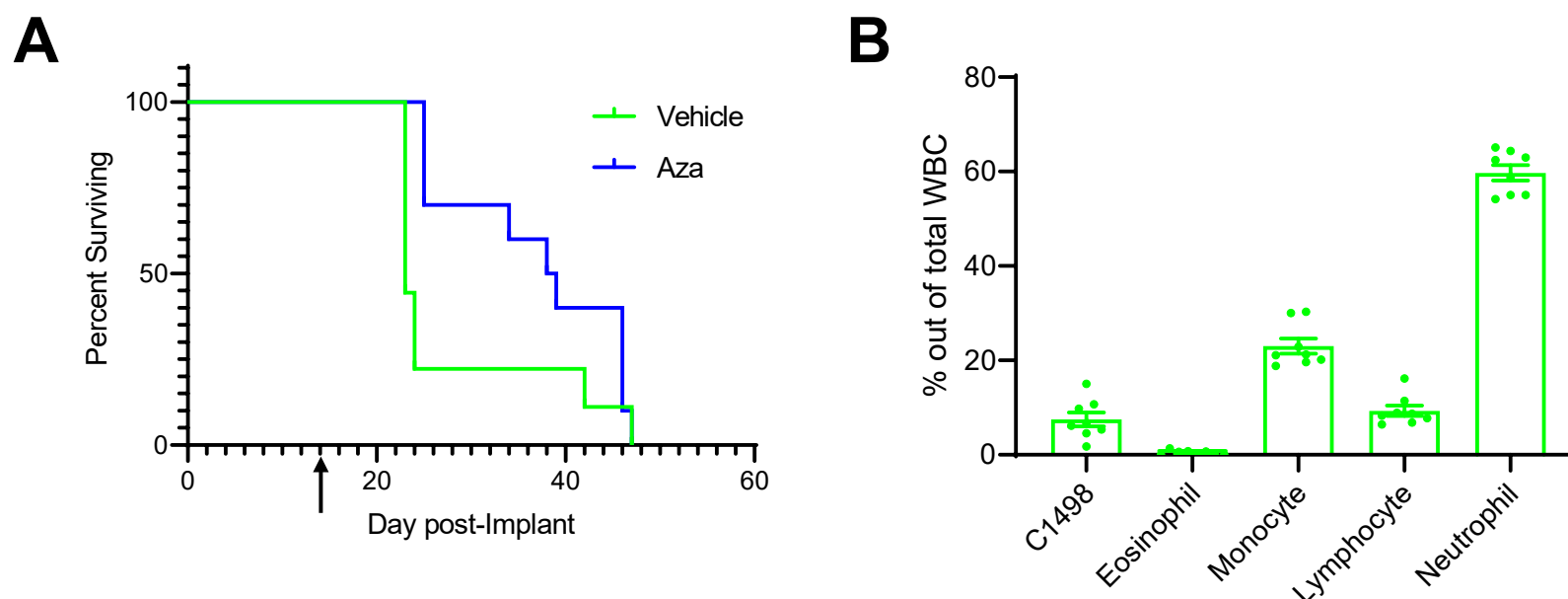
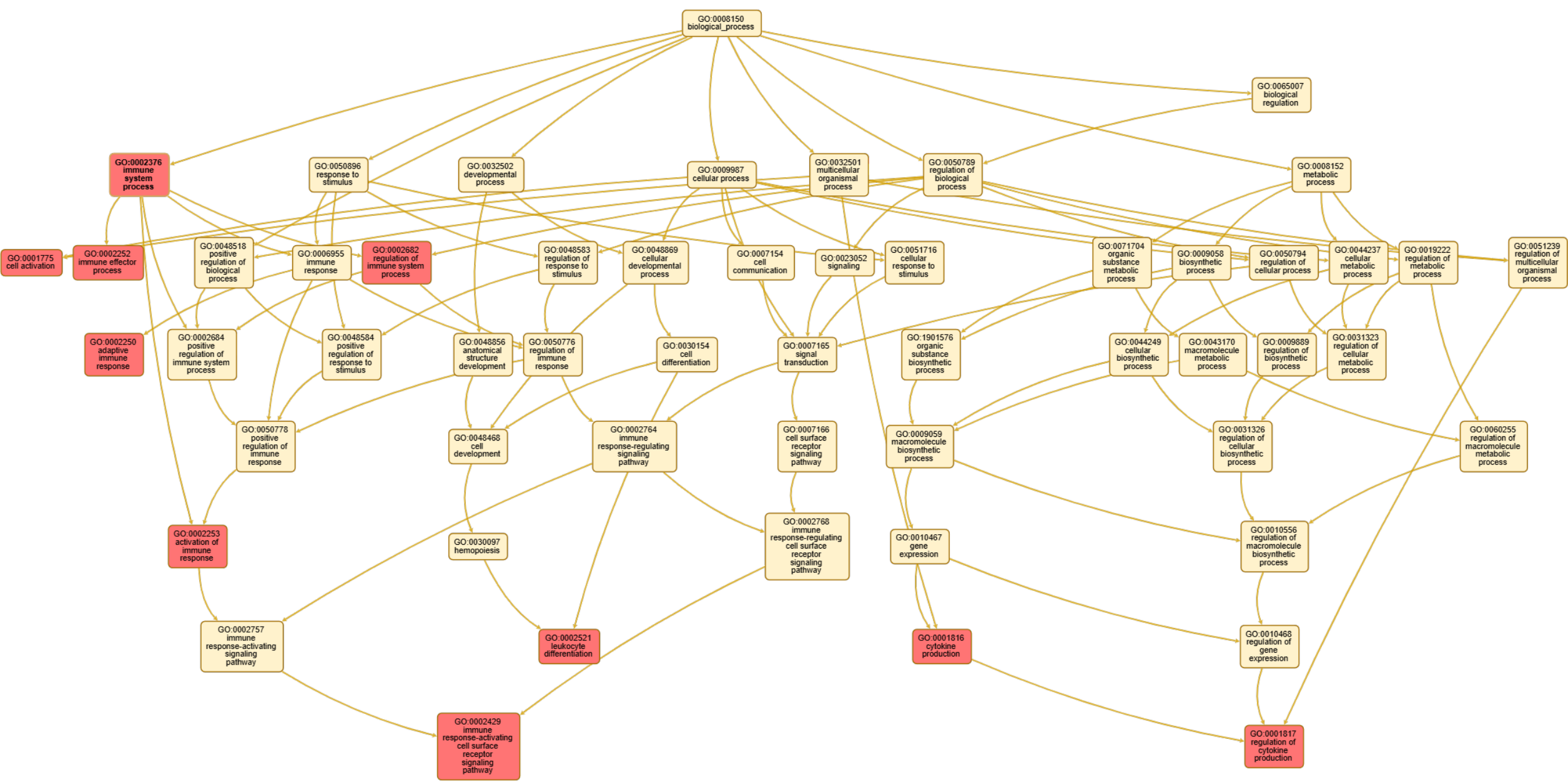




Supplemental Figure 1. Survival and Hematologic Profiles of Leukemic Vehicle- and AZA-treated Immunodeficient Mice. C1498 leukemia cells (80,000) were implanted in NSG immunodeficient mice via tail vein injection. Treatment with DMSO in diluent (Vehicle) (n=9) or 5mg/kg/mouse AZA (n=10) by intraperitoneal injection began on day 3 after implantation and continued thrice weekly until survival endpoints. **(A)** Mice were euthanized once they showed signs of terminal disease state and survival was recorded for each mouse and displayed as a Kaplan-Meier curve. Statistical significance was analyzed using the Log-rank (Mantel-Cox) test. The arrow ($\uparrow$) indicates the timepoint at which retroorbital blood was drawn to assess hematologic profiles. **(B)** Drawn blood was stained and smeared for complete blood counts. Manually counted WBCs for C1498-Vehicle mice are shown as percentages of total WBC counted. Blood from C1498-AZA mice showed an extremely low WBC count that could not accurately be displayed graphically.

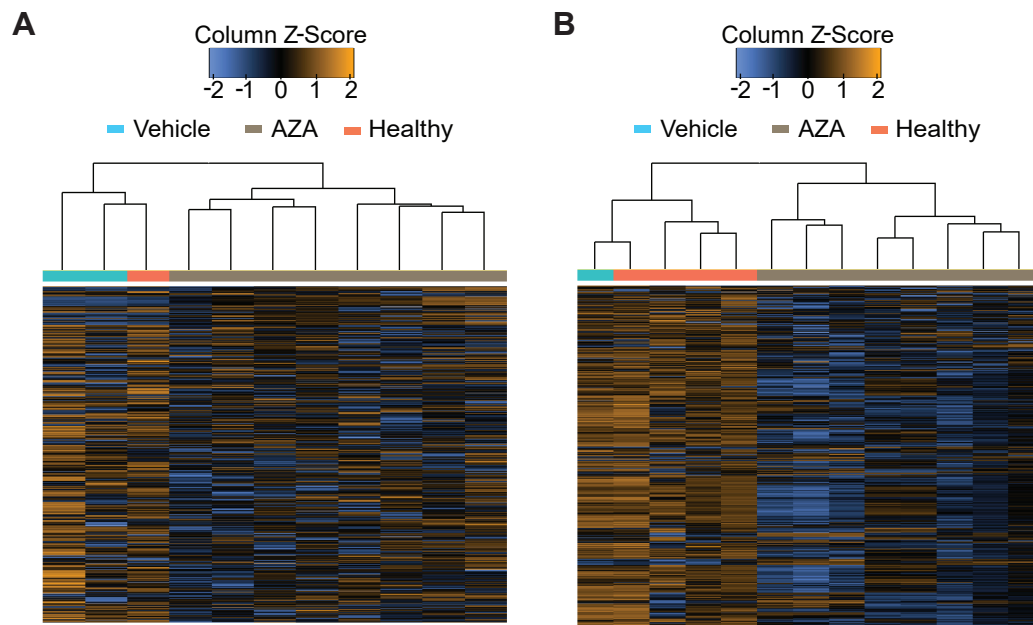


Enriched Gene Ontology Categories

GO Identification	GO Name
GO:0001775	Cell Activation
GO:0001816	Cytokine Production
GO:0001817	Regulation of Cytokine Production
GO:0002250	Adaptive Immune Response
GO: 0002252	Immune Effector Process

GO Identification	GO Name
GO:0002253	Activation if Immune Response
GO:0002376	Immune System Process
GO:0002429	Immune Response-Activating Cell Surface Receptor Signaling Pathway
GO:0002521	Leukocyte Differentiation
GO:0002682	Regulation of Immune System Process

Supplemental Figure 2. Map and Listing of Gene Ontologies Enriched in the Mouse PanCancer Immune Profiling Panel. Genes to be probed for expression were analyzed for Network Topology using the WEB-based Gene Set Analysis Toolkit (WebGestalt). The mapping of enriched gene ontologies is shown in red with the linked ancestor ontologies in off-white. The top ten enriched ontologies are shown with their Gene Ontology (GO) identification number.



Supplemental Figure 3. Heatmap of total reads for all genes by sample using the Mouse PanCancer Immune Profiling Panel. Total reads for each gene by sample from (A) whole blood or (B) whole spleen of C1498-vehicle, C1498-AZA, and Healthy mice.

Supplemental Table 1. “Panel Plus” user added genes to the Mouse PanCancer Immune Profiling panel with optimized probe target sequence followed by the complete gene list from the Mouse PanCancer Immune Profiling Panel.

“Panel Plus” Genes

Customer Identifier	Accession	Position	Target Sequence
abat	NM_001170978.1	3561-3660	GAGCCACAGTGTTCATATACAGATACTTCCGCAGGTCCTTAGAGTTCAAAGGGTTTAAATCCAGGACATAAGCAGAAATCGCTCTCTTTAGTGAAGGGAGC
Akt1	NM_001165894.1	899-998	GCCATGAAGATCCTCAAGAAGGAGGTCATCGTCGCCAAGGATGAGGTTGCCCAACGCTTACTGAGAACCGTGTCTGCAGAACTCTAGGCATCCCTTCC
Bad	NM_007522.3	1147-1246	TTTCGAGGCCTTAGGAAAAAAAAAGAGGATCGCTGTGTCCCTTTAACAGGGAGAAAGAGCTGACGTACAGCTTGAGTCCCTTCCGGTGCGTGCAATAGCCAC
bbc3	NM_133234.1	1462-1561	CCCCAATCCCCATCCATCTCATTGCATAGGTTTAGAGAGAGACGCTGTGACCACGTGCATTCAATTTGGGGGGTGGGAGATATTGGCGGAAGCCACCCAG
birc3	NM_007464.3	426-525	CCCTGTCATCTCACCATGAACATGTTCAAGACAGCGCCTTTCTAGCCAAGCTGATGAAGAGTGCTGACACCTTTGAGTTGAAGTATGACTTTTCCTGTG
blm	NM_001042527.2	265-364	AAAGATGTGAACGTGTCTGAGGCCTTTTCATTCACTGAGTCTCCACTCCACAAACCAAAGCAGCAGGCAAAGATTGAAGGCTTCTTTAAACATTTCCCTG
casp9	NM_015733.4	1676-1775	ATAACTGTCCTGCTAAGATAGGATTTTGAAGTGGGGCAGGCTGCTCTTTCCCTTTGGCGATGCAAACATGCTCCTAGCAGCTTTCAGGTTGTAGGGCAAT
ctnnb1	NM_007614.2	2976-3075	TTGGTCGAGGAGTAACAATACAAATGGATTTGGGGAGTGACTCACGCAGTGAAGAATGCACACGAATGGATCACAAGATGGCGTTATCAAACCCTAGCCT
dbn1	NM_019813.4	2571-2670	CGAAATTTAAACATGGCAATAAATGGCTCGTGGGCTCTGGCTCCCTGGGACCCTTCCCTTCTCTTTACCCTCGCTGCTTGGTCAGAAGGAATTATCAG
ddx52	NM_030096.2	501-600	AGGAAAAGGTCAACTTCTTTCCGGAACAAGCACAAGATACATGTCCAAGGAACTGATCTTCCTGACCCAATTGCTACATTTACGCAACTTGACCAGGAATA
mdm2	NM_010786.4	1665-1764	GTCATGTTTCACGTGTGCAAAGAAGCTAAAAAAGAAACAAGCCCTGCCAGTGTGCAGACAGCCAATCCAAATGATTGTGCTAACTTACTTCACTAG
pdk4	NM_013743.2	1356-1455	AGCGGATGACGCCTGACATTTTACGGGATCAAAGTGGGTCTGTGGCATTGCTGCTTCGTGAATGTGTGTGGACTCTAGTTTCCGCAAACAACGCAACAC
psmb5	NM_011186.1	335-434	TGCAGCTTCTGGGAGCGGTTGTTGGCTCGGCAGTGTGCAATCTATGAGCTTCGCAATAAGGAACGCATCTCGGTCGCAGCAGCCTCCAAACTGCTCGCTA
psmc4	NM_011874.2	1147-1246	TCGACCTGGAAGACTATGTGGCCCGTCCAGATAAGATTTTCAAGGAGCCGATATCACTCCATCTGTGAGGAGAGTGGAATGTTGGCTGTCCGTGAGAACCG
Ripk1	NM_009068.3	3186-3285	GCTTTGGCCTTGTGGCCATTCTGGCACTCATTGGCACTTCATCCTCCTTTGTTGGCTATCCTGTACTCAGTAGGATATTTGGGAACATTCCTGGCCTC
Ripk3	NM_019955.1	271-370	CACAGAACATGGAACCATGATGTAGCAGTCAAGATCGTGAAGTCAAGAGAAGATATCCTGGGAGGTGAAGGCTATGGTTAATCTTCGTAATGAGAACGTTT
rock1	NM_009071.2	416-515	AAGTTGGTTGAACTTGCTTTCCGCTGCGGGCAAGAAGGTATCGTCACAAGTAGCAGCATCATGTGCACTGGGGACAGTTTTGAGACTCGGTTTGAAAAA
slc24a3	NM_053195.2	2271-2370	CAGGAGAGGGTCCGCTGATGGCAGGAAGGTTTGTGTTTGTGTTGGGAGTGAGTCCTAGGTTACGGGGGCTCAGGGAAATTGTTTAATTTAGAGGGGGCGCTTTT
tnfsf9	NM_009404.3	293-392	GCTCTATGGCCTAGTCGCTTTGTTTTGCTGCTTCTGATCGCCGCCTGTGTTCCATCTTCACCCGCACCGAGCCTCGGCCAGCGCTCACAATCACCACC
ubb	NM_011664.4	1324-1423	TCCTCCGTCTGAGGGGTGGCTATTAATTATTCGGTCTGCATTCCAGTGGGCAGTGATGGCATTACTCTGCACTCTAGCCACTTGCCCCAATTTAAGTTT

Mouse PanCancer Immune Profiling Panel

Official Symbol	Accession	Target Sequence
A2m	NM_175628.3	AGAGGACATGTATGGCTTCTTAAAGGATATGGGCTTAAAGGTATTCACCAACTTGAACATCCGTAACCCAAAGTCTGTGAACGCCTTGGAGTCAATAAA
Abca1	NM_013454.3	CTCCTTGTCATCTCTAGCCAGGATATTGAGCATCCTCTCCAGAGCAAAAAGCGACTCCACATAGAAGACTACTGTCTCTCAGACAACACTTGACCAA

Abcb1a	NM_011076.1	AAGGGGCTACAGGGTCTAGGCTTGCTGTGATTTTCCAGAACATAGCAAATCTTGGGACAGGAATCATCATATCCCTAATCTATGGCTGGCACTAACACT
Abcg1	NM_009593.1	GCGGCCGTGAACATCGAATTCAAGGACCTTTCTACTCTGTACCCGAGGGGCCCTGGTGGGAAGAA GAAAGGATACAAGACCTTTTGAAAGGGATCTCTG
Abl1	NM_009594.4	ATTGCTCTGGGAGATTGCTACCTATGGCATGTCACCTTACCCGGGAATTGACCTGTCTCAGGTTTATGAGCTGCTGGAAAAAGACTACCGCATGGAGCGC
Ada	NM_007398.3	GACATGGTTATCACACCATCGAGGATGAAGCTCTCTACAACAGACTACTGAAAGAAAACATGCAC TTTGAGGTCTGCCCCTGGTCCAGCTACCTCACAGG
Adora2a	NM_009630.2	ACTATGAAAGGCAGGGTGCCAGAGTGTGGGCTCACGTCTCAGGATTGAGTTTAGAGACATCAAG TCATGGACCCGAGCTGGATAGTTCAGAGCTGCCCTG
Aicda	NM_009645.2	AATCGTGAAAGAACTTTCAAAGCCTGGGAAGGGCTACATGAAAATTCTGTCCGGCTAACCCAGACA ACTTCGGCGCATCCTTTTGCCCTTGACGAAGTCG
Aire	NM_009646.1	TCCAGGAACCCGAGGGGGCCGTGGAAGGGATCCTTATCCAGCAGGTGTTTGAGTCAGGAAGATCC AAGAAGTGCATTAGGTTGGGGGAGAGTTTTATACA
Akt3	NM_011785.3	GTTGTCATGTTAGCAAGCGCAGCTCCAATTCACAGATCATTGCCTGCGTTTTCTTTTGACCCATGTG CAAGGAATGTACACACCCATTAGAATCATGCAC
Alcam	NM_009655.1	ATTTATCCTTAAACCCAAGTGGGGAGGTGACCAAGCAGATTGGCGATACCCTGCCTGTGTCATGC ACAATATCTGCAAGTAGGAACGCGACTGTGGTGTG
Ambp	NM_007443.3	CCACAAATCCAAATGGAACATAACCTTGGAATCCTATGTGGTCCACACCAACTATGACGAATATGC CATTTTCCTTACCAAGAAGTCCAGCCACCACCAC
Amica1	NM_001005421.4	TTTCAAAGGACAATTTACCAACTCCTCCAAGTATAAGGGTCAGCAGGGCATCCTGAATGGAAA TCAGCTGGTGATCATTGTGGGGATCGTCTGTGCCA
Angpt1	NM_009640.3	GGGCTGGAAGGAGTATAAAATGGGTTTTGGGAATCCCTCTGGTGAATATTGGCTTGGGAACGAG TTCATTTTTGCAATAACCAGTCAGAGGCAGTACATG
Angpt2	NM_007426.3	GAAGAATGTTCCGTGGGAGTTCAGCAGTAAATAACTGGAAAACAGAACACTTAGATGGTGCAGA TAAATCTTGGGACCACATTCCTCTAAGCACGGTTTC
Anp32b	NM_130889.2	AAGATATCAGCACCTTGAGCCGTTGAAAAGGTTGGATTGTCTGAAAAGCCTGGATCTGTTTGGC TGTGAGGTCACTAACCGGAGTGATTACCGAGAAAC
Anxa1	NM_010730.2	GGCTATGCTAAAACTCCAGCTCAGTTTGATGCAGATGAACTCCGTGGTGCCATGAAGGGACTTG GAACAGATGAAGACACTCTCATTGAGATTTTGACA
Apoe	NM_009696.3	GCTAAGGACTTGTTTCGGAAGGAGCTGACTGGCCAATCACAATTGCGAAGATGAAGGCTCTGTG GGCCGTGCTGTTGGTCACATTGCTGACAGGATGCCT
App	NM_007471.2	GTGAGCGACGCCCTTCTCGTGCCGACAAGTGCAAGTTCCTACACCAGGAGCGGATGGATGTTTG TGAGACCCATCTTCACTGGCACACCGTCGCCAAAG
Arg1	NM_007482.3	GTACATTGGCTTGCAGACGTAGACCCTGGGGAACACTATATAATAAAAACTCTGGGAATTAAGT ATTTCTCCATGACTGAAGTAGACAAGCTGGGGATT
Arg2	NM_009705.2	GGCTCTCCAGGTTGGGATGCCACCTAAAAGACTTTGGAGACTTGAGTTTTACTAATGTCCCACAAG ATGATCCCTACAATAATCTGGTTGTGTATCCTCG
Atf1	NM_007497.3	GAAGCTCCGAAAAGATAGAGTGCTCAAGGAATGGACTTTCAGCAGTTTAAATAGAAATAATGGTC AGCAACGAAAATGGCAGGCGACGTTAGTGAAGCAG
Atf2	NM_001284371.1	AGAGCAGCAGCTTCAAGATGCCGACAAAAAAGGAAAAGTGTGGGTTCAGTCCTTAGAGAAGAAAG CAGAAGACTTGAGTTCACTAAATGGCCAGCTGCAGG
Atg10	NM_025770.3	GGGTTCTCATTAAACATGGAGGATGAGTTCTTTGGAGAAAAAAGCTTCCAGCATTATTGTGCAGAA TTCATCAGACATTCACAGCAGATAGGCGATGGCTG
Atg12	NM_026217.1	CATGGCAGCACTCCTAGCATTGAGGAAGTGGAACAAGCAGACTGAAAGTTTAAGACTGTGTGG GCTACAGAGTGAGATTGTCTACCTCTGGGGGAAAA
Atg16l1	NM_001205391.1	CGTTCGAGGAGATCATTCTGCAGTATACCAAGTTGCTGGAAAAGTCAGATCTTCATTAGTATTGA CCCAGAACTACAAGCAGAAAAAGCATGACATGCC
Atg5	NM_053069.5	CATTACCAAAAAACATCCAGAGGTTACTGGAACCTCTACCACAGTAAGGAAAGTTTGCTGCACTCTC TCGATGGCTGCTTGGAGACTCCTGCTGTTGATT
Atg7	NM_028835.1	TGCAGGGAGCTAGAGACGTGACACATAGCATCATCTTTGAAGTGAACTTCCAGAAATGGCATT AGCCCAGATTGTCCTAAAGCTGTTGGCTGGGAGAA

