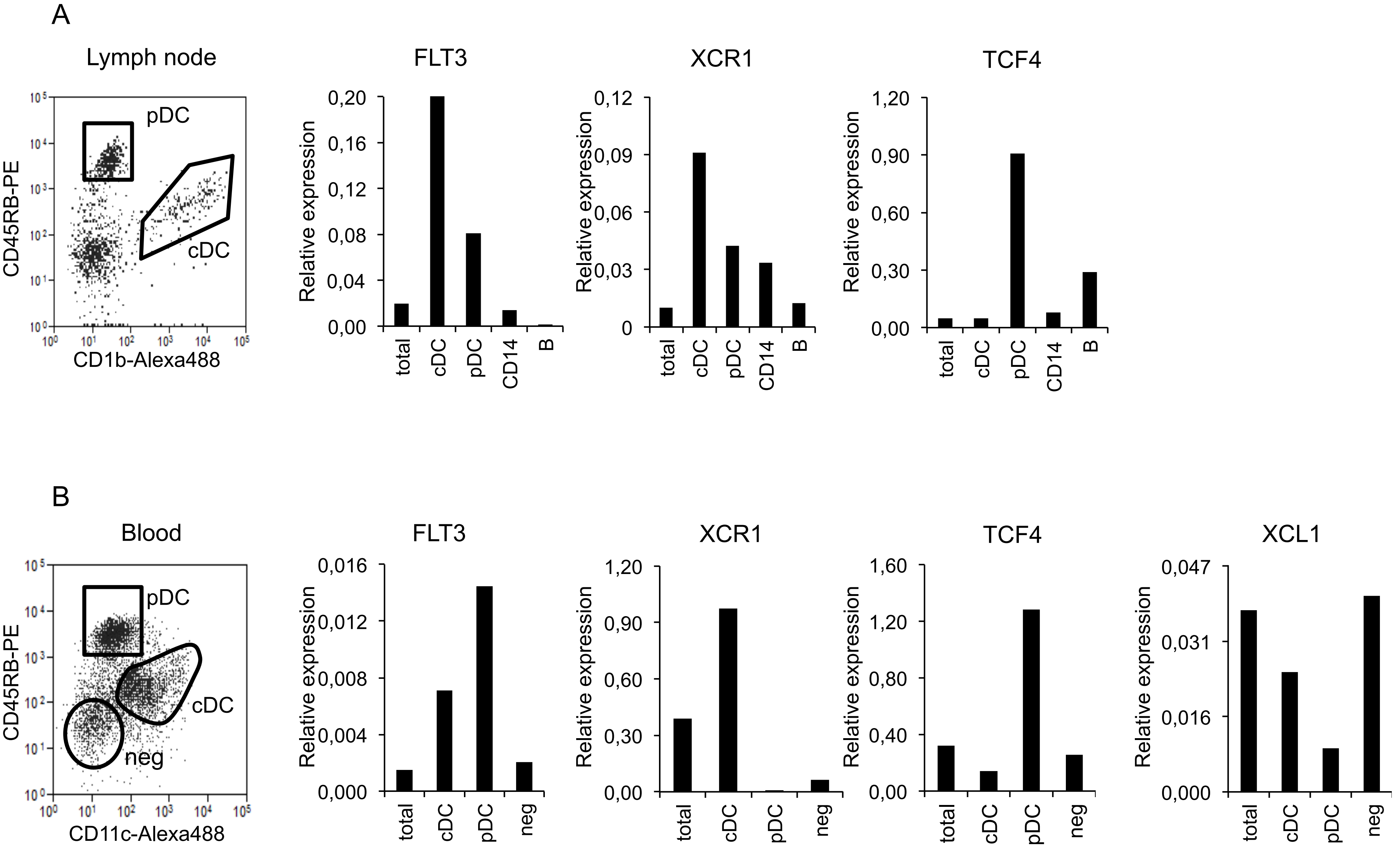
A
Lymph node
CD45RB-PE
CD1b-Alexa488
pDC
cDC
10^0
10^1
10^2
10^3
10^4
10^5
FLT3
Relative expression
0,20
0,16
0,12
0,08
0,04
0,00
total
cDC
pDC
CD14
B
XCR1
Relative expression
0,12
0,09
0,06
0,03
0
total
cDC
pDC
CD14
B
TCF4
Relative expression
1,20
0,90
0,60
0,30
0,00
total
cDC
pDC
CD14
B
B
Blood
CD45RB-PE
CD11c-Alexa488
pDC
cDC
neg
FLT3
Relative expression
0,016
0,012
0,008
0,004
0,000
total
cDC
pDC
neg
XCR1
Relative expression
1,20
0,90
0,60
0,30
0,00
total
cDC
pDC
neg
TCF4
Relative expression
1,60
1,20
0,80
0,40
0,00
total
cDC
pDC
neg
XCL1
Relative expression
0,047
0,031
0,016
0,000
total
cDC
pDC
neg

Figure S1

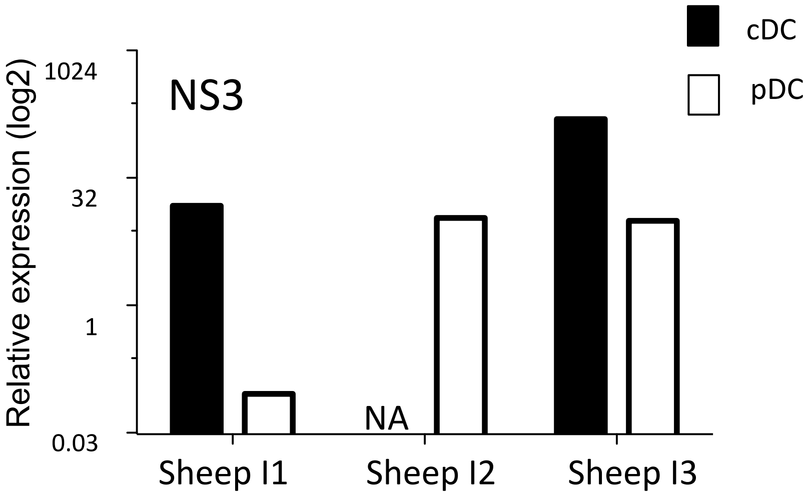
NS3
Relative expression (log2)
1024
32
1
0.03
NA
Sheep I1
Sheep I2
Sheep I3
■ cDC
□ pDC

Figure S2

Supplementary legends

Figure S1. Characterization of sheep cDCs and pDCs in lymphoid organs. A. Lymph node: LD local lymph node cells were stained with anti CD45RB, CD1b, CD8, TCRγ/δ, B, and CD11b mAbs followed by anti-mouse IgG Alexa Fluor 488-conjugated goat Fab or by anti-mouse isotype-specific PE- and Alexa Fluor 647-conjugated goat IgG (see materials and methods). On the resulting gate generated on FSC^{hi} cells and from excluded CD8^{+}TCRγ/δ^{+}B^{+}CD11b^{+} LD cells, the pDC and cDC gates were established based on isotype controls. Blood B cells and monocytes were sorted using the DU2-104 and anti-CD14 mAbs (not shown). A qPCR was performed on the sorted subsets and total LD cells using ovine specific primers for the GAPDH, FLT3, XCR1, TCF4 and XCL1 mRNA detection. DC canonic gene expressions were assessed by qRT-PCR relatively to GAPDH and arbitrary units were calculated by the $2^{-\Delta CT}$ method. **B.** Blood: LD blood cells were labeled as in A except that the anti-CD11c replaced the anti-CD1b mAb. The CD11c^{-}CD45RB^{-} cells (neg cells) were used as controls and may include activated CD8^{+} T cells and/or NK cells, as attested by their high XCL1 expression. Similar results were found with spleen and blood DCs. Sorting and qPCR analyses of canonic DC gene expression on lymph nodes, spleen and blood were done with 2 different sheep and gave similar results.

Figure S2. Viral BTV RNA detection in lymph node cDCs and pDCs. Total RNA extracted from the pDCs of three BTV- infected sheep (sheep I1, I2, I3) and from the cDCs of two BTV- infected sheep (sheep I1 and sheep I3) was processed for BTV RNA detection by qRT-PCR and normalized with GAPDH (ADIAVET® BTV Real-time

A352). Arbitrary units were calculated by the $2^{-\Delta CT}$ method. NA: total RNA from lymph node cDC not available for sheep I2

Table S1. DEG in blood pDCs upon BTV infection*

Official gene symbol	Approved name	Control sheep 1 (log2)	Control sheep 3 (log2)	Infected sheep 1 (log2)	Infected sheep 2 (log2)	Minimal fold change (log2)	Minimal fold change
AHNAK	AHNAK NUCLEOPROTEIN	6.77	6.84	4.70	5.28	-1.49	0.35
AIF1	ALLOGRAFT INFLAMMATORY FACTOR 1	0.26	0.34	2.46	2.49	2.12	4.36
ALOX5AP	ARACHIDONATE 5-LIPOXYGENASE-ACTIVATING PROTEIN	-0.71	-1.07	1.12	1.11	1.81	3.51
ANG	ANGIOGENIN, RIBONUCLEASE, RNASE A FAMILY, 5	1.37	0.02	3.34	3.85	1.97	3.92
ANXA2	ANNEXIN A2 PSEUDOGENE 3; ANNEXIN A2; ANNEXIN A2 PSEUDOGENE 1	6.21	6.28	4.51	4.80	-1.41	0.38
APEX2	APEX NUCLEASE (APURINIC/APYRIMIDINIC ENDONUCLEASE) 2	5.36	4.99	3.48	3.95	-1.04	0.49
APP	AMYLOID BETA (A4) PRECURSOR PROTEIN	-0.86	-1.40	0.25	0.32	1.11	2.16
ASPM	ASP (ABNORMAL SPINDLE) HOMOLOG, MICROCEPHALY ASSOCIATED	2.10	1.88	0.11	0.84	-1.04	0.49
ATF3	ACTIVATING TRANSCRIPTION FACTOR 3	-1.50	-1.22	-0.03	0.52	1.19	2.28
BAG3	BCL2-ASSOCIATED ATHANOGENE 3	-1.12	-1.00	0.13	0.34	1.13	2.18
BHLHE40	BASIC HELIX-LOOP-HELIX FAMILY, MEMBER E40	3.74	4.51	2.10	2.20	-1.54	0.34
BIN1	BRIDGING INTEGRATOR 1	2.63	2.83	1.47	1.60	-1.04	0.49
BMP2K	BMP2 INDUCIBLE KINASE	0.91	1.30	-0.12	-0.11	-1.02	0.49
BRK1	BRICK1, SCAR/WAVE ACTIN-NUCLEATING COMPLEX SUBUNIT	2.54	2.93	0.76	1.45	-1.08	0.47
BTK	BRUTON AGAMMAGLOBULINEMIA TYROSINE KINASE	3.77	3.87	2.12	2.31	-1.46	0.36
C12orf11	CHROMOSOME 12 OPEN READING FRAME 11	1.55	1.59	0.25	0.50	-1.06	0.48
C12orf65	CHROMOSOME 12 OPEN READING FRAME 65	3.20	3.34	1.22	1.97	-1.23	0.43
C15orf38	CHROMOSOME 15 OPEN READING FRAME 38	1.13	1.82	-0.89	-1.02	-2.02	0.25
C15orf48	CHROMOSOME 15 OPEN READING FRAME 48	0.21	0.11	1.77	1.34	1.12	2.18
C15orf57	CHROMOSOME 15 OPEN READING FRAME 57	4.27	4.37	2.94	3.21	-1.06	0.48
C18orf22	CHROMOSOME 18 OPEN READING FRAME 22	3.89	3.82	2.33	2.75	-1.07	0.48
C1orf116	CHROMOSOME 1 OPEN READING FRAME 116	-1.39	-1.19	1.90	2.65	3.09	8.49
C3	SIMILAR TO COMPLEMENT C3 PRECURSOR; COMPLEMENT COMPONENT 3; HYPOTHETICAL PROTEIN LOC100133511	-0.68	-0.52	0.66	1.21	1.18	2.26
C4orf47	CHROMOSOME 4 OPEN READING FRAME 47	1.82	1.98	0.70	0.45	-1.12	0.46
C5AR1	COMPLEMENT COMPONENT 5A RECEPTOR 1	-1.09	-1.14	0.08	0.12	1.17	2.25
C5orf62	MSTP150	-1.89	-1.73	-0.68	-0.57	1.05	2.07
CCL2	CHEMOKINE (C-C MOTIF) LIGAND 2	-0.76	-0.35	2.96	1.01	1.36	2.56
CCL4	CHEMOKINE (C-C MOTIF) LIGAND 4	-0.10	0.19	2.04	2.33	1.85	3.61
CCR7	CHEMOKINE (C-C MOTIF) RECEPTOR 7	-1.59	-1.38	0.17	0.24	1.55	2.93
CD109	CD109 MOLECULE	1.35	2.03	-0.90	-0.18	-1.54	0.34
CD14	CD14 MOLECULE	1.10	1.01	2.94	2.90	1.80	3.47
CD4	CD4 MOLECULE	-1.10	-1.33	0.06	0.62	1.16	2.24
CD5	CD5 MOLECULE	2.23	1.76	3.59	4.14	1.36	2.57
CD83	CD83 MOLECULE	0.33	0.78	2.71	2.40	1.62	3.07
CDC25B	CELL DIVISION CYCLE 25 HOMOLOG B	2.65	2.64	1.21	1.54	-1.10	0.47
CDC42	CELL DIVISION CYCLE 42 (GTP BINDING PROTEIN, 25KDA); CELL DIVISION CYCLE 42 PSEUDOGENE 2	1.99	2.42	-0.35	-0.21	-2.20	0.22
CDH1	CADHERIN 1, TYPE 1, E-CADHERIN	2.05	2.42	0.40	0.94	-1.11	0.46
CDH4	CADHERIN 4, TYPE 1, R-CADHERIN	-1.14	-1.38	0.24	0.86	1.38	2.61
CDKN1C	CYCLIN-DEPENDENT KINASE INHIBITOR 1C (P57, KIP2)	2.42	1.30	4.91	5.53	2.49	5.61
CEBPD	CCAAT/ENHANCER BINDING PROTEIN (C/EBP), DELTA	1.11	0.30	2.63	2.86	1.53	2.88

CENPC1	centromere protein C 1	1.41	1.64	0.11	0.33	-1.09	0.47
CFB	complement factor B	-1.37	-1.31	0.02	0.43	1.32	2.50
CFP	complement factor properdin	-0.53	-0.48	2.21	1.43	1.91	3.75
CHST2	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	5.38	5.36	2.31	3.20	-2.16	0.22
CISH	cytokine inducible SH2-containing protein	-0.72	-0.93	0.58	0.84	1.30	2.47
CKAP2L	cytoskeleton associated protein 2-like	1.18	0.78	-0.30	-0.25	-1.02	0.49
CKAP4	cytoskeleton-associated protein 4	4.79	4.99	3.05	3.60	-1.19	0.44
CLDND1	claudin domain containing 1	3.65	4.00	2.28	2.59	-1.06	0.48
CLEC6A	C-type lectin domain family 6, member A	-1.34	-1.22	0.44	-0.18	1.04	2.05
COX7A1	cytochrome c oxidase subunit VIIa polypeptide 1	1.96	1.39	3.37	4.22	1.41	2.65
CRIP1	cysteine-rich protein 1	9.97	10.03	8.17	8.80	-1.17	0.44
CRIP2	cysteine-rich protein 2	6.50	6.61	4.01	4.93	-1.57	0.34
CSF2RA	colony stimulating factor 2 receptor, alpha, low-affinity	0.35	-1.15	1.40	1.36	1.02	2.02
CTBP2	C-terminal binding protein 2	-0.97	-1.18	0.19	0.21	1.16	2.23
CTLA4	cytotoxic T-lymphocyte-associated protein 4	0.38	-0.63	2.43	3.30	2.05	4.13
CTSB	cathepsin B	0.50	-0.44	1.63	2.33	1.13	2.19
CXCL10	chemokine (C-X-C motif) ligand 10	-0.99	0.24	2.49	3.34	2.25	4.76
CXCR6	chemokine (C-X-C motif) receptor 6	0.38	0.52	1.76	2.33	1.25	2.38
CXCR7	chemokine (C-X-C motif) receptor 7	-1.49	-1.24	0.08	0.34	1.32	2.50
DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides	3.06	3.57	1.71	1.88	-1.18	0.44
DCK	deoxycytidine kinase	1.83	1.95	0.42	0.59	-1.24	0.42
DDIT4	DNA-damage-inducible transcript 4	0.45	0.58	1.74	1.69	1.11	2.15
DEPDC6	DEP domain containing 6	-0.37	-1.14	0.90	0.81	1.18	2.26
DHX16	DEAH (Asp-Glu-Ala-His) box polypeptide 16	1.22	1.27	-0.03	-0.12	-1.25	0.42
DUSP5	dual specificity phosphatase 5	3.11	2.87	4.55	5.22	1.44	2.71
EAF2	ELL associated factor 2	5.64	5.54	3.93	4.49	-1.05	0.48
EGLN3	egl nine homolog 3	2.61	2.91	0.78	0.91	-1.70	0.31
EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	-0.16	0.00	1.56	2.09	1.56	2.95
Eif2s3x	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa pseudogene	3.45	3.40	2.13	2.32	-1.07	0.47
EMILIN2	elastin microfibril interfacer 2	-1.62	-1.31	-0.28	0.03	1.03	2.04
ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	1.43	1.21	-0.51	-0.25	-1.45	0.37
F13A1	coagulation factor XIII, A1 polypeptide	-0.77	-1.02	0.50	0.31	1.08	2.12
FAM159B	SFRS12-interacting protein 1; family with sequence similarity 159, member B	2.29	2.55	1.01	1.14	-1.15	0.45
FAM3B	family with sequence similarity 3, member B	-0.24	-0.39	0.77	0.80	1.01	2.01
FCER2	Fc fragment of IgE, low affinity II, receptor for (CD23)	1.14	0.06	2.28	2.14	1.01	2.01
FCGRT	Fc fragment of IgG, receptor, transporter, alpha	5.08	4.94	3.49	3.70	-1.24	0.42
FEM1B	fem-1 homolog b	1.41	1.68	0.06	0.32	-1.09	0.47
FGFR1	fibroblast growth factor receptor 1	4.97	4.94	2.59	2.98	-1.96	0.26
FUT3	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group)	0.92	0.32	2.48	2.18	1.26	2.40
FXYD6	FXYD domain containing ion transport regulator 6	-0.21	-1.34	1.85	1.63	1.84	3.57
FYB	FYN binding protein (FYB-120/130)	-0.87	-1.34	0.24	0.60	1.11	2.17
GADD45B	growth arrest and DNA-damage-inducible, beta	1.33	1.62	3.34	4.07	1.72	3.29
GANAB	glucosidase, alpha ; neutral AB	0.82	0.80	-0.37	-0.39	-1.17	0.44
GATC	glutamyl-tRNA(Gln) amidotransferase, subunit C homolog	2.25	2.59	0.58	1.20	-1.05	0.48

GBP1	GUANYLATE BINDING PROTEIN 1, INTERFERON-INDUCIBLE, 67KDA	-0.73	0.66	3.58	1.74	1.08	2.11
GCLC	GLUTAMATE-CYSTEINE LIGASE, CATALYTIC SUBUNIT	-0.52	-0.09	1.08	1.46	1.17	2.24
GLS	GLUTAMINASE	1.27	1.51	0.06	-0.23	-1.20	0.43
GNPNAT1	GLUCOSAMINE-PHOSPHATE N-ACETYLTRANSFERASE 1	2.12	2.16	0.62	1.05	-1.07	0.47
GNS	GLUCOSAMINE (N-ACETYL)-6-SULFATASE	-0.16	-0.45	1.13	0.95	1.11	2.15
GOLGB1	GOLGIN B1, GOLGI INTEGRAL MEMBRANE PROTEIN	4.61	4.54	2.86	3.25	-1.29	0.41
GPR125	G PROTEIN-COUPLED RECEPTOR 125	2.62	2.51	0.77	0.90	-1.61	0.33
GPR18	G PROTEIN-COUPLED RECEPTOR 18	0.76	1.03	-0.37	-0.47	-1.14	0.45
GRAP	GRB2-RELATED ADAPTOR PROTEIN	2.20	2.42	1.08	0.85	-1.11	0.46
GTF2A1	GENERAL TRANSCRIPTION FACTOR IIA, 1, 19/37KDA	3.61	3.68	1.73	2.42	-1.19	0.44
GZMB	GRANZYME B (GRANZYME 2, CYTOTOXIC T-LYMPHOCYTE-ASSOCIATED SERINE ESTERASE 1)	0.45	1.17	3.24	2.82	1.65	3.15
HAO1	HYDROXYACID OXIDASE (GLYCOLATE OXIDASE) 1	-0.80	-0.96	0.83	0.87	1.63	3.09
HDDC3	HD DOMAIN CONTAINING 3	3.00	2.80	1.40	1.79	-1.01	0.50
HKR1	GLI-KRUPPEL FAMILY MEMBER HKR1	-1.17	-1.79	1.65	3.50	2.82	7.07
HLA-DRB1	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DR BETA 4; MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DR BETA 1	5.37	6.21	7.38	7.24	1.03	2.05
HOPX	HOP HOMEOBOX	0.60	0.82	-1.00	-1.51	-1.60	0.33
HSPA12A	HEAT SHOCK 70KDA PROTEIN 12A	0.98	1.31	-0.35	-0.37	-1.33	0.40
HSPA1A	HEAT SHOCK 70KDA PROTEIN 1A; HEAT SHOCK 70KDA PROTEIN 1B	3.80	4.10	1.55	1.93	-1.87	0.27
HSPB1	HEAT SHOCK 27KDA PROTEIN-LIKE 2 PSEUDOGENE; HEAT SHOCK 27KDA PROTEIN 1	1.91	1.28	5.47	5.11	3.20	9.22
HSPH1	HEAT SHOCK 105KDA/110KDA PROTEIN 1	0.04	0.29	1.45	2.06	1.16	2.24
HYAL2	HYALURONOGLUCOSAMINIDASE 2	-0.50	-0.98	1.21	1.17	1.67	3.18
IFNG	INTERFERON, GAMMA	-1.19	-1.64	-0.10	-0.18	1.01	2.02
IGH@	IMMUNOGLOBULIN HEAVY CONSTANT GAMMA 1 (G1M MARKER)	5.35	5.36	3.72	3.96	-1.38	0.38
IGHA1	IMMUNOGLOBULIN HEAVY CONSTANT ALPHA 1	11.61	11.64	9.91	10.29	-1.32	0.40
IGHE	IMMUNOGLOBULIN HEAVY CONSTANT EPSILON	7.54	6.23	3.89	5.08	-1.15	0.45
IGHG1	IMMUNOGLOBULIN HEAVY CONSTANT GAMMA 1 (G1M MARKER)	8.23	8.35	6.16	6.27	-1.96	0.26
Ighv	IMMUNOGLOBULIN HEAVY VARIABLE	5.06	5.08	3.43	3.63	-1.43	0.37
IGL@	IMMUNOGLOBULIN LAMBDA VARIABLE 2-11	4.70	4.35	2.58	2.75	-1.60	0.33
IGLL1	IMMUNOGLOBULIN LAMBDA-LIKE POLYPEPTIDE 1	5.93	5.78	4.51	4.45	-1.27	0.41
IGLV	IMMUNOGLOBULIN LAMDA-VARIABLE	6.58	5.96	4.69	4.76	-1.20	0.44
IL12RB1	INTERLEUKIN 12 RECEPTOR, BETA 1	2.15	2.67	0.89	0.89	-1.26	0.42
IL8	INTERLEUKIN 8	-1.84	-1.61	0.33	0.97	1.95	3.86
INF2	INVERTED FORMIN, FH2 AND WH2 DOMAIN CONTAINING	0.93	1.00	-0.31	-0.28	-1.22	0.43
INPP1	INOSITOL POLYPHOSPHATE-1-PHOSPHATASE	2.92	3.14	1.70	1.69	-1.22	0.43
IQCB1	IQ MOTIF CONTAINING B1	2.92	3.31	1.55	1.90	-1.02	0.49
ISG15	ISG15 UBIQUITIN-LIKE MODIFIER	1.44	0.93	7.26	7.48	5.83	56.76
ITGB1	INTEGRIN, BETA 1 (FIBRONECTIN RECEPTOR, BETA POLYPEPTIDE, ANTIGEN CD29 INCLUDES MDF2, MSK12)	6.20	6.62	4.22	5.05	-1.15	0.45
JHDM1D	JUMONJI C DOMAIN CONTAINING HISTONE DEMETHYLASE 1 HOMOLOG D	1.51	1.57	0.25	0.12	-1.26	0.42
KCNA3	POTASSIUM VOLTAGE-GATED CHANNEL, SHAKER-RELATED SUBFAMILY, MEMBER 3	2.81	2.55	0.82	1.26	-1.29	0.41
KIAA0528	KIAA0528	4.06	4.38	2.69	3.06	-1.00	0.50
KIAA1370	KIAA1370	2.07	2.39	0.90	0.80	-1.18	0.44
KLF3	KRUPPEL-LIKE FACTOR 3	3.05	3.04	1.66	1.99	-1.05	0.48
KLF4	KRUPPEL-LIKE FACTOR 4	-0.17	0.31	1.54	2.52	1.23	2.34

LGALS1	LECTIN, GALACTOSIDE-BINDING, SOLUBLE, 1	1.60	0.69	3.62	4.07	2.02	4.06
LIPA	LIPASE A, LYSOSOMAL ACID, CHOLESTEROL ESTERASE	0.92	0.54	3.52	3.84	2.60	6.06
LOC750761	LOC750761	0.69	0.63	2.06	2.14	1.37	2.58
LRP1	LOW DENSITY LIPOPROTEIN-RELATED PROTEIN 1 (ALPHA-2-MACROGLOBULIN RECEPTOR)	-0.94	-1.18	0.76	0.86	1.70	3.25
LRRC33	LEUCINE RICH REPEAT CONTAINING 33	1.20	1.56	-0.14	0.02	-1.18	0.44
LTF	LACTOTRANSFERRIN	-1.50	-1.69	0.45	0.47	1.94	3.85
LY6E	LYMPHOCYTE ANTIGEN 6 COMPLEX, LOCUS E	1.35	-0.48	2.79	3.07	1.44	2.72
LYZ	LYSOZYME	0.72	1.35	3.45	3.60	2.10	4.29
MAFB	V-MAF MUSCULOAPONEUROTIC FIBROSARCOMA ONCOGENE HOMOLOG B	-1.67	-1.40	0.67	0.76	2.07	4.21
MBD4	METHYL-CPG BINDING DOMAIN PROTEIN 4	4.31	4.72	2.72	3.10	-1.21	0.43
MEF2C	MYOCYTE ENHANCER FACTOR 2C	3.54	3.72	2.25	1.92	-1.29	0.41
METTL14	METHYLTRANSFERASE LIKE 14	2.69	2.87	0.73	1.47	-1.23	0.43
MLH3	MUTL HOMOLOG 3	0.49	0.75	-0.54	-0.69	-1.03	0.49
MND1	MEIOTIC NUCLEAR DIVISIONS 1 HOMOLOG	5.06	4.45	2.50	3.05	-1.41	0.38
MPZL1	MYELIN PROTEIN ZERO-LIKE 1	2.32	2.50	0.84	1.23	-1.09	0.47
MS4A8B	MEMBRANE-SPANNING 4-DOMAINS, SUBFAMILY A, MEMBER 8B	-1.43	-1.34	0.14	0.30	1.48	2.80
MT1A	METALLOTHIONEIN 1A	-2.12	-1.91	-0.65	-0.25	1.26	2.39
MT2A	METALLOTHIONEIN 2A	1.77	0.55	3.86	4.54	2.09	4.26
MX1	MYXOVIRUS (INFLUENZA VIRUS) RESISTANCE 1, INTERFERON-INDUCIBLE PROTEIN P78	2.59	2.17	5.81	5.79	3.20	9.18
MX2	MYXOVIRUS (INFLUENZA VIRUS) RESISTANCE 2	-0.04	-0.18	5.16	5.42	5.20	36.77
MYLIP	MYOSIN REGULATORY LIGHT CHAIN INTERACTING PROTEIN	1.16	1.19	2.38	2.61	1.19	2.28
MYOF	MYOFERLIN	-0.99	-1.33	0.77	1.46	1.76	3.40
NDRG1	N-MYC DOWNSTREAM REGULATED 1	0.30	-0.51	1.71	3.01	1.41	2.66
NEK6	NIMA (NEVER IN MITOSIS GENE A)-RELATED KINASE 6	2.57	2.49	0.92	0.88	-1.58	0.33
NFAT5	NUCLEAR FACTOR OF ACTIVATED T-CELLS 5, TONICITY-RESPONSIVE	4.16	4.65	2.98	3.05	-1.12	0.46
NFIL3	NUCLEAR FACTOR, INTERLEUKIN 3 REGULATED	-0.20	-0.31	1.44	1.75	1.63	3.10
NFKBIA	NUCLEAR FACTOR OF KAPPA LIGHT POLYPEPTIDE GENE ENHANCER IN B-CELLS INHIBITOR, ALPHA	3.45	4.33	5.50	5.80	1.17	2.26
NMRAL1	NMRA-LIKE FAMILY DOMAIN CONTAINING 1	4.58	4.51	2.53	3.08	-1.42	0.37
NMT2	N-MYRISTOYLTRANSFERASE 2	2.26	2.56	0.30	0.35	-1.90	0.27
NT5E	5'-NUCLEOTIDASE, ECTO (CD73)	0.62	0.90	-0.84	-0.48	-1.10	0.47
NUP43	NUCLEOPORIN 43KDA	1.79	1.96	0.20	0.68	-1.11	0.46
NUPR1	NUCLEAR PROTEIN, TRANSCRIPTIONAL REGULATOR, 1	1.96	2.14	0.60	0.28	-1.37	0.39
PACSIN1	PROTEIN KINASE C AND CASEIN KINASE SUBSTRATE IN NEURONS 1	-0.75	-1.43	0.31	0.37	1.05	2.08
PARP2	POLY (ADP-RIBOSE) POLYMERASE 2	2.80	3.26	1.66	1.13	-1.14	0.46
PIGR	POLYMERIC IMMUNOGLOBULIN RECEPTOR	-1.95	-1.79	-0.58	-0.40	1.22	2.32
PLA2G16	PHOSPHOLIPASE A2, GROUP XVI	2.26	1.73	3.79	3.55	1.29	2.45
PLAC8	PLACENTA-SPECIFIC 8	7.27	5.92	8.41	9.38	1.15	2.22
PLCB2	PHOSPHOLIPASE C, BETA 2	1.88	1.50	0.37	0.21	-1.13	0.46
PLOD1	PROCOLLAGEN-LYSINE 1, 2-OXOGLUTARATE 5-DIOXYGENASE 1	-0.92	-1.15	0.84	1.32	1.76	3.40
PPM1B	PROTEIN PHOSPHATASE 1B (FORMERLY 2C), MAGNESIUM-DEPENDENT, BETA ISOFORM	1.61	1.79	0.17	0.34	-1.27	0.42
PRDX3	PEROXIREDOXIN 3	4.85	5.06	2.86	3.70	-1.16	0.45
PRSS23	PROTEASE, SERINE, 23	-1.67	-1.73	-0.21	-0.66	1.01	2.01
PTX3	PENTRAXIN-RELATED GENE, RAPIDLY INDUCED BY IL-1 BETA	-2.05	-2.04	-0.75	-0.73	1.29	2.45

RAB27A	RAB27A, member RAS oncogene family	3.14	2.91	1.68	1.82	-1.10	0.47
RABEPK	Rab9 effector protein with kelch motifs	1.97	1.97	0.44	0.97	-1.00	0.50
RAD51L1	RAD51-like 1	4.59	3.89	2.84	2.31	-1.05	0.48
RGS1	regulator of G-protein signaling 1	1.87	1.33	2.91	4.32	1.04	2.05
RGS18	regulator of G-protein signaling 18	2.42	2.90	0.88	1.35	-1.07	0.48
RGS2	regulator of G-protein signaling 2, 24kDa	0.83	0.24	3.01	3.36	2.17	4.50
RHOH	ras homolog gene family, member H	2.62	2.93	1.37	1.60	-1.02	0.49
RNASE4	ribonuclease, RNase A family, 4	1.01	-0.20	2.76	3.27	1.75	3.36
RNF212	ring finger protein 212	0.09	0.05	1.66	1.32	1.23	2.34
RRAS2	related RAS viral (r-ras) oncogene homolog 2	2.43	2.91	0.87	0.87	-1.56	0.34
RSAD2	radical S-adenosyl methionine domain containing 2	-1.89	-1.76	-0.05	-0.26	1.50	2.83
RSRC1	arginine/serine-rich coiled-coil 1	3.19	3.10	1.33	1.89	-1.21	0.43
RTP4	receptor (chemosensory) transporter protein 4	3.12	2.82	5.38	5.38	2.26	4.79
S100A12	S100 calcium binding protein A12	0.36	0.82	3.09	3.09	2.27	4.82
S100A4	S100 calcium binding protein A4	2.05	2.27	4.80	4.45	2.18	4.53
S100A8	S100 calcium binding protein A8	-0.27	0.98	3.77	3.86	2.79	6.92
S100A9	S100 calcium binding protein A9	-1.37	-0.83	2.72	2.43	3.26	9.58
SBK1	SH3-binding domain kinase 1	5.51	5.74	4.38	4.02	-1.12	0.46
SDF2L1	stromal cell-derived factor 2-like 1	6.91	6.77	4.97	5.65	-1.12	0.46
SELPLG	selectin P ligand	2.95	3.13	1.35	1.89	-1.06	0.48
SERINC4	serine incorporator 4	1.65	1.74	3.25	3.18	1.44	2.71
SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	-1.83	-1.56	-0.44	-0.27	1.12	2.17
SHISA5	shisa homolog 5	-0.32	-0.44	0.90	1.06	1.22	2.32
SLC11A1	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	0.08	-0.08	2.75	2.27	2.19	4.57
SLC40A1	solute carrier family 40 (iron-regulated transporter), member 1	-1.59	-1.53	-0.02	-0.39	1.14	2.20
SMAD6	SMAD family member 6	0.07	0.07	-0.94	-1.00	-1.01	0.50
SMC4	structural maintenance of chromosomes 4	3.32	3.35	1.73	2.24	-1.08	0.47
SMYD2	SET and MYND domain containing 2	-0.12	-0.26	1.12	2.12	1.24	2.36
SNTB2	syntrophin, beta 2	2.86	2.86	1.63	1.76	-1.09	0.47
SNX10	sorting nexin 10	3.73	3.90	2.41	2.57	-1.16	0.45
SOCS2	suppressor of cytokine signaling 2	-1.37	-1.26	1.49	2.03	2.76	6.76
SOCS3	suppressor of cytokine signaling 3	-1.86	-1.61	-0.51	-0.48	1.11	2.16
SPEG	SPEG complex locus	1.55	0.39	5.57	5.10	3.56	11.76
SPRY1	sprouty homolog 1, antagonist of FGF signaling	-1.29	-1.33	-0.09	-0.21	1.09	2.12
ST3GAL1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	6.92	7.16	5.59	5.74	-1.18	0.44
STAT4	signal transducer and activator of transcription 4	1.57	1.05	2.96	3.38	1.40	2.64
SULT1A1	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	0.02	0.21	1.28	1.28	1.06	2.09
TCEA3	transcription elongation factor A (SII), 3	-1.80	-1.73	0.00	1.81	1.73	3.32
TDG	similar to G/T mismatch-specific thymine DNA glycosylase; thymine-DNA glycosylase	2.77	2.82	0.52	1.17	-1.61	0.33
TESC	tescalcin	4.37	4.57	2.95	2.64	-1.42	0.37
THBS1	thrombospondin 1	-0.79	-1.37	1.04	0.50	1.29	2.45
TIPIN	TIMELESS interacting protein	2.51	2.16	-0.02	0.27	-1.89	0.27
TLR10	toll-like receptor 10	2.12	3.36	0.92	0.57	-1.20	0.44

TM9SF2	TRANSMEMBRANE 9 SUPERFAMILY MEMBER 2	-2.06	-1.73	2.10	2.49	3.83	14.22
TMEM51	TRANSMEMBRANE PROTEIN 51	-1.67	-1.58	-0.25	0.32	1.33	2.52
TNF	TUMOR NECROSIS FACTOR (TNF SUPERFAMILY, MEMBER 2)	2.52	1.82	3.59	4.70	1.07	2.11
TNFAIP3	TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 3	4.19	3.78	5.82	6.18	1.64	3.11
TNFRSF13B	TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY, MEMBER 13B	3.53	3.55	1.67	2.20	-1.33	0.40
TNFRSF17	TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY, MEMBER 17	1.32	1.75	-0.31	-0.17	-1.49	0.36
TNFSF13B	TUMOR NECROSIS FACTOR (LIGAND) SUPERFAMILY, MEMBER 13B	-1.50	-1.53	-0.02	-0.33	1.17	2.24
TRAF3	TNF RECEPTOR-ASSOCIATED FACTOR 3	4.37	4.66	2.76	3.05	-1.33	0.40
Trg1	TRNA GLYCINE1	2.38	1.73	3.78	4.58	1.40	2.64
TRIB2	TRIBBLES HOMOLOG 2	5.00	5.24	3.57	3.62	-1.38	0.38
TRIM50	TRIPARTITE MOTIF-CONTAINING 50	-1.34	-1.15	0.23	-0.05	1.10	2.14
TSPAN13	TETRASPANIN 13	3.27	3.31	1.98	1.85	-1.29	0.41
UBE2D4	UBIQUITIN-CONJUGATING ENZYME E2D 4	2.05	2.51	0.84	0.96	-1.10	0.47
UBE2H	UBIQUITIN-CONJUGATING ENZYME E2H	4.07	4.09	2.50	2.57	-1.50	0.35
UBE2L6	UBIQUITIN-CONJUGATING ENZYME E2L 6	2.45	2.07	4.86	4.97	2.41	5.31
UNC119B	UNC-119 HOMOLOG B	2.16	2.19	0.73	0.86	-1.30	0.41
VCL	VINCULIN	4.52	4.54	2.85	3.33	-1.19	0.44
VPS13D	VACUOLAR PROTEIN SORTING 13 HOMOLOG D	2.29	0.01	5.23	5.10	2.81	7.00
VWA5A	VON WILLEBRAND FACTOR A DOMAIN CONTAINING 5A	-1.64	-1.38	-0.23	-0.15	1.15	2.22
WDR34	WD REPEAT DOMAIN 34	3.21	3.05	1.36	2.01	-1.05	0.48
XAF1	XIAP ASSOCIATED FACTOR 1	0.44	-0.02	3.08	3.01	2.58	5.97
XIST	X (INACTIVE)-SPECIFIC TRANSCRIPT	4.69	4.58	-0.69	-1.26	-5.27	0.03
ZBTB10	ZINC FINGER AND BTB DOMAIN CONTAINING 10	0.13	0.28	1.85	2.18	1.58	2.98
ZBTB32	ZINC FINGER AND BTB DOMAIN CONTAINING 32	2.63	2.67	0.65	1.39	-1.24	0.42
ZFYVE27	ZINC FINGER, FYVE DOMAIN CONTAINING 27	3.53	3.50	2.07	2.47	-1.03	0.49
ZNF207	ZINC FINGER PROTEIN 207	4.43	4.50	2.57	3.27	-1.16	0.45

* The genes presenting a minimum fold change >2 and <0.5 in the 2 infected samples relatively to the 2 control samples were considered as DEG.

Table S2. DEG in lymph node pDCs upon BTV infection*

Official gene symbol	Approved name	Raw.pValue	Adj.pValue	Mean fold change (log2)	Mean fold change
AADAT	AMINOADIPATE AMINOTRANSFERASE	0.00016351	0.00377906	-1.20	0.44
ABCA4	ATP-BINDING CASSETTE, SUB-FAMILY A (ABC1), MEMBER 4	0.00198906	0.01646099	-1.43	0.37
ABCC10	ATP-BINDING CASSETTE, SUB-FAMILY B (MDR/TAP), MEMBER 10	2.928E-06	0.00045085	1.52	2.86
ABCF1	ATP-BINDING CASSETTE, SUB-FAMILY F (GCN20), MEMBER 1	4.0622E-05	0.00185521	1.16	2.24
ABHD11	ABHYDROLASE DOMAIN CONTAINING 11	0.0001175	0.00316259	1.10	2.15
ABHD5	ABHYDROLASE DOMAIN CONTAINING 5	0.00184816	0.01581043	-1.26	0.42
ACAA2	ACETYL-COA ACYLTRANSFERASE 2	0.00105287	0.01133196	1.20	2.30
ACAT1	ACETYL-COA ACETYLTRANSFERASE 1	1.6518E-06	0.00033494	-1.33	0.40
ACOT7	ACYL-COA THIOESTERASE 7	0.0002258	0.00441947	2.18	4.55
ACSL3	ACYL-COA SYNTHETASE LONG-CHAIN FAMILY MEMBER 3	1.2843E-07	0.00012069	-2.16	0.22
ADAM8	ADAM METALLOPEPTIDASE DOMAIN 8	6.6556E-05	0.00229519	-1.18	0.44
ADK	ADENOSINE KINASE	0.00716391	0.03237038	-1.04	0.49
AHSA1	AHA1, ACTIVATOR OF HEAT SHOCK 90KDA PROTEIN ATPASE HOMOLOG 1	5.4762E-07	0.00020821	1.91	3.76
ALDH1A1	ALDEHYDE DEHYDROGENASE 1 FAMILY, MEMBER A1	0.00027673	0.00503415	-2.05	0.24
AMZ2	ARCHAELYSIN FAMILY METALLOPEPTIDASE 2	2.628E-05	0.00148024	-1.36	0.39
ANK3	ANKYRIN 3, NODE OF RANVIER	2.7999E-05	0.00155412	-1.19	0.44
ANKRD10	ANKYRIN REPEAT DOMAIN 10	5.2647E-06	0.00061209	1.41	2.65
ANP32A	ACIDIC (LEUCINE-RICH) NUCLEAR PHOSPHOPROTEIN 32 FAMILY, MEMBER A	0.00428575	0.0248675	1.37	2.59
ANTXR2	ANTHRAX TOXIN RECEPTOR 2	0.00018846	0.00408519	1.70	3.25
AP3S2	ADAPTOR-RELATED PROTEIN COMPLEX 3, SIGMA 2 SUBUNIT	8.0435E-05	0.00252217	1.01	2.02
APLP2	AMYLOID BETA (A4) PRECURSOR-LIKE PROTEIN 2	0.00017421	0.00391343	-1.04	0.48
APOBEC3H	APOLIPOPROTEIN B MRNA EDITING ENZYME, CATALYTIC POLYPEPTIDE-LIKE 3H	0.00020922	0.00429392	-2.12	0.23
ARG2	ARGINASE, TYPE II	0.00012254	0.00321637	-1.12	0.46
ARHGAP30	RHO GTPASE ACTIVATING PROTEIN 30	0.00597236	0.02957032	-1.16	0.45
ARID3A	AT RICH INTERACTIVE DOMAIN 3A (BRIGHT-LIKE)	0.00026513	0.00490736	1.01	2.01
ARL2	ADP-RIBOSYLATION FACTOR-LIKE 2	7.6211E-05	0.00244632	-1.10	0.47
ARL4C	ADP-RIBOSYLATION FACTOR-LIKE 4C	4.3511E-06	0.00056557	-1.45	0.37
ARPC3	ACTIN RELATED PROTEIN 2/3 COMPLEX, SUBUNIT 3, 21KDA	0.00059231	0.007874	-1.29	0.41
ARPC5L	ACTIN RELATED PROTEIN 2/3 COMPLEX, SUBUNIT 5-LIKE	8.2225E-06	0.00078155	1.46	2.75
ASF1B	ASF1 ANTI-SILENCING FUNCTION 1 HOMOLOG B	0.00133711	0.01303511	1.12	2.18
ASNS	ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING)	0.00075263	0.00910576	1.02	2.03
ATP8B1	ATPASE, AMINOPHOSPHOLIPID TRANSPORTER, CLASS I, TYPE 8B, MEMBER 1	0.00798805	0.03419081	-1.08	0.47
AURKB	AURORA KINASE B	0.0006679	0.00847875	1.23	2.35
AZI2	5-AZACYTIDINE INDUCED 2	3.0188E-06	0.00045909	1.22	2.33
AZIN1	ANTIZYME INHIBITOR 1	0.00124125	0.01243538	-1.19	0.44
B4GALT1	UDP-GAL:BETAGLCNAC BETA 1,4- GALACTOSYLTRANSFERASE, POLYPEPTIDE 1	4.9907E-06	0.00060556	-1.49	0.36
BAG2	BCL2-ASSOCIATED ATHANOGENE 2	4.0152E-05	0.00184482	1.39	2.61
BAMBI	BMP AND ACTIVIN MEMBRANE-BOUND INHIBITOR	8.3932E-05	0.00258388	-1.58	0.33
BAT1	DEAD (ASP-GLU-ALA-ASP) BOX POLYPEPTIDE 39B	7.5769E-05	0.00244632	1.01	2.02
BATF	BASIC LEUCINE ZIPPER TRANSCRIPTION FACTOR, ATF-LIKE 3	3.5354E-06	0.00051206	1.89	3.70
BATF3	BASIC LEUCINE ZIPPER TRANSCRIPTION FACTOR, ATF-LIKE 3	5.525E-05	0.00209535	2.28	4.87
BC017643	CHROMOSOME 17 OPEN READING FRAME 62 ORTHOLOG	0.00021881	0.00436958	1.04	2.06
BCAS2	HYPOTHETICAL LOC496329	6.7174E-05	0.0022989	-1.31	0.40
BCL11B	B-CELL CLL/LYMPHOMA 11B (ZINC FINGER PROTEIN)	0.0014892	0.01389437	-1.99	0.25
BIRC5	BACULOVIRAL IAP REPEAT-CONTAINING 5	0.00382763	0.02338714	1.65	3.14
BLMH	BLEOMYCIN HYDROLASE	0.00259523	0.01899077	-1.13	0.46
BMP2	BONE MORPHOGENETIC PROTEIN 2	0.00066865	0.00847875	1.00	2.00
BNIP3L	BCL2/ADENOVIRUS E1B 19KDA INTERACTING PROTEIN 3-LIKE	0.00024991	0.00475087	-1.21	0.43
BRD2	BROMODOMAIN CONTAINING 2	0.00228953	0.01787431	-1.03	0.49
BRD8	BROMODOMAIN CONTAINING 8	0.00055493	0.00760994	1.32	2.51
BSG	BASIGIN (OK BLOOD GROUP)	0.0004337	0.00660811	1.33	2.51
BTG1	B-CELL TRANSLOCATION GENE 1, ANTI-PROLIFERATIVE	6.6386E-05	0.00229454	-2.07	0.24
BTG2	BTG FAMILY, MEMBER 2	0.00172089	0.0150972	-1.19	0.44
BTK	TYROSINE-PROTEIN KINASE BTK	1.5923E-06	0.00033494	1.73	3.32
BXDC2	BRX1, BIOGENESIS OF RIBOSOMES, HOMOLOG	1.974E-05	0.0012798	1.21	2.32
C10H15ORF 23	CHROMOSOME 15 OPEN READING FRAME 23	2.4041E-05	0.00139548	1.19	2.28
C13ORF15	CHROMOSOME 13 OPEN READING FRAME 15	1.1578E-06	0.00029346	-1.73	0.30
C16ORF53	CHROMOSOME 16 OPEN READING FRAME 53	9.1938E-05	0.00272023	1.17	2.25
C16ORF88	TESTIS-SPECIFIC GENE 118 PROTEIN	0.00071507	0.00881269	1.23	2.35

C19ORF33	CHROMOSOME 19 OPEN READING FRAME 33	0.00011046	0.0030377	-1.28	0.41
C19ORF40	CHROMOSOME 19 OPEN READING FRAME 40	4.6821E-06	0.00058847	1.24	2.36
C19ORF50	CHROMOSOME 19 OPEN READING FRAME 50	2.1461E-05	0.00132312	1.24	2.37
C1ORF124	CHROMOSOME 1 OPEN READING FRAME 124	7.6729E-05	0.00244632	1.02	2.03
C1ORF38	CHROMOSOME 1 OPEN READING FRAME 38	6.156E-06	0.00063971	1.64	3.12
C22ORF28	CHROMOSOME 22 OPEN READING FRAME 28	6.2367E-05	0.00218544	1.12	2.18
C3	COMPLEMENT COMPONENT 3	1.915E-05	0.0012798	1.36	2.57
C3ORF37	CHROMOSOME 3 OPEN READING FRAME 37	3.8041E-05	0.0017911	-1.25	0.42
C4ORF27	CHROMOSOME 4 OPEN READING FRAME 27	0.00022264	0.00439319	1.35	2.55
C6ORF145	CHROMOSOME 6 OPEN READING FRAME 145	0.00069002	0.00866176	-1.03	0.49
C7	COMPLEMENT COMPONENT 7	2.0793E-05	0.00131211	-1.36	0.39
C7ORF10	WAS PROTEIN FAMILY HOMOLOG 1	0.00062504	0.00812439	1.36	2.57
C7ORF30	CHROMOSOME 7 OPEN READING FRAME 30	1.1536E-05	0.00096416	-1.32	0.40
C8H9ORF3	CHROMOSOME 9 OPEN READING FRAME 3 ORTHOLOG	1.2793E-06	0.00031137	-2.60	0.16
C9H6ORF203	CHROMOSOME 6 OPEN READING FRAME 203 ORTHOLOG	0.00083894	0.00980073	1.08	2.11
C9ORF23	CHROMOSOME 9 OPEN READING FRAME 23 ORTHOLOG	0.00048388	0.00703814	1.02	2.03
C9ORF46	CHROMOSOME 9 OPEN READING FRAME 46 ORTHOLOG	1.5063E-06	0.00032934	-1.51	0.35
CAD	CARBAMOYL-PHOSPHATE SYNTHETASE 2, ASPARTATE TRANSCARBAMYLASE, AND DIHYDROOROTASE	6.7338E-05	0.0022989	1.10	2.14
CAPN3	CALPAIN 3	0.00318658	0.02125121	-2.22	0.21
CASC4	CANCER SUSCEPTIBILITY CANDIDATE 4	0.00015593	0.00368107	-1.21	0.43
CASP7	CASPASE 7, APOPTOSIS-RELATED CYSTEINE PEPTIDASE	0.01125126	0.04019022	1.31	2.48
CAST	CALPASTATIN	0.00013097	0.00330865	-1.09	0.47
CCDC138	COILED-COIL DOMAIN CONTAINING 13	0.00028435	0.00514811	-1.60	0.33
CCDC34	COILED-COIL DOMAIN CONTAINING 34	0.01573147	0.04778737	1.08	2.11
CCDC90B	COILED-COIL DOMAIN CONTAINING 90B	1.8742E-07	0.00013573	-1.68	0.31
CCL4	CHEMOKINE (C-C MOTIF) LIGAND 4-LIKE 1	0.00159361	0.01452975	-1.03	0.49
CCL5	CHEMOKINE (C-C MOTIF) LIGAND 5	0.00035723	0.00585424	2.15	4.44
CCNA2	CYCLIN A2	7.4E-05	0.00240469	2.16	4.46
CCNB2	CYCLIN B2	0.00025443	0.00479655	1.02	2.03
CCND1	CYCLIN D1	5.6137E-05	0.00210943	-1.25	0.42
CCNDBP1	CYCLIN D-TYPE BINDING-PROTEIN 1	2.3205E-05	0.00136928	1.30	2.46
CCNL1	MINICHROMOSOME MAINTENANCE COMPLEX COMPONENT 2	4.4134E-05	0.00191768	-1.41	0.38
CCNY	CYCLIN Y	0.00027891	0.0050677	-1.36	0.39
CCR7	CHEMOKINE (C-C MOTIF) RECEPTOR 7	3.723E-06	0.00051945	-1.41	0.38
CCT3	CHAPERONIN CONTAINING TCP1, SUBUNIT 3 (GAMMA)	9.9728E-05	0.00284139	1.51	2.86
CCT8	CHAPERONIN CONTAINING TCP1 SUBUNIT 8	4.5841E-06	0.00058679	1.43	2.70
CD109	CD109 MOLECULE	0.00011211	0.0030609	-1.21	0.43
CD2	CD2 MOLECULE	1.5489E-05	0.00116114	-1.97	0.25
CD2AP	CD2-ASSOCIATED PROTEIN	9.7634E-05	0.00280765	-1.02	0.49
CD3EAP	FAMILY WITH SEQUENCE SIMILARITY 76, MEMBER A	7.1624E-05	0.00236795	-1.17	0.44
CD40	CD40 MOLECULE, TNF RECEPTOR SUPERFAMILY MEMBER 5	0.0044423	0.0253639	1.32	2.50
CD83	CD83 MOLECULE	2.9129E-06	0.00045085	-1.95	0.26
CD97	CD97 MOLECULE	0.01485246	0.04657241	1.02	2.03
CDC2	CYCLIN-DEPENDENT KINASE 1	0.0001681	0.00384422	1.87	3.66
CDC20	CELL DIVISION CYCLE 20 HOMOLOG	6.1248E-06	0.00063971	1.54	2.91
CDC42EP5	CDC42 EFFECTOR PROTEIN (RHO GTPASE BINDING) 5	0.01546914	0.04742557	-1.02	0.49
CDCA3	CELL DIVISION CYCLE ASSOCIATED 3	0.0007534	0.00910783	1.59	3.02
CDCA5	CELL DIVISION CYCLE ASSOCIATED 5	0.00029191	0.00520864	1.35	2.54
CDCA7	CELL DIVISION CYCLE ASSOCIATED 7	0.01599669	0.04816051	1.13	2.18
CDK2AP2	CYCLIN-DEPENDENT KINASE 2 ASSOCIATED PROTEIN 2	4.4782E-05	0.0019293	-1.11	0.46
CDKN1A	CYCLIN-DEPENDENT KINASE INHIBITOR 1A (P21)	1.1538E-05	0.00096416	-3.65	0.08
CEACAM1	CARCINOEMBRYONIC ANTIGEN-RELATED CELL ADHESION MOLECULE 1 (BILIARY GLYCOPROTEIN)	1.6091E-05	0.00118991	1.09	2.13
CEBPD	CCAAT/ENHANCER BINDING PROTEIN (C/EBP), DELTA	5.228E-05	0.0020705	-1.09	0.47
CENPF	CENTROMERE PROTEIN F, 350/400KA	0.01350999	0.04442763	1.16	2.23
CHD8	CHROMODOMAIN HELICASE DNA BINDING PROTEIN 8	5.1997E-05	0.00206467	1.21	2.32
CHGA	CHROMOGRANIN A (PARATHYROID SECRETORY PROTEIN 1)	2.1118E-05	0.00131622	1.18	2.27
CHMP4A	CHROMATIN MODIFYING PROTEIN 4A	9.0426E-06	0.00082991	1.64	3.11
CHORDC1	CYSTEINE AND HISTIDINE-RICH DOMAIN (CHORD) CONTAINING 1	3.2367E-05	0.001662	1.25	2.38
CHRNB1	CHOLINERGIC RECEPTOR, NICOTINIC, BETA 1	0.00010252	0.00289274	-1.02	0.49
CHST12	CARBOHYDRATE (CHONDROITIN 4) SULFOTRANSFERASE 12	1.1029E-05	0.00095994	1.07	2.10
CHST3	CARBOHYDRATE (CHONDROITIN 6) SULFOTRANSFERASE 3	7.0695E-05	0.00235259	-1.92	0.26
CHTF8	CTF8, CHROMOSOME TRANSMISSION FIDELITY FACTOR 8 HOMOLOG	9.0588E-06	0.00082991	1.57	2.97
CIITA	DOWNSTREAM NEIGHBOR OF SON	2.1085E-05	0.00131622	1.84	3.59
CIRH1A	CIRRHOSIS, AUTOSOMAL RECESSIVE 1A	9.9273E-05	0.00283787	1.64	3.13
CISD1	CDGSH IRON SULFUR DOMAIN 1	0.00431915	0.02491867	1.13	2.18
CISH	CYTOKINE INDUCIBLE SH2-CONTAINING PROTEIN	5.6098E-05	0.00210943	1.23	2.34
CKAP2L	CYTOSKELETON ASSOCIATED PROTEIN 2-LIKE	0.00309791	0.02094392	1.02	2.03
CKS2	CDC28 PROTEIN KINASE REGULATORY SUBUNIT 2	0.00694255	0.03185948	1.14	2.20

CLDN4	claudin 4	1.1681E-05	0.00096546	-1.02	0.49
CLK2	CDC-like kinase 2	1.7442E-05	0.00124031	1.67	3.19
CNOT6L	CCR4-NOT transcription complex, subunit 6-like	0.00084984	0.00989614	-1.06	0.48
COMMD8	COMM domain containing 8	6.3003E-05	0.00220011	1.38	2.61
COPB2	coatomer protein complex, subunit beta 2 (beta prime)	0.00181711	0.01567475	1.21	2.31
COPS4	COP9 constitutive photomorphogenic homolog subunit 4	8.9641E-05	0.00269809	1.63	3.09
CPEB1	cytoplasmic polyadenylation element binding protein 1	1.4554E-05	0.00111113	-1.38	0.39
CPSF7	cleavage and polyadenylation specific factor 7, 59kDa	0.00032072	0.00548977	1.02	2.03
CSRNP2	cysteine-serine-rich nuclear protein 2	2.9001E-05	0.00157057	-1.49	0.36
CTDSP2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	8.4687E-05	0.00259663	1.12	2.17
CTSC	cathepsin C	3.1714E-05	0.00165741	-1.32	0.40
CTSH	cathepsin H	1.4612E-05	0.00111113	1.36	2.57
CTSZ	cathepsin Z	7.7233E-05	0.0024521	1.69	3.24
CWF19L1	CWF19-like 1, cell cycle control	1.9565E-05	0.0012798	1.01	2.01
CXCR4	chemokine (C-X-C motif) receptor 4	4.7925E-08	7.6385E-05	-2.02	0.25
CXCR6	chemokine (C-X-C motif) receptor 6	0.00012119	0.00321637	1.77	3.42
CXCR7	chemokine (C-X-C motif) receptor 7	3.2468E-05	0.001662	-3.18	0.11
CYBB	cytochrome b-245, beta polypeptide	0.00039811	0.00628702	1.10	2.14
CYP2U1	cytochrome P450, family 2, subfamily u, polypeptide 1	0.00066064	0.00845706	-1.01	0.50
CYP51A1	cytochrome P450, family 51, subfamily A, polypeptide 1	5.4921E-06	0.00061869	-2.15	0.23
DAAM1	dishevelled associated activator of morphogenesis 1	0.01074873	0.03918184	-2.13	0.23
DCAF13	WD repeats and SOF domain containing 1	1.2424E-05	0.00099825	1.34	2.54
DCTN2	dynactin 2	0.00278953	0.01968331	1.04	2.05
DDC	dopa decarboxylase (aromatic L-amino acid decarboxylase)	0.00061666	0.00805683	-1.09	0.47
DDX1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	2.8008E-05	0.00155412	1.06	2.09
DDX23	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23	0.00073481	0.00900458	1.09	2.12
DDX39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39A	0.00025978	0.00486549	1.28	2.43
DDX5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	0.00163734	0.01469987	1.24	2.35
DENND4A	DENN/MADD domain containing 4A	1.6216E-06	0.00033494	-1.93	0.26
DGCR2	DiGeorge syndrome critical region gene 2	8.1777E-05	0.00254851	-1.00	0.50
DICER1	dicer 1, ribonuclease type III	0.0002582	0.00484177	1.05	2.07
DLGAP5	discs, large homolog-associated protein 5	0.00081485	0.00962502	1.16	2.23
DLST	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	0.0005563	0.00761572	1.13	2.18
DNAJA3	DnaJ (Hsp40) homolog, subfamily A, member 3	0.000331	0.00558077	1.01	2.02
DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9	5.6141E-06	0.0006232	-2.02	0.25
DNAJC14	DnaJ (Hsp40) homolog, subfamily C, member 14	3.3027E-05	0.00166314	1.33	2.52
DNASE2	deoxyribonuclease II	2.1843E-05	0.00133945	1.43	2.69
DPCD	deleted in primary ciliary dyskinesia homolog	0.0004284	0.00654782	1.17	2.25
Dpf2	D4, zinc and double PHD fingers family 2	0.00056046	0.00761764	1.19	2.28
DUSP11	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	0.0001037	0.00291498	-1.67	0.32
DUSP3	dual specificity phosphatase 3	1.1153E-06	0.00028749	-1.48	0.36
DUSP5	dual specificity phosphatase 5	7.3181E-07	0.00023125	-2.47	0.18
EAPP	E2F-associated phosphoprotein	1.804E-05	0.00124703	1.06	2.08
EIF1AD	eukaryotic translation initiation factor 1A domain containing	5.7863E-05	0.00212187	1.18	2.27
EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	1.1895E-05	0.00097783	1.54	2.91
EIF2AK3	eukaryotic translation initiation factor 2-alpha kinase 3	7.5067E-06	0.00073242	-2.20	0.22
EIF2B3	eukaryotic translation initiation factor 2B, subunit 3 gamma, 58kDa	0.00489721	0.02665597	1.18	2.26
EIF2B4	eukaryotic translation initiation factor 2B, subunit 4 delta, 67kDa	8.3786E-05	0.00258388	1.20	2.30
EIF4A1	eukaryotic translation initiation factor 4A isoform 1	0.00055173	0.00760025	-1.19	0.44
ELOF1	elongation factor 1 homolog	2.5716E-05	0.00146414	1.12	2.18
ELOVL4	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3)-like 4	0.00062703	0.00812943	-1.19	0.44
EMD	emerin	3.6518E-05	0.00175749	-1.24	0.42
EMILIN2	elastin microfibril interfacer 2	0.00041281	0.00640818	-1.08	0.47
ERRFI1	ERBB receptor feedback inhibitor 1	1.0761E-06	0.00028376	-2.78	0.15
ESPL1	extra spindle pole bodies homolog 1	0.00793326	0.03403499	1.06	2.08
ETV3	ets variant 3	1.8349E-06	0.00035323	-1.77	0.29
EXOC6	COBL-like 1	0.00090906	0.01033901	-1.03	0.49
EXOSC10	exosome component 10	1.2472E-05	0.00099825	-2.02	0.25
EXOSC7	exosome component 7	0.00022524	0.00441416	1.16	2.24
EXOSC9	exosome component 9	6.5889E-07	0.00023125	1.59	3.02
FADS3	fatty acid desaturase 3	1.1121E-05	0.00095994	1.34	2.54
FAM100B	family with sequence similarity 100, member B; predicted gene 7367	0.00135835	0.01314941	1.10	2.15
FAM149A	family with sequence similarity 149, member A	0.00238228	0.01815473	-1.57	0.34
FAM33A	spindle and kinetochore associated complex subunit 2	0.00079622	0.00948228	-1.22	0.43

