

## Supplemental Figure Legends:

**Supplemental Figure 1:** a) FACS plots showing how populations were defined, gated, and sorted for experiments. KSL: Lin<sup>-</sup> cKit<sup>hi</sup> Sca1<sup>+</sup>; CDP: Lin<sup>-</sup>, CD11c<sup>-</sup>, cKit<sup>lo</sup>, FcγRII/III<sup>-</sup>, Flt3<sup>+</sup>, CD115<sup>+</sup>; cDC: CD19<sup>-</sup>, CD3<sup>-</sup>, NK<sup>-</sup>, CD11c<sup>+</sup> CD45RA<sup>-</sup>; pDC: CD19<sup>-</sup>, CD3<sup>-</sup>, NK<sup>-</sup>, CD11c<sup>lo</sup>, CD45RA<sup>+</sup>; CMP: Lin<sup>-</sup> cKit<sup>hi</sup>, Sca1<sup>-</sup>, CD34<sup>+</sup>, FcγRII/III<sup>lo/-</sup>; GMP: Lin<sup>-</sup> cKit<sup>hi</sup>, Sca1<sup>-</sup>, CD34<sup>+</sup>, FcγRII/III<sup>hi</sup>; Myeloid/monocytes: CD19<sup>-</sup>, Mac1<sup>+</sup>, Gr1<sup>+</sup>; B lineage: Mac1<sup>-</sup>, CD3<sup>-</sup>, CD19<sup>+</sup>, CD45RA<sup>+</sup>. Splenic DC stained negative for other lineage markers (CD3, CD19 and NK<sup>-</sup>) but positive for expression of CD11c (as DCs express CD11c<sup>+</sup>), MHCII (for cDCs) and B220<sup>+</sup> and/or PDCA-1<sup>+</sup> (for pDC).

b) CD19<sup>+</sup> B lineage cells, CD11c<sup>+</sup> DC, and Mac1<sup>+</sup> Gr-1<sup>+</sup> monocytes were sorted from pooled spleens of B6 control mice. 10<sup>5</sup> cells were double sorted from each population and used for Western blot analysis to determine C/EBP $\alpha$  expression (top panel) as compared to HSP-90 (control, bottom panel).

c) Immunofluorescence of sorted cell populations. 2x10<sup>5</sup> cells were used to generate cytopins. These slides were then fixed and stained for C/EBP $\alpha$  and DAPI from normal 8 week old mice (magnification, 1000). B cells were sorted as a negative control, whereas, monocytes are known to express C/EBP $\alpha$ .

d) Immunofluorescence of cultured cell populations. 1x10<sup>6</sup> cells were used to generate cultures for 7 days. Cell were placed onto slides and were then fixed and stained for CD11c, CD11b or CD8 and DAPI (magnification, 1000).

e) FACS plots showing cDC and pDC from cultures at Day 7 from control or C/EBP $\alpha$  floxed whole bone marrow.

**Supplemental Figure 2:** Analysis of mice following deletion of C/EBP $\alpha$ .

a) qRT-PCR showing loss of C/EBP $\alpha$  RNA in total lysed bone marrow 14 days after poly(IC) injection of MxCre<sup>-</sup> or MxCre<sup>+</sup> C/EBP $\alpha$  floxed/floxed mice. The excision of C/EBP $\alpha$  was further confirmed by the loss of C/EBP $\alpha$  expression measured by quantitative RT-PCR. Following DNase treatment, RNA expression was assessed for C/EBP $\alpha$  and normalized to the housekeeping gene beta2-microglobulin using Taqman RT-PCR. Data are the mean  $\pm$  SD of four experiments.

b) Bone marrow KSL (cKithi Sca1<sup>+</sup> Lin<sup>-</sup>), CDP (Lin<sup>-</sup>, CD11c<sup>-</sup>, FcγRII/III<sup>-</sup>, cKit<sup>+</sup>, Flt3<sup>+</sup>, CD115<sup>+</sup>), or splenic myeloid cells (Gr1<sup>+</sup>, Mac1<sup>+</sup>) were gated from viable cells from MxCre-C/EBP $\alpha$ fl/fl or MxCre<sup>+</sup>C/EBP $\alpha$ fl/fl poly(IC) treated mice 14 days after the last of three injections.

c) Viable cells from poly(IC) treated MxCre<sup>-</sup> or MxCre<sup>+</sup> C/EBP $\alpha$ fl/fl mice 14 days after the last injection, dot plots show lack of MSCFR (CD115) expression and SSC-A high cells in C/EBP $\alpha$ fl/fl marrow cells.

**Supplemental Figure 3:** Deletion of C/EBP $\alpha$  in late stages of DC differentiation.

a) Sorted DC from control (lanes 2, 3 and 5, 6) or CD11c-Cre x C/EBP $\alpha$ fl/fl (lanes 4, 5 and 8, 9) spleen were tested for excision of C/EBP $\alpha$  by PCR as described earlier. The ladder (far left) is 100bp with darker bands at 500bp and 1000bp and excised band should be present at ~400bp.

b) Absolute numbers of cDCs pDCs were calculated from percentages of the cell populations defined as in (A, left panels) from total bone marrow, splenocytes, thymocytes and lymphnodes. The numbers of cDC represent mean  $\pm$  SD from three independent experiments with three mice per group.

c) CD11c-Cre<sup>+</sup> x CEBP $\alpha$ /fl/fl and CEBP $\alpha$ /fl/fl mice were analyzed for the ability of DC to uptake antigen in vivo. Mice were injected i.p. with green fluorescent labeled 0.5-um latex beads and sacrificed after 16 hours. DC (CD19/B220<sup>-</sup>, CD3<sup>-</sup>, NK<sup>-</sup>, CD11c<sup>+</sup>) cells were analyzed for fluorescence distribution due to bead uptake. CEBP $\alpha$ /fl/fl splenic DC had 18 $\pm$ 5% fluorescence due to beads as compared to 22 $\pm$ 4% in the CD11c-Cre<sup>+</sup> x CEBP $\alpha$ /fl/fl splenic DC. Data representative of 2 experiments each with 3 mice per group.

d) Analysis of RNA from cDC of CD11c-Cre<sup>+</sup> C/EBP $\alpha$ /fl/fl and C/EBP $\alpha$ /fl/fl spleens was conducted using SABiosciences murine dendritic cell specific array. These populations were double sorted from CD11c-Cre<sup>+</sup> and control mice and RNA was isolated following DNase treatment. The array plate is pre-coated with primers for DC specific transcripts. The plot shows the distribution of RNA detected compared to control. C/EBP $\alpha$  is highlighted by a red circle, confirming that it is indeed excised in the CD11c-Cre<sup>+</sup> system and differs greatly in expression compared with control DC. A list of other significant genes that are decreased as well as increased can be seen listed to the right.

**Supplemental Figure 4:** Expression of PU.1 does not rescue DC differentiation from C/EBP $\alpha$  deficient KSL.

a) Expression of C/EBP $\alpha$ , C/EBP $\beta$ , PU.1, IRF4, IRF8, Id2 by relative quantitative real-time RT-PCR of RNA from sorted KSL (cKit<sup>Hi</sup>, Sca1<sup>+</sup>, Lin<sup>-</sup>). Values normalized to the control KSL. Data are averages of three independent experiments (error bars, s.e.m.).

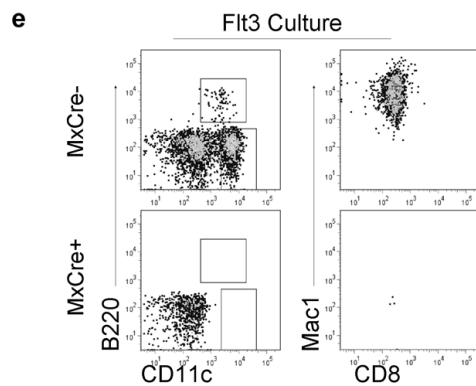
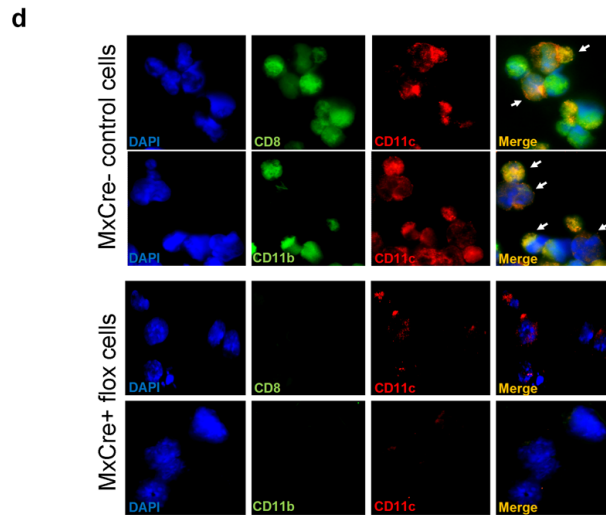
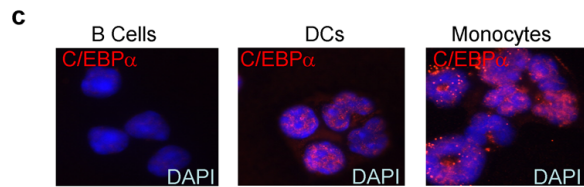
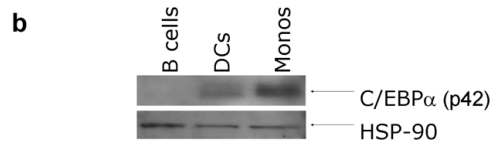
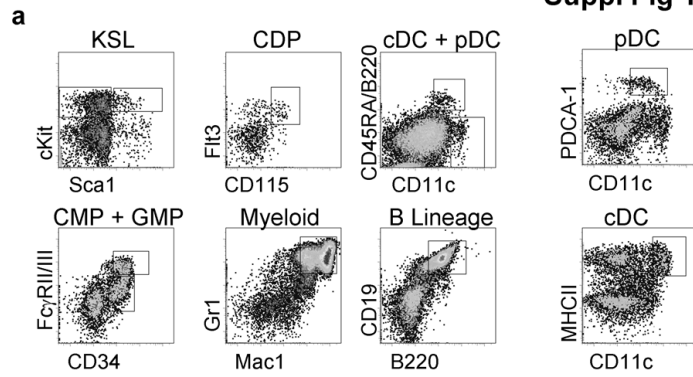
b) KSL from control or MxCre<sup>+</sup> C/EBP $\alpha$  flox/flox or MxCre<sup>+</sup> PU.1 flox/flox polyI:C treated mice were sorted and transduced with a retrovirus expressing PU.1-YFP. Cells were cultured in Flt3L differentiation conditions for 8 days. The top left panel shows typical numbers of YFP<sup>+</sup> PU.1

expressing cells after transduction of KSL cells and culture. KSL from control mice uniformly differentiated into DC (top middle panel, with the box indicating CD11c<sup>+</sup> cells. YFP<sup>+</sup> C/EBP $\alpha$  deleted KSL can be seen in the top right panel (x-axis, CD11c; y-axis, FSC), but PU.1 alone could not rescue CD11c<sup>+</sup> DC in KSL depleted for C/EBP $\alpha$ . PU.1 flox deleted KSL were used to demonstrate that the PU.1 retrovirus could rescue DC differentiation, bottom panels. These representative plots were taken from triplicate wells of two separate experiments.