Atm	NM_00749 9.2	TTCCTCAAAGTGAAAGTCATGACATTTGGATAAAGACACTGACGTGTGCCTTTCTGGACAGTGGA GGCATAAACAGTGAAATTCTCCAGTTATTAAAGCC
Axl	NM_00946 5.3	GAGATTCTAAAGGTCCACAGTCTAGAGTATTAGGTACGACTCCAAGGGTGGGCGCTTGTAGCCAT CCTAAGTCCTTTCCCTCCTTAAGCACCTATGCTCC
Batf	NM_01676 7.2	ACTGGACTCTCCCAGGGAAGTCGAGCCAATGTACTGGACCCAAAAAATGACAAGTCAACCCTGGA CTGTCATGAATGATGCCCAAATACACAGCACAGA
Bax	NM_00752 7.3	CATAAATTATGACATTTTCTGGGATGAATGGGGGAAGGGGAAAGGCATTTTCTTACTTTTGTA TTATTGGGAGGGGTGGGAATGGTGGCCTGGGGAG
Bcl10	NM_00974 0.1	TTTAGCAGTAAGCTGTTGTGTTTCAGGAAAGCTGGACACGGGAAAGCTGCCGACACACTCAGCAG TGTCCTCACTCCTTAGTTCTGAGAAGCCGTCGGGT
Bcl2	NM_00974 1.3	GGCCTTCTTTGAGTTCGGTGGGGTTCATGTGTGTGGAGAGCGTCAACAGGGAGATGTCACCCCTG GTGGACAACATCGCCCTGTGGATGACTGAGTACCTG
Bcl2l1	NM_00974 3.4	GAGCAACCGGGAGCTGGTGGTGCAGTTTCTCTCTCTACAAGCTTTCCAGAAAGGATACAGCTGGA GTCAGTTTAGTGATGTCTGAAGAGAATAGGACTGAG
Bcl6	NM_00974 4.3	ACGTTGTCATCGTGGTGAGCCGTGAGCAGTTTAGAGCCATAAGACAGTGCTCATGGCCTGCAGC GGCCTGTTCTACAGTATCTTCACTGACCAGTTGAA
Bid	NM_00754 4.3	AATCATGCACACGACTTATCTGTGTGGTGTGAGTTACTCAGGCTCTTGCTACGGAATGCAAAGA ACAACCTCACATACCAGTGTCAAACAGAATGCACA
Birc5	NM_00968 9.2	GGCTTCATCCACTGCCCTACCGAGAACGAGCCTGATTTGGCCCAGTGTTTTTCTGCTTTAAGGAA TTGGAAGGCTGGGAACCCGATGACAACCCGATAG
Blk	NM_00754 9.2	AAGGATTGTGTTAGAACTTACCTCCAGTTGTGTTTCAGACCCCGATAGTCCCGAAATCAGTCTGACC AGTTAGCGATGGACAGGATGTCAGGCTGTCATAA
Blnk	NM_00852 8.4	CTGAAGAGGCCTTGACAGATCCAACAAGGATGGATCGTTTCTTATTCGGAAGAGCTCTGGCCAT GATCCAAGCAGCCGTACACCCTAGTTGCGTTCTT
Bmi1	NM_00755 2.4	TCTCGAGGTTTTTCATGGTGTACCTAAGACAAAAGACATCTCACCTCTATGATGGACTTACTTCTG AGAGTGCCTTGAGGCACTTATGGCTTACTAAG
Bst1	NM_00976 3.3	TCATGAACTCAGCCTCAGCATCTATGCGGAGGGAGAGCGCATCTCTTCATGCAATAGGAGACGCC AGCCTTCTCATTTCTCTTAGTAGCTTTGGCTTC
Bst2	NM_19809 5.2	CAGCTCCATGGTGGTCTCCAGCCTACTGGTGCTCAAAGTGCTACTGTTCTGCTCTTTTGAGGACT CATTAGTTGGCAGGTCACAGTTGTTGAAGTCAC
Btk	NM_01348 2.2	GAAGAGCCCTGGACATCTAGGAATGCCTTTCTTCTCTCGTTCCCTGGCATACTGCTCTAAGCAAAG GTCAAGGGATTTCTGTGCCTAGTATTACCCATAA
Btla	NM_00103 7719.2	AGTGCCTGCCATGCTTGGGACTCCTCGTTATTTAGGGAATTCTTCATCCTCCATCTGGGCCTCTG GAGCATCCTTTGTGAGAAAGCTACTAAGAGGAAT
C1qa	NM_00757 2.2	CAGTGCCCGGCTTCTATTACTTCAACTTCCAAGTGATCTCCAAGTGGGACCTTTGTCTGTTTATCAA GTCTTCTCCGGGGGCCAGCCAGGGATTCCCT
C1qb	NM_00977 7.2	GTGCCAACAGCATCTTCACTGGCTTTCTGCTTTTCCCTGACATGGATGCGTAATCACGGGGTCAAA TTACACCTATCCAACACCATCTTCTGCCTCCCT
C1qbp	NM_00757 3.2	TCCTGAGGATGAGATTGGACACGAAGATGAGGCCGAGAGTGATATTTTCTCTATCAAGGAAGTTA GCTTTCAGGCCACTGGTGACTCTGAGTGGAGGGAT
C1ra	NM_02314 3.3	CAATGAGACCTTCTATGGCCAAGGCCTCATGGGTTATGTCAGCGGATTCGGGATAACAGAAGATA AGTTAGCTTTGATCTCAGGTTTCGTGAGTGCCT
C1s1	NM_14493 8.2	GGCAGGGTTGATCACTGAGCCGTGTTGGTTATTCAGTTACTATTGCTAACAACATGGCAGAAACC CTTCTATCTTGCCTATTCCACAGGGATATCTTAT
C2	NM_01348 4.2	ATGGTGTCTGGACTTTCTGCCACTTTAACATGGTCACTGACTCCTTTATTAGTCTGAACTTCCTGT CTAATACCTCTGAGCGTTCTCACTCCTGGATAC
C3	NM_00977 8.2	AAGACTTCCTAAAGAGGCAAGTGCTGACCAGTGAGAAGACAGTGTTGACAGGAGCCAGTGGACA TCTGAGAAGCGTCTCCATCAAGATTCCAGCCAGTAA
C3ar1	NM_00977 9.2	ATAAGCCAATCTGGTGCCAGAATCATCGAAACGTGAGAACCGCCTTCGCCATCTGTGGATGTGTC TGGGTGGTAGCCTTTGTGATGTGTGTGCCGTATT
C4b	NM_00978 0.2	GTGCAGACCGATCAGCCTATCTATAATCCGGGGCAGCGGGTTCGTTATCGGGTCTTTGCACTGGA TCAAAAGATGCGCCCATCCACTGATTTCTCACCA

C5ar1	NM_007577.3	CATTGCTCCTCACCATTCCATCCTTCGTGTACCGGGAGGCATATAAGGACTTCTACTCAGAGCACA CTGTATGTGGTATTAACCTATGGTGGGGGTAGCTT
C6	NM_016704.2	CTGATTGACAAGAGTGAAGCCTGTTTCTGTGACCACTACCCATGGACTCACTGGTCCAGCTGTTCT AAGTCCTGCAATTCTGGAACCCAGAGCAGACAGA
C7	XM_356827.6	AGACAAATGTGAAAATGTGGCTAACCCTTCCTGCAACATTGATAAGCCTCCTCCCAACATAGAAGT TACCGGTTATGGTTACAACGTAGTTACTGGCCAG
C8a	NM_146148.2	TGGCATGTACGCCAAGTTCATCAATGACTATGGCACCCACTACATCACCTCTGGAACCATGGGTG GCATTTATGAATATGTTATGGTGCTTGACAAAGAG
C8b	NM_133882.2	GTTACTGCCTGTGCTGGAGGAAGTTTCGGTATTGGTGGTATGGTCTATAAAGTCTATGTCAAAGT GGGCGTTTCCGCAAAGAAATGCAGTGACATTATGA
C8g	NM_027062.1	GAGCGGCGAGTCAGGGAAGCCAACCTGACAGAAGATCAGATTCTTTCTTTCCCAAGTATGGTTT CTGCGAGACTGCGGACCAATTACACATCCTGAACG
C9	NM_013485.1	TCCTTGCTCAAACAAAGGTTTCGCTCAAGAAGCATTTTAGCCTTCGGACAGTTTAATGGGAAAAAG CTGTGTTGATGTTTTGGGAGACAGACAAGGCTGT
Camp	NM_009921.2	AACCCGGCCGCTGATTCTTTTGACATCAGCTGTAACGAGCCTGGTGCACAGCCCTTTCGGTTCAAG AAAATTTCCCGGCTGGCTGGACTTCTCCGCAAAG
Card11	NM_175362.2	ATTGTTGGACATTCTTCACACCAAGGGACAAAGGGGCTATGTGGTCTTCCTGGAGAGCCTGGAGT TTTACTACCCAGAACTTTACAACTGGTGACTGGA
Card9	NM_001037747.1	ACAGGCCACAAGGGCTACGTGGCTTTCCTCGAGAGCCTGGAGCTCTACTACCCTCAGTTATACCG GAAAGTCACTGGCAAGGAGCCAGCACGCGTCTTCT
Casp1	NM_009807.2	GACAATAAATGGATTGTTGGATGAACCTTTAGAGAAGAGAGTGCTGAATCAGGAAGAAATGGAT AAAATAAACTTGCAAACATTACTGCTATGGACAAG
Casp3	NM_009810.2	GAGGCTGACTTCTGTATGCTTACTCTACAGCACCTGGTTACTATTCTGGAGAAATTCAAAGGAC GGGTCGTGGTTCATCCAGTCCCTTTCAGCATGC
Casp8	NM_009812.2	TTTCATTAGGCTTGCCAAGGAAGTAACTTCAGAAAGGAGTGCCTGATGAGGCAGGCTTCGAGC AACAGAACCACTTTAGAAGTGATTTCATCATCT
Ccl1	NM_011329.2	ATGCTTACGGTCTCCAATAGCTGCTGCTTGAACACCTGAAGAAAGAGCTTCCCCTGAAGTTTATC CAGTGTTACAGAAAGATGGGCTCCTCCTGTCTGT
Ccl11	NM_011330.3	CAACCTCCTCTCTTGACACTAACCCAGAGCCTAAGAACTGCTTGATTCTTCTCTTTCCTAAGACGT GCTCTGAGGGAATATCAGCACCAGTCGCCCAAG
Ccl12	NM_011331.2	ATGAAGATTTCCACACTTCTATGCCTCCTGCTCATAGCTACCACCATCAGTCCTCAGGTATTGGCTG GACCAGATGCGGTGAGCACCCAGTCACGTGCT
Ccl17	NM_011332.2	TCTGTGCAGACCCCAAAGACAAACATGTGAAGAAGGCCATCAGATTGGTGAAAAACCCAAGGCC ATGACCTTCCCGCTGAGGCATTTGGAGACGCCAGGG
Ccl19	NM_011888.2	CTTCTGCCAAGAACAAAGGCAACAGCACCAAGGAGCCCTGTGTCTTGAGTAAAGAGATGTGA ATCACTCTGGCCCAGGAAACCAAGGACCAGAAGAGA
Ccl2	NM_011333.3	TCTTCAGCACCTTTGAATGTGAAGTTGACCCGTAAATCTGAAGCTAATGCATCCACTACCTTTTCCA CAACCACCTCAAGCACTTCTGTAGGAGTGACCA
Ccl20	NM_016960.1	GCAGCAAGCAACTACGACTGTTGCCTCTCGTACATACAGACGCCTCTTCCTTCAGAGCTATTGTG GGTTTCACAAGACAGATGGCCGATGAAGCTTGTG
Ccl21a	NM_011124.4	TTAAGTACAGCCAGAAGAAAAATCCCTACAGTATTGTCCGAGGCTATAGGAAGCAAGAACCAAGT TTAGGCTGTCCCATCCCGGCAATCCTGTTCTCACC
Ccl22	NM_009137.2	CCAAGAATCAACTCCACCCCTCTCAACCACATGCTAGGGTCTTTTACTTTCTCTGCCCCACACCTT TGACTCCTTGCTGTGTAGCTGATAGTCGAAG
Ccl24	NM_019577.4	CTGGATGCCAAGAAAAACCAGCCTTCTAAAGGGGCCAAGGCAGTGAGAACCAAGTTTGCTGTCC AGAGACGCCGTGGCAATAGCACCGAGGTTTAGCCGC
Ccl25	NM_009138.3	TTCCGCCAGAAAGTAGTGTGTGGGAATCCAGAGGACATGAATGTGAAGAGGGCGATGAGAATCT TGACAGCTAGGAAAAGGCTAGTCCACTGGAAGAGCG
Ccl26	NM_001013412.2	CAGCTATAAGTTCACCGACAAGAGCTGCACCAGTGACGGTGTGATATTCTTTACAAAAACAGGTA AGCAATTCTGTGTCCAGCCAGGGGCCAAATGGGTG
Ccl27a	NM_001048179.1	GCCTCTGCCCTCCAGCACTAGCTGCTGTACTCAGCTCTATAGACAGCCACTCCAAGCAGGCTGCT GAGGAGGATTGTCCACATGGAAGTGCAGGAGGCC

Ccl28	NM_02027 9.3	GCTGCTGTCATCCTTCATGTTAAACGTAGAAGAATCTGCATCAGCCCGCACAATCGTACTTTGAAG CAGTGGATGAGAGCCTCAGAGGTAAAGAAGAATG
Ccl3	NM_01133 7.1	TCTGTACCTGCTCAACATCATGAAGGTCTCCACCACTGCCCTTGCTGTTCTTCTGTACCATGAC ACTCTGCAACCAAGTCTTCTCAGCGCCATATGG
Ccl4	NM_01365 2.1	TTCTCAGCACCAATGGGCTCTGACCCTCCCACTTCTGCTGTTTCTTTACACCTCCCGGCAGCTTC ACAGAAGCTTTGTGATGGATTACTATGAGACCA
Ccl5	NM_01365 3.3	GTCGTGTTTGTCACTCGAAGGAACCGCCAAGTGTGTGCCAACCAGAGAAGAAGTGGGTTCAAG AATACATCAACTATTTGGAGATGAGCTAGGATAGAG
Ccl6	NM_00913 9.2	ATGTAGCCACAGGACTGTCTCTTTCTTCAGATTTCATAGAACTACGGGGCCAGTCTGAAACTGGGCT CTTGGGGTGAAATTATCTCACTCACTCACCTTGA
Ccl7	NM_01365 4.2	ACAGAAGGATCACCAGTAGTCGGTGTCCCTGGGAAGCTGTTATCTTCAAGACAAAGAAGGGCAT GGAAGTCTGTGCTGAAGCCCATCAGAAAGTGGGTCTGA
Ccl8	NM_02144 3.2	ACCTGCTGCTTTCATGTACTAAAGCTGAAGATCCCCCTTCGGGTGCTGAAAAGCTACGAGAGAAT CAACAATATCCAGTGCCCCATGGAAGCTGTGGTTT
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Ccnd3	NM_00763 2.2	GCCATGATGGTCAGAGAAATACAAACAGGTAAATCCACACACCAGCATTTCTTTTGAAGTCCCTCT TCTGTCCGGGGCTCCAACCTTCTCAGTTGCCAAA
Ccr1	NM_00991 2.4	CTTCTGATTACAGCCATAGGTGTCAACCAAGGAAGGTCTAAGAAGAGAATGAGGAGACAGTATA TAGCTCTCAAGACTGATACTGACAGTTCTTACAGT
Ccr2	NM_00991 5.2	ATGAACTAACATAGACAGCTCAGGATTAACAGGGACTTGTGGTTTGTGGTCTGTGGGCTTATCCA AGCATGGTGATTTAGACTCTAAGGTCCGTCTGGAT
Ccr3	NM_00991 4.4	TGACTTTTGCTACTATCACCAGTATCATTACCTGGGGCCTTGCAGGACTGGCAGCATTGCCTGAAT TTATCTTCCATGAGTCTCAAGACAGCTTTGGAGA
Ccr4	NM_00991 6.2	CTACTACGCCGCCGACCAGTGGGTTTTTGGACTAGGTCTGTGCAAGATCGTTTCATGGATGTACCT GGTGGGCTTCTACAGCGGCATCTTCTTCATCATG
Ccr5	NM_00991 7.5	GGAGCAGGGAGAACGAGTCTTTTATCAGGGCCGGGAAATATGCACAAAGAGACTTGAGGCAGG TGCCATGACCCATATGCAAAGGGACGACACAGGGCC
Ccr6	NM_00119 0333.1	CTACCGTTCTGGGCAGTTACTCATGCCACCAACACTTGGGTTTTTACGCGATGCACTGTGTAACTG ATGAAAGGCACATATGCGGTCAACTTTAACTGTG
Ccr7	NM_00771 9.2	CCCAGATGGTTTTTGGGTTCTAGTGCCTATGCTGGCTATGAGTTTCTGCTACCTCATTATCATCCG TACCTTGCTCCAGGCACGCAACTTTGAGCGGAA
Ccr8	NM_00772 0.2	GTTCTTCATCACCTAATGAGTGTGGACAGGTATCTGGCTATTGTCCACGCTGTCTATGCCATCAA GGTGAGGACGGCCAGCGTGGGCACAGCCCTGAGT
Ccr9	NM_00991 3.6	TATACCATCATCATTACATACCTTGGTACAGGCCAAGAAGTCATCCAAGCACAAGGCCCTCAAGGTG ACCATCACTGTCCTCACTGTCTTCATTATGTCTC
Ccr12	NM_01746 6.4	TGTTTGCGGTGGGTCTCTTGGACAACGTGCTGGCGGTGTTTATCTTGGTGAAATACAAAGGACTC AAGAATCTGGGGAACATCTACTTCCTAAACCTGGC
Cd14	NM_00984 1.3	CTAGACGAGGAAAGTTGTTCTGCAACTTCTCAGATCCGAAGCCAGATTGGTCCAGCGCTTTCAAT TGTTTGGGGCGGCGAGATGTGGAATTGTACGGCG
Cd160	NM_00116 3496.1	CAACTAGAACAGCTTAGGGTTAAAAGGGATCCTGAGACAGATGGCATCACTGAAAAGTCATCTC AGTTGGTGTTACCATAGAACAAAGCTACACCATCA
Cd163	NM_05309 4.2	TCACGGCACTCTTGGTTTGTGGAGCCATTCTATTGGTCCCTCCTATTGTCTTCTCTGTGGACTCT GAAGCGACGACAGATTACAGCGACTTACAGTTTC
Cd164	NM_01689 8.2	ATATTGAAGAAGTCCACATGGAAGACGCTGTTCCAGGATCTTTACCTTTCAAAGGATGCATACA GGATATTTTGGAGCATCATCTCGAAGAAAAGTC
Cd180	NM_00853 3.2	AGGGTTTGAAGAACTCTACGATCCAGTCTCTTGGCTGGGGACATTTGAGGACATGGATGACGAA GATATTAGTCTGCCGTGTTTGAAGGTCTCTGTGA
Cd19	NM_00984 4.2	CTCAGCGTTGGGCTGCTGGCCTAGGGAGTGTCCCTGGGTCTATGGAAATCCACGCATTCAAGTC CAGGATACTGGAGCTCAGAGCCATGAAACAGGACT
Cd1d1	NM_00763 9.3	GTTTTATGGGATTTGCACTGAACTAGAAAGCATACTTCTGCCCAAACAGACGCTCTGAGGTTAGT TGGCAAGTGTAAGTCCAACACCAACCTGGCTGT

Cd1d2	NM_00764 0.2	GGAATGCTTCGGAAGCTTTTTTCATGTAGCATTTC AAGGAAAATATGCCGTGAGATTCCGGGGA ACATCTTGGCAGAGGGTCTAGGGGCCCCATCTTG
Cd2	XM_006500 959.1	ACTGTTTTCTGTACTCTTCCCTATTCTGGTGGAAGAAGGGATCAGAACTCTTATGCCACTGATAA CTGTTGAGTGTCTAGGCGGCTTTCCTGAACCCA
Cd200	NM_01081 8.3	CCCTGCCATCTCCTGGAAGGGTACTGGGACAGGAATTGAGAATAGTACCGAGAGTCACTTCCATT CAAATGGGACTACATCTGTCAACCAGCATCCTCCGG
Cd200r1	NM_02132 5.3	AAGCTACTTCAGCTATTGAGGAGGATGAAATGCAGCCTTATGCTAGCTATACAGAGAAGAGCAAT CCACTCTATGATACTGTGACTAAGGTGGAGGCATT
Cd207	NM_14494 3.3	ATGTCAACAAGCTGCTCAAACAACAGAGTGACATTCTGGAGATGGTGGCTCGAGGCTGGAAGTA TTTCTCGGGGAACCTTCTATTACTTTTCACGCACCCC
Cd209e	NM_13090 5.2	CCAGTTGGGGAGTGGACTTTCATCATGCGTTTCCAGTTCCTACTCCCTGTCTATGGGCATGGAA ATCTTAGTATTACCTCTGGGACTCATCAGTCTCC
Cd22	NM_00104 3317.2	CTCTGACCTGTGGACTGAATTTCTCTGCTTTGGGTATGACATCCTCTTGAAGTGGTTCCTAGAAG ATTCTGAGATCACCTCCATCACCTCTTCTGTCAC
Cd244	NM_01872 9.2	TACAGACAAAAGATGTTTCTGTTCAATGGAAGAAGACAGAACAGGGCTCACACAGAAAAATTGA GATCCTGAATTGGTATAATGATGGTCCCAGTTGGTC
Cd247	NM_00111 3391.2	GCTTTGGTCTGCTGGATCCCAAACCTGCTACTTGCTAGATGGAATCCTCTTCATCTACGGAGTCAT CATCACAGCCCTGTACCTGAGAGCAAAATTGAG
Cd27	NM_00103 3126.2	CTGGGGGAGGACTCTGCTGCCGGATGTGTGAGCCAGGTACATTCTTTGTGAAGGACTGTGAACA AGACAGAACAGCTGCTCAGTGTGATCCCTGTATACC
Cd274	NM_02189 3.2	TGAACTAATATGTCAGGCCGAGGGTTATCCAGAAGCTGAGGTAATCTGGACAAACAGTGACCACC AACCCGTGAGTGGGAAGAGAAGTGTCAACCACTTCC
Cd276	NM_13398 3.4	TGGTCCATAGACCACCCACAGCCTTACTTTTCCAATGGACTTAATTCCCATCATCCTGCAGCCTCAT TTCTCCAGTGACACGATACACGAACCATCCTGC
Cd28	NM_00764 2.4	TCTGTCTCTCTTTCTCTCTGTGCATATGTCTCCCCTCCCTCACTTCTCTGTCTTTCTCTCTCCCT CTCTCTGTCTTTCTCTGTGTCTCTCTGT
Cd33	NM_00111 1058.1	ATGACACAGGAATGTACTTCTTCAAGTGGTCAGAGAACCTTTTGTGAGATATTCTTACAAAAAAA GCCAGCTGTCACTGCATGTGACCTCTCTATCACG
Cd34	NM_00111 1059.1	CTGATTATTGCTTAATAATAGCAGCTTTGAGATGACATCACCCACCGAGCCATATGCTTACACAT CATCTTCTGCTCCGAGTGCCATTAAGGGAGAAAT
Cd36	NM_00764 3.3	GGGACCATTGGTGATGAAAAAGCAGAAATGTTCAAAACACAAGTGACTGGGAAAATCAAGCTCC TTGGCATGGTAGAGATGGCCTTACTTGGGATTGGAG
Cd37	NM_00764 5.4	GTA TAGGCGGCCTGATTTTCTGCTTCGGCACCTGGATCCTCATTGACAAGACCAGCTTCGTGTCC TTTGTGGGTTTGTCTTCGTGCCACTGCAGACTT
Cd38	NM_00764 6.4	TATTCACATGGTAAACCTGAGGTCATAGGGTCATTATAGGGAAGGTGCTGTGTGGGAACTACCCA CGTGCCCTGTGCTTTAATCTTTAACTCAACACATC
Cd3d	NM_01348 7.2	CTGTGTGGAGCTAGACTCGGGCACCATGGCTGGTGTCTTTCATTGACCTCATCGCAACTCTGCT CCTGGCTTTGGGCGTCTACTGCTTTCAGGACAT
Cd3e	NM_00764 8.4	TGAGTACTGTGTGGAGGTGGACCTGACAGCAGTAGCCATAATCATCATTGTTGACATCTGTATCA CTCTGGGCTTGCTGATGGTCATTTACTTGGAGC
Cd3eap	NM_14582 2.2	ACCTGTCATTAAAGCTGTCGCTGGCCCGCCTGTTTGGAATGGGGTTCTGCCTCTTATTCTCCTGGCT GAGGAGCTTCGGGTGTCTGGGTCTACATGAGG
Cd3g	NM_00985 0.2	GCATTGAGCTAAACATAGGCACCATATCCGGCTTTATCTTCGCTGAGGTCATCAGCATCTTCTTCT TGCTCTTGGTGTATATCTCATTGCGGGACAGGA
Cd4	NM_01348 8.2	AAGAGGTGTCCGTACAAAAGTCCACCAAAGACCTCAAGCTCCAGCTGAAGGAAACGCTCCCACTC ACCCTCAAGATACCCAGGTCTCGCTTCAGTTTGC
Cd40	NM_01161 1.2	GCTGCCCAAACCCGTTACCTGATTTTGATCCCTGGGACTTCATGGTAAAAGGGAGAGAAACAAA TCCAGAGGGTTGTCATTTGACCTCCATGTGTGCTC
Cd40lg	NM_01161 6.2	AGCAGTGGATCTGAGAGAATCTTACTCAAGGCGGCAATACCCACAGTTCTCCAGCTTTGCGA GCAGCAGTCTGTTCACTTGGGCGGAGTGTGTAAT
Cd44	NM_00985 1.2	TCGCTTTGGGTGTGTCTTCGCGCGCTCCCTCCCTCTTAGGTCACTCACTCTTCAAAGCCTGGAAT AAAAACCACAGCCAACCTCCGAAGCGGTCTCAT

