERANT_MACROPHAGE_DN	409	19	0.0465	5.21E-09	5.52E-07
CHANG_IMMORTALIZED_BY_HPV31_DN	65	9	0.1385	5.69E-09	5.97E-07
REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECULES	413	19	0.046	6.09E-09	6.32E-07
WILCOX_RESPONSE_TO_PROGESTERONE_DN	66	9	0.1364	6.54E-09	6.71E-07
KAAB_HEART_ATRIUM_VS_VENTRICLE_UP	249	15	0.0602	7.07E-09	7.18E-07
GABRIELY_MIR21_TARGETS	289	16	0.0554	7.41E-09	7.45E-07
CHICAS_RB1_TARGETS_CONFLUENT	567	22	0.0388	8.63E-09	8.59E-07
KEGG_DILATED_CARDIOMYOPATHY	92	10	0.1087	8.94E-09	8.80E-07
LOPEZ_MBD_TARGETS	957	29	0.0303	9.79E-09	9.54E-07
CHIARADONNA_NEOPLASTIC_TRANSFORMATION_CDC25_UP	120	11	0.0917	9.91E-09	9.56E-07

Supplementary Table 3 - GO term List for zap70^{y442} downregulated genes

Zap70^{y442} vs wt downregulated genes associated Go Terms					
Gene Set Name	# Genes in Gene Set (K)	# Genes in Overlap (k)	k/K	p-value	FDR q-value
PLASMA_MEMBRANE	1426	72	0.0505	1.49E-33	2.16E-30
MEMBRANE	1994	83	0.0416	8.78E-33	6.38E-30
MEMBRANE_PART	1670	75	0.0449	1.18E-31	5.72E-29
PLASMA_MEMBRANE_PART	1158	61	0.0527	2.17E-29	7.89E-27
INTRINSIC_TO_MEMBRANE	1348	63	0.0467	1.73E-27	5.03E-25
INTEGRAL_TO_MEMBRANE	1330	62	0.0466	5.40E-27	1.31E-24
INTRINSIC_TO_PLASMA_MEMBRANE	991	54	0.0545	9.43E-27	1.96E-24
INTEGRAL_TO_PLASMA_MEMBRANE	977	53	0.0542	3.57E-26	6.49E-24
ANATOMICAL_STRUCTURE_DEVELOPMENT	1013	46	0.0454	1.03E-19	1.67E-17
SIGNAL_TRANSDUCTION	1634	57	0.0349	7.16E-19	1.04E-16
SYSTEM_DEVELOPMENT	861	41	0.0476	2.17E-18	2.81E-16
MULTICELLULAR_ORGANISMAL_DEVELOPMENT	1049	45	0.0429	2.32E-18	2.81E-16
SYSTEM_PROCESS	563	32	0.0568	9.67E-17	1.08E-14
ESTABLISHMENT_OF_LOCALIZATION	870	37	0.0425	3.73E-15	3.87E-13
TRANSPORT	795	34	0.0428	4.37E-14	4.24E-12
RECEPTOR_ACTIVITY	583	29	0.0497	8.26E-14	7.51E-12
CELL_SURFACE_RECEPTOR_LINKED_SIGNAL_TRANSDUCTION_GO_0007166	641	30	0.0468	1.46E-13	1.25E-11
CYTOPLASM	2131	56	0.0263	2.60E-13	2.10E-11
NERVOUS_SYSTEM_DEVELOPMENT	385	23	0.0597	7.94E-13	6.07E-11
ENZYME_LINKED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	140	15	0.1071	2.10E-12	1.53E-10
EXTRACELLULAR_REGION	447	23	0.0515	1.65E-11	1.14E-09
PROTEIN_METABOLIC_PROCESS	1231	38	0.0309	2.63E-11	1.74E-09
TRANSMEMBRANE_RECEPTOR_ACTIVITY	418	22	0.0526	2.97E-11	1.88E-09
EXTRACELLULAR_MATRIX_PART	57	10	0.1754	7.03E-11	4.26E-09
PROTEIN_KINASE_ACTIVITY	285	18	0.0632	1.02E-10	5.94E-09
BIOPOLYMER_METABOLIC_PROCESS	1684	44	0.0261	1.42E-10	7.95E-09
PHOSPHOTRANSFERASE_ACTIVITY_ALCOHOL_GROUP_AS_ACCEPTOR	334	19	0.0569	1.83E-10	9.84E-09
NEUROLOGICAL_SYSTEM_PROCESS	379	20	0.0528	2.27E-10	1.18E-08
TRANSFERASE_ACTIVITY_TRANSFERRING_PHOSPHORUS_CONTAINING_GROUPS	424	21	0.0495	2.55E-10	1.28E-08
KINASE_ACTIVITY	369	19	0.0515	9.66E-10	4.64E-08
BASEMENT_MEMBRANE	37	8	0.2162	9.89E-10	4.64E-08
PROTEINACEOUS_EXTRACELLULAR_MATRIX	98	11	0.1122	1.14E-09	5.16E-08
PROTEIN_COMPLEX	816	28	0.0343	1.22E-09	5.37E-08
TRANSMEMBRANE_TRANSPORTER_ACTIVITY	375	19	0.0507	1.26E-09	5.39E-08
EXTRACELLULAR_MATRIX	100	11	0.11	1.41E-09	5.87E-08
MACROMOLECULAR_COMPLEX	945	30	0.0317	1.87E-09	7.56E-08
SUBSTRATE_SPECIFIC_TRANSPORTER_ACTIVITY	392	19	0.0485	2.61E-09	1.03E-07
CELL_CELL_SIGNALING	404	19	0.047	4.27E-09	1.63E-07
EXTRACELLULAR_REGION_PART	338	17	0.0503	1.05E-08	3.91E-07
CELL_DEVELOPMENT	577	22	0.0381	1.18E-08	4.29E-07
SUBSTRATE_SPECIFIC_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	344	17	0.0494	1.36E-08	4.82E-07
REGULATION_OF_DEVELOPMENTAL_PROCESS	440	19	0.0432	1.68E-08	5.82E-07
CELLULAR_PROTEIN_METABOLIC_PROCESS	1117	31	0.0278	2.24E-08	7.57E-07
CELLULAR_MACROMOLECULE_METABOLIC_PROCESS	1131	31	0.0274	2.96E-08	9.79E-07
ORGAN_DEVELOPMENT	571	21	0.0368	4.68E-08	1.51E-06
TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_SIGNALING_PATH	83	9	0.1084	5.09E-08	1.61E-06
LYMPHOCYTE_ACTIVATION	61	8	0.1311	6.28E-08	1.94E-06
INTRACELLULAR_ORGANELLE_PART	1192	31	0.026	9.50E-08	2.88E-06
ORGANELLE_PART	1197	31	0.0259	1.04E-07	3.09E-06
LEUKOCYTE_ACTIVATION	69	8	0.1159	1.68E-07	4.88E-06

Supplementary Table 4 - PCR primers

tcrb and *igm* transcript expression primers			
Gene	PCR #	Forward Primer	Reverse Primer
eef1a1l1	1	atggcacggtgacaacatgct	ccacattaccacgacggatg
Vb14.5-Cb1	1	gaatccaatgtgacgttaacatgc	aagatgacaaggccatacagtc
	2	catgatcataaggaccactacag	gtccgctcttagcaatggtc
V16C1	1	ctcctaattcaaagtatgaggcaac	tagtctgctggatatggtgtact
	2	ctcctaattcaaagtatgaggcaac	cttgctgtccaacaaaccatgctac
V27C1	1	ccagcaaacagacaacacactc	tagtctgctggatatggtgtact
	2	ccagcaaacagacaacacactc	cttgctgtccaacaaaccatgctac
igVH1-Cm	1	gatggacgtgttacaatttgg	acatgaaggttgctgatccac
	2	cctcctcagactctgtggtga	ttgctgatccaccttctaattc
IgVH1-Cm	1	catgacaatggatattgtgtcc	acatgaaggttgctgatccac
	2	ctctgttggtgtcaaacactg	ttgctgatccaccttctaattc
igVH4-Cm	1	caagatgaagaatgctctctg	acatgaaggttgctgatccac
	2	tgtcaaagtatggagtcga	ttgctgatccaccttctaattc
in situ hybridization primers			
hbae1	1	ctccaggatgttgattgtctac	gccaagctatttaggtgacactatagctgagaggaacttgtccattg
lyz	1	tttgtgtctggcgtggatg	gccaagctatttaggtgacactatagaggctcggaggctttgtttg
rag2	1	acatcattttcggcggatac	gccaagctatttaggtgacactatagtggagcagaaggctttcagg