FAM49A	FAMILY WITH SEQUENCE SIMILARITY 49, MEMBER A	0.00196662	0.01635062	-1.01	0.50
FAM53C	FAMILY WITH SEQUENCE SIMILARITY 3, MEMBER C	0.000138	0.00344623	-1.11	0.46
FAM58A	FAMILY WITH SEQUENCE SIMILARITY 13, MEMBER A	1.8299E-05	0.00125924	1.22	2.33
FAM83D	FAMILY WITH SEQUENCE SIMILARITY 83, MEMBER D	0.00046454	0.00685893	-2.01	0.25
FARSA	PHENYLALANYL-TRNA SYNTHETASE, ALPHA SUBUNIT	5.3702E-05	0.00209535	1.25	2.38
FBP1	FRUCTOSE-1,6-BISPHOSPHATASE 1	0.00013589	0.00340458	-1.23	0.43
FBXO33	F-BOX PROTEIN 33	0.00056684	0.00766945	-1.16	0.45
FCER1A	FC FRAGMENT OF IGE, HIGH AFFINITY I, RECEPTOR FOR; ALPHA POLYPEPTIDE	0.00012184	0.00321637	-2.44	0.18
FCER2	FC FRAGMENT OF IGE, LOW AFFINITY II, RECEPTOR FOR (CD23)	1.559E-06	0.00033394	-1.77	0.29
FCGR2B	FC FRAGMENT OF IGG, LOW AFFINITY IIB, RECEPTOR (CD32)	0.00023626	0.00457127	1.86	3.62
FH	FUMARATE HYDRATASE	0.00017367	0.00391291	1.51	2.84
FIZ1	FLT3-INTERACTING ZINC FINGER 1	0.00309862	0.02094392	-1.01	0.50
FKBP4	FK506 BINDING PROTEIN 4, 59KDA	1.4492E-05	0.00111113	1.93	3.82
FKBP4	FK506 BINDING PROTEIN 4, 59KDA	1.4492E-05	0.00111113	1.93	3.82
FNDC3B	FIBRONECTIN TYPE III DOMAIN CONTAINING 3B	0.00095576	0.010624	-1.07	0.48
FOS	C-FOS PROTEIN	9.529E-06	0.0008626	-1.45	0.37
FOSL2	FOS-LIKE ANTIGEN 2	7.5045E-09	2.5141E-05	-4.45	0.05
FRAT2	FREQUENTLY REARRANGED IN ADVANCED T-CELL LYMPHOMAS 2	0.00031729	0.00544829	-1.02	0.49
FXYD6	FXYD DOMAIN CONTAINING ION TRANSPORT REGULATOR 6	4.5684E-05	0.00194628	2.12	4.35
GADD45A	GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE, ALPHA	2.7152E-07	0.00014747	-2.28	0.21
GADD45B	GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE, BETA	4.0898E-05	0.00185662	-1.58	0.33
GALK1	GALACTOKINASE 1	0.00041793	0.0064396	1.12	2.18
GALNT3	UDP-N-ACETYL-ALPHA-D-GALACTOSAMINE:POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE 3 (GALNAC-T3)	2.332E-05	0.00136928	-1.06	0.48
GAPT	GRB2-BINDING ADAPTOR PROTEIN, TRANSMEMBRANE	1.107E-05	0.00095994	1.47	2.77
GARS	GLYCYL-TRNA SYNTHETASE	8.5275E-05	0.00260414	1.52	2.87
GCLC	GLUTAMATE-CYSTEINE LIGASE, CATALYTIC SUBUNIT	0.00038786	0.00620255	1.45	2.73
GDE1	GLYCEROPHOSPHODIESTER PHOSPHODIESTERASE 1	0.0015174	0.01408361	1.01	2.02
GEM	GTP BINDING PROTEIN OVEREXPRESSED IN SKELETAL MUSCLE	2.7043E-06	0.00044604	-2.01	0.25
GEMIN7	GEM (NUCLEAR ORGANELLE) ASSOCIATED PROTEIN 7	1.4983E-05	0.00113365	1.06	2.09
GFM1	G ELONGATION FACTOR, MITOCHONDRIAL 1	3.9862E-06	0.00053721	1.44	2.72
GH2	GROWTH HORMONE 2	0.00082018	0.00965424	-1.43	0.37
GLTPD1	GLYCOLIPID TRANSFER PROTEIN DOMAIN CONTAINING 1	0.00020474	0.0042536	-1.00	0.50
GLUL	GLUTAMATE-AMMONIA LIGASE	0.00115268	0.01186243	-1.23	0.43
GMFG	GLIA MATURATION FACTOR, GAMMA	0.00017609	0.00393223	1.13	2.18
GNE	GLUCOSAMINE (UDP-N-ACETYL)-2-EPIMERASE/N-ACETYLMANNOSAMINE KINASE	0.00030288	0.00531861	-1.26	0.42
GNL3	GUANINE NUCLEOTIDE BINDING PROTEIN-LIKE 3 (NUCLEOLAR)	0.00020591	0.00427211	1.38	2.61
GOLGB1	GOLGIN B1, GOLGI INTEGRAL MEMBRANE PROTEIN; SIMILAR TO GIANTIN	0.00070242	0.00872748	-1.02	0.49
GOSR2	GOLGI SNAP RECEPTOR COMPLEX MEMBER 2	4.7618E-05	0.00196787	1.05	2.08
GPR171	G PROTEIN-COUPLED RECEPTOR 171	2.3224E-05	0.00136928	-1.80	0.29
GPR98	G PROTEIN-COUPLED RECEPTOR 98	4.2166E-06	0.00055576	-2.56	0.17
GRASP	GRP1 (GENERAL RECEPTOR FOR PHOSPHOINOSITIDES 1)-ASSOCIATED SCAFFOLD PROTEIN	5.6512E-05	0.00211198	-1.46	0.36
GSN	GELSOLIN (AMYLOIDOSIS, FINNISH TYPE)	4.9069E-06	0.00060556	-1.40	0.38
GSTZ1	GLUTATHIONE TRANSFERASE ZETA 1	6.7651E-05	0.0022989	-1.05	0.48
GUCY1B3	GUANYLATE CYCLASE 1, SOLUBLE, BETA 3	4.2999E-07	0.00019517	-5.14	0.03
GZMB	GRANZYME B (GRANZYME 2, CYTOTOXIC T-LYMPHOCYTE-ASSOCIATED SERINE ESTERASE 1)	1.9763E-05	0.0012798	1.54	2.91
GZMH	GRANZYME H (CATHEPSIN G-LIKE 2, PROTEIN H-CCPX)	5.5971E-06	0.0006232	2.14	4.42
HBA1	HEMOGLOBIN, ALPHA 1	0.0002035	0.0042454	-1.49	0.36
HCLS1	HEMATOPOIETIC CELL-SPECIFIC LYN SUBSTRATE 1	0.0002936	0.00521613	1.64	3.11
HEATR6	HEAT REPEAT CONTAINING 6	2.4333E-05	0.00140708	1.05	2.07
HERC1	HECT (HOMOLOGOUS TO THE E6-AP (UBE3A) CARBOXYL TERMINUS) DOMAIN AND RCC1 (CHC1)-LIKE DOMAIN (RLD) 1	2.9209E-05	0.00157522	1.22	2.34
HERPUD1	HOMOCYSTEINE-INDUCIBLE, ENDOPLASMIC RETICULUM STRESS-INDUCIBLE, UBIQUITIN-LIKE DOMAIN MEMBER 1	5.8181E-05	0.00212187	-1.92	0.26
HHEX	HEMATOPOIETICALLY EXPRESSED HOMEOBOX	0.00040569	0.00635381	1.15	2.21
HIGD1A	HIG1 HYPOXIA INDUCIBLE DOMAIN FAMILY, MEMBER 1A	0.00010395	0.00291665	-1.68	0.31
HIRIP3	HIRA INTERACTING PROTEIN 3	0.00011288	0.00307646	1.02	2.03
HKR1	HKR1, GLI-KRUPPEL ZINC FINGER FAMILY MEMBER	0.00019956	0.00420349	2.87	7.31
HLA-B	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS I, B	0.00110268	0.01161645	2.33	5.03
HLA-C	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS I, C; MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS I, B	0.00028536	0.00516017	2.43	5.38
HLA-DRB1	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II, DR BETA 1	0.00373511	0.02306273	1.15	2.22
HMGA1	HIGH MOBILITY GROUP AT-HOOK 1	3.2239E-05	0.001662	1.68	3.21
HMGCR	3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE	1.304E-06	0.00031137	-1.87	0.27
HNRNPA2B1	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2/B1	0.00044237	0.00668083	-1.08	0.47
HNRNPK	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K	0.00154856	0.01424711	-1.06	0.48

HNRNPU	heterogeneous nuclear ribonucleoprotein U	0.00012513	0.00323088	1.14	2.20
HOMEZ	homeobox and leucine zipper encoding	4.5688E-05	0.00194628	1.10	2.15
HPS3	Hermansky-Pudlak syndrome 3	3.5873E-06	0.00051468	-1.58	0.33
HRSP12	heat-responsive protein 12	3.6047E-05	0.00174585	-1.47	0.36
HSP90AA2	heat shock protein 90kDa alpha (cytosolic), class A member 2; heat shock protein 90kDa alpha (cytosolic), class A member 1	1.0822E-06	0.00028376	2.64	6.25
HSP90AB1	heat shock 90kDa protein 1, beta	1.8015E-05	0.00124703	2.23	4.69
HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	0.00020079	0.00420598	-1.56	0.34
HSPA9	heat shock protein 9	0.0001081	0.0030032	-1.06	0.48
HSPB1	heat shock 27kDa protein 1	1.5872E-07	0.00012069	4.32	19.93
HSPD1	heat shock 60kDa protein 1 (chaperonin)	6.7386E-05	0.0022989	1.72	3.30
HSPE1	heat shock 10kDa protein 1 (chaperonin 10)	0.00056034	0.00761764	1.14	2.21
HSPH1	heat shock 105kDa/110kDa protein 1	1.3757E-06	0.00031699	1.82	3.53
HTRA2	HtrA serine peptidase 2	7.513E-06	0.00073242	1.17	2.25
HYAL1	hyaluronoglucosaminidase 1	1.5308E-07	0.00012069	-2.26	0.21
HYAL2	hyaluronoglucosaminidase 2	4.4627E-07	0.00019517	-2.71	0.15
IARS2	isoleucyl-tRNA synthetase 2, mitochondrial	1.7761E-05	0.00124703	1.19	2.28
ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	1.9881E-05	0.0012798	-2.10	0.23
IER3	immediate early response 3	0.00012571	0.00324044	-2.12	0.23
IFITM1	interferon induced transmembrane protein 1 (9-27)	0.00166391	0.01483021	1.42	2.67
IFITM3	interferon induced transmembrane protein 3 (1-8U)	0.00501668	0.02693984	1.16	2.24
IFRD1	interferon-related developmental regulator 1	8.921E-06	0.00082726	-1.25	0.42
Ige	immunoglobulin E	0.00011888	0.00318846	-2.98	0.13
IGH@	immunoglobulin heavy locus	0.00900659	0.03606135	1.07	2.10
IGLL1	immunoglobulin lambda variable group	0.00711519	0.03225272	1.44	2.71
IL16	interleukin 16 (lymphocyte chemoattractant factor)	0.00055	0.00759703	1.32	2.50
IL18BP	interleukin 18 binding protein	7.3563E-06	0.00072646	1.39	2.62
IL2RG	interleukin 2 receptor, gamma	0.00385527	0.02347115	1.06	2.09
IL32	interleukin 32	0.00091013	0.01033901	1.08	2.12
IMP4	IMP4, U3 small nucleolar ribonucleoprotein, homolog	3.7061E-05	0.0017724	1.07	2.10
IRF2	interferon regulatory factor 2	0.00033535	0.00562908	1.01	2.01
IRF5	interferon regulatory factor 5	0.00159986	0.01455186	1.24	2.36
ITFG1	integrin alpha FG-GAP repeat containing 1	0.00082704	0.0097088	-1.05	0.48
ITGA5	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	6.4357E-07	0.00023125	-2.18	0.22
ITM2B	integral membrane protein 2B	0.00021346	0.00434007	-1.03	0.49
JAG1	jagged 1	0.0005794	0.00774981	-1.94	0.26
JMJD1C	jumonji domain containing 1C	0.00036742	0.005948	-1.12	0.46
JOSD1	Josephin domain containing 1	2.6144E-06	0.00044178	-1.57	0.34
JUND	jun D proto-oncogene	9.0803E-07	0.00026055	-1.67	0.32
KCNA3	potassium voltage-gated channel, shaker-related subfamily, member 3	0.00010626	0.00297598	-1.28	0.41
KDR	kinase insert domain receptor (a type III receptor tyrosine kinase)	4.3467E-05	0.00189413	-1.77	0.29
KIAA0101	KIAA0101	0.00867439	0.03553884	1.20	2.29
KIAA1967	KIAA1967	0.00029055	0.00520864	1.14	2.21
KLF10	Kruppel-like factor 10	0.00085134	0.00990321	-1.05	0.48
KLF3	Kruppel-like factor 3	0.00022272	0.00439319	-1.16	0.45
KLF4	Kruppel-like factor 4	1.6833E-05	0.00121327	-1.63	0.32
KLHDC3	kelch domain containing 3	3.9238E-06	0.00053721	1.26	2.39
KPNA2	karyopherin alpha 2	0.00014828	0.00358923	1.44	2.72
KYNU	Kynureninase	4.13E-05	0.00186933	1.14	2.20
LAMP2	lysosomal-associated membrane protein 2	6.0078E-05	0.00214228	1.24	2.36
LDHA	lactate dehydrogenase A	2.9349E-06	0.00045085	-1.90	0.27
LGALS1	lectin, galactoside-binding, soluble, 1	2.3976E-07	0.00014662	3.09	8.50
LIMA1	LIM domain and actin-binding protein 1	4.6676E-05	0.00195549	-1.42	0.37
LINS1	lines homolog	6.9815E-05	0.00233351	1.35	2.54
LIPA	lysosomal acid lipase A	5.9997E-05	0.00214228	2.48	5.58
LITAF	SET and MYND domain containing 2	8.8973E-06	0.00082726	1.44	2.71
LOC100626076	0	0.00032793	0.00553519	-2.27	0.21
LOC508070	0	0.01691646	0.04943989	-1.05	0.48
LOC510193	apolipoprotein L, 3-like	1.7781E-06	0.00034669	-1.42	0.37
LOC750761	0	0.00021507	0.00436095	-1.28	0.41
LONP2	lon peptidase 2, peroxisomal	0.00015965	0.00372389	1.31	2.48
LRRC25	leucine rich repeat containing 25	0.00017505	0.00392058	1.15	2.22
LY6E	lymphocyte antigen 6 complex, locus E	0.00105689	0.01135916	1.13	2.20
LYST	lysosomal trafficking regulator	6.7896E-06	0.00068783	1.75	3.35
LZIC	leucine zipper and CTNNBIP1 domain containing	7.6346E-06	0.00073953	1.19	2.28
MAN1C1	mannosidase, alpha, class 1C, member 1	0.009167	0.03636197	-1.09	0.47
MAP3K2	mitogen-activated protein kinase kinase kinase 2	0.00010822	0.0030032	-2.15	0.23

MAP7D1	MAP7 domain containing 1	6.8294E-06	0.00068783	1.07	2.09
MARS	methionyl-tRNA synthetase	0.00065516	0.00839396	1.21	2.31
MAZ	MYC-associated zinc finger protein (purine-binding transcription factor)	6.578E-06	0.0006714	1.38	2.61
MCM3	minichromosome maintenance complex component 3	0.00019677	0.00417939	1.07	2.10
MDC1	mediator of DNA-damage checkpoint 1	0.0001098	0.00303597	1.13	2.19
MED1	mediator complex subunit 1	3.8191E-05	0.00179263	1.09	2.12
MED25	Spi-B transcription factor (Spi-1/PU.1 related)	0.00068863	0.00866176	-1.15	0.45
MED30	mediator complex subunit 30	0.00026451	0.00490588	-1.01	0.50
MED8	mediator complex subunit 8	1.0414E-05	0.0009208	1.25	2.37
METTL12	methyltransferase like 12	4.243E-05	0.00188274	1.11	2.16
MICAL1	microtubule associated monoxygenase, calponin and LIM domain containing 1	0.00941607	0.03690829	1.03	2.05
MIER2	mesoderm induction early response 1, family member 2	0.00117576	0.01204107	-1.04	0.49
MIF	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	0.00136242	0.01318045	1.06	2.08
MKNK2	MAP kinase interacting serine/threonine kinase 2	2.0424E-05	0.00129965	-1.89	0.27
MORF4L1	ubiquitin specific peptidase 15	4.2039E-05	0.00188274	-1.13	0.46
MOV10	Mov10l1, Moloney leukemia virus 10-like 1, homolog	0.00333975	0.02187379	1.13	2.18
MOXD1	monooxygenase, DBH-like 1	5.9605E-05	0.00214228	-1.38	0.38
MPP1	membrane protein, palmitoylated 1, 55kDa	0.000345	0.00574671	1.10	2.15
MPRIP	myosin phosphatase Rho interacting protein	9.4316E-05	0.00276369	1.09	2.13
MPZL1	myelin protein zero-like 1	3.0769E-05	0.00161358	-1.64	0.32
MRPL2	mitochondrial ribosomal protein L2	0.00023245	0.00451169	1.24	2.37
MRPL28	mitochondrial ribosomal protein L28	0.00012859	0.00327578	1.10	2.15
MRPL45	mitochondrial ribosomal protein L45	0.00010951	0.00303365	1.24	2.36
MRPL48	mitochondrial ribosomal protein L48	5.9505E-06	0.00063971	1.11	2.16
MRPL51	mitochondrial ribosomal protein L51	0.0003597	0.00587211	1.29	2.45
MRPS11	mitochondrial ribosomal protein S11	1.2122E-05	0.00098586	1.01	2.01
MRPS12	mitochondrial ribosomal protein S12	3.6287E-05	0.00175191	1.09	2.13
MRPS5	mitochondrial ribosomal protein S5	0.00048639	0.00703814	1.08	2.11
MRRF	mitochondrial ribosome recycling factor	9.2668E-06	0.00084389	1.54	2.92
MSH6	mutS homolog 6	0.00330492	0.0217685	1.07	2.10
MT1A	metallothionein 1A	1.452E-05	0.00111113	1.17	2.25
MT2A	metallothionein 2A	0.00013318	0.00334774	1.65	3.14
MTCH2	mitochondrial carrier homolog 2	2.0087E-06	0.00037861	1.90	3.74
MTMR9	myotubularin related protein 9	0.00023837	0.00460051	-1.04	0.49
MT-ND3	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	1.3701E-06	0.00031699	-1.46	0.36
MX2	myxovirus (influenza virus) resistance 2	0.00538416	0.02786058	2.01	4.03
MYBL2	v-myb myeloblastosis viral oncogene homolog like 2	0.00022394	0.00441145	1.52	2.87
MYC	transcription factor protein	0.00020643	0.00427423	2.02	4.05
MYL6	myosin, light chain 6B, alkali, smooth muscle and non-muscle	0.00106108	0.01137092	1.51	2.84
MYLIP	myosin regulatory light chain interacting protein	0.00012267	0.00321637	-1.36	0.39
MYOF	myoferlin	0.00887405	0.03594315	1.67	3.18
MYST1	MYST histone acetyltransferase 1	4.2287E-05	0.00188274	1.05	2.07
N6AMT2	N-6 adenine-specific DNA methyltransferase 2 (putative)	5.0182E-06	0.00060556	1.27	2.42
NAA10	N(alpha)-acetyltransferase 10, NatA catalytic subunit	5.9204E-05	0.00214228	1.04	2.06
NAP1L5	nucleosome assembly protein 1-like 5	3.2551E-06	0.00048533	-2.51	0.18
NARF	nuclear prelamin A recognition factor	0.00102578	0.01114256	-1.12	0.46
NCAPH	non-SMC condensin I complex, subunit H	0.00025452	0.00479655	1.05	2.06
NCF1	neutrophil cytosolic factor 1	0.00042333	0.00648344	1.01	2.02
NCF4	neutrophil cytosolic factor 4, 40kDa	0.00017237	0.00389722	1.23	2.34
NCOA2	nuclear receptor coactivator 2	3.3545E-05	0.00166717	-1.73	0.30
NCOA3	nuclear receptor coactivator 3	0.01052306	0.0387308	-1.12	0.46
NCS1	neuronal calcium sensor 1	0.00566765	0.02868031	-1.40	0.38
NDE1	External NADH-ubiquinone oxidoreductase 1, mitochondrial	0.00251992	0.01863048	1.10	2.14
NDEL1	nudE nuclear distribution gene E homolog like 1	7.5346E-07	0.00023125	-2.77	0.15
NDNL2	necdin-like 2	2.5667E-07	0.00014662	-4.06	0.06
NDRG1	N-myc downstream regulated 1	0.0031844	0.0212498	-1.16	0.45
NDUFAF4	mitochondrially encoded NADH dehydrogenase 1	0.01509473	0.04693531	1.02	2.03
NDUFS2	hypothetical protein MGC130896	0.00181333	0.01565989	1.15	2.21
NEDD4L	Nedd4 protein	0.000143	0.0035152	-1.07	0.47
NEDD9	neural precursor cell expressed, developmentally down-regulated gene 9	4.999E-06	0.00060556	-1.25	0.42
NFIL3	nuclear factor, interleukin 3 regulated	0.00033219	0.00558851	-1.21	0.43
NGDN	neuroguidin, EIF4E binding protein	0.00037355	0.00601795	1.17	2.25
NGFRAP1	nerve growth factor receptor (TNFRSF16) associated protein 1	4.6495E-05	0.0019533	-1.74	0.30
NGRN	neugrin, neurite outgrowth associated	1.7535E-05	0.00124031	1.57	2.96
NKG7	natural killer cell group 7 sequence	0.00726356	0.0325662	1.16	2.24

NLRC5	NLR family, CARD domain containing 5	0.0021645	0.01723443	1.41	2.66
NME6	non-metastatic cells 1, protein (NM23A) expressed in	2.1224E-05	0.00131745	1.09	2.13
NOP56	NOP56 ribonucleoprotein homolog	0.00552359	0.02820558	1.24	2.36
NPC2	Niemann-Pick disease, type C2	0.00011951	0.00319414	-1.17	0.44
NPM3	nucleophosmin/nucleoplasmin 3	7.4894E-05	0.00242856	1.59	3.01
NQO2	NAD(P)H dehydrogenase, quinone 2	0.00110298	0.01161645	-1.28	0.41
NR4A1	nuclear receptor subfamily 4, group A, member 1	4.7746E-07	0.00019517	-2.36	0.19
NRD1	nardilysin, N-arginine dibasic convertase, NRD convertase 1	7.6028E-07	0.00023125	-1.62	0.32
NTHL1	nth endonuclease III-like 1	0.00070164	0.00872488	1.02	2.03
NUCB2	nucleobindin 2	3.6868E-05	0.00176872	-1.42	0.37
NUDC	nuclear distribution gene C homolog	0.00069378	0.00866969	1.15	2.22
NUDT5	nudix (nucleoside diphosphate linked moiety X)-type motif 6	0.00053641	0.00747051	1.27	2.40
NUP85	nucleoporin 85kDa	7.0583E-05	0.00235259	1.42	2.68
NUP98	nucleoporin 98kDa	9.7836E-05	0.00280765	-1.09	0.47
NXF1	nuclear RNA export factor 1	0.00042053	0.00645353	1.23	2.34
OGDH	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	5.8816E-06	0.00063971	-1.89	0.27
Ogt	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	0.00183401	0.01576687	1.11	2.16
OR3A1	olfactory receptor, family 3, subfamily A, member 1	0.00097425	0.0107599	1.20	2.30
ORMDL3	ORM1-like 3	1.371E-05	0.00107862	-1.35	0.39
OSTN	osteocrin	4.2069E-06	0.00055576	-2.20	0.22
OXCT1	3-oxoacid CoA transferase 1	0.00020896	0.00429392	1.07	2.10
P4HA2	prolyl 4-hydroxylase, alpha polypeptide II	0.00034384	0.00573995	1.55	2.93
P4HB	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide	0.00015154	0.00364335	-1.29	0.41
PA2G4	proliferation-associated 2G4, 38kDa	0.001034	0.01119223	1.14	2.20
PACRG	high mobility group box 1	2.9343E-05	0.00157684	1.13	2.18
PACS1	phosphofurin acidic cluster sorting protein 1	0.00021133	0.00431395	-1.10	0.47
PAF1	Rtf1, Paf1/RNA polymerase II complex component, homolog	0.00019658	0.00417939	-1.19	0.44
PALLD	palladin, cytoskeletal associated protein	0.00048038	0.00700547	-1.05	0.48
PAPOLA	poly (A) polymerase alpha	1.6219E-05	0.00119156	1.01	2.02
PCYOX1	prenylcysteine oxidase 1	6.015E-05	0.00214228	1.04	2.05
PDE4B	phosphodiesterase 4B, cAMP-specific	3.345E-09	1.6957E-05	-3.85	0.07
PDEA	phosphodiesterase 7A	2.5689E-07	0.00014662	-2.86	0.14
PDHB	Pyruvate dehydrogenase E1 component subunit beta	8.2715E-05	0.00256706	1.21	2.31
PER1	period homolog 1	1.6475E-06	0.00033494	-2.38	0.19
PFDN2	prefoldin subunit 2	0.0168611	0.04937193	-1.74	0.30
PGM3	phosphoglucomutase 3	1.7534E-05	0.00124031	-1.90	0.27
PHACTR1	phosphatase and actin regulator 1	0.00039227	0.00622844	-1.04	0.48
PHKG2	phosphorylase kinase, gamma 2	2.2717E-05	0.00136015	-1.57	0.34
PIAS1	protein inhibitor of activated STAT, 1	0.00012012	0.00319919	1.01	2.01
PICALM	phosphatidylinositol binding clathrin assembly protein	8.8352E-05	0.00267289	-1.04	0.49
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	3.7906E-05	0.00179031	-1.28	0.41
PIN1	peptidylprolyl cis/trans isomerase, NIMA-interacting 1	9.0646E-05	0.00270302	1.00	2.00
PITPNA	phosphatidylinositol transfer protein, alpha	0.00015525	0.00368011	1.17	2.24
PITX3	paired-like homeodomain transcription factor 3	0.00140934	0.01348848	-1.25	0.42
PKD2	polycystic kidney disease 2	0.01109061	0.03987954	-1.02	0.49
PKM2	pyruvate kinase, muscle	0.00332833	0.02184356	1.15	2.22
PLAGL1	pleiomorphic adenoma gene-like 1	7.2414E-06	0.00072452	-1.40	0.38
PLCB2	phospholipase C, beta 2	5.4324E-06	0.00061869	-1.24	0.42
PLDN	pallidin homolog	0.00061723	0.0080574	1.01	2.02
PLK2	polo-like kinase 2	1.1415E-05	0.00096416	-1.54	0.34
PLOD1	procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1	6.8809E-08	8.3038E-05	2.19	4.55
PLXNC1	plexin C1	7.3607E-05	0.00239718	1.49	2.81
POMT2	protein-O-mannosyltransferase 2	2.4792E-05	0.00142281	-1.03	0.49
PPM1M	protein phosphatase, Mg2+/Mn2+ dependent, 1M	0.00019132	0.00410954	1.17	2.25
PPRC1	peroxisome proliferator-activated receptor gamma, coactivator-related 1	0.00023063	0.00450109	1.16	2.23
PRC1	proteasome C9 1	0.00175856	0.0153174	1.38	2.61
PRMT5	similar to protein arginine N-methyltransferase 5 (predicted)	5.1755E-05	0.00206467	1.78	3.45
PRNP	prion protein	0.00083573	0.00978586	-1.21	0.43
PSAP	prosaposin	4.9359E-05	0.00200581	-1.10	0.47
PSMB3	proteasome (prosome, macropain) subunit, beta type, 3	4.9848E-05	0.00201619	1.00	2.00
PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)	0.00016071	0.00373373	1.29	2.44
PSMC5	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	0.00090531	0.01032085	1.06	2.09
PSMG1	proteasome (prosome, macropain) assembly chaperone 1	0.00012382	0.00322997	1.16	2.23
PSPH	phosphoserine phosphatase	1.37E-05	0.00107862	1.09	2.13
PTCD3	Pentatricopeptide repeat domain 3	0.00030872	0.00537794	1.03	2.04

PTGER4	prostaglandin receptor EP4 subtype	0.0008424	0.00981699	-1.14	0.46
PTGS2	cyclooxygenase-2	1.8726E-05	0.0012798	-1.22	0.43
PTOV1	prostate tumor overexpressed 1	9.9173E-07	0.00027528	1.76	3.38
PTPMT1	protein tyrosine phosphatase, mitochondrial 1	0.00073786	0.00900458	1.00	2.00
PTPN2	protein tyrosine phosphatase, non-receptor type 2	2.4901E-05	0.00142368	-1.23	0.43
PUS3	pseudouridylate synthase 3	1.9399E-05	0.0012798	1.37	2.58
RAB11FIP3	RAB11 family interacting protein 3 (class II)	0.00236998	0.01813925	-1.15	0.45
RAB1B	RAB1B, member RAS oncogene family	0.01117911	0.0400688	-1.13	0.46
RAB32	RAB40C, member RAS oncogene family	6.5785E-05	0.00228413	1.23	2.34
RAB3GAP1	guanylate binding protein 2, interferon-inducible	0.00040509	0.00635381	-1.61	0.33
RAB40B	RAB40C, member RAS oncogene family	0.00026103	0.00487093	-1.05	0.48
RAB43	RAB43, member RAS oncogene family	0.00268434	0.01928698	-1.05	0.48
RAB7A	RAB7A, member RAS oncogene family	3.6872E-06	0.00051945	-1.44	0.37
RABEPK	Rab9 effector protein with kelch motifs	2.0521E-05	0.00130036	1.27	2.41
RAD51L1	RAD51-like 1	0.00656285	0.03107808	-1.44	0.37
RANBP2	RAN binding protein 2	3.7196E-06	0.00051945	-2.67	0.16
RASSF2	Ras association (RalGDS/AF-6) domain family member 2	0.007575	0.03323384	1.05	2.07
RASSF5	Ras association (RalGDS/AF-6) domain family member 5	0.00015536	0.00368011	-1.34	0.39
RB1	retinoblastoma 1	0.00045981	0.00683554	1.07	2.10
RBM3	RNA binding motif (RNP1, RRM) protein 3	4.1923E-05	0.00188274	-1.85	0.28
RBM48	chromosome 7 open reading frame 64 ortholog	6.064E-05	0.00214568	1.29	2.45
RDX	radixin	0.00036529	0.00592882	1.06	2.09
REG3G	regenerating islet-derived 3 gamma	0.01686203	0.04937193	-1.05	0.48
RFC2	replication factor C (activator 1) 2, 40kDa	0.00015758	0.00369818	1.51	2.86
RFC3	replication factor C (activator 1) 3, 38kDa	3.233E-05	0.001662	1.41	2.66
RGAG4	retrotransposon gag domain containing 4	2.2019E-05	0.00133947	-1.05	0.48
RGMB	RGM domain family, member B	0.00014153	0.00349415	-1.28	0.41
RGS1	regulator of G-protein signaling 1	0.0001948	0.00415889	-1.04	0.48
RGS2	regulator of G-protein signaling 2, 24kDa	0.0065981	0.03115277	-2.05	0.24
RHOF	ras homolog gene family, member F	0.00020036	0.00420598	1.21	2.32
RHOT2	family with sequence similarity 195, member A	0.00019501	0.00415889	1.21	2.31
RNF113A	ring finger protein 113A	2.3886E-05	0.00139177	1.38	2.60
RNF144B	ring finger protein 144B	4.529E-05	0.00194568	-1.18	0.44
RNF19A	ring finger protein 19A	0.00072976	0.00896459	1.04	2.06
RNMT	RNA (guanine-7-) methyltransferase	0.0001563	0.00368107	1.03	2.05
ROBLD3	late endosomal/lysosomal adaptor, MAPK and MTOR activator 2	0.00045056	0.0067442	1.33	2.51
RPL10	ribosomal protein L10	0.00611479	0.02998938	-1.30	0.41
RPL5	60S ribosomal protein L5-B	0.00046841	0.00688936	1.18	2.26
RPS24	ribosomal protein S24	1.124E-05	0.00095994	-1.49	0.36
RPS6KA6	ribosomal protein S6 kinase, 90kDa, polypeptide 6	7.7167E-06	0.00074276	-1.46	0.36
RRM2	ribonucleotide reductase M2	0.001617	0.01464966	1.28	2.42
RRP7A	ribosomal RNA processing 7 homolog A	0.00465841	0.0259126	-1.38	0.38
RTP4	receptor (chemosensory) transporter protein 4	1.1659E-05	0.00096546	2.23	4.68
RUFY3	RUN and FYVE domain containing 3	2.8103E-05	0.00155412	1.21	2.31
RUNX2	runt related transcription factor 2	2.8375E-05	0.00155786	1.02	2.03
RYBP	RING1 and YY1 binding protein	2.7276E-06	0.00044604	-1.57	0.34
SACM1L	SAC1 suppressor of actin mutations 1-like	8.8878E-06	0.00082726	-1.54	0.34
SAMHD1	SAM domain and HD domain 1	1.7666E-06	0.00034669	1.56	2.95
SAMSN1	SAM domain, SH3 domain and nuclear localization signals 1	2.8861E-05	0.00157057	-1.20	0.44
SAP30BP	similar to transcriptional regulator protein; SAP30 binding protein	0.00028639	0.00517277	1.21	2.31
SC5DL	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog)-like	0.00170306	0.01504806	-1.09	0.47
SCARB2	scavenger receptor class B, member 2	0.00653204	0.03101446	-1.18	0.44
SCNM1	sodium channel modifier 1	0.00012482	0.00323088	1.01	2.01
SDC4	syndecan 4	4.3142E-05	0.00189079	-1.13	0.46
SDF2L1	stromal cell-derived factor 2-like 1	0.00024517	0.00468999	-1.08	0.47
SDHAF1	succinate dehydrogenase complex assembly factor 1	0.00013062	0.00330865	1.24	2.36
SDHAF2	succinate dehydrogenase complex assembly factor 1	6.1151E-05	0.00215039	1.14	2.21
SDHC	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	0.00029249	0.00520864	1.13	2.18
SEC11C	SEC11 homolog C	0.00317406	0.02120877	-1.47	0.36
SEC24D	SEC24 family, member D	0.00018644	0.00407297	-1.41	0.38
SEC61A1	Sec61 alpha 2 subunit	0.00268393	0.01928698	-1.30	0.41
SEC61G	Sec61 gamma subunit	0.00027287	0.00498774	-1.08	0.47
SELENBP1	selenium binding protein 1	8.9771E-05	0.00269809	-1.60	0.33
Selk	selenoprotein k	2.7601E-06	0.00044654	-1.67	0.31
SEMA4D	hypothetical protein LOC738112; sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	0.00274875	0.01949769	-1.00	0.50
SEPHS1	selenophosphate synthetase 1	7.1225E-05	0.00236505	1.22	2.33

SEPX1	SELENOPROTEIN X, 1	0.00019523	0.00415889	1.14	2.21
SERPINB1	SERPIN PEPTIDASE INHIBITOR, CLADE B, MEMBER 1	0.01152665	0.04075733	-1.10	0.47
SERPINB2	SERPIN PEPTIDASE INHIBITOR, CLADE B, MEMBER 2	3.5314E-07	0.00017902	-2.53	0.17
SERPINE1	SERPIN PEPTIDASE INHIBITOR, CLADE E (NEXIN, PLASMINOGEN ACTIVATOR INHIBITOR TYPE 1), MEMBER 1	0.00107971	0.01146944	-1.27	0.41
SERTAD1	SERTA DOMAIN CONTAINING 1	0.00118291	0.01207361	-1.07	0.48
SF3B1	SPLICING FACTOR 3B, SUBUNIT 1, 155KDA	0.0001691	0.00385554	-1.09	0.47
SFRS5	HYPOTHETICAL PROTEIN MGC78772	6.3516E-06	0.00065267	-1.59	0.33
SFXN4	SIDEROFLEXIN 4	0.0002728	0.00498774	1.01	2.02
SGCE	SARCOGLYCAN, EPSILON	1.3104E-06	0.00031137	-2.08	0.24
SGPP1	SPHINGOSINE-1-PHOSPHATE PHOSPHATASE 1	0.00017104	0.00388825	-1.19	0.44
SH2B1	SH2B ADAPTOR PROTEIN 1	5.6176E-05	0.00210943	1.15	2.22
SHISA5	SHISA HOMOLOG 5	1.6534E-05	0.0012032	1.07	2.10
SIRPA	SIGNAL-REGULATORY PROTEIN ALPHA	0.00039235	0.00622844	-1.03	0.49
SIRT7	SIRTUIN 7	0.00011502	0.00310708	1.11	2.15
SKA1	SPINDLE AND KINETOCHORE ASSOCIATED COMPLEX SUBUNIT 1	0.00057162	0.0077042	1.01	2.02
SKP2	S-PHASE KINASE-ASSOCIATED PROTEIN 2 (P45)	0.00309779	0.02094392	1.01	2.02
SLAIN1	SLAIN MOTIF FAMILY, MEMBER 1	0.00206486	0.01683792	-1.30	0.41
SLC15A4	SOLUTE CARRIER FAMILY 15, MEMBER 4	0.00012197	0.00321637	1.27	2.41
SLC25A28	SOLUTE CARRIER FAMILY 25, MEMBER 28	0.0007972	0.00948652	-1.20	0.44
SLC29A1	SOLUTE CARRIER FAMILY 29 (NUCLEOSIDE TRANSPORTERS), MEMBER 1	3.2567E-05	0.001662	1.03	2.04
SLC2A1	SOLUTE CARRIER FAMILY 2 (FACILITATED GLUCOSE TRANSPORTER), MEMBER 1	1.1103E-07	0.00011256	-2.84	0.14
SLC2A3	SOLUTE CARRIER FAMILY 2 (FACILITATED GLUCOSE TRANSPORTER), MEMBER 3	4.0851E-07	0.00019517	-3.97	0.06
SLC39A10	SOLUTE CARRIER FAMILY 39 (ZINC TRANSPORTER), MEMBER 10	2.4127E-07	0.00014662	1.92	3.78
SLC44A4	SOLUTE CARRIER FAMILY 44, MEMBER 4	0.01674803	0.04917065	-1.41	0.38
SLC4A1AP	SOLUTE CARRIER FAMILY 4 (ANION EXCHANGER), MEMBER 1, ADAPTOR PROTEIN	6.897E-05	0.00231209	1.02	2.03
SLC4A7	SOLUTE CARRIER FAMILY 4, SODIUM BICARBONATE COTRANSPORTER, MEMBER 7	2.1012E-05	0.00131622	-1.65	0.32
SLC6A5	NEUROEPITHELIAL CELL TRANSFORMING 1	0.00024056	0.00461928	-1.21	0.43
SLC7A1	SOLUTE CARRIER FAMILY 7 (CATIONIC AMINO ACID TRANSPORTER, Y+ SYSTEM), MEMBER 1	3.9249E-08	7.4613E-05	-2.76	0.15
SLC9A3R1	SOLUTE CARRIER FAMILY 9 (SODIUM/HYDROGEN EXCHANGER), MEMBER 3 REGULATOR 1	0.00010667	0.00297867	-1.29	0.41
SLPI	SECRETORY LEUKOCYTE PEPTIDASE INHIBITOR	0.00383173	0.02340282	-1.90	0.27
SNAI1	SNAIL HOMOLOG 1	6.1062E-06	0.00063971	-1.63	0.32
SNAP25	SYNAPTOSOMAL-ASSOCIATED PROTEIN, 25KDA	0.00026313	0.00489799	-1.54	0.34
SNAPC3	SMALL NUCLEAR RNA ACTIVATING COMPLEX, POLYPEPTIDE 3, 50KDA	0.00016787	0.00384422	1.13	2.19
SNHG12	SMALL NUCLEOLAR RNA HOST GENE 12 (NON-PROTEIN CODING)	0.0002088	0.00429392	-1.13	0.46
SNRK	SNF RELATED KINASE	1.0195E-08	2.5842E-05	-3.71	0.08
SNRPA1	SMALL NUCLEAR RIBONUCLEOPROTEIN POLYPEPTIDE A	0.00024188	0.00463281	1.26	2.40
SNRPN	SMALL NUCLEAR RIBONUCLEOPROTEIN POLYPEPTIDE N	0.00013876	0.00345951	1.02	2.03
SNUPN	SNURPORTIN 1	2.2252E-05	0.00134292	1.26	2.40
SOCS2	SUPPRESSOR OF CYTOKINE SIGNALING 2	2.9274E-06	0.00045085	-1.90	0.27
SOCS3	SUPPRESSOR OF CYTOKINE SIGNALING 3	4.704E-05	0.00195678	1.59	3.02
SOD1	SUPEROXIDE DISMUTASE	0.00049665	0.00713223	-1.01	0.49
SP100	SP100 NUCLEAR ANTIGEN	0.00019526	0.00415889	1.12	2.18
SPATA20	SPERMATOGENESIS ASSOCIATED 20	0.00057496	0.00772846	1.03	2.04
SPEG	SPEG COMPLEX LOCUS	2.0414E-06	0.00037861	3.30	9.85
SPINT2	SERINE PEPTIDASE INHIBITOR, KUNITZ TYPE, 2	0.00012243	0.00321637	-1.16	0.45
SPP1	SECRETED PHOSPHOPROTEIN 1	4.8766E-07	0.00019517	-2.10	0.23
SQLE	SQUALENE EPOXIDASE	1.7114E-05	0.00122766	-1.77	0.29
SQSTM1	SEQUESTOSOME 1	0.00012831	0.00327401	-2.23	0.21
SRRM1	SERINE/ARGININE REPETITIVE MATRIX 1	0.00842108	0.03509668	-1.06	0.48
SSR1	SIGNAL SEQUENCE RECEPTOR, ALPHA (TRANSLOCON-ASSOCIATED PROTEIN ALPHA)	6.1075E-06	0.00063971	-1.61	0.33
ST3GAL2	ST6 BETA-GALACTOSAMIDE ALPHA-2,6-SIALYLTRANFERASE 2	0.00071028	0.00877778	-1.19	0.44
ST6	ST6 (ALPHA-N-ACETYL-NEURAMINYL-2,3-BETA-GALACTOSYL-1,3)-N-ACETYLGALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE 2	0.00038852	0.00620646	1.51	2.86
STAT4	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1	0.00250701	0.01858023	-1.27	0.41
STIP1	STRESS-INDUCED-PHOSPHOPROTEIN 1;	0.00019031	0.00410286	1.44	2.71
STK17A	SERINE/THREONINE KINASE 17A	3.9916E-06	0.00053721	-1.69	0.31
STOML2	STOMATIN (EPB72)-LIKE 2	2.6014E-05	0.00147072	1.36	2.57
STUB1	STIP1 HOMOLOGY AND U-BOX CONTAINING PROTEIN 1, E3 UBIQUITIN PROTEIN LIGASE	0.00069811	0.00869193	1.27	2.41
STX11	SYNTAXIN 11	0.00018213	0.00402265	-1.37	0.39
SYTL2	SYNAPTOTAGMIN-LIKE 2	0.00850368	0.03520935	-1.12	0.46
TAC1	TACHYKININ 1	0.00064011	0.00826305	-2.44	0.18
TAF2	TAF2 RNA POLYMERASE II, TATA BOX BINDING PROTEIN (TBP)-	0.00011117	0.00305128	-1.19	0.44

	associated factor, 150kDa				
TAF7	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa	1.0175E-05	0.00090489	1.32	2.50
TCEA3	transcription elongation factor A (SII), 3	0.00065197	0.00836717	2.08	4.23
TCEAL1	transcription elongation factor A (SII)-like 1	5.0551E-06	0.00060556	-1.94	0.26
TCOF1	Treacher Collins-Franceschetti syndrome 1	4.6172E-05	0.0019533	1.18	2.26
TESC	tescalcin	0.0011942	0.01213993	-1.21	0.43
TGIF2	TGFB-induced factor homeobox 2	0.00014905	0.0035981	-1.06	0.48
TGM2	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	0.00379868	0.02333211	2.17	4.51
TIAL1	TIA1 cytotoxic granule-associated RNA binding protein-like 1	5.0638E-05	0.00204272	1.18	2.26
TIAM1	T-cell lymphoma invasion and metastasis 1	0.00040028	0.00630165	-1.02	0.49
TIFA	TRAF-interacting protein with forkhead-associated domain	7.7179E-05	0.0024521	1.66	3.16
TIMM23	translocase of inner mitochondrial membrane 23 homolog	6.7793E-05	0.0022989	1.14	2.20
TIMM50	translocase of inner mitochondrial membrane 50 homolog	0.00019047	0.00410286	1.04	2.06
TIPARP	TCDD-inducible poly(ADP-ribose) polymerase	5.3128E-06	0.00061209	1.24	2.35
TLE1	transducin-like enhancer of split 1 (E(sp1) homolog)	1.9945E-05	0.0012798	-1.01	0.50
TLE3	transducin-like enhancer of split 3 (E(sp1) homolog)	5.8062E-05	0.00212187	-1.04	0.49
TLR7	toll-like receptor7	4.2463E-05	0.00188274	1.47	2.76
TM9SF2	transmembrane 9 superfamily member 2	9.0277E-10	6.8647E-06	3.32	9.98
TMBIM6	transmembrane BAX inhibitor motif containing 6	0.00045199	0.006759	-1.22	0.43
TMED1	transmembrane emp24 protein transport domain containing 1	6.1226E-05	0.00215039	-1.46	0.36
TMEM167A	transmembrane protein 167A	0.00067327	0.00849714	-1.01	0.50
TMEM41B	transmembrane protein 41B	3.7712E-05	0.00179031	-1.69	0.31
TMEM51	transmembrane protein 51	1.0718E-06	0.00028376	1.68	3.20
TMEM55B	transmembrane protein 55B	0.00015195	0.00364499	1.31	2.48
TMEM86B	transmembrane protein 86B	0.00021486	0.00436095	1.33	2.51
TNFAIP3	tumor necrosis factor, alpha-induced protein 3	4.946E-05	0.00200581	-1.46	0.36
TNFRSF13B	tumor necrosis factor receptor superfamily, member 13B	9.6533E-05	0.00279065	2.05	4.13
TOMM20	translocase of outer mitochondrial membrane 20 homolog	0.00070794	0.00876733	-1.04	0.49
TOMM5	translocase of outer mitochondrial membrane 5 homolog	7.3487E-06	0.00072646	1.55	2.93
TP53	tumor protein p53	0.00211734	0.01704309	1.29	2.45
TP53INP2	tumor protein p53 inducible nuclear protein 2	5.0227E-08	7.6385E-05	-3.80	0.07
TPM1	tropomyosin 1 (alpha)	1.4566E-05	0.00111113	1.44	2.71
TPM4	tropomyosin 4	0.00137239	0.01325159	-1.11	0.46
TPRKB	TP53RK binding protein	0.00022047	0.00438285	-1.69	0.31
TRAPPC6B	trafficking protein particle complex 6B	0.00056854	0.00767883	-1.19	0.44
TRIAP1	TP53 regulated inhibitor of apoptosis 1	1.4602E-05	0.00111113	1.12	2.17
TRIP12	thyroid hormone receptor interactor 12	0.00238753	0.01815473	1.11	2.17
TRIP13	similar to thyroid hormone receptor interactor 13	0.01519413	0.047052	1.25	2.38
TSC22D2	TSC22 domain family, member 2	1.7378E-06	0.00034669	-1.54	0.34
TSEN34	tRNA splicing endonuclease 34 homolog	0.00157365	0.01437358	1.07	2.10
TSPAN31	tetraspanin 31	0.00815728	0.03445999	1.08	2.11
Tspan6	tetraspanin 6	0.00249855	0.01856248	-1.38	0.38
TUBA1A	tubulin, alpha 1	0.00015035	0.00362365	-1.08	0.47
TUBA4A	tubulin, alpha 4a	0.00102648	0.01114256	-1.40	0.38
TUBB2B	tubulin, beta 2B	0.00021795	0.00436958	1.67	3.17
TXNL4A	thioredoxin-like 4A	0.00029118	0.00520864	1.12	2.18
UBE2C	ubiquitin-conjugating enzyme E2C	0.00186373	0.01591447	1.63	3.09
UBE2L6	ubiquitin-conjugating enzyme E2L 6	5.2826E-06	0.00061209	2.35	5.11
UBE2S	ubiquitin-conjugating enzyme E2S	0.0009598	0.01064674	1.22	2.32
UBFD1	ubiquitin family domain containing 1	6.0668E-05	0.00214568	1.10	2.14
UCP2	uncoupling protein 2 (mitochondrial, proton carrier)	6.6997E-05	0.0022989	-1.23	0.43
UGGT1	UDP-glucose glycoprotein glucosyltransferase 1	0.00055736	0.00761572	-1.22	0.43
ULBP3	ULBP17 protein	0.00342277	0.02215986	2.82	7.08
UTP3	UTP3, small subunit (SSU) processome component, homolog	9.0221E-05	0.00270095	1.02	2.03
UTRN	utrophin	9.1677E-05	0.00271777	-1.35	0.39
VAPA	Vesicle-associated membrane protein-associated protein A	9.2993E-05	0.00274078	-1.21	0.43
VPS52	vacuolar protein sorting 52 homolog	1.5499E-05	0.00116114	1.12	2.18
WARS	tryptophanyl-tRNA synthetase	0.00188684	0.0160129	1.36	2.57
WDR45L	WDR45-like	2.1998E-05	0.00133947	-1.70	0.31
WDR6	WD repeat domain 6	0.00010806	0.0030032	-1.11	0.46
WDR67	WD repeat domain 67	0.00137757	0.01327742	-1.20	0.43
XAF1	XIAP associated factor 1	6.0013E-05	0.00214228	1.29	2.45
XBP1	X-box binding protein 1	0.00071109	0.00877778	-1.15	0.45
XIST	X (inactive)-specific transcript (non-protein coding)	4.6338E-05	0.0019533	-1.08	0.47
XRCC2	X-ray repair complementing defective repair in Chinese hamster cells 2	3.4021E-05	0.001675	1.28	2.43
XRN1	5'-3' exoribonuclease 1	0.0002622	0.00488663	-1.03	0.49
ZBTB10	zinc finger and BTB domain containing 10	5.2537E-07	0.00020487	-2.05	0.24
ZBTB38	zinc finger and BTB domain containing 38	0.00078407	0.00939495	-1.01	0.50

ZCCHC7	NUCLEAR FACTOR (ERYTHROID-DERIVED 2)-LIKE 1	6.8098E-05	0.0022989	1.32	2.49
ZFAND5	ZINC FINGER, AN1-TYPE DOMAIN 5	9.0126E-05	0.00270095	-1.58	0.34
ZFP36L2	ZINC FINGER PROTEIN 36, C3H TYPE-LIKE 2	7.9837E-07	0.00023807	-1.96	0.26
ZNF295	ZINC FINGER PROTEIN 295	3.37E-05	0.0016694	-1.30	0.41
ZNF32	ZINC FINGER PROTEIN 32	5.2581E-06	0.00061209	1.21	2.31
ZNF329	ZINC FINGER PROTEIN 329	0.00011502	0.00310708	1.18	2.26
ZNF691	ZINC FINGER PROTEIN 691	0.0007917	0.00944322	1.01	2.01
ZNF75D	ZINC FINGER PROTEIN 75D	3.1263E-07	0.00016395	1.99	3.97
ZP3	ZONA PELLUCIDA GLYCOPROTEIN 3	1.7928E-05	0.00124703	-1.55	0.34
ZRANB1	ZINC FINGER, RAN-BINDING DOMAIN CONTAINING 1	0.00540519	0.02790714	-1.10	0.47
ZWINT	ZW10 INTERACTOR	0.00044674	0.00671348	-1.41	0.38

* The genes that were significantly modulated ($p < 0.05$ with Benjamini-Hochberg correction for multiple testing) and showed a mean fold expression value > 2 or < 0.5 upon BTV infection were selected.

Table S3. DEG in lymph node cDCs upon BTV infection*

Official gene symbol	Approved Name	Raw.pValue	Adj.pValue	Mean log fold change	Mean fold change
AADAT	AMINOADIPATE AMINOTRANSFERASE	0.0013924	0.02262348	-1.01	0.50
ABCC5	ATP-BINDING CASSETTE, SUB-FAMILY C (CFTR/MRP), MEMBER 5	0.00075753	0.0175036	1.26	2.40
ABCF1	ATP-BINDING CASSETTE, SUB-FAMILY F (GCN20), MEMBER 1	0.000779	0.00170347	1.03	2.05
ABCG2	ATP-BINDING CASSETTE, SUB-FAMILY G (WHITE), MEMBER 2	8.3947E-06	0.01623605	-1.81	0.28
ABLIM1	ACTIN BINDING LIM PROTEIN 1	0.0008471	0.00576711	-1.26	0.42
ACAD8	ACYL-COA DEHYDROGENASE FAMILY, MEMBER 8	4.0252E-05	0.01883736	-1.68	0.31
ACADL	ACYL-COENZYME A DEHYDROGENASE, LONG-CHAIN	9.9855E-06	0.00284121	-1.85	0.28
ACBD6	ACYL-COA BINDING DOMAIN CONTAINING 6	0.00234446	0.00292013	-1.06	0.48
ACTN1	ACTININ, ALPHA 1	0.00069268	0.03590749	-1.19	0.44
ACTR1A	ARP1 ACTIN-RELATED PROTEIN 1 HOMOLOG A, CENTRACTIN ALPHA	0.00114955	0.04502366	1.16	2.23
ACVR2B	ACTIVIN A RECEPTOR, TYPE IIB	1.2186E-05	0.0075114	1.64	3.12
ADA	ADENOSINE DEAMINASE	0.00146017	0.01910066	-1.91	0.27
ADAMTSL4	ADAMTS-LIKE 4	0.00123146	0.02066057	1.44	2.71
ADM	ADRENOMEDULLIN	3.8742E-05	1.4935E-05	-1.32	0.40
AGPAT6	1-ACYLGLYCEROL-3-PHOSPHATE O-ACYLTRANSFERASE 6 (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE, ZETA)	0.00042567	0.01223742	1.59	3.01
AHSA1	AHA1, ACTIVATOR OF HEAT SHOCK 90KDA PROTEIN ATPASE HOMOLOG 1	6.6146E-06	0.01883506	3.01	8.05
ALOX5AP	ARACHIDONATE 5-LIPOXYGENASE ACTIVATING PROTEIN	1.7719E-05	0.01775296	-1.83	0.28
AMICA1	ADHESION MOLECULE, INTERACTS WITH CXADR ANTIGEN 1	0.00042033	0.00481401	-1.66	0.32
AMN	AMNIONLESS HOMOLOG	0.00016426	0.01601083	-1.05	0.48
ANGPT1	ANGIOPOIETIN 1	0.00015547	0.03039685	-1.36	0.39
ANKRD10	ANKYRIN REPEAT DOMAIN 10	7.7695E-05	0.00351812	1.20	2.29
ANP32A	ACIDIC (LEUCINE-RICH) NUCLEAR PHOSPHOPROTEIN 32 FAMILY, MEMBER A	0.000865	0.01219909	1.17	2.25
ANTXR2	ANTHRAX TOXIN RECEPTOR 2	8.0525E-06	0.00340771	1.74	3.35
ANXA2	ANNEXIN A2	0.00022481	0.00141885	1.52	2.87
AP2B1	ADAPTOR-RELATED PROTEIN COMPLEX 2, BETA 1 SUBUNIT	0.00044773	0.00703815	1.19	2.29
AQP3	AQUAPORIN 3	0.00240516	0.0029256	-2.30	0.20
ARG2	ARGINASE, TYPE II	0.00264698	0.00451601	-1.36	0.39
ARPC5L	ACTIN RELATED PROTEIN 2/3 COMPLEX, SUBUNIT 5-LIKE	8.476E-05	0.0083592	1.56	2.95
ARPP19	CAMP-REGULATED PHOSPHOPROTEIN, 19KDA	4.0655E-05	0.00153089	1.00	2.01
ARRDC3	ARRESTIN DOMAIN CONTAINING 3	1.8033E-06	0.0044758	2.36	5.13
ASAH1	N-ACYLETHANOLAMINE ACID AMIDASE	0.0001416	0.02028111	1.07	2.10
ATP6V0A2	ATPASE, H+ TRANSPORTING, LYSOSOMAL V0 SUBUNIT A2	7.2083E-05	0.00085702	-1.07	0.48
B4GALT3	UDP-GAL:BETAGLCNAC BETA 1,4- GALACTOSYLTRANSFERASE, POLYPEPTIDE 3	4.8198E-05	0.00438495	1.13	2.19
BAG2	BCL2-ASSOCIATED ATHANOGENE 2	9.2114E-06	0.01674812	2.28	4.86
BAG3	BCL2-ASSOCIATED ATHANOGENE 3	8.9916E-08	0.01692436	3.46	11.04
BAMBI	BMP AND ACTIVIN MEMBRANE-BOUND INHIBITOR HOMOLOG	2.3122E-05	0.00153814	-1.31	0.40
BANF1	BARRIER TO AUTOINTEGRATION FACTOR 1	6.7173E-06	0.01883506	1.40	2.64
BATF	BASIC LEUCINE ZIPPER TRANSCRIPTION FACTOR, ATF-LIKE 3	1.125E-05	0.00203201	2.33	5.04
BBS1	DIPEPTIDYL-PEPTIDASE 3	0.00096338	0.00273279	1.16	2.23
BCAM	BASAL CELL ADHESION MOLECULE	1.5232E-05	0.00182009	1.68	3.21
BCAP31	B-CELL RECEPTOR-ASSOCIATED PROTEIN 31	9.6867E-05	0.0044758	1.61	3.06
BCKDHB	BRANCHED CHAIN KETO ACID DEHYDROGENASE E1, BETA POLYPEPTIDE	0.00236036	0.00709679	-1.49	0.36
BCL11B	B-CELL CLL/LYMPHOMA 11B (ZINC FINGER PROTEIN)	7.5485E-05	0.00161019	-1.13	0.46
BCL2L15	BCL2-LIKE 15	0.00212717	0.00020392	1.04	2.05
BHLHE40	BASIC HELIX-LOOP-HELIX FAMILY, MEMBER E40	1.4943E-05	0.02867446	-1.69	0.31
BIRC2	BACULOVIRAL IAP REPEAT CONTAINING 2	0.00097852	0.00185535	1.20	2.30
BLZF1	BASIC LEUCINE ZIPPER NUCLEAR FACTOR 1	2.6595E-05	0.00393669	1.19	2.27
BNIP3L	BCL2/ADENOVIRUS E1B 19KDA INTERACTING PROTEIN 3-LIKE	0.00016846	0.03049423	-1.04	0.49
BRD8	BROMODOMAIN CONTAINING 8	0.00299382	0.03834153	1.26	2.40
BRP44	BRAIN PROTEIN 44	5.7466E-05	0.03124483	-1.07	0.48
BST2	BONE MARROW STROMAL CELL ANTIGEN 2	1.1834E-05	0.0372401	1.66	3.15
BTG2	BTG FAMILY, MEMBER 2	0.00358506	0.00632575	-1.28	0.41
C12ORF30	N(ALPHA)-ACETYLTRANSFERASE 25, NATB AUXILIARY SUBUNIT	0.00032279	0.003745	-1.18	0.44
C13ORF15	CHROMOSOME 13 OPEN READING FRAME 15	0.00026819	0.00353302	-1.31	0.40
C14ORF73	CHROMOSOME 14 OPEN READING FRAME 73	0.00171528	0.02027197	-1.60	0.33
C19ORF2	CHROMOSOME 19 OPEN READING FRAME 2	0.00020616	0.00550335	-1.11	0.46
C19ORF40	CHROMOSOME 19 OPEN READING FRAME 40	0.00147527	0.00087238	1.03	2.04
C19ORF42	CHROMOSOME 19 OPEN READING FRAME 42	0.00217649	0.01518777	1.44	2.71
C1ORF128	CHROMOSOME 1 OPEN READING FRAME 128	0.0020696	0.02912791	1.22	2.33
C20ORF30	CHROMOSOME 20 OPEN READING FRAME 30	0.00118867	0.00877753	1.11	2.17
C4ORF34	CHROMOSOME 4 OPEN READING FRAME 34	0.00253455	0.00906022	-1.01	0.50
C4ORF34	CHROMOSOME 4 OPEN READING FRAME 34	0.00022276	0.01886295	-1.23	0.43

C5ORF32	CHROMOSOME 5 OPEN READING FRAME 32 ORTHOLOG	3.5454E-05	0.04369729	1.21	2.31
C6ORF106	CHROMOSOME 6 OPEN READING FRAME 106	0.00260315	0.00953203	1.28	2.42
C6ORF145	CHROMOSOME 6 OPEN READING FRAME 145	5.383E-06	0.00154486	-1.99	0.25
CALCA	CALCITONIN-RELATED POLYPEPTIDE ALPHA	0.00342086	0.04466367	-1.14	0.45
CAPN3	CALPAIN 3, (P94)	1.0629E-05	0.0433421	-1.36	0.39
CASP5	CASPASE 9, APOPTOSIS-RELATED CYSTEINE PEPTIDASE	0.00218344	0.00518424	1.47	2.77
CAST	CALPASTATIN	0.00013812	0.03365912	-1.12	0.46
CCNI	CYCLIN I	0.00458903	0.01170479	1.49	2.81
CCT3	CHAPERONIN CONTAINING TCP1, SUBUNIT 3 (GAMMA)	4.0416E-06	0.02827435	1.85	3.60
CD200	CD200 ANTIGEN; SIMILAR TO MRC OX-2 ANTIGEN HOMOLOG	0.00514801	0.04052306	1.27	2.41
CD3E	CD3 ANTIGEN, EPSILON POLYPEPTIDE	0.00403569	0.00801919	-1.15	0.45
CD5	CD5 MOLECULE	0.00036411	0.01468279	-1.22	0.43
CD6	CD6 MOLECULE	0.00071316	0.00914501	-1.03	0.49
CD97	CD97 MOLECULE	8.6345E-06	0.02339505	-1.64	0.32
CDCA7	CELL DIVISION CYCLE ASSOCIATED 7	5.4455E-05	0.02908622	1.49	2.81
CDK7	CYCLIN-DEPENDENT KINASE 7	0.0050567	0.0206834	1.06	2.08
CDV3	CDV3 HOMOLOG	0.00470155	0.0317246	-1.32	0.40
CEACAM8	CARCINOEMBRYONIC ANTIGEN-RELATED CELL ADHESION MOLECULE 8	2.8102E-06	0.0083034	1.54	2.90
CEBPD	CCAAT/ENHANCER BINDING PROTEIN (C/EBP), DELTA	0.00028413	0.00322862	1.14	2.20
CEP78	CENTROSOMAL PROTEIN 78KDA	0.00443738	0.03213367	-1.04	0.49
CES1	CARBOXYLESTERASE 1	0.0001092	0.00124038	-1.46	0.36
CHD8	CHROMODOMAIN HELICASE DNA BINDING PROTEIN 8	0.00059939	0.01106353	1.24	2.36
CHES1L1	CHECKPOINT SUPPRESSOR 1-LIKE 1	9.5483E-05	0.04026941	-1.31	0.40
CHMP4A	CHROMATIN MODIFYING PROTEIN 4A	0.00395425	0.00912934	1.14	2.21
CHMP4B	CHROMATIN MODIFYING PROTEIN 4B	0.00020773	0.02609455	1.06	2.08
CHORDC1	CYSTEINE AND HISTIDINE-RICH DOMAIN (CHORD) CONTAINING 1	0.00099285	0.00199372	1.54	2.92
CHTF8	CTF8, CHROMOSOME TRANSMISSION FIDELITY FACTOR 8 HOMOLOG	0.0017759	0.04385173	1.02	2.03
CITED2	CBP/P300-INTERACTING TRANSACTIVATOR, WITH GLU/ASP-RICH CARBOXY-TERMINAL DOMAIN, 2	0.00013852	0.00194493	-1.37	0.39
CKAP4	CYTOSKELETON-ASSOCIATED PROTEIN 4	4.7064E-06	0.02752311	2.10	4.29
CLCN6	CHLORIDE CHANNEL 6	0.00039406	0.01081912	-1.59	0.33
CLDN4	CLAUDIN 4	0.00026297	0.0011361	-1.15	0.45
CLIC4	CHLORIDE INTRACELLULAR CHANNEL 4	0.00206914	0.01016117	-1.02	0.49
CLK2	CDC-LIKE KINASE 2	0.00230929	0.0083034	1.32	2.50
CNN2	CALPONIN 2	4.5803E-05	0.01864012	1.02	2.03
CNO	CAPPUCCINO HOMOLOG	0.00114682	0.01859361	-1.01	0.50
COLEC11	COLLECTIN SUB-FAMILY MEMBER 11	2.9552E-06	0.03782395	-3.15	0.11
COMMD8	COMM DOMAIN CONTAINING 8	0.00026353	0.00370702	1.16	2.23
COPS4	COP9 (CONSTITUTIVE PHOTOMORPHOGENIC) HOMOLOG, SUBUNIT 4 (ARABIDOPSIS THALIANA)	0.00095453	0.04669615	1.20	2.30
CPPED1	CALCINEURIN-LIKE PHOSPHOESTERASE DOMAIN CONTAINING 1	0.00246334	0.00225939	-1.57	0.34
CSNK1D	CASEIN KINASE 1, DELTA	0.00063416	0.00399364	1.28	2.43
CSRP2	CYSTEINE AND GLYCINE-RICH PROTEIN 2	0.00059678	0.00525317	-1.42	0.37
CST7	CYSTATIN F (LEUKOCYSTATIN)	5.3836E-05	0.00524706	2.46	5.49
CTNNBL1	CATENIN, BETA LIKE 1	0.00024068	0.00856955	-1.36	0.39
CTSB	CATHEPSIN B	0.00025617	0.00712006	1.25	2.37
CTSD	CATHEPSIN D	0.00021471	0.01696415	1.36	2.56
CTSH	CATHEPSIN H	0.0009873	0.04342064	1.42	2.67
CTSZ	CATHEPSIN Z	0.0045427	0.01060703	1.33	2.52
CUL1	CULLIN 1	1.4421E-05	0.02179983	1.34	2.53
CXCL10	CHEMOKINE (C-X-C MOTIF) LIGAND 10	0.00282278	0.00495236	1.31	2.48
CXCL5	CHEMOKINE (C-X-C MOTIF) LIGAND 5	0.00281706	0.00913784	-1.27	0.42
CXCR4	CHEMOKINE (C-X-C MOTIF) RECEPTOR 4	8.4834E-05	0.01399381	-1.31	0.40
CYB5A	CYTOCHROME B5 TYPE A (MICROSOMAL)	0.00026635	0.0127329	1.72	3.28
CYB5B	CYTOCHROME B5 TYPE B (OUTER MITOCHONDRIAL MEMBRANE)	0.00034575	0.01603807	1.26	2.39
CYP51A1	CYTOCHROME P450, FAMILY 51, SUBFAMILY A, POLYPEPTIDE 1	5.1232E-05	0.00814251	-1.29	0.41
DAAM1	DISHEVELLED ASSOCIATED ACTIVATOR OF MORPHOGENESIS 1	0.00351677	0.00385418	-1.26	0.42
DDX5	DEAD (ASP-GLU-ALA-ASP) BOX POLYPEPTIDE 5	0.00046384	0.00459436	1.40	2.65
DDX5	DEAD (ASP-GLU-ALA-ASP) BOX POLYPEPTIDE 5	0.00058546	0.03419898	-1.19	0.44
DENND4A	DENN/MADD DOMAIN CONTAINING 4A	0.00012097	0.00198929	-1.44	0.37
DERL2	DER1-LIKE DOMAIN FAMILY, MEMBER 2	0.00022211	0.03624641	1.49	2.81
DGAT1	DIACYLGLYCEROL O-ACYLTRANSFERASE HOMOLOG 1	1.9721E-05	0.0107555	1.34	2.53
DKK3	DICKKOPF HOMOLOG 3	0.0011477	0.01989582	-1.05	0.48
DLC1	DELETED IN LIVER CANCER 2	0.00031274	0.00200486	-1.01	0.50
DNAJB1	DNAJ (HSP40) HOMOLOG, SUBFAMILY B, MEMBER 1	2.5432E-07	0.00260718	1.84	3.57
DNAJB2	DNAJ (HSP40) HOMOLOG, SUBFAMILY B, MEMBER 2	4.4363E-05	0.00489157	1.14	2.21
DNAJC14	DNAJ (HSP40) HOMOLOG, SUBFAMILY C, MEMBER 14	0.00517686	0.01887553	1.06	2.08
DOK2	DOCKING PROTEIN 2, 56KDA	1.8561E-05	0.0175036	1.28	2.43
DOPEY1	DOPEY FAMILY MEMBER 1	5.8823E-05	0.03729952	-1.08	0.47
DUSP5	DUAL SPECIFICITY PHOSPHATASE 5	0.00010121	0.00611555	-1.17	0.45

DYSF	DYSFERLIN, LIMB GIRDLE MUSCULAR DYSTROPHY 2B (AUTOSOMAL RECESSIVE)	0.00010006	0.01765533	2.23	4.68
EBI3	EPSTEIN-BARR VIRUS INDUCED 3	0.00128867	0.00087238	-1.25	0.42
ECM1	EXTRACELLULAR MATRIX PROTEIN 1	0.00070024	0.0218432	1.19	2.29
EGR3	EARLY GROWTH RESPONSE 3	0.00017011	0.02499928	-2.15	0.22
EIF1AD	EUKARYOTIC TRANSLATION INITIATION FACTOR 1A DOMAIN CONTAINING	9.0498E-05	0.00385961	1.44	2.72
EIF2AK2	EUKARYOTIC TRANSLATION INITIATION FACTOR 2-ALPHA KINASE 2	0.00026532	0.04020006	1.71	3.26
EIF4A1	EUKARYOTIC TRANSLATION INITIATION FACTOR 4A, ISOFORM 1	9.8324E-05	0.01674812	-1.63	0.32
EIF4B	SIMILAR TO EUKARYOTIC TRANSLATION INITIATION FACTOR 4H; EUKARYOTIC TRANSLATION INITIATION FACTOR 4B	2.576E-05	0.00087238	-1.06	0.48
EIF4E	EUKARYOTIC TRANSLATION INITIATION FACTOR 4E	0.00053116	8.2329E-05	1.40	2.64
EIF6	EUKARYOTIC TRANSLATION INITIATION FACTOR 6	0.00046376	0.0018681	1.04	2.05
ELOVL7	ELOVL FAMILY MEMBER 7, ELONGATION OF LONG CHAIN FATTY ACIDS	1.6781E-05	0.0018681	-2.56	0.17
ENPP2	ECTONUCLEOTIDE PYROPHOSPHATASE/PHOSPHODIESTERASE 2	0.00078529	0.01817823	-2.39	0.19
EPAS1	ENDOTHELIAL PAS DOMAIN PROTEIN 1	0.00445513	0.02965666	-1.09	0.47
ERBB3	V-ERB-B2 ERYTHROBLASTIC LEUKEMIA VIRAL ONCOGENE HOMOLOG 3	0.00116158	0.00282783	-1.00	0.50
ESRP2	EPITHELIAL SPLICING REGULATORY PROTEIN 2	0.00033199	0.00632575	2.02	4.06
EXOC6	COBL-LIKE 1	0.00391361	0.00153089	-1.96	0.26
EZR	EZRIN	0.00088741	0.00385418	-1.16	0.45
FADS1	FATTY ACID DESATURASE 3	0.00326284	0.00416645	-1.47	0.36
FADS2	FATTY ACID DESATURASE 2	9.9712E-05	0.00226807	-2.72	0.15
FAM105A	FAMILY WITH SEQUENCE SIMILARITY 105, MEMBER A	0.00021149	0.00290395	-1.49	0.35
FAM107B	FAMILY WITH SEQUENCE SIMILARITY 107, MEMBER B	1.3271E-05	0.02205636	-1.67	0.31
FAM189B	FAMILY WITH SEQUENCE SIMILARITY 189, MEMBER B	4.9122E-05	0.04583222	1.03	2.04
FAM32A	FAMILY WITH SEQUENCE SIMILARITY 32, MEMBER A	0.00031622	0.00402356	1.11	2.16
FAM3B	FAMILY WITH SEQUENCE SIMILARITY 3, MEMBER B	7.9453E-05	0.00402356	-1.53	0.35
FAM43A	FAMILY WITH SEQUENCE SIMILARITY 43, MEMBER A	0.00292113	0.00087238	-1.28	0.41
FAM83D	FAMILY WITH SEQUENCE SIMILARITY 83, MEMBER D	1.3745E-05	0.00020392	-1.56	0.34
FAM98A	FAMILY WITH SEQUENCE SIMILARITY 98, MEMBER A	0.0002417	0.00325289	1.21	2.31
FAS	FAS (TNF RECEPTOR SUPERFAMILY MEMBER 6)	0.00011692	0.013635	1.66	3.15
FCGR2B	FC FRAGMENT OF IGG, LOW AFFINITY IIB, RECEPTOR (CD32)	0.00034038	0.00909006	2.07	4.19
FGF2	FIBROBLAST GROWTH FACTOR 2	0.00033624	0.03041615	-1.12	0.46
FGL2	FIBRINOGEN-LIKE 2	0.00110285	0.00147818	1.16	2.23
FKBP10	FK506 BINDING PROTEIN 10, 65 KDA	1.4633E-05	0.00284121	-2.31	0.20
FKBP4	FK506 BINDING PROTEIN 4, 59KDA	1.2652E-07	0.00260718	3.09	8.51
FKBP5	FK506 BINDING PROTEIN 5	2.4515E-05	0.0096489	-1.25	0.42
FLOT1	FLOTILLIN 1	8.7487E-05	0.00426148	1.31	2.48
FMNL2	FORMIN-LIKE 2	0.0001794	0.02978708	-1.30	0.41
FOSL2	FOS-LIKE ANTIGEN 2	0.0009892	0.00491207	-1.38	0.38
GALK1	GALACTOKINASE 1	0.00343497	0.04020006	1.03	2.05
GAPDH	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE	0.00083568	0.01696415	-1.21	0.43
GCHFR	GTP CYCLOHYDROLASE I FEEDBACK REGULATOR	0.00130128	0.00550816	1.41	2.66
GNAS	GNAS (GUANINE NUCLEOTIDE BINDING PROTEIN, ALPHA STIMULATING) COMPLEX LOCUS	0.00195878	0.00214459	1.08	2.11
GPR98	G PROTEIN-COUPLED RECEPTOR 98	0.00084706	0.0180252	-1.03	0.49
GPX3	GLUTATHIONE PEROXIDASE 3 (PLASMA)	0.00085792	0.01458439	-2.10	0.23
GRASP	GRP1 (GENERAL RECEPTOR FOR PHOSPHOINOSITIDES 1)-ASSOCIATED SCAFFOLD PROTEIN	2.3799E-06	0.00793146	-1.50	0.35
GSN	GELSOLIN (AMYLOIDOSIS, FINNISH TYPE)	0.00102007	0.00442405	-1.49	0.36
GTF2H2	GENERAL TRANSCRIPTION FACTOR IIH, POLYPEPTIDE 2, 44KDA	0.00013029	0.00895172	1.10	2.14
GUCY1B3	GUANYLATE CYCLASE 1, SOLUBLE, BETA 3	0.00164876	0.04367285	-2.64	0.16
HAO1	HYDROXYACID OXIDASE 1,	0.00322033	0.0474755	-1.48	0.36
HCK	HEMOPOIETIC CELL KINASE	0.00089648	0.01440116	1.31	2.49
HDAC1	HISTONE DEACETYLASE 1	0.00404387	0.0317246	1.30	2.46
HDDC3	HD DOMAIN CONTAINING 3	0.00390423	0.00385418	-1.05	0.48
HEATR6	HEAT REPEAT CONTAINING 6	0.00075767	0.02440263	1.11	2.16
HERPUD1	HOMOCYSTEINE-INDUCIBLE, ENDOPLASMIC RETICULUM STRESS-INDUCIBLE, UBIQUITIN-LIKE DOMAIN MEMBER 1	7.8365E-06	0.02000651	-1.61	0.33
HEY1	HAIRY/ENHANCER-OF-SPLIT RELATED WITH YRPW MOTIF 1	5.4673E-05	0.00087238	-1.69	0.31
HIGD2A	HIG1 HYPOXIA INDUCIBLE DOMAIN FAMILY, MEMBER 2A	2.7892E-05	0.01253851	1.08	2.11
HIST1H2BN	HISTONE CLUSTER 1, H2BM	0.00013804	0.04497009	1.53	2.88
HLA-A	MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS I, A	0.00368364	0.01257997	1.11	2.16
HMGCL	3-HYDROXYMETHYL-3-METHYLGLUTARYL-COA LYASE	0.00097891	0.00245626	1.27	2.42
HMGN1	HIGH-MOBILITY GROUP NUCLEOSOME BINDING DOMAIN 1	1.5654E-05	0.01106353	1.20	2.29
HMGN3	HIGH MOBILITY GROUP NUCLEOSOMAL BINDING DOMAIN 3	1.8868E-05	0.02205636	1.07	2.11
HS3ST1	HEPARAN SULFATE (GLUCOSAMINE) 3-O-SULFOTRANSFERASE 1	0.00224063	0.00072151	1.15	2.22
HSP90AA2	HEAT SHOCK PROTEIN 90KDA ALPHA (CYTOSOLIC), CLASS A MEMBER 2; HEAT SHOCK PROTEIN 90KDA ALPHA (CYTOSOLIC), CLASS A MEMBER 1	5.0152E-06	0.02281934	3.89	14.79

HSP90AB1	HEAT SHOCK 90KDA PROTEIN 1, BETA	5.6714E-06	0.01284872	3.30	9.86
HSPA4L	HEAT SHOCK 70KDA PROTEIN 4-LIKE	1.224E-05	0.01860425	2.38	5.21
HSPA6	HEAT SHOCK 70KDA PROTEIN 4	1.2407E-05	0.02812122	3.92	15.18
HSPB1	HEAT SHOCK 27KDA PROTEIN 1	1.6241E-08	0.00451601	4.77	27.38
HSPD1	HEAT SHOCK 60KDA PROTEIN 1 (CHAPERONIN)	2.7222E-07	0.03187818	2.83	7.09
HSPE1	HEAT SHOCK 10KDA PROTEIN 1 (CHAPERONIN 10)	1.556E-05	0.00102442	2.26	4.80
HSPH1	HEAT SHOCK 105KDA/110KDA PROTEIN 1	2.0145E-06	0.01039226	3.01	8.05
ID3	INHIBITOR OF DNA BINDING 3, DOMINANT NEGATIVE HELIX-LOOP-HELIX PROTEIN	1.9089E-05	0.0252377	-1.46	0.36
ID4	INHIBITOR OF DNA BINDING 4, DOMINANT NEGATIVE HELIX-LOOP-HELIX PROTEIN	2.9979E-05	0.00639813	-1.57	0.34
IDO1	INDOLEAMINE 2,3-DIOXYGENASE 1	0.00098473	0.00102442	1.96	3.88
IGF2	INSULIN-LIKE GROWTH FACTOR 2 (SOMATOMEDIN A)	0.00021338	0.00105921	-1.16	0.45
IGFBP4	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 4	0.00027887	0.01292628	-1.32	0.40
IGHV@	IMMUNOGLOBULIN HEAVY LOCUS	5.2127E-05	0.0018247	2.04	4.11
IGSF8	IMMUNOGLOBULIN SUPERFAMILY, MEMBER 1	6.4793E-05	0.03323756	-1.62	0.33
IL1B	INTERLEUKIN 1, BETA	0.00051104	0.00163569	-2.41	0.19
IL27	APOLIPOPROTEIN B RECEPTOR	7.5877E-05	0.0044758	2.23	4.69
IL2RG	INTERLEUKIN 2 RECEPTOR, GAMMA	0.00025762	0.0096697	1.77	3.42
IL4R	INTERLEUKIN 4 RECEPTOR	0.00235001	0.03922855	1.35	2.55
IL8	INTERLEUKIN 8	0.00035085	0.00429584	-2.97	0.13
IMPA1	INOSITOL(MYO)-1(OR 4)-MONOPHOSPHATASE 1	0.00496656	0.00525317	-1.01	0.50
ING4	INHIBITOR OF GROWTH FAMILY, MEMBER 4	0.00134264	0.04681602	1.06	2.08
IP6K2	DIPHOSPHOINOSITOL PENTAKISPHOSPHATE KINASE 2	0.00094198	0.00338984	1.27	2.41
IRF2	INTERFERON REGULATORY FACTOR 2	6.0146E-05	0.00385418	1.28	2.42
IRF4	INTERFERON REGULATORY FACTOR 4	6.0449E-05	0.00075523	1.05	2.08
IRF8	INTERFERON REGULATORY FACTOR 8	1.3462E-06	0.00493628	-2.26	0.22
ITFG1	INTEGRIN ALPHA FG-GAP REPEAT CONTAINING 1	0.00094998	0.02049928	-1.08	0.47
JAG1	JAGGED 1	9.857E-05	0.00211828	-1.59	0.33
JAGN1	JAGUNAL HOMOLOG 1	2.4358E-05	0.00416645	1.53	2.89
KANK1	KN MOTIF AND ANKYRIN REPEAT DOMAINS 1	0.00226419	0.02533813	-1.53	0.35
KCNAB2	POTASSIUM VOLTAGE-GATED CHANNEL, SHAKER-RELATED SUBFAMILY, BETA MEMBER 2	6.6994E-07	0.00730612	-2.81	0.14
KCNJ2	POTASSIUM INWARDLY-RECTIFYING CHANNEL, SUBFAMILY J, MEMBER 2	3.2161E-05	0.00370702	-1.30	0.41
KCTD10	POTASSIUM CHANNEL TETRAMERISATION DOMAIN CONTAINING 10	0.00286381	0.00385961	1.05	2.07
KIAA0323	KH AND NYN DOMAIN CONTAINING	0.00028995	0.02750815	1.00	2.01
KIF15	KINESIN FAMILY MEMBER 15	6.7766E-05	0.03663162	-1.00	0.50
KLF4	KRUPPEL-LIKE FACTOR 4	0.00023328	0.00275565	-1.61	0.33
KLF5	KRUPPEL-LIKE FACTOR 5	6.6568E-06	0.01864012	-1.95	0.26
KPNA2	KARYOPHERIN (IMPORTIN) ALPHA 2;	0.00017843	0.00153089	1.14	2.20
KTELC1	KTEL (LYS-TYR-GLU-LEU) CONTAINING 1	0.00099527	0.00395998	1.15	2.21
KYNU	KYNURENINASE (L-KYNURENINE HYDROLASE)	0.00021992	0.00370702	1.36	2.57
LAMP1	LYSOSOMAL-ASSOCIATED MEMBRANE PROTEIN 1	7.3598E-05	0.00385418	1.40	2.65
LAMP2	LYSOSOMAL-ASSOCIATED MEMBRANE PROTEIN 2	0.0002512	0.00262939	1.43	2.69
LBR	LAMIN B RECEPTOR	3.2162E-05	0.02220559	-1.70	0.31
LCAT	LECITHIN-CHOLESTEROL ACYLTRANSFERASE	0.00078663	0.00245626	1.26	2.39
LCP1	LYMPHOCYTE CYTOSOLIC PROTEIN 1 (L-PLASTIN)	0.0002025	0.03968942	1.06	2.09
LFNG	LFNG O-FUCOSYLPEPTIDE 3-BETA-N-ACETYLGLUCOSAMINYLTRANSFERASE	0.00010974	0.00310767	-1.22	0.43
LGALS1	LECTIN, GALACTOSE BINDING, SOLUBLE 1	2.9236E-06	0.0218432	2.11	4.32
LMNA	LAMIN A/C	8.85E-05	0.00966499	-1.25	0.42
LMO7	LIM DOMAIN 7	1.6651E-05	0.00153814	-1.11	0.46
LONP2	LON PEPTIDASE 2, PEROXISOMAL	0.00058211	0.00678869	1.28	2.42
LRP1	LOW DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1	0.00184999	0.00625359	-1.46	0.36
LRRN1	LEUCINE RICH REPEAT NEURONAL 1	1.4278E-06	0.03389324	-1.98	0.25
LSR	LIPOLYSIS STIMULATED LIPOPROTEIN RECEPTOR	0.00088775	0.00048516	-1.44	0.37
LYST	LYSOSOMAL TRAFFICKING REGULATOR	0.00092079	0.00048516	1.09	2.13
M6PR	MANNOSE-6-PHOSPHATE RECEPTOR (CATION DEPENDENT)	0.00174715	0.01696415	1.16	2.23
MAFG	V-MAF MUSCULOAPONEUROTIC FIBROSARCOMA ONCOGENE HOMOLOG G	0.00073494	0.00020392	-1.04	0.49
MAN2C1	MANNOSIDASE, ALPHA, CLASS 2C, MEMBER 1	0.00056627	0.0044758	-1.01	0.50
MAP2K1	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1	0.0003526	0.00525317	-1.03	0.49
MAP4K2	MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE KINASE 2	0.00046975	0.01855599	-1.06	0.48
MAP7D1	MAP7 DOMAIN CONTAINING 1	0.00253344	0.02022632	1.06	2.08
MAPK11	MITOGEN-ACTIVATED PROTEIN KINASE 11	1.1861E-06	0.03604289	1.94	3.83
MAPK14	MITOGEN-ACTIVATED PROTEIN KINASE 14	0.00142509	0.0463822	1.01	2.01
MCMBP	MINICHROMOSOME MAINTENANCE COMPLEX BINDING PROTEIN	0.00269333	0.0460489	-1.66	0.32
MED6	MEDIATOR COMPLEX SUBUNIT 6	5.1132E-05	0.00372851	1.17	2.24
MED8	MEDIATOR COMPLEX SUBUNIT 8	0.00159336	0.00489157	1.01	2.02
MERTK	C-MER PROTO-ONCOGENE TYROSINE KINASE	9.0528E-05	0.01468279	-1.48	0.36

METTL7A	METHYLTRANSFERASE LIKE 7A	2.7886E-06	0.03691547	-2.09	0.23
MGEA5	SIMILAR TO MENINGIOMA EXPRESSED ANTIGEN 5 (HYALURONIDASE)	1.8843E-05	0.04343983	1.37	2.59
MORF4L2	MORTALITY FACTOR 4 LIKE 2	2.8007E-05	0.00428415	1.64	3.20
MOV10	MOV10L1, MOLONEY LEUKEMIA VIRUS 10-LIKE 1, HOMOLOG	0.00095664	0.01399381	1.33	2.52
MPZL1	MYELIN PROTEIN ZERO-LIKE 1	0.00204844	0.01883506	-1.24	0.42
MRC1	MANNOSE RECEPTOR, C TYPE 1	0.00531453	0.00632575	-1.47	0.36
MRPL1	MITOCHONDRIAL RIBOSOMAL PROTEIN L1	0.00044272	0.00372249	1.11	2.16
MRPL14	MITOCHONDRIAL RIBOSOMAL PROTEIN L14	0.00480669	0.00431753	1.13	2.18
MRPL18	MITOCHONDRIAL RIBOSOMAL PROTEIN L18	0.00044812	0.00102442	1.23	2.35
MRPL34	MITOCHONDRIAL RIBOSOMAL PROTEIN L34	2.2011E-05	0.00539712	1.05	2.07
MRPS11	MITOCHONDRIAL RIBOSOMAL PROTEIN S11	0.0003652	0.0493792	1.05	2.06
MRRF	MITOCHONDRIAL RIBOSOME RECYCLING FACTOR	0.00134184	0.00233427	1.15	2.23
MT2A	METALLOTHIONEIN 2A	0.00111425	0.01191051	2.13	4.37
MTA3	METASTASIS ASSOCIATED 1 FAMILY, MEMBER 3	6.1379E-05	0.00426148	1.01	2.02
MT-ND2	MITOCHONDRIALLY ENCODED NADH DEHYDROGENASE 2	7.0194E-05	0.0328315	-1.56	0.34
MT-ND3	NADH DEHYDROGENASE (UBIQUINONE) FE-S PROTEIN 1, 75KDA (NADH-COENZYME Q REDUCTASE)	3.7835E-06	0.00170347	-2.11	0.23
MT-ND5	MITOCHONDRIALLY ENCODED NADH DEHYDROGENASE 5	2.3701E-06	0.00385961	-2.07	0.24
MX2	MYXOVIRUS (INFLUENZA VIRUS) RESISTANCE 2	3.8605E-06	0.01936126	3.42	10.71
MXRA7	MATRIX-REMODELLING ASSOCIATED 7	9.1256E-06	0.03389324	-1.76	0.29
MYC	V-MYC MYELOCYTOMATOSIS VIRAL ONCOGENE HOMOLOG	0.00345432	0.00385418	-1.14	0.46
MYD88	MYELOID DIFFERENTIATION PRIMARY RESPONSE GENE (88)	7.7801E-05	0.00912934	1.28	2.43
MYST1	MYST HISTONE ACETYLTRANSFERASE 1	0.00256845	0.00678869	1.01	2.01
N4BP2L1	NEDD4 BINDING PROTEIN 2-LIKE 1	9.4648E-06	0.00020392	1.31	2.48
NAGA	N-ACETYLGALACTOSAMINIDASE, ALPHA-	0.00166946	0.00782856	1.10	2.15
NAMPT	NICOTINAMIDE PHOSPHORIBOSYLTRANSFERASE	0.00023036	0.01468279	-1.17	0.44
NASP	NUCLEAR AUTOANTIGENIC SPERM PROTEIN (HISTONE-BINDING)	0.00010116	0.0175036	-1.48	0.36
NAT10	N-ACETYLTRANSFERASE 10	0.00364139	0.02667232	-1.16	0.45
NCS1	NEURONAL CALCIUM SENSOR 1	0.00029375	0.00040365	-1.08	0.47
NDRG1	N-MYC DOWNSTREAM REGULATED GENE 1	2.5086E-05	0.00102442	-1.56	0.34
NDUFS1	NADH DEHYDROGENASE (UBIQUINONE) FE-S PROTEIN 1, 75KDA (NADH-COENZYME Q REDUCTASE)	0.00067541	0.00442405	-1.34	0.40
NDUFV2	NADH DEHYDROGENASE (UBIQUINONE) FLAVOPROTEIN 2, 24KDA	1.1398E-05	0.00680435	1.62	3.08
NEDD9	NEURAL PRECURSOR CELL EXPRESSED, DEVELOPMENTALLY DOWN-REGULATED GENE 9	4.3248E-05	0.01612454	-1.86	0.28
NEIL3	NEI LIKE 3	0.00012023	0.0314194	-1.16	0.45
NGFRAP1	NERVE GROWTH FACTOR RECEPTOR (TNFRSF16) ASSOCIATED PROTEIN 1	7.6084E-05	0.01261829	-1.85	0.28
NGRN	NEUGRIN, NEURITE OUTGROWTH ASSOCIATED	0.00016429	0.00225939	1.76	3.40
NKG7	NATURAL KILLER CELL GROUP 7 SEQUENCE	0.00277563	0.01066198	1.09	2.13
NLRC5	NLR FAMILY, CARD DOMAIN CONTAINING 5	0.00371414	0.00639813	1.07	2.10
NMI	N-MYC (AND STAT) INTERACTOR	6.9206E-05	0.00822753	1.18	2.27
NOL3	NUCLEOLAR PROTEIN 3 (APOPTOSIS REPRESSOR WITH CARD DOMAIN)	1.6297E-05	0.01859361	1.69	3.22
NPLOC4	NUCLEAR PROTEIN LOCALIZATION 4 HOMOLOG	4.4441E-05	0.01902281	1.31	2.52
NR4A1	NUCLEAR RECEPTOR SUBFAMILY 4, GROUP A, MEMBER 1	8.9261E-05	0.01558698	-1.95	0.26
NSA2	*NSA2* ribosome biogenesis homolog	0.00011219	0.01106121	-1.18	0.44
NUDC	NUCLEAR DISTRIBUTION GENE C HOMOLOG	0.00520554	0.04200999	1.20	2.29
NUPR1	NUCLEAR PROTEIN, TRANSCRIPTIONAL REGULATOR, 1	1.3425E-06	0.00428824	2.18	4.52
NXF1	NUCLEAR RNA EXPORT FACTOR 1	0.00117	0.0218432	1.47	2.78
NXN	NUCLEOREDOXIN	4.9058E-06	0.00233427	1.81	3.51
P4HA2	PROLYL 4-HYDROXYLASE, ALPHA POLYPEPTIDE II	0.00529587	0.01106121	1.05	2.07
PAF1	RTF1, PAF1/RNA POLYMERASE II COMPLEX COMPONENT, HOMOLOG	5.4021E-05	0.00153089	-1.04	0.49
PALLD	PALLADIN, CYTOSKELETAL ASSOCIATED PROTEIN	0.00272825	0.02572013	-1.54	0.34
PAPD5	PAP ASSOCIATED DOMAIN CONTAINING 5	6.4519E-05	0.00233427	1.14	2.21
PARP14	POLY (ADP-RIBOSE) POLYMERASE FAMILY, MEMBER 14	0.00029164	0.03393221	1.01	2.01
PARP9	POLY (ADP-RIBOSE) POLYMERASE FAMILY, MEMBER 9	8.3213E-06	0.0005689	1.49	2.80
PBXIP1	PRE-B-CELL LEUKEMIA HOMEOBOX INTERACTING PROTEIN 1	0.00090436	0.00754784	-1.02	0.49
PDE4B	PHOSPHODIESTERASE 4B, CAMP-SPECIFIC	8.0531E-06	0.00260718	-2.24	0.21
PDE4D	PHOSPHODIESTERASE 4D, CAMP-SPECIFIC	5.8066E-05	0.03903799	-1.05	0.48
PDK4	PYRUVATE DEHYDROGENASE KINASE, ISOZYME 4	0.00338346	0.01093752	1.32	2.50
PDLIM4	PDZ AND LIM DOMAIN 4	0.00017775	0.01601083	-2.12	0.23
PFDN2	PREFOLDIN SUBUNIT 2	0.00078976	0.00906022	-1.70	0.31
PFKL	PHOSPHOFRUCTOKINASE, LIVER	0.00021407	0.02314472	-1.24	0.42
PGCP	PLASMA GLUTAMATE CARBOXYPEPTIDASE	3.3921E-05	0.04992563	-1.56	0.34
PGM3	PHOSPHOGLUCOMUTASE 3	4.3874E-05	0.0156222	-1.61	0.33
PGS1	PHOSPHATIDYLGLYCEROPHOSPHATE SYNTHASE 1	2.6998E-05	0.02344764	1.45	2.73
PHACTR1	PHOSPHATASE AND ACTIN REGULATOR 1	2.8584E-05	0.0075114	-1.47	0.36
PHKG2	PHOSPHORYLASE KINASE, GAMMA 2	1.2588E-06	0.00426148	-2.18	0.22
PHYH	PHYTANOYL-COA 2-HYDROXYLASE	0.00379461	0.03056508	1.79	3.46
PIAS1	PROTEIN INHIBITOR OF ACTIVATED STAT, 1	0.00113382	0.01468279	1.46	2.75

PIAS3	protein inhibitor of activated STAT, 3	0.00323267	0.01675604	1.06	2.08
PICALM	phosphatidylinositol binding clathrin assembly protein	9.7153E-05	5.8781E-05	-1.25	0.42
PITPNA	phosphatidylinositol transfer protein, alpha	0.00096338	0.01468279	1.09	2.13
PLA2G2A	phospholipase A2, group IIA	3.8078E-05	0.01106353	3.28	9.74
PLCB2	phospholipase C, beta 2	0.0013623	0.04343983	-1.55	0.34
PLEKHJ1	pleckstrin homology domain containing, family J member 1	0.00129857	0.02716827	1.19	2.28
PLOD1	procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1	3.8213E-05	0.03534727	3.20	10.78
POLR1D	polymerase (RNA) I polypeptide D, 16kDa	0.00015267	0.01764188	1.07	2.11
POLR2H	polymerase (RNA) II (DNA directed) polypeptide H	0.00013405	0.01039226	1.10	2.15
PON2	paraoxonase 2	0.00169463	0.01883506	1.10	2.14
PPARG	peroxisome proliferator-activated receptor gamma	0.00334329	0.02288489	1.19	2.28
PPP1CC	protein phosphatase 1, catalytic subunit, gamma isoform	5.6605E-05	0.00717306	-1.30	0.41
PPP1R16B	protein phosphatase 1, regulatory (inhibitor) subunit 16B	4.5356E-05	0.01406117	-1.40	0.38
PPP3CA	protein phosphatase 3, catalytic subunit, alpha isozyme	8.6962E-05	0.02758013	1.01	2.01
PRDM1	PR domain containing 1, with ZNF domain	6.5406E-07	0.00385418	1.58	2.98
PRDX2	peroxiredoxin 2	0.00194148	0.00411584	1.30	2.47
PRKAG1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	0.00500821	0.03187818	1.01	2.02
PRKCDBP	protein kinase C, delta binding protein	0.00510194	0.02004247	1.24	2.36
PSMB9	transmembrane 9 superfamily member 2	0.00076112	0.0018681	-1.00	0.50
PSMC4	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	0.00093229	0.02041869	1.08	2.11
PSPC1	paraspeckle component 1; paraspeckle protein 1 pseudogene	5.2673E-05	0.04308805	-1.09	0.47
PSPH	phosphoserine phosphatase	2.2127E-05	0.01648521	1.20	2.29
PTGES3	prostaglandin E synthase 3 (cytosolic)	0.00149337	0.00199372	1.11	2.17
PTGS2	prostaglandin-endoperoxide synthase 2	0.00021748	0.00712006	-1.66	0.32
PTMA	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	0.00047428	0.00290395	-1.46	0.36
PTOV1	prostate tumor overexpressed 1	0.00010109	0.04065153	1.62	3.08
PTPLAD1	protein tyrosine phosphatase-like A domain containing 1	0.00059079	0.01305222	1.45	2.74
PXN	paxillin	3.0338E-05	0.03275664	-1.49	0.36
PYGL	liver glycogen phosphorylase	4.1243E-05	0.0018681	1.05	2.07
PYHIN1	interferon, gamma-inducible protein 16	3.6148E-05	0.02322825	2.43	5.40
RAB7B	RAB7B, member RAS oncogene family	6.8454E-05	0.02118548	-1.43	0.37
RAB8A	RAB8A, member RAS oncogene family	0.00011265	0.00222702	1.07	2.10
RAB9A	RAB40C, member RAS oncogene family	0.00447247	0.00679417	1.65	3.13
RABEPK	Rab9 effector protein with kelch motifs	0.00053663	0.01257997	1.74	3.34
RAD23A	RAD23 homolog A	0.00098213	0.03082988	-1.04	0.49
RASSF2	Ras association (RalGDS/AF-6) domain family member 2	0.00013893	0.03251635	1.54	2.92
RASSF5	Ras association (RalGDS/AF-6) domain family member 5	4.5038E-05	0.00251171	-1.46	0.36
RBM3	RNA binding motif (RNP1, RRM) protein 3	5.5754E-05	0.00141885	-1.95	0.26
RBM39	RNA binding motif protein 39	0.00104907	0.00518424	1.05	2.07
RBM48	chromosome 7 open reading frame 64 ortholog	0.00036315	0.00202909	1.15	2.22
RETSAT	retinol saturase (all-trans-retinol 13,14-reductase)	0.00567887	0.03464997	-1.10	0.47
RFC2	replication factor C (activator 1) 2, 40kDa	0.00010611	0.02549955	1.72	3.29
RGMB	RGM domain family, member B	2.0568E-05	0.00801373	-1.82	0.28
RIPK1	receptor-interacting serine-threonine kinase 2	6.9924E-05	0.02827435	1.32	2.49
RIPK3	receptor-interacting serine-threonine kinase 3	3.938E-06	0.0017708	1.86	3.62
RNASE4	angiogenin, ribonuclease, RNase A family, 5	3.0684E-05	0.00102442	-1.65	0.32
RNF114	ring finger protein 114	0.00135661	0.04658188	1.01	2.01
RNF216L	ring finger protein 216-like	0.00018558	0.04094377	1.02	2.02
ROBLD3	late endosomal/lysosomal adaptor, MAPK and MTOR activator 2	0.00389896	0.01106353	1.16	2.23
RPL18A	ribosomal protein L18a	0.00269638	0.00385961	-1.03	0.49
RPL6	ribosomal protein L6	0.00053492	0.04625839	-1.03	0.49
RPS4X	ribosomal protein S4, X-linked	7.6848E-05	0.00632575	-1.26	0.42
RRP7A	ribosomal RNA processing 7 homolog A	0.00319952	0.00912934	-1.09	0.47
RTN3	reticulon 3	2.0337E-05	0.03017159	-1.34	0.39
RTP4	receptor (chemosensory) transporter protein 4	7.465E-07	0.00087238	2.94	7.66
RYBP	RING1 and YY1 binding protein	1.0081E-05	0.01860025	-1.45	0.37
S100A10	S100 calcium binding protein A10	8.7231E-05	0.01468279	1.13	2.19
S100A4	S100 calcium binding protein A4	0.00104521	0.00385961	-1.42	0.37
S1PR3	sphingosine-1-phosphate receptor 3	0.00094877	0.00816314	-1.36	0.39
SAP30	Sin3A-associated protein, 30kDa	0.00011217	0.03365428	-1.93	0.26
SARM1	sterile alpha and TIR motif containing 1	0.00065437	0.00481401	-1.24	0.42
SATB1	SATB homeobox 1	0.00286281	0.00913784	-1.00	0.50
SBNO2	strawberry notch homolog 2	0.00036003	0.00385418	1.19	2.29
SCAND1	SCAN domain containing 1	4.8941E-05	0.0127329	-2.07	0.24
SDC2	syndecan 2	3.5736E-05	0.01462027	-1.16	0.45
SDF2L1	stromal cell-derived factor 2-like 1	0.00423094	0.00230817	-1.03	0.49

SDHAF1	SUCCINATE DEHYDROGENASE COMPLEX ASSEMBLY FACTOR 1	6.8801E-05	0.02027197	1.04	2.05
SDHAF2	SUCCINATE DEHYDROGENASE COMPLEX ASSEMBLY FACTOR 1	0.00130023	0.00022809	1.07	2.11
SDHC	SUCCINATE DEHYDROGENASE COMPLEX, SUBUNIT C, INTEGRAL MEMBRANE PROTEIN, 15KDA	2.0507E-05	0.00521065	1.01	2.01
SEMA4D	SEMA DOMAIN, IMMUNOGLOBULIN DOMAIN (IG), TRANSMEMBRANE DOMAIN (TM) AND SHORT CYTOPLASMIC DOMAIN, (SEMAPHORIN) 4D	0.00247055	0.002665	-1.28	0.41
SERF1A	SMALL EDRK-RICH FACTOR 1A (TELOMERIC); SMALL EDRK-RICH FACTOR 1B (CENTROMERIC)	8.1677E-06	0.00214459	1.21	2.32
SERPINB1	SERPIN PEPTIDASE INHIBITOR, CLADE B (OVALBUMIN), MEMBER 1	0.00025991	0.0180252	-1.31	0.40
SERPINE1	SERPIN PEPTIDASE INHIBITOR, CLADE E (NEXIN, PLASMINOGEN ACTIVATOR INHIBITOR TYPE 1), MEMBER 1	0.00015434	0.00524706	-1.68	0.31
SERPINH1	SERPIN PEPTIDASE INHIBITOR, CLADE H (HEAT SHOCK PROTEIN 47), MEMBER 1, (COLLAGEN BINDING PROTEIN 1)	8.5354E-06	0.00195948	3.37	10.30
SESN2	SESTRIN 2	0.00078921	0.01023203	-1.12	0.46
SFRS5	SPLICING FACTOR, ARGININE/SERINE-RICH 5	0.00065697	0.00878802	-1.02	0.49
SGMS1	SPHINGOMYELIN SYNTHASE 1	0.00021731	0.00423504	1.09	2.13
SH3D20	RHO GTPASE ACTIVATING PROTEIN 27	0.00040514	0.00709679	1.16	2.24
SHISA5	SHISA HOMOLOG 5	1.2135E-07	0.01066198	3.48	11.17
SIK3	SIK FAMILY KINASE 3	0.00084671	0.00020392	1.34	2.53
SLAMF1	SIGNALING LYMPHOCYTIC ACTIVATION MOLECULE FAMILY MEMBER 1	0.00059668	0.00733418	1.20	2.29
SLAMF7	SLAM FAMILY MEMBER 7	5.043E-07	0.01742992	2.72	6.59
SLC15A4	SOLUTE CARRIER FAMILY 15, MEMBER 4	0.0007072	0.02752311	1.44	2.70
SLC2A1	SOLUTE CARRIER FAMILY 2 (FACILITATED GLUCOSE TRANSPORTER), MEMBER 1	1.4898E-06	0.01916645	-2.07	0.24
SLC38A2	SOLUTE CARRIER FAMILY 38, MEMBER 2	2.944E-05	0.03601084	-1.59	0.33
SLC39A6	SOLUTE CARRIER FAMILY 39 (ZINC TRANSPORTER), MEMBER 6	0.00250188	0.04099942	1.04	2.06
SLC44A4	SOLUTE CARRIER FAMILY 44, MEMBER 4	0.00055585	0.03369073	-1.29	0.41
SLC4A7	SOLUTE CARRIER FAMILY 4, SODIUM BICARBONATE COTRANSPORTER, MEMBER 7	0.00045397	0.00205232	-1.65	0.32
SLC7A1	SOLUTE CARRIER FAMILY 7 MEMBER 1	1.83E-05	0.00225939	-1.73	0.30
SLC7A6OS	SOLUTE CARRIER FAMILY 7, MEMBER 6 OPPOSITE STRAND	0.00033652	0.00117341	1.08	2.12
SMAGP	SMALL CELL ADHESION GLYCOPROTEIN	4.0138E-06	0.00128732	1.88	3.67
SNAP25	SYNAPTOSOMAL-ASSOCIATED PROTEIN, 25KDA	2.047E-05	0.00022999	-1.29	0.41
SNRK	SNF RELATED KINASE	0.00015615	0.00205232	-1.41	0.38
SNRPC	SMALL NUCLEAR RIBONUCLEOPROTEIN POLYPEPTIDE C	7.3356E-05	0.00709679	1.01	2.02
SNX12	SORTING NEXIN 12	0.00014178	0.00815927	1.10	2.14
SPARC	SECRETED PROTEIN, ACIDIC, CYSTEINE-RICH (OSTEONECTIN)	0.00143789	0.00942443	-1.48	0.36
SPRY1	SPROUTY HOMOLOG 1, ANTAGONIST OF FGF SIGNALING	0.00100558	0.01093752	-1.65	0.32
SQLE	SQUALENE EPOXIDASE	5.2481E-05	0.01859361	-2.01	0.25
SSNA1	SJOGREN SYNDROME NUCLEAR AUTOANTIGEN 1	0.00183977	0.00912934	1.02	2.02
STAT4	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1	3.8116E-05	0.00297834	-1.21	0.43
STAT2	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 2, 113KDA	0.00019858	0.00856955	1.25	2.38
STIP1	STRESS-INDUCED-PHOSPHOPROTEIN 1	6.493E-05	0.00141885	2.05	4.15
SULT1A1	SULFOTRANSFERASE FAMILY, CYTOSOLIC, 1A, PHENOL-PREFERRING, MEMBER 1	7.9488E-06	0.00731426	1.47	2.77
SUOX	SULFITE OXIDASE	0.00035876	0.01894375	-1.69	0.31
SUPT4H1	SUPPRESSOR OF TY 4 HOMOLOG 1	0.00173689	0.00827868	1.75	3.36
SYTL2	SYNAPTOTAGMIN-LIKE 2	0.0004455	0.02491994	-1.55	0.34
TBCB	TUBULIN FOLDING COFACTOR B	0.00143106	0.00297834	1.02	2.03
TBL1X	TRANSDUCIN (BETA)-LIKE 1X-LINKED	6.7346E-05	0.00087238	1.28	2.43
TCF7	TRANSCRIPTION FACTOR 7 (T-CELL SPECIFIC, HMG-BOX)	0.0001864	0.02671852	-1.57	0.34
TCIRG1	T-CELL, IMMUNE REGULATOR 1, ATPASE, H+ TRANSPORTING, LYSOSOMAL V0 SUBUNIT A3	0.00288033	0.00075523	1.01	2.01
TES	TESTIS DERIVED TRANSCRIPT (3 LIM DOMAINS)	8.6038E-07	0.01835302	1.90	3.74
TESC	TESCALCIN; SIMILAR TO TESCALCIN	0.00018716	0.01455568	-1.47	0.36
TGFBI	TRANSFORMING GROWTH FACTOR, BETA-INDUCED, 68KDA	0.0023776	0.0257968	1.63	3.09
TGM2	TRANSGLUTAMINASE 2 (C POLYPEPTIDE, PROTEIN-GLUTAMINE-GAMMA-GLUTAMYLTRANSFERASE)	0.00552053	0.0109434	-1.02	0.49
THYN1	THYMOCYTE NUCLEAR PROTEIN 1	0.00368356	0.0328315	-1.07	0.48
TIAL1	TIA1 CYTOTOXIC GRANULE-ASSOCIATED RNA BINDING PROTEIN-LIKE 1	0.00035169	0.00495236	-1.20	0.43
TIMM22	TRANSLOCASE OF INNER MITOCHONDRIAL MEMBRANE 22 HOMOLOG	0.00059504	0.00225939	1.06	2.08
TM9SF2	TRANSMEMBRANE 9 SUPERFAMILY MEMBER 2	7.7302E-09	0.0021861	2.98	7.91
TMEM120A	TRANSMEMBRANE PROTEIN 120A	0.00022239	0.00340771	1.10	2.14
TMEM134	TRANSMEMBRANE PROTEIN 134	0.00059198	0.00405847	-1.18	0.44
TMEM18	TRANSMEMBRANE PROTEIN 18	0.00036433	0.00431753	-1.04	0.49
TMEM55B	TRANSMEMBRANE PROTEIN 55B	0.00448652	0.00087238	1.39	2.62
TMEM62	TRANSMEMBRANE PROTEIN 62	0.00189363	0.00161019	1.14	2.21
TNNT3	TROPONIN T TYPE 3	0.00032322	0.03741692	-1.05	0.48
TOR3A	TORSIN FAMILY 3, MEMBER A	0.00145339	0.00852404	1.81	3.50
TRAC	T CELL RECEPTOR ALPHA CONSTANT	0.00481973	0.03869901	-1.48	0.36

TRAF3IP3	TNF RECEPTOR-ASSOCIATED FACTOR 3	0.00069623	0.00262939	-1.29	0.41
TRAF5	TNF RECEPTOR-ASSOCIATED FACTOR 5	0.00025599	0.00369505	1.18	2.27
TRAPPC2L	TRAFFICKING PROTEIN PARTICLE COMPLEX 2-LIKE	0.00577126	0.00574987	1.01	2.01
TRAPPC3	TRAFFICKING PROTEIN PARTICLE COMPLEX 3	0.00065949	0.00703815	1.14	2.20
TRAPPC5	TRAFFICKING PROTEIN PARTICLE COMPLEX 5	0.00149092	0.0055805	-1.01	0.50
TRIM5	TRIPARTITE MOTIF-CONTAINING 5	0.00571162	0.00116573	1.25	2.38
TRIM50	TRIPARTITE MOTIF CONTAINING 50	0.00310288	0.04739857	1.66	3.17
TRIM8	TRIPARTITE MOTIF CONTAINING 8	0.00085611	0.0330276	-1.22	0.43
TRIP12	THYROID HORMONE RECEPTOR INTERACTOR 12	0.00095521	0.01818957	1.65	3.13
TSPAN17	TETRASPANIN 17	0.00018909	0.00815927	1.35	2.55
TSPAN33	TETRASPANIN 33	0.00385802	0.00073629	1.06	2.09
TXNL4A	THIOREDOXIN-LIKE 4A	2.4226E-05	0.00518424	1.14	2.20
TYK2	TYROSINE KINASE 2	0.00232848	0.00389521	1.28	2.43
UBAP1	UBIQUITIN ASSOCIATED PROTEIN 1	0.00016639	0.00385418	1.12	2.17
UBE2D4	UBIQUITIN-CONJUGATING ENZYME E2D 4 (PUTATIVE)	0.0005424	0.00649472	-1.45	0.37
UBE2Z	UBIQUITIN-CONJUGATING ENZYME E2Z	0.00198196	0.02346202	1.44	2.71
UBP1	UPSTREAM BINDING PROTEIN 1 (LBP-1A)	0.000342	0.00822753	-1.08	0.47
UCHL3	UBIQUITIN CARBOXYL-TERMINAL ESTERASE L3 (UBIQUITIN THIOLESTERASE)	0.0001731	0.00356378	-1.16	0.45
UCK2	URIDINE-CYTIDINE KINASE 2	0.00257153	0.0055805	-1.16	0.45
UGDH	UDP-GLUCOSE DEHYDROGENASE	0.00053737	0.00385961	-2.84	0.14
UNC119B	UNC-119 HOMOLOG B	0.0010136	0.01936187	1.11	2.16
UNG	URACIL-DNA GLYCOSYLASE	6.2517E-05	0.02216045	-1.05	0.48
UTRN	UTROPHIN	0.00111757	0.00750623	-1.38	0.38
VAMP8	VESICLE-ASSOCIATED MEMBRANE PROTEIN 8	0.00439437	0.01399381	1.20	2.29
VEGFA	VASCULAR ENDOTHELIAL GROWTH FACTOR A	1.2341E-05	0.00449503	-1.94	0.26
VPS13D	VACUOLAR PROTEIN SORTING 13 D	0.00018719	0.00233427	2.37	5.18
WARS	TRYPTOPHANYL-TRNA SYNTHETASE	0.00098184	0.00051603	1.59	3.00
XAF1	XIAP ASSOCIATED FACTOR 1	1.44E-05	0.00489157	1.99	3.96
XDH	XANTHINE DEHYDROGENASE	0.00243758	0.0055805	1.06	2.08
XIST	X-INACTIVE SPECIFIC TRANSCRIPT	9.8205E-10	0.00323494	-5.47	0.02
XPO1	EXPORTIN 1	2.5304E-06	0.03130162	1.62	3.08
YPEL3	YIPPEE-LIKE 2	0.00017042	0.00153351	1.23	2.35
ZDHHC4	ZINC FINGER, DHHC-TYPE CONTAINING 4	0.00398015	0.00154486	1.05	2.06
ZFYVE21	EARLY ENDOSOME ANTIGEN 1	0.00023268	0.01696415	1.85	3.60
ZG16B	ZYMOGEN GRANULE PROTEIN 16 HOMOLOG B	0.00268162	0.01558698	-1.78	0.29
ZNF313	RING FINGER PROTEIN 114	0.00101319	0.00075523	1.00	2.01
ZNF32	ZINC FINGER PROTEIN 32	2.991E-05	0.00288981	1.08	2.11
ZNF75D	ZINC FINGER PROTEIN 75D	0.001186	0.01427228	1.05	2.07
ZWINT	ZW10 INTERACTOR	0.00047976	0.0229459	-1.32	0.40

* The genes that were significantly modulated ($p < 0.05$ with Benjamini-Hochberg correction for multiple testing) and showed a mean fold expression value > 2 or < 0.5 upon BTV infection were selected.

Table S4. DEG in spleen cDCs upon BTV infection*

Official gene symbol	Approved name	Control sheep 1 (log2)	Control sheep 2 (log2)	Control sheep 3 (log2)	Infected sheep 1 (log2)	Infected sheep 2 (log2)	Minimal fold change (log2)	Minimal fold change
ADD3	ADDUCIN 3 (GAMMA)	4.87	3.83	4.19	2.04	1.75	-1.79	0.29
AHNAK	AHNAK NUCLEOPROTEIN	6.98	6.59	6.05	4.76	4.27	-1.29	0.41
ARHGAP9	RHO GTPASE ACTIVATING PROTEIN 9	3.95	3.57	4.00	1.25	1.07	-2.32	0.20
ARSB	ARYLSULFATASE B	1.58	0.74	1.46	-0.73	-0.53	-1.27	0.41
ASF1B	ASF1 ANTI-SILENCING FUNCTION 1 HOMOLOG B	1.34	1.65	1.36	0.05	0.23	-1.11	0.46
BAMBI	BMP AND ACTIVIN MEMBRANE-BOUND INHIBITOR HOMOLOG	1.47	0.90	2.32	-0.59	-0.81	-1.49	0.35
BATF3	BASIC LEUCINE ZIPPER TRANSCRIPTION FACTOR, ATF-LIKE 3	5.72	6.44	6.27	7.79	7.61	1.17	2.25
BCL2L11	BCL2-LIKE 11 (APOPTOSIS FACILITATOR)	-0.33	-0.01	0.24	1.48	1.73	1.23	2.35
BLVRB	BILIVERDIN REDUCTASE B (FLAVIN REDUCTASE (NADPH))	4.12	4.89	4.49	6.96	6.64	1.75	3.37
BMP7	BONE MORPHOGENETIC PROTEIN 7	-1.90	-2.06	-1.82	-0.62	-0.32	1.20	2.30
C12orf75	CHROMOSOME 12 OPEN READING FRAME 75	2.83	1.45	1.85	-0.24	0.26	-1.20	0.44
C13orf15	CHROMOSOME 13 OPEN READING FRAME 15	3.57	2.62	3.46	1.23	0.19	-1.39	0.38
C6orf132	CHROMOSOME 6 OPEN READING FRAME 132	1.16	0.96	0.95	-0.50	-0.84	-1.45	0.37
CALD1	CALDESMON 1	-1.15	-0.89	-0.55	0.53	0.84	1.08	2.12
CASP7	CASPASE 7, APOPTOSIS-RELATED CYSTEINE PEPTIDASE	3.12	3.23	3.68	4.87	4.94	1.19	2.29
CCL5	CHEMOKINE (C-C MOTIF) LIGAND 5	2.34	1.59	2.89	-0.65	0.15	-1.44	0.37
CD19	CD19 MOLECULE	2.34	2.01	2.23	0.08	-0.19	-1.93	0.26
CD1E	CD1E MOLECULE	1.97	1.39	1.91	-0.05	-0.06	-1.44	0.37
CD22	CD22 MOLECULE	1.59	1.82	1.58	0.08	0.30	-1.28	0.41
CD247	CD247 MOLECULE	2.34	2.25	2.72	-0.76	0.51	-1.73	0.30
CD3D	CD3D MOLECULE, DELTA (CD3-TCR COMPLEX)	3.86	2.87	4.19	1.62	0.75	-1.25	0.42
CD3E	CD3E MOLECULE, EPSILON (CD3-TCR COMPLEX)	6.14	5.81	6.94	3.78	2.88	-2.03	0.24
CD3G	CD3G MOLECULE, GAMMA (CD3-TCR COMPLEX)	0.52	1.01	1.20	-0.79	-1.31	-1.31	0.40
CD52	CD52 MOLECULE	3.04	2.20	2.86	-0.70	-0.13	-2.33	0.20
CD6	CD6 MOLECULE	3.62	3.29	3.93	2.22	1.00	-1.06	0.48
CD69	CD69 MOLECULE	2.30	0.56	2.37	-0.65	-1.13	-1.21	0.43
CD79A	CD79A MOLECULE, IMMUNOGLOBULIN-ASSOCIATED ALPHA	3.85	3.49	3.25	1.57	2.06	-1.20	0.44
CD9	CD9 MOLECULE	2.08	1.65	1.76	-0.34	-0.38	-1.99	0.25
CDKN2D	CYCLIN-DEPENDENT KINASE INHIBITOR 2D (P19, INHIBITS CDK4)	5.84	4.42	4.67	3.34	3.32	-1.09	0.47
CFI	COMPLEMENT FACTOR I	-1.86	-1.82	-1.85	-0.70	0.79	1.11	2.16
CLNK	CYTOKINE-DEPENDENT HEMATOPOIETIC CELL LINKER	2.04	2.60	3.26	4.53	4.36	1.10	2.14
CSF1R	COLONY STIMULATING FACTOR 1 RECEPTOR	3.08	3.30	2.33	0.52	1.05	-1.28	0.41
CXCL10	CHEMOKINE (C-X-C MOTIF) LIGAND 10	4.29	4.84	4.77	7.43	6.70	1.85	3.61
CXCL2	CHEMOKINE (C-X-C MOTIF) LIGAND 2	2.37	0.36	0.79	-0.88	-0.94	-1.24	0.42
DDIT4	DNA-DAMAGE-INDUCIBLE TRANSCRIPT 4	2.56	2.51	2.45	1.21	0.59	-1.24	0.42
DNAJB6	DNAJ (HSP40) HOMOLOG, SUBFAMILY B, MEMBER 6	3.95	3.53	3.89	5.81	5.09	1.14	2.21
DUSP1	DUAL SPECIFICITY PHOSPHATASE 1	3.81	4.16	3.75	0.43	2.67	-1.07	0.47
DUSP5	DUAL SPECIFICITY PHOSPHATASE 5	5.52	3.14	3.99	1.34	1.85	-1.29	0.41
DYSF	DYSFERLIN, LIMB GIRDLE MUSCULAR DYSTROPHY 2B (AUTOSOMAL RECESSIVE)	-1.44	-1.10	-1.43	0.07	0.51	1.17	2.25
EIF2AK2	EUKARYOTIC TRANSLATION INITIATION FACTOR 2-ALPHA KINASE 2	-0.54	-0.27	0.04	1.77	2.60	1.74	3.33

EMP3	EPITHELIAL MEMBRANE PROTEIN 3	3.88	4.04	3.19	1.19	1.44	-1.75	0.30
ERG	V-ETS ERYTHROBLASTOSIS VIRUS E26 ONCOGENE	1.01	0.92	1.34	-0.82	-1.04	-1.74	0.30
ESYT1	FAMILY WITH SEQUENCE SIMILARITY 62 (C2 DOMAIN CONTAINING), MEMBER A	1.29	0.77	1.11	-0.26	-0.31	-1.02	0.49
ETS1	V-ETS ERYTHROBLASTOSIS VIRUS E26 ONCOGENE HOMOLOG 1 (AVIAN)	3.60	2.85	3.69	0.60	0.23	-2.24	0.21
FAM129C	FAMILY WITH SEQUENCE SIMILARITY 129, MEMBER C	5.96	4.72	4.13	3.06	1.62	-1.08	0.47
FAM149A	FAMILY WITH SEQUENCE SIMILARITY 149, MEMBER A	4.34	2.36	2.97	0.51	0.11	-1.85	0.28
FCER1A	FC FRAGMENT OF IGE, HIGH AFFINITY I, RECEPTOR FOR; ALPHA POLYPEPTIDE	4.03	2.73	3.57	0.27	-0.16	-2.46	0.18
FGL2	FIBRINOGEN-LIKE 2	3.25	4.03	4.53	5.62	5.61	1.08	2.11
FLNA	FILAMIN A, ALPHA (ACTIN BINDING PROTEIN 280)	1.49	1.54	1.18	-0.42	-0.27	-1.45	0.37
FMNL2	FORMIN-LIKE 2	1.04	0.61	1.05	2.68	2.33	1.28	2.43
FOSB	FBJ MURINE OSTEOSARCOMA VIRAL ONCOGENE HOMOLOG B	1.21	1.40	1.23	-0.33	0.05	-1.16	0.45
FTSJD1	FTSJ METHYLTRANSFERASE DOMAIN CONTAINING 1	0.07	0.06	0.12	1.37	1.18	1.06	2.09
GAPDH	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE-LIKE 6; HYPOTHETICAL PROTEIN LOC100133042; GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE	7.97	8.71	8.11	4.85	6.19	-1.78	0.29
GAS1	GROWTH ARREST-SPECIFIC 1	1.04	1.73	1.88	3.69	2.89	1.01	2.02
GIMAP6	GTPASE, IMAP FAMILY MEMBER 6	2.08	1.93	2.44	0.61	0.90	-1.03	0.49
GKAP1	G KINASE ANCHORING PROTEIN 1	1.35	0.61	1.41	2.53	2.71	1.12	2.17
GNB2L1	GUANINE NUCLEOTIDE BINDING PROTEIN (G PROTEIN), BETA POLYPEPTIDE 2-LIKE 1	9.55	9.58	9.60	8.07	8.48	-1.08	0.47
HERC5	HECT DOMAIN AND RLD 5	2.07	1.94	2.33	4.26	3.78	1.44	2.72
HINT2	HISTIDINE TRIAD NUCLEOTIDE BINDING PROTEIN 2	0.83	1.69	1.08	-0.65	-0.31	-1.14	0.45
HSPA4L	HEAT SHOCK 70KDA PROTEIN 4-LIKE	-1.51	-1.50	-1.35	-0.11	0.19	1.24	2.37
HSPB1	HEAT SHOCK 27KDA PROTEIN-LIKE 2 PSEUDOGENE; HEAT SHOCK 27KDA PROTEIN 1	5.66	8.13	6.49	9.29	9.26	1.13	2.19
HSPE1	HEAT SHOCK 10KDA PROTEIN 1 (CHAPERONIN 10)	7.15	7.18	7.14	8.72	8.81	1.54	2.91
ID3	INHIBITOR OF DNA BINDING 3, DOMINANT NEGATIVE HELIX-LOOP-HELIX PROTEIN	2.97	2.27	3.12	1.10	0.92	-1.16	0.45
IDH3G	ISOCITRATE DEHYDROGENASE 3 (NAD+) GAMMA	3.87	4.29	3.80	1.22	2.74	-1.05	0.48
IDO1	INDOLEAMINE 2,3-DIOXYGENASE 1	-0.72	0.65	-0.14	1.72	2.77	1.06	2.09
IGF2	INSULIN-LIKE GROWTH FACTOR 2 (SOMATOMEDIN A); INSULIN; INS-IGF2 READTHROUGH TRANSCRIPT	1.15	0.54	1.77	-0.67	-1.68	-1.22	0.43
IGHG1	IMMUNOGLOBULIN HEAVY CONSTANT GAMMA 1	4.47	2.78	4.64	0.81	0.60	-1.97	0.26
IL18	INTERLEUKIN 18 (INTERFERON-GAMMA-INDUCING FACTOR)	-1.83	-1.21	-1.61	0.56	-0.14	1.07	2.10
IL1RN	INTERLEUKIN 1 RECEPTOR ANTAGONIST	1.23	0.72	0.77	-0.29	-0.37	-1.01	0.50
IL27	INTERLEUKIN 27	-0.06	-0.11	-0.10	2.80	1.80	1.87	3.65
IL8	INTERLEUKIN 8	3.27	0.60	1.52	-0.49	-1.17	-1.09	0.47
IRF4	INTERFERON REGULATORY FACTOR 4	1.92	2.46	1.18	-0.07	0.12	-1.06	0.48
ISG15	ISG15 UBIQUITIN-LIKE MODIFIER	3.38	2.46	2.69	7.10	6.79	3.41	10.63
ITGAD	INTEGRIN, ALPHA D	2.31	2.80	3.22	-0.04	-0.40	-2.34	0.20
KCNE3	POTASSIUM VOLTAGE-GATED CHANNEL, ISK-RELATED FAMILY, MEMBER 3	1.53	1.15	0.65	-0.35	-0.89	-1.01	0.50
KIF26A	KINESIN FAMILY MEMBER 26A	-1.37	-1.07	-0.98	0.53	0.47	1.45	2.73
KLF4	KRUPPEL-LIKE FACTOR 4 (GUT)	8.22	7.10	7.27	4.80	4.29	-2.30	0.20
LAP3	LEUCINE AMINOPEPTIDASE 3	4.33	4.67	4.38	6.08	6.10	1.41	2.65
LCK	LYMPHOCYTE-SPECIFIC PROTEIN TYROSINE KINASE	2.56	1.86	2.76	-0.43	-0.25	-2.11	0.23
LIMCH1	LIM AND CALPONIN HOMOLOGY DOMAINS 1	4.15	4.67	3.69	1.12	2.31	-1.38	0.38
LYST	LYSOSOMAL TRAFFICKING REGULATOR	3.76	3.92	3.97	6.00	5.94	1.97	3.92
MAGED4B	MELANOMA ANTIGEN FAMILY D, 4B; MELANOMA ANTIGEN FAMILY D, 4	1.51	1.43	1.38	-0.07	0.13	-1.26	0.42
MAGOH	MAGO-NASHI HOMOLOG, PROLIFERATION-ASSOCIATED (DROSOPHILA)	2.07	1.91	2.26	3.56	3.71	1.30	2.46

MAP1LC3A	MICROTUBULE-ASSOCIATED PROTEIN 1 LIGHT CHAIN 3 ALPHA	2.44	2.79	2.58	0.79	1.43	-1.02	0.49
MATN2	MATRILIN 2	0.21	1.55	1.31	2.90	3.30	1.35	2.55
MBP	MYELIN BASIC PROTEIN	-0.72	0.08	-0.83	1.72	1.32	1.23	2.35
MED25	MEDIATOR COMPLEX SUBUNIT 25	2.58	1.65	1.53	0.24	-0.05	-1.29	0.41
METTL8	METHYLTRANSFERASE LIKE 8	1.96	2.39	2.88	4.45	4.52	1.58	2.99
MGMT	O-6-METHYLGUANINE-DNA METHYLTRANSFERASE	1.00	1.02	0.76	-0.25	-0.70	-1.00	0.50
MT2A	METALLOTHIONEIN 2A	4.20	4.37	3.85	6.18	6.02	1.65	3.14
MX1	MYXOVIRUS (INFLUENZA VIRUS) RESISTANCE 1, INTERFERON-INDUCIBLE PROTEIN P78	3.28	2.39	3.06	5.77	5.33	2.04	4.13
MX2	MYXOVIRUS (INFLUENZA VIRUS) RESISTANCE 2	3.03	2.42	2.14	6.67	6.62	3.59	12.04
MXRA7	MATRIX-REMODELLING ASSOCIATED 7	2.93	1.57	2.76	0.22	0.35	-1.23	0.43
N4BP2L1	NEDD4 BINDING PROTEIN 2-LIKE 1	0.51	0.73	1.03	2.38	2.09	1.07	2.09
NCALD	NEUROCALCIN DELTA	2.21	1.47	2.00	0.20	0.47	-1.00	0.50
NOTCH3	NOTCH HOMOLOG 3	6.51	4.12	4.98	1.57	1.10	-2.55	0.17
NQO2	NAD(P)H DEHYDROGENASE, QUINONE 2	2.91	2.86	2.51	0.43	1.06	-1.44	0.37
NR4A1	NUCLEAR RECEPTOR SUBFAMILY 4, GROUP A, MEMBER 1	3.74	4.12	2.95	0.42	1.86	-1.09	0.47
NUDT9	NUDIX (NUCLEOSIDE DIPHOSPHATE LINKED MOIETY X)-TYPE MOTIF 9	0.61	0.88	0.88	3.48	2.25	1.37	2.58
P4HA2	PROLYL 4-HYDROXYLASE, ALPHA POLYPEPTIDE II	3.02	2.88	3.17	5.18	5.62	2.01	4.04
PARP14	POLY (ADP-RIBOSE) POLYMERASE FAMILY, MEMBER 14	2.77	2.46	2.36	4.13	3.98	1.22	2.32
PARP9	POLY (ADP-RIBOSE) POLYMERASE FAMILY, MEMBER 9	3.13	2.82	3.01	4.18	4.24	1.04	2.06
PDLIM4	PDZ AND LIM DOMAIN 4	0.55	1.00	1.63	2.94	3.07	1.31	2.47
PGM1	PHOSPHOGLUCOMUTASE 1	5.17	4.59	5.49	3.42	3.43	-1.16	0.45
PIWIL4	PIWI-LIKE 4	0.59	1.52	0.79	2.59	2.84	1.07	2.10
PLA2G16	PHOSPHOLIPASE A2, GROUP XVI	3.35	2.61	3.03	5.14	4.83	1.48	2.79
PLCB2	PHOSPHOLIPASE C, BETA 2	4.23	4.27	3.95	2.65	2.94	-1.01	0.50
PPIC	PEPTIDYLPROLYL ISOMERASE C (CYCLOPHILIN C)	0.44	0.79	-0.07	1.83	3.06	1.03	2.05
PPIF	PEPTIDYLPROLYL ISOMERASE F	0.79	1.50	1.13	-0.52	-0.28	-1.07	0.48
PRAM1	PML-RARA REGULATED ADAPTOR MOLECULE 1	2.83	2.77	2.55	1.12	0.33	-1.42	0.37
PSPC1	PARASPECKLE COMPONENT 1; PARASPECKLE PROTEIN 1 PSEUDOGENE	2.37	2.09	2.36	0.08	0.91	-1.17	0.44
PTPLAD1	PROTEIN TYROSINE PHOSPHATASE-LIKE A DOMAIN CONTAINING 1	1.40	1.83	1.77	3.67	3.19	1.36	2.57
PTPLB	PROTEIN TYROSINE PHOSPHATASE-LIKE (PROLINE INSTEAD OF CATALYTIC ARGININE), MEMBER B	1.10	0.75	1.04	2.26	2.16	1.06	2.09
RAB30	RAB30, MEMBER RAS ONCOGENE FAMILY	3.54	4.04	4.66	5.71	5.94	1.05	2.07
RASGRP2	RAS GUANYL RELEASING PROTEIN 2 (CALCIUM AND DAG-REGULATED)	1.07	1.26	0.74	-0.29	-0.27	-1.01	0.50
RGL1	RAL GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR-LIKE 1	-0.05	0.12	0.39	1.61	1.88	1.22	2.33
RHOB	RAS HOMOLOG GENE FAMILY, MEMBER B	5.30	4.50	5.00	2.69	3.48	-1.02	0.49
RNASE6	RIBONUCLEASE, RNASE A FAMILY, K6	3.46	2.97	3.18	1.16	0.82	-1.80	0.29
RPS24	RIBOSOMAL PROTEIN S24	-0.09	0.71	0.76	2.67	2.41	1.65	3.14
RSRC2	ARGININE/SERINE-RICH COILED-COIL 2	1.91	1.81	2.01	3.44	3.17	1.15	2.22
RTP4	RECEPTOR (CHEMOSENSORY) TRANSPORTER PROTEIN 4	2.36	1.26	1.98	5.18	4.47	2.12	4.33
RUNX2	RUNT-RELATED TRANSCRIPTION FACTOR 2	3.17	2.44	2.73	1.23	1.31	-1.13	0.46
SARM1	STERILE ALPHA AND TIR MOTIF CONTAINING 1	3.41	3.37	2.94	1.51	1.90	-1.05	0.48
SCD	STEAROYL-COA DESATURASE (DELTA-9-DESATURASE)	3.03	2.95	3.21	1.60	1.88	-1.07	0.48
SEMA4D	SEMA DOMAIN, IMMUNOGLOBULIN DOMAIN (IG), TRANSMEMBRANE DOMAIN (TM) AND SHORT CYTOPLASMIC DOMAIN, (SEMAPHORIN) 4D	5.24	4.72	5.46	3.53	2.46	-1.19	0.44
SEPT1	SEPTIN 1	1.44	0.94	1.01	-0.31	-0.07	-1.01	0.50

SEPT5	SEPTIN 5	1.45	2.08	1.49	0.16	-0.96	-1.28	0.41
SERPINH1	SERPIN PEPTIDASE INHIBITOR, CLADE H (HEAT SHOCK PROTEIN 47), MEMBER 1, (COLLAGEN BINDING PROTEIN 1)	-0.81	-0.87	-0.83	3.28	3.87	4.09	17.04
SLAMF7	SLAM FAMILY MEMBER 7	4.63	4.84	5.09	6.70	6.61	1.53	2.88
SLC27A5	SOLUTE CARRIER FAMILY 27 (FATTY ACID TRANSPORTER), MEMBER 5	-1.23	-0.75	-1.17	0.31	0.69	1.07	2.09
SMAGP	SMALL TRANS-MEMBRANE AND GLYCOSYLATED PROTEIN	2.36	2.29	2.19	0.84	1.10	-1.09	0.47
SOCS3	SUPPRESSOR OF CYTOKINE SIGNALING 3	0.41	-0.42	0.02	2.81	2.11	1.71	3.26
SPEG	SPEG COMPLEX LOCUS	1.81	1.93	1.00	6.54	6.01	4.08	16.94
SPINT2	SERINE PEPTIDASE INHIBITOR, KUNITZ TYPE, 2	3.57	2.48	2.56	0.25	1.40	-1.07	0.48
SPTBN2	SPECTRIN, BETA, NON-ERYTHROCYTIC 2	2.69	2.27	2.25	0.28	0.44	-1.80	0.29
SSR4	SIGNAL SEQUENCE RECEPTOR, DELTA (TRANSLOCON-ASSOCIATED PROTEIN DELTA)	6.18	5.69	5.65	2.72	4.62	-1.03	0.49
ST6	SIALYLTRANSFERASE 6	5.62	4.66	4.63	0.93	3.27	-1.36	0.39
STAB1	STABILIN 1	2.39	3.05	2.88	5.13	5.07	2.02	4.05
SYTL2	SYNAPTOTAGMIN-LIKE 2	0.35	0.35	0.58	-0.70	-1.12	-1.05	0.48
TARP	TCR GAMMA ALTERNATE READING FRAME PROTEIN; T CELL RECEPTOR GAMMA VARIABLE 9; T CELL RECEPTOR GAMMA CONSTANT 1	0.95	0.69	1.44	-0.35	-0.54	-1.04	0.49
TCF4	TRANSCRIPTION FACTOR 4	2.78	1.79	1.81	-0.08	0.37	-1.42	0.37
TCF7	TRANSCRIPTION FACTOR 7 (T-CELL SPECIFIC, HMG-BOX)	2.34	1.36	2.40	0.24	0.24	-1.12	0.46
TECR	GLYCOPROTEIN, SYNAPTIC 2	3.07	3.23	2.93	1.15	1.83	-1.10	0.47
TESC	TESCALCIN	2.67	1.52	2.44	-0.19	-0.45	-1.70	0.31
TFCP2	TRANSCRIPTION FACTOR CP2	3.03	2.52	3.06	4.46	4.17	1.11	2.16
TIE1	TYROSINE KINASE WITH IMMUNOGLOBULIN-LIKE AND EGF-LIKE DOMAINS 1	3.27	1.96	2.26	-0.42	0.46	-1.50	0.35
TM9SF2	TRANSMEMBRANE 9 SUPERFAMILY MEMBER 2	-1.83	-1.87	-2.12	2.38	2.20	4.03	16.29
TMEM154	TRANSMEMBRANE PROTEIN 154	2.36	1.13	1.44	-0.09	-0.19	-1.22	0.43
TPI1	TPI1 PSEUDOGENE; TRIOSEPHOSPHATE ISOMERASE 1	5.16	4.92	4.94	2.86	3.77	-1.15	0.45
TRAC	T CELL RECEPTOR ALPHA CONSTANT;	1.34	1.92	1.95	0.13	-0.76	-1.20	0.43
TRANK1	LUPUS BRAIN ANTIGEN 1	-1.04	-0.65	-0.68	0.39	0.96	1.04	2.06
TRD@	T CELL RECEPTOR DELTA LOCUS	0.64	0.84	1.09	-0.48	-0.94	-1.12	0.46
TRIO	TRIPLE FUNCTIONAL DOMAIN (PTPRF INTERACTING)	3.33	3.67	3.88	5.79	5.27	1.38	2.61
TRIP6	THYROID HORMONE RECEPTOR INTERACTOR 6	-0.71	-0.35	-0.44	0.93	0.73	1.09	2.13
TRPS1	TRICHORHINOPHALANGEAL SYNDROME I	1.13	0.93	1.43	-0.16	-0.33	-1.09	0.47
UNG	URACIL-DNA GLYCOSYLASE	2.29	1.89	2.63	0.57	0.87	-1.03	0.49
VIM	VIMENTIN	7.85	7.63	7.76	6.38	6.00	-1.25	0.42
VMP1	VACUOLE MEMBRANE PROTEIN 1	0.11	0.00	0.15	1.40	1.42	1.25	2.37
VPS13D	VACUOLAR PROTEIN SORTING 13 HOMOLOG D	3.59	2.96	3.16	5.80	5.28	1.69	3.22
WNT2B	WINGLESS-TYPE MMTV INTEGRATION SITE FAMILY, MEMBER 2B	4.39	4.15	3.81	2.44	2.79	-1.03	0.49
XDH	XANTHINE DEHYDROGENASE	-1.21	-0.25	-0.60	2.63	1.76	2.02	4.05
XIST	X (INACTIVE)-SPECIFIC TRANSCRIPT	5.15	5.19	4.93	-0.79	-1.59	-5.72	0.02
XPO1	EXPORTIN 1	1.57	1.44	1.84	3.18	2.91	1.07	2.10
ZBTB16	ZINC FINGER AND BTB DOMAIN CONTAINING 16	1.24	1.34	0.79	-0.65	-0.48	-1.27	0.42
ZCCHC24	ZINC FINGER, CCHC DOMAIN CONTAINING 24	2.46	2.04	1.93	0.05	-0.25	-1.87	0.27
ZNFX1	ZINC FINGER, NFX1-TYPE CONTAINING 1	-1.03	-0.84	-0.89	0.38	0.59	1.22	2.33

* The genes presenting a minimum fold change >2 and <0.5 in the 2 infected samples relatively to the 3 control samples were considered as DEG.

Table S5. Fold changes of gene expression upon BTV infection obtained in microarray and in qPCR analyses

Gene	Microarrays Fold Change	qPCR Fold Change
Blood pDC		
CCR7	2.93[1]	26.17[3]
CXCL10	4.76[1]	16.11[3]
EIF2AK2	2.95[1]	7.78[3]
IFNG	2.02[1]	35.75[3]
IL8	3.86[1]	19.97[3]
TNF	2.11[1]	40.22[3]
Lymph node pDC		
CCL5	4.44[2]	6.3[3]
CCR7	0.38[2]	0.44[3]
EIF2AK2	2.91[2]	3.75[3]
Id2	0.23[2]	0.50[3]
STK17	0.31[2]	0.52[3]
Lymph node cDC		
CXCL10	2.4[2]	7.11[3]
EIF2AK2	3.26[2]	19.69[3]
IDO1	3.88[2]	6.77[3]
IL1b	0.19[2]	0.13[3]
IL8	0.13[2]	0.64[3]
IRF8	0.22[2]	0.27[3]
Spleen cDC		
BATF3	2.9[1]	7.6[3]
CCL5	0.2[1]	0.08[3]
CLEC9A	3[1]	13.6[3]
CXCL10	5.4[1]	24.25[3]
GATA3	0.3[1]	0.41[3]

[1] minimal fold change

[2] mean fold change

[3] fold between expression in one of the infected versus one of the control sheep DC

Table S6. Canonical pathways enriched in blood pDCs, node pDCs, node cDCs and spleen cDCs upon BTV infection.

Ingenuity Canonical Pathways	**-log (p-value)**	**Ratio**	**Molecules**
Blood pDCs			
Inflammation			
Role of Hypercytokinemia/hyperchemokinemia in the Pathogenesis of Influenza	4.76E00	1.36E-01	CXCL10, IL8, IFNG, CCL4, CCL2, TNF
Acute Phase Response Signaling	2.26E00	3.93E-02	SOCS3, RRAS2, NFKBIA, SOCS2, CFB, SERPINA1, TNF
IL-6 Signaling	4.03E+00	7.26E-02	IL8, SOCS3, RRAS2, NFKBIA, TNFRSF1A, NFKBIE, CD14, TNF, HSPB1
Immune response			
Dendritic Cell Maturation	2.76E00	3.86E-02	NFKBIA, NFKBIE, HLA-DRB1, CD83, IGHG1, STAT4, TNF, CCR7, PLCB2
Antigen Presentation Pathway	1.11E00	5.00E-02	IFNG, HLA-DRB1
Communication between Innate and Adaptive Immune Cells	1.24E01	1.38E-01	IFNG, IL8, CD4, HLA-DRB1, CD83, IGHG1, CCL3, CD8B, TNFRSF17, CXCL10, TLR10, CCL4, CCL15, TNFRSF13B, TNF, TNFSF13B, CCR7
Crosstalk between Dendritic Cells and Natural Killer Cells	2.26E00	5.26E-02	IFNG, HLA-DRB1, CD83, TNF, CCR7
IL-12 Signaling and Production in Macrophages	2.74E00	4.49E-02	PPARG, IFNG, LYZ, IL12RB1, SERPINA1, S100A8, STAT4, TNF
Signalling pathways			
Role of PKR in Interferon Induction and Antiviral Response	3.86E00	1.09E-01	IFNG, TRAF3, NFKBIA, EIF2AK2, TNF
NF-κB Signaling	4.3E00	5.71E-02	TLR10, TRAF3, RRAS2, NFKBIA, TNFAIP3, EIF2AK2, TNF, TNFSF13B, TNFRSF17, FGFR1
LXR/RXR Activation	2.97E00	5.15E-02	LYZ, MYLIP, CD14, SERPINA1, S100A8, TNF, CCL2
JAK/Stat Signaling	2.82E00	7.14E-02	SOCS3, RRAS2, CISH, SOCS2, STAT4
Glucocorticoid Receptor Signaling	2.68E00	3.4E-02	IL8, IFNG, NFAT5, RRAS2, NFKBIA, CCL2, HSPA1A/HSPA1B, CDKN1C, GTF2A1, TNF
VDR/RXR Activation	1.76E00	4.94E-02	CXCL10, IFNG, CD14, KLF4
Phospholipase C Signaling	1.97E00	3.08E-02	ITGB1, BTK, PLCB2, NFAT5, RRAS2, AHNAK, MEF2C, RHOH
P53 signaling	4.86E-01	2.08E-02	GADD45B,THBS1
p38 MAPK Signaling	1.22E00	3.42E-02	CDC25B,MEF2C,TNF,HSPB1
PPAR Signaling	9.4E-01	2.86E-02	RRAS2,NFKBIA,TNF

Lymph node pDCs			
Inflammation			
Role of Hypercytokinemia/hyperchemokinemia in the Pathogenesis of Influenza	3.77E-01	4.55E-02	CCL4, CCL5
Acute Phase Response Signaling	2.89E-01	3.37E-02	SOCS3, FOS, PIK3R1, SOCS2, SERPINE1, HNRNPK
IL-6 Signaling	2.53E-01	3.23E-02	SOCS3, FOS, PIK3R1, HSPB1
Immune response			
Dendritic Cell Maturation	1.47E00	5.31E-02	STAT4, PLCB2, CD40, HLA-C, PIK3R1, IL32, HLA-B, HLA-DRB1, CD83, FCGR2B, CCR7
Antigen Presentation Pathway	2.94E00	1.5E-01	CIITA, HLA-B, NLRC5, HLA-DRB1, PSMB8, HLA-C
Communication between Innate and Adaptive Immune Cells	3.03E00	9.17E-02	CCL4, CD40, TLR7, HLA-B, HLA-DRB1, CD83, CCL5, TNFRSF13B, CCR7, HLA-C
Crosstalk between Dendritic Cells and Natural Killer Cells	2.03E00	8.42E-02	IL2RG, CD40, TLR7, HLA-B, HLA-DRB1, CD83, CCR7, HLA-C
IL-12 Signaling and Production in Macrophages	0.5	3.85E-02	STAT4, FOS, CD40, PIK3R1, RAB7A, PCYOX1
Signalling pathways			
Role of PKR in Interferon Induction and Antiviral Response	4.02E-01	4.35E-02	TP53, EIF2AK2
NF-κB Signaling	6.82E-01	4.57E-02	AZI2,CD40,PIK3R1,BMP2,KDR,TLR7,TNFAIP3,EIF2AK2
LXR/RXR Activation	5.9E-01	4,41E-02	MYLIP,ARG2, PCYOX1, PTGS2, HMGCR, CYP51A1
JAK/Stat Signaling	2.73E00	1.14E-01	SOCS3, PIK3R1, PIAS1, CDKN1A, CISH, SOCS2, STAT4, FOS
Glucocorticoid Receptor Signaling	1.75E00	5.44E-02	MED1, PIK3R1, HSPA9, SLPI, TAF7, CCL5, HSPA5, NCOA3, FOS, HSP90AB1, NCOA2, CDKN1A, FKBP4, PTGS2, SERPINE1, TAF2
VDR/RXR Activation	4.16E00	1.36E-01	SERPINB1, SPP1, NCOA2, GADD45A, MED1, RUNX2, CDKN1A, CCL5, KLF4, PSMC5, NCOA3
Phospholipase C Signaling	4.09E-01	3.46E-02	TGM2, BTK, PLCB2, MPRIP, MYL6, RHOT2, ITGA5, FCGR2B, RHOF
p53 Signaling	3.51E00	1.15E-01	TP53, RB1, PLAGL1, GADD45B, GADD45A, MED1, PIK3R1, CDKN1A, GNL3, CCND1, BIRC5
p38 MAPK Signaling	7.42E-01	5.13E-02	TP53, MYC, RPS6KA6, TIFA, MKNK2, HSPB1
PPAR Signaling	4.02E-0	3.81E-02	FOS, HSP90AB1, MED1, PTGS2

Lymph nodes cDCs			
Inflammation			
Role of Hypercytokinemia/hyperchemokinemia in the Pathogenesis of Influenza	9.56E-01	6.82E-02	CXCL10, IL8, IL1B
Acute Phase Response Signaling	7.36E-01	3.93E-02	MAPK14, RIPK1, MYD88, IL1B, SERPINE1, MAP2K1, MAPK11
IL-6 Signaling	1.37E00	5.65E-02	VEGFA, IL8, MAPK14, IL1B, MAP2K1, MAPK11, HSPB1
Immune response			
Dendritic cell maturation	1.64E00	4.83E-02	MAPK14, HLA-A, MYD88, IL1B, STAT2, IRF8, FCGR2B, STAT4, MAPK11, PLCB2
Antigen Presentation Pathway	1.11E00	7.50E-02	PSMB9, HLA-A, NLRC5
Communication between Innate and Adaptive Immune Cells	6.19E-01	3.67E-02	CXCL10, IL8, HLA-A, IL1B
Crosstalk between Dendritic Cells and Natural Killer Cells	3.67E-01	3.16E-02	IL2RG, HLA-A, FAS
IL-12 Signaling and Production in Macrophages	1.12E00	4.49E-02	PPARG, STAT4, MAPK14, MYD88, IRF8, MAP2K1, MAPK11
Signaling pathways			
Role of PKR in Interferon Induction and Antiviral Response	1.00E+00	6.52E-02	MAPK14, TRAF5, EIF2AK2
NF-κB Signaling	4.95E-01	3.43E-02	RIPK1, MYD88, HDAC1, IL1B, TRAF5, EIF2AK2
LXR/RXR Activation	6.08E-01	3.68E-02	LCAT, IL1B, ARG2, PTGS2, CYP51A1
JAK/Stat Signaling	1.97E00	8.57E-02	STAT4, PIAS3, PIAS1, TYK2, STAT2, MAP2K1
Glucocorticoid Receptor Signaling	4.45E00	6.46E-02	IL8, CD3E, CDK7, HSPA6, GTF2H2, MAPK11, PRKAG1, MAPK14, HSP90AB1, FKBP4, PTGES3, IL1B, POLR2H, PTGS2, SERPINE1, STAT4, FKBP5, MAP2K1, PPP3CA
VDR/RXR Activation	4.33E-01	3.70E-02	CXCL10, SERPINB1, KLF4
Phospholipase C Signaling	7.64E-01	3.46E-02	TGM2, PLCB2, GNAS, CD3E, HDAC1, PLA2G2A, FCGR2B, MAP2K1, PPP3CA
p53 Signaling	5.87E-01	4.17E-02	MAPK14, HDAC1, CSNK1D, FAS
p38 MAPK Signaling	1.89E00	6.84E-02	MYC, MAPK14, HMGN1, IL1B, PLA2G2A, MAPK11, FAS, HSPB1
PPAR Signaling	1.8E00	6.67E-02	PPARG, HSP90AB1, IL1B, PTGS2, MAP2K1, CITED2, SCAND1

Spleen cDCs			
Inflammation			
Role of Hypercytokinemia/hyperchemokinemia in the Pathogenesis of Influenza	4.41E00	1.14E-01	CXCL10, IL8, IL18, IL1RN, CCL5
Acute Phase Response Signaling	1.22E00	2.25E-02	SOCS3, IL18, TCF4, IL1RN
IL-6 Signaling	2.46E00	4.03E-02	IL8, SOCS3, IL18, IL1RN, HSPB1
Immune response			
Communication between Innate and Adaptive Immune Cells	4.83E00	6.42E-02	CXCL10, IL8, IL18, TRD, IL1RN, IGHG1, CCL5
Dendritic Cell Maturation	1.72	2.42E-02	PLCB2, IL18, TRD, IL1RN, IGHG1
Crosstalk between Dendritic Cells and Natural Killer Cells	7.32E-01	2.11E-02	IL18, CD69
IL-12 Signaling and Production in Macrophages	-		
Signaling pathways			
Role of PKR in Interferon Induction and Antiviral Response	5.29E-01	2.17E-02	EIF2AK2
NF-κB Signaling	1.81E00	2.86E-02	LCK, IL18, TRD, IL1RN, , EIF2AK2
LXR/RXR Activation	1.01E00	2.21E-02	SCD, IL18, IL1RN
JAK/Stat Signaling	3.52E-01	1.43E-02	SOCS3
Glucocorticoid Receptor Signaling	2.62E00	2.72E-02	CD247, IL8, CD3G, CD3E, DUSP1, IL1RN, CCL5, CD3D
VDR/RXR Activation	2.3E00	4.94E-02	CXCL10, RUNX2, CCL5, KLF4
Phospholipase C Signaling	5.09E00	6.54E-02	CD247, PLCB2, TRD, CD3E, GNB2L1, CD3D, CD79A, CD3G, LCK, AHNAK, RHOB
p53 Signaling	-		
p38 MAPK Signaling	1.71E00	3.42E-02	IL18, DUSP1, IL1RN, HSPB1
PPAR Signaling	7.03E-01	1.90E-02	IL18, IL1RN

Table S7. Biological functions modulated in blood pDCs upon BTV infection

Functions	p-Value	Z-score	Genes[1]	#
Blood pDCs				
Inflammatory response	1.57E-16	2.224	AIF1, ALOX5AP, APP, ATF3, C5AR1, CCL2, CCL4, CCR7, CD14, CD4, CDC42, CSF2RA, CXCL10, CXCR7, HYAL2, IFNG, IGHE, IL12RB1, IL8, ISG15, KLF4, LGALS1, LIPA, LTF, LYZ, NAD+, NFIL3, NT5E, NUPR1, PIGR, PTX3, RAB27A, RGS1, S100A4, S100A8, S100A9, SELPLG, SERPINA1, SLC11A1, SOCS3, STAT4, THBS1, TLR10, TNF, TNFAIP3	45
Permeability of vasculature	1.14E-05	2.200	CCL4, IFNG , LRP1, PTX3, THBS1, TNF	6
Chemotaxis of leucocytes	4.32E-11	2.418	AIF1, APP, C5AR1, CCL2, CCL4, CCR7, CD4, CDC42, CSF2RA, CXCL10, CXCR7, IFNG, IL12RB1, IL8, LGALS1, PIGR, RGS1, S100A4, S100A8, S100A9, SELPLG, SERPINA1, SOCS3, THBS1, TNF	25
Immune response of cells	5.27E-07	2.064	APP, CD14, CD4, CDC42, CTLA4, CXCL10, IFNG, IGHG1, ITGB1, LTF, PTX3, RRAS2, SELPLG, SLC11A1, THBS1, TNF, TNFRSF17, UBE2L6	18
Activation of antigen presenting cells	2.13E-09	3.241	APP, ATF3, BTK, CCL2, CCL4, CD4, CXCL10, IFNG, IL8, KLF4, LRP1, LTF, NFIL3, S100A9, SLC11A1, STAT4, THBS1, TNF	18
Cell survival	4.32E-13	1,189	ANG, APP, BHLHE40, BTK, CCL2, CCL4, CD4, CDH1, CDKN1C, CEBPD, CISH, CSF2RA, CTSB, CXCL10, CXCR7, DCK, DUSP5, EGLN3, EMILIN2, FGFR1, GADD45B, GCLC, GZMB, HSPA1A/HSPA1B, HSPB1, IFNG, IL8, INPP1, ITGB1, LRP1, LTF, MBD4, MEF2C, MX1, NAD+, NDRG1, NFAT5, NFIL3, NFKBIA, NUPR1, PLAC8, PPM1B, S100A4, SMAD6, SOCS2, SOCS3, STAT4, THBS1, TNF, TNFAIP3, TNFRSF13B, TNFRSF17, TNFSF13B, TRAF3, VCL	55
Killing of cells	3.08E-08	2.011	APP, CTLA4, CXCL10, GZMB, HSPA1A/HSPA1B, IFNG, IGHG1, ITGB1, LGALS1, LTF, NFAT5, NFKBIA, NUP43, TNF, TNFSF13B	15
Phagocytosis	3.44E-06	2,074	APP, CD14, CD4, CDC42, CXCL10, FCER2, IFNG, IGHG1, ITGB1, PTX3, RRAS2, SELPLG, SLC11A1, THBS1, TNF	15
Inhibition of virus	4.88E-07	2.581	CCL4, EIF2AK2, IFNG , LYZ, MX1, RNASE4, TNF	7
Lymph node pDCs				
Inflammatory response	4.22E-06	-1.778	ABCF1, ADAM8, B4GALT1, CCL4, CCL5, CCND1, CCR7, CD40, CD97, CDKN1A, CIITA, CXCR4, CXCR7, CYBB, FCGR2B, FOS, GADD45A, GSN, HSPD1, HYAL1, HYAL2, IER3, IL16, KDR, KLF4, LGALS1, LIPA, LYST, MIF, MPP1, NAD+, NCF1, NEDD9, NFIL3, NUP85, PDE4B, PRNP, PTGER4, PTGS2, PTPN2, RGS1, SERPINB1, SERPINE1, SLPI, SOCS3, SPP1, STAT4, TAC1, TGM2, TIAM1, TLR7, TNFAIP3, TP53, XBP1, ZP3	55
Chemotaxis of leukocytes	2.63E-04	-2.597	B4GALT1, CCL4, CCL5, CCND1, CCR7, CD40, CDKN1A, CXCR4, CXCR7, GSN, HSPD1, IL16, KDR, LGALS1, LYST, MPP1, NEDD9, NUP85, PDE4B, PRNP, RGS1, SERPINB1, SERPINE1, SLPI, SOCS3, SPP1, TAC1, TIAM1	28
Cell survival	4.15E-10	-1.183	ADK, ANTXR2, AURKB, BAMBI, BIRC5, BMP2, BRD2, BTK, CASP7, CCL4, CCL5, CCNA2, CCND1, CD2AP, CD40, CD82, CDK1, CDKN1A, CEACAM1, CEBPD, CISH, CLDN4, CLK2, COPB2, CXCR4, CXCR7, CYBB, DICER1, DUSP5, EIF2AK3, EMILIN2, FCER1A, FH, FOS, GADD45A, GADD45B, GALNT3, GCLC, GMFG, GZMB, HERPUD1, HHEX, HMGA1, HSP90AB1,	98

			HSPA5, HSPB1, HSPD1, ID2, IL2RG, ITGA5, JAG1, JUND, KDR, MED, MIF, MYBL2, MYC, NAD+, NDRG1, NDUFAF4, NEDD9, NFIL3, NGFRAP1, NR4A1, OGT, P4HB, PIK3R1, PIN1, PITX3, PKM, PLAGL1, PLK2, PPM1M, PRNP, PSMC5, PTGS2, RB1, RRM2, SEMA4D, SERPINB2, SERPINE1, SGPP1, SIRPA, SLC2A1, SLPI, SNRPA1, SOCS2, SOCS3, SOD1, SPP1, SQSTM1, STAT4, TGM2, TNFAIP3, TNFRSF13B, TP53, XBP1, XRCC2	
Lymph nodes cDCs				
Inflammatory response	2.24E-06	-2.049	ABCF1, ADA, ALOX5AP, AMICA1, ANGPT1, CALCA, CD200, CD97, CXCL10, CXCL5, CXCR4, FCGR2B, FGF2, FLOT1, GNAS, GSN, HCK, HSPD1, IDO1, IL1B, IL4R, IL8, KLF4, LGALS1, LYST, MAP2K1, MAPK14, MYD88, NEDD9, NMI, NUPR1, PDE4B, PLA2G2A, PON2, PPARG, PTGS2, RIPK3, S100A4, S1PR3, SBNO2, SERPINB1, SERPINE1, SGMS1, STAT4, TGM2, VEGFA	46
Chemotaxis of leucocytes	5.51E-06	-2.165	AMICA1, ANGPT1, CALCA, CXCL10, CXCL5, CXCR4, FLOT1, GNAS, GSN, HCK, HSPD1, IL1B, IL4R, IL8, LGALS1, LYST, MAPK14, MYD88, NEDD9, PDE4B, PON2, PPARG, S100A4, S1PR3, SERPINB1, SERPINE1, VEGFA	27
Shock response	1.92E-06	-2.55	CALCA, CEACAM8, CLIC4, ENPP2, FAS, GUCY1B3, HCK, IL1B, IRF4, MYD88, PDE4B, PDE4D, PRDX2, PTGS2, S1PR3, SERPINE1, TGM2	17
Immune response of cells	3.23E-04	-0.832	CD200, CNN2, CXCL10, FAS, FCGR2B, GSN, HCK, IRF2, IRF8, MAPK14, MERTK, MRC1, MYC, MYD88, PPARG, PRDM1, PXN, SERPINE1, TCIRG1, TGM2	20
Binding of lipids	2.24E-04	2.23	ANXA2, DNAJB1, FAS, FKBP4, FKBP5, HSP90AB1, IL8, PTGES3, STIP1	9
Activation of antigen presenting cells	5.07E-07	-0.442	ANGPT1, CD200, CTSH, CXCL10, FAS, HCK, HSPD1, IL1B, IL4R, IL8, IRF4, KLF4, LRP1, MAP2K1, MERTK, MYD88, PLA2G2A, PSMB9, PTGS2, SBNO2, STAT4, VEGFA	22
Cell survival	2.73E-09	-0.448	ABCG2, ACVR2B, ANGPT1, ANTXR2, AQP3, ASAH1, BAMBI, BANF1, BCAP31, BHLHE40, CCNI, CD3E, CEBPD, CLDN4, CLK2, CTSB, CXCL10, CXCR4, DUSP5, EGR3, EIF4E, ERBB3, EZR, FAS, FGF2, FKBP5, HCK, HDAC1, HERPUD1, HMGN1, HSP90AB1, HSPB1, HSPD1, ID4, IGF2, IL1B, IL27, IL2RG, IL4R, IL8, JAG1, KLF5, LMNA, LRP1, MAP2K1, MAPK14, MTA3, MYC, MYD88, NDRG1, NEDD9, NGFRAP1, NR4A1, NUPR1, PARP14, PLA2G2A, PPARG, PPP1CC, PPP1R16B, PPP3CA, PSMC4, PTGS2, RIPK1, S100A4, S1PR3, SEMA4D, SERPINE1, SLC2A1, SPARC, STAT2, STAT4, TCF7, TGM2, TYK2, UNG, VEGFA, XDH, XPO1	78
Killing of cells	6.58E-05	1.723	ADM, CALCA, CTSD, CXCL10, FAS, FGF2, LGALS1, MAPK14, MGEA5, MYD88, NR4A1, PLA2G2A, PPARG, SLAMF1, SLAMF7	15
Inhibition of virus	4.97E-04	1.075	BST2, EIF2AK2, IL27, PTMA, RNASE4, TRIM5	6
Spleen cDCs				
Cell survival	7,53E-09	-2.279	BAMBI, BCL2L11, BMP7, CASP7, CCL5, CD19, CD22, CD3E, CD79A, CD82, CD9, CDKN2D, CSF1R, CXCL10, DUSP1, DUSP5, FCER1A, FLNA, GNB2L1, HSPB1, IGF2, IL18, IL27, IL8, LCK, MBP, MGMT, MX1, NR4A1, PARP14, SEMA4D, SOCS3, TCF7, TIE1, UNG, XDH, XPO1	37
Killing of cells	9,44E-06	0.796	BCL2L11, CASP7, CXCL10, ETS1, IGHG1, IL18, MBP, MGMT, NR4A1, SLAMF7	10
Inhibition of virus	3,61E-04	0.957	CCL5, EIF2AK2, IL27, MX1	4

[1] The downmodulated genes are underlined. The unmarked genes are upregulated.

Table S8. Predicted upstream regulators modulated in DCs upon BTV infection

Upstream regulators	**Z-score**	**p-Value**	**Genes**
Blood pDCs			
C5	2,428	2,23E-07	ATF3,C5AR1,CCL2,CCL4,IL8,ITGB1,NFKBIA,SOCS3,TNF,TNFAIP3
CCL5	2,400	9,29E-05	C5AR1,CCL2,CCL4,IFNG,IL8,TNF
CCL13	2,610	4,92E-06	CCL4,CD14,CTSB,CXCL10,IFNG,KLF4,TNF
CXCL2	0	3,20E-04	CCL4,CXCL10,TNF
CSF2	3,278	2,71E-07	ALOX5AP,C5AR1,CCL2,CCL4,CCR7,CD14,CD83,CISH,CSF2RA,CTLA4,CXCL10,HSPH1,IFNG,IL8,NFKBIA,SOCS2,SOCS3,TNF
IFNG	3,278	2,71E-07	ALOX5AP,C5AR1,CCL2,CCL4,CCR7,CD14,CD83,CISH,CSF2RA,CTLA4,CXCL10,HSPH1,IFNG,IL8,NFKBIA,SOCS2,SOCS3,TNF
IFNA	3,278	2,71E-07	ALOX5AP,C5AR1,CCL2,CCL4,CCR7,CD14,CD83,CISH,CSF2RA,CTLA4,CXCL10,HSPH1,IFNG,IL8,NFKBIA,SOCS2,SOCS3,TNF
IFNB1	2,060	1,96E-10	BHLHE40,CCL2,CCL4,CD14,CD83,CXCL10,EIF2AK2,IFNG,IL8,ISG15,MX1,RNASE4,RSAD2,STAT4,THBS1,TNF,VCL,XIST
IL1A	3,160	1,08E-09	APP,CCL2,CCL4,CD83,CXCL10,FGFR1,GBP1,IL8,ITGB1,NFKBIA,PTX3,S100A12,S100A8,S100A9,TNF,TNFAIP3
IL1B	5,018	6,39E-19	AIF1,APP,ATF3,CCL2,CCL4,CCR7,CD14,CD83,CDKN1C,CEBPD,CISH,CTSB,CXCL10,DDIT4,DUSP5,ENPP2,F13A1,FCER2,GADD45B,GBP1,GCLC,HSPA1A/HSPA1B,HSPB1,IFNG,IL8,ISG15,ITGB1,MT2A,MX1,NFIL3,NFKBIA,PIGR,PTX3,RSAD2,S100A8,S100A9,SOCS2,SOCS3,STAT4,THBS1,TNF,TNFAIP3,UBE2L6
IL3	1,843	8,63E-07	CCL2,CD14,CD83,CISH,CTLA4,EIF2AK2,FCER2,FGFR1,GADD45B,GZMB,IL8,PLCB2,SOCS3,STAT4,TNF
IL6	3,695	2,28E-11	ANG,APP,ATF3,C5AR1,CCL2,CCL4,CCR7,CD14,CD83,CEBPD,CISH,CXCL10,GADD45B,GZMB,HLA-DRB1,IFNG,IL8,LTF,S100A9,SERPINA1,SOCS2,SOCS3,STAT4,THBS1,TNF,TNFRSF17,TRAF3
IL12B	3,385	6,65E-13	CEBPD,CXCL10,DUSP5,GZMB,IFNG,IL8,S100A8,S100A9,SELPLG,SOCS3,STAT4,TNF
IL15	2,326	1,63E-08	BRK1,CCL2,CCL4,CD5,CD83,CISH,CXCR6,DUSP5,FYB,GZMB,IFNG,IL8,ITGB1,MX1,NFKBIA,SELPLG,SOCS2,TNF,TNFRSF17
IL17A	2,590	5,92E-05	CCL2,CCL4,CEBPD,IFNG,IL8,ISG15,S100A8,SOCS3,TNF
IL18	2,802	1,66E-07	CCL2,CCL4,CCR7,CD83,CXCL10,GADD45B,GZMB,IFNG,IL12RB1,IL8,TNF

IL23A	2,140	2,77E-05	CXCL10,IFNG,S100A8,S100A9,TNF
IL27	2,373	1,43E-06	CEBPD,CTLA4,CXCL10,GZMB,IFNG,MX1,SOCS3,TNF,TNFSF13B
TGFB1	0,812	2,35E-16	AHNAK,ALOX5AP,ANXA2,APP,ASUN,BHLHE40,BIN1,CCL2,CCL4,CCR7,CD14,CD83,CDH1,CDKN1C,CRIP2,CTLA4,CTSB,CXCL10,CXCR6,DDIT4,F13A1,FXYD6,GADD45B,GBP1,GCLC,GNS,GZMB,HLA-DRB1,HSPA1A/HSPA1B,HSPB1,IFNG,IL8,ITGB1,KLF4,MEF2C,MS4A8B,MYOF,NFKBIA,NT5E,NUPR1,PLOD1,PTX3,RSAD2,S100A4,SERPINA1,SHISA5,SMAD6,SMC4,SNTB2,SOCS3,SPEG,SPRY1,THBS1,TNF,TNFAIP3,TNFSF13B,VCL
TNF	3,157	7,83E-18	ALOX5AP,APP,ATF3,BHLHE40,C5AR1,CCL2,CCL4,CCR7,CD14,CD4,CD5,CD83,CDC42,CEBPD,CFB,CHST2,CISH,CTLA4,CTSB,CXCL10,CXCR7,DUSP5,ENPP2,FCER2,FCGRT,FGFR1,FUT3,GADD45B,GBP1,GLS,HSPA1A/HSPA1B,IFNG,IL8,ISG15,ITGB1,KLF4,MT1A,MX1,NFKBIA,PIGR,PLA2G16,PRSS23,PTX3,RGS1,RGS2,RNASE4,S100A8,S100A9,SELPLG,SOCS3,STAT4,THBS1,TNF,TNFAIP3,TNFSF13B,TRAF3,UBE2H,VCL
TNFSF10	2,425	1,74E-05	CD14,EIF2AK2,IFNG,IL8,ISG15,TNF,TNFAIP3
TNFSF13		7,22E-03	IGHA1,IGHE,IGHG1
TNFSF12	2,843	1,07E-07	CCL2,CSF2RA,CXCL10,IL8,NFKBIA,PTX3,S100A8,S100A9,TNF
leukotriene D4	2,744	4,57E-08	ATF3,CCL2,CCL4,IL8,KLF4,NDRG1,RGS2,TNF
prostaglandin E1		1,46E-02	CD14,IFNG
NOS2	1,718	6,61E-06	APP,CCL2,CCL4,CD14,COX7A1,IFNG,IGHG1,ISG15,NFKBIA,PIGR,TNF
Lymph node pDCs			
C5	-1,303	1,42E-02	CCL4,CCL5,CCND1,CYBB,FCGR2B,SERPINE1,SOCS3,TNFAIP3
CCL5	-0,705	0,000183	CCL4,CCL5,CD40,CD97,FOS,HMGA1,SERPINB2,SOD1,SQLE
CCL13	-1,231	3,93E-02	CCL4,CCL5,KDR,KLF4,SDC4
CXCL12	0,280	6,21E-03	CD82,CXCR4,CXCR6,FOS,HCLS1,JMJD1C,MSH6,NR4A1,PTGS2,SOCS3,TP53
CSF2	2,852	1,57E-	ADAM8,BIRC5,BSG,CCL4,CCNA2,CCND1,CCR7,CD40,CD83,CD97,CDC20,CDCA3,CDCA5,CDK1,CDKN1A,CEACAM1,CIITA,CISH,CTSC,CXCR4,CYBB,FCGR2B,FOS,HSPH1,ID2,IER3,IL16,IL32,IRF2,IRF5,LAMP2,MCM3,MYC,NCAPH,PRC1,PTGER4,PTGS2,RB1,RB

		17	M3,RRM2,SKA1,SOCS2,SOCS3,TGM2,TP53,TPM4,TRIP13,UBE2C,XBP1
IFNG	2,406	3,50E-15	ARG2,BTG1,CASP7,CCL4,CCL5,CCNA2,CCND1,CD2,CD40,CD83,CDKN1A,CEACAM1,CEBPD,CHST3,CIITA,CISH,CTSC,CTSH,CTSZ,CXCR4,CYBB,DDX5,DUSP5,EIF2AK2,FBP1,FCER2,FCGR2B,FOS,GFM1,GLUL,GZMB,HLA-B,HLA-C,HLA-DRB1,HMGCR,HSP90AB1,HSPB1,HSPD1,IER3,IFITM1,IFITM3,IL18BP,IL32,IRF2,IRF5,ITGA5,JAG1,KDR,KLF10,KLF4,KYNU,LDHA,MIF,MX2,MYC,NEDD9,NLRC5,NUP98,PHACTR1,PRNP,PSMB8,PTGS2,RB1,RTP4,RUNX2,SAMHD1,SDC4,SIRPA,SLC29A1,SLC2A1,SLPI,SNAP25,SOCS2,SOCS3,SP100,SPP1,SQLE,STAT4,STX11,TAC1,THEMIS2,TLR7,TP53,UBE2L6,WARS,XIST
IFNA2	2,309	1,26E-09	BIRC5,CDKN1A,CEACAM1,CISH,EIF2AK2,GEM,GZMB,HLA-B,HLA-C,IFITM1,IFITM3,IRF5,LY6E,MT2A,MYC,SOCS2,SOCS3,SP100,STAT4,THEMIS2,TP53,UBE2L6,XAF1
IFNB1	1,101	4,48E-04	CCL4,CCL5,CD40,CD83,CDKN1A,DICER1,EIF2AK2,FOS,GZMH,HMGCR,IFITM1,MYC,PTGS2,SERPINB2,SQLE,STAT4,TLR7,XIST
IL1A	-1,704	4,19E-03	CCL4,CCL5,CD40,CD83,FOS,IL32,ITGA5,LDHA,MYC,PTGS2,SERPINE1,SPP1,TAC1,TNFAIP3
IL1B	-0,951	1,78E-11	ADAM8,BMP2,BTG2,CCL4,CCL5,CCR7,CD40,CD82,CD83,CDKN1A,CEBPD,CISH,CTSZ,CXCR4,CYBB,DDX5,DUSP5,ERRFI1,FCER2,FCGR2B,FOS,GADD45A,GADD45B,GCLC,GEM,HLA-B,HLA-C,HSPB1,IER3,IFRD1,IL16,IL32,ITGA5,KDR,KLF10,LDHA,MIF,MT2A,MYC,NCOA2,NFIL3,NR4A1,P4HB,PDE4B,PSMB8,PTGS2,RUNX2,SDC4,SERPINB2,SERPINE1,SLC2A1,SNAP25,SOCS2,SOCS3,SPP1,STAT4,TAC1,TGM2,TNFAIP3,UBE2L6
Il3	-0,714	7,77E-03	CDKN1A,CISH,FOS,MYC,NFIL3,TP53
IL6	-1,544	9,71E-10	BIRC5,BTG2,CASP7,CCL4,CCNA2,CCND1,CCR7,CD40,CD83,CD97,CDK1,CDKN1A,CEBPD,CIITA,CISH,CTSC,CXCR4,FOS,GADD45A,GADD45B,GZMB,HLA-C,HLA-DRB1,HSPA5,IFITM3,KDR,MYC,NUCB2,PRNP,PSMB8,PTGER4,PTGS2,RB1,SERPINE1,SNAI1,SOCS2,SOCS3,SPP1,SRSF5,STAT4,TAC1,TGM2,WARS,XBP1
IL12B	0,056	6,47E-03	CCL5,CEBPD,DUSP5,GZMB,SOCS3,STAT4
IL15	1,002	1,70E-07	BAMBI,BTG1,CCL4,CCL5,CD2,CD40,CD83,CEACAM1,CISH,CKS2,COPB2,CXCR4,CXCR6,DUSP11,DUSP5,GARS,GZMB,HNRNPA2B1,HSPE1,IFITM1,IL2RG,IL32,MIF,MYC,PA2G4,PDE4B,PSAP,PSMB8,SOCS2,SP100,XBP1
IL17	0		
IL18	0,174	1,79E-03	BSG,CCL4,CCL5,CCR7,CD40,CD83,GADD45B,GZMB,IL18BP,IL32,PTGS2
IL23	0		

IL27	2,184	3,17E-03	CEBPD,CIITA,FOS,GZMB,HLA-B,HLA-C,MYC,PTGS2,SOCS3
TGFB1	-2,685	1,77E-15	ABCF1,ACAA2,ACSL3,ADK,ASNS,BAMBI,BNIP3L,BSG,BTG1,CCL4,CCL5,CCNA2,CCND1,CCR7,CD40,CD83,CDK1,CDKN1A,CEACAM1,CHST3,CIITA,CLDN4,CLK2,CTSC,CTSH,CXCR4,CXCR6,CYBB,DDX5,FCER1A,FNDC3B,FOS,FOSL2,FXYD6,GADD45A,GADD45B,GARS,GCLC,GEM,GSN,GZMB,HLA-DRB1,HMGA1,HSPA5,HSPB1,ID2,IER3,IFRD1,ITGA5,JAG1,JUND,KDR,KLF10,KLF4,LDHA,LITAF,MSH6,MYBL2,MYC,MYL6,MYOF,NCF1,NCOA3,NEDD9,NR4A1,NUCB2,PA2G4,PDHB,PLAGL1,PLK2,PLOD1,PLXNC1,PSPH,PTGER4,PTGS2,RB1,RBM3,RGCC,RUNX2,RYBP,SAMHD1,SDC4,SELENBP1,SERPINB1,SERPINB2,SERPINE1,SERTAD1,SHISA5,SIRPA,SLC2A1,SLC2A3,SLC7A1,SNAI1,SOCS3,SPEG,SPP1,SRSF5,STK17A,STOML2,TGM2,TNFAIP3,TP53,TPM1,TUBA1A,XBP1,ZFP36L2
TNF	-0,950	1,43E-12	ADAM8,B4GALT1,BIRC5,BMP2,BTG1,BTG2,CASP7,CCL4,CCL5,CCND1,CCR7,CD40,CD82,CD83,CDC42EP5,CDKN1A,CEBPD,CIITA,CISH,CTSC,CTSZ,CXCR4,CXCR7,CYBB,DDX5,DENND4A,DUSP5,EXOSC7,FCER2,FCGR2B,FOS,GADD45A,GADD45B,GOSR2,HERC1,HLA-B,HLA-C,HMGCR,HSP90AB1,HSPD1,IER3,IL16,IL18BP,IL32,IRF5,ITGA5,JAG1,JUND,KDR,KLF10,KLF4,KYNU,LDHA,LITAF,MAN1C1,MCM3,MIF,MT1A,MYC,MYL6,NCF1,NCOA2,NEDD9,NPM3,NR4A1,NUCB2,NUP98,P4HB,PDE4B,PLK2,PSMB8,PTGS2,RAB32,RGS1,RGS2,RRM2,RUNX2,SDC4,SERPINB1,SERPINB2,SERPINE1,SLC2A1,SLC7A1,SLPI,SOCS3,SOD1,SPP1,SQLE,SQSTM1,STAT4,TAC1,TGM2,TLR7,TNFAIP3,TP53,UCP2
TNFSF10	-0,077	8,12E-05	BIRC5,CXCR4,EIF2AK2,FOS,HLA-C,IFITM1,PTGS2,SP100,TNFAIP3,TP53
TNFSF13B	-1,188	4,28E-02	CCL4,FCGR2B,MYC,TP53
TNFSF12	0		
leukotriene D4	-2,543	1,35E-06	BMP2,CCL4,FOSL2,GEM,KLF4,NDRG1,NEDD9,NR4A1,PTGS2,RGS2
prostaglandin E2	-2,509	4,05E-09	BIRC5,BTG1,CASP7,CCL4,CCL5,CCND1,CCR7,CD40,CD83,CEBPD,CHGA,CXCR4,FOS,FOSL2,GZMB,IL16,IL2RG,ITGA5,MYC,NFIL3,PTGER4,PTGS2,RGS2,RUNX2,SOCS2,SOCS3,UCP2
NOS2	0		
Lymph node cDCs			
C5	-2,404	3,19E-02	FCGR2B,IL1B,IL27,IL8,SERPINE1,VEGFA
CCL5	-2,219	1,82E-02	CD97,IL1B,IL8,NAMPT,SQLE
CCL13	-0,394	1,31E-02	CTSB,CXCL10,IL1B,KLF4,PPARG

CXCL12	0		
CSF2	-0,386	2,67E-05	ADA,ALOX5AP,CD97,CXCL10,CXCR4,DOK2,EGR3,FAS,FCGR2B,HSPH1,IDO1,IL1B,IL8,IRF2,IRF4,LAMP2,LCP1,MRC1,MYC,PPARG,PTGS2,RBM3,TGM2
IFNG	2,692	3,41E-19	ADM,ALOX5AP,ARG2,ARPP19,BIRC2,BST2,CALCA,CASP5,CD200,CEBPD,CLIC4,CTSB,CTSD,CTSH,CTSZ,CXCL10,CXCR4,CYB5A,DDX5,DUSP5,EBI3,EGR3,EIF2AK2,FAS,FCGR2B,FGF2,FGL2,FKBP5,GCHFR,HLA-A,HSP90AB1,HSPB1,HSPD1,IDO1,IGFBP4,IL1B,IL27,IL4R,IL8,IRF2,IRF4,IRF8,JAG1,KLF4,KYNU,MAP2K1,MAPK14,MRC1,MX2,MYC,MYD88,NAMPT,NEDD9,NLRC5,NMI,NUPR1,PHACTR1,PLA2G2A,PPARG,PRDM1,PRDX2,PSMB9,PTGS2,RIPK1,RTP4,S100A10,S1PR3,SERPINH1,SLAMF1,SLC2A1,SMAGP,SNAP25,SQLE,STAT2,STAT4,TRIM8,VEGFA,WARS,XIST
IFNA2	2,688	1,50E-03	BST2,CXCL10,EIF2AK2,FAS,FGF2,HLA-A,IL1B,MT2A,MYC,STAT4,XAF1
IFNB1	3,286	1,72E-07	BHLHE40,BST2,CXCL10,DKK3,EIF2AK2,FGF2,IDO1,IL1B,IL27,IL8,IP6K2,MYC,MYD88,NMI,PDK4,PTGS2,RNASE4,SQLE,STAT2,STAT4,XIST
IL1A	-1,448	2,70E-03	BIRC2,CXCL10,CXCL5,FAS,FGF2,IL1B,IL8,MYC,PPARG,PTGS2,SERPINE1,SPARC
IL1B	-1,270	6,23E-12	ABCG2,ADM,ANGPT1,BIRC2,BTG2,CALCA,CEBPD,CTSB,CTSZ,CXCL10,CXCL5,CXCR4,DDX5,DUSP5,EBI3,EIF4E,ENPP2,EPAS1,FAS,FCGR2B,FGF2,FKBP5,GCHFR,HSPB1,ID3,IGFBP4,IL1B,IL27,IL8,KIF15,LCP1,MAPK14,MT2A,MYC,NAMPT,NR4A1,PDE4B,PLA2G2A,PPARG,PSMB9,PTGS2,S100A10,SERPINE1,SLAMF1,SLC2A1,SNAP25,SPARC,STAT4,TGM2,UGDH,VEGFA
IL3	-2,622	6,43E-08	ADA,BNIP3L,CD97,CITED2,DOK2,EGR3,EIF2AK2,FAS,FCGR2B,FOSL2,IL1B,IL8,MYC,PFKL,PLCB2,PSMC4,RBM3,RPL6,SLC2A1,STAT4,TIAL1,TYK2,VEGFA,YPEL3
IL6	-0,827	1,25E-07	ABCC5,ABCG2,BST2,BTG2,CALCA,CD97,CEBPD,CES1,CXCL10,CXCL5,CXCR4,FAS,IDO1,IGF2,IGFBP4,IL8,IRF4,LCAT,MERTK,MYC,MYD88,NAMPT,PLA2G2A,PPARG,PSMB9,PTGS2,SERPINE1,SRSF5,STAT4,TGM2,TYK2,VEGFA,WARS
IL12B	-0,388	2,45E-04	CEBPD,CXCL10,DUSP5,IL1B,IL8,STAT2,STAT4
IL15	-0,569	7,49E-05	AQP3,BAMBI,CD5,CXCR4,DUSP5,FAS,GAPDH,GNAS,HSPE1,ID4,IL2RG,IL8,MYC,MYD88,NAGA,PDE4B,PSMB9,PYGL,RAB8A,TCF7,TRIM5
IL17A	-1,059	2,70E-02	CEBPD,CXCL5,FAS,IL1B,IL8,JAG1,PTGS2,VEGFA
IL18	-0,363	2,69E-02	CXCL10,FAS,IDO1,IL1B,IL8,PTGS2,VEGFA
IL23	0		
IL27	1,457	7,43E-03	CEBPD,CXCL10,HLA-A,IL1B,MYC,PTGS2,STAT2
TGFB1	-2,051	2,81E-15	ABCF1,ABCG2,ACTN1,ADM,ALOX5AP,ANGPT1,ANXA2,BAMBI,BHLHE40,BNIP3L,CALCA,CITED2,CLDN4,CLIC4,CLK2,CNN2,CPQ,CSRP2,CTSB,CTSD,CTSH,CXCL10,CXCR4,DDX5,DKK3,ECM1,EGR3,ESRP2,FAS,FGF2,FOSL2,GNAS,GSN,HEY1,HSPB1,ID3,ID4,IGF2,IGFBP4,IL1B,IL4R,IL8,JAG1,KLF4,LBR,LCAT,LSR,MAP2K1,MAPK14,MGEA5,MRC1,MYC,MYD88,NAMPT,NEDD9,NR4A1,NUPR1,PDE4D,PDLIM4,PLOD1,PPARG,PSPH,PTGS2,PXN,RAB9A,RBM3,RGCC,RYBP,S

			100A10,S100A4,S1PR3,SBNO2,SERPINB1,SERPINE1,SERPINH1,SHISA5,SLAMF1,SLC2A1,SLC7A1,SPARC,SPRY1,SRSF5,TGFBI,TGM2,UCK2,VEGFA,XDH
TNF	-1,338	5,63E-11	ABCG2,ADM,ALOX5AP,ANGPT1,AQP3,BCKDHB,BHLHE40,BIRC2,BST2,BTG2,CALCA,CD5,CEBPD,CITED2,CLIC4,CST7,CTSB,CTSZ,CXCL10,CXCL5,CXCR4,DDX5,DENND4A,DGAT1,DUSP5,EBI3,ENPP2,FADS1,FAS,FCGR2B,FGF2,HDAC1,HMGN3,HSP90AB1,HSPD1,IDO1,IGF2,IGFBP4,IL1B,IL4R,IL8,IRF4,IRF8,JAG1,KLF4,KLF5,KYNU,LCAT,MAPK14,MYC,MYD88,NAMPT,NEDD9,NR4A1,PDE4B,PLA2G2A,PPARG,PRDM1,PSMB9,PTGS2,RIPK1,RNASE4,S1PR3,SDC2,SERPINB1,SERPINE1,SLC2A1,SLC7A1,SPARC,SQLE,STAT4,SUPT4H1,TGM2,TYK2,VEGFA
TNFSF10	-0,555	2,84E-04	ANGPT1,BIRC2,CXCR4,EIF2AK2,HLA-A,IL8,PTGS2,VEGFA
TNFSF13B	-1,406	2,99E-03	FCGR2B,IL8,MYC,NAMPT,PRDM1
TNFSF12	0		
leukotriene D4	-2,559	9,47E-08	EGR3,FOSL2,IL8,KCNJ2,KLF4,NDRG1,NEDD9,NR4A1,PDK4,PTGS2
prostaglandin E2	-2,436	5,55E-07	ANGPT1,CEBPD,CST7,CXCL10,CXCR4,FAS,FOSL2,IDO1,IGFBP4,IL1B,IL27,IL2RG,IL8,IRF4,LMNA,MRC1,MYC,PPARG,PTGS2,VEGFA
NOS2	0,32	0,0262	CD3E,FAS,IL1B,PTGS2,SERPINH1,TCF7,TNNT3,TOR3A,VEGFA
Spleen cDCs			
C5	-1,384	1,39E-03	CCL5,CXCL2,IL27,IL8,SOCS3
CCL5	-2,173	0,000181	CCL5,CXCL2,DUSP1,IL8,PPIF
CCL13	-1,481	8,72E-06	CCL5,CXCL10,CXCL2,ETS1,KLF4,TIE1
Cxcl12	-2,236	2,34E-07	CCL5,CD69,CD9,RUNX2,VIM,ZBTB16
CSF2	-1,043	2,33E-04	BCL2L11,CD69,CSF1R,CXCL10,IDO1,IL1RN,IL8,IRF4,PPIF,SOCS3,TCF4
IFNG	1,705	5,03E-11	BCL2L11,CASP7,CCL5,CSF1R,CXCL10,CXCL2,DUSP1,DUSP5,EIF2AK2,FGL2,FOSB,GNB2L1,HSPB1,IDO1,IGHG1,IL18,IL1RN,IL27,IL8,IRF4,ISG15,KLF4,MX1,MX2,NCALD,NOTCH3,RHOB,RTP4,RUNX2,SERPINH1,SMAGP,SOCS3,XIST
IFNA2	2,688	1,50E-03	BST2,CXCL10,EIF2AK2,FAS,FGF2,HLA-A,IL1B,MT2A,MYC,STAT4,XAF1
IFNB1	2,162	3,36E-06	CCL5,CXCL10,CXCL2,EIF2AK2,GAS1,IDO1,IL27,IL8,ISG15,MX1,XIST
IL1A	-1,597	5,69E-03	CCL5,CXCL10,CXCL2,IL18,IL1RN,IL8
IL1B	-1,126	3,25E-08	CCL5,CD82,CXCL10,CXCL2,DDIT4,DUSP1,DUSP5,FOSB,HERC5,HSPB1,ID3,IL18,IL1RN,IL27,IL8,ISG15,MT2A,MX1,NR4A1,RHOB,RUNX2,SOCS3,VIM
IL3	-2,251	3,40E-06	BCL2L11,CD247,CD3D,CD3G,CD69,CSF1R,EIF2AK2,EMP3,FCER1A,IL8,PLCB2,SOCS3
IL6	-1,502	6,24E-05	BCL2L11,CASP7,CD79A,CDKN2D,CXCL10,CXCL2,DUSP1,IDO1,IGF2,IL1RN,IL8,IRF4,SOCS3,VIM
IL12B	-0,577	4,57E-06	CCL5,CDKN2D,CXCL10,DUSP5,IL8,SOCS3
IL15	-2,069	4,96E-06	BAMBI,BCL2L11,CCL5,CD69,CXCL2,DUSP5,ETS1,GAPDH,HSPE1,IL8,LCK,MX1,TCF7

IL17A	-0,782	7,87E-03	CCL5,CXCL2,IL8,ISG15,SOCS3
IL18	0,303	6,70E-05	BCL2L11,CCL5,CD69,CXCL10,IDO1,IL18,IL8
IL23		1,83E-02	IL8,IRF4
IL27	2,205	1,10E-03	CXCL10,IL18,MX1,SOCS3,VIM
TGFB1	-0,671	2,04E-10	AHNAK,BAMBI,BCL2L11,CALD1,CCL5,CD69,CSF1R,CXCL10,CXCL2,DDIT4,DNAJB6,DUSP1,ETS1,FCER1A,FLNA,FOSB,GAS1,GNB2L1,HSPB1,ID3,IGF2,IL18,IL1RN,IL8,KLF4,MGMT,NOTCH3,NR4A1,PDLIM4,RGCC,RHOB,RUNX2,SCD,SERPINH1,SOCS3,SPEG,VIM,XDH
TNF	0,362	3,54E-09	BCL2L11,CASP7,CCL5,CD247,CD69,CD82,CSF1R,CXCL10,CXCL2,DUSP1,DUSP5,ERG,ETS1,FOSB,HERC5,IDO1,IGF2,IL18,IL1RN,IL8,IRF4,ISG15,KLF4,MBP,MGMT,MX1,NR4A1,PLA2G16,PPIF,RUNX2,SCD,SLC27A5,SOCS3,TIE1,VIM
TNFSF10	-0,152	2,98E-04	BCL2L11,EIF2AK2,IL1RN,IL8,ISG15
TNFSF13		7,22E-03	IGHA1,IGHE,IGHG1
TNFSF12	-0,711	2,65E-03	CCL5,CXCL10,CXCL2,IL8
leukotriene D4	-2,183	3,56E-05	CXCL2,DUSP1,IL8,KLF4,NR4A1
prostaglandin E2	-0,714	3,91E-07	CASP7,CCL5,CD69,CXCL10,ETS1,IDO1,IGHG1,IL27,IL8,IRF4,RUNX2,SOCS3
NOS2	2,135	1,09E-04	CD3E,CXCL2,IGHG1,IL1RN,ISG15,LCK,SERPINH1,TCF7