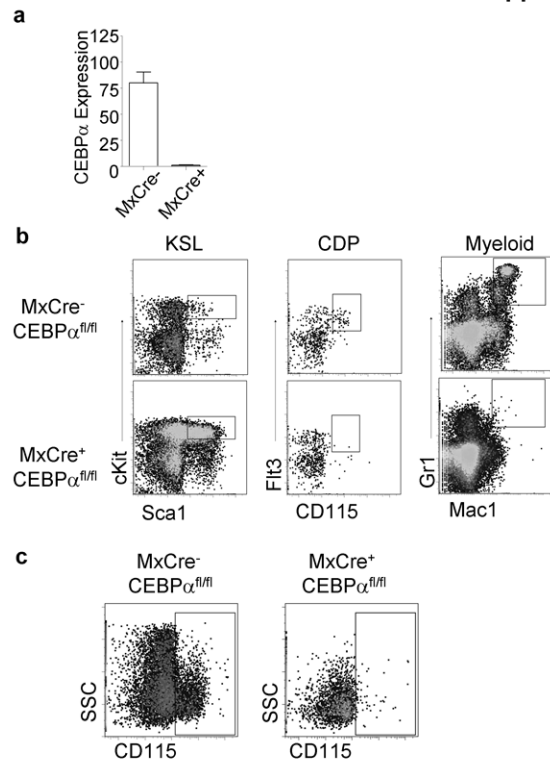
**Supplemental Table 1:** cDC (CD19/CD3/NK<sup>-</sup>, CD11c<sup>+</sup> MHCII<sup>+</sup>) from CD11c-Cre<sup>+</sup> C/EBP $\alpha$ fl/fl and C/EBP $\alpha$ fl/fl spleens were analyzed using SABiosciences murine dendritic cell specific array (PAMM-406A). This table lists of significant altered genes of 84 total that are decreased or increased in the CD11c-Cre x C/EBP $\alpha$ fl/fl splenic DC relative to control C/EBP $\alpha$ fl/fl splenic DC. These data are generated from Supplemental Figure 3C.

**Supplemental Table 2:** List of up and down regulated genes from array data comparing C/EBP $\alpha$  conditional knock-out MPP to CDP. Genes that were also expressed in MPP were subtracted as they may not pertain to dendritic cell differentiation. This approach was done using the dchip software, see Methods.

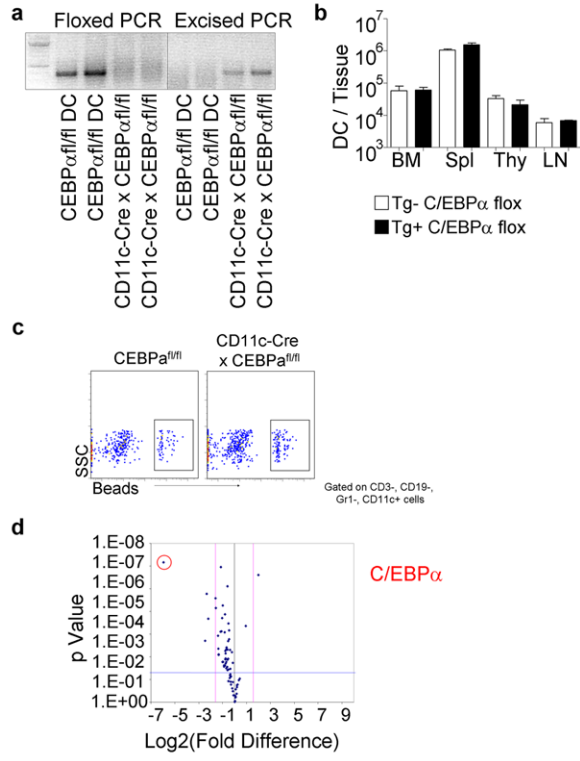
**Suppl Fig 1**



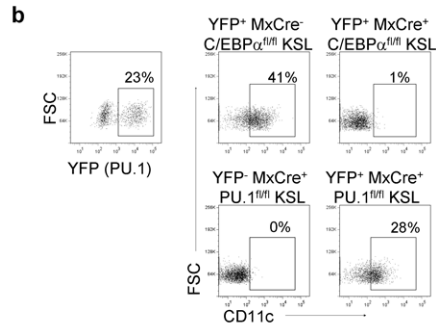
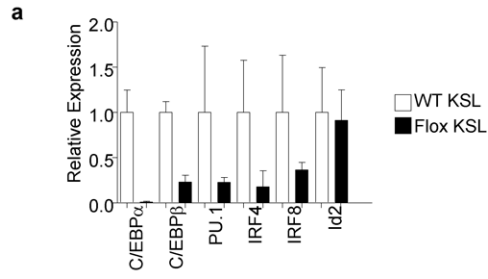
Suppl Fig 2



**Suppl Fig 3**



Suppl Fig 4





Supplementary Table 1

Symbol	Log2(FC)	p Value
Cebpa	-5.893	6.84E-07
Ccr2	-2.462	2.10E-04
Adamdec1	-2.461	1.97E-03
Ccr5	-2.129	7.79E-06
Il6	-1.587	2.44E-05
Cd209a	-1.487	1.38E-04
Ifit3	-1.253	5.50E-04
Cd2	-1.239	1.30E-03
Ccl19	-1.120	3.27E-03
Tlr1	-1.048	1.44E-03
Ccr1	-1.020	1.71E-04
Stk4	-1.001	1.21E-03
Fcgr1	-0.987	1.07E-05
Csf1r	-0.862	2.08E-03
Vcl	-0.839	1.04E-03
Il16	-0.791	5.79E-03
Ifngr1	-0.714	8.67E-03
B2m	-0.699	7.21E-03
Itgb2	-0.649	3.64E-03
Fas	-0.627	5.63E-03
Relb	-0.599	3.36E-04
Fcer1g	-0.582	8.61E-04
Fcer2a	-0.575	5.17E-03
Nfkb2	-0.538	9.39E-04
Lyn	-0.532	2.71E-05
Tlr2	-0.516	1.25E-07
Nfkb1	-0.421	4.19E-04
Tap2	-0.375	6.58E-03
Pdia3	0.673	4.33E-04
Ccl2	1.057	5.85E-03
Ifng	2.029	1.37E-05

Supplementary Table 2

gene name	fold change	lower bound of FC
0610009O20Rik: RIKEN cDNA 0610009O20 gene	-1.99	-1.36
1110002B05Rik: RIKEN cDNA 1110002B05 gene	1.82	1.29
1110004M10Rik: RIKEN cDNA 1110004M10 gene	-5.65	-1.49
1110020G09Rik: RIKEN cDNA 1110020G09 gene	1.80	1.42
1110059E24Rik: RIKEN cDNA 1110059E24 gene	-2.04	-1.68
1190002H23Rik: RIKEN cDNA 1190002H23 gene	2.77	1.87
1700029I15Rik: RIKEN cDNA 1700029I15 gene	-7.99	-2.07
1700030K09Rik: RIKEN cDNA 1700030K09 gene	-2.90	-1.55
1700037H04Rik: RIKEN cDNA 1700037H04 gene	-4.67	-1.53
1700052K11Rik: RIKEN cDNA 1700052K11 gene	-5.66	-2.00
1700097N02Rik: RIKEN cDNA 1700097N02 gene	2.04	1.64
1700097N02Rik: RIKEN cDNA 1700097N02 gene	1.87	1.47
1810013L24Rik: RIKEN cDNA 1810013L24 gene	-5.24	-1.39
2010309G21Rik /// Igl-C2: RIKEN cDNA 2010309G21	-9.40	-5.11
2310016E02Rik: RIKEN cDNA 2310016E02 gene	2.00	1.28
2310044G17Rik: RIKEN cDNA 2310044G17 gene	-2.71	-1.82
2310044G17Rik: RIKEN cDNA 2310044G17 gene	-6.51	-2.25
2410001C21Rik: RIKEN cDNA 2410001C21 gene	5.89	3.55
2510039O18Rik: RIKEN cDNA 2510039O18 gene	1.81	1.26
2610005L07Rik: cadherin 11 pseudogene	-2.08	-1.32
2610044O15Rik: RIKEN cDNA 2610044O15 gene	-1.77	-1.28
2810002D19Rik: RIKEN cDNA 2810002D19 gene	-3.14	-1.73
2810405K02Rik: RIKEN cDNA 2810405K02 gene	2.23	1.39
2810407C02Rik: RIKEN cDNA 2810407C02 gene	-2.44	-1.28
2810421E14Rik: RIKEN cDNA 2810421E14 gene	-5.41	-3.38
2810455D13Rik: RIKEN cDNA 2810455D13 gene	-2.57	-1.72
2900072G11Rik: RIKEN cDNA 2900072G11 gene	-3.28	-1.96
3110080O07Rik: RIKEN cDNA 3110080O07 gene	-2.97	-1.75
4833408D11Rik: RIKEN cDNA 4833408D11 gene	-2.42	-1.41
4833420G17Rik: RIKEN cDNA 4833420G17 gene	-2.00	-1.49
4833438C02Rik: RIKEN cDNA 4833438C02 gene	-2.63	-1.67
4921509J17Rik: RIKEN cDNA 4921509J17 gene	-4.42	-2.40
4921513D23Rik: RIKEN cDNA 4921513D23 gene	-2.95	-1.58
4922501C03Rik: RIKEN cDNA 4922501C03 gene	-8.46	-2.30
4930402E16Rik: RIKEN cDNA 4930402E16 gene	4.90	2.58
4930447I22Rik: RIKEN cDNA 4930447I22 gene	-12.22	-3.10
4930453N24Rik: RIKEN cDNA 4930453N24 gene	-20.61	-7.78
4930547N16Rik: RIKEN cDNA 4930547N16 gene	-1.75	-1.35
4933433G19Rik: RIKEN cDNA 4933433G19 gene	-6.74	-2.29
5031425E22Rik: RIKEN cDNA 5031425E22 gene	-3.14	-2.16

5430435G22Rik: RIKEN cDNA 5430435G22 gene	26.31	17.26
5430437P03Rik: RIKEN cDNA 5430437P03 gene	2.07	1.30
5830405N20Rik: RIKEN cDNA 5830405N20 gene	-9.59	-1.56
6230424C14Rik: RIKEN cDNA 6230424C14 gene	22.32	12.46
6330509M05Rik: RIKEN cDNA 6330509M05 gene	1.71	1.31
6720422M22Rik: RIKEN cDNA 6720422M22 gene	-9.30	-5.36
8430427H17Rik: RIKEN cDNA 8430427H17 gene	-7.55	-3.62
9030203C11Rik: RIKEN cDNA 9030203C11 gene	-2.92	-1.97
9030418K01Rik: RIKEN cDNA 9030418K01 gene	-2.23	-1.62
9130604C24Rik: RIKEN cDNA 9130604C24 gene	6.69	2.67
9230108I15Rik: RIKEN cDNA 9230108I15 gene	-3.58	-2.16
9430020K01Rik: RIKEN cDNA 9430020K01 gene	-3.02	-2.14
9530028C05: hypothetical protein 9530028C05	-3.26	-2.04
9530028C05: hypothetical protein 9530028C05	-3.90	-2.50
9530051E23Rik: RIKEN cDNA 9530051E23 gene	-7.44	-2.15
9630025I21Rik: RIKEN cDNA 9630025I21 gene	-3.43	-1.56
A130078K24Rik: RIKEN cDNA A130078K24 gene	-3.53	-1.48
A130082M07Rik /// Tcra: RIKEN cDNA A130082M07	-7.10	-2.28
A130082M07Rik /// Tcra: RIKEN cDNA A130082M07	-24.87	-7.61
A130088B03Rik: RIKEN cDNA A130088B03 gene	-14.38	-7.90
A730089K16Rik: RIKEN cDNA A730089K16 gene	-11.27	-6.41
A930001N09Rik: RIKEN cDNA A930001N09 gene	2.31	1.42
AA408296: expressed sequence AA408296	-6.44	-2.33
Aak1: AP2 associated kinase 1	-2.59	-1.92
Aasdhppt: amino adipate-semialdehyde	-1.78	-1.27
Abcf3: ATP-binding cassette, sub-family F (GCN20)	-2.59	-1.72
Abhd5: abhydrolase domain containing 5	-2.20	-1.62
Abtb1: ankyrin repeat and BTB (POZ) domain	-2.20	-1.64
Abtb2: ankyrin repeat and BTB (POZ) domain	-4.90	-3.10
Acad9: acyl-Coenzyme A dehydrogenase family	-9.03	-2.56
Acap1 /// LOC100045877: ArfGAP with coiled-coil,	-1.84	-1.26
Acbd6: acyl-Coenzyme A binding domain containing 6	-1.92	-1.42
Acly: ATP citrate lyase	-2.22	-1.26
Actr10: ARP10 actin-related protein 10 homolog	-1.90	-1.26
Actr10: ARP10 actin-related protein 10 homolog	-3.28	-1.99
Actr1a: ARP1 actin-related protein 1 homolog A,	-1.97	-1.47
Adam17: a disintegrin and metallopeptidase domain	-2.41	-1.65
Adcy6: adenylate cyclase 6	-3.29	-1.64
Add1: adducin 1 (alpha)	-2.07	-1.38
Adh5: alcohol dehydrogenase 5 (class III), chi	-1.90	-1.41
Adipor1: adiponectin receptor 1	-1.68	-1.33
Adprh: ADP-ribosylarginine hydrolase	1.76	1.31
Adrm1: adhesion regulating molecule 1	-2.63	-1.37
Adrm1: adhesion regulating molecule 1	-2.02	-1.41

Afp: alpha fetoprotein	-8.67	-4.05
Afp: alpha fetoprotein	-12.81	-4.80
Ahctf1: AT hook containing transcription factor 1	-2.30	-1.60
AI415730: expressed sequence AI415730	-4.31	-2.27
AI465300: expressed sequence AI465300	-4.07	-2.34
AI480526: expressed sequence AI480526	-3.19	-1.87
AI661453: expressed sequence AI661453	-9.23	-5.02
Aifm2: apoptosis-inducing factor, mitochondrion-	-4.41	-2.94
Akap12: A kinase (PKA) anchor protein (gravin) 12	-6.01	-1.98
Akr1b3: aldo-keto reductase family 1, member B3	-1.64	-1.37
Alas1: aminolevulinic acid synthase 1	3.25	2.44
Alas1: aminolevulinic acid synthase 1	2.96	2.00
Als2: amyotrophic lateral sclerosis 2	-33.78	-13.64
Amd1: S-adenosylmethionine decarboxylase 1	3.19	1.55
Amn1: antagonist of mitotic exit network 1 homolog	-2.57	-1.34
Amn1: antagonist of mitotic exit network 1 homolog	-2.62	-1.34
Amn1: antagonist of mitotic exit network 1 homolog	-13.92	-6.63
Ampd2: adenosine monophosphate deaminase 2	-1.79	-1.40
Anapc4: anaphase promoting complex subunit 4	-1.58	-1.29
Ankrd13b: ankyrin repeat domain 13b	-3.33	-2.00
Ankrd17: ankyrin repeat domain 17	-15.83	-6.53
Ankrd32: ankyrin repeat domain 32	-1.88	-1.29
Ankzf1: ankyrin repeat and zinc finger domain	-4.28	-2.66
Anxa7: annexin A7	-2.09	-1.53
Ap3m1: adaptor-related protein complex 3, mu 1	-2.81	-1.56
Ap3s1: adaptor-related protein complex 3, sigma 1	4.27	2.85
Apbb3: amyloid beta (A4) precursor protein-binding,	-2.72	-1.27
Apob48r: apolipoprotein B48 receptor	-1.86	-1.29
Appl1: adaptor protein, phosphotyrosine interaction,	-2.45	-1.34
Arf6: ADP-ribosylation factor 6	-1.85	-1.44
Argef1: ADP-ribosylation factor guanine nucleotide-	-3.17	-1.31
Arfp2: ADP-ribosylation factor interacting protein 2	-2.75	-1.65
Arhgap5: Rho GTPase activating protein 5	-2.13	-1.27
Arhgap6: Rho GTPase activating protein 6	-15.58	-8.93
Arhgef2: rho/rac guanine nucleotide exchange factor	-1.61	-1.27
Arhgef4: Rho guanine nucleotide exchange factor	-6.25	-3.33
Arl2: ADP-ribosylation factor-like 2	1.86	1.35
Armc8: armadillo repeat containing 8	-2.02	-1.28
Arpc1b: actin related protein 2/3 complex, subunit 1B	2.13	1.31
Arpp19 /// LOC632823: cAMP-regulated	2.05	1.45
Arpp21: cyclic AMP-regulated phosphoprotein, 21	-6.25	-3.93
Atl3: atlastin GTPase 3	-2.22	-1.53
Atmin: ATM interactor	-2.45	-1.52
Atp10d: ATPase, class V, type 10D	-3.19	-1.60

Atp13a1: ATPase type 13A1	-1.79	-1.31
Atp1b1: ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, beta 1	3.63	2.42
Atp1b1: ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, beta 1	3.22	1.99
Atp5g2: ATP synthase, H <sup>+</sup> transporting, mitochondrial	1.61	1.30
Atp6v0c: ATPase, H <sup>+</sup> transporting, lysosomal V0	2.33	1.86
Atp6v0e: ATPase, H <sup>+</sup> transporting, lysosomal V0	1.95	1.32
Atpif1: ATPase inhibitory factor 1	-5.36	-3.04
Atrnl1: Attractin like 1	-3.76	-1.80
Atxn2 /// LOC100047323: ataxin 2 /// similar to ataxin	-14.92	-5.42
AU020177: expressed sequence AU020177	-12.93	-5.61
AU041133: expressed sequence AU041133	-4.01	-1.92
AU041474: expressed sequence AU041474	-2.06	-1.29
Auts2: Autism susceptibility candidate 2	-3.13	-2.30
Aven: apoptosis, caspase activation inhibitor	2.04	1.42
AW552393: expressed sequence AW552393	-3.98	-2.57
B630019K06Rik: RIKEN cDNA B630019K06 gene	-4.99	-2.47
B830007D08Rik: RIKEN cDNA B830007D08 gene	-3.80	-2.93
B930041F14Rik: RIKEN cDNA B930041F14 gene	6.21	3.78
B930041F14Rik: RIKEN cDNA B930041F14 gene	2.95	1.98
Baz2b: bromodomain adjacent to zinc finger domain,	-9.19	-3.80
Bbs2: Bardet-Biedl syndrome 2 (human)	-3.86	-2.29
Bbs9: Bardet-Biedl syndrome 9 (human)	-3.27	-2.10
Bbx: bobby sox homolog (Drosophila)	-4.19	-1.58
BC024814: cDNA sequence BC024814	-2.25	-1.62
BC026590: cDNA sequence BC026590	-2.58	-1.85
BC029214: cDNA sequence BC029214	-2.66	-1.53
BC049807: cDNA sequence BC049807	-5.66	-3.10
BC055324: cDNA sequence BC055324	-1.99	-1.49
BC064078: cDNA sequence BC064078	2.76	1.78
BC064078: cDNA sequence BC064078	2.73	1.68
Bcas2: breast carcinoma amplified sequence 2	-6.59	-4.80
Bcdin3d: BCDIN3 domain containing	-5.96	-3.87
Bcl11b: B-cell leukemia/lymphoma 11B	-14.39	-2.02
Bend5: BEN domain containing 5	-6.32	-3.87
Best1: bestrophin 1	-10.33	-4.83
Bfar: bifunctional apoptosis regulator	-1.78	-1.27
Birc2: baculoviral IAP repeat-containing 2	-2.50	-1.68
Bmf: BCL2 modifying factor	-5.72	-1.56
Bmi1: Bmi1 polycomb ring finger oncogene	-1.78	-1.29
Bptf: bromodomain PHD finger transcription factor	-2.07	-1.30
Brd1 /// LOC100045983: bromodomain containing 1	-2.48	-1.27
Brd2: bromodomain containing 2	2.15	1.36
Brp44: brain protein 44	1.73	1.35
Brwd1: bromodomain and WD repeat domain	-2.72	-1.50