Cd46	NM_010778.3	TGAGGCCCTTCTGTTTCTGCTGTCTCATTTATCTGATGCCTGTGAACTACCACGGCCATTTGAAGCTATGGAAGTCAAGGGTACACCTAAACTCTTTTAT
Cd47	NM_010581.3	CTCCTGCTGCTGCGGTTCAAGTCAACTACTGTTTAGTAACGTCAACTCCATAGAGTTCACTTCATGC AATGAAACTGTGGTCATCCCTTGATCGTCCGT
Cd48	NM_007649.4	TGCGTGAAACTGAGAACGAGTTGAAGATAACCCTGGAAGTATTTGATCCTGTGCCCCAAGCCTTCC ATAGAAATCAATAAGACTGAAGCGTCGACTGATTC
Cd5	NM_007650.3	ACCAGAACATGTCTTTCCATCGAAGCCACACAGCAACTGTGCGGTCCCAAGTTGAGAACCCAACA GCCTCTCATGTGGACAATGAATACAGCCAGCCTCC
Cd53	NM_007651.3	ATGGCATCAGTTATTCTGGGTCAAAAGTTCAATTTCCACCCAGGGCAAAATTACACAACAGGCATA TGACTTCTAGGAAGTTGAGATCATTGATGGCCAC
Cd55	NM_010016.2	ACAGTTAAAGTTTCAGCAACCCAGCATGTACCTGTTACCAAGACAACAGTACGTCATCCAATAAGA ACATCTACAGACAAAGGAGAGCCTAACACAGGTG
Cd59b	NM_181858.1	CGATTAGACGTGGCAGGCATACAAAGCAAATGCTGTCTAGTGGGACTTGTGTAACAAAAATCTTGA CGGATTAGAAGAGCCAAACAACGCAGAAACTTCTCT
Cd6	NM_001037801.2	GAAGTGCCTTCAGAGTTCCAGTCACGATAGAATCTTCTGTGCCGGTGAGCGTGAAGGATAAGGA CTCACAAGGGCTGACACTTCTCATTCTCTGTATTG
Cd63	NM_001042580.1	GTGGGATTGATCGCCATTGGTGTAGCGGTTCAAGTTGTCTTGAAGCAGGCCATTACCCATGAGAC TACTGCTGGCTCGCTGTTGCCTGTGGTCATCATTG
Cd68	NM_009853.1	AGCCCGAGTACAGTCTACCTGGACTACATGGCGGTGGAATACAATGTGTCCTTCCCACAGGCAGC ACAGTGGACATTTCATGGCGCAGAATTCATCTCTTC
Cd69	NM_001033122.3	GCAGATTTCAAAGTGCTGGAAAGAAAAGTGCAATACGTGTAGTGGCAGATCTCTGTCAGGACAC ACCCTGTGGTTTGACCTTGAATAACTCCAGTCTTG
Cd7	NM_009854.1	CTCAGGCTTACAATGTGATTTACTTTGAAGACCGGCAGGAGCCACAGTAGACAGGACCTTCTCA GGCCGAATTAATTTCTCTGGTTCCAGAAGAACCT
Cd70	NM_011617.1	CGCTGACATACCTGGTCCACGGAGATGTCCTCTGTACCAACCTCACCTGCCTCTGCTGCCGTCC CGCAACGCTGATGAGACCTTCTTTGGAGTTCACT
Cd74	NM_001042605.1	ATGGATAACATGCTCCTTGGGCCTGTGAAGAACGTTACCAAGTACGGCAACATGACCCAGGACCA TGTGATGCATCTGCTCACGAGGTCTGGACCCCTGG
Cd79a	NM_007655.3	AAATAACAGGAAGTCTCTTGGGGAAGTCCCCACCCCAATTGAAATGCTGGTTTATCTCCCTTATAG GGCCTCACCTCCTCATGTCCCAAAGCAAGGGGG
Cd79b	NM_008339.2	CAGACCCAGAATGGCTCTGTCTACACCCTCACTATCCAAAACATCCAGTACGAGGATAATGGTATC TACTTCTGCAAGCAGAAATGTGACAGCGCCAACC
Cd80	NM_009855.2	TGGCTTTCCCATCATGTTCTCAAAGCATCTGAAGCTATGGCTTGAATTGTCAGTTGATGCAGG ATACACCACTCCTCAAGTTTCCATGTCCAAGGCT
Cd81	NM_133655.2	GGCATCTGGGGCTTCGTAACAAAGACCAGATCGCCAAGGATGTGAAGCAGTTCTATGACCAGG CCCTTCAGCAAGCTGTGATGGATGATGATGCCAACA
Cd83	NM_009856.2	CCAGATAGTTTAGTCTGGGTTGAATACAATGGATGTGAAGTTGCTTGGGGAAAGCTGAATGTAGT GAATACATTGGCAACTCTACTGGGCTGTTACCTTG
Cd84	NM_001252472.1	CGCCATCTGTGGATCTGGTTCCTTTGCCTACAAACCTGGTCTGAAGCAGCAGGAAAAGATGCAGA CCCGGTGGTAATGAATGGGATTCTTGGGGAGTCAG
Cd86	NM_019388.3	CAAAACATAAGCCTGAGTGAGCTGGTAGTATTTTGGCAGGACCAGCAAAAAGTTGGTTCTGTACGA GCACTATTTGGGCACAGAGAACTTGATAGTGTGA
Cd8a	NM_001081110.2	CCACCTTCGTTGTCTATATGGCTTCATCCACAACAAGATAACGTGGGACGAGAAGCTGAATTCGT CGAAACTGTTTTCTGCCATGAGGGACACGAATAA
Cd8b1	NM_009858.2	GCCACCTCATGAATAAAGTTTTCTGCAAACAGTTTCAGGGCTCTCAGCAGCCATCTTACTCTCTCAG GCCTTGCCGTGGGTTTGGGAGGCTGTTGGCTCA
Cd9	NM_007657.3	CAGCTTTTGAAAGTTTCCAGGTTAAGCCCTGCCCTGAAGCCATCAGTGAGGTCTTCAACAACAA GTTCCACATCATTGGAGCAGTGGGTATCGGCATCG
Cd96	NM_032465.2	AACCCTGTGGTAGAGTTGAGGTTTTTGGACACGAATAGGGTGGCTAGCGTTTGCTTAGCTAGAAA CAGCAATCGCCTCCTGTGATCATTACAGAAATGCT
Cd97	NM_011925.1	CGTGGCCATCTCAATGGCAGTTGTCAAATGGATGGCTATGGGCATGCAACATACTGCTGGCTGG ACTTTAGGAAGCAGGGCTTTCTCTGGAGCTTTTCG

Cd99	NM_025584.2	CCGCCGTGAAATCACCGCCTGCACCGCCCCTCGCCGCTGCATCAGTGATGTCACTACTGCCAAAGA CTCCGCCCACAACCTGACCTCTGACCCCGGTGACA
Cdh1	NM_009864.2	TCGAAGTGCCCGAAGACTTTGGTGTGGGTGAGGAAATCACATCTTATACCGCTCGAGAGCCGGAC ACGTTTCATGGATCAGAAGATCACGTATCGGATTG
Cdh5	NM_009868.3	CAGCAACTTCACCCCTATAAAACAACCATGACAACACCGCCAACATCACGGTCAAGTATGGGCAGTT TAATCGGGAGCATGCCAAGTTCCACTACCTGCCC
Cdk1	NM_007659.3	CCAGATCTCTGTTGGGAAGTAACTGGGTAAACAAAAGCCGTTGCACTGGTTTGACAGCTAACAAC GTTGGTACTTTGTATTGAGAAGGAATGAGGTAGCG
Cdkn1a	NM_007669.4	AATACCGTGGGTGTCAAAGCACTTAGTGGGTCTGACTCCAGCCCCAAACATCCCTGTTTCTGTAAC ATCCTGGTCTGGACTGTCTACCCTTAGCCCGCAC
Ceacam1	NM_001039185.1	CAAGGGAAACACTACGGCTATAGACAAAGAAATTGCACGATTTGTACCAAATAGTAATATGAATT TCACGGGGCAAGCATACAGCGGCAGAGAGATAATA
Cebpb	NM_009883.3	CGGGCACCGCGCGCACGCACCTGCACAGCGCACCGGGTTTCGGGACTTGATGCAATCCGGATCA AACGTGGCTGAGCGCGTGTGGACACGGGACTGACGC
Cfb	NM_008198.2	GGTCGGGCCTCTGGTGGACTCCGTGAACATCAATGCCTTAGCTTCCAAAAAGGACAATGAGCATC ATGTGTTTAAAGTCAAGGATATGGAAGACCTGGAG
Cfd	NM_013459.1	AGTGTCAATCATGAACCGGACAACCTGCAATCTGCGCACGTACCATGACGGGGTAGTCACCATT ACATGATGTGTGCAGAGAGCAACCGCAGGGACACT
Cfh	NM_009888.3	GAAATTCTCTGCACACCACCGCAGTGGAATAATGGAGATGGTATAAATGTGAAACCAGTTTACAA GGAGAATGAAAGATACCACTATAAGTGTAAAGCATG
Cfi	NM_007686.2	TTCCTTAATTTATGGGAGAACAAAAACAGAGGGACTTGTTCAAGTCAAACCTTGTTGGACCAAGATG AGAGAATGTTTCATATGTAAAAACAGCTGGAGCATG
Cfp	NM_008823.3	CGGCCGCAAATTTAATGGGAAGCCATGTGCTGGAAAACCTCCAGGATATTCGACACTGCTATAACA TCCATAACTGTATCATGAAAGTTTCATGGTCACAG
Chil3	NM_009892.2	ATTGTGGGATTTCCAGCATATGGGCATACCTTTATCCTGAGTGACCCTTCTAAGACTGGAATTGGT GCCCCACAAATTAGTACTGGCCACCAGGAAAGT
Chit1	NM_027979.1	GGAGGCAGTTTCGGTCTTTCCAGGGATGTGGATCCCAACCTGTGTACCCACGTCATCTTTGCTTT TGCTGGAATGGACAACCATCAGCTCAGCACTGTG
Chuk	NM_001162410.1	TCGTTTAGAGCTAAGTTCCAAAAACAGAGAGCGATGGTGCCATGAAATCCAGATCATGAAAAAGT TGGACCATGCGAATGTTGTAAAGGCCTGTGATGTC
Ciita	NM_007575.2	TGCAGCCACTGGCCATGGATGACGAGGTCCTTGATTATATCGTGAGGCAGCCAGACCGTGTCTG CTCATCCTAGATGCTTTGAGGAGCTAGAGGCCCA
Cklf	NM_029295.2	GAAAGAGCCATTAATCGAGAAGGCTTGAAAGAGAGGCGTGACTGTTGGGTCTGTGGGCAAGATG GAGACTCCACGGCCGGTCGTAAGCCGTCGGCCCTC
Clec4a2	NM_001170332.1	ATGGGCATTTCGATTATTGTTATCCAACATTACACAGACACCTGGGAAATTCTACAGGTTACAG AATTTAAGTGGGCAGCAAATGGTTATGCATACAC
Clec4n	NM_001190320.1	CTGAAGCGGAGCAGAATTTTCATACCCAGCAGCTGAATGAGTCACTTTCTACTTCTGGGTCTTT CGGATCCACAAGGTAATGGCAAATGGCAATGGAT
Clec5a	NM_001038604.1	CGCTGGATCAACAACCTCTGTGTTCAATGGCAATGTTACCAATCAGGACCAGAACTTCGACTGTGTC ACTATAGGTCTGACGAAGACATATGATGCTGCAT
Clec7a	NM_020008.2	GGATGAAGAAGCTGAGACTTTTGTAATTGTTCATCTTCACAAAGATGGTGGCACTATCTCCAGTTA GGAAGTCACTAGACATGGAGTGAGGGCAGCTCAA
Clu	NM_013492.2	TTAATAAGGAGATTGAGAACGCCGTCCAGGGAGTGAAGCACATAAAAACTCTCATAGAAAAAAC AACGCAGAGCGCAAGTCCTTGCTCAACAGTTTGA
Cma1	NM_010780.2	GAGGGAGAATTAACCTCTGGAGCTTTTGCCAGCCTGTGAGGAAATCTGGAAGTGAATAGTGCAG GTTTTGTGTGCCATGCGATCTGGCCTGTCTGTAGTT
Cmah	NM_001111110.2	CATCGAGGATTTAGATGGAAGGTCCGTTAAATGCACAAAGCACAACCTGGAAGTTAGACGTGAGC ACCATGAAATATATCAACCCTCCAGGGAGCTTCTGT
Cmklr1	NM_008153.3	TCGCCACCTTCAAGATGAAGAAGACCGTGAACACTGTGTGGTTTGTCAACCTGGCTGTGGCCGAC TTCCTGTTCAACATCTTTTGCCGATGCACATCAC
Cmpk2	NM_020557.4	AAAACTGGGGACTGAGCAGTTTGCTTCTCTGACTGACTGAGCCAGCTGCGGCTGCTGATTC ATTTCTGCCTGGCCATGTACCAACTTCTTGGGATA

Col1a1	NM_00774.2.3	CAATGGTGAGACGTGGAAACCCGAGGTATGCTTGATCTGTATCTGCCACAATGGCACGGCTGTGTGCGATGACGTGCAATGCAATGAAGAACTGGACTGT
Col3a1	NM_00993.0.1	CAAGACAGTCTTTGAATATCAAACACGCAAGGCAATGAGACTACCCATCATAGATATCGCACCCCTATGACATTGGGGGCTCTGATCAAGAATTTGGTGTG
Col4a1	NM_00993.1.2	CTCCAGGGATCACAGGTTCAAAGGGAGATATGGGACTGCCCGGAGTTCAGGATTTCAAGGTCA GAAAGGGCTTCCTGGTCTGCAGGGAGTGAAAGGAGA
Colec12	NM_13044.9.2	TAACCCAGGTTCCAGCAGAGGAACCTTATCTCAAATCTGCAGCAGTCTGTGGATGACACAAGCCTG GCCATCCAGCGAATTAAGAATGATTTCCAAAATCT
Cr2	NM_00775.8.2	TGGTTTATAGAAATCCGTCTTTGTAAAGAAATCACCTGCCACCACCTCCTGTTATACACAACGGG ACACATACATGGAGTTCCTCAGAAGATGTCCCAT
Creb1	NM_00103.7726.1	TTCTGTCTGGACAGTTCACCAGATTCTCCAGAAGGCTTTCAAACGGCTAAAGTTTGATCTTTGTCCT GCTGAGCTTGCTGGGAAGGAGATAGCATAAAAG
Creb5	NM_17272.8.2	CATGGAGGTGGCCAGGCTGGTGCCTCATCTGAGTAGTTCTGATTTATATTTTCAGCAATGTCCAC GGACTTGCCATTACGGAAAGCAGATCAAACCCA
Crebbp	NM_00102.5432.1	TTGGATATTGCTGTGGACGAAAGTATGAGTTCTCCCCACAGACTTTGTGCTGTTACGGAAAGCAG CTGTGTACAATTCCTCGTGATGCAGCCTACTACAG
Crp	NM_00776.8.4	TTGTATTTCCAAGGAGTCAGATACTTCCTATGTGTCTCTGGAAGCAGAGTCAAAGAAGCCACTGA ACACCTTTACTGTGTGTCTCCATTTCTACACTGC
Csf1	NM_00111.3530.1	TCCAGCTGCTGGAGAAGATCAAGAACTCTTTAATGAAACAAAGAATCTCCTTGAAAAGGACTGG AACATTTTACCAAGAACTGCAACAACAGCTTTGC
Csf1r	NM_00103.7859.2	GTACAAGCAGAAGCCGAAGTACCAGGTGCGCTGGAAGATCATCGAGAGATACGAAGGCAATAG CTACACCTTCATTGACCCTACTCAGTTGCCCTACAAT
Csf2	NM_00996.9.4	CTGAATCCAGCTTCTCAGACTGCTGCTTTTGTGCCTGCGTAATGAGCCAGGAAGTTGGAATTTCTG CCTTAAAGGGACCAAGAGATGTGGCACAGCCACA
Csf2rb	NM_00778.0.4	ATTGCGTGTCTGCATTGCTATGAGATGGGTTGCCGAGCCACACCTGTCTTTGGGTCCCTGTTTGCA GGGGTCTTTGCTGTAAGTGACACGTGCCTTTGT
Csf3	NM_00997.1.1	TTGTTCTCCTGCTTAGAGCAGAGAGAGAAGGCTCTTGTGTCTCCTCTGTGGAGGCCAGGGAAGGA GATGGGTAAATACCAAGTATTGATTCTGCTGCTGC
Csf3r	NM_00125.2651.1	CCCAGCCTTCTGCCTCAGGGCTATCTCATTGAGTGGGAAATGAGTTCTCCAGCTACAATAACAGC TATAAGTCCTGGATGATAGAACCTAACGGGAACA
Cspg4	NM_13900.1.2	TGGAGCTAGACATCTGGGAGCCCAAACCCGGAATGTTTACCCTGTTGGACGTGGTGAACCGT AAGGCCCGCTTTGTTACGATGGCTCTGAAGACAC
Ctla4	NM_00984.3.3	TGGACTCGAGGTCCTGCACCAACTGGCTTGGAACTAGATGAGGCTGTCACAGGGCTCAGTTGCA TAAACCGATGGTGATGGAGTGTAACCTGGGTCTTT
Ctsg	NM_00780.0.1	CTATGGAAGCAACAATGGTAACCTCCAGCTGTATTACCAAAATCCAGAGCTTCATGCCCTGGAT CAAAAGAACAATGAGACGCTTTCACCAAGATAT
Ctsh	NM_00780.1.2	TGTCATAAACTCCAGATAAAGTAAACCATGCAGTCTGGCGGTTGGCTATGGAGAACAGAATGG ATTACTCTACTGGATTGTGAAAACTCTTGGGGCT
Ctsl	NM_00998.4.3	TTCTTGTCGCGAGCTAGCCGCCTCAGGTGTTTGAACCATGAATCTTTTACTCCTTTTGGCTGTCCTC TGCTTGGGAACAGCCTTAGCTACTCCAAAATT
Ctss	NM_02128.1.2	AGACGCTTCCTATCCCTACAAAGCCACGGATGAAAAGTGTCACTATAACTCAAAAAATCGAGCTG CCACGTGTTCAAGGTACATTAGCTCCCGTTTGGT
Ctsw	NM_00998.5.4	GCCGTCTGAGCATCTTTGCCACAATCTGGCTCAGGCTCAAAGGCTACAGCAAGAAGACTTGGGT ACAGCTGAGTTTGGAGAGACTCCATTAGTGACCT
Cx3cl1	NM_00914.2.3	CGTTCCTCCATTTGTGTACTCTGCTGCCGGGTCAGCACCTCGGCATGACGAAATGCGAAATCATGT GCGACAAGATGACCTCACGAATCCCAGTGGCTTT
Cx3cr1	NM_00998.7.3	TCCTGTGTTGGTTGTGATAACCATTTCAAAGTCTCTCCAGCCTGTTGCTCACGGCGGCATGTCT GATATCTCCTTGGCAGTCTGTATGTTTGTGTCGA
Cxcl1	NM_00817.6.1	TGCTAGTAGAAGGGTGTGTGCGAAAAGAAGTGCAGAGAGATAGAGTTTAGTATTATGTTTTGTA TGTATTAGGGTGAGGACATGTGTGGGAGGCTGTGT
Cxcl10	NM_02127.4.1	AGGACGGTCCGCTGCAACTGCATCCATATCGATGACGGGCCAGTGAGAATGAGGGCCATAGGGA AGCTTGAAATCATCCCTGCGAGCCTATCTGCCAC

Cxcl11	NM_019494.1	TTAAGGCGTCAAACATGTGACATCCTGGGAACGTCTGACTGTGAGCCCTCCAATAAGAACTCTGTGCCAGGAACCTGACCCTCTGCTGTCTTGGAACAT
Cxcl12	NM_021704.3	CTGAAAATCCTCAACACTCCAACTGTGCCCTTCAGATTGTTGCACGGCTGAAGAACAAACAGACAAGTGTGCATTGACCCGAAATTAAAGTGATCC
Cxcl13	NM_018866.2	CTGAGAGGGAATGCTCAAGCTCCGTTGCATACCCAACCCACATCCTTGTTCTTAAGAAAGGCTATTGAGAACAGGCATTTAGTGACAACCCACTTCAG
Cxcl14	XM_006517307.1	GTGGACGGGTCCAAGTGTAAGTGTTCGGGAAGGGGGCCCAAGATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCACACTGCGAGG
Cxcl15	NM_011339.2	AGAGAATATTTCCCTTTCCAATTTCGGGAGACCTCTAGACACTTTGCTGATTTAGCTCACAACAGTGATAGGAATTTTCTACGGGACTCCAGTGAAGTCAG
Cxcl16	NM_023158.6	CGCAGGGTACTTTGGATCACATCCGAAAATACCTGAAAGCATTTTCATCGTTGTCCATTCTTTATCAGGTTCCAGTTGCAGTCCAAAAGCGTGTGTGGGGG
Cxcl2	NM_009140.2	GGTGGGGGTGGGGACAAATAGATGCAGTCGGATGGCTTTTCATGGAAGGAGTGTGCATGTTCACATCATTTTTTTGTAAGCACCGAGGAGAGTAGAACAGC
Cxcl3	NM_203320.2	ACTCTCAAGGATGGTCAAGAAGTTTGCCTCAACCCCCAAGGCCCCAGGCTTCAGATAATCATCAAGAAGATACTGAAGAGCGGCAAGTCCAGCTGAGCCG
Cxcl5	NM_009141.2	CCCAGTGAAGATAAGAAGAAAGGGCTGATTCTCTCCACCCACGGATTTTCTTTATGAACTCCCTGCTTTGATGAGAAAAGGGAAACCATTGTCCCTGAAG
Cxcl9	NM_008599.2	TAGAACTCAGCTCTGCCATGAAGTCCGCTGTTCTTTTCTCTTGGGCATCATCTTCTGGAGCAGTGTGGAGTTCGAGGAACCTAGTGATAAGGAATGC
Cxcr1	NM_178241.4	TCTCTTAGGAGCCCACTTGATTGAAGATACTTGCGAACGCCGAATGACATTGACCAGGCCCTGTATATTACTGAGATCCTGGGCTTTTCTCATAGTTGT
Cxcr2	NM_009909.3	CCTTGCCTGTCTGGGCTGCATCTAAAGTAAATGGATGGACTTTTGGCTCAACCCTGTGCAAGATATTCTCATACGTGAAGGAGGTTACCTTCTACAGCAG
Cxcr3	NM_009910.2	GTTGTATGGGGTCTCTGTCTGCTCTTTGCCCTCCAGATTTTCATCTACCTATCAGCCAACTACGATCAGCGCCTCAATGCCACCCATTGCCAGTACAACT
Cxcr4	NM_009911.3	GTTTCAATTCCAGCATATAATGGTGGGTCTCGTCTGCCCGGCATCGTCATCCTCTCCTGTTACTGCATCATCATCTCTAAGCTGTCACACTCCAAGGGC
Cxcr5	NM_007551.2	ACCGTGCCTTTCTCTTAACCAAGCAGAAAGCTGAAACCGATCTACTTTAGGTAGCTGTCTGGTTCCAACCTAACAGCATTGGGTGAGCCCCATGTTACT
Cxcr6	NM_030712.4	AGTGAGGAGATATCCACTATGGTTCTTGTTATACAGATGACTCTGGGGTTCTTCTGCCATTGCTCCTATGATTCTGTGCTACTCAGGCATTATCAAGA
Cybb	NM_007807.2	ACAGAAGACTCTGTATGGACGGCCCAACTGGGATAACGAGTTCAAGACCATTGCAAGTGAACACCCTAACACCACAATAGGCGTTTTCTGTGTGGCCCT
Cyfp2	NM_001252459.1	TATGAGAATAAGATGTACCTGACGCCCAGTGAAAAGCACATGTTGCTCAAGGTGATGGGCTTTGGTCTCTATCTGATGGACGGAAATGTCAGTAACATTT
Cyld	NM_001276279.1	CTATGACGATCCGGACATCTCAGCTGGGAAGATCAAGCAGTTCTGTAAGACCTGCAGCACTCAGGTTCACCTTCATCCCAGGAGGTTGAATCATTCTTAT
Ddx58	NM_172689.3	GTACACATCACATTTGCGGAAATACAACGATGCACTCATCATCAGTGAGGATGCACAGATGACAGACGCTCTAAATTACCTCAAAGCCTTCTTCCACGAT
Ddx60	NM_001081215.1	TGCCTTGGTGGAGAAATTGGAGCGGAAATCTGGGAGCATCTCCTTGTTATGATCCGATGTCCCTTTTGCGCCCTTTCAGCTACCATTAGCAACCCTCAGC
Defb1	NM_007843.3	GGTGTGGCATTCTCACAAGTCTTGACGAAGAACAGATCAATACAAATGCCTTCAACATGGAGGATTCTGTCTCCGCTCCAGCTGCCCATCTAATACCA
Dll4	NM_019454.2	TGGCAATGTCTCCACGCCGGTATTGGGCACCAACTCCTTCGTCGTCAGGGACAAGAATAGCGGCA GTGGTCGCAACCCTCTGCAGTTGCCCTTCAATTC
Dmbt1	XM_006507298.1	GTTCACTTCTCAATCAAGCAGTCCCACACCTGATGTGTTCTACCCAAGTACCAAACCACAGCAGAGCAGACAACCGTTTCTGATTATACAACAATAGG
Dock9	XM_976068.1	AGCTGATCGAGCCACTGGACTACGAAAATGTCATCGTGCAGAAGAAGACGCAGATCCTAAACGACTGCCTGCGGGAGATGCTCCTCTTCCCTTATGATGA
Dpp4	NM_001159543.1	AAGAGGGGATCACTATTTATGTGATGTGGTGTGGGCTACAGAAGAAAGAATTTCACTACAGTGGCTCAGGAGGATTCAGAACTATTCCGTGATGGCTATC

Dusp4	NM_17693.3.4	ACTGGGTGCCGTTGAGATTTTCTGCCGTGAATCATTTGGTAAGGCCAGATCAGAACCAGATCACTGAAGATGAACTAAAAATGAATCTCCCTCTCGCGG
Dusp6	NM_02626.8.2	TCAGTTCCTCTTGAGCAGCATCGACCAGGCTGCTTTCTTTCTGTGTGTGGCCCCGGGTGTCAAAAGTGTCACCAGCTGTCTGTGTTAGACAAGGTTGCCA
Ebi3	NM_01576.6.2	ATGTACTGGGCTGCTCCGAAGCACTGGATAATTCACTTGACTTCTTCAGACCTCAATTTCCAACCCTGTGGGATGATCTTTCTTCTTCTGCCGGTGCGGG
Ecsit	NM_00125.3897.1	GCCCTTTCAGGAACTCCCTTTGCTCAGGTGTCCCTCCAGGCTCTACGAGGCCTTCACTGTAGTGCA GCTACACACAAGGATGAGCCGTGGTTGGTTCCTC
Egfr	NM_20765.5.2	TGCTACAAACATCAAACACTTCAAATACTGCACTGCCATCAGCGGGGACCTTCACATCCTGCCAGTGGCCTTTAAGGGGGATTCTTTCACGCGCACTCT
Egr1	NM_00791.3.5	CGGCAGCAGCGCCTTCAATCCTCAAGGGGAGCCGAGCGAACAACCCTATGAGCACCTGACCACAGAGTCCTTTCTGACATCGCTCTGAATAATGAGAAG
Egr2	NM_01011.8.2	CAGCTCTGTCCCACCTTCTCACGGACGGCCTTCCGAAACTTAGGCCATTTGAAGGGAGTTGACTGTCACTCCAAGAAATGGGGGAGCAAAAAGAGGGCT
Egr3	NM_01878.1.2	CCAGGATTACCAATCGGCCAAGCCGGCCTTGGACAGCAATCTTTCCCATGATTCTGACTACAACTGTACCACCATCCCAACGACATGGGCTCCATT
Elane	NM_01577.9.2	AGGTTGGGCACAAACAGACCATCACCCAGTGTGCTACAAGAGCTCAATGTGACAGTGGTGACTAACATGTGCCGCCGTCTGTGAACGTATGCACTCTGG
Elk1	NM_00792.2.4	AGGGTCTCATCTTTGCCATAACTTACCAGTTGGGATACACTTGCTGGCCATCAAGTCTCAAGGATCTACCTGGTTCTACCTTGGGATTACAAGCATGTAC
Emr1	NM_01013.0.1	TGATGAGTGCACCCAAGATCCATTACAATGTGGACTGAATTCTGTCTGCACCAATGTACCAGGCTCTACATCTGTGGCTGCCTCCCTGACTTTCAAATG
Eng	NM_00114.6350.1	ATTTTCCCGGAATGCTGTACATCTGGAGCTGACTCTTCAGGCATCCAAGCAAAATGGCACGGAGACCCAGGAGGTGTTCTGGTCCTCGTTTCGAACAA
Entpd1	NM_00984.8.3	CAAACCCAGTCCAAGCCTGCCCTTTGGATAGGAGAGTTTTCTAAAGTAGATAAAATATGTGCTAAAGCCAAAGAGTCCTTGCCAAGGAGCTTATGTGCTCG
Eomes	NM_01013.6.2	ACTGAAAAGGTCGTTCAAGGTGCTGGATTGATTCATTTATGGGAAACGAGAAATGTTTCAGAAAAAGCAGGCTATGAAGAACGAGTGCCCGGTGCTATTAA
Ep300	NM_17782.1.6	TGGGACCTTTCTGGAGAATCGAGTGAATGACTTTCTGAGGCGACAAAATCACCTGAATCAGGAGAGGTCACTGTTGCGGTTGTTTCATGCTTCTGACAAA
Epcam	NM_00853.2.2	TGAAATTTGTA CTGTAATAACAAGCAGCTGGACACCGGCATTACCGATCGTAAAATTAGACGAACGCTTTATAGGTGCAGGTCCAGTGTGGTACTCAGA
Epsti1	NM_02949.5.2	CTCAGCCCAGGAAGCTAACCTGTGAGAAAGTCCAAGGGTGTCGGGTAGAGAATGAATGAGGAA GTTCTCTGAACCCAGCGGGTGTTAAAGAGAAATCG
Erbp2	NM_00100.3817.1	AGATCACAGGTTACCTATACATTTACAGCATGGCCAGAGAGCTTCCAAGACCTCAGTGTCTTCCAGAACCTTCGGGTCAATTCGGGGACGGATTCTCCATGA
Ets1	NM_00103.8642.1	GAAAGAGGATGTGAAACCATATCAGGTTAATGGAGCCAACCTACCTACCCAGAATCCTGTTACACCTCGGATTACTTCATCAGTACGGTATCGAGCAT
Ewsr1	NM_00796.8.3	ATATGCACAGACCACCCAGGCATATGGGCAACAAAGCTATGGAACCTATGGACAGCCTACTGATGTCAGCTATACTCAGGCTCAGACCACTGCCACCTAC
F12	NM_02148.9.2	CCTCACTGGGAAACATTGCCAGAAAGAGAAATGCTTTGAGCCTCAGCTTCTCAAGTTCTTCCACGA GAATGAGCTATGGTTTAGAACGGGGCCAGGAGGT
F13a1	NM_00116.6391.1	TTTCTTCTTGCAAAGCCAGAGAAAGGTCTTTCATCTTGACCTGCAGCCAAGGAACTGCCTGCCAAATTTACAGATTACCTTGTGAGAAGATGTGGCC
F2rl1	NM_00797.4.4	GCTGGCCATGTACTTCATCTGCTTTGCTCCTAGCAACCTTCTGCTCGTAGTGCATTATTTCTAATCAAACCCAGAGGCAGAGCCACGTCTACGCCCTC
Fadd	NM_01017.5.5	TTAAGTGGCAGTATTGAGTTACTACTGTTGCAGGGCTTTGGGCCACCAAAGAACTTATCCCTTTGTACAGAGTCCCTTCAACCAGTTGGGGATTAAA
Fap	NM_00798.6.2	CTCTGGCGATATTCATACACAGCGACATACTACATCTACGACCTTCAGAATGGGGAATTTGTAAGAGGATACGAGCTCCCTCGTCCAATTCACTATCTAT
Fas	NM_00798.7.2	CCAATTGTATTTATATATCGAAAGTACCGGAAAAGAAAGTGCTGGAAAAGGAGACAGGATGACCCTGAATCTAGAACCTCCAGTCGTGAAACCATACCA

FasI	NM_010177.3	CATTTAACAGGGAACCCCCACTCAAGGTCCATCCCTCTGGAATGGGAAGACACATATGGAACCGCTCTGATCTCTGGAGTGAAGTATAAGAAAGGTGGCC
Fcer1a	NM_010184.1	GAGAAATCTGTACTGACCTTGGACCCACCATGGATTAGAATATTTACAGGAGAGAAAGTGACCCTTTCCTGCTATGGGAACAATCACCTTCAAATGAACT
Fcer1g	NM_010185.4	CTATAGCCAGCCGTGAGAAAGCAGATGCTGTCTACACGGGCCTGAACACCCGGAGCCAGGAGACATATGAGACTCTGAAGCATGAGAAACCACCCAGTA
Fcer2a	NM_001253737.1	CCCAATCAAAATACACCATCACATCATAGCCAGTCTAACAGACCGCCCTTTTTCTCTTCATAAAATTACACCTGCAACCAGGCGTAGTGGTGCAGGCCT
Fcgr1	NM_010186.5	GAGACAGTTCACACAATGGTTTATCAACGGAACAGCCGTTGAGATCTCCACGCCTAGTTATAGCATCCCAGAGGCCAGTTTTTCAGGACAGTGGCGAATA
Fcgr2b	NM_001077189.1	TTGGTCCCAATGGTTGACTGTACTAATGACTCCCATAACTTACAGCTTCCCAACTCAAGACTCTTCTGCTATCGATCCCACTGCCACTAAAATTAATC
Fcgr3	NM_010188.5	TCTGACCTCCACCATCCACCATGGCAGGTGCACACAATAAATTAATTAATGTCATGTATATTTTTAAACAAGAGACAGGGGCAGGCTAAGGGTTGATGGCAT
Fcgr4	NM_144559.1	GGCGATCCAGGGTCTCCATCCATGTTTCCACCGTGGCATCAAATCACATTCTGCCTGCTGATAGGACTCTTGTTTGCAATAGACACAGTGCTGTATTCT
Fez1	NM_183171.4	GAAGCTCTGAATGGCAACAGCTCTGACATTGAGATTCATGAGAAGGAAGAAGAAGAGTTCAATGAGAAGAGTGAAAAAGACTCTGGCATCAATGAGGAGC
Flt3	NM_010229.2	CGCCCTACAGGCCGTTGCTTCGCTGGACTTTTCTCTAGATGCTGTCTGCCATTACTCCAAAGTGACTTCTATAAAATCAAACCTCTCCTCGCACAGGTGG
Flt3l	NM_013520.2	GGTCTAAGATGCAAACGCTTCTGGAGGACGTCAACACCGAGATACATTTTGTACCTCATGTACCTTCCAGCCCCTACCAGAATGTCTGCGATTCTGCCA
Fn1	NM_010233.1	TCCAGACCCTACCGTGGACCAGGTTGATGATACTTCCATTGTTGTTGGTGGAGTAGACCCCAGGCACCTATCACAGGGTATAGAATTGTCTATTACCT
Fos	NM_010234.2	AGCTGGTGCATTACAGAGAGGAGAAACACGTCTTCCCTCGAAGGTTCCCGTCGACCTAGGGAGGACCTTACCTGTTCTGTGAAACACACCAGGCTGTGGGC
Foxj1	NM_008240.3	TAAGCCCCTAGGGCCTTTCCCTGGTCCATCACCTGCACAAGGGAGGCTACAAACCTTCCAGCCTGACTTGAGGCTAAGAGCATCAGGAAGATGGGGTGT
Foxp3	NM_054039.2	TGCCTTCAGACGAGACTTGGAAGACAGTCACATCTCAGCAGCTCCTCTGCCGTTATCCAGCCTGCCCTTGACAAGAACCCAATGCCAACCTAGGCCAG
Fpr2	NM_008039.2	GTGAGAGATTTATTCAATCCCTGCCTTATAGTCTTGAGAGAGCCCTGAGTGAGGATTCTGGTCAAAACAGTGATTCAAGCACCAAGTTCTACTTCACCTCC
Fut7	NM_001177367.1	GATGCCTTTGTACAGTGGACGACTTCAGCTCTGCCCGTGAAGTGGCTGTCTTCTCTCGTCAGCATGAATGAGAGTCGTTATCGTGGCTTCTTTGCTTGGC
Fyn	NM_008054.2	TTCTTATCCGCGAGAGCGAAACCACCAAAGGTGCCTACTCACTTTCCATCCGTGATTGGGATGATATGAAAGGGGACCACGTCAAACATTATAAAATCCG
Gata3	NM_008091.3	CATGCGTGAGGAGTCTCCAAGTGTGCGAAGAGTTCCTCCGACCCCTTCTACTTGCGTTTTTCGCAGGAGCAGTATCATGAAGCCCCGAAAGCGACAGATCT
Gbp2b	NM_010259.2	TCAAGAACATGCCTCCACCTCGATCATGCACCATACTTTAAAATCTGAACAGACTAAAGCTCTCTACCCTGTTTCCACTCATCAAGGAAAAAACTTCGGG
Gbp5	NM_153564.2	TCGTTCAAGGATGAGGGTGAATTTTTCCAGAAAGAATTGGAGAGCCTACTAAGTGCAAAGCAGGATGAGATTTGTAAGAAGAACGCGGATGCTTCTGCAG
Gfi1	NM_010278.2	CAAAGCTCATCATGGTTAGTCCCCTTCACTTCTTCCCGGAGCTGCTGGAGGAGATGAACTCCCGTTTCTAAGGTCAACCCAGAGTGGGAACCGCAGCA
Glycam1	NM_008134.2	ACTTCAAATGAAGACTCAGCCACAGATGCCATTCCAGCTGCCAGTCCACTCCCACCAGCTACACAGTGAGGAGAGTACTTCCAGTAAGGACCTTTCC
Gpi1	NM_008155.4	CGACCAACTCTATTGTGTTTACCAAGCTGACACCCTTCACTTCTGGGGGCCTTGATTGCCATGTATGAGCACAAGATCTTTGTTGAGGGCATCATGTGGGA
Gpr183	NM_183031.2	CAGCCAGGGTATTAATGCCTCTGCATTACAGCCTGGTCTTCATCATTGGGCTGGTGGGAAACCTGCTGGCCTTGGTTGTCATTGTTCAAAACAGAAAAA
Gpr44	XM_006526695.1	ATCAGAATGGGTGGTTCTGAAGAGTGCAGGAGCGCTGTCTTCTGAGCATCCCATGACACTGACAGTGCAGCTTGAAGGGATGTCTCACAGCAGAAAGAGA

Gtf3c1	NM_20723.9.1	ACCAACGGCATGCTAGACCAGCCTGATCATTTTTCTTTCAAGGACCTGGATAGCAGTGACCCTTCA AATGACCTGGTGGCATTTTTCTTTGGACAGCCCTG
Gzma	NM_01037.0.2	CTGTGCTGGCGCTTTGATTGAAAAGAACTGGGTGTTGACTGCTGCCACTGTAACGTGGGAAAGA GATCTAAGTTCATTCTTGGGGCTCACTCAATCAAT
Gzmb	NM_01354.2.2	TTCTGCCACCATGCTGTGACAACCCAACTGACATCTTCCTATGGAAGTTTGGCCTCTCCACAAAAG AAGTAGAATGTTTGCATTGGAGCTGGGCATGCTC
Gzmk	NM_00819.6.1	CATCCCATTCTCAGCACTTCAGTCCGGTTCCGCATCGCATGACATCATGCTGATAAAGCTTCGCACT GCTGCAGAACTAAACAAGAATGTCCAAGTCTT
Gzmm	NM_00850.4.2	CAGAACCTGAAGCTGGTGCTTGGCCTGCACAACCTCCATGATCTCCAAGATCCTGGCCTCACCTTC TACATCCGGGAAGCCATTAACACCCTGGCTACA
H2-Aa	NM_01037.8.2	TCAGAAATAGCAAGTCAGTCGACAGCGGTGTTTATGAGACCAGCTTCTTCGTCAACCGTGACTATT CCTTCCACAAGCTGTCTTATCTCACCTTCATCCC
H2-Ab1	NM_20710.5.2	AAGGCATTTCTGTGTACCAGTTCATGGGCGAGTGCTACTTCACCAACGGGACGCAGCGCATACGAT ATGTGACCAGATACATCTACAACCGGGAGGAGTAC
H2-D1	NM_01038.0.3	GTGACAGACGATGTGTTCAAGTCTCTCTGTGACATCCAGAGCCCTCAGTTCTCTTTACACAACAT TGCTGATGTTCCCTGTGAGCTTGGGTTCAAGTGT
H2-DMa	NM_01038.6.3	AGCTGTGATGGGCTGACCTTCCAGGCTTTCTCTTATTTAAACTTCACACCGGAACCCTTTGACCTT TACTCTGCACTGTGACACACGAGATTGACCGC
H2-DMb1	NM_01038.7.2	CTCTATTCAGGTCCCTTCTCTGAAATAAATATTAGTAGTTTGGGGGGGTATTTATAATGAAGTCTG TCCCAGGTGGGGGAGCTGAGGTGAGCTGAAATGA
H2-DMb2	NM_01038.8.4	TTTGGGGTGCTGTCTAGATTGGCTGAAATAATTTCAAATATCCTCAACGAACAGGAGAGCCTTATT CATCGCTTGCAAACGGGCTTCAGGACTGTGCCA
H2-Ea-ps	NM_01038.1.2	ATCATGAAGGGTATTAATAAACGCAATGTTGTAGAACGCCGACAAGGAGCCCTGTGAGATACCT GGAGGCAATGCCTTCAGTTAAAGTTCAGTGAAGAAA
H2-Eb1	NM_01038.2.2	AAACATGTCCTGCTTGGCCACATCCCTCCAGAGACACTGCTCTTCCAGGACCTGGCTCCTCTGA TTCTCCACCCTGGAGATCTGTGCTCCTGATGGCT
H2-K1	NM_00100.1892.2	TCTTCCCTTCCACAGCCAACCTTGCTGGTTCAAGCAAACTGAGGGACATCTGTAGCCTGTCAGC TCCATGCTACCCTGACCTGCAACTCCTCACTTCC
H2-M3	NM_01381.9.2	GAGTCTCCTCTCCATACCTGTGTCTCCTCTTTTCTCACCTGTACCACAGGGGGATCCAGGACTTCT TCATCCCTGTGGAACTTTAGGTTTCTATGGGC
H2-Ob	NM_01038.9.3	TTTCTATGAGTTAGCATCTGATGCAGACTTGGGGTGAGACTCTAGTCTGATTGTTTTGGAGTCTGG AGGAGGCCATGACCTTTTCTGGAGTTACAGTGTA
H2-Q1	NM_01039.0.3	TACTACAACCAGAGCAAGGGCGGCATTACACCTTCCAGAAGTTGTCTGGCTGTGATCTGGGGTC AGATGGGCGCCTTCAAAGCGGGTACCTGCAGTTCC
H2-Q10	NM_01039.1.4	TGAGCCCCTCACCTGAGATGGGAACCTCCTCCTTCCACTGACTCTATCATGTCACACATTGCTGAT CTGCTGTGGCCATCATTAAAGCTCTGGTGGTAT
H2-Q2	NM_01039.2.2	ACCTGGCAGCACTGAAGACCCGAAGCAAGTTGGAGCAGGCTGGTCTTGACAGAGAAGCGCAGGG CCTACCTGGAGGTCGATTGCTTGACGTGGCTCCGCAG
H2-T23	NM_01039.8.3	CCTACGATGGCCAGGATTACATCTCCCTGAACGAGGACCTGCGTTCCTGGACCGGAATGACATA GCCTCACAGATCTCTAAGCACAAAGTCAGAGGCACT
H60a	NM_01040.0.2	GGGCAAGGAGTTGGCCAGTTTTCAAAGGTAATTAGGAATATATGGCAAGTACAGCCAGTGATTT GGATGGAGCTGGCAAAGTAAGACACAATTTAATGTG
Hamp	NM_03254.1.1	AAGAGAGACACCAACTTCCCCATCTGCATCTTCTGCTGTAAATGCTGTAACAATTCCAGTGTGGT ATCTGTTGCAAAACATAGCCTAGAGCCACATCCT
Havcr2	NM_13425.0.2	TGGAAAATGCTTATGTGTTTGAAGTTGGTAAGAATGCCTATCTGCCCTGCAGTTACACTCTATCTA CACCTGGGGCACTTGTGCCTATGTGCTGGGGCAA
Hc	NM_01040.6.1	CTACACACTGAATTTGGTCGCTACTCCTCTTTTCTGTGAAGCCCGGGATTCCATTTTCCATCAAGGCA CAGGTTAAAGATTCACTCGAGCAGGCGGTAGGA
Hck	NM_01040.7.3	GAGGACTTCACAATCTCTTTCTGACTCTAGTCATCTGCAATCCGCCACTCTCAGGGCCTCCAAGTTG GTATGTCTCATTGCTGGAATGACTGAATTCA
Hcst	NM_01182.7.3	CATCGGCAGGTTCTGCTCCGGATGTGGGACTCTGTCTCTGCCACTCCTGGCAGGCCTAGTGGCT GCAGATGCGGTCATGTCACTCCTAATTGTAGGGT

Herc6	NM_025992.2	CCACAACATCATAGAAGGAATTGGTGGCCGTGTTTCACAGATAGAGTGCGCAAGTTATCACACCAT TGCATATGTCTACACCACTGGTCAGGTGGTATCTT
Hif1a	NM_010431.2	ACCATGATATGTTTACTAAAGGACAAGTCACCACAGGACAGTACAGGATGCTTGCCAAAAGAGGT GGATATGTCTGGGTGAAACTCAAGCAACTGTCAT
Hmgb1	NM_010439.3	GTGGGACTATTAGGATCAAGCAATCTGAACGTCTGTCTTGAAGGACTGATAGAAAAGTACCTTC TAATCCTTACACGAGGACTCTCCTTTAACCGCCAT
Hras	NM_008284.2	CAAATGTTCAAGCTTCCCTTGCTGTGTGTATCTGGGGCTCCTGAGGTATCATCTGGAGCGTCAGTG ACACCTTCGGAGCCTTGTGGTTCATGAACCTAAG
Hsd11b1	NM_008288.2	CAGGTCCCTGTTTGATGGCAGTTATGAAAAATTACCTCCTCCCGATCCTGGTGCTCTTCTGGCCTA CTACTACTATTCTACAAATGAAGAGTTCAGACC
Hspb2	NM_024441.3	CTGTCTACCTCCCGTGGTGATTCCATAAATCCACCACACCCAGAGGGAGCAGCATCCCTGGGAG ATGGCATCGGTGCATGGTCCACAGTGTATGGTTTG
Icam1	NM_010493.2	CACATGGGTCGAGGGTTTCTCTACTGGTCAGGATGCTTTTCTCATAAGGGTCGACTTTTTTACCA GTCACATAAACACTATGTGGACTGGCAGTGGTTC
Icam2	NM_010494.1	GAAGTGGAACAGTTCTTAGTCTCAAACGTCTCAAAGACACGGTCTTCTTTGCCATTTACAGTG TTCGGGAAAGCAGCACTCGGAGAGTCTCAACATC
Icam4	NM_023892.2	GGATTCTTGGTGGTGAGCCTGAGAAGAGGTGGCCGAGTGATTTATCATGAAAGCCTGGAGCGCT TCACCGGTTCAAGTTGGCTAATGTCACTTTGACCT
Icos	NM_017480.1	TTCACAATGGAGGTGTACAGATTTCTTGTAATACCCTGAGACTGTCCAGCAGTTAAAAATGCGAT TGTTCAAGAGAGAGAGAAAGTCCTCTGCGAACTCAC
Icosl	NM_015790.3	CCCCACAGACGCCATTTCAACTTGAGTGGTCTGTATGTCTATTGGCAAATCGAAAACCCAGAAGTT TCGGTGACTTACTACCTGCCTTACAAGTCTCCAG
Ido1	NM_008324.1	ACATGGACATTCTGTTCTCATTTCTGGTGGGGACTGCGACAAGGGCTTCTTCTCGTCTCTCTATT GGTGGAAATCGCAGCTTCTCTGCAATCAAAGC
Ifi27	NM_026790.2	GGTTCCTGTTTGAAACTTAACTGGTCTCATGGCGTTTTCGGGCACAGGGACACTGGTGGCTTCC ATTGTCTCCAAGATGACATCTTCAGCAGCCATGG
Ifi35	NM_027320.4	GTCTCTCCCTATGTGAGTGGTGAGATCCAGAAAGCCGAGATCAAATTCCAGCAAGCCCCTCATTCA GTGCTGGTGACAAATATTCTGATGTCATGGATG
Ifi44	NM_133871.2	CTGACAGATACCAGTTCGATTCCATGAAACCAATCACATCAAACCATCCGAACATATCCCATGACC CACTGCTGAAGGACAGAATTAAGTGTGTTTT
Ifi44l	NM_031367.1	ACTGGTAACCTGGCTCCTTTCTAAAGCACTGCCTTTTGGGAAACCCTCAGCTGTAGTTCACTGGGG TGTTGGGGACCATTTTCTAGCCCTGACATGTA
Ifih1	NM_027835.2	GCTGCTAAAGACGGAAATCGCAAAGATCGCGTCTGTGCAGAACATTTGAGGAAGTACAACGAAG CCCTACAAATCAACGACACGATCCGAATGATTGATG
Ifit1	NM_008331.2	AACAGGGCCTTGACAGGCATCACCTTCTCTGGCTACTTACATTATCAAAAAGGGCTCTGCTACAAG CAACAAATCTCCCAACTGAGGACATCCCGAAACA
Ifit2	NM_008332.2	ACAACGAGTAAGGAGTCACTGGAGAGCAATCTGCGACAGCTAAAATGCCATTTACCTGGAACCT GATAGCAGAAGATGAGTCCTTGATGAGTTTGAGG
Ifit3	NM_010501.1	AATTGTGGTGGATTCTTGGCAGTTGCAGGGATAAAGGAGTGGCTGAATGGTTTTGGGGTTTGGG AGGCAACGCACTTTGGGGCACAGGCAGGCTTTTCT
Ifitm1	NM_001112715.1	CCTCCACCGCCAAGTGCCTGAACATCAGCTCCCTGTTCTTACCATCCTCACGGCCATCGTCGTCAT CGTTGTCTGTGCCATTAGATGATGTGAGATGTC
Ifitm2	NM_030694.1	GCTTCTCCAAGCTATGAGACAATCAAAGAGGAGTACGGGGTGAAGTGAAGTGGGGGAACCCAGC AACTCAGCTGTTGTGAGGACCACCGTATCAACATG
Ifna1	NM_010502.2	CTGGCGGTGCTGAGCTACTGGCCAACCTGCTCTCTAGGATGTGACCTTCTCAGACTCATAACCTC AGGAACAAGAGAGCCTTGACACTCTGGTACAAA
Ifna2	NM_010503.2	TAACCTCAGGAACAAGAGGGCCTTGAAGTCTGGCACAGATGAGGAGGCTCCCTTTCTCTCTCT GCCTGAAGGACAGGCAGGACTTTGGATTCCCCCTG
Ifna4	NM_010504.2	CAGAAGGCTCAAGCCATCCTTGTGCTAAGAGATCTTACCAGCAGATTTGAACCTCTTACATCA AAAGACTTGTCTGCTACTTGAATGCAACTCTAC
Ifnar1	NM_010508.1	TGGGAAAACACTTCCAATACTAAGATAAGCATGGAGAAGGATGGCCCAGAGTTCACCTCAAGA ACCTGCAGCCGCTGACTGTGTACTGTGTCCAGGCCA

Ifnar2	NM_001110498.1	TCCTCTTGAGCCGCCAGAATTTGAGATCGTTGGCTTTACAGACCACATAAACGTGACGATGGAATT TCCACCTGTCACTTCCAAAATAATCCAGGAAAAG
Ifnb1	NM_010510.1	GATGAACTCCACCAGCAGACAGTGTCTGAAGACAGTACTAGAGGAAAAGCAAGAGGAAAGAT TGACGTGGGAGATGTCCTCACTGCTCTCCACTTGA
Ifng	NM_008337.1	CTAGCTCTGAGACAATGAACGCTACACACTGCATCTTGGCTTTCAGCTCTTCCTCATGGCTGTTTC TGGCTGTTACTGCCACGGCACAGTCATTGAAAG
Ifngr1	NM_010511.2	AAGCATAATGTTACCTAAGTCCTTGCTCTGTGTTGTAAGAGTCCACGTTAGAGACAAAACCTGA ATCGAAGTATTCATTGTACACCCGCCAGCCA
Ifnl2	NM_001024673.2	GCCACCAGGCTCCAGTGGAAGCAAAGGATTGCCACATTGCTCAGTTCAAGTCTCTGTCCCCAAA AGAGCTGCAGGCCTTCAAAAAGGCCAAGGATGCCA
Igf1r	NM_010513.2	CGTATGAGAACTTCATGCATCTGATCATTGCTCTGCCGTTGCCATCCTGCTGATCGTTGGGGGGC TGGTTATCATGCTGTATGTCTTCATAGAAAAGAG
Igf2r	NM_010515.1	TGCATCTGCTTGCCAGATGAAATATGAAAATCATGAGGGCTCCTTGGCAGAGACTGTATCCATCA GTAACCTGGGAGTTGCAAAGATAGGCCCTGTGGTG
Igll1	NM_001190325.1	GTGGAGAAGAGTGTGTACCTGCTGAGTGTCTTAGACCACAATCCTCCCTGAAGCCTCAGGGGC CTGGATCTGAAGTGCCAGAAAAAGTTGTTTTTGT
Ikbkb	NM_010546.2	CTTACCCTGCTGAGTGACATCGCATCGGCTCTTAGATACCTTACGAAAACAGAATCATCCATCGA GACCTGAAGCCAGAAAACATCGTTCTGCAGCAAG
Ikbke	NM_019777.3	TGGGAGCCTGCTGAGCGTGCTGGAAGACCCTGAGAACACGTTCTGGGCTTCTGAAGAGGAGTTC CTAGTGGTGCTGCGCTGTGTGGTGGCTGGCATGAAC
Ikbkg	NM_178590.2	TGCCAACAGATGGCTGAGGACAAGGCCTCTGTGAAAGCTCAGGTGACATCATTGCTCGGAGAACT CCAGGAGAGCCAGAGCCGTTTGGAGGCTGCCACCA
Ikzf1	NM_001025597.1	GATTCCAGTGCCCTCAAGTTGTGTTTAAGTAGCTATCAGAGGCAAGAGGGTTCCTAAGAGCAGG TTGACCTGTTGGCGACAGATGGCAATCACCATTTC
Ikzf2	NM_011770.4	AATTATGGAAGTGTGATCTAAAAACGGTTTGACAGTGGAGCACCAGAGAGGATGTCCACCACTCA CTTGCCCTTCGGTACGACTAAGCTCTGAGTTTGCG
Il10	NM_010548.1	GGGCCCTTTGCTATGGTGTCTTTCAATTGCTCTCATCCCTGAGTTCAGAGCTCCTAAGAGAGTTGT GAAGAAACTCATGGGTCTTGGGAAGAGAAACCA
Il10ra	NM_008348.2	TGTTGTCGCGTTTGCTCCATTCTCGTCACGATCTCCAGCCTGAGCCTAGAATTCATTGCATACGG GACAGAACTGCCAAGCCCTTCTATGTGTGGTT
Il11	NM_008350.2	GCGCTGGGACATTGGGATCTTTGCAGTTCCTGGTGTGCTGACAAGGCTTCGAGTAGACTTGATG TCCTACCTCCGGCATGTACAATGGCTGCGCCGTGC
Il11ra1	NM_010549.3	GGGTCCCACAACCTCAGTGGAGCGGGAGACAGTTCTTAGCCTGTAGGAGGAAGTCTTGGAGGCCA TGGGCACTCAGTCACTGTGATTATCAAGATGAGCAG
Il12a	NM_008351.1	TCATGAAGACATCACACGGGACCAAACCAGCACATTGAAGACCTGTTTACCACTGGAACCTACACA AGAACGAGAGTTGCCTGGCTACTAGAGAGACTTCT
Il12b	NM_008352.1	TCGTAGAGAAGACATCTACCGAAGTCCAATGCAAAGGCGGGAATGTCTGCGTGCAAGCTCAGGA TCGCTATTACAATTCTCGTGACGAAGTGGGCATG
Il12rb1	NM_008353.2	TGAACCTCTCCGGGGCCACCTATGACCTGAATGTGCTCGCCAAAACCTCGTTTCGGTCGCAGCACCA TCCAGAAGTGGCACCTTCTGCCAAGAGCTCAC
Il12rb2	NM_008354.3	CTTCTGCACCCACTCACATTAACATAGTGGACCTATGTGGCACTGGGTTGCTGGCTCCTCACCAGG TCTCTGCAAAGTCGGAGAACATGGACAACATTCT
Il13	NM_008355.2	AGCTACACAAAGCAACTGTTTCGCCACGGCCCTTCTAATGAGGAGAGACCATCCCTGGGCATCTC AGCTGTGGACTCATTTTCTTTCTCACATCAGAC
Il13ra1	NM_133990.4	CTCAAACCGACCGACATAATATTTTAGAGGTTGAAGAGGACAAATGCCAGAATTCCGAATCTGAT AGAAACATGGAGGGTACAAGTTGTTTCCAACCTCCC
Il13ra2	NM_008356.3	GACCCATTCCACCAAGGTGTTACCTTATGAAATTGTGATCCGAGAAGACGATATTTCTGGGAGT CTGCCACAGACAAAACGATATGAAGTTGAAGAG
Il15	NM_008357.2	CTTGCAAACAGCACTCTGTCTTCTAACAAGAATGTAGCAGAATCTGGCTGCAAGGAATGTGAGGA GCTGGAGGAGAAAACCTTCACAGAGTTTTTGCAA
Il15ra	NM_008358.2	CTTTCCTGGCCTGGTACATCAAATCAAGGCAGCCTTCTAGCCGTGCCGTGTTGAGGTGGAAACC ATGGAAACAGTACCAATGACTGTGAGGGCCAGCAG

II16	NM_010551.3	TGCGAGACAAAGCTGTTGGATGAAAAGGCCAGTAAGCTTTACTCCATCAGCAGCCAGCTATCATC TGCTGTCATGAAATCCCTGCTGTGCCTTCCATCTT
II17a	NM_010552.3	ACCTCAAAGTCTTTAACTCCCTTGGCGCAAAAGTGAGCTCCAGAAGGCCCTCAGACTACCTCAACC GTTCCACGTCACCCTGGACTCTCCACCGCAATGA
II17b	NM_019508.1	CCATGGGGGTACAGCATCAACCACGACCCAGCCGCATCCCTGCGGACTTGCCCCGAGGCGCGGTG CCTATGTTTGGGTTGCGTGAATCCCTTCACCATGC
II17f	NM_145856.2	TGTGAAGCCCGATCTCCAAGTCTTTATGCTTTCTAGGACTCTCAGTAAGGTGTGCATGGCATTCTT GCAGCTCTGCAGTAGATATAGCTTGAACCTTCTG
II17ra	NM_008359.1	CCCCAAAACCTGACCCCGTCTTCCCCAAAAAACATCTATATCAATCTTAGTGTTTCCTCTACCCAGC ACGGAGAATTAGTCCCTGTGTTGCATGTTGAGT
II17rb	NM_019583.3	GCCAGGGAGAACTCTCAGGATCTGTTCCCTCTTGCCCTTAACTCTTTGTAGTGATTTCAGCAGCC AGACGCATCTGCACAAATACCTGGTGGTCTATC
II18	NM_008360.1	ACTTTGGCCGACTTCACTGTACAACCGCAGTAATACGGAATATAAATGACCAAGTTCTCTTCGTTG ACAAAAGACAGCCTGTGTTGAGGATATGACTGA
II18r1	NM_001161842.1	AGATGGTTCAAAGGCAGTGCTTCACATGAGTATAGAGAGCTGAACAACAGAAGCTCGCCAGAG TCACTTTTCATGATCACACCTTGAATTCTGGCCAG
II18rap	NM_010553.2	CTTGAAGTCGGTCCACGCCAGTTCAGGTTCTGGACCCAAATTCGTTACCACATGCCTGTGAAGAA CTCCAACAGGTTTATGTTCAACGGGCTCAGAATT
II19	NM_001009940.1	TCTAGGAGAACTGAACATACTTTTAGCCTGGATTGACAGGAATCATCTGGAAACTCCTGCAGCCT GACACGAAACGCCTCGTCTGATTATCTAAATAACG
II1a	NM_010554.4	ACCTCTGAAACGTCAAAGATGTCCAACCTTCACCTTCAAGGAGAGCCGGGTGACAGTATCAGCAAC GTCAAGCAACGGGAAGATTCTGAAGAAGAGACGGC
II1b	NM_008361.3	GTTGATTCAAGGGGACATTAGGCAGCACTCTCTAGAACAGAACCTAGCTGTCAACGTGTGGGGG ATGAATTGGTCATAGCCCGCACTGAGGTCTTTCATT
II1r1	NM_001123382.1	CTTCTTCGGAGTAAAAGATAAACTGTTGGTGAGGAATGTGGCTGAAGAGCACAGAGGGGACTAT ATATGCCGTATGTCCTATACGTTCCGGGGGAAGCAA
II1r2	NM_010555.4	AGAAACGCATCCCCTGTGAGCAAATGTCTGTGGAACCTCAAGGTCTTTAAGAATACTGAAGCATC TCTGCCTCATGTCTCCTACTTGCAAATCTCAGCTC
II1rap	NM_008364.2	ACAGTCAAACCTGCAGCTGTTCTCTGTGACTGATTAAGCGACATACTGCCTTCCTGCTACTAAACCC CATTGCTCTCATCTCAGGTAATGGAGATCATAT
II1rapl2	NM_030688.1	TGGATGGCTGCATTGATTGGTCGGTGGATCTCAAGACATACATGGCTTTGGCAGGTGAACCTGTC CGAGTGAAATGTGCCCTTTTCTACAGTTATATCCG
II1rl1	NM_001025602.2	ATAGGAAAACCAGCAAGTATTGCCTGTTGAGCTTGCTTTGGCAAAGGCTCTCACTTCTTGGCTGAT GTCCTGTGGCAGATTAACAAAACAGTAGTTGGAA
II1rl2	NM_133193.3	AGGAAGTTGAGTATGGAAGAAGGATCCCTAACATCACGTATCCAAAGAACAACCTCCATTGAAGTT CCAATTGGCTCCACCCTCATCGTGAACCTGCAATAT
II1rn	NM_031167.5	CAACCAGCTCATTGCTGGGTACTTACAAGGACCAAATATCAAACCTAGAAGAAAAGATAGACATGG TGCCTATTGACCTTCATAGTGTGTTCTTGGGCATC
II2	NM_008366.3	TCTTCAGTGCCTAGAAAGATGAACCTTGACCTCTGCGGCATGTTCTGGATTTGACTCAAAGCAAAA GCTTTCAATTGGAAGATGCTGAGAATTCATCAGC
II21	NM_021782.2	ATGGCCTGGGGGATGTTTTGATCTAAGGAAAAAGGTGTCTGTACCTCACAGTGCCTTTAAACA AGCAGAGATCCCGTGTAACGCCCTAAGATAGCACA
II21r	NM_021887.1	TATGGTACACGTGCCATATGCGCTTGCTCAATTCCTGTCCGATGAAGTTTTATTGTCAATGTGAC GGACCAGTCTGGCAACAACCTCCAAGAGTGTGG
II22	NM_016971.1	AGAAGAATGTCAGAAGGCTGAAGGAGACAGTGAAAAAGCTTGAGAGAGTGGAGAGATCAAG GCGATTGGGGAACTGGACCTGCTGTTTATGTCTCTGAG
II22ra1	NM_178257.1	ACTCCTTCTCGGGCGCCGTGCTCTTTCCATGGGTTTCTCGTCGGCTTGCTCTGTTATCTGGGCTA CAAATACATCACCAGCCACCTGTACCTCTAA
II22ra2	NM_178258.5	TAAGCATTGCCTTCTAGGTCTCCTCATCATACTCTTGAGCAGTGCAACAGAAATACAACCAGCTCG TGTATCTCTGACGCCCCAGAAGGTCCGATTTTCAG
II23a	NM_031252.1	CAAGGACAACAGCCAGTTCTGCTTGCAAAGGATCCGCCAAGGTCTGGCTTTTTATAAGCACCTGCT TGACTCTGACATCTTCAAAGGGGAGCCTGCTCTA

II23r	NM_14454.8.1	AAGTATTTGGTATGGGTCCAAGCTGTCAATTCCTAGGCATGGAGAACTCACAACAACTACACGTC CATCTGGATGATATAGTGATACCTTCTGCGTCCA
II24	NM_05309.5.2	CATAGTCATCATGTCACAACTACAGCCAGTAAGGACAATTCCATGCTTCCCATTAGTGAGAGTGC ACACCAGCGTTTTTGTCTGTTCCGCAGAGCATTC
II25	NM_08072.9.2	TTGGGGAGAACTCTGACTTTTGCATTTTGGGAAGCACTTTTGGGAAGGAGCAGGTTCCGCTTGT GCTGCTAGAGGATGCTGTTGTGGCATTTTCTACTC
II27	NM_14563.6.1	GCCATGAGGCTGGATCTCCGGGACCTGCACAGGCACCTCCGCTTTCAGGTGCTGGCTGCAGGATT CAAATGTTCAAAGGAGGAGGAGGACAAGGAGGAAG
II2ra	NM_00836.7.2	AAGGAATTGGTCTATATGCGTTGCTTAGGAACTCCTGGAGCAGCAACTGCCAGTGCACCAGCAA CTCCCATGACAAATCGAGAAAGCAAGTTACAGCTC
II2rb	NM_00836.8.3	TTATTTTATGTGTTCTTGGGCGATGCTGGTCTATGTAAGGGGTGGGGGCGCGGGGTGATTGAAG TGAGGGCTCCTTCTATGTTGCTTTGGGGACCTTGT
II2rg	NM_01356.3.3	ATCCAATGCTCACTGCCTTCCCTTGGGGCTAAGTTTCGATTTCTGTCCCATGTAAGTCTTTTCTGT TCCATATGCCCTACTTGAGAGTGTCCCTTGCC
II3	NM_01055.6.4	TGCAGCTCTATTGTCAAGGAGATTATAGGGAAGCTCCCAGAACCTGAACTCAAACTGATGATGA AGGACCCTCTCTGAGGAATAAGAGCTTTCGGAGAG
II34	NM_00113.5100.1	TGGTGAGTCTCAATGCCACTGAGTCTGTGATGGATGTACTTCTCGAGGGCCACCCGTCCTGGAAG TATCTACAGGAGGTTCCAGACATTGCTGGAGAACGT
II3ra	NM_00836.9.1	GGGTGACGTGCACTACCGGATGTTCTGGCGTGATGTGCGGCTCGGTCTGCCACAACCGCGAGT GTCCACACTACCACAGCCTTGATGTCAACACCGCT
II4	NM_02128.3.1	TGCTTGAAGAAGAACTCTAGTGTTCTCATGGAGCTGCAGAGACTCTTTCGGGCTTTTCGATGCCTG GATTCATCGATAAGCTGCACCATGAATGAGTCCA
II4ra	NM_01055.7.1	CCCACAGCAGTGCTGACGTTCTAAGTCTGGGCTTTCCTAGCTGATGTTGTCCTACCTACTCAGTC CCATTTTGTCCACCGAATAGACCTGTCACTCAA
II5	NM_01055.8.1	CAATGAGACGATGAGGCTTCTGTCCCTACTCATAAAAATCACCAGCTATGCATTGGAGAAATCTT TCAGGGGCTAGACATACTGAAGAATCAAAGTCTC
II5ra	NM_00837.0.2	ACATGTCCCTGTGTTCCATAGGCCTGTTCAAGGAAATGTCTAAGCCAAAGTAAGTTTAAGTCACCG TGCTGGGGTGAAAAAGATGGTTCAGATGACGAA
II6	NM_03116.8.1	CTCTCTGCAAGAGACTTCCATCCAGTTGCCTTCTTGGGACTGATGCTGGTGACAACCACGGCCTTC CCTACTTCACAAGTCCGGAGAGGAGACTTCACAG
II6ra	NM_01055.9.2	CACCTCACTGCCACCTTGGCCTTCCTTGCTTTACGTTTGACTGAGTGGCCTCAGATGCTTTCCCTG GGGCTTTGAGGAATCCAGTGATGTTAGTGGTCA
II6st	NM_01056.0.2	AGAAGCAAACAACAAGAAGCCTTGTCAGATGACCTGAAGTCCGTGGACCTGTTCAAGAAGGAG AAAGTGAGTACAGAAGGGCACAGCAGTGGCATCGGG
II7	NM_00837.1.2	AAACATTCAATTGGTGAACCACTGGGGGAGTGGAAGTGTCTGTTTTAGACTGGAGATACTGGAGG GCTCACGGTGATGGATAATGCTCTTGAAAACAAGA
II7r	NM_00837.2.3	GTTTCCTGGACTGCCAGATTCATGAGGTGAAAGGCGTTGAAGCCAGGGACGAGGTGGAAAGTTT TCTGCCCAATGATCTTCTGCACAGCCAGAGGAGTT
II9	NM_00837.3.1	TCTGTTTTGCTCTTCAGTTCTGTGCTGGGCCAGAGATGCAGCACCACATGGGGCATCAGAGACAC CAATTACCTTATTGAAAATCTGAAGGATGATCCAC
IIf3	NM_01056.1.2	GAGGTTGAGGTGGACGGACAGAAGTTTCAAGGTGCTGGTTCAAACAAAAGGTGGCAAAGGCTT ATGCTGCACTTGCCGCATTAGAAAACTTTTCCCTG
Inpp5d	NM_00111.0192.1	GCCGTCCTGGTGCGACCGAGTCTCTGGAAGTCTACCCGCTGGTGCATGTGGTCTGTCAGTCCTA TGGCAGTACCAGTGACATCATGACGAGTGACCAC
Irak1	NM_00836.3.2	AGGTGGAACAGCTATCAAGGTTTCGTCACCCAAATATCGTAGACTTTGCTGGCTACTGTGCAGAG AGTGGCTTATACTGCCTTGTTATGGCTTCTTGCC
Irak2	NM_00111.3553.1	AGAAAGGCTTTTGGGTTTGGCCGGAGACAGGCTTTTCTGGAGTGAAGCAGATGTCGTCCAAGCAA CTGAGGACTTTGACCAAAGCCACCGAATCAGCGAG
Irak3	NM_02867.9.3	AGCCCACCATCATTACCACCGGCACTTAATGCTAGTCTTCTGCTAGGGATACTGACAGTCTATTTG CTCCCATGGTCATAGGGAAGTTGCTCAAATGC
Irak4	NM_02992.6.5	TTGATCCTCAAGAAGGGTGGAAGAAATTAGCAGTAGCTATCAAAAAGCCGTCCGGCGACGACAG ATACAATCAGTTCCATATAAGGAGATTCTGAAGCCTT

Irf1	NM_008390.1	TGTTCCGGAGCTGGGCCATTACACAGGCCGATACAAAGCAGGAGAAAAAGAGCCAGATCCCAA GACATGGAAGGCCAAACTTCCGTTGTGCCATGAACTC
Irf2	NM_008391.2	GCCATGAATTCCCTGCCCCGACATTGAGGAAGTGAAGGACAGAAGCATAAAGAAAGGAAACAACG CCTTCAGAGTCTACCGGATGCTGCCCTTATCCGAAC
Irf3	NM_016849.4	GAAAGAAGTGTTGCGGTTAGCTGCTGACAATAGCAAGGACCCTTATGACCCTCATAAAGTGTATG AGTTTGTGACTCCAGGGGCGCGGGACTTCGTACAT
Irf4	NM_013674.1	AAGGGACTTGTTCTTAGGTCCAGTCTAGGCTATCATGTCCTGATCCTGCACTCTCTCTGAGTAGA CCCTACATCCTGTTTGTCTCCTCTTCTTGCCCTT
Irf5	NM_012057.3	CCTTTAGTACCACGGAGTCCAATTACCCCAGGGTAGCCAACTTTTAAGGTTGCCCCAATTCTTCTA GCAAAACCTGCCAAGGAGTGTTGTGGGGGCTTTC
Irf7	NM_016850.2	CGCTGTGCACTCCACAGCACAGGGCGTTTTATCTTGCGCCAAGACAATTCAGGGGATCCAGTTGA TCCGCATAAGGTGTACGAACCTAGCCGGGAGCTTG
Irf8	NM_008320.3	GCAGGGAGAGTCACTCATCTGCTTTTGTCTGAGAGAAGGAGAGCTTCTCCGTTTGTCAACTTTGTA ACAAGCTGGGTTACATGCTCCACGCAGCTAGAGA
Irgm2	NM_019440.2	TCCAGAGACTCCTTCATAGACACGCCAAAGGTCTCTTTCATAGTGATTCTAGATCCTGCCAACC TGCCAACCAATATTAACACAGGCACTCAGGG
Isg15	NM_015783.1	GGTCTTTCTGACGCAGACTGTAGACACGCTTAAGAAGAAGGTGTCCAGCGGAACAAGTCACGAA GACCAGTTCTGGCTGAGCTTCGAGGGAAGGCCCATG
Isg20	NM_020583.5	AAGCTGGTGGTGGGCCATGACCTGAAGCACGACTTCAATGCCCTGAAGGAGGATATGAGCAAGT ACACCATCTATGACACGTCCACAGACAGGCTGCTGT
Itch	NM_008395.2	GACAAAGAGCCAACAGAGACGATGGGAGATTGTGTCAGTTTGTCTTGATGGGCTGCAAGTAGAAG CTGAGGTTGTTACTAACGGTGAAACGTCATGCTCCG
Itga1	NM_001033228.3	ATTGAAGTCTAAAGAAGACTCAGTTTACGAGGCTGATCTGCAGTACCGTGTACCCTTGATTGCT GAGGCAGATATCACGGAGCTTTTTTCTGGAAC
Itga2	NM_008396.2	ATTTACAATGGTCACCAGGGTACCATTGCGACCAAGTACTCCCAGAAAATCCTTGGGTCCAATGGA GCCTTAGGAGACATCTCCAGTCTTTGGAAGGT
Itga2b	NM_010575.2	CCGTTGCTCTTCGACCTCAGGGATGAGACACGAAACCTAGGCTTCCAAATTTTCAAACCTTCAA GACCGGGCAAGGACTTGGGGCGTCGGTCGTCAGC
Itga4	NM_010576.3	AATTTGTTGAGACCACTGGTCACTTGGACAGTCCCTTACTTCAACAGGGTGGAGCTTTGATCTTCA GGCTACTGGCCTTAGTCATCTGACAAGACTTAGA
Itga5	NM_010577.3	CAGGCACCAGTCTCTGGGGTGGCCTTCGGTTCACTGTTCTCATCTTCAAGACACAAAGAAAACCA TCCAGTTTGACTTTAGATCCTCAGCAAGAACCT
Itga6	NM_008397.3	CAGTGGGGCTGTAGTTTTGCTAAAAAGAGACATGAAGTCCGCGCATCTGCTCCCTGAGTATATAT TTGACGGAGAAGGCCTGGCTTCTCGTTTGGCTAT
Itgae	NM_008399.1	CCAGACTGAGTTTGATCTTCAAGAGAGCCGGGACATTAACGCCTCCCTTGCCAAAGTTCAGAGCA TCGTTCAAGTGAAGGAAGTCACTAAGACCGCCTCA
Itgal	NM_008400.2	TAACCCGCTACATCATCGGGATTGGCAAGCATTTTGTGAGCGTACAAAAGCAAAGACGCTCCAC ATATTTGCCTCAGAACCTGTAGAGGAATTTGTGAA
Itgam	NM_008401.2	ATCTGGACACTGAACATCCCATGACCTTCCAAGAGAATGCAAAAGGCTTTGGACAGAGTGTGGTC CAGCTTGGCGGAACCAAGTGTGGTTGTTGCAGCCCC
Itgax	NM_021334.2	GGGCCTGTCCCTTGCTGCTGCCACCAACCTTCTGGCTGTTGGCTTGTGGTCCTACTGTGCACCA CACATGCAGAGAGAATATATACTTGACAGGGCTC
Itgb1	NM_010578.1	CTGTGATAGGTCTAATGGCTTAATTTGTGGAGGCAATGGCGTGTGCAGGTGTCGTGTTTGTGAAT GCTATCCCAATTACACTGGCAGTGCATGTGACTGT
Itgb2	NM_008404.4	GCTCGGTTTCTTTCCGCCATTATATCAAGTCTGCCAGGGTTTCCAGGGACTTGTCTCCGACCTGCA CAATCTTGCCGAGAGCCCTAAGAATTGTCCCG
Itgb3	NM_016780.2	TGGGAATGTATCTCTCTGTGTGTACTTATGTGTGTGACGAGTGTGGGGAAATGTGTAATTTAAAA CTTGTGATGTGTCTCACAGGCAGAGCTCCACAGCC
Itgb4	NM_001005608.2	TGCCACCCTTGTCGCCGTCTGGTAAACATCACCATTATCAAGGAACAAGCTAGTGGGGTAGTGT CCTTCGAGCAGCCTGAATACTCGGTGAGTCGTGGA
Itk	NM_010583.3	GCGCTGGGTGCTGACCCTTAAAGAAGAAACGAGGAATAACAACAGCCTGGTATCCAAGTATCACC CTAATTTCTGGATGGATGGGCGGTGGAGGTGCTGC

Jak1	NM_14614.5.2	CATAGCAAAGGACTGTGCCGCTGGCATATTGATCTCAGATAAAAACTTGTGGACTTGGCTGACAC TCTCCCTTGCCCTGAAATCTCAATGTCTATTCACT
Jak2	NM_00841.3.2	GATCCAAGACTATCACATTTTAACCCGGAAGCGAATCAGGTACAGATTCGCAGATTCATTAGCA ATTCAGTCAATGTAAAGCCACTGCCAGGAACCTA
Jak3	NM_01058.9.5	TTCTCTTTTGGGGACTACTTGGCTGAGGATTTATGTGTGCGAGCTGCCAAGGCCTGTGGCATCCTG CCTGTTTATCATTTCGCTTTTCGCTCTGGCCACTG
Jam3	NM_02327.7.4	GCAGTGAATCTCAAATCCAGCAACCGAAACCCAGTGGTACATGAATTTGAAAGTGTGGAATTGTC TTGCATCATTACGGAATCACAGACAAGTGACCCTA
Jun	NM_01059.1.2	CGCGACCAGAACGATGGACTTTTCGTTAACATTGACCAAGAACTGCATGGACCTAACATTCGATCT CATTCACTATTAAAGGGGGGTGGGAGGGGTACA
Kdr	NM_01061.2.2	TTAAATTGTACAGCGAGAACAGAGCTCAATGTGGGGCTTGATTTACCTGGCACTCTCCACCTTCA AAGTCTCATCATAAGAAGATTGTAAACCGGGATG
Kit	NM_00112.2733.1	CAGTTTCCCTGCATGTCGCTCACTGTCTAGAATTTACTCAAAGCCGCCACAGAGGCTTAGCGGAGT GAAGTGCCGAAGGACCTCTTTATTTGGAGTCCTC
Klra1	NM_01665.9.3	ACAAAGTCTCACTTCTCTGTGTTAAATCCTTCATTGCTGAAACAGCTTCTTTCCAGGAATTCTC ATCACAACACATGTACAAAACCTCATAGAAGA
Klra15	NM_01379.3.2	ATCAATCATTCATCTGTATTTGTGGGAAGAGATTGGACAAATTCCTCATTGACTCTCTGACAAGT GTAAAGGTAAAAAATGAATTTTCTGACTCTC
Klra17	NM_13320.3.4	CCCATAACTGCAGGATCTATTATCTTACCAGAATCTTTCAGGGTAGAGACACAGGCACCATTTT AACAGAGAACACACTCTACATACACCCATGATGA
Klra2	NM_00117.0851.1	CCGTCAAGAGTACCAGGTCATGAAAAATGACAGCTCCTTAATGGAAGAAATGTTAAGAAATAAGT CTTCAGAGTGTAAGGCCCTCAATGATAGCCTGCAC
Klra20	NM_05315.0.2	CCCTGGAAGCTCATTGTGATAGCTTGTGGAATCCTCTGTTTTCTCTCCTGGTAACTGTTGTATTGT TGGCAATAAAAAATCAACAAAAACATGAACTGC
Klra21	NM_05315.1.1	AGGCATCCATCCTTTCTACAGGCATCACTTCAGGGTGGAGACACAGAACATACCTCTACTTATCCC ATAAGATGAGTGAGCAGGAGGTCACTTTCCCAAC
Klra27	XM_916590.3	ATGAAGATGAACTGTCTTTTATCTCCATTGAGTGCCAAGTAAACACCTCTTTTTTAGGATTGCTTT TTGGAACCTGGAAGTGAGGCTGCCTGAGATGAG
Klra3	NM_01064.8.2	GAGGGGCAGAAAATCATGAGGTTGAGTATCACCCGGTGGAAATTTAGTTCGACTTTCAATTTTG AAACTCGTAGGAGATCTAAACCAGAAAACGCCAAC
Klra4	NM_01064.9.3	GAAGACACTTTCTCAGCTGTGAGATTCCATAAGTCTTCAGGGTTGCAGAACGAGATGAGGCTCAA GGAGACACGGAAGCCTGAAAAAGCTCGCCTCAGAG
Klra5	NM_00846.3.2	GTGAGCCATGAGGAGATTCAAGGGCCCGGAGAAGCTGGCTACAGAAAGTGTTAGTACCCTGGC AGCTCACTGTGAGATCGCTTGAATCTTCTGTTTCC
Klra6	NM_00846.4.2	ACTTTCCACCAAAGTTAAAGAACATAGACTGCTGTGAATAGAGACAAAGCTGCAAGAGCATTGGG ACTGTTCTCTGGTATCTAACTTGCAGAACAGAGGC
Klra7	NM_00111.0323.1	GTCCCTGGAAGCTCATTGTGATAGCTTGTGGAATCCTCTGTTTCTCTCCTGGTAACTGTTGCAT TGTTGGCAATAACGATTTTTCAGCATAGTCAAC
Klrb1	NM_00109.9918.1	AGACCTTGGGCTGACGGTCTGGTTGACTGTAATTTGAAAGGAGCCACTTTGCTGCTCATTCAAGAT GAAGAAGAATTGAGATTATTGCAGAACTTCTCAA
Klrb1c	NM_00852.7.2	GGTGTGGGAACAGAGCAGAGCATTACAGAGGACTTTCTTTTGCTTATTTACCTCAAAGGCCTTG GAGTTTGTCCCTTCTCACCACCAGTTAAGTGTTG
Klrc1	NM_00113.6068.1	ACCAAGGGGTCTCGCAGCTCCATTTCACTCATCGAGCAGGAAATCATCTATTCGGAATTCAGCTT TCAAAAATCCTTCTCAGGAGCATCCCTGGATCTGC
Klrc2	NM_01065.3.4	TTGTTTCTCCATATGCTGAACTGAAGAAGCAGATCCACCCCTTCTTGTTAGAACCAGAAAGGCT CACACGCCTTGCTCTCAAAGCACAGCCTTGTC
Klrd1	NM_01065.4.2	AGTTATCAGGCCAGAGCACTGCATTGTTTACAGTCCAAGCAAAAGCGTTTCTGCTGAATCCTGTGA AAATAAAAACCGTTACATCTGTAAGAACTGCCT
Klrg1	NM_01697.0.1	TGGATAAAGTTTATTTAATGGATACCCACCCTGCAGATAGCCACCCTGGCTCTCTCATCCCTTCT CTGCCATCTCTGTCAAAGATATGTAGAAAATA
Klrk1	NM_00108.3322.1	ATAAGAGGAAGATACCCTATAGAAAAACTCAAATATCTCCAATGTTGCTTGTTCGAGTCCTTGCT ATAGCCTTGGCAATTCGATTACCCTTAACACAT

Lag3	NM_00847.9.1	GGTGCCCTCTCCCTGTTCTTTTGGTGGCCGGGGCCTTTGGCTTTCACTGGTGGAGAAAACAGTTGCTACTGAGAAGATTTTCTGCCTTAGAACATGGGA
Lamp1	NM_01068.4.2	AGTGATTTCAGTCTTGTGTTGGCGTTCAGGGTGGCCCTGTCTCTGCACTGTGTACAATAATAGATTCACACTGCTGACGTGTCTTGACGCGTAGGTGGG
Lamp2	NM_001017959.1	GTGCCTTTTCATTTTAAACATCAACCCTGCCACAACCAACTTACCGGCAGCTGTCAACCTCAAAGTGCTCAACTTAGGCTGAACAACAGCCAAATTAAGT
Lamp3	NM_17735.6.3	AGACAGTAGTTGGGCATTCTTCAAGTGTGTGAGTGTGAGCAGAGCATCCAGCTGTGAGCTCAGCTTCAAATGAAAACAATGAATATCCACCTTCAGGCCTT
Lbp	NM_00848.9.2	CCATCTCAGATTATGCCTTCAACATAGCCAGCCGGGTTTATCACCAGGCTGGGTACCTGAATTTTTCCATCACAGATGACATGTTACCACATGACTCCGG
Lck	NM_01069.3.2	TCGGGCATCAAGTTGAATGTCAACAACTTTTGACATGGCAGCCCAGATTGCAGAGGGCATGGCGTTCATCGAAGAACAGAATTACATACATCGGGACC
Lcn2	NM_00849.1.1	GCAGGCAATGCGGTCCAGAAAAAACAGAAGGCAGCTTACGATGTACAGCACCATCTATGAGCTACAAGAGAACAATAGCTACAATGTACCTCCATCC
Lcp1	NM_001247984.1	TGCCCAGCCATATTACCAAGCCTCACTTTGCTGGTACTACGGAAGCTTTTGCCACCCTAAAATTCCTGGAATTGGGGCATTGATATGTGCCAATAATCT
Lgals3	NM_001145953.1	ACAGGAGAGTCATTGTGTGTAACACGAAGCAGGACAATAACTGGGGAAAGGAAGAAAGACAGTCAGCCTTCCCCTTTGAGAGTGGCAAACCATTCAAAAT
Lif	NM_00850.1.2	ACATCTTTCACCTGGAAGCATTGACTTCCACCGAGCATAGTAGGTAGTGTGTCTGGACCAGAGAAAAAGGGATGGGGCATTTTGCAGTTTATCCAGAGAG
Lilra5	NM_001081239.2	AACACCTGGGTACTTGGGTGGAAAATTCTTCTATGGCCAATCATCCTGTTATCACTTCACCTAGATGTATACTTTGGCTGACAGTCTCCTCTGTCTCCC
Litaf	NM_01998.0.1	TCCTGTCTCAGCTCCTGGCCTGTGAAGGTCTCCTTCTCATACAGTTTCTGGGAACTCCCTTTGTTCTAAACACAGATGAAAGTTACTTGGCAGGGAG
Lrp1	NM_00851.2.2	GAGCAGATGGCAATCGACTGGCTGACGGGAAACTTCTACTTTGTCGACGACATTGACGACAGGATCTTTGTCTGTAACCGAAACGGGGACACCTGTGTCA
Lrrn3	NM_01073.3.2	GCATTTCAAGGATATGATGGAAATTTGCCTCCCTCTTATAGCTCCTGAGAGCTTTCCTTCTGACCTGGATGTAGAAGCTGACAGCTATGTGTGCTTCAC
Lta	NM_01073.5.1	AAGAGGGGAAAAATAGAAAGCCGTGAGATGACAACTAGGTCCCAGACACAAAGGTGTCTCACCTCAGACAGGACCCATCTAAGAGAGAGATGGCGAGAGA
Ltb	NM_00851.8.2	ATCAGGGACGTGCGGTTGAGAAGATCATTGGCTCAGGAGCACAGGCTCAGAAAAGACTGGATGACAGCAAACCGTCGTGCATCTTGCCCTCACCCTCTAG
Ltbr	NM_01073.6.3	AGAGAAGGGGAGGATGGGGCCTTGGGTAGCGTTAGCATGTGTGGAGGAGAGTTTGGGAACAGGAGAAAAACGACAAGTGATTATGAGTTGTAATCACA
Ltf	NM_00852.2.3	TGCGTATGGGTGACCATGTATGCCTCAACATAAGTTTGCACATGACTGTGTGCACTCCTTGCACTGATGTTGCATAGGACTGTGTACTTGCACTAATGC
Ltk	NM_00852.3.2	GAGGTTTCACCAGCCAATGTCACTCTACTCAGAGCCCTTGGCCATGGTGCCTTTGGGGAAGTGTA CGAGGGACTAGTGACTGGTCTTCTGGGGACTCCA
Ly86	NM_01074.5.2	CCAGGGACAGATGTTCCAGACCCAACAGATGTAATAAACCTCAAAAATCTATTTCTGAGGACCTGAGTAGTCTTGAAGCCCTATTGTAGTACCT
Ly9	NM_00853.4.2	ACGGTGGTGGAAACAATGTGACATACACATGGATGCCTCTACAAAACAAAGCTGTCATGTCCCAAGGGAAGTCGCACCTCAACGTCTCCTGGGAAAGTGG
Ly96	NM_001159711.1	ATTCTCTTTTCGACGCTGCTTCTCCCATATTGACTGAATCTGAGAAGCAACAGTGGTTCTGCAACTCCTCCGATGCAATTATTTCTACAGTTATTGTG
Lyn	NM_01074.7.1	CATTGAGACTAGCCTATTGTAGGTAGTTGGGAAAGCAGCCTTGGAGGAGCTAACTATCTCATGCCAGGACCCTCTGTGTTCTGGTTCCTGATGGACGTG
Lyve1	NM_05324.7.4	AGGTGCCGACCTCGTGCAAGACCTTTCATTTCTACATGCAGAATCATGGGCGTTGCCCTTGTTGGGCAGAAACAAAACCCACAGATGAATTTACAGAA
Lyz2	NM_01737.2.3	TTGTGAGTTTGCCAGAACTCTGAAAAGGAATGGAATGGCTGGCTACTATGGAGTCAGCCTGGCCGACTGGGTGTGTTTAGCTCAGCACGAGAGCAATTAT
Maf	NM_001025577.2	CTGGCAATGAACAATTCCGACCTGCCACCAAGTCCCTGGCCATGGAATATGTTAATGACTTCGATCTGATGAAGTTTGAAGTGAAAAAGGAACCGGTGG

Map2k1	NM_008927.3	CTTTGTGCTTGGGGCTATTTGTCTGTTTCATCAAAACACATGCCAGGCTGAACTACAGTGAAACCCTA GTGACCTGGGTGGTCGTTCTTACTGATGTTTGCA
Map2k2	NM_023138.4	GTCGGCACAGTGGCCGCTGCCTCTGGGGACAGTGATGCTGTTTGTGTGGCAGGGGACCTATGCC CATGCATTTGAAAACCAACAAAATGAAGAAAGAG
Map2k4	NM_009157.4	CTCGCCACAGACACCATGTGCAATAAGACTGGTGTTTCGTTTCCATCATGTCTGTATACTTCTGTCATC TAGACTGTGCATCCCTGTAATACCTGACTGATC
Map3k1	NM_011945.2	CAGCAGATTCTTCCGCTTACAAAGATTGGCCGAGCCATGGATTGAGGTGTTTGAATGGAAC CGTTGGCTGCTTATTCTCTAGAACTGGAACGTAA
Map3k5	NM_008580.4	CATCATCCTCTACTGCGATACTAATTCCGATTCACTCCAGTCCCTGAAGGAAATTATTTGCCAGAAG AATACTGTGTGCACCGGGAACCTACACCTTCATC
Map3k7	NM_009316.1	ATAACACGCCGGAAACCTTCGATGAGATCGGTGGCCAGCTTTCAGAATCATGTGGGCTGTTCA TAATGGCACTCGACCACCACTGATCAAAAATTTAC
Map4k2	NM_009006.2	TTGATGCTCATGTGCAAAAGCAGCTTCAGCCACCCAAGCTAAGAGATAAGACGCGTTGGACCCA GAATTTCCACCACTTCCTCAAGCTGGCCCTAACCA
Mapk1	NM_011949.3	TGTGCAGAGACCAATGTCCAAGTGTACATCCTTTGATTGAACGAAATCTGTTGTGACCTCTGAGT TGTATTCCATGAAGAGAATGCTACCCAGAAGATA
Mapk11	NM_011161.5	GTGTACCTCGTGACGACCCTGATGGGCGCCGACCTGAATAACATCGTCAAGTGTGAGGCCCTGAG CGATGAGCATGTTCAATTCCTGTCTACCAGCTGC
Mapk14	NM_001168513.1	GTGCTGCTTTTGATACAAAGACGGGGCATCGTGTGGCAGTTAAGAAGCTGTCGAGACCGTTTCAG TCCATCATTACGCCAAAAGGACCTACCGAGAGTT
Mapk3	NM_011952.2	ACCTTAATTGCATCATTAAACATGAAGGCCCGAAACTACCTGCAGTCTCTGCCCTCGAAAACCAAGG TGGCTTGGGCCAAGCTCTTTCCTAAATCTGACTC
Mapk8	NM_016700.3	GAAAACAGGCCTAAATACGCTGGATATAGCTTTGAGAACTGTTCCCCGATGTGCTTTTCCAGCT GACTCAGAGCATAACAACTTAAAGCCAGTCAGG
Mapkapk2	NM_008551.1	GTAGCCTCTGCTTGCCCTTCTTGCCACGATTAACCCACTCTTGTCGAGTCTCTGAAATTTTATGCC ATTTCTCAATGGGCTGTCCACTCCACGGTGAG
Marco	NM_010766.2	GCACAGAAGACAGAGCCGATTTTGACCAAGCTATGTTCCCTGTGATGGAGACCTTCGAAATCAAT GATCCAGTGCCCAAGAAGAGAAATGGGGGGACCTT
Masp1	NM_008555.2	CCCGGAGGGGTTTGAATCAAGCTTTACTTCATGCACTTCAACTTGGAATCCTCTATCTTTGTGAA TACGACTATGTGAAGGTAGAAACAGAAGACCAG
Masp2	NM_010767.3	TCACTGGGTCCCAGCCTAAAGGTCACCTTCCACTCCGACTACTCCAATGAGAAGCCGTTACAGGG TTTGAGGCCTTCTATGCAGCGGAGGATGTGGATG
Mavs	NM_144888.1	CAGAACTCAGGCTGGGCTTGCATCAGTTCACCTTTCCCTGGCCTTTAGCAGATGTCTAGCTTCTC TAGTCTTGTTCCCAATGTAGATAGCGGGCAGCT
Mbl2	NM_010776.1	CCCTGAGAACTGGGTGCTCTTCTCTGAGTGAAAAAGTTGAAAGAAGTATTTTGTGAGCAGT GTAAAAAGATGAGCCTTGACAGAGTGAAGGCCCT
Mcam	NM_023061.2	CCAGTGGCTTGACACCTTGAAGAGTGTTCTGAGTGACGCCTAGTTAAGGAAGACAAAGATGCC CAGTTTTACTGTGAACTCAGCTACCGGCTACCCAG
Mef2c	NM_001170537.1	TTCTACTACTAAAGGTATCAATGGAACATGAAGACGAGTATTTAGGCAGAAGCAAAACAGGAAAC CATCCTTACAAACATGCTTACCTGCACATCTGTTT
Mefv	NM_001161790.1	CACAGGGATTCCAGAGCATTCCATGGTGCTGGATGAAAAACATTGAGAAACATGTCTTCCAAAA CATCGTTGATTGGGGAGGAGAGATGCCCTACATCA
Mertk	NM_008587.1	AGGGACTTACAAAGAGCTTTCTGAAGAAGTCAGCCAGAATGGCAGCTGGGCTCAGATTCCTGTCC AAATCCACAATGCCACCTGCACAGTGAGAATCGCG
Mfge8	NM_008594.2	GCAACTTGGACAACAACCTCCACAAGAAGAACATCTTCGAGAAACCCTTCATGGCTCGCTACGTG CGTGTCCTCCAGTGTCTGGCATAACCGCATCAC
Mif	NM_010798.2	AACTATTACGACATGAACGCTGCCAACGTGGGCTGGAACGGTTCCACCTTCGCTTGAGTCCTGGC CCCACTTACCTGCACCGCTGTTCTTTGAGCCTCGC
Mill2	NM_153760.2	AAAAATGAAAGCCAGTTCTGGAAAGCCCAGAGAATTGAGACCAGCAGTCTACTGTTGATCTTAG GGCTGCTCCTTAGAGACTCACGGGGATCCAGCATC
Mme	NM_008604.3	TGCTCGACTGATTGAGAATATGGATGCCTCTGTTGAGCCATGTACAGACTTCTTCAAGTATGCTTG TGGAGGCTGGTTGAAACGCAACGTCAATCCCGAG

Mmp9	NM_01359.2	CCTCTACAGAGTCTTTGAGTCCGGCAGACAATCCTTGCAATGTGGATGTTTTGATGCTATTGCTGAGATCCAGGGCGCTCTGCATTTCTCAAGGACGG
Mnx1	NM_01994.4.1	AAGTGACCTAGAACTTGAACCCTCCTTTGGAGACAACCATTCTGCTGAAAATTTAAACAGAGGGAGGAAAAAGGTGTTATGCCTATGTATGGGGGGGG
Mpo	NM_01082.4.2	AGTACCGATCTTACAACGACTCAGTAGACCCTCGAATCGCCAATGTCTTCACCAACGCTTTCGGTTATGGCCACACCCTCATCCAACCCTTCATGTTCCG
Mpped1	NM_17261.0.3	CCTGGCTACACACGTTTTGTCTGTGTTTCTGACACTCACTCAAGGACAGATCCCATTCAAATGCCCTACGGCGATGTGCTGATCCACGCTGGGGACTTCA
Mr1	NM_00820.9.4	TTACAAGTAGATCACAGAGTATCAGAGCCGCAAGCAACTTTCTCACCTAAGCAGGAGATGTCTTCTAAAATGTCATAGACTTGAGCATTAGCCTTCACTC
Mrc1	NM_00862.5.1	GTTCCGAAATGTTGAAGGGAAGTGGCTTTGGTTGAACGACAATCCTGTCTCCTTTGTCAACTGGA AACAGGCGATCCCTCTGGTGAACGGAATGATTGT
Ms4a1	NM_00764.1.5	GCAACCTGCTCCAAAAGTGAACCTCAAAAGGACATCTTCACTGGTGGGCCCCACACAAAGCTTCTTCATGAGGGAATCAAAGGCTTTGGGGGCTGTCCAA
Ms4a2	NM_00127.6330.1	ACAGAAAATAGGAGCAGAGCAGATCTTGCTCTCCAAATCCACAAGAATCCTCCAGTGACCTGACATTGAACTCTTGAAGCATCTCCTGCCAAAGCAG
Msln	NM_01885.7.1	AACAAGCCAAGGGGCTGGCTATGGCTGTAAGACAGAAGAACATTACACTCCGGGGACATCAGCTGCGTTGTCTGGCACGTCGCCTTCTAGGCACCTCAC
Msr1	NM_00111.3326.1	GATTTCGTCAGTCCAGGAACATGGGAATTCAGTGGATGCAATCTCCAAGTCCTTGACAGAGTCTGATATGACACTGCTTGATGTTCAACTCCATACAGAA
Mst1r	NM_00907.4.1	GATACTCCTTATTGCTCTTCTGGTCTTGATCCTGCTTGCTGGCTGTGCTGGCCGTTGCCCTGATCTTTAACTCCCGAAGACGGA AAAAGCAGCTAGGTGCT
Muc1	NM_01360.5.1	AACGGAGATTTTCTGGGGATCTCTAGCATCAAGTTCAGGTCAGGCTCCGTGGTGGTAGAATCGAC TGTGGTTTTCCGGGAGGGTACTTTTAGTGCCTCTG
Mx1	NM_01084.6.1	TGGCAGAGAGACTGACTGAGGAGCTCACCTCCCACATCTGTAAATCACTGCCACTATTGGAAGATCAAATAAATAGCAGTCATCAGAGTGCAAGCGAGGA
Mx2	NM_01360.6.1	TGTCCTTCCCTGTGTTTCTGGATTGTGATTACAGGACAGAAGGGCTCCTGCCTTTCCTGGTAGCTATACCACCAGCCTTTATGCTCTGATAAGTGCTAG
Myc	NM_01084.9.4	CCCTCAACGTGAACTTCACCAACAGGAAGTATGACCTCGACTACGACTCCGTACAGCCCTATTTCA TCTGCGACGAGGAAGAGAATTCTATCACCAGCA
Myd88	NM_01085.1.2	GCTGCAGGCTCAGCTGTTTTCTCCCCAGCAGCGAGGTTTGCATCTTCTTATTCCTTTCACGTTCTCTACCATAGAGGCAATGTCATGGTCCCTCTCAGGG
Ncam1	NM_00111.3204.1	ATGCTGTGATTGTCTGTGATGTGGTCAGCTCCCTGCCTCCAACCATCATCTGGAAACACAAAGGCCGAGATGTCATTCTGAAAAAAGACGTCCGGTTCAT
Ncf4	NM_00867.7.2	TCATGGATCGCATGGAAGCGCCAAGAGCAGAGGCCTTGTTTGACTTCACTGGGAACAGCAAATTG GAGCTAAGTTTCAAAGCTGGAGATGTGATCTTCT
Ncr1	NM_01074.6.3	ACACCCAACCTCTGGGTTTATCCACAGCCTGAGGTAACCTTGGGGGAGAATGTTACCTTCTTTTGC CAACTGAAGACTGCCACAAGCAAATTCTTTCTGC
Nefl	NM_01091.0.1	ATAACCAGCGGCTACTCTCAGAGCTCGCAGGTCTTCGGCCGTTCTGCTTACAGTGGCTTGACAGAGCAGTCCCTACTTGATGTCTGCTCGCTCTTCCAG
Nfatc1	NM_01679.1.4	ATCCCGTTGCTTCCAGAAAATAACATGCGAGCCATCATCGACTGTGCTGGGATCCTGAAGCTCAGAAACTCTGATATTGAGCTGAGGAAAAGGGGAGACAG
Nfatc2	NM_00103.7177.1	GGATCCTTAAGCCGCACGCCTTCTACCAAGTACACAGGATCACTGGGAAAACGGTCACCACCACGAGCTATGAGAAGATCGTAGGCAACACCAAGGTCCT
Nfatc3	NM_01090.1.2	GGGCTCACATTGTCTTGAAGTTCCTCCCTATCATAACCCAGCAGTTACATCTGCCGTGCAGGTGC ACTTTTATCTTTGCAATGGCAAGAGGAAAAAAG
Nfatc4	NM_02369.9.3	ACAAGCGGGTGTCCCGACCAAGTCCAGGTCTACTTTTACGTCTCCAATGGACGGAGGAAGCGCAGT CCTACCCAAAGTTTCAAGTTCCTACCTGTGGTCTT
Nfkb1	NM_00868.9.2	GTCTTACACTTAGCCATCATCCACCTCCACGCTCAGCTTGAGGGATCTGCTGGAAGTCACATCTGGTTTGATCTCTGATGACATCATCAACATGAGAA
Nfkb2	NM_01940.8.2	CCTATCACAAGATGAAGATCGAGAGGCCTGTAACGGTGTTCTGCGAGCTGAAACGCAAGCGTGGGGCGATGTCTCGGACTCCAAACAGTTCACATATTA

Nfkbia	NM_010907.2	CTGCAGGCCACCAACTACAATGGCCACACGTGTCTGCACCTAGCCTCTATCCACGGCTACCTGGCCATCGTGGAGCACTTGGTGACTTTGGGTGCTGATG
Nlrc5	NM_001033207.3	CCCAGGCTTAGGAGTTAACCTGACCTTGGGAGAGTTCGCACTCATCTCTTCTTCTGGTTTAAGG GACAAAGCCGAGCTACAGGTTTAGGGATAAGTAC
Nlrp3	NM_145827.3	ACGTGTACATCACATTCCTCTATGGTATGCCAGGAGGACAGCCTTGAAGAAGAGTGATGGGTTT GCTGGGATATCTCTCCCGCATCTCCATTTGTA AAA
Nod1	NM_172729.2	TGGATCATCTCCGTTGTTTCCAGCACTTCCAGACGGTCTTCGAGGGCTCCTCTTCACAGTTGCCGG ACTGTGCTGTGACCCTGACCGATGTCTTTCTGC
Nod2	NM_145857.2	TCCTTCTTGACCATCTGACCGTGTCTGTAACTTTGATGGCTTGGACGAGTTCAAGTTCCGGTT CACCGACCGGGAGCGCCACTGCTCTCCAATTGA
Nos2	NM_010927.3	CCCCCTCCTCCACCCTACCAAGTAGTATTGTACTATTGTGGACTACTAAATCTCTCTCCTCTCCTCC CTCCCTCTCTCCCTTTCTCCCTTCTTCTCC
Notch1	NM_008714.2	TGAGATTGATGTTAATGAGTGCATCTCCAACCCATGTGAGAATGATGCCACTTGCCTGGACCAGAT TGGGGAGTTCCAATGCATATGTATGCCAGGTTAT
Nrp1	NM_008737.2	GGATCCGCTCCTCTTCAGGCGTTCTATCCATGGTCTTTTACACTGACAGCGCAATAGCAAAGAAG GTTTCTCAGCCAACTACAGTGTGCTACAGAGCAG
Nt5e	NM_011851.3	AAGCATGACTCTGGTGATCAAGATATCAGCGTGGTTTCTGAATACATCTCAAAAAATGAAAGTAGTT TACCCAGCCGTTGAAGGGCGGATCAAGTTCTCTG
Nup107	NM_134010.2	CCAACCAAGAGGACAATTTTGGTACTGCTACACCAAGAAGCCAGATCATTCTCGAACGCCAAGC TCCTTTCGACAGCCTTTTGTACTCCATCGAGCCG
Oas2	NM_145227.3	GCCCTAAGAGGCTGCTCCGATGGTACCCTTGTCTCTTCATGGACTGCTTCCAACAGTTCCAGGAT CAGATAAAATACCAAGATGCATACCTTGACGTCA
Oas3	NM_145226.2	CCGGGGCCTGGCCTGACTTTTGAGTTTTCTCAGTCAAAGGCGTCCAGGATCTTACAGTTTCGTCTG GCATCGGCAGACGGAGAACACTGGATAGATGTTA
Oasl1	NM_145209.3	GGGTACCCAGGAAATTTCTCTCCATCCTTCAGCGAGCTGCAGCGAACTTCGTGAAGCATCGGCC GACGAAGCTGAAGAGCCTCCTTCGGTTGGTCAAAC
Osm	NM_001013365.2	CACGGTCCACTACAACACCAGATGTCTTTAATACCAAGATAGGCAGCTGTGGCTTTCTCTGGGGAT ACCATCGTTTCATGGGCTCAGTGGGGAGGGTCTT
Pax5	NM_008782.2	TGAATCAGCTTGGGGGGGTTTTTGTGAATGGACGGCCACTCCAGATGTAGTCCGCCAAAGGATA GTGGAACCTGCCCATCAAGGTGTGAGGCCCTGCGA
Pdcd1	NM_008798.1	AGCAGGCTTCCCGGTTTCTATTGTCAAGGTGCAGAGCTGGGGCCTAAGCCTATGTCTCTCTGA ATCCTACTGTTGGGCACTTCTAGGGACTTGAGACA
Pdcd1lg2	NM_021396.2	ATTGTTAGGGCACTTGAGGGTGGGCGTTCTGGAAGTCCTTTCAGGTTAGTGTGTTGGGGGCAGGG TTGCTCAGAATACATAAAGGTGCTAACTTAACTGC
Pdgfc	NM_019971.2	GTTGTCACTATATCTGGTAATGGGAGCATCCACAGCCCGAAGTTTCTCATACATACCCAAGAAAT ATGGTGCTGGTGTGGAGATTAGTTGCAGTAGATG
Pdgfrb	NM_008809.1	CTCAAGGACAACCGTACCTTGGGTGACTCCGGCGCTGGCGAGTTAGTTTTGTCTACTCGCAACAT GTCTGAGACCCGGTACGTGTGAGAACTGATCCTGG
Pecam1	NM_008816.2	ACACCTGCAAAGTGGAATCAAACCGTATCTCCAAAGCCAGTAGCATCATGGTCAACATAACAGAG CTGTTTCCCAAGCCGAAGTTAGAGTTCTCCTCCAG
Pik3cd	XM_003945690.1	CCCACCAACTCTGAAATAGGAAACGTGTCTGTGTGTGTATGTATGTATGCCATGTTATTTATTG AAAAGAGTCTAGGTGCTCTCTGGTGTGGCTG CAG
Pik3cg	NM_020272.2	CTGAATCTCTGGACCTGTGCCTTCTGCCTTACGGTTGCATCTCAACTGGTGACAAAATAGGAATGA TCGAGATTGTAAAGGATGCCACAACGATCGTCA
Pin1	NM_023371.3	CTTCTTAGACTTGACACAGGGGATTCTGGGTTATTGCTGCAGTAGGGAATGGCAGCCTCCTGATT ATAGCCAAACAGTCATCTATGATTTAGAGCAAGTT
Pla2g1b	NM_011107.1	GAGGACTTCATCTGCAACTGTGACCGTGAGGCCGCCATCTGCTTCTCCAAGGTCCCGTACAACAA GGAATACAAAAACCTTGACACCGGGAAATTTCTGTT
Pla2g6	NM_001199023.1	CCCACAGAGGATGCAGTTCTTCGGACGCCTCGTCAACACCCTCAGTAGCGTCACCAACTTGTCTC GAACCCATTCCGGGTGAAGGAGGTGTCCCTGACT
Plau	NM_008873.2	CAAGTCTAGGTATTTCCCTAACTCCAGACTGTGATGCGGGGCCATTTGGTCTTCCATGTGATGCTC CACGTGAATGTATCATTCCCGGGCGTGACCCGTG

Plaur	NM_011113.3	TTCTTTGGACCTCAGTTTTTCCATGAACCAGAAGAGAATTGGAACAAGGGCTGCGGGCAGCAGGG GCCTCTTAGTTGAGATAATATTGTTGCTGTTATTA
Pmch	NM_029971.2	GAAGATACTGCAGAAAGATCCGTTGTCGCCCCTTCTCTGGAACAATACAAAAACGACGAGAGCGG TTTCATGAACGATGATGACAATAAGAATTCAAAGA
Pml	NM_008884.5	TCCGCGACAATTCAGTGAGCAGCTTCCTCGACAGTACGCGCAAGTCCAATATCTTCTGCTCCAATA CCAACCACCGCAACCCTGCGCTGACTGACATCTA
Pnma1	NM_027438.3	CGTGCAAGATGTTGCTCGTGTGCTTGGGTTTCAGAACCTGCTCCAGCTCCAGGCCCGGAAATGC CAGCAGAGATGCTCAACTATATTTTGGATAATGTT
Pou2af1	NM_011136.2	TGCTGGAGAAGCATAACACTTGCTGTTGAGTGTTTTGCTGTCTCCTAGTGCTTTGCTCCTGAAGTG GATGTGTCTTTGGGAAGTGGCCATTGTTACTA
Pou2f2	NM_001163556.1	GCCCCGAGAGGCCGAGAAGCAAAGTCTGGACTCCCCGTGAGAGCACACAGACACCGAAAGAAAT GGACCCGACATTAACCATCAGAACCCCCAGAATAAA
Pparg	NM_011146.1	ACCAAGTGACTCTGCTCAAGTATGGTGTCCATGAGATCATCTACACGATGCTGGCCTCCCTGATGA ATAAAGATGGAGTCTCATCTCAGAGGGCCAAGG
Ppbp	NM_023785.2	TATCGAACTGCGCTGCAGATGTACGAATACCATCTCTGGAATCCCATTCAATTCTATCTCCCTTG AATGTGTACAGGCCAGGAGTCACTGTGCTGAT
Prdm1	NM_007548.3	CCAATGGCTTGAGCACCATGAACAACATCAATGGTATCAACAACCTCAGCCTCTTCCCTAGGTTGT ATCCCGTCTACAGTAACCTCCTTAGTGGCAGCAG
Prf1	NM_011073.2	ACAGCTACTGATGCCTACCTAAAGGTCTTCTTTGGTGGCCAGGAGTTCAGGACCGGTGTCGTGTG GAACAATAACAATCCCCGGTGGACTGACAAGATGG
Prg2	NM_008920.4	CTTCTGACTCCAAAAGCCCATTGATGGATGAGAACTTGCTAGGGATGCAGAGATATCAGGACCA GAAGGAGAAGAGTGTCTCCAGGGGAAGAGCTAAT
Prkcd	NM_011103.2	AGGACCACCTGTTCTTCGTGATGGAGTTTCTCAATGGGGTGACCTGATGTTCCACATTCAGGACA AAGGCCGCTTGAAGTCTACCGGGCTACGTTTTA
Prkce	NM_011104.2	CCCGAAAATTTGATGAGCCTCGTTCTCGGTTCTATGCCGCAGAGGTCACATCAGCCCTCATGTTTC TCCACCAGCACGGAGTGATCTACAGGGATTTGAA
Psen1	NM_008943.2	GTAGCTAGTATCCAATAACCCAGGGGTTTCTCATGTGATGCAAATACTACGTGTCCAACCAATCA GTGCTGTCAACGGGCTGCCATAGCTCCTTCGATG
Psen2	NM_001128605.1	CAAGTATCGATGCTACAAGTTCATCCATGGCTGGCTGATCATGTCCTCCCTGATGCTCCTCTTCTG TTCACCTACATCTACCTCGGGGAAGTGCTCAAG
Psma2	NM_008944.2	CAGTGGGGATTAAAGCTGCAAATGGCGTAGTATTAGCAACCGAGAAAAAGCAGAAATCCATCCT GTATGATGAAAGGAGTGTTCAAGGTGGAGCCCAT
Psemb10	NM_013640.3	AACCACAGGAGGCTTCTTTTCGAGAACTGCCAGAGGAATGCGTCCTTGGAAACACGTCTTCCG GGACTTCGGGTTCTCATGCACGCAAGACCGGGAC
Psemb7	NM_011187.1	ACGAGAGCAACTGAAGGGATGGTTGTTGCTGACAAAACTGTTCAAAAATTCATTTCATATCTCCT AATATTTATTGCTGTGGTGCTGGGACAGCTGCAG
Psemb8	NM_010724.2	CCTGAGGTCCTTTGGTGGTGACCAGGAAAGGAATGTTCAAATTGAGATGGCCACGGCACAACCA CACTCGCCTTCAAGTTCAGCATGGCGTCATCGTG
Psemb9	NM_013585.2	TTCACCACAGATGCCATCACTCTGGCCATGAACCGAGATGGCTCTAGTGGGGGTGTCATCTACCT GGTCACCATCACAGCTGCTGGTGTGGACCATCGAG
Psmd7	NM_010817.2	ATTGCTAAATGGAATTCATGGATCCCATACAATGCCGCCCAACACTTGAGCTTGGACCTTGTGAA CTTTTGAGACCACACCACCTTTTGACCTGTAAC
Ptgd2	NM_009962.2	GAAGCCGCTCTGTCCACTCTTGGAGGAGATGGTCCAGCTTCAAACCACAGCAACTCTAGCCTCC GCTACATCGACCACGTGTCGGTGCTGTTGCACGGG
Ptgs2	NM_011198.3	CCATCAGTTTTTCAAGACAGATCATAAGCGAGGACCTGGGTTACCCGAGGACTGGGCCATGGAG TGGACTTAAATCACATTTATGGTGAAACTCTGGAC
Ptprc	NM_011210.3	AGTGGATGTCTATGGTTATGTTGTCAAGCTAAGGCGACAGAGGTGTCTGATGGTGCAAGTGGAG GCACAGTATATCCTGATTCATCAGGCTTTAGTGGA
Pvr	NM_027514.2	CGAACACGGGTGACTTTCCCAACTCTGTAAAGCGCCAGGGCAATATGCTTCTAATCTCCACCGTAG AGGATGGTCTCAATAACACGGTCATTGTGTGCGA
Pvrl2	NM_001159724.1	GCCGATCCTGCTGCCAGTGACCCTCTGTGCGCTACCCTCCAGAAGTATCCATCTCCGGCTATGA TGACAACTGGTACCTTGGCCGAGTGAGGCCATA

Pycard	NM_02325.4	TGAAGATCGTATTGTGTGAATATAAACACGGGTGCATGTCTGCACAGAAGCTTGAAGACAACTC CAGAGTTCTGTTTCTTACCTTGAGGTAGGGAGGAG
Raet1c	NM_00901.8.1	TACACAGAGAATATGAGCTGGAGATCAGCTAATGATGAATCAGGGGTATCATGAATAAATGGA ACGATGATGGGGACCTTGTGCAACGATTGAAATACT
Rag1	NM_00901.9.2	GAAGCACGGGAGTGGGCCCCGAGTTCCAGAAAAGGCCGTTCTGTTTCTTTTACAGTCATGAGAA TTACGATAGAGCATGGTTCACAGAACGTGAAGGTG
Rel	NM_00904.4.2	ATGGTACAGTTTTACCAGAAATGCCCAGGTCTTCAGGAGTTCAGGGCAAGCTGAACCTTACTATT CTTCATGCGGGTCCATCTCGAGTGGATTGCCACA
Rela	NM_00904.5.4	GAGGCTGACCTCTGCCCAGACCGCAGTATCCATAGCTTCAGAACCTGGGGATCCAGTGTGTGAA GAAGCGAGACCTGGAGCAAGCCATTAGCCAGCGAA
Relb	NM_00904.6.2	TTCTCTTTGAGCCCATTTTACAGAATGCTGAGTCCGAAGAGGAAAAGGGGCTCCTGCAGATGGAC CCCTTCTCAGGACAGATTCTCAGAGATTGTACATA
Reps1	NM_00111.1065.1	ACACTGTAAAGGATCTCCCTCTCCCACGATTTGTTGCTTCAAAGAATGAACAGGAATCTCGCCTTG CAGCCTCTATTCTTCAGATTCTGAAAACAGGG
Ripk2	NM_13895.2.3	CCAGGGACATCGACCTGACACCAGTGAGGAGAATTTGCCATTTGATATACCTCATCGAGGTCTCA TGATCTCTCTAATACAGAGTGGATGGGCGCAAAAC
Rora	NM_01364.6.1	GTGTCAAAATGATCAAATTGTGCTTCTAAAAGCAGGCTCGCTAGAGGTGGTGTATTATTAGGATGT GCCGTGCCTTGACTCTCAGAACACACCGTGTAC
Rorc	NM_01128.1.2	GGGGCCTCCTGCCACCTTGAGTATAGTCCAGAACGAGGCAAAGCTGAAGGCAGAGACAGCATCT ATAGCACTGACGGCCAACCTTACTCTTGAAGATGTG
Rps6	NM_00909.6.3	GATTAAACCTAGGCCTCAGTCATGCTTCCAGTCACTGGTACTGATTTGTATGCACCCGCTTAGGT GTGAAGGTAGTTTTGGTGTGTATACAAGTAGC
Rrad	NM_01966.2.2	GAACCCAGCTTGTGGACAGGACTCTGCCTTTCTCTATGCGGGTGTCTGTGCCCTGGAGGGAGGCT GTTCAATATGTTGCTGTTTGTGTACATGCAGATT
Rsad2	NM_02138.4.4	AGCCTTATCCGGGAGAGATGGTTCAAGGACTATGGGGAGTATTTGGACATTCTTGCTATCTCTG CGACAGCTTCGATGAGCAGGTTAATGCTCTGATTG
Runx1	NM_00111.1021.1	ACAGTGGAGGACTTGGTCAAAATCCAGTTGTTCTACAACGTATGAAGCCTAACCGCTGGTTCTGA CATACATGTGCTCAAAATGATCTGGTTGTTTGGAT
Runx3	NM_01973.2.2	GATGTGCCGATGGAACGGTGGTGACCGTGATGGCCGGCAATGATGAGAACTACTCCGCCGAGC TGCGCAACGCTTCCGCTGTCATGAAGAACCAAGTGG
S100a8	NM_01365.0.2	TGGACATCAATAGTGACAATGCAATTAACCTTCGAGGAGTTCCTTGCGATGGTGATAAAAGTGGGT GTGGCATCTCACAAAGACAGCCACAAGGAGTAGCA
S100b	NM_00911.5.3	ACCGAGAATCAAAATTCTGCTCGGCAGACTTCTCCTTTCAGGATGATCGCTTTGTTCTGGAGGAC AGAGGAGGGGAATGGCCAGAGTCTTTTCTAGTT
Saa1	NM_00911.7.3	GGCAAAGACCCCAATTACTACAGACCTCCTGGACTGCCTGACAAATACTGAGCGTCCTCCTATTAG CTCAGTAGGTTGTGCTGGGGGCTGAGGGTGGGG
Sbno2	NM_18342.6.1	GAGTGCAGACCGTGCCATTCAACAGTTTGCCCGCACCCACAGGTCCAACCAGGTCTCAGCACCCG AGTACGTCTTCTTATCTCAGAACTGGCAGGGGAG
Sele	NM_01134.5.2	TCAGTGGCTGCCGAAGTATTCTTGAACATTGTGTTCTGTGTCCTGGCACTGAAGCCAGCATGAGAT CCATCATTCTTATGTCAGCTCAAGGGTCAAAAGG
Sell	NM_00116.4059.1	GTCCAAGTGTGCTTTCAACTGTTCTGAGGGAAGAGAGCTACTTGGGACTGCAGAAACACAGTGTG GAGCATCTGGAACTGGTCATCTCCAGAGCCAATC
Selplg	NM_00915.1.3	GCTTTCCAGGTCCCTGGCTTGGAGGGATGGTCTTCTTTGGGCCCGTGTGAACCAACGAGTTTC CGTACAGTGACAGAATGACCTCGCGCTGCGGCCT
Serpinb2	NM_00117.4170.1	TGGGCTTTATCCTTTCCGTGTGAACTCGCATGAGAGCATACCTGTCCAGATGATGTTCTCCATGC AAAGCTGAACATTGGATACATAAAGGACCTGAAG
Serping1	NM_00977.6.3	TCTGCCATCTCCTTTGGCCGAAGCTTACCCATCTTTGAGGTGCAGCGACCTTTCCTCTTCTGCTCT GGGACCAGCAACACAGGTTCCCACTTTCATGG
Sh2b2	NM_01882.5.3	GGAAATGCCTGAAAAGGACAACACATTTGTGCTCAAGGTGGAGAACGGAGCAGAATACATCCTG GAAACGATAGACTCACTGCAGAAGCACTCGTGGGTG
Sh2d1a	NM_01136.4.3	TTGTATCAAGGTTACATCTACACATATCGAGTGTCCAGACAGAAACAGGTTCTTGGAGTGCCGA GACAGCACCTGGAGTACATAAAAGATTTTCCGGA

Sh2d1b1	NM_012009.4	ATCTAAGGATACTGAAGGAGCAAACATGTCCTTCTACCTGTGAGGTCGTGGTCCTGATGGGGGC TGTGACCCAACCTGAAACTGTAGTTTTTTTACCT
Sigirr	NM_023059.3	CTGGGTCAGCGCCAATTCTCAGAGATTGTGTCCAGTGTCTGGTGCTCAACTTGACCAATGCAGA GGACTATGGAACCTTCACCTGTTCTGTCTGGAAT
Siglec1	NM_011426.3	ATTGGCTTCAGGAGGGACCGGCTTCTCACTCCAGTTCCTGGTGACTACACGGGCTCACGCTGGT GCTTACTTTTTGCCAGGTGCATGATACACAAGGCAC
Slamf1	NM_013730.4	AAGTGTGGTTCTCTGATTAAGTCAAAGCAACACTGTTTGGAATGCTGCTGTAAAGTGCCTGGA ATACTCAGAGGAACCTGTCCCAGGGAGGTTTTTTT
Slamf6	NM_030710.2	CCAAGAATGCTGTGAGCAATTTGTCAGTCTCTGTTTCGACCCAGAGTCTCTGCAAAGGGGTTCTAA CTAATCCACCCTGGAATGCAGTATGGTTTATGAC
Slamf7	NM_144539.5	TACCGTGCAGAGATTTACAGTACATCGAGTCAGGCTTCTTAATCCAGGAGTATGTGCTGCATGTC TACAAGCATTGTCAAGGCCCAAGGTCACCATAG
Slc11a1	NM_013612.2	CATGTACTTCTGATTGAGGCCACCATCGCCCTATCGGTGTCCTTCATCATCAACCTCTTCGTCATG GCTGTTTTTGGTCAGGCCTTCTACCAGCAAACC
Slc7a11	NM_011990.2	CCGGGGTCGGTTTTCTTATCACCTTGACTGGGGTCCCTGCATATTATCTTTCATTGTATGGGACAA GAAACCCAAGTGGTTCAGACGATTATCAGACAG
Smad2	NM_010754.4	TCACAGCTTGGATTTGCAGCCAGTTACTTACTCGGAACCTGCATTCTGGTGTTCAATCGCATACTAT GAACTAAACCAGAGGGTTGGAGAGACCTTCCAT
Smad3	NM_016769.3	GTGTATCGCCACCTGACTCCTTGTTTAATGACAGAGGTCTGGGATGTCACAGTCCAAAAGGAAAG TGCCTTTCTCCATGGCTGGAGTATGGAGTTTACCT
Smad4	NM_008540.2	TCCTAGGGAGAAGGTTTTGTATAAAACACTAAAAGCAGTGTCACTCTGCCTGCTGCTTCACTGTTC TGCAAGGTGGCAGTACTTCAACTGAAATAATGAA
Smn1	NM_011420.2	GAAACCTGTGTCGTGGTTTATACTGGATATGAAACAGAGAGGAGCAAACTTATCTGACCTACT TTCCCCGACCTGTGAAGTAGCTAATAGTACAGAAC
Smpd3	NM_021491.3	TAAGTTGAAAGAGCAGCTACACGGCTACTTCGAGTACATCCTGTATGATGTTGGGGTCTACGGTT GTCATGGTTGCTGCAATTTCAAATGTCTCAACAGC
Snai1	NM_011427.2	TCACTGCCAGGACTCCTTCCAGCCTTGGTCCGGGGACCTGTGGCGTCCATGTCTGGACCTGGTTCC TGCTTGGCTCTCTTGGTGGCCTTTGCCGACGGTG
Socs1	NM_009896.2	CAGCTTGTGTCTGGGGCCAGGACCTGAATTCCACTCCTACCTCTCCATGTTTACATATTTCCAGTAT CTTTGCACAAACCAGGGGTCGGGGAGGGTCTCT
Socs3	NM_007707.2	CCGCGACAGCTCGGACCAGCGCCACTTCTTCACGTTGAGCGTCAAGACCCAGTCGGGGACCAAGA ACCTACGCATCCAGTGTGAGGGGGGCAGCTTTTCG
Spink5	NM_001081180.1	TTCCAGCTCCTCTAGGGACTCTGACATGTGCAAAAACCTACCGAATATTACCCAGAATGGGTTATCT TTGCCCAAAGAATCTAAACCCTGTCTGTGGTGAT
Spn	NM_001037810.1	GCAACCAGTTCTGTGGAGAGTTCCAGTGTGGCCCGTGGCACCTCAGTTTCCAGCAGAAAAACATC CACGACGTCTACCCAAGATCCCATACCACCAGGT
Spp1	NM_009263.3	TGAATCTGACGAATCTCACCATTGCGATGAGTCTGATGAGACCGTCACTGCTAGTACACAAGCAG ACACTTTCACCTCCAATCGTCCCTACAGTCGATGTC
St6gal1	NM_001252506.1	GCCAGGCATCCTCATCTTCTCCATAAGTCATTTTATGGCTGCTCTCTGGTTACCACTGCTTGAAG GAGTGTTTTTATTCAACAGGCCAGCCTGCTTC
Stat1	NM_009283.3	ACGCTGGGAACAGAACTAATGAGGGGCTCTCATTGTCACCGAAGAACTTCACTCTCTTAGCTTTG AAACCCAGTTGTGCCAGCCAGGCTTGGTGATTGA
Stat2	NM_019963.1	AGTGGGACCACTACAGCTCAGACTCCAATCACTTTTTATTACAGCATAACTGCGAAAATTCAGCC GGGATATTCAGACCTTTCCAATGGCCCTACCCA
Stat3	NM_213659.2	GGGGTCACTTTCACTTGGGTGGAAAAGGACATCAGTGGCAAGACCCAGATCCAGTCTGTAGAGC CATACACCAAGCAGCAGCTGAACAACATGTCATTTG
Stat4	NM_011487.4	TAGAGACCAGCTCATTACCTGTCGTGATGATTTCTAATGTCAGCCAACTACCTAATGCATGGGCAT CCATCATTTGGTACAATGTATCAACTAACGACTC
Stat5b	NM_011489.3	TGAGGGTGTACCTGGACATGGGAGAGGTTTTTAACTGGAAAGTGTGTCCCCTATCTGCATGCTGG TCTCTCTCTCTCTGCCCAACTCTTGCAACCCAAA
Stat6	NM_009284.2	CATTGTATAAGACAGCAACCCAGTATCATTTGGGGAGTAACTATGTGGCTGTGACATGCATAAAG CTCTAGCCTGGGTAACCTGATGCTTCCAGTGTTTC

Syk	NM_001198977.1	TGAGGCTTCGCAATTACTACTACGACGTGGTTAACTAACAGCTCCGGCGCCTGTCCGTGCACACCA CGGATTCCCAAGCGATCACAGGAAATTCATTCAG
Syt17	NM_138649.1	AACTGGAAAACGCCAGCCTAGTATTCACAGTGTTTCGGCCACAACATGAAAAGCAGCAATGACTTC ATCGGGAGGATCGTCATCGGCCAGTATTCCTCCGG
Tab1	NM_025609.2	TGTGCAAATCTACAGTGGATGGGTACAGGTTACACAGCTAAACATGGACCACACCACCGAGAAC GAGGACGAGCTCTTTCGGCTTTCGCAACTGGGTTT
Tal1	NM_011527.2	CCGATCTATCCTAAAGCTAGGCCTGCCTATAATGAAGTTCAAGCTCATGAAACAAAGTGCGCAGA AGTCCTGTGTATCTGTCATTGTATTGGTGTCACTC
Tank	NM_011529.1	CAATCAAAGGTGAGACGACAAGAAGTTTCTTCTGGAAAAGAATCCGCCAAGGGTCTCAACATCCC TCTGCATCACGAAAGGGATAATATAGAGAAGACTT
Tap1	NM_001161730.1	TGGCCATTCCCTTCTTCACGGGCCGCATCACTGACTGGATTCTTCAGGATAAGACAGTTCCTAGCT TCACCCGCAACATATGGCTCATGTCCATTCTCAC
Tap2	NM_011530.2	TCCAGGCCGGACCTGCCTTTCCTCATAGCTGCCTTCTTCTTCTTGTGGTGGCTGTGTGGGGGGAG ACATTAATCCCTCGCTATTCCGGGTCGTGAATTG
Tapbp	NM_009318.2	AGGGAGTTTCAGGTCAGTCGGGGTTACTTGGCGGGGCTTTGTTGAGAGAACTAAATATAAGAAC ACACATGCGTAGAGTCCAGGGTTGAGAAGAACCAG
Tbk1	NM_019786.4	ATACACTGTTCTAGAGGAGCCGTCCAATGCGTATGGACTTCCAGAATCAGAATTTCTCATTGTCTT ACGAGATGTGGTGGGCGGGATGAATCATCTCCGA
Tbx21	NM_019507.1	CACTAAGCAAGGACGGCGAATGTTCCATTCTGTCTTCACCGTGGCTGGGCTGGAGCCCACAA GCCATTACAGGATGTTTGTGGATGTGGTCTTGGTG
Tcf7	NM_009331.3	CTTCCCAAGAAGCTCACCAGCATTAACTAGTCAATATAGTTGGCCTAAACCCAGTGTGCACC CTTCTATCAGGCTCTTCCAGTTCATTTCAG
Tdo2	NM_019911.2	AGAGTCTACAGTTCGGCTGCTGAAAATAAGATTGGTGTCTTCAGAGCTTGAGAGTCCCTTAC AACAGGAAACACTATCGTGATAACTTTGGAGGAGA
Tek	NM_013690.2	GAGACCATCATTTGCCAGATATTGGTGTCTTAAACAGGATGCTGGAAGAACGGAAGACATACG TGAACACCACACTGTATGAGAAGTTTACCTATGCA
Tfe3	NM_172472.3	GAGGACTCTGTGCTGACCTTATTCTTGGGGAAGGGAACAGATTTTGACCTAGATCAAGTGTAAC TAGGTCCTCACCTTGGGACGACCTTGCTTTTCT
Tfeb	NM_001161723.1	CCTACCACCTGCAACAGTCCCAGCATCAGAAGGTTCCGGAGTATCTGTCTGAGACCTATGGGAAC AAGTTTGCTGCCACGTGAGCCCAGCCCAAGGTTT
Tfrc	NM_011638.3	CTGAACCAGTTCAAAACAGATATCAGGGATATGGGTCTAAGTCTACAGTGGCTGTATTCCGCTCG TGGAGACTACTTCCGTGCTACTTCTAGACTAACAA
Tgfb1	NM_011577.1	GGAGTTGTACGGCAGTGGCTGAACCAAGGAGACGGAATACAGGGCTTTCGATTCAGCGCTCACT GCTCTGTGACAGCAAAGATAACAACTCCACGTGG
Tgfb2	NM_009367.1	CCCAAAGCCAGAGTGGCCGAGCAGCGGATTGAACTGTATCAGATCCTTAAATCCAAAGACTTAAC ATCTCCACCCAGCGCTACATCGATAGCAAGGTTG
Tgfb3	NM_009368.2	TCATGTAATTAGTTTCTGGGCCAGCACTAGCTATCTCAGGTCCCTTAGAGATGCTGGACTCAAAA GCAGAGGTCAGAATTGGTTCTCTCATGTATTCCC
Tgfb1	NM_009370.2	TCAGAAGTAGTGGCCAGCTGTGTCTCTAGTAGGACAGTAAAGGCATGAAGCTCAGCCTGTAATCC TGCTACTACAGTAGTACTCCAGAAGTGCCTTGAGG
Tgfb2	NM_009371.2	TGTGCAAGTTTTGCGATGTGAGACTGTCCACTTGCGACAACCAGAAGTCTGCTGAGCAACTGC AGCATCACGGCCATCTGTGAGAAGCCGCATGAAGT
Thbd	NM_009378.3	CCCTTTGACATGACAATAGGACATTGCTATCTTGAGACATACTGGGCCACATTCATAGCTTTCCAA GGATGTATGTGGTCTGCCTCAACATATCAGAGC
Thbs1	NM_011580.3	TGGAGAGCGCGGAGCTGGATGTACCCATCCAGAGCATCTTCACCAGGGATCTGGCCAGCGTTGC CAGGCTCCGAGTTGCAAAGGGAGATGTCAATGACAA
Thy1	NM_009382.3	ACTTTTGTGAGCTTCAAGTCTCGGGCGCAATCCCATGAGCTCCAATAAAAGTATCAGTGTGTATA GAGACAAGCTGGTCAAGTGTGGCGGCATAAGCCT
Ticam1	NM_174989.4	TCCAGTCTCTTCCCCACAGTCCCAATCCTTTCATCAGCCTCCTCCCAGCCCCACAGACTCCAGGA CCTCAGCCTCTCATTATTCACCATGCCAGATG
Ticam2	NM_173394.2	TTCTAAGAAATGCTTAGACGTGAGTCTGCTTCCAAGAAATCTGTGGCACACAAGAAAGGTACACT TCTGCAGCCCTAGGATTGGGCTACTTTCGAATGAC

Tie1	NM_011587.2	GGGCTCAAGATGAACGCAGCCATCAAGATGCTAAAAGAGTATGCGTCTGAAAATGACCATCGAGACTTTGCAGGTGAACTAGAAGTTCTGTGCAAACCTAG
Tigit	NM_001146325.1	GCAGAAGATGACTATGCTGACCCACAGGAATACTTTAATGTCCTGAGCTACAGAAGCCTAGAGAGCTTCATTGCTGTATCGAAGACTGGCTAACGACAGC
Timd4	NM_178759.4	GAATCATCTCCAGGAAGTCAACAAAATATACACTTTTGGGGAAGGTCCAGTTTGGTGAAGTGTCCTTGACCATCTCAAAACCAATCGAGGTGACAGTGG
Tirap	NM_001177846.1	AGGAGGTGCAAACCCATGCAATCTACCTGGAATCGGCTGTCTTACCATTTTATGACTTTGTTTGCCTAGCTGACGGATCTCAAATGCCCTCTGGCCAG
Tlr1	NM_030682.1	TCAGCACTACGATCGGTTTGGAACTGTCTAACATCAAGTGTGTGCTTGAAGACCAGGGCTGCTCTTATTTCTTACGTGCTTTGTCAAAGCTTGGAAAGAA
Tlr2	NM_011905.2	GCAGGCGGTCACTGGCAGGAGATGTGTCCGCAATCATAGTTTCTGATGGTGAAGGTTGGACGGCAGTCTCTGCGACCTAGAAGTGGAAGATGTCTGTTT
Tlr3	NM_126166.2	TTTCTCTGGGCTGAAGTGGACAAATCTCACCCAGCTCGATCTTTCCTACAACAACCTCCATGATGTCGGCAACGGTTCCTTCTCCTATCTCCCAAGCCTG
Tlr4	NM_021297.2	AACGGCAACTTGGACCTGAGGAGAACAAACTCTGGGGCCTAAACCCAGTCTGTTTGCAATTAATAATGCTACAGCTCACCTGGGGCTCTGCTATGGAC
Tlr5	NM_016928.2	CTGGGGACCCAGTATGCTAACTTGACCATTGGTCCAGGGGCTTTCAGAAACCTGCCAATCTTAGGATCTTGACTTGGGCCAAAGCCAGATCGAAGTCT
Tlr6	NM_011604.3	ACCTGGATGTCTCACACAATCGGTTGCAAAACATCTCTTGCTGCCCTATGGCGAGCCTGAGGCATCTAGACCTCTCATTCAATGACTTTGATGTACTGCC
Tlr7	NM_133211.3	TCTGCAGGAGCTCTGTCTTGAGTGGCCTGCAAATCCACAGGCTCACCCATACTTCTGGCAGTGCCTGAAAAATGCCCTGACCACAGACAATCATGTGGC
Tlr8	NM_133212.2	TCCATAAAGCGAACTATTCCAGAAGCTATCCTTGAGCAGATAAAGGCACAACTCCCTTGTGATTGCAGAATGCAACCATCGTCAACTGCATGAAGTTCC
Tlr9	NM_031178.2	GGCCACAATTTAGTTTTGTGACCCATCTGTCCATGCTACAGAGCCTTAGCCTGGCACACAATGACATTCATACCCGTGTGTCTCACATCTCAACAGCA
Tmed1	NM_010744.3	GCGAGTTCACATTTCTGTTCCCGCCGGGAGAAAGCAGTGTCTTATCAGTCCGCACCGGCCAATGCTAGTCTTGAGACCGAGTACCAGGTGATCGGAGG
Tmem173	NM_028261.1	GCAGACTTCCAACCCTCCAGCTTCTGGTCACGTGTGTTCAATGGGAGCTTAAGTAGATGGCGAGAGGGAGAAGGAACATTTGTTCTGTTAGCTGTATACA
Tnf	NM_013693.1	TTCCTGAGTTCTGCAAAGGGAGAGTGGTCAGGTTGCCTCTGTCTCAGAATGAGGCTGGATAAGATCTCAGGCCTTCTACCTTCAGACCTTTCCAGACTC
Tnfaip3	NM_009397.2	GGCTGAACAACCTTCTTCTCAGGCTTTGTATTTGAGCAATATGCGGAAAGCTGTGAAGATACGAGAGAGAACCCAGAAAGACATTTTCAAACCTACCAAT
Tnfrsf10b	NM_020275.3	CTGGTTCACATAAGATCCCATAATAATGTGCAGGATGGCTAAACTTGCTGAGAGCTGACTCTGTGGTCTCCTGTCCAGATTCTAGCGATATTCATTACTA
Tnfrsf11a	NM_009399.3	ATCTCTGTGGTAGTAGTGGCTGCCATCATCTTCGGCGTTTACTACAGGAAGGGAGGGAAAGCGCTGACAGCTAATTTGTGGAATTGGGTCAATGATGCTT
Tnfrsf11b	NM_008764.3	CCGGAGTGTCCCAAAGCCCCACCACTAGCTCCCAAGGTTCTAAAAAGGAACAAGGTTTGTCCAGACAGAGACTAATAGATCAAAGGCAGGGCATACTTC
Tnfrsf12a	NM_001161746.1	AGCCTCAATCTGGGTCAAAAGCGACCCATACTAAGGAACTGCAGCATTTGCACAAGGGAATCTCTTGTTCCCCACAAGTCTTGGCAGTCTGGCTGACTT
Tnfrsf13b	NM_021349.1	GTCCAGGATTGAGGCTAAGTAGCGACCAGCTGACTCTCTACTGCACACTGGGGGTCTGCCTCTGCGCCATCTTCTGCTGTTTCTTGGTGGCCTTGGCCTC
Tnfrsf13c	NM_028075.2	AATGCACTGCGGGTGGCTCATTACTGAGCATAACTTTTGCTTCAGGGGACCTGATGCCTCTGGACTTCATGGGCATCTGTATTACGTGCACATCCTACA
Tnfrsf14	NM_178931.2	ACAGACACCACCTGCTCCTCCAGGTGCTCTACTACGTTGTGTCCATCCTTTTGCCACTTGTGATAGTGGGAGCTGGGATAGCTGGATTCTCATCTGCA
Tnfrsf17	NM_011608.1	CCTCATGGCGCAACAGTGTTTCCACAGTGAATATTTTGACAGTCTGCTGCATGCTTGCAAACCGTGTCACTTGCGATGTTCCAACCCTCTGCAACCTGT
Tnfrsf18	NM_009400.2	CTCCCTCAACAGTGCGGGAAGTGGGTGTATGAGAGCGGTGAGTTACGATTGGGCCCTATGGCTGCCTTCTCATTTGACAGCTCTGTTGGAGTAGGGTC

Tnfrsf1a	NM_011609.2	CTCCTTGCCAAGCTGACAAGGACACGGTGTGTGGCTGTAAGGAGAACCAGTTCCAACGCTACCTGAGTGAGACACACTTCCAGTGCCTGGACTGCAGCCC
Tnfrsf1b	NM_011610.3	GTGTGTGTCCATGTTTGCATGTATGTGTGTGCCAGTGTGTGGAGGCCAGAGGTTGGCTTTGGGTGTGTTTGATCACTCTCAGTTACTGAGGCAGGGCTCT
Tnfrsf4	NM_011659.2	ATGGTGAGCCGCTGTGATCATACCAGGGATACTCTATGTCATCCGTGTGAGACTGGCTTCTACAATGAAGCTGTCAATTATGATACCTGCAAGCAGTGTA
Tnfrsf8	NM_009401.2	GAGCCCCGGGTATCCACGGAACACACCAATAACAGGATTGAGAAAACTACATCATGAAGGCCGACACAGTGATCGTGGGCTCTGTAAAACTGAAGTCC
Tnfrsf9	NM_001077508.1	TCTTCAGAGCAGTTCAAGGGCCTGCTTCTCCTGTTTCCTCTGTGTCAGGCTTTTCAATAAAAAAGGCCGTTTAGGAAAGGGACAAAGCACTGTGAGGTGGG
Tnfsf10	NM_009425.2	GTTCACCATGCTTGCTTTGTCCAGATTGCGACTGTCACCCAGTCCTCTGGCTCTTCCATCTGTCTGTCCACTCCACCTACCAAGATGTTGAACACTTGTT
Tnfsf11	NM_011613.3	CCAGCGAGGCAAGCCTGAGGCCAGCCