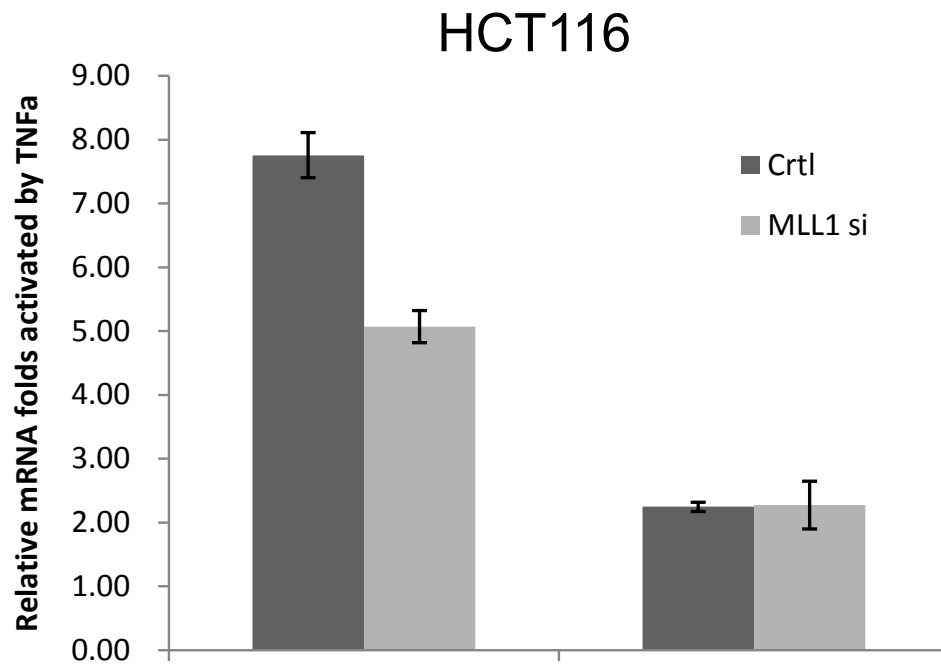
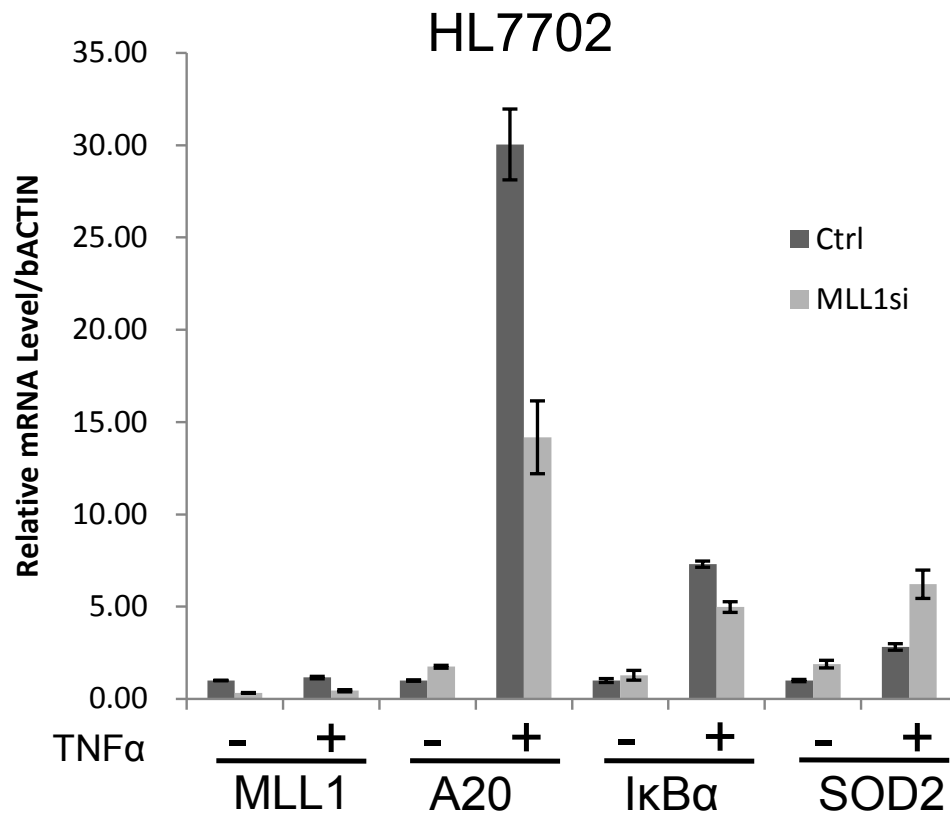


Sup. Fig. 1 The basal mRNA level of NF-κB targeting genes in wide type and *Mll1*^{-/-} cells.

The wide type and *Mll1*^{-/-} cell were harvested and RT-PCR was performed to analyze the expression of indicated genes. Totally 40 reported NF-κB targeting genes were assayed (only part of data were presented). Among them, the expression of Ptges was significantly reduced.

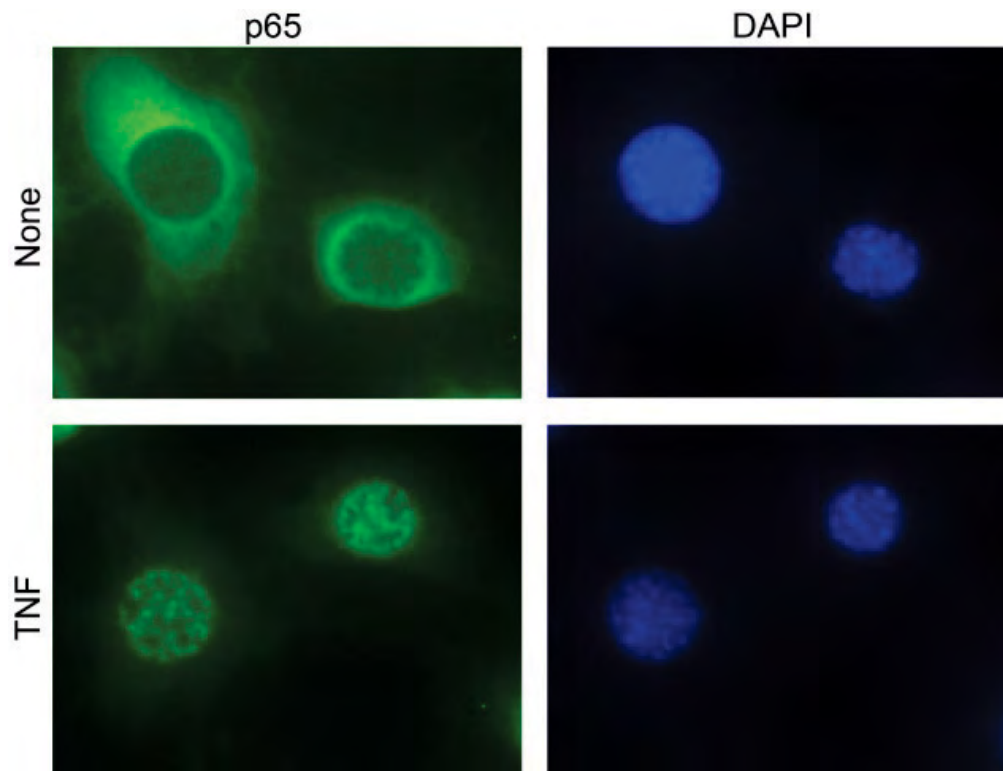


Sup. Fig. 2 MLL1 regulated the activation of I κ B α in HCT116 cell. HCT116 cell was transiently transfected with MLL1 siRNA and treated by TNF α 72hr after transfection. The elevated levels of I κ B α and SOD2 mRNA were monitored by real time PCR.

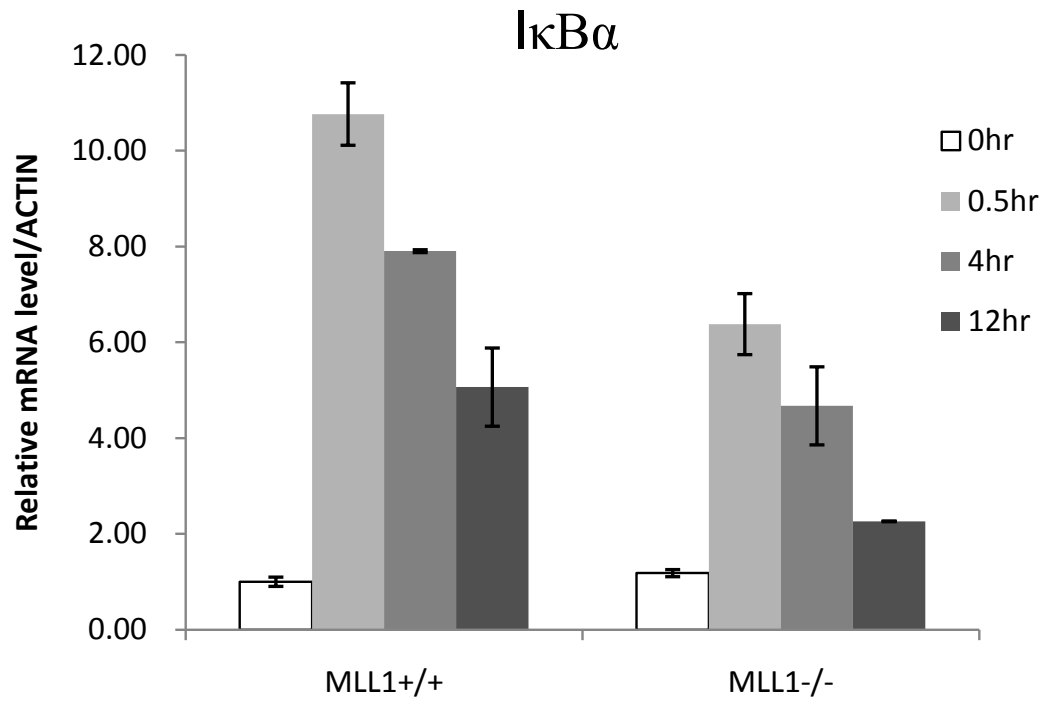


Sup. Fig. 3 MLL1 regulated the activation of NFκB downstream genes in HL7702 cell.

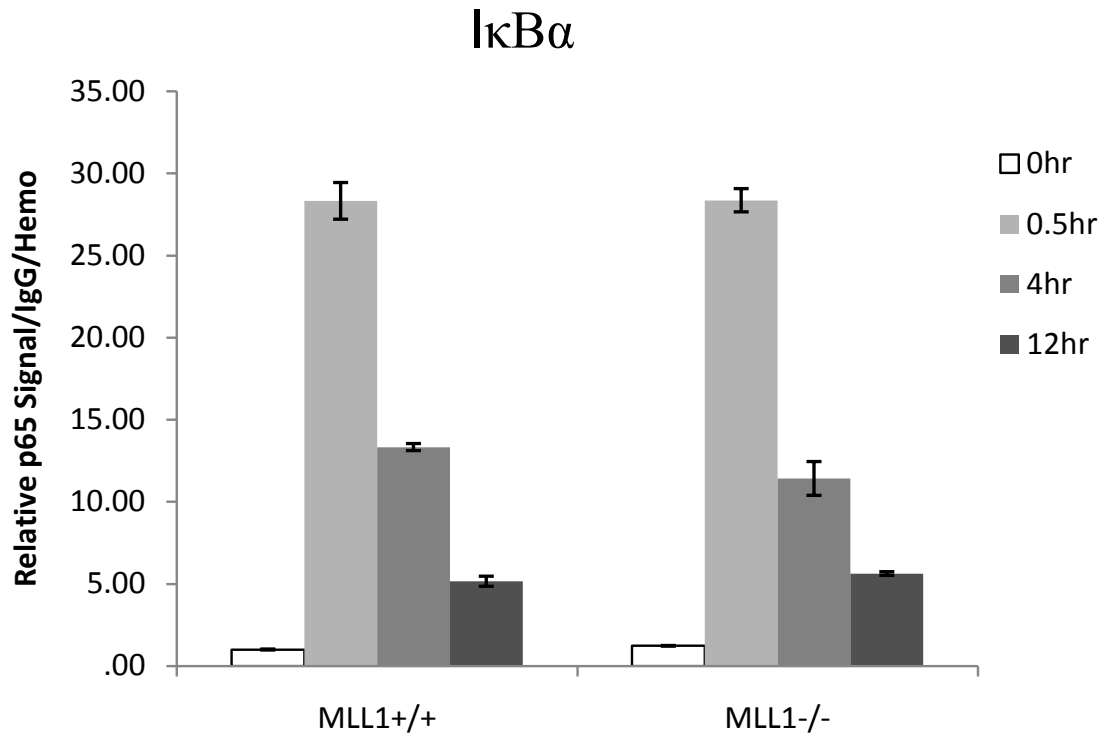
Immortalized liver cell HL7702 was transiently transfected with MLL1 siRNA and treated by TNFα 72hr after transfection. The elevated mRNA levels of indicated genes were assayed by real time PCR.



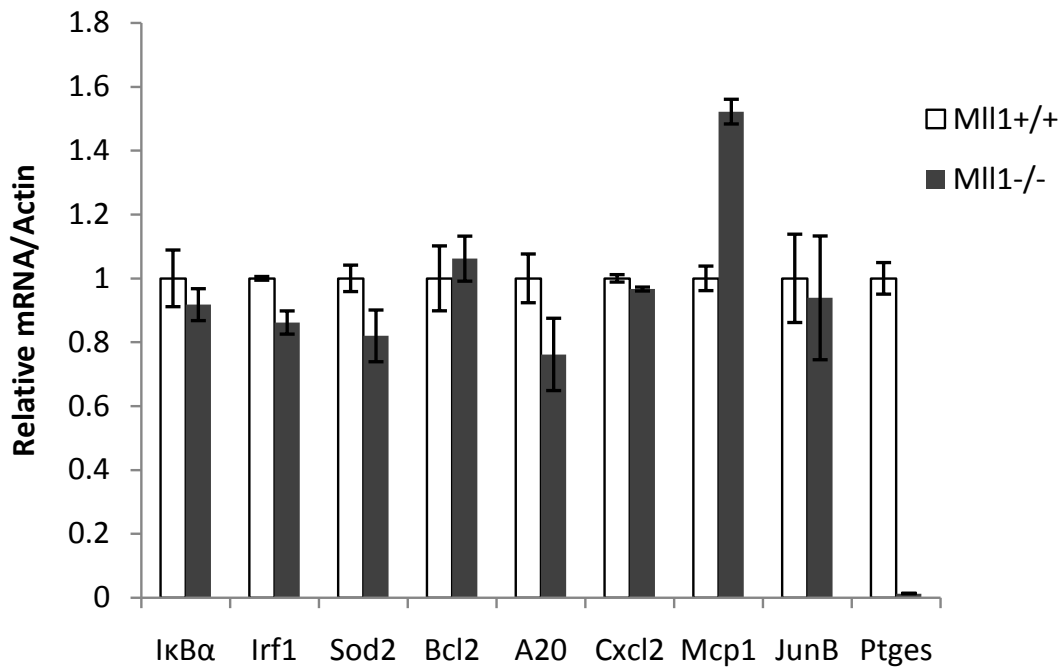
Sup. Fig. 4 NF- κ B was translocated into nuclear in *Mll1*^{-/-} cell. Immunofluorescent staining experiment was performed to study the localization of p65 in *Mll1*^{-/-} cell. p65 is localized in the cytoplasm (upper) and translocated into nuclear (lower) after TNF α treatment, which is no difference from wide type cell.



Sup. Fig. 5 The $I\kappa B\alpha$ mRNA level at different time points after TNF α treatment. $MLL1^{+/+}$ and $MLL1^{-/-}$ cells were treated with TNF and harvested at 0hr, 0.5hr, 4hr and 12hr. The $I\kappa B\alpha$ mRNA levels were analyzed.

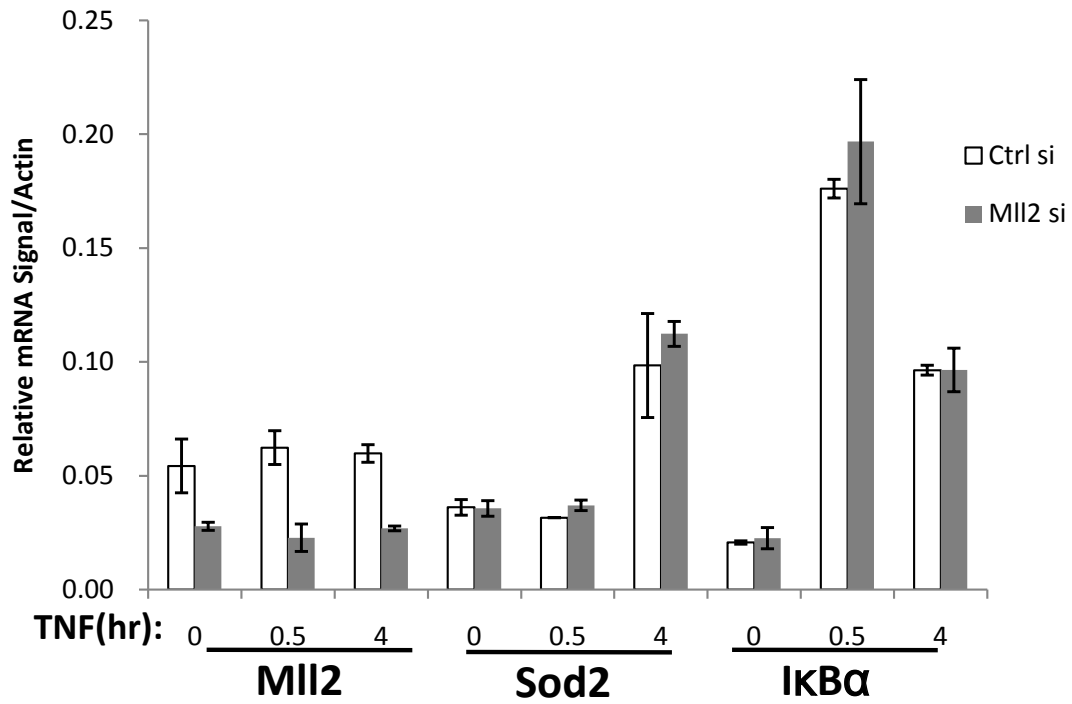


Sup. Fig. 6 The bound p65 amount on $I\kappa B\alpha$ promoter at different time points after TNF α treatment. *MLL1*^{+/+} and *MLL1*^{-/-} cells were treated with TNF and harvested at 0hr, 0.5hr, 4hr and 12hr. The amount of p65 protein on $I\kappa B\alpha$ promoter was analyzed by CHIP assay.



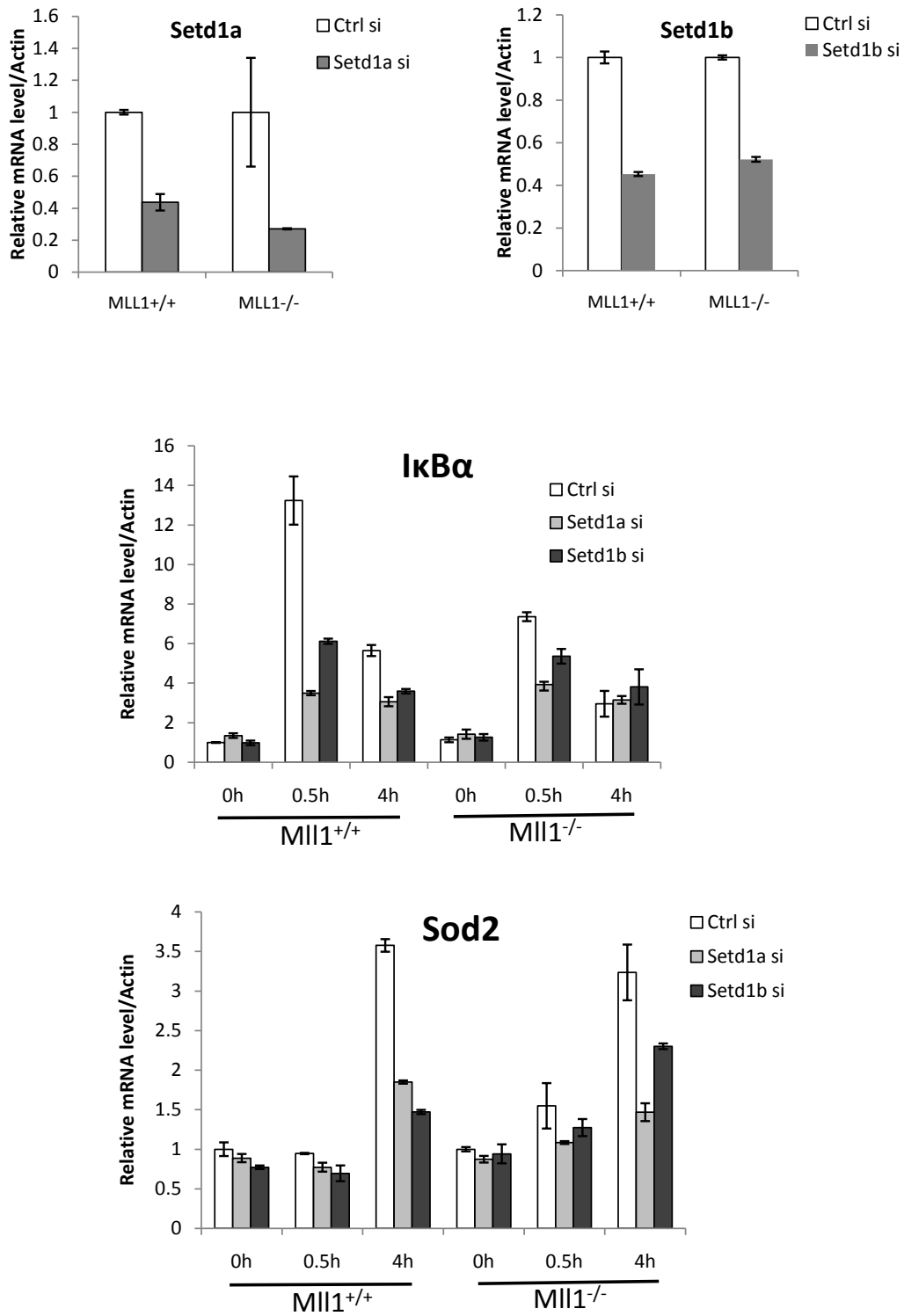
Sup. Fig. 7 The amount of Wdr5 on Ikbα increased upon TNFα treatment in *Mll1*^{-/-} cell.

ChIP assay was performed to analyze the amount of Wdr5 on Ikbα promoter. Wdr5 bound Ikbα promoter in wide type MEF and increased upon TNFα treatment. The bound Wdr5 decreased in *Mll1*^{-/-} cell, but still increased after treatment.



Sup. Fig. 8 Mll2/HRX2 did not regulate the expression of *Ikbα* and *Sod2* in MEF cell.

Mll2 was knocked down by siRNA in MEF cell and the mRNA levels of indicated genes were assayed by quantitative PCR following reverse transcription.



Sup. Fig. 9 Setd1a and Setd1b regulated the expression of the expression of *IκBα* and *Sod2* in MEF cell. *Setd1a* and *Setd1b* were knocked down in *Mll1*^{+/+} and *Mll1*^{-/-} cells by siRNA respectively. The up panels showed the knockdown effect assayed by real time PCR. The middle and bottom showed that the expression of both *IκBα* (middle) and *Sod2* (bottom) were impaired with *Setd1a* or *Setd1b* deficiency.

Supplementary Table 1

The sequences of primers used in the study

Primers for RT PCR		
Gene	Forward primer	Reverse Primer
mb-Actin	aggtcatcactattggcaac	agaggtctttacggatgtca
mWdr82	CTCTAGCAGCGATGATGACT	GGTCCACACCGTACTTCTTA
mM111	ATGGGGAATGATGACAAGT	GGTGACAGGCTTAATTGGT
mM112	AGCACAGTGTGGAGCTG	AGCTGGTACAGAAGAGCAAG
mM113	CAAGCCTTATTTGATTCCAC	GTTCTTCCATTTGGCATATT
mM114	CATGGTGCCTGAAGATGT	TCTCTGATGCTGATGACGTA
mSet1A	GTCATGGGCAACATCATT	TGAGGAGTGTAAAGCCATT
mp65	ATGGCTACTATGAGGCTGAC	GTCTCGCTTCTTCACACACT
mB94	ATACCTACTTGCTGCTGCTC	GACACCTTGAAGCTCCTGT
mPGES	TACAGGAGTGACCCAGATGT	CGAGGAAGAGGAAAGGATAG
mikBa	TCCTCAACTCCAGAACAAC	GGGTATTTCTCGAAAGTCT
mSOD2	ACACCATTTTCTGGACAAAC	CAAAGTCACGCTTGATAGC
mMCP1	CTGGAGCATCCACGTGTT	CATCTTGCTGGTGAATGAG
mIAP1	ATAGAACACGCCAAATGGT	GCTTGAATCTCATCAACAAAC
mCox2	GTACCCGGACTGGATTCTAT	GGCTTCAGCAGTAATTTGAT
mJunB	CAGCTACTTTTCGGGTCAG	GATCAAGCGCTCCAGTTC
mC-myc	tagtgctgcatgaggagac	caccacatcaatttcttctct
mIL6	cacatgttctctggaatc	catcgttgttcatacaatcag
mTap1	ACTCCTGCTTATCTTGGATG	CTTGGGGCTCTCATACAG
mTAPBP	TCTACCTGGCTACGGTACAC	GTGCTGGTGTAGAGACTC
mTraf1	ATGAGAGGAGAATACGATGC	GGTTGTTCTGGTCAAGTAGC
mTraf2	ACCGCTACTGCTCCTTCT	TACAGGCCTTCATAGACACA
mTraf3	AAGCATCATCAAAGACAAGG	ATTCCGACAGTAGACCTGAA
mGch1	TAGTGATTGAAGCGACACAC	TGGTGTAGTGACAGTCTTG
mGfpt2	CCGAGGTTATGATGTTGACT	GGTGACGACAGTCTTGTGAT
mKlrc2	GCTGAACTGAAGAAGCAGAT	TTGGACAATGAGGACAAG
mIcam1	CACGCTACCTCTGCTCCT	GGATGGATGGATACCTGAG
mI127ra	TTCTGCTGTCGCTGATGT	GACCGACGCTGTAGCACT
mNFkB1	CTGAGTCCTGCTCCTTCTAA	CTGTGTAGCCCATCTGTTG
mNFkB2	TGGACACATACAGGAAGACC	CAATAGACCCACCAAGTCC
mcRel	AGAACTGTGGAAGTGTGAGG	GTCATTCAACACAAAACGAA
mTrim16	GAACTCAAGTGTCTGCCATT	TGTCACAGGCATATTGAAGA
mTnip1	CTGTCACCACCGACATCT	GTAGCAGGATGTACCTGGAC
mCyb5	GTCTAATTCAGTTGGTGGA	AAGTCAATCTTCTGCCATGT

mPsmb9	ACGGAAGAAGTCCACACC	GAATCAGAGCCCACCAC
mCxc12	ACGGAAGAACCAAAGAGAA	AAATAAGTGAACTCTCAGACAGC
mTNFa	TACTGAACTTCGGGGTGAT	GCCATAGAAGTATGAGAGG
mBID	CCTTCAACCAAGGAAGAATA	CGAGATGTCTGGCAATGT
mCtgf	GTGTGTGACGAGCCCAAG	GCCAAATGTGTCTTCCAGT
hb-Actin	GATCCACATCTGCTGGAAG	CAGCACAATGAAGATCAAGA
hWdr82	CTCCATCGTGCTCTATGACT	GATGAGGTCCACACCATATT
hMLL1	cgggaaaagtattacgacag	cacacgagtgattgatgaag
hMl12	TGTGCTCTATGCCAACATTA	TTCTCCAGAGCTTCATGATT
hMLL3	gtttggagtatcgacagcat	tatccagaaagaccattgct
hMl14	GACTGGAAAGCAGAAGTCTC	AGCCACACGTTCTCTAAATC
hSetd1A	acagtgacctgctgaaactc	acgtattcgatgacctctc
hSetd1b	acagtgacctgctcaagttc	acgtactcgatgacctctc
hp65	CTGGAGCAGGCTATCAGTC	ACAGCATTCAGGTCGTAGTC
hB94	ACCTACATGCTGCTGCTC	CCATACCCTGCAGCTCAC
hIkBa	GTCTTGGGTGCTGATGT	GAGAATAGCCCTGGTAGGTAA
hSOD2	GCACGTTACTACCTTCAGT	CTCCAGTTGATTACATTCC
hI16	AACCTGAACCTTCAAAGAT	ACTCCAAAAGACCAGTGATG
hcIAP1	GCCATCTAGTGTCCAGTTC	AGCATTTGACATCATCATTG
hcIAP2	TCAAGTTCAAGCCAGTTACC	GACTCTGCATTTTCATCTCC
hCox2	CCAGACAAGCAGGCTAATAC	TGATAGCCACTCAAGTGTTG
hJunB	CGACGACTCATACACAGCTA	TCGGTTTCAGGAGTTGTAG
hTap1	GTGGTCCTCTCCTCTTTG	TGAGCCATCTGTAGAAATCC
hTAPBP	GTCCCTGTCTCTGCTCCT	CTCCACGAACCAACACTC
hTraf1	CCACCTCTATCCACCAGAG	CAGGGTCTGCTGAAGCTC
hTraf2	CAAGATTGAAGCCCTGAGTA	ATCTCCAAGACCTTCTGCTC
hTraf3	GGAGAGCGTGGACAAGAG	CACACTCAGCATCTGGTCAT
hGch1	CTACCAGGAGACCATCTCAG	TATGTCCTTACAATCACCA
hGfpt2	ACAAGCTCTCCACAGAACAG	CCTCTTCATCCGTGTCTTAC
hKlrc2	TATGACTGCCAAGGTTACTG	ATCAGGACAATGCAAATGAT
hIcam1	GTGACCATCTACAGCTTCC	TCACACTTACTGTACCTC
hI127ra	CTCTCACCAACCTCTCTTTG	ACCAGTAGCTCCGTGCTC
hNFkB1	TGGTATCAGACGCCATCTA	GCTGTCTGTCCATTCTTAC
hNFkB2	AATTGAACTCCTCATTGTG	CCTCTCTGCTTAGGCTGTT
hcRel	TTCTGACCAGGAAGTTAGTGA	TTTGCTTTATTGCCGTAAGT
hTrim16	ACACCATAGTCTCCCTGGAT	GATGGCATTTCATTCAACT
hTnip1	AATGCAAGGGATAAAGATGT	TTGTCCTTCACTAGCTCCTC
hCyb5	ACAAGGTGTACGATTTGACC	GTTCTCAGTAGCGTCACCTC
hPsmb9	ATCGAGAGGACTTGCTGTC	GGTTCCATATACCTGACCT
hCxc12	CAAGAACATCCAAAGTGTGA	CCATTCTTGAGTGTGGCTAT

hCtgf	GAGTGGGTGTGTGACGAG	CGTGTCTTCCAGTCGGTA
Primers for ChIP		
Name	Forward	Reverse
mHemob	CTTTGGGCATCTAGCTTTTA	AATCCTTGCAAGAAACAAAA
mIkBapro	GAGGACTTTCCAGCCACTCA	GCTCGTCCTCCACTGAGAAG
mSOD2proF	AGTCTCAGGGGCAACAAAGA	GCCCCTCTGACCCAGTTAAT
mI16pro	gggatgtctgtagctcattc	gcagagaggaacttcatagc
mTnip1pro	CCTGCAGAAGCTCAGAAA	ACGAGGTGATCTGAAGATGT
mA20pro	catggatgtgacgtggaa	cggagaaactcctaggtc
mMcp1pro	ccacagtttctctcttccac	atcacctggataagtgatg

Supplementray Table 2 Differential expressed genes of MEF wide type cell with or without TNF α

ID	ACCESSION NUMBER	NAME	TNF	Ctrl	FOLDCHANGE
17260	NM 001170537.1	myocyte enhancer factor 2C	0.0000	0.0449	0.0000
73887	XR 106601.1	RIKEN cDNA 4930417022 gene	0.0000	0.2437	0.0000
73887	XR 106411.1	RIKEN cDNA 4930417022 gene	0.0000	0.2437	0.0000
100504427	XR 104672.1	predicted gene 13404	0.0182	0.2388	0.0762
100504427	XR 107364.1	predicted gene 13404	0.0183	0.2211	0.0826
78445	XR 106969.1	RIKEN cDNA C330013E15 gene	0.1018	0.7192	0.1416
78445	XR 105710.1	RIKEN cDNA C330013E15 gene	0.1018	0.7192	0.1416
442801	NM 177566.3	Rho guanine nucleotide exchange factor (GEF) 15	0.0255	0.1455	0.1749
69903	NM 028544.1	Ras interacting protein 1	0.0564	0.2390	0.2360
100342	NM 175307.6	family with sequence similarity 46, member B	0.1406	0.5044	0.2788
56379	NM 019659.3	potassium inwardly-rectifying channel, subfamily J, member 1	0.0931	0.3286	0.2832
56379	NM 001168354.1	potassium inwardly-rectifying channel, subfamily J, member 1	0.0930	0.3284	0.2832
11606	NM 007428.3	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	0.1926	0.6801	0.2832
14747	NM 008153.3	chemokine-like receptor 1	0.8669	2.5226	0.3437
22403	NM 016873.2	WNT1 inducible signaling pathway protein 2	0.4007	1.0714	0.3740
11754	NM 009675.2	amine oxidase, copper containing 3	0.1870	0.4676	0.3999
100503611	XM 003084596.1	-	0.6688	1.4808	0.4516
100039781	NM 027511.1	histidine rich carboxyl terminus 1	2.1003	4.5465	0.4620
64929	NM 022886.2	sciellin	0.6556	1.2876	0.5092
22417	NM 009523.1	wingless-related MMTV integration site 4	2.9543	5.6667	0.5213
56745	NM 019959.2	Clq and tumor necrosis factor related protein 1	1.6079	3.0580	0.5258
100042198	XR 104937.1	predicted gene 3716	0.9085	1.7203	0.5281
100042198	XR 107688.1	predicted gene 3716	1.0012	1.8815	0.5321
15902	NM 010496.3	inhibitor of DNA binding 2	12.2842	22.8301	0.5381
105844	NM 130859.2	caspase recruitment domain family, member 10	1.7540	3.2205	0.5446
70788	NM 027551.2	kelch-like 30 (Drosophila)	2.9826	5.4573	0.5465
23882	NM 011817.2	growth arrest and DNA-damage-inducible 45 gamma	12.7631	23.2863	0.5481
68169	NM 172399.3	RIKEN cDNA A930038C07 gene	3.8765	7.0064	0.5533

14181	NM 008009.3	fibroblast growth factor binding protein 1	3.7718	6.8084	0.5540
329540	NM 001001986.2	RIKEN cDNA 8430427H17 gene	1.1553	2.0751	0.5567
13653	NM 007913.5	early growth response 1	1.1868	2.1249	0.5585
12159	NM 007554.2	bone morphogenetic protein 4	4.9474	8.7537	0.5652
71093	NM 153778.3	atonal homolog 8 (Drosophila)	4.1587	7.3353	0.5669
17130	NM 008542.3	MAD homolog 6 (Drosophila)	2.3821	4.1757	0.5705
329540	NM 001134300.2	RIKEN cDNA 8430427H17 gene	1.0585	1.8549	0.5706
68404	NM 153529.1	neuritin 1	9.8921	17.1447	0.5770
76969	NM 023850.2	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	10.1686	17.5478	0.5795
231861	NM 001122730.1	trinucleotide repeat containing 18	3.2867	5.5961	0.5873
223650	NM 144848.2	epiplakin 1	0.6346	1.0706	0.5928
231861	NM 178242.2	trinucleotide repeat containing 18	2.4112	4.0547	0.5947
271221	NM 198642.2	RIKEN cDNA 5031414D18 gene	3.7752	6.2986	0.5994
74760	NM 144538.2	RAB3A interacting protein (rabin3)-like 1	5.1150	8.3631	0.6116
380912	NM 199029.2	zinc finger protein 395	2.6201	4.2724	0.6133
14200	NM 010212.3	four and a half LIM domains 2	13.6753	22.2197	0.6155
15426	NM 010466.2	homeobox C8	6.8197	11.0521	0.6171
77889	NM 029999.4	limb-bud and heart	3.1456	5.0193	0.6267
19252	NM 013642.3	dual specificity phosphatase 1	15.8758	25.1264	0.6318
70445	NM 054042.2	CD248 antigen, endosialin	11.5292	18.1946	0.6337
21825	NM 011580.3	thrombospondin 1	51.2370	80.6369	0.6354
16582	NM 010631.2	kinesin family member C3	4.3592	6.7345	0.6473
16582	NM 001145831.1	kinesin family member C3	4.1775	6.4013	0.6526
16582	NM 001145832.1	kinesin family member C3	4.7334	7.1883	0.6585
170676	NM 001040611.1	paternally expressed 10	3.8115	5.7253	0.6657
170676	NM 130877.2	paternally expressed 10	3.8115	5.7253	0.6657
67306	NM 173181.3	family with sequence similarity 164, member A	24.2472	36.0316	0.6729
104445	NM 027219.3	CDC42 effector protein (Rho GTPase binding) 1	18.9825	27.8494	0.6816
53881	NM 017391.3	solute carrier family 5 (inositol transporters), member 3	13.5437	19.4589	0.6960
18596	NM 001146268.1	platelet derived growth factor receptor, beta polypeptide	13.0414	18.5416	0.7034

18596	NM 008809.2	platelet derived growth factor receptor, beta polypeptide	13.0684	18.5585	0.7042
57265	NM 020510.2	frizzled homolog 2 (Drosophila)	11.0146	15.6363	0.7044
94242	NM 001168333.1	tubulointerstitial nephritis antigen-like 1	43.7188	61.8658	0.7067
14313	NM 008046.2	follistatin	26.5054	37.4681	0.7074
94242	NM 023476.3	tubulointerstitial nephritis antigen-like 1	40.5717	57.2028	0.7093
20410	NM 011366.2	sorbin and SH3 domain containing 3	18.2764	25.7422	0.7100
20346	NM 009152.3	sema domain, immunoglobulin domain (Ig), short basic domain, secr	11.6199	16.1153	0.7210
11826	NM 007472.2	aquaporin 1	78.5188	108.0738	0.7265
100503984	XR 107221.1	-	704.9197	524.9652	1.3428
75788	NM 001038627.1	SMAD specific E3 ubiquitin protein ligase 1	30.0263	22.2618	1.3488
75788	NM 029438.3	SMAD specific E3 ubiquitin protein ligase 1	29.9830	22.2181	1.3495
100503946	XR 107210.1	-	736.1257	543.3139	1.3549
15364	NM 010441.2	high mobility group AT-hook 2	151.6343	110.8795	1.3676
83946	NM 001081216.1	pleckstrin homology domain interacting protein	11.8800	8.6521	1.3731
328949	NM 001085373.1	mutated in colorectal cancers	10.4393	7.5425	1.3841
328949	NM 001085374.1	mutated in colorectal cancers	10.6870	7.7204	1.3843
19791	NR 003278.1	18S ribosomal RNA	499.2789	360.4836	1.3850
17118	NM 008538.2	myristoylated alanine rich protein kinase C substrate	27.3839	19.6516	1.3935
67073	NM 025951.2	phosphatidylinositol 4-kinase type 2 beta	21.1863	15.2003	1.3938
218454	NM 172589.2	lipoma HMGIC fusion partner-like 2	26.8897	19.2346	1.3980
67073	NM 028744.2	phosphatidylinositol 4-kinase type 2 beta	20.6771	14.7820	1.3988
215449	NM 024457.2	RAS related protein 1b	314.0320	224.2397	1.4004
16880	NM 013584.2	leukemia inhibitory factor receptor	10.2795	7.3299	1.4024
18828	NM 008880.2	phospholipid scramblase 2	56.8543	40.5030	1.4037
26921	NM 008696.2	mitogen-activated protein kinase kinase kinase kinase 4	39.3240	27.9976	1.4046
20348	NM 013657.5	sema domain, immunoglobulin domain (Ig), short basic domain, secr	60.1780	42.8094	1.4057
12977	NM 001113530.1	colony stimulating factor 1 (macrophage)	124.2404	87.9714	1.4123
226525	NM 177644.5	RAS protein activator like 2	4.7036	3.3242	1.4150
16476	NM 010591.2	Jun oncogene	19.2680	13.5904	1.4178
12977	NM 007778.4	colony stimulating factor 1 (macrophage)	159.7792	112.5273	1.4199

14182	NM 001079909.1	fibroblast growth factor receptor 1	20.2126	14.2323	1.4202
14182	NM 010206.2	fibroblast growth factor receptor 1	19.9201	13.9416	1.4288
24136	NM 015753.3	zinc finger E-box binding homeobox 2	6.3854	4.4639	1.4304
14182	NM 001079908.1	fibroblast growth factor receptor 1	19.8939	13.9006	1.4312
13486	NM 026106.4	down-regulator of transcription 1	29.4534	20.5493	1.4333
208846	NM 172464.2	dishevelled associated activator of morphogenesis 1	7.5518	5.2661	1.4341
12977	NM 001113529.1	colony stimulating factor 1 (macrophage)	163.4552	113.8839	1.4353
208846	NM 026102.2	dishevelled associated activator of morphogenesis 1	7.4237	5.1657	1.4371
17936	NM 008667.3	Ngfi-A binding protein 1	18.9093	13.1578	1.4371
78388	NM 080638.3	major vault protein	18.0370	12.4491	1.4489
20912	NM 011504.1	syntaxin binding protein 3A	13.6674	9.4132	1.4520
140780	NM 080708.1	BMP2 inducible kinase	6.9804	4.8030	1.4533
54216	NM 001122758.1	protocadherin 7	11.4650	7.8501	1.4605
21664	NM 009344.3	pleckstrin homology-like domain, family A, member 1	32.8883	22.4914	1.4623
12457	NM 009834.2	CCR4 carbon catabolite repression 4-like (<i>S. cerevisiae</i>)	9.8646	6.7216	1.4676
22762	NM 011766.5	zinc finger protein, multitype 2	17.5195	11.8835	1.4743
20971	NM 011521.2	syndecan 4	59.1218	39.9927	1.4783
30953	NM 001113419.1	schwannomin interacting protein 1	11.1351	7.5303	1.4787
268396	NM 177364.3	SH3 and PX domains 2B	12.3986	8.3803	1.4795
15979	NM 010511.2	interferon gamma receptor 1	44.6664	30.1706	1.4805
16195	NM 010560.3	interleukin 6 signal transducer	62.4263	42.1626	1.4806
30953	NM 001113421.1	schwannomin interacting protein 1	11.9842	8.0936	1.4807
14042	NM 010162.2	exostoses (multiple) 1	51.4466	34.5395	1.4895
16423	NM 010581.3	CD47 antigen (Rh-related antigen, integrin-associated signal tran	49.6476	33.2580	1.4928
380711	NM 001015046.2	RAP1 GTPase activating protein 2	6.7583	4.5178	1.4959
18412	NM 011018.2	sequestosome 1	389.4593	260.1461	1.4971
23872	NM 011809.3	E26 avian leukemia oncogene 2, 3' domain	33.3136	22.1853	1.5016
21928	NM 009396.2	tumor necrosis factor, alpha-induced protein 2	28.1665	18.7552	1.5018
20496	NM 009194.3	solute carrier family 12, member 2	53.6863	35.5881	1.5085
30953	NM 001113420.1	schwannomin interacting protein 1	15.3918	10.1965	1.5095

30953	NM 013928.5	schwannomin interacting protein 1	14.5393	9.6318	1.5095
54216	NM 018764.2	protocadherin 7	21.5416	14.2519	1.5115
16362	NM 001159396.1	interferon regulatory factor 1	16.5818	10.9424	1.5154
18933	NM 001025570.1	paired related homeobox 1	10.5276	6.9171	1.5220
268515	NM 198423.3	BAH domain and coiled-coil containing 1	4.7554	3.1148	1.5267
71409	NM 172409.2	formin-like 2	8.1921	5.3624	1.5277
110521	NM 007772.2	human immunodeficiency virus type I enhancer binding protein 1	3.0667	1.9942	1.5379
52552	NM 001081009.1	poly (ADP-ribose) polymerase family, member 8	13.5426	8.7941	1.5400
18481	NM 008778.2	p21 protein (Cdc42/Rac)-activated kinase 3	7.0763	4.5827	1.5441
170737	NM 133206.3	zinc and ring finger 1	6.7605	4.3767	1.5447
16362	NM 008390.2	interferon regulatory factor 1	17.1987	11.0824	1.5519
102626	NM 178907.3	mitogen-activated protein kinase-activated protein kinase 3	9.9259	6.3906	1.5532
99382	NM 178890.3	ankyrin repeat and BTB (POZ) domain containing 2	5.5385	3.5475	1.5612
433022	NM 001134480.1	phosphatidylinositol-specific phospholipase C, X domain containing	2.1635	1.3833	1.5640
98376	NM 178883.5	golgin, RAB6-interacting	10.4566	6.6407	1.5746
100463512	NM 001190732.1	-	113.7580	72.2355	1.5748
18933	NM 175686.3	paired related homeobox 1	22.8892	14.5037	1.5782
52118	NM 027514.2	poliovirus receptor	18.4506	11.6816	1.5795
21356	NM 001025313.1	TAP binding protein	24.8124	15.6451	1.5859
12608	NM 009883.3	CCAAT/enhancer binding protein (C/EBP), beta	30.1458	19.0011	1.5865
21356	NM 009318.2	TAP binding protein	24.8915	15.6753	1.5879
18933	NM 011127.2	paired related homeobox 1	22.7663	14.3271	1.5890
14538	NM 133219.1	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	3.2357	2.0359	1.5893
67338	NM 001164569.1	ring finger and FYVE like domain containing protein	10.5859	6.6496	1.5920
170737	NM 001168622.1	zinc and ring finger 1	6.1730	3.8729	1.5939
16177	NM 008362.2	interleukin 1 receptor, type I	2.8510	1.7883	1.5942
12837	NM 007739.2	collagen, type VIII, alpha 1	32.0221	20.0786	1.5948
67338	NM 001164570.1	ring finger and FYVE like domain containing protein	10.7568	6.7268	1.5991
67338	NM 001007465.3	ring finger and FYVE like domain containing protein	11.0411	6.9021	1.5997
16177	NM 001123382.1	interleukin 1 receptor, type I	2.8175	1.7552	1.6053

67338	NM 026097.3	ring finger and FYVE like domain containing protein	10.6633	6.6350	1.6071
12192	NM 007564.5	zinc finger protein 36, C3H type-like 1	13.5355	8.4117	1.6091
20620	NM 152804.2	polo-like kinase 2 (Drosophila)	226.8847	140.7800	1.6116
67338	NM 001164571.1	ring finger and FYVE like domain containing protein	10.9996	6.8126	1.6146
15980	NM 008338.3	interferon gamma receptor 2	48.4175	29.8441	1.6223
18033	NM 008689.2	nuclear factor of kappa light polypeptide gene enhancer in B-cell	34.4185	21.1595	1.6266
58244	NM 021433.3	syntaxin 6	21.9780	13.5074	1.6271
231549	NM 178701.3	leucine rich repeat containing 8D	12.1910	7.4796	1.6299
231549	NM 001122768.1	leucine rich repeat containing 8D	12.1168	7.4340	1.6299
75234	NM 029219.1	ring finger protein 19B	20.7091	12.7049	1.6300
74194	NM 028810.2	Rho family GTPase 3	29.4216	17.9490	1.6392
192657	NM 138953.2	elongation factor RNA polymerase II 2	22.6277	13.6865	1.6533
22031	NM 001048206.1	TNF receptor-associated factor 3	10.4963	6.3396	1.6557
20352	NM 013659.4	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM)	6.6758	4.0122	1.6639
14573	NM 010275.2	glial cell line derived neurotrophic factor	5.8571	3.5149	1.6663
22031	NM 011632.2	TNF receptor-associated factor 3	10.5627	6.3387	1.6664
16362	NM 001159393.1	interferon regulatory factor 1	10.8842	6.5247	1.6682
236285	NM 173414.3	LanC lantibiotic synthetase component C-like 3 (bacterial)	6.3554	3.8088	1.6686
75296	NM 201230.4	Fgfr1 oncogene partner	13.8136	8.2592	1.6725
114774	NM 054056.2	PRKC, apoptosis, WT1, regulator	17.2460	10.2983	1.6746
19288	NM 008987.3	pentraxin related gene	48.8220	29.0910	1.6783
320924	NM 178793.4	collagen and calcium binding EGF domains 1	11.1861	6.6199	1.6898
16155	NM 008349.5	interleukin 10 receptor, beta	17.5100	10.3314	1.6948
19225	NM 011198.3	prostaglandin-endoperoxide synthase 2	27.0702	15.9376	1.6985
19734	NM 011267.3	regulator of G-protein signaling 16	7.4345	4.3718	1.7005
75599	NM 029357.3	protocadherin 1	3.0870	1.8115	1.7041
387609	NM 199449.2	zinc fingers and homeoboxes 2	3.1821	1.8640	1.7072
672511	XM 001476651.2	ring finger protein 213	5.8450	3.4128	1.7127
672511	XM 001477846.2	ring finger protein 213	5.8450	3.4128	1.7127
100504142	XR 106553.1	predicted gene, 20084	240.3367	140.3107	1.7129

100504142	XR 105374.1	predicted gene, 20084	240.3367	140.3107	1.7129
380855	NM 001013769.1	regulator of sex limited protein 1	4.7169	2.7497	1.7154
260315	NM 001081035.1	neuron navigator 3	0.9002	0.5237	1.7191
100504290	XR 105381.1	predicted gene, 20152	21.0056	12.0925	1.7371
100504290	XR 106558.1	predicted gene, 20152	21.1812	12.1505	1.7432
100125931	NR 030676.1	RIKEN cDNA A130049A11 gene	3.6301	2.0793	1.7458
72747	NM 028341.4	tetratricopeptide repeat domain 39C	7.9645	4.5361	1.7558
15273	NM 010437.2	human immunodeficiency virus type I enhancer binding protein 2	5.4886	3.1134	1.7629
408065	NM 001001186.3	zinc finger protein 456	1.9103	1.0698	1.7856
229675	NM 172684.2	rosbin, round spermatid basic protein 1	5.7704	3.1845	1.8120
20308	NM 011338.2	chemokine (C-C motif) ligand 9	17.2538	9.4835	1.8193
26399	NM 011943.2	mitogen-activated protein kinase kinase 6	7.2214	3.9488	1.8287
53970	NM 017395.2	regulatory factor X, 5 (influences HLA class II expression)	2.0734	1.1278	1.8385
16477	NM 008416.2	Jun-B oncogene	10.6419	5.7279	1.8579
319622	NM 001033380.3	inositol 1,4,5-triphosphate receptor interacting protein-like 2	44.3796	23.7390	1.8695
73683	NM 001111111.1	autophagy related 16 like 2 (S. cerevisiae)	2.2595	1.2060	1.8736
231830	NM 174850.3	MICAL-like 2	28.4579	15.1649	1.8766
20656	NM 013671.3	superoxide dismutase 2, mitochondrial	28.3965	15.0895	1.8819
13874	NM 007950.2	epiregulin	17.2754	9.1729	1.8833
108767	NM 001033225.2	proline-rich nuclear receptor coactivator 1	9.7834	5.1865	1.8863
223881	NM 172612.3	Rho family GTPase 1	63.4554	33.5264	1.8927
75985	NM 029494.2	RAB30, member RAS oncogene family	7.7293	4.0790	1.8949
671535	NM 001163576.1	poly (ADP-ribose) polymerase family, member 10	5.1870	2.7172	1.9090
18174	NM 008732.2	solute carrier family 11 (proton-coupled divalent metal ion trans	28.1269	14.7291	1.9096
671535	NM 001163575.1	poly (ADP-ribose) polymerase family, member 10	5.3393	2.7918	1.9125
64292	NM 022415.3	prostaglandin E synthase	6.7331	3.4511	1.9510
67844	NM 026405.3	RAB32, member RAS oncogene family	67.8149	34.7469	1.9517
12125	NM 009754.3	BCL2-like 11 (apoptosis facilitator)	4.2829	2.1795	1.9651
100503984	XR 104558.1	-	24.2867	12.2887	1.9763
100503984	XR 104553.1	-	25.6072	12.9568	1.9763

100503984	XR 104554.1	-	24.1888	12.2392	1.9763
100503984	XR 104561.1	-	25.5255	12.9155	1.9763
100503984	XR 104562.1	-	27.3260	13.8265	1.9763
100503984	XR 104560.1	-	24.7879	12.5423	1.9763
100503984	XR 104557.1	-	25.0726	12.6863	1.9763
100503984	XR 104555.1	-	24.7369	12.5165	1.9763
100503984	XR 104563.1	-	28.2008	14.2479	1.9793
100503984	XR 104559.1	-	24.3228	12.2887	1.9793
100503984	XR 104556.1	-	24.0312	12.1414	1.9793
230073	NM 172689.3	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	1.7282	0.8609	2.0074
12125	NM 207681.2	BCL2-like 11 (apoptosis facilitator)	4.3432	2.1615	2.0094
74732	NM 001163590.1	syntaxin 11	3.1775	1.5791	2.0123
270118	NM 001013813.3	mastermind like 2 (Drosophila)	2.6256	1.2998	2.0200
74732	NM 001163591.1	syntaxin 11	3.3312	1.6469	2.0227
319909	NM 001126490.1	isthmin 1 homolog (zebrafish)	1.1413	0.5635	2.0253
12125	NM 207680.2	BCL2-like 11 (apoptosis facilitator)	4.2339	2.0894	2.0264
212168	NM 172503.3	zinc finger, SWIM domain containing 4	4.6611	2.2975	2.0287
108797	NM 175366.3	mex3 homolog B (C. elegans)	6.2886	3.0933	2.0330
70701	NM 001081205.1	NIPA-like domain containing 1	0.9605	0.4717	2.0363
17082	NM 001025602.2	interleukin 1 receptor-like 1	31.0010	15.1780	2.0425
67916	NM 080555.2	phosphatidic acid phosphatase type 2B	17.1256	8.3487	2.0513
74732	NM 029075.1	syntaxin 11	3.1328	1.5202	2.0607
100503392	XR 107188.1	-	3.8623	1.8678	2.0679
100503392	XR 105978.1	-	3.8623	1.8678	2.0679
22038	NM 011636.2	phospholipid scramblase 1	44.7919	21.5776	2.0758
100502974	XR 107727.1	predicted gene, 19481	4.4408	2.1310	2.0839
18174	NM 001146161.1	solute carrier family 11 (proton-coupled divalent metal ion trans	32.4984	15.5207	2.0939
16878	NM 001039537.1	leukemia inhibitory factor	6.5125	3.0480	2.1366
17082	NM 010743.2	interleukin 1 receptor-like 1	53.3054	24.9395	2.1374
16878	NM 008501.2	leukemia inhibitory factor	6.2228	2.9103	2.1382

100503392	XR 107187.1	-	4.1181	1.9161	2.1492
100503392	XR 105977.1	-	4.1181	1.9161	2.1492
57875	NM 020581.2	angiopoietin-like 4	1.9028	0.8847	2.1509
100503984	XR 104572.1	-	3.1527	1.4563	2.1648
100503984	XR 104565.1	-	3.1695	1.4641	2.1648
192656	NM 138952.3	receptor (TNFRSF)-interacting serine-threonine kinase 2	45.2043	20.8356	2.1696
209086	NM 010156.3	sterile alpha motif domain containing 9-like	14.2532	6.5460	2.1774
100503984	XR 104570.1	-	12.4206	5.6963	2.1805
100503984	XR 104569.1	-	12.3266	5.6532	2.1805
100503984	XR 104567.1	-	11.8513	5.3866	2.2001
11796	NM 007464.3	baculoviral IAP repeat-containing 3	3.6884	1.6753	2.2016
100503984	XR 104568.1	-	12.2280	5.5361	2.2088
100503984	XR 104566.1	-	12.1348	5.4939	2.2088
326623	NM 177371.3	tumor necrosis factor (ligand) superfamily, member 15	0.7176	0.3218	2.2300
270118	NM 173776.3	mastermind like 2 (Drosophila)	3.0188	1.3528	2.2315
50908	NM 001097617.1	complement component 1, s subcomponent	1.7196	0.7684	2.2380
239650	NM 177716.3	expressed sequence AI836003	2.8046	1.2457	2.2514
50908	NM 144938.2	complement component 1, s subcomponent	1.6859	0.7465	2.2584
15937	NM 133662.2	immediate early response 3	34.3661	15.1534	2.2679
100503551	XR 107722.1	predicted gene 15817	2.1234	0.9284	2.2872
100503551	XR 106291.1	predicted gene 15817	2.1234	0.9284	2.2872
70737	NM 001037711.2	cingulin	1.3052	0.5654	2.3084
16206	NM 008377.2	leucine-rich repeats and immunoglobulin-like domains 1	25.1269	10.8787	2.3097
170677	NM 130878.2	cadherin-related family member 1	0.4505	0.1901	2.3701
20312	NM 009142.3	chemokine (C-X3-C motif) ligand 1	0.7390	0.3097	2.3860
319236	NM 001146007.1	tripartite motif-containing 12C	0.5071	0.2124	2.3877
12521	NM 001136055.1	CD82 antigen	2.6123	1.0928	2.3903
12521	NM 007656.4	CD82 antigen	2.4983	1.0321	2.4206
20821	NM 001082552.1	tripartite motif-containing 21	1.5322	0.6264	2.4462
215113	NM 173388.1	solute carrier family 43, member 2	2.7445	1.1175	2.4559

18034	NM 019408.3	nuclear factor of kappa light polypeptide gene enhancer in B-cell	58.9402	23.9000	2.4661
18034	NM 001177370.1	nuclear factor of kappa light polypeptide gene enhancer in B-cell	62.8664	25.4739	2.4679
12609	NM 007679.4	CCAAT/enhancer binding protein (C/EBP), delta	4.0962	1.6596	2.4683
20821	NM 009277.3	tripartite motif-containing 21	1.5457	0.6238	2.4778
18034	NM 001177369.1	nuclear factor of kappa light polypeptide gene enhancer in B-cell	62.2524	25.1053	2.4797
230738	NM 153159.2	zinc finger CCCH type containing 12A	15.0109	6.0299	2.4894
71683	NM 001048207.1	glycophorin C	15.8227	6.3333	2.4983
21929	NM 001166402.1	tumor necrosis factor, alpha-induced protein 3	13.3463	5.3201	2.5087
21929	NM 009397.3	tumor necrosis factor, alpha-induced protein 3	13.1228	5.2182	2.5148
100048759	XM 003086792.1	-	5.9885	2.3270	2.5735
434438	NM 001135198.1	coiled-coil domain containing 36	0.5216	0.2005	2.6017
12266	NM 009778.2	complement component 3	5.8334	2.2281	2.6180
18812	NM 011118.2	prolactin family 2, subfamily c, member 3	33.4373	12.7137	2.6300
17533	NM 008625.2	mannose receptor, C type 1	1.5246	0.5760	2.6469
107849	NM 181852.1	prolactin family 2, subfamily c, member 5	14.0089	5.2485	2.6691
20568	NM 011414.3	secretory leukocyte peptidase inhibitor	4.1181	1.5329	2.6864
18811	NM 031191.1	prolactin family 2, subfamily c, member 2	36.9197	13.7408	2.6869
19260	NM 008979.1	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	2.8108	1.0421	2.6973
71816	NM 027934.2	ring finger protein 180	0.4627	0.1715	2.6980
80859	NM 001159395.1	nuclear factor of kappa light polypeptide gene enhancer in B-cell	6.1356	2.2726	2.6998
80859	NM 030612.3	nuclear factor of kappa light polypeptide gene enhancer in B-cell	5.6188	2.0768	2.7055
18208	NM 008744.2	netrin 1	4.8428	1.7853	2.7125
80859	NM 001159394.1	nuclear factor of kappa light polypeptide gene enhancer in B-cell	5.8570	2.1589	2.7130
666317	NM 001045532.1	Prolactin family 2, subfamily c, member 1	5.0628	1.8389	2.7531
57783	NM 021327.2	TNFAIP3 interacting protein 1	30.0159	10.7610	2.7893
545551	NR 033629.1	cDNA sequence BC021767	1.0428	0.3723	2.8010
630663	XM 904245.4	predicted gene 7040	9.9369	3.4792	2.8561
11988	NM 007514.3	solute carrier family 7 (cationic amino acid transporter, y+ syst	0.2404	0.0840	2.8632
11988	NM 001044740.1	solute carrier family 7 (cationic amino acid transporter, y+ syst	0.2411	0.0842	2.8632
20556	NM 011408.1	schlafen 2	2.7381	0.9423	2.9058

16997	NM 013589.3	latent transforming growth factor beta binding protein 2	0.2106	0.0708	2.9733
630663	XM 001473551.2	predicted gene 7040	13.9888	4.6690	2.9961
16149	NM 001042605.1	CD74 antigen (invariant polypeptide of major histocompatibility c	1.3238	0.4284	3.0899
16149	NM 010545.3	CD74 antigen (invariant polypeptide of major histocompatibility c	1.4713	0.4657	3.1592
19698	NM 009046.2	avian reticuloendotheliosis viral (v-rel) oncogene related B	14.9871	4.7315	3.1675
233552	NM 201352.2	glycerophosphodiester phosphodiesterase domain containing 5	1.9709	0.6096	3.2333
12051	NM 033601.3	B-cell leukemia/lymphoma 3	3.6036	1.0416	3.4595
21822	NM 011579.3	T-cell specific GTPase 1	0.3563	0.1027	3.4689
14239	NM 010226.2	forkhead box S1	0.9542	0.2751	3.4689
20306	NM 013654.3	chemokine (C-C motif) ligand 7	342.8538	98.8195	3.4695
56489	NM 019777.3	inhibitor of kappaB kinase epsilon	6.0930	1.7114	3.5602
20296	NM 011333.3	chemokine (C-C motif) ligand 2	#####	433.7946	3.7885
100039796	NM 001145164.1	T-cell specific GTPase 2	0.3427	0.0896	3.8229
21942	NM 001077508.1	tumor necrosis factor receptor superfamily, member 9	0.6437	0.1624	3.9645
14102	NM 007987.2	Fas (TNF receptor superfamily member 6)	9.7176	2.4512	3.9645
626578	NM 001039646.2	guanylate-binding protein 10	0.3242	0.0818	3.9645
18035	NM 010907.2	nuclear factor of kappa light polypeptide gene enhancer in B-cell	66.4125	16.4009	4.0493
16193	NM 031168.1	interleukin 6	4.9981	1.2276	4.0716
18606	NM 001136077.1	ectonucleotide pyrophosphatase/phosphodiesterase 2	0.9115	0.2233	4.0811
56619	NM 019948.2	C-type lectin domain family 4, member e	0.7095	0.1718	4.1296
320207	NM 177320.2	phosphoinositide-3-kinase, regulatory subunit 5, p101	1.8842	0.4464	4.2214
21942	NM 011612.2	tumor necrosis factor receptor superfamily, member 9	0.6532	0.1521	4.2948
238393	NM 001033335.3	serine (or cysteine) peptidase inhibitor, clade A, member 3F	0.4199	0.0978	4.2948
18606	NM 015744.2	ectonucleotide pyrophosphatase/phosphodiesterase 2	1.0805	0.2447	4.4150
102502	NM 001033210.3	plastin 1 (I-isoform)	0.6961	0.1561	4.4600
238393	NM 001168294.1	serine (or cysteine) peptidase inhibitor, clade A, member 3F	0.4282	0.0960	4.4600
238393	NM 001168295.1	serine (or cysteine) peptidase inhibitor, clade A, member 3F	0.4726	0.1060	4.4600
100702	NM 194336.2	guanylate binding protein 6	0.4128	0.0916	4.5051
14102	NM 001146708.1	Fas (TNF receptor superfamily member 6)	3.5421	0.7798	4.5426
18788	NM 011111.4	serine (or cysteine) peptidase inhibitor, clade B, member 2	1.0686	0.2336	4.5744

21942	NM 001077509.1	tumor necrosis factor receptor superfamily, member 9	0.7267	0.1535	4.7353
12363	NM 007609.2	caspase 4, apoptosis-related cysteine peptidase	12.0475	2.5167	4.7871
18788	NM 001174170.1	serine (or cysteine) peptidase inhibitor, clade B, member 2	1.0608	0.2177	4.8730
214854	NM 153408.2	neutralized homolog 3 homolog (Drosophila)	7.3203	1.4660	4.9933
14468	NM 010259.2	guanylate binding protein 1	0.2915	0.0512	5.6989
547253	NM 001039530.3	poly (ADP-ribose) polymerase family, member 14	0.1528	0.0249	6.1449
18037	NM 008690.3	nuclear factor of kappa light polypeptide gene enhancer in B-cell	6.8181	1.1019	6.1878
17384	NM 019471.2	matrix metallopeptidase 10	1.4331	0.2305	6.2170
14469	NM 010260.1	guanylate binding protein 2	1.6490	0.2627	6.2771
22029	NM 009421.3	TNF receptor-associated factor 1	10.6692	1.6442	6.4890
630294	NM 001177467.1	predicted gene 7030	0.7952	0.1203	6.6074
240675	NM 172840.2	von Willebrand factor A domain containing 2	0.1288	0.0186	6.9378
100503422	XM 003085129.1	predicted gene, 19684	0.4659	0.0672	6.9378
100503422	XM 003085162.1	predicted gene, 19684	0.4665	0.0672	6.9378
547347	NM 001034909.3	predicted gene 6034	0.3064	0.0442	6.9378
17392	NM 010809.1	matrix metallopeptidase 3	0.3270	0.0388	8.4245
17386	NM 008607.2	matrix metallopeptidase 13	1.1358	0.1348	8.4245
20715	NM 009251.1	serine (or cysteine) peptidase inhibitor, clade A, member 3G	2.0601	0.2310	8.9200
16819	NM 008491.1	lipocalin 2	18.0602	1.9871	9.0887
216799	NM 145827.3	NLR family, pyrin domain containing 3	0.1689	0.0179	9.4156
17395	NM 013599.2	matrix metallopeptidase 9	0.1347	0.0113	11.8934
414084	NM 001001495.2	TNFAIP3 interacting protein 3	3.2149	0.2488	12.9226
15945	NM 021274.1	chemokine (C-X-C motif) ligand 10	5.3800	0.4071	13.2149
20311	NM 009141.2	chemokine (C-X-C motif) ligand 5	337.7799	24.9941	13.5144
22329	NM 011693.3	vascular cell adhesion molecule 1	21.2693	1.3054	16.2930
14825	NM 008176.3	chemokine (C-X-C motif) ligand 1	319.9473	18.5556	17.2426
12981	NM 009969.4	colony stimulating factor 2 (granulocyte-macrophage)	0.6228	0.0349	17.8401
408066	XR 001629.2	cDNA sequence BC067074	0.1007	0.0044	22.7956
16165	NM 008356.3	interleukin 13 receptor, alpha 2	0.5735	0.0231	24.7779
20297	NM 016960.2	chemokine (C-C motif) ligand 20	56.3419	1.6931	33.2767

20210	NM 011315.3	serum amyloid A 3	4.6446	0.1358	34.1934
20297	NM 001159738.1	chemokine (C-C motif) ligand 20	55.8253	1.6142	34.5847
71132	NM 001042418.1	calcium-binding tyrosine-(Y)-phosphorylation regulated (fibroushe	0.1741	0.0000	Inf
14728	NM 013532.2	leukocyte immunoglobulin-like receptor, subfamily B, member 4	0.2769	0.0000	Inf
20310	NM 009140.2	chemokine (C-X-C motif) ligand 2	0.4951	0.0000	Inf
13982	NM 007956.4	estrogen receptor 1 (alpha)	0.0662	0.0000	Inf
18126	NM 010927.3	nitric oxide synthase 2, inducible	1.2452	0.0000	Inf
16365	NM 008392.1	immunoresponsive gene 1	0.1381	0.0000	Inf
15894	NM 010493.2	intercellular adhesion molecule 1	0.1407	0.0000	Inf
408066	XR 035217.2	cDNA sequence BC067074	0.0759	0.0000	Inf
100503281	XR 108224.1	-	0.4655	0.0000	Inf

Supplementary Table 3 Differential expressed genes of MLL1-/- MEF cell with or without TNF α

ID	ACCESSION NUMBER	NAME	TNF	Ctrl	FOLDCHANGE
12695	NM_001005787.1	InaD-like (Drosophila)	0.0000	0.1546	0.0000
100045736	XM_001474842.2	-	0.0722	1.2501	0.0578
100039589	XM_003084688.1	predicted gene 2329	0.0722	1.1112	0.0650
380698	NM_199152.2	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	0.0023	0.0260	0.0867
245607	NM_001163016.1	G protein-coupled receptor associated sorting protein 2	0.0274	0.2769	0.0991
245607	NM_001163017.1	G protein-coupled receptor associated sorting protein 2	0.0275	0.2780	0.0991
245607	NM_001163015.1	G protein-coupled receptor associated sorting protein 2	0.0272	0.2742	0.0991
100503347	XM_003086491.1	predicted gene, 19648	0.0400	0.2308	0.1734
19784	NR_004439.1	ribonuclease P RNA-like 2	0.2223	1.2111	0.1836
24131	NM_011918.4	LIM domain binding 3	0.2466	0.6916	0.3566
24131	NM_001039072.2	LIM domain binding 3	0.2533	0.7001	0.3618
24131	NM_001039071.2	LIM domain binding 3	0.2561	0.7079	0.3618
24131	NM_001039074.2	LIM domain binding 3	0.2509	0.6936	0.3618
24131	NM_001039073.2	LIM domain binding 3	0.2624	0.7148	0.3671
19017	NR_027710.1	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	0.1675	0.4523	0.3702
19017	NM_008904.2	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	0.1683	0.4545	0.3702
11754	NM_009675.2	amine oxidase, copper containing 3	0.2003	0.5324	0.3762
100047224	XM_003086950.1	-	1.6493	4.3521	0.3790
195727	NM_001081052.1	Nance-Horan syndrome (human)	0.3465	0.7773	0.4458
223650	NM_144848.2	epiplakin 1	0.2347	0.5250	0.4471
668066	XM_001004338.2	predicted gene 14418	1.5995	3.4546	0.4630
243385	NM_183183.2	GPRIN family member 3	1.6040	3.3894	0.4732
244867	NM_175535.3	Rho GTPase activating protein 20	1.5055	3.0903	0.4872
625703	XM_904090.4	-	1.7629	3.5234	0.5003
13838	NM_007936.3	Eph receptor A4	1.0641	2.1247	0.5008

231861	NM_178242.2	trinucleotide repeat containing 18	3.0532	6.0066	0.5083
242481	NM_172868.2	paralemmin 2	1.5201	2.9836	0.5095
240427	NM_053099.2	SET binding protein 1	0.7680	1.4917	0.5149
66395	NM_009643.1	AHNAK nucleoprotein (desmoyokin)	96.8238	183.5819	0.5274
67393	NM_133687.2	CXXC finger 5	2.4654	4.5681	0.5397
330938	NM_178118.2	DIX domain containing 1	6.9659	12.5231	0.5562
100503159	XR_108047.1	-	6.5701	11.6379	0.5645
26408	NM_008580.4	mitogen-activated protein kinase kinase kinase 5	1.8536	3.2225	0.5752
231861	NM_001122730.1	trinucleotide repeat containing 18	3.9304	6.6259	0.5932
17309	NM_010795.3	mannoside acetylglucosaminyltransferase 3	5.4516	9.0626	0.6016
100042862	XM_003085879.1	predicted gene 4076	234.2826	388.2562	0.6034
100042862	XM_001478943.2	predicted gene 4076	246.8104	408.8011	0.6037
11630	NM_172393.2	absent in melanoma 1	11.4334	18.8011	0.6081
214137	NM_172525.2	Rho GTPase activating protein 29	6.1049	9.9728	0.6122
271564	NM_173028.3	vacuolar protein sorting 13A (yeast)	3.3181	5.4093	0.6134
68861	NM_001033145.2	RIKEN cDNA 1190002N15 gene	18.2794	28.9826	0.6307
77057	NM_029858.2	stonin 1	13.2659	20.9501	0.6332
54127	NM_016844.2	ribosomal protein S28	718.3538	452.7200	1.5868
667682	XM_991853.3	predicted gene 8759	1085.2008	683.1858	1.5884
14455	NR_002840.2	growth arrest specific 5	65.1405	40.7494	1.5986
671641	XM_001479052.2	predicted gene 10063	1981.0625	1234.7892	1.6044
100042561	XM_003086748.1	predicted gene 10177	175.4771	109.3654	1.6045
100042561	XM_001478520.2	predicted gene 10177	175.4771	109.3654	1.6045
100046297	XM_001477362.2	-	703.1160	436.4319	1.6111
100043718	XM_001480721.2	predicted gene 4604	236.1249	146.3981	1.6129
14775	NM_008160.5	glutathione peroxidase 1	92.2788	57.2039	1.6132
12859	NM_009942.2	cytochrome c oxidase, subunit Vb	141.0200	87.3991	1.6135
54217	NM_018730.3	ribosomal protein L36	284.0859	175.7512	1.6164
30055	NM_013895.4	translocase of inner mitochondrial membrane 13 homolog (yeast)	59.4914	36.7882	1.6171

635470	XM_003086282.1	predicted gene 14407	157.9373	97.5871	1.6184
100046079	XM_001475417.2	-	166.5536	102.7729	1.6206
27370	NM_013765.2	ribosomal protein S26	1431.4740	881.8388	1.6233
67673	NM_026305.2	transcription elongation factor B (SIII), polypeptide 2	147.6390	90.6721	1.6283
665533	XM_003086398.1	predicted gene 13004	529.7444	324.9924	1.6300
665533	XM_977600.2	predicted gene 13004	529.7444	324.9924	1.6300
546695	XM_003086080.1	predicted gene, 16519	106.6450	65.3828	1.6311
545487	XM_619852.4	predicted gene 14439	156.3150	95.8047	1.6316
16206	NM_008377.2	leucine-rich repeats and immunoglobulin-like domains 1	49.2302	30.1324	1.6338
20335	NM_011343.3	SEC61, gamma subunit	104.4851	63.9293	1.6344
19981	NM_009084.4	ribosomal protein L37a	536.2309	328.0250	1.6347
18034	NM_001177370.1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2, p49/p100	74.7410	45.7093	1.6351
15980	NM_008338.3	interferon gamma receptor 2	35.3064	21.5783	1.6362
18034	NM_001177369.1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2, p49/p100	73.8610	45.0676	1.6389
18034	NM_019408.3	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2, p49/p100	70.1387	42.7890	1.6392
72338	NM_028203.1	WD repeat domain 89	77.4768	47.2237	1.6406
57294	NM_027015.4	ribosomal protein S27	683.5674	415.9998	1.6432
100043813	NM_001190258.1	predicted gene 9846	676.2565	411.5506	1.6432
100048613	XM_001480380.2	-	107.3612	65.2260	1.6460
67126	NM_025983.3	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, epsilon subunit	97.9056	59.4226	1.6476
12857	NM_009941.2	cytochrome c oxidase subunit IV isoform 1	312.4543	189.3574	1.6501
27425	NM_013795.5	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit g	227.3541	137.6219	1.6520
100042348	XM_001478455.2	predicted gene 10221	234.8841	142.1616	1.6522
230075	NM_001033305.2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6	89.4306	54.0857	1.6535
100503897	XR_107153.1	predicted gene, 19947	161.3130	97.2955	1.6580
100503897	XR_105996.1	predicted gene, 19947	161.3130	97.2955	1.6580

69878	NM_027246.1	small nuclear ribonucleoprotein polypeptide F	105.8570	63.8354	1.6583
17133	NM_010755.3	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian)	22.5600	13.5280	1.6677
12010	NM_009735.3	beta-2 microglobulin	363.5380	217.7566	1.6695
99382	NM_178890.3	ankyrin repeat and BTB (POZ) domain containing 2	7.1917	4.3023	1.6716
12866	NM_009945.3	cytochrome c oxidase, subunit VIIa 2	156.6245	93.5164	1.6748
666642	XM_985134.3	predicted pseudogene 8210	93.1370	55.5507	1.6766
629750	NR_033523.1	predicted gene 11517	130.3621	77.7199	1.6773
13014	NM_007793.3	cystatin B	234.4187	139.6702	1.6784
751556	NR_030451.1	microRNA 682	435.4102	259.3550	1.6788
100040259	NM_001111330.1	predicted pseudogene 16379	248.8759	147.5966	1.6862
57294	NR_033727.1	ribosomal protein S27	344.5862	204.2557	1.6870
192657	NM_138953.2	elongation factor RNA polymerase II 2	15.9917	9.4558	1.6912
66491	NM_025593.1	polymerase (RNA) II (DNA directed) polypeptide L	17.0794	10.0725	1.6956
67945	NM_018860.4	ribosomal protein L41	2637.6470	1554.9638	1.6963
17392	NM_010809.1	matrix metalloproteinase 3	42.4850	24.9785	1.7009
233016	NM_144923.3	biliverdin reductase B (flavin reductase (NADPH))	32.8141	19.2852	1.7015
19944	NM_009082.2	ribosomal protein L29	110.8143	64.9454	1.7063
21929	NM_001166402.1	tumor necrosis factor, alpha-induced protein 3	9.5689	5.5609	1.7208
67184	NM_023312.2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	19.4337	11.2887	1.7215
20656	NM_013671.3	superoxide dismutase 2, mitochondrial	29.2301	16.9286	1.7267
223881	NM_172612.3	Rho family GTPase 1	87.7922	50.8359	1.7270
21929	NM_009397.3	tumor necrosis factor, alpha-induced protein 3	9.4206	5.4543	1.7272
665964	XM_980604.3	predicted gene 7866	522.4457	302.1944	1.7288
22186	NM_019883.3	ubiquitin A-52 residue ribosomal protein fusion product 1	1030.7802	595.3682	1.7313
100039782	XM_003086738.1	predicted gene 10709	131.6384	76.0086	1.7319
665964	XM_003086743.1	predicted gene 7866	530.0628	305.8558	1.7330
11927	NM_009720.2	ATX1 (antioxidant protein 1) homolog 1 (yeast)	63.5819	36.6762	1.7336
67916	NM_080555.2	phosphatidic acid phosphatase type 2B	23.7194	13.6538	1.7372
17319	NM_010798.2	macrophage migration inhibitory factor	600.4224	343.1800	1.7496

230073	NM_172689.3	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	9.9966	5.7019	1.7532
20422	NM_009169.2	split hand/foot malformation (ectrodactyly) type 1	189.0396	107.7058	1.7551
629957	XM_003086273.1	predicted gene 14303	507.7795	289.1612	1.7560
100504654	XR_105586.1	predicted gene 10736	1840.2606	1046.0660	1.7592
100504654	XR_105587.1	predicted gene 10736	1911.2104	1086.3963	1.7592
100504654	XR_106826.1	predicted gene 10736	1778.6007	1010.8844	1.7595
100504654	XR_106827.1	predicted gene 10736	1844.7812	1048.4987	1.7595
100038969	XM_001472037.2	predicted gene 14958	1600.4838	908.9360	1.7608
626048	XM_001473380.2	predicted pseudogene 6646	1601.3925	908.9360	1.7618
100503567	XM_003085762.1	predicted gene 11694	209.1386	118.6965	1.7620
100503567	XM_003085509.1	predicted gene 11694	209.1386	118.6965	1.7620
434460	XM_001477611.2	predicted gene 5623	96.9986	54.7627	1.7713
434460	XM_001477346.2	predicted gene 5623	96.9986	54.7627	1.7713
20200	NM_011313.2	S100 calcium binding protein A6 (calyclin)	729.7546	411.8745	1.7718
67067	NM_001164216.1	reactive oxygen species modulator 1	41.9669	23.6771	1.7725
12864	NM_053071.2	cytochrome c oxidase, subunit VIc	211.6069	119.3407	1.7731
665032	XM_974069.2	predicted gene 13841	123.4288	69.4725	1.7767
665032	XM_991641.2	predicted gene 13841	123.1820	69.3078	1.7773
66379	NM_183256.3	RIKEN cDNA 2310016M24 gene	34.5307	19.4212	1.7780
434843	XM_486761.5	predicted pseudogene 5642	1693.9502	952.3672	1.7787
665463	XM_977110.3	predicted pseudogene 7643	1693.9502	952.3672	1.7787
665611	XM_978135.3	predicted pseudogene 7711	1693.9502	952.3672	1.7787
665522	XM_977540.3	predicted pseudogene 7671	1693.9502	952.3672	1.7787
665579	XM_977918.3	predicted pseudogene 7698	1693.9502	952.3672	1.7787
665032	XM_003085349.1	predicted gene 13841	123.6729	69.4848	1.7799
665032	XM_003086489.1	predicted gene 13841	123.4220	69.3181	1.7805
382265	XM_356374.5	predicted gene 5167	99.8413	56.0350	1.7818
100043714	XM_003086243.1	predicted pseudogene 10774	55.6842	31.2394	1.7825
100043714	XM_001480774.2	predicted pseudogene 10774	55.6842	31.2394	1.7825
629957	XM_894924.4	predicted gene 14303	818.9727	458.8247	1.7849

54405	NM_019443.2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1	40.6538	22.7750	1.7850
20198	NM_011311.2	S100 calcium binding protein A4	2385.4436	1331.7804	1.7912
17991	NM_010885.4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2	116.5165	64.9515	1.7939
66142	NM_025379.2	cytochrome c oxidase subunit VIIb	88.5289	49.2034	1.7992
100039782	XM_001473311.2	predicted gene 10709	98.9061	54.9447	1.8001
13198	NM_007837.3	DNA-damage inducible transcript 3	21.3312	11.8400	1.8016
11839	NM_009704.3	amphiregulin	13.9534	7.7248	1.8063
319238	XR_107318.1	RIKEN cDNA 9330123L03 gene	5.1955	2.8542	1.8203
20090	NM_009093.2	ribosomal protein S29	601.5951	330.0521	1.8227
433941	XM_003086189.1	predicted gene 5561	108.9998	59.7879	1.8231
433941	XM_001478364.2	predicted gene 5561	108.9998	59.7879	1.8231
56187	NM_019519.2	Rab geranylgeranyl transferase, a subunit	6.1415	3.3628	1.8263
100503055	XM_003085327.1	-	50.2746	27.5242	1.8266
100043718	XM_003086523.1	predicted gene 4604	237.7590	130.0606	1.8281
320415	NM_177157.4	GTP cyclohydrolase I feedback regulator	84.2406	46.0753	1.8283
11983	NM_007512.3	ATPase inhibitory factor 1	56.6753	30.9422	1.8317
622707	XM_001475711.2	predicted gene 6344	71.2296	38.8333	1.8342
102644	NM_178644.3	OAF homolog (Drosophila)	35.9188	19.5807	1.8344
17873	NM_008655.1	growth arrest and DNA-damage-inducible 45 beta	19.2499	10.4934	1.8345
66169	NM_025394.3	translocase of outer mitochondrial membrane 7 homolog (yeast)	68.1720	36.9712	1.8439
68949	NM_001081005.1	RIKEN cDNA 1500012F01 gene	60.4516	32.7572	1.8454
72655	XM_986352.2	small nucleolar RNA host gene 5	46.3329	25.0715	1.8480
217344	NM_172572.3	rhomboid 5 homolog 2 (Drosophila)	4.4054	2.3712	1.8578
13197	NM_007836.1	growth arrest and DNA-damage-inducible 45 alpha	9.3944	5.0447	1.8622
66915	NR_028108.1	myeloma overexpressed 2	27.9426	15.0044	1.8623
217344	NM_001167680.1	rhomboid 5 homolog 2 (Drosophila)	4.6732	2.5079	1.8634
72655	XM_925560.3	small nucleolar RNA host gene 5	46.0753	24.7247	1.8635
12609	NM_007679.4	CCAAT/enhancer binding protein (C/EBP), delta	11.3447	6.0813	1.8655
69920	NM_027259.1	polymerase (RNA) II (DNA directed) polypeptide I	22.6379	12.1145	1.8687

18036	NM_010908.4	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta	11.1049	5.9397	1.8696
20308	NM_011338.2	chemokine (C-C motif) ligand 9	17.4949	9.3368	1.8738
100503653	XR_104731.1	predicted gene 14036	102.2717	54.5805	1.8738
13167	NM_007830.4	diazepam binding inhibitor	152.6526	81.3535	1.8764
14790	NM_013535.1	gene rich cluster, C10 gene	20.6090	10.9587	1.8806
66915	NM_001163425.1	myeloma overexpressed 2	47.8378	25.2243	1.8965
68040	NM_024215.2	zinc finger protein 593	5.6453	2.9763	1.8968
17384	NM_019471.2	matrix metalloproteinase 10	36.3866	19.1835	1.8968
66481	NM_025587.2	ribosomal protein S21	735.2156	386.8005	1.9008
69895	NR_028574.1	small nucleolar RNA host gene 8	27.6465	14.5265	1.9032
83673	NR_002896.3	small nucleolar RNA host gene (non-protein coding) 1	128.6195	67.4759	1.9062
18049	NM_013609.2	nerve growth factor	16.0144	8.3903	1.9087
22272	NM_025352.2	ubiquinol-cytochrome c reductase, complex III subunit VII	90.2122	47.2625	1.9087
30059	NM_013899.2	translocase of inner mitochondrial membrane 10 homolog (yeast)	56.7326	29.7171	1.9091
100041286	XR_106636.1	predicted gene 11974	25.8980	13.5425	1.9123
100041286	XR_105435.1	predicted gene 11974	25.8980	13.5425	1.9123
74732	NM_001163590.1	syntaxin 11	7.2620	3.7881	1.9170
100504319	XM_003086228.1	-	207.0361	107.9865	1.9172
100504319	XM_003084494.1	-	207.0361	107.9865	1.9172
100503669	XM_003086525.1	-	83.2977	43.3896	1.9198
100503669	XM_003084644.1	-	83.2977	43.3896	1.9198
13167	NM_001037999.2	diazepam binding inhibitor	135.1238	70.3696	1.9202
74732	NM_001163591.1	syntaxin 11	7.5787	3.9447	1.9212
20568	NM_011414.3	secretory leukocyte peptidase inhibitor	83.3139	43.3349	1.9226
80859	NM_030612.3	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	3.9502	2.0538	1.9233
19698	NM_009046.2	avian reticuloendotheliosis viral (v-rel) oncogene related B	14.7822	7.6782	1.9252
100041859	XM_003086090.1	predicted gene 3550	55.8534	28.9648	1.9283
100041859	XM_001477476.2	predicted gene 3550	55.8534	28.9648	1.9283

22038	NM_011636.2	phospholipid scramblase 1	49.7638	25.7935	1.9293
15040	NM_010398.3	histocompatibility 2, T region locus 23	10.7368	5.5581	1.9317
68763	NR_015536.1	RIKEN cDNA 1110038B12 gene	160.2223	82.5510	1.9409
18049	NM_001112698.1	nerve growth factor	18.6172	9.5834	1.9427
74732	NM_029075.1	syntaxin 11	7.0690	3.6370	1.9436
80859	NM_001159395.1	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	4.3422	2.2293	1.9478
100503826	XR_107649.1	predicted gene 13075	22.0599	11.3206	1.9487
100503826	XR_104900.1	predicted gene 13075	22.0599	11.3206	1.9487
66141	NM_025378.2	interferon induced transmembrane protein 3	157.5462	80.6882	1.9525
80859	NM_001159394.1	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	4.1437	2.1155	1.9587
68763	NR_027943.1	RIKEN cDNA 1110038B12 gene	142.2872	72.5673	1.9608
12578	NM_001040654.1	cyclin-dependent kinase inhibitor 2A	33.7588	17.1650	1.9667
100045766	XM_001474415.2	predicted gene 10126	123.5835	62.6092	1.9739
100045766	XM_003084933.1	predicted gene 10126	123.5835	62.6092	1.9739
434394	XM_915072.3	predicted gene 5614	78.8342	39.9309	1.9743
436081	XM_001004069.3	predicted gene 5745	26.9668	13.5951	1.9836
436081	XM_488179.5	predicted gene 5745	26.9668	13.5951	1.9836
100503585	XM_003086438.1	-	334.0994	168.0256	1.9884
100503585	XM_003084617.1	-	334.0994	168.0256	1.9884
12578	NM_009877.2	cyclin-dependent kinase inhibitor 2A	34.1776	17.0990	1.9988
381155	XR_035375.1	RIKEN cDNA 9630014M24 gene	3.0137	1.5066	2.0003
66293	NR_027819.1	RIKEN cDNA 1810032008 gene	8.9850	4.4602	2.0145
11435	NM_007389.4	cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle)	1.8119	0.8826	2.0529
100504928	XR_106975.1	-	1.9112	0.9253	2.0655
230738	NM_153159.2	zinc finger CCCH type containing 12A	6.5553	3.1600	2.0745
108153	NM_001003911.2	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 7	4.0967	1.9739	2.0755
320207	NM_177320.2	phosphoinositide-3-kinase, regulatory subunit 5, p101	15.2432	7.3159	2.0836
19260	NM_008979.1	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	6.3087	2.9870	2.1120

668092	XM_994269.1	predicted gene 8973	58.7021	27.6645	2.1219
15937	NM_133662.2	immediate early response 3	58.4487	27.5021	2.1252
434394	XM_486208.5	predicted gene 5614	73.9478	34.7634	2.1272
76964	NM_029816.2	RIKEN cDNA 2610028H24 gene	3.8487	1.8077	2.1291
12916	NM_001110853.1	cAMP responsive element modulator	2.4338	1.1359	2.1427
12916	NM_001110857.1	cAMP responsive element modulator	2.2933	1.0690	2.1453
72275	NM_028179.1	RIKEN cDNA 2200002D01 gene	25.1042	11.6382	2.1571
56695	NM_025580.2	paroxysmal nonkinesigenic dyskinesia	8.5520	3.9558	2.1619
668092	XM_003085977.1	predicted gene 8973	58.2089	26.8741	2.1660
100504742	XM_003086332.1	-	117.6074	52.9206	2.2223
18037	NM_008690.3	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	18.0281	8.0801	2.2312
12856	NM_001017429.2	cytochrome c oxidase, subunit XVII assembly protein homolog (yeast)	25.4228	11.3069	2.2484
66594	NM_025650.2	ubiquinol-cytochrome c reductase, complex III subunit XI	101.8100	44.6566	2.2798
57783	NM_021327.2	TNFAIP3 interacting protein 1	43.2784	18.8918	2.2909
18788	NM_011111.4	serine (or cysteine) peptidase inhibitor, clade B, member 2	5.7035	2.4563	2.3220
20361	NM_011352.2	sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (semaphorin) 7A	3.0227	1.3017	2.3222
18788	NM_001174170.1	serine (or cysteine) peptidase inhibitor, clade B, member 2	5.7580	2.4547	2.3457
546663	XM_915258.4	predicted pseudogene 5963	278.1877	118.0584	2.3564
546663	XM_001002128.3	predicted pseudogene 5963	278.1877	118.0584	2.3564
545551	NR_033629.1	cDNA sequence BC021767	1.5344	0.6482	2.3673
100504629	XM_003086098.1	predicted gene, 17669	12.2776	5.1640	2.3775
319689	XM_003086426.1	predicted gene, 17739	1.6810	0.7050	2.3844
319689	XM_003084614.1	predicted gene, 17739	1.6810	0.7050	2.3844
12051	NM_033601.3	B-cell leukemia/lymphoma 3	4.2058	1.7639	2.3844
100503758	XR_106535.1	predicted gene, 19876	75.6369	31.6424	2.3904
100503758	XR_105417.1	predicted gene, 19876	75.6369	31.6424	2.3904
26434	NM_023043.2	prion protein dublet	1.4915	0.6234	2.3924
17748	NM_013602.3	metallothionein 1	125.7142	52.4440	2.3971

69221	NR_030738.1	RIKEN cDNA 2410006H16 gene	63.5934	26.4643	2.4030
257632	NM_145857.2	nucleotide-binding oligomerization domain containing 2	1.7822	0.7220	2.4684
18035	NM_010907.2	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	54.3012	21.8327	2.4871
16193	NM_031168.1	interleukin 6	2.7637	1.0995	2.5137
16878	NM_001039537.1	leukemia inhibitory factor	9.2464	3.6711	2.5187
233552	NM_201352.2	glycerophosphodiester phosphodiesterase domain containing 5	3.5449	1.4074	2.5188
17395	NM_013599.2	matrix metalloproteinase 9	1.1058	0.4378	2.5261
16878	NM_008501.2	leukemia inhibitory factor	8.9014	3.5099	2.5361
110332	NM_173449.3	RIKEN cDNA 4921523A10 gene	1.8618	0.7240	2.5715
20306	NM_013654.3	chemokine (C-C motif) ligand 7	144.0293	55.3655	2.6014
69749	XR_107112.1	RIKEN cDNA 2410004N09 gene	15.6704	5.9801	2.6204
69749	XR_105940.1	RIKEN cDNA 2410004N09 gene	15.6704	5.9801	2.6204
26434	NM_001126338.1	prion protein dublet	1.7468	0.6616	2.6404
11796	NM_007464.3	baculoviral IAP repeat-containing 3	2.7367	1.0242	2.6721
17750	NM_008630.2	metallothionein 2	39.0333	14.5985	2.6738
12363	NM_007609.2	caspase 4, apoptosis-related cysteine peptidase	4.9157	1.8070	2.7204
56489	NM_019777.3	inhibitor of kappaB kinase epsilon	10.8508	3.9800	2.7264
17386	NM_008607.2	matrix metalloproteinase 13	8.4810	3.0902	2.7445
74013	NM_028713.1	raftlin family member 2	0.7582	0.2700	2.8084
14727	NM_008147.1	glycoprotein 49 A	3.6912	1.2974	2.8451
20296	NM_011333.3	chemokine (C-C motif) ligand 2	752.1989	255.4061	2.9451
57875	NM_020581.2	angiopoietin-like 4	1.7842	0.5978	2.9848
227659	NM_001177627.1	solute carrier family 2 (facilitated glucose transporter), member 6	2.6249	0.8495	3.0899
76773	NM_029734.1	WDYHV motif containing 1	8.4159	2.7215	3.0924
22329	NM_011693.3	vascular cell adhesion molecule 1	58.3048	18.8018	3.1010
22029	NM_009421.3	TNF receptor-associated factor 1	17.6218	5.5043	3.2014
24088	NM_011905.3	toll-like receptor 2	4.2713	1.3168	3.2437
751530	NR_030494.1	-	48.9708	14.9388	3.2781

227659	NM_172659.2	solute carrier family 2 (facilitated glucose transporter), member 6	2.9099	0.8859	3.2847
75614	XR_105882.1	RIKEN cDNA 2610019E17 gene	6.6720	2.0256	3.2938
414084	NM_001001495.2	TNFAIP3 interacting protein 3	6.7889	2.0214	3.3584
100217453	NR_028548.1	small nucleolar RNA, C/D box 16A	18.7832	5.4721	3.4325
14468	NM_010259.2	guanylate binding protein 1	1.7816	0.5121	3.4792
16149	NM_010545.3	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	1.1287	0.3215	3.5105
14102	NM_007987.2	Fas (TNF receptor superfamily member 6)	13.0013	3.6861	3.5271
14728	NM_013532.2	leukocyte immunoglobulin-like receptor, subfamily B, member 4	6.6386	1.8586	3.5719
16819	NM_008491.1	lipocalin 2	7.4081	2.0432	3.6257
14469	NM_010260.1	guanylate binding protein 2	2.7460	0.6852	4.0077
14528	NM_008102.3	GTP cyclohydrolase 1	1.8177	0.4504	4.0358
103142	NM_153133.2	retinol dehydrogenase 9	0.4608	0.1107	4.1606
100047734	XM_003086912.1	-	2.0998	0.4282	4.9036
408066	XR_035217.2	cDNA sequence BC067074	0.1158	0.0223	5.2008
408066	XR_001629.2	cDNA sequence BC067074	0.1333	0.0244	5.4608
15945	NM_021274.1	chemokine (C-X-C motif) ligand 10	3.9956	0.7027	5.6862
24108	NM_023137.3	ubiquitin D	1.2580	0.2103	5.9809
20311	NM_009141.2	chemokine (C-X-C motif) ligand 5	14.5530	1.9858	7.3284
14825	NM_008176.3	chemokine (C-X-C motif) ligand 1	67.9688	9.1431	7.4339
20297	NM_001159738.1	chemokine (C-C motif) ligand 20	2.3793	0.2933	8.1133
20297	NM_016960.2	chemokine (C-C motif) ligand 20	2.4925	0.2922	8.5293
80287	NM_030255.3	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 3	0.7682	0.0844	9.1014
80287	NM_001160415.1	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 3	0.7372	0.0810	9.1014
55932	NM_018734.3	guanylate binding protein 3	0.9028	0.0755	11.9618
73474	NR_027900.2	small nucleolar RNA host gene (non-protein coding) 9	3.6795	0.2721	13.5221
434775	XR_001556.2	predicted gene 5636	0.2217	0.0142	15.6024
20210	NM_011315.3	serum amyloid A 3	2.6337	0.0000	Inf
18606	NM_001136077.1	ectonucleotide pyrophosphatase/phosphodiesterase 2	0.2264	0.0000	Inf

16069	NM_152839.3	immunoglobulin joining chain	0.2944	0.0000	Inf
630294	NM_001177467.1	predicted gene 7030	0.4033	0.0000	Inf
399570	XR_104919.1	RIKEN cDNA A730085A09 gene	0.1518	0.0000	Inf
229320	NM_153385.2	clarin 1	0.3093	0.0000	Inf
229320	NM_153384.2	clarin 1	0.3005	0.0000	Inf
229320	NM_153386.2	clarin 1	0.3428	0.0000	Inf
12642	NM_009890.1	cholesterol 25-hydroxylase	0.4174	0.0000	Inf