Bscl2: Bernardinelli-Seip congenital lipodystrophy 2	1.59	1.41
Btrc: beta-transducin repeat containing protein	-4.30	-2.80
C1qb: complement component 1, q subcomponent,	-12.15	-4.58
C1qb: complement component 1, q subcomponent,	-36.40	-19.27
C230037E05Rik: RIKEN cDNA C230037E05 gene	-10.22	-5.54
C230096C10Rik: RIKEN cDNA C230096C10 gene	1.86	1.39
C77080: expressed sequence C77080	-10.62	-2.64
C87436: expressed sequence C87436	-2.77	-1.83
Calm3: calmodulin 3	2.52	1.64
Camk1d: calcium/calmodulin-dependent protein	3.09	1.66
Camk2a: calcium/calmodulin-dependent protein	-11.78	-6.07
Camkk1: calcium/calmodulin-dependent protein	-11.83	-2.75
Cand2: cullin-associated and neddylation-dissociated	-3.30	-2.32
Cap1: CAP, adenylate cyclase-associated protein 1	2.13	1.33
Car12: carbonic anhydrase 12	-5.26	-2.56
Card11: caspase recruitment domain family, member	-8.52	-4.59
Carhsp1: calcium regulated heat stable protein 1	-2.40	-1.72
Carm1: coactivator-associated arginine	-1.59	-1.25
Cblb: Casitas B-lineage lymphoma b	-1.69	-1.29
Cbx2: chromobox homolog 2 (Drosophila Pc class)	-1.59	-1.38
Cbx5: chromobox homolog 5 (Drosophila HP1a)	2.56	1.41
Ccdc111: coiled-coil domain containing 111	-2.07	-1.57
Ccdc40: coiled-coil domain containing 40	-7.17	-4.32
Ccdc45: coiled-coil domain containing 45	-1.68	-1.26
Ccdc88a: coiled coil domain containing 88A	1.79	1.32
Ccdc93: coiled-coil domain containing 93	-2.25	-1.38
Ccnj1: cyclin J-like	-18.91	-7.31
Ccp1 /// LOC100135765: cell cycle progression 1 ///	-3.70	-1.87
Ccr12: chemokine (C-C motif) receptor-like 2	-4.17	-1.43
Cct4: chaperonin containing Tcp1, subunit 4 (delta)	-2.04	-1.29
Cd38: CD38 antigen	-3.87	-2.43
Cd3eap: CD3E antigen, epsilon polypeptide	-4.12	-1.61
Cd47: CD47 antigen (Rh-related antigen, integrin-	-1.76	-1.37
Cd55: CD55 antigen	-11.26	-5.59
Cd55: CD55 antigen	-18.40	-6.76
Cd68: CD68 antigen	2.86	1.59
Cd99l2: CD99 antigen-like 2	-5.20	-1.46
Cdad1: cytidine and dCMP deaminase domain	-1.91	-1.41
Cdc16: CDC16 cell division cycle 16 homolog	-2.05	-1.57
Cdkn2aip: CDKN2A interacting protein	1.57	1.28
Cdkn3: cyclin-dependent kinase inhibitor 3	2.28	1.76
Cds2: CDP-diacylglycerol synthase (phosphatidate	5.28	3.20
Cebpg: CCAAT/enhancer binding protein (C/EBP),	-6.02	-1.36
Cenpp: centromere protein P	-1.97	-1.31

Cep55: centrosomal protein 55	1.96	1.50
Chml: choroideremia-like	-13.42	-6.79
Chordc1: cysteine and histidine-rich domain	-2.36	-1.28
Chpt1: choline phosphotransferase 1	-4.11	-2.53
Chst15: carbohydrate (N-acetylgalactosamine 4-	-2.06	-1.50
Ckap4: cytoskeleton-associated protein 4	2.48	1.46
Clcn6: chloride channel 6	-1.59	-1.27
Cltb /// LOC100046457: clathrin, light polypeptide	-2.45	-1.58
Cmtm7: CKLF-like MARVEL transmembrane domain	2.42	1.62
Cnot4: CCR4-NOT transcription complex, subunit 4	2.93	1.86
Cnot6: CCR4-NOT transcription complex, subunit 6	-1.91	-1.38
Cntn2: contactin 2	-6.29	-4.30
Commd7 /// LOC674161: COMM domain containing 7	-2.92	-1.86
Cox10: COX10 homolog, cytochrome c oxidase	-2.07	-1.67
Cox16: COX16 cytochrome c oxidase assembly	3.20	1.51
Cox4nb: COX4 neighbor	-4.84	-2.94
Cox5b: cytochrome c oxidase, subunit Vb	-9.83	-4.03
Csnk2a1: casein kinase 2, alpha 1 polypeptide	2.28	1.34
Ctcf: CCCTC-binding factor	3.88	2.06
Cul7: cullin 7	-2.11	-1.37
Cxcr4: chemokine (C-X-C motif) receptor 4	1.87	1.27
Cxxc5: CXXC finger 5	1.82	1.27
Cyb5b: cytochrome b5 type B	-1.83	-1.43
Cybb: cytochrome b-245, beta polypeptide	11.45	8.72
Cyp11a1: cytochrome P450, family 11, subfamily a,	-27.42	-9.19
D030056L22Rik: RIKEN cDNA D030056L22 gene	1.90	1.33
D18Ertd653e: DNA segment, Chr 18, ERATO Doi	-3.19	-2.22
D19Wsu162e: DNA segment, Chr 19, Wayne State	-2.01	-1.29
D1Bwg0212e: DNA segment, Chr 1, Brigham &	-3.16	-1.67
D1Ertd622e: DNA segment, Chr 1, ERATO Doi 622,	2.34	1.50
D3Ertd751e: DNA segment, Chr 3, ERATO Doi 751,	-6.21	-3.83
D930001B02: hypothetical protein D930001B02	-3.79	-1.87
Dcaf17: DDB1 and CUL4 associated factor 17	-1.76	-1.27
Dcp1b: DCP1 decapping enzyme homolog b	-2.15	-1.31
Dcun1d3: DCN1, defective in cullin neddylation 1,	-3.72	-2.01
Ddb1: damage specific DNA binding protein 1	1.92	1.35
Ddx1: DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	-2.18	-1.29
Ddx3x: DEAD/H (Asp-Glu-Ala-Asp/His) box	-1.90	-1.35
Ddx3y: DEAD (Asp-Glu-Ala-Asp) box polypeptide 3,	80.90	31.58
Ddx3y: DEAD (Asp-Glu-Ala-Asp) box polypeptide 3,	38.14	8.35
Ddx42: DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	6.88	3.21
Ddx6: DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	2.85	1.63
Ddx60: DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	-16.94	-8.24
Deaf1: deformed epidermal autoregulatory factor 1	-2.16	-1.49

Dennd1b: DENN/MADD domain containing 1B	-2.55	-1.63
Dennd5b: DENN/MADD domain containing 5B	-3.71	-2.72
Dgcr8: DiGeorge syndrome critical region gene 8	-1.95	-1.41
Dgka: diacylglycerol kinase, alpha	-2.36	-1.67
Dgke: diacylglycerol kinase, epsilon	-4.23	-2.69
Dgkg: diacylglycerol kinase, gamma	3.43	2.26
Dhdds: dehydrodolichyl diphosphate synthase	-6.58	-1.91
Dhps: deoxyhypusine synthase	-2.27	-1.38
Dhx30: DEAH (Asp-Glu-Ala-His) box polypeptide 30	-2.22	-1.82
Dicer1: Dicer1, Dcr-1 homolog (Drosophila)	-2.29	-1.44
Dicer1: Dicer1, Dcr-1 homolog (Drosophila)	-2.33	-1.80
Dis3l2: DIS3 mitotic control homolog	-5.05	-2.49
Dlg2: discs, large homolog 2 (Drosophila)	32.29	12.58
Dna2: DNA replication helicase 2 homolog (yeast)	2.87	2.02
Dnaja1: DnaJ (Hsp40) homolog, subfamily A, member	-2.23	-1.41
Dnajb12: DnaJ (Hsp40) homolog, subfamily B,	-3.89	-2.16
Dnajb14: DnaJ (Hsp40) homolog, subfamily B,	4.91	3.14
Dnajc10 /// LOC100047007: DnaJ (Hsp40) homolog,	1.87	1.33
Dnajc2: DnaJ (Hsp40) homolog, subfamily C, member	-1.75	-1.30
Dnm1l: dynamin 1-like	-16.03	-1.77
Dnm1l: dynamin 1-like	-14.91	-3.73
Dnm2: dynamin 2	-1.58	-1.27
Dstn: destrin	2.41	1.58
Dtx4: deltex 4 homolog (Drosophila)	2.20	1.60
Dusp7: dual specificity phosphatase 7	6.90	3.42
Dynlt3: dynein light chain Tctex-type 3	-1.78	-1.31
Dynlt3: dynein light chain Tctex-type 3	-2.89	-1.45
E030037K03Rik: RIKEN cDNA E030037K03 gene	-8.88	-3.85
E130012A19Rik: RIKEN cDNA E130012A19 gene	-6.75	-2.10
E130112L23Rik: RIKEN cDNA E130112L23 gene	-8.69	-3.40
E130112L23Rik: RIKEN cDNA E130112L23 gene	-7.86	-4.12
E130304F04Rik: RIKEN cDNA E130304F04 gene	-8.30	-5.03
E2f8: E2F transcription factor 8	1.96	1.41
Ecm1: extracellular matrix protein 1	-6.20	-2.88
Efnb1: ephrin B1	-2.93	-1.48
Efr3b: EFR3 homolog B (S. cerevisiae)	-26.03	-7.71
Egfl8: EGF-like domain 8	-6.56	-2.13
Eif2ak2: eukaryotic translation initiation factor 2-alpha	-1.96	-1.29
Eif2c3: eukaryotic translation initiation factor 2C, 3	-4.01	-1.79
Eif2s3y: eukaryotic translation initiation factor 2,	45.93	14.23
Eif4ebp2: eukaryotic translation initiation factor 4E	-14.39	-7.44
Eif4g1: eukaryotic translation initiation factor 4,	-2.21	-1.37
Eif5a: eukaryotic translation initiation factor 5A	1.65	1.37
Elac1: elaC homolog 1 (E. coli)	-2.27	-1.49



Elac1: elaC homolog 1 (E. coli)	-4.61	-1.83
Elane: elastase, neutrophil expressed	41.63	17.51
Elovl6: ELOVL family member 6, elongation of long	-2.74	-2.10
Eno1 /// Gm5506 /// LOC100047043: enolase 1, alpha	-1.73	-1.37
Eno1: enolase 1, alpha non-neuron	-1.76	-1.36
Enpp4: ectonucleotide pyrophosphatase	-5.29	-1.85
Epb4.115: erythrocyte protein band 4.1-like 5	-27.15	-12.73
Eps8 /// LOC632638: epidermal growth factor	-2.76	-2.00
Erc1: ELKS/RAB6-interacting/CAST family member 1	-10.40	-3.29
Erdr1: erythroid differentiation regulator 1	4.45	1.72
Esam: endothelial cell-specific adhesion molecule	-18.10	-4.74
Ets2: E26 avian leukemia oncogene 2, 3' domain	-4.63	-1.74
Evi5: ecotropic viral integration site 5	3.12	1.76
Exoc6: exocyst complex component 6	-1.96	-1.36
F11r: F11 receptor	-8.99	-3.73
F730047E07Rik: RIKEN cDNA F730047E07 gene	1.77	1.34
Fads1: fatty acid desaturase 1	-2.14	-1.57
Faf1: Fas-associated factor 1	-1.90	-1.28
Fam100a: family with sequence similarity 100,	-2.12	-1.38
Fam101b: family with sequence similarity 101,	7.99	4.59
Fam105a: family with sequence similarity 105,	21.68	7.90
Fam149b: family with sequence similarity 149,	-2.97	-2.15
Fam160b1: family with sequence similarity 160,	2.43	1.57
Fam175a: family with sequence similarity 175,	-2.15	-1.45
Fam53c: family with sequence similarity 53, member C	-1.89	-1.28
Fam69b: family with sequence similarity 69, member	-1.86	-1.56
Fancc: Fanconi anemia, complementation group B	-2.11	-1.61
Fbx17: F-box and leucine-rich repeat protein 17	6.71	3.38
Fbxo17: F-box protein 17	-4.55	-2.94
Fbxo45: F-box protein 45	-2.67	-1.61
Fbxo7: F-box protein 7	-2.11	-1.62
Fbxw5: F-box and WD-40 domain protein 5	-2.27	-1.54
Fcf1: FCF1 small subunit (SSU) processome	-2.37	-1.31
Fcho2: FCH domain only 2	2.30	1.28
Fli1: Friend leukemia integration 1	2.58	1.27
Flot1: flotillin 1	-2.48	-1.99
Flywch1: FLYWCH-type zinc finger 1	-1.97	-1.41
Fmn13: formin-like 3	1.52	1.27
Fndc3a: fibronectin type III domain containing 3A	-1.83	-1.49
Foxp1: Forkhead box P1	2.20	1.52
Foxp1: forkhead box P1	2.05	1.42
Foxp4: forkhead box P4	-3.38	-1.34
Foxp4: forkhead box P4	-2.33	-1.49
Fyb: FYN binding protein	-2.45	-1.79

Gadd45g: growth arrest and DNA-damage-inducible	-8.63	-2.50
Gak: cyclin G associated kinase	-2.26	-1.41
Galm: galactose mutarotase	-5.60	-2.98
Galnt11: UDP-N-acetyl-alpha-D-	-14.04	-5.41
Galnt2: UDP-N-acetyl-alpha-D-	-1.58	-1.26
Galnt6: UDP-N-acetyl-alpha-D-	-3.95	-2.77
Gata3: GATA binding protein 3	-42.10	-16.37
Gbp4 /// Gbp8: guanylate binding protein 4 ///	-23.95	-7.79
Gcnt2: glucosaminyl (N-acetyl) transferase 2, I-	1.96	1.42
Gemin5: gem (nuclear organelle) associated protein 5	-3.78	-1.88
Gemin8: gem (nuclear organelle) associated protein 8	-3.77	-1.56
Ggps1 /// LOC100045315: geranylgeranyl	-2.36	-1.56
Ghr: growth hormone receptor	-25.55	-9.15
Gimap4: GTPase, IMAP family member 4	-6.81	-3.42
Gimap4: GTPase, IMAP family member 4	-13.33	-5.38
Glis2: GLIS family zinc finger 2	-2.82	-1.83
Glt8d1: glycosyltransferase 8 domain containing 1	-2.01	-1.44
Gltscr2: glioma tumor suppressor candidate region	-3.73	-2.57
Gm10035 /// Higd1c /// Mettl7a1 /// Mettl7a2 ///	3.01	1.38
Gm10883 /// Gm1420 /// Gm7202 /// Igk /// Igk-C ///	-13.81	-3.05
Gm10883: predicted gene 10883	-13.53	-3.61
Gm11560 /// LOC100045189 /// Ybx1: CCAAT-	-3.34	-1.25
Gm5141: predicted gene 5141	-1.50	-1.29
Gm5312 /// Rpl18: predicted gene 5312 /// ribosomal	-2.91	-1.71
Gm5918: predicted gene 5918	-4.49	-1.95
Gm7380 /// Gm9385 /// Rpl24: predicted gene 7380 ///	2.58	1.27
Gmcl1: germ cell-less homolog 1 (Drosophila)	-1.99	-1.44
Gmnn: geminin	2.15	1.49
Gnb1l: guanine nucleotide binding protein (G protein),	-3.43	-2.04
Golgb1: golgi autoantigen, golgin subfamily b,	-2.13	-1.26
Gpam: glycerol-3-phosphate acyltransferase,	-1.63	-1.36
Gpatch4: G patch domain containing 4	-2.77	-1.31
Gpc4: glypican 4	22.77	7.72
Gpd2: glycerol phosphate dehydrogenase 2,	-1.95	-1.28
Gphn: gephyrin	2.16	1.54
Gpr172b: G protein-coupled receptor 172B	-2.01	-1.39
Gpr172b: G protein-coupled receptor 172B	-2.14	-1.44
Gpr172b: G protein-coupled receptor 172B	-2.78	-1.93
Gpr68: G protein-coupled receptor 68	-17.67	-6.39
Gprasp1: G protein-coupled receptor associated	-7.74	-2.32
Gpx4: glutathione peroxidase 4	1.83	1.31
Grina: glutamate receptor, ionotropic, N-methyl D-	-1.99	-1.27
Grpel2: GrpE-like 2, mitochondrial	-2.86	-1.49
Gtf2i: general transcription factor II I	-2.74	-1.64

Gvin1: GTPase, very large interferon inducible 1	-1.92	-1.39
H2-D1: histocompatibility 2, D region locus 1	-4.65	-3.52
H2-DMb2: histocompatibility 2, class II, locus Mb2	3.84	2.69
H2-M3: histocompatibility 2, M region locus 3	1.83	1.34
Hars2: histidyl-tRNA synthetase 2, mitochondrial	-2.62	-1.84
Hbb-b2: hemoglobin, beta adult minor chain	-3.60	-2.50
Hcfc2: host cell factor C2	-4.38	-2.02
Hdac7: histone deacetylase 7	-1.75	-1.35
Heatr6: HEAT repeat containing 6	-1.85	-1.37
Hells: helicase, lymphoid specific	2.49	1.38
Helz: helicase with zinc finger domain	-8.74	-1.75
Herc5: hect domain and RLD 5	-2.70	-1.44
Herc5: hect domain and RLD 5	-8.30	-2.99
Hivep2: human immunodeficiency virus type I	-5.55	-1.87
Hk1: hexokinase 1	-6.72	-2.69
Hmgb1: high mobility group box 1	2.10	1.50
Hmgb1: high mobility group box 1	2.51	1.36
Hmgcs1: 3-hydroxy-3-methylglutaryl-Coenzyme A	-1.80	-1.30
Hn1l: hematological and neurological expressed 1-like	1.98	1.51
Hnrnpd: heterogeneous nuclear ribonucleoprotein D	-1.62	-1.26
Hnrnpd: heterogeneous nuclear ribonucleoprotein D	-4.53	-3.15
Hoxb4: homeobox B4	-3.58	-2.08
Hp: haptoglobin	24.74	3.73
Hsh2d: hematopoietic SH2 domain containing	-2.85	-1.98
Iah1: isoamyl acetate-hydrolyzing esterase 1 homolog	1.89	1.37
Icam4: intercellular adhesion molecule 4, Landsteiner-	-8.22	-3.77
Id2: inhibitor of DNA binding 2	-2.58	-1.28
Igbp1: immunoglobulin (CD79A) binding protein 1	-2.26	-1.28
Igh-2 /// Igh-VJ558 /// LOC544903: immunoglobulin	-3.88	-1.66
Igh-2 /// Igh-VJ558 /// LOC544903: immunoglobulin	-4.43	-1.97
Igh-2 /// Igh-VJ558 /// LOC544903: immunoglobulin	-4.73	-2.05
Igh-6: Immunoglobulin heavy chain 6 (heavy chain of	10.28	6.23
Igh-VJ558: Immunoglobulin heavy chain (J558 family)	-37.88	-13.76
Igkv14-111: Immunoglobulin kappa chain variable 14-	-14.51	-4.76
Ikbkap: inhibitor of kappa light polypeptide enhancer	-1.89	-1.46
Ikbkb: inhibitor of kappaB kinase beta	-2.22	-1.48
Ikbkg: inhibitor of kappaB kinase gamma	-2.08	-1.43
Il17ra: interleukin 17 receptor A	2.15	1.68
Il17re: interleukin 17 receptor E	-6.72	-3.07
Il18rap: interleukin 18 receptor accessory protein	-5.61	-2.60
Il1rl2: interleukin 1 receptor-like 2	-5.34	-1.29
Impad1: inositol monophosphatase domain containing	-1.88	-1.30
Ino80c: INO80 complex subunit C	-2.51	-1.59
Inpp5b: inositol polyphosphate-5-phosphatase B	-2.41	-1.39

Iqce: IQ motif containing E	-3.26	-2.46
Irf4: interferon regulatory factor 4	-5.90	-2.11
Irgm2: immunity-related GTPase family M member 2	-2.36	-1.35
Itgb5: integrin beta 5	2.84	1.83
Itpkb: inositol 1,4,5-trisphosphate 3-kinase B	-3.24	-1.74
Itpr1p: inositol 1,4,5-triphosphate receptor interacting	2.43	1.69
Kcnn4: potassium intermediate/small conductance	-1.91	-1.46
Kcnq1ot1: KCNQ1 overlapping transcript 1	-2.71	-1.72
Kdelc2: KDEL (Lys-Asp-Glu-Leu) containing 2	2.34	1.53
Kdm1a: lysine (K)-specific demethylase 1A	-2.81	-1.71
Kdm4b: lysine (K)-specific demethylase 4B	-5.66	-2.87
Khsrp: KH-type splicing regulatory protein	2.99	1.80
Kif3a: kinesin family member 3A	-3.54	-2.05
Kif3b: kinesin family member 3B	-3.61	-2.42
Klf7: Kruppel-like factor 7 (ubiquitous)	-4.23	-1.41
Klf7: Kruppel-like factor 7 (ubiquitous)	-2.99	-1.74
Klhl12: kelch-like 12 (Drosophila)	-4.36	-2.93
Klhl17: kelch-like 17 (Drosophila)	-1.83	-1.38
Krit1: KRIT1, ankyrin repeat containing	-2.40	-1.44
Krr1: KRR1, small subunit (SSU) processome	-2.17	-1.34
Krt10: keratin 10	2.72	1.86
Ksr1: kinase suppressor of ras 1	-3.11	-1.72
Kti12: KTI12 homolog, chromatin associated	-2.08	-1.48
L2hgdh: L-2-hydroxyglutarate dehydrogenase	-2.58	-1.60
Lamc1: laminin, gamma 1	-5.89	-2.53
Lancl1: LanC (bacterial lantibiotic synthetase	-2.03	-1.69
Lars2: leucyl-tRNA synthetase, mitochondrial	-2.12	-1.75
Leng1: leukocyte receptor cluster (LRC) member 1	-2.28	-1.34
Leptol1: leptin receptor overlapping transcript-like 1	1.94	1.41
Lgals4: lectin, galactose binding, soluble 4	-4.35	-2.70
Lgals8: lectin, galactose binding, soluble 8	-3.72	-1.60
Lilrb3: leukocyte immunoglobulin-like receptor,	3.07	2.35
Lins2: lines homolog 2 (Drosophila)	-3.82	-1.33
LOC100040377: similar to SR protein related family	-3.09	-2.03
LOC100045503 /// Tmem108: hypothetical protein	-4.96	-2.49
LOC100045677 /// Mcm3: similar to DNA replication	1.54	1.27
LOC100046166 /// Tbrg4: similar to Transforming	-3.86	-2.25
LOC100046672 /// Wars: similar to Wars protein ///	-1.80	-1.34
LOC100047009 /// Pus7: hypothetical protein	-2.37	-1.47
LOC100047324 /// Sesn1: similar to Sesn1 protein ///	-1.87	-1.36
LOC100048307 /// Slc35f2: similar to Solute carrier	-8.49	-3.79
LOC433064 /// Ppih: similar to peptidyl prolyl	1.95	1.42
LOC636537 /// Ssr1: similar to signal sequence	2.05	1.25
LOC677224 /// Ubash3b: similar to RIKEN cDNA	-2.33	-1.48

Lrp5: low density lipoprotein receptor-related protein 5	-4.76	-2.80
Lrrc1: leucine rich repeat containing 1	-2.67	-1.75
Lrrc28: leucine rich repeat containing 28	-2.18	-1.44
Lsm12: LSM12 homolog (S. cerevisiae)	3.35	1.25
Luc7l: Luc7 homolog (S. cerevisiae)-like	-1.91	-1.46
Lztf11: leucine zipper transcription factor-like 1	-3.44	-2.56
Mad111: mitotic arrest deficient 1-like 1	-4.84	-2.65
Man1a2: mannosidase, alpha, class 1A, member 2	-2.92	-1.68
Map2k5: mitogen-activated protein kinase kinase 5	-2.66	-1.81
Mapk11: mitogen-activated protein kinase 11	-4.19	-1.96
Mapk8: mitogen-activated protein kinase 8	-1.83	-1.27
Mars: methionine-tRNA synthetase	-2.19	-1.63
Marvel2: MARVEL (membrane-associating) domain	-9.39	-4.57
Matn2: matrilin 2	-4.89	-2.64
Mbd2: Methyl-CpG binding domain protein 2	7.37	4.25
Mbd5: methyl-CpG binding domain protein 5	-3.41	-2.40
Mbtps2 /// Yy2: membrane-bound transcription factor	-1.98	-1.51
Mbtps2: membrane-bound transcription factor	-2.05	-1.49
Mcf2l: mcf.2 transforming sequence-like	-2.59	-1.47
Mdfi: MyoD family inhibitor	-9.93	-3.33
Mdm4: transformed mouse 3T3 cell double minute 4	-2.21	-1.37
Mecp2: methyl CpG binding protein 2	2.80	1.89
Mef2c: myocyte enhancer factor 2C	2.11	1.47
Metrn: meteorin, glial cell differentiation regulator	1.92	1.49
Mettl13: methyltransferase like 13	-5.53	-3.19
Mettl2: methyltransferase like 2	1.94	1.31
Mettl8: methyltransferase like 8	-2.45	-1.78
Mfsd2b: major facilitator superfamily domain	-5.22	-3.26
Mfsd6: major facilitator superfamily domain containing	-1.64	-1.35
Mfsd8: major facilitator superfamily domain containing	-3.66	-2.34
Mgat4a: mannoside acetylglucosaminyltransferase 4,	-2.55	-1.42
Mlec: malectin	-2.72	-1.61
Mllt11: myeloid/lymphoid or mixed-lineage leukemia	-1.90	-1.46
Mospd2: motile sperm domain containing 2	2.11	1.29
Mpa2l: macrophage activation 2 like	-4.64	-2.52
Mrps5: mitochondrial ribosomal protein S5	1.84	1.26
Msh6: mutS homolog 6 (E. coli)	-1.64	-1.26
Mt2: metallothionein 2	7.93	3.90
Mthfd2l: methylenetetrahydrofolate dehydrogenase	-5.53	-4.13
Muc1: mucin 1, transmembrane	-14.81	-3.24
Mxd4: Max dimerization protein 4	-2.27	-1.58
Mycbp: c-myc binding protein	-2.98	-1.56
Mycn: v-myc myelocytomatosis viral related	-4.76	-2.86
Myl4: myosin, light polypeptide 4	-2.75	-1.65

Myo6: myosin VI	-12.16	-6.90
N4bp2: NEDD4 binding protein 2	3.07	1.34
Naa35: N(alpha)-acetyltransferase 35, NatC auxiliary	-1.75	-1.27
Naa50: N(alpha)-acetyltransferase 50, NatE catalytic	-1.68	-1.30
Nanp: N-acetylneuraminic acid phosphatase	1.80	1.28
Nap1l1: nucleosome assembly protein 1-like 1	1.92	1.42
Nbn: nibrin	-2.09	-1.34
Ncbp2: nuclear cap binding protein subunit 2	1.68	1.26
Nde1: nuclear distribution gene E homolog 1	-1.83	-1.31
Ndufa12: NADH dehydrogenase (ubiquinone) 1 alpha	-1.69	-1.41
Ndufa3: NADH dehydrogenase (ubiquinone) 1 alpha	1.79	1.37
Ndufb9: NADH dehydrogenase (ubiquinone) 1 beta	2.03	1.59
Ndufs1: NADH dehydrogenase (ubiquinone) Fe-S	-1.86	-1.51
Nedd9: neural precursor cell expressed,	2.10	1.40
Nedd9: neural precursor cell expressed,	2.16	1.33
Neil3: nei like 3 (E. coli)	5.37	3.63
Nfatc1: nuclear factor of activated T-cells,	-1.88	-1.32
Nlk: nemo like kinase	-2.37	-1.85
Nr2c1: nuclear receptor subfamily 2, group C,	-1.75	-1.43
Nr2c2: nuclear receptor subfamily 2, group C,	-15.43	-5.36
Nr3c1: nuclear receptor subfamily 3, group C,	1.85	1.30
Nrarp: Notch-regulated ankyrin repeat protein	-6.74	-1.79
Nrarp: Notch-regulated ankyrin repeat protein	-18.08	-4.79
Nrp1: neuropilin 1	30.65	11.59
Nt5dc3: 5'-nucleotidase domain containing 3	-2.20	-1.40
Nudc: nuclear distribution gene C homolog	2.02	1.43
Nup133: nucleoporin 133	-2.60	-1.68
Nynrin: NYN domain and retroviral integrase	-20.21	-9.33
Oasl1: 2'-5' oligoadenylate synthetase-like 1	-6.69	-3.21
Ociad2: OCIA domain containing 2	-2.86	-1.38
Ogt: O-linked N-acetylglucosamine (GlcNAc)	-2.86	-1.89
Optn: optineurin	-12.85	-5.98
Orc3l: origin recognition complex, subunit 3-like	-2.02	-1.54
Orc4l: origin recognition complex, subunit 4-like	-2.71	-1.53
Osbpl5: oxysterol binding protein-like 5	-8.76	-4.08
Osbpl9: oxysterol binding protein-like 9	-1.74	-1.26
Osgepl1: O-sialoglycoprotein endopeptidase-like 1	-1.97	-1.55
Osm: oncostatin M	-2.87	-1.57
Oxa1l: oxidase assembly 1-like	-2.42	-1.69
Oxr1: oxidation resistance 1	-2.03	-1.37
P2rx1: purinergic receptor P2X, ligand-gated ion	-5.71	-3.25
P2rx7: purinergic receptor P2X, ligand-gated ion	3.41	1.78
P2rx7: purinergic receptor P2X, ligand-gated ion	2.34	1.25
Pabpn1: poly(A) binding protein, nuclear 1	1.76	1.31

Pacs1: phosphofurin acidic cluster sorting protein 1	-1.75	-1.41
Pak1: p21 protein (Cdc42/Rac)-activated kinase 1	2.80	1.56
Panx1: pannexin 1	-1.97	-1.33
Papolg: poly(A) polymerase gamma	-1.90	-1.35
Papss2: 3'-phosphoadenosine 5'-phosphosulfate	2.87	1.43
Parp14: poly (ADP-ribose) polymerase family,	-3.45	-2.44
Parp3: poly (ADP-ribose) polymerase family, member	-2.07	-1.45
Pcdh7: Protocadherin 7	-26.91	-11.56
Pcmt1: protein-L-isoaspartate (D-aspartate) O-	-1.55	-1.31
Pcnx: pecanex homolog (Drosophila)	-7.66	-3.46
Pcyt1a: phosphate cytidyltransferase 1, choline,	2.25	1.39
Pdcd1lg2: programmed cell death 1 ligand 2	-14.32	-1.52
Pde7a: phosphodiesterase 7A	1.96	1.26
Pdk2: pyruvate dehydrogenase kinase, isoenzyme 2	-10.07	-4.02
Peci: peroxisomal delta3, delta2-enoyl-Coenzyme A	-1.96	-1.26
Pex1: peroxisomal biogenesis factor 1	-2.02	-1.53
Pf4: platelet factor 4	-3.21	-1.43
Pfkp: phosphofructokinase, platelet	2.04	1.50
Pgm2l1: phosphoglucomutase 2-like 1	-1.93	-1.48
Pgr: progesterone receptor	-10.82	-2.89
Phc1: polyhomeotic-like 1 (Drosophila)	-1.82	-1.35
Pias2: protein inhibitor of activated STAT 2	-3.16	-1.71
Pign: Phosphatidylinositol glycan anchor biosynthesis,	-1.89	-1.32
Pigo: phosphatidylinositol glycan anchor biosynthesis,	-2.39	-1.84
Pigo: phosphatidylinositol glycan anchor biosynthesis,	-2.53	-2.02
Pigx: phosphatidylinositol glycan anchor biosynthesis,	-2.31	-1.30
Pik3cb: phosphatidylinositol 3-kinase, catalytic, beta	-2.24	-1.26
Pik3cd: phosphatidylinositol 3-kinase catalytic delta	3.39	2.06
Pitpnc1: phosphatidylinositol transfer protein,	-2.30	-1.75
Pitrm1: pitrilysin metallopeptidase 1	-1.78	-1.47
Pkd1: polycystic kidney disease 1 homolog	-2.16	-1.65
Pla2g4a: phospholipase A2, group IVA (cytosolic,	-2.02	-1.54
Plk1s1: polo-like kinase 1 substrate 1	-2.12	-1.54
Plxdc2: plexin domain containing 2	-14.36	-8.67
Plxnc1: plexin C1	2.58	1.43
Plxnd1: plexin D1	2.56	2.03
Pmpcb: peptidase (mitochondrial processing) beta	-1.78	-1.26
Pnpla6: Patatin-like phospholipase domain containing	14.40	5.77
Pnpt1: polyribonucleotide nucleotidyltransferase 1	-2.54	-1.66
Pofut2: protein O-fucosyltransferase 2	-6.73	-2.49
Polr3k: polymerase (RNA) III (DNA directed)	-2.43	-1.33
Pon3: paraoxonase 3	-2.39	-1.47
Pot1a: protection of telomeres 1A	-21.20	-11.10
Ppm1a: protein phosphatase 1A, magnesium	-8.52	-2.05

Ppm1l: protein phosphatase 1 (formerly 2C)-like	-8.37	-4.46
Ppp1r16b: protein phosphatase 1, regulatory	-2.82	-1.93
Ppp1r3b: protein phosphatase 1, regulatory (inhibitor)	-2.41	-1.67
Ppp3cc: protein phosphatase 3, catalytic subunit,	-6.56	-3.86
Pqlc3: PQ loop repeat containing	2.09	1.27
Prc1: protein regulator of cytokinesis 1	-2.16	-1.39
Prkag2: protein kinase, AMP-activated, gamma 2	-2.16	-1.50
Prkcb: protein kinase C, beta	-5.05	-2.79
Prkch: protein kinase C, eta	-4.65	-2.23
Prmt2: protein arginine N-methyltransferase 2	-2.19	-1.34
Prrc1: proline-rich coiled-coil 1	-10.45	-3.59
Psd3: pleckstrin and Sec7 domain containing 3	-3.56	-2.36
Psmb9: proteasome (prosome, macropain) subunit,	1.80	1.38
Psmc3ip: proteasome (prosome, macropain) 26S	1.73	1.30
Psmd3: proteasome (prosome, macropain) 26S	2.02	1.62
Pten: phosphatase and tensin homolog	-1.86	-1.29
Pter: phosphotriesterase related	-3.38	-2.09
Ptgr2: prostaglandin reductase 2	9.90	5.00
Ptgs1: prostaglandin-endoperoxide synthase 1	6.69	3.28
Ptov1: prostate tumor over expressed gene 1	-2.22	-1.37
Ptp4a1: protein tyrosine phosphatase 4a1	-2.09	-1.27
Ptpn12: protein tyrosine phosphatase, non-receptor	-2.03	-1.49
Ptpn18: protein tyrosine phosphatase, non-receptor	-1.83	-1.25
Ptpn2: protein tyrosine phosphatase, non-receptor	-5.79	-1.33
Ptpn23: protein tyrosine phosphatase, non-receptor	-3.43	-1.81
Ptpn3: protein tyrosine phosphatase, non-receptor	-7.79	-3.46
Pum2: pumilio 2 (Drosophila)	2.08	1.42
Purb: Purine rich element binding protein B	-16.69	-3.15
Pvr: poliovirus receptor	-2.67	-1.33
Pvr: poliovirus receptor	-4.30	-1.74
Pxmp4: peroxisomal membrane protein 4	-2.69	-1.70
Qprt: quinolinate phosphoribosyltransferase	-4.41	-2.44
Qser1: glutamine and serine rich 1	-1.81	-1.30
Rab11b: RAB11B, member RAS oncogene family	-3.67	-1.78
Rab2a: RAB2A, member RAS oncogene family	-1.86	-1.51
Rab2a: RAB2A, member RAS oncogene family	-2.46	-1.70
Rab4a: RAB4A, member RAS oncogene family	-6.82	-3.62
Rab6b: RAB6B, member RAS oncogene family	-10.89	-5.46
Rabep1: rabaptin, RAB GTPase binding effector	-2.44	-1.35
Rabl3: RAB, member of RAS oncogene family-like 3	-9.98	-3.30
Rasal3: RAS protein activator like 3	-1.65	-1.34
Rassf7: Ras association (RalGDS/AF-6) domain	2.63	1.82
Rb1: retinoblastoma 1	2.00	1.37
Rbks: ribokinase	1.77	1.32



Rbm41: RNA binding motif protein 41	-2.11	-1.55
Rbms2: RNA binding motif, single stranded	-2.90	-1.90
Rc3h2: ring finger and CCCH-type zinc finger	-1.95	-1.64
Rc3h2: ring finger and CCCH-type zinc finger	-10.18	-7.12
Rcor1: REST corepressor 1	-2.24	-1.30
Rcor3: REST corepressor 3	4.66	2.21
Rdm1: RAD52 motif 1	1.72	1.37
Reck: reversion-inducing-cysteine-rich protein with	-6.07	-1.97
Reep6: receptor accessory protein 6	-6.28	-3.39
Rfc2: replication factor C (activator 1) 2	-1.64	-1.28
Rfc4: replication factor C (activator 1) 4	-1.79	-1.34
Rg9mtd2: RNA (guanine-9-) methyltransferase	-1.80	-1.30
Rheb1: Ras homolog enriched in brain like 1	-1.95	-1.38
Rian: RNA imprinted and accumulated in nucleus	-16.61	-2.38
Rnf144b: ring finger protein 144B	2.07	1.68
Rnf7: ring finger protein 7	1.92	1.31
Rora: RAR-related orphan receptor alpha	-7.47	-1.52
Rpl39l: ribosomal protein L39-like	6.29	3.55
Rpl41: ribosomal protein L41	-1.33	-1.27
Rpp40: ribonuclease P 40 subunit (human)	-1.94	-1.29
Rps2: ribosomal protein S2	1.75	1.31
Rps4y2: ribosomal protein S4, Y-linked 2	3.56	2.17
Rps6ka1: ribosomal protein S6 kinase polypeptide 1	2.19	1.68
Rpsud2: RNA pseudouridylate synthase domain	-3.25	-1.45
Rpsud2: RNA pseudouridylate synthase domain	-6.41	-3.49
Rras2: related RAS viral (r-ras) oncogene homolog 2	-5.76	-3.01
Rreb1: ras responsive element binding protein 1	-3.72	-1.25
Runx1: runt related transcription factor 1	5.81	2.70
S100a1: S100 calcium binding protein A1	2.85	1.42
S100a10: S100 calcium binding protein A10	2.38	1.42
Sap18: Sin3-associated polypeptide 18	-2.96	-1.57
Sar1a: SAR1 gene homolog A (S. cerevisiae)	-2.20	-1.45
Satb1: special AT-rich sequence binding protein 1	-1.82	-1.31
Sbno1: sno, strawberry notch homolog 1 (Drosophila)	1.95	1.31
Scand3: SCAN domain containing 3	-13.25	-3.51
Scarb1: scavenger receptor class B, member 1	2.01	1.42
Scrn3: secernin 3	-4.79	-3.21
Sdccag8: serologically defined colon cancer antigen 8	-3.79	-1.60
Sdha: succinate dehydrogenase complex, subunit A,	-1.92	-1.53
Sec63: SEC63-like (S. cerevisiae)	-2.28	-1.71
Sel1l: sel-1 suppressor of lin-12-like (C. elegans)	-1.77	-1.54
Sell: selectin, lymphocyte	1.86	1.33
Senp2: SUMO/sentrin specific peptidase 2	-1.92	-1.34
Sephs1: selenophosphate synthetase 1	-4.10	-2.26

Sept2: septin 2	-2.12	-1.27
Serbp1: serpine1 mRNA binding protein 1	-2.26	-1.43
Serf2: small EDRK-rich factor 2	-2.20	-1.55
Serpine2: serine (or cysteine) peptidase inhibitor,	-10.08	-3.78
Serpini1: serine (or cysteine) peptidase inhibitor,	-5.38	-3.10
Sfrs16: splicing factor, arginine/serine-rich 16	-1.97	-1.46
Sfrs18: splicing factor, arginine/serine-rich 18	1.99	1.45
Sfrs2ip: splicing factor, arginine/serine-rich 2,	-2.25	-1.44
Sh2d5: SH2 domain containing 5	-2.60	-1.67
Shapin: SHANK-associated RH domain interacting	-2.45	-1.68
Shfm1: split hand/foot malformation (ectrodactyly)	2.11	1.52
Shisa2: shisa homolog 2 ( <i>Xenopus laevis</i> )	-9.73	-5.30
Shmt1: serine hydroxymethyltransferase 1 (soluble)	-4.78	-1.30
Shmt2: serine hydroxymethyltransferase 2	2.35	1.36
Siglecg: sialic acid binding Ig-like lectin G	2.39	1.35
Ska1: spindle and kinetochore associated complex	2.08	1.52
Slc16a12: solute carrier family 16 (monocarboxylic	-28.61	-13.00
Slc16a13: solute carrier family 16 (monocarboxylic	-3.22	-2.16
Slc19a2: solute carrier family 19 (thiamine	-2.89	-1.79
Slc20a1: solute carrier family 20, member 1	-2.61	-1.87
Slc25a37: solute carrier family 25, member 37	-2.61	-1.71
Slc35b4: solute carrier family 35, member B4	-1.98	-1.29
Slc35b4: solute carrier family 35, member B4	-2.28	-1.79
Slc37a1: solute carrier family 37 (glycerol-3-	-4.65	-2.40
Slc38a10: solute carrier family 38, member 10	-1.88	-1.31
Slc38a2: solute carrier family 38, member 2	-4.02	-1.81
Slc4a11: solute carrier family 4, sodium bicarbonate	13.95	5.58
Slc5a3: solute carrier family 5 (inositol transporters),	-2.48	-1.45
Slc7a7: solute carrier family 7 (cationic amino acid	-1.99	-1.30
Slc9a3r2: solute carrier family 9 (sodium/hydrogen	4.08	1.88
Slfn10: schlafen 10	-4.83	-2.83
Slfn8: schlafen 8	-2.18	-1.47
Sltm: SAFB-like, transcription modulator	-2.76	-1.80
Smug1: single-strand selective monofunctional uracil	-3.77	-2.28
Smyd5: SET and MYND domain containing 5	-4.92	-1.46
Snap23: synaptosomal-associated protein 23	-2.76	-1.52
Snopc3: small nuclear RNA activating complex,	-2.88	-1.67
Snx19: sorting nexin 19	-1.77	-1.30
Soat1: sterol O-acyltransferase 1	4.94	3.05
Socs2: suppressor of cytokine signaling 2	-19.79	-4.55
Son: Son DNA binding protein	2.06	1.54
Son: Son DNA binding protein	-2.26	-1.47
Sos2: son of sevenless homolog 2 ( <i>Drosophila</i> )	-1.70	-1.26
Sox13: SRY-box containing gene 13	-5.17	-2.67

Sparc: secreted acidic cysteine rich glycoprotein	-17.33	-8.93
Spata24: spermatogenesis associated 24	-1.89	-1.52
Spcs2: signal peptidase complex subunit 2 homolog	1.97	1.28
Srrd: SRR1 domain containing	-4.20	-2.59
Sssca1: Sjogren's syndrome/scleroderma autoantigen	-4.31	-2.35
Sstr2: somatostatin receptor 2	-9.89	-4.22
St3gal1: ST3 beta-galactoside alpha-2,3-	-9.67	-2.23
St6gal1: beta galactoside alpha 2,6 sialyltransferase 1	-14.42	-5.19
St7: suppression of tumorigenicity 7	-1.92	-1.39
Stx17: syntaxin 17	-2.20	-1.40
Stx3: syntaxin 3	1.88	1.35
Stx3: syntaxin 3	-2.43	-1.54
Stx3: syntaxin 3	-6.80	-3.13
Stx5a: syntaxin 5A	-2.19	-1.78
Stxbp1: syntaxin binding protein 1	-3.65	-2.32
Styx: serine/threonine/tyrosine interaction protein	-2.10	-1.44
Surf1: surfeit gene 1	-1.81	-1.27
Susd1: sushi domain containing 1	-1.93	-1.34
Taf1a: TATA box binding protein (Tbp)-associated	-2.30	-1.46
Taok1: TAO kinase 1	1.94	1.25
Tbc1d15: TBC1 domain family, member 15	2.54	1.30
Tbc1d20: TBC1 domain family, member 20	3.12	1.74
Tbc1d5: TBC1 domain family, member 5	-8.47	-4.42
Tbc1d8b: TBC1 domain family, member 8B	-2.55	-1.55
Tbl1x: transducin (beta)-like 1 X-linked	-1.59	-1.29
Tcea2: transcription elongation factor A (SII), 2	-3.75	-2.61
Tcf25: transcription factor 25 (basic helix-loop-helix)	-1.72	-1.26
Tcf3: transcription factor 3	2.05	1.26
Tcfec: transcription factor EC	3.29	1.86
Tcn2: transcobalamin 2	-2.04	-1.47
Tcn2: transcobalamin 2	-2.01	-1.48
Tcrb-J: T-cell receptor beta, joining region	-12.55	-2.01
Tcrg-V1: T-cell receptor gamma, variable 1	-7.87	-2.54
Tdrd3: tudor domain containing 3	-1.90	-1.38
Telo2: TEL2, telomere maintenance 2, homolog	-2.01	-1.25
Telo2: TEL2, telomere maintenance 2, homolog	-2.20	-1.28
Tex2: testis expressed gene 2	2.50	1.68
Tfdp2: transcription factor Dp 2	-2.39	-1.45
Tgfb1: transforming growth factor, beta induced	2.71	1.79
Tgfb3: transforming growth factor, beta receptor III	9.30	4.30
Thap2: THAP domain containing, apoptosis	-2.51	-1.86
Thbd: thrombomodulin	1.95	1.30
Thnsl1: threonine synthase-like 1 (bacterial)	-3.54	-2.01
Thsd1: thrombospondin, type I, domain 1	-3.56	-1.48

Tia1: cytotoxic granule-associated RNA binding	-1.92	-1.49
Tia1: cytotoxic granule-associated RNA binding	-2.13	-1.56
Timm8a1: translocase of inner mitochondrial	-2.13	-1.37
Timm8b: translocase of inner mitochondrial	1.92	1.40
Tinf2: Terf1 (TRF1)-interacting nuclear factor 2	-2.43	-1.77
Tiprl: TIP41, TOR signalling pathway regulator-like	-2.84	-1.59
Tjp1: tight junction protein 1	-5.71	-1.46
Tjp2: tight junction protein 2	-1.89	-1.36
Tjp2: tight junction protein 2	-2.58	-1.70
Tlcd1: TLC domain containing 1	-51.15	-7.89
Tlcd2: TLC domain containing 2	-2.24	-1.70
Tlr7: toll-like receptor 7	-8.45	-5.48
Tlr7: toll-like receptor 7	-17.41	-9.21
Tmbim4: transmembrane BAX inhibitor motif	2.23	1.49
Tmem14a: transmembrane protein 14A	-3.65	-2.10
Tmem151a: transmembrane protein 151A	19.58	7.17
Tmem161a: transmembrane protein 161A	-3.05	-1.43
Tmem19: transmembrane protein 19	-2.11	-1.42
Tmem206: transmembrane protein 206	-2.50	-1.44
Tmem215: transmembrane protein 215	-103.12	-11.30
Tmem62: transmembrane protein 62	-3.52	-1.92
Tmem86a: transmembrane protein 86A	1.90	1.28
Tmprss3: transmembrane protease, serine 3	-5.01	-2.91
Tnfaip8l2: tumor necrosis factor, alpha-induced	-1.78	-1.27
Tnfsf10: tumor necrosis factor (ligand) superfamily,	-23.20	-4.74
Tnfsf14: tumor necrosis factor (ligand) superfamily,	-2.75	-2.04
Tnik: TRAF2 and NCK interacting kinase	-6.21	-3.35
Tnik: TRAF2 and NCK interacting kinase	-9.94	-3.69
Tnni2: troponin I, skeletal, fast 2	3.23	2.09
Tomm70a: translocase of outer mitochondrial	-1.97	-1.38
Top2b: topoisomerase (DNA) II beta	-2.99	-1.76
Tor1aip1: torsin A interacting protein 1	1.80	1.46
Tox: thymocyte selection-associated high mobility	-13.33	-4.40
Tpm2: tropomyosin 2, beta	-2.14	-1.49
Tpm3: tropomyosin 3, gamma	1.85	1.25
Tpr: translocated promoter region	-1.89	-1.33
Trappc1: trafficking protein particle complex 1	2.25	1.30
Trat1: T cell receptor associated transmembrane	-13.87	-6.45
Trem12: triggering receptor expressed on myeloid	-1.92	-1.28
Trem12: triggering receptor expressed on myeloid	-2.13	-1.61
Trf: transferring	-1.89	-1.27
Trim34: tripartite motif-containing 34	-2.48	-1.49
Trim34: tripartite motif-containing 34	-2.94	-1.68
Trim8: Tripartite motif-containing 8	-23.83	-7.53

Trmt1: TRM1 tRNA methyltransferase 1 homolog	-1.69	-1.35
Trmu: tRNA 5-methylaminomethyl-2-thiouridylate	-2.00	-1.38
Trp53bp1: transformation related protein 53 binding	-3.42	-2.07
Trp53i11: transformation related protein 53 inducible	-6.96	-3.67
Trpc2: transient receptor potential cation channel,	-1.77	-1.35
Tsc22d1: TSC22 domain family, member 1	-4.21	-2.40
Tshz1: teashirt zinc finger family member 1	1.75	1.30
Tspyl2: TSPY-like 2	-2.54	-1.74
Tstd2: thiosulfate sulfurtransferase (rhodanese)-like	-2.33	-1.82
Ttc14: tetratricopeptide repeat domain 14	-2.81	-1.52
Ttc19: tetratricopeptide repeat domain 19	-3.08	-1.70
Ttc3: tetratricopeptide repeat domain 3	2.28	1.62
Ttpal: tocopherol (alpha) transfer protein-like	-5.64	-2.32
Tuft1: tuftelin 1	-3.57	-1.78
Tusc1: tumor suppressor candidate 1	1.68	1.36
Ubp2l: ubiquitin associated protein 2-like	-2.17	-1.26
Ube2b: ubiquitin-conjugating enzyme E2B, RAD6	-2.33	-1.56
Ube2c: ubiquitin-conjugating enzyme E2C	2.56	1.77
Ube2i: ubiquitin-conjugating enzyme E2I	-8.85	-3.48
Ubqln2: ubiquilin 2	-10.12	-4.00
Ubxn11: UBX domain protein 11	-7.51	-3.93
Ulk2: Unc-51 like kinase 2 (C. elegans)	-3.03	-2.13
Usp36: ubiquitin specific peptidase 36	2.72	1.27
Usp40: ubiquitin specific peptidase 40	-3.07	-2.25
Usp9x: ubiquitin specific peptidase 9, X chromosome	-3.12	-1.27
Vamp5: vesicle-associated membrane protein 5	-8.88	-5.54
Vars2: valyl-tRNA synthetase 2, mitochondrial	-3.67	-2.19
Vav1: vav 1 oncogene	1.83	1.32
Vcam1: vascular cell adhesion molecule 1	-27.23	-5.05
Vcpip1: valosin containing protein (p97)/p47 complex	-5.35	-1.83
Vmn2r84: Vomeronasal 2, receptor 84	-17.85	-2.06
Vopp1: vesicular, overexpressed in cancer,	-1.73	-1.38
Vps13a: vacuolar protein sorting 13A (yeast)	-6.51	-2.69
Vps37a: vacuolar protein sorting 37A (yeast)	-3.61	-1.30
Vps4a: vacuolar protein sorting 4a (yeast)	1.54	1.27
Vps4b: vacuolar protein sorting 4b (yeast)	-6.54	-3.37
Vps54: vacuolar protein sorting 54 (yeast)	-1.82	-1.26
Vps54: vacuolar protein sorting 54 (yeast)	-3.75	-2.42
Wbp5: WW domain binding protein 5	2.34	1.58
Wdr37: WD repeat domain 37	-3.56	-2.36
Wdr37: WD repeat domain 37	-4.16	-2.53
Wdr48: WD repeat domain 48	-1.89	-1.38
Wipf1: WAS/WASL interacting protein family, member	1.89	1.27
Wrnip1: Werner helicase interacting protein 1	-2.06	-1.68

Wwp1: WW domain containing E3 ubiquitin protein	-2.16	-1.30
Xist: inactive X specific transcripts	-4.49	-3.09
Xpot: exportin, tRNA (nuclear export receptor	-1.74	-1.41
Xrcc3: X-ray repair complementing defective repair in	-1.84	-1.37
Ypel1: yippee-like 1 (Drosophila)	8.40	3.59
Ywhaz: tyrosine 3-monooxygenase/tryptophan 5-	1.73	1.33
Zbtb33: zinc finger and BTB domain containing 33	-2.12	-1.32
Zdhhc23: zinc finger, DHHC domain containing 23	-3.43	-2.30
Zdhhc3: zinc finger, DHHC domain containing 3	-2.25	-1.72
Zfp157: zinc finger protein 157	-4.33	-3.01
Zfp191: zinc finger protein 191	-2.82	-1.38
Zfp238: zinc finger protein 238	1.96	1.34
Zfp260: zinc finger protein 260	-28.39	-7.95
Zfp316: zinc finger protein 316	-11.70	-7.04
Zfp354c: zinc finger protein 354C	-7.27	-4.35
Zfp367: zinc finger protein 367	1.99	1.57
Zfp386: zinc finger protein 386 (Kruppel-like)	-2.30	-1.27
Zfp414: zinc finger protein 414	1.73	1.51
Zfp429: zinc finger protein 429	-2.53	-1.62
Zfp445: zinc finger protein 445	-3.49	-1.47
Zfp592: zinc finger protein 592	1.86	1.36
Zfp599: zinc finger protein 599	-5.24	-2.22
Zfp64: Zinc finger protein 64	-5.58	-2.85
Zfp704: zinc finger protein 704	-2.91	-1.61
Zfp706: zinc finger protein 706	2.40	1.56
Zfp709: zinc finger protein 709	-3.72	-2.74
Zfp764: zinc finger protein 764	-2.26	-1.63
Zfp783: zinc finger protein 783	-4.65	-2.87
Zfp810: zinc finger protein 810	-1.74	-1.28
Zfp826: zinc finger protein 826	-1.85	-1.38
Zfp871: zinc finger protein 871	2.75	1.68
Zfp91: zinc finger protein 91	-2.83	-1.89
Zfp94: zinc finger protein 94	-10.92	-4.39
Zfyve1: zinc finger, FYVE domain containing 1	-3.13	-1.56
Zfyve16: zinc finger, FYVE domain containing 16	-3.97	-2.10
Zkscan17: zinc finger with KRAB and SCAN domains	-1.63	-1.29
Zmym3: zinc finger, MYM-type 3	-8.70	-4.20
Zmynd17: zinc finger, MYND domain containing 17	-3.92	-1.74
Zscan12: zinc finger and SCAN domain containing 12	-2.40	-1.73
Zswim7: zinc finger, SWIM-type containing 7	-2.59	-1.86
Zufsp: zinc finger with UFM1-specific peptidase	-1.91	-1.26
Zwint: ZW10 interactor	-3.71	-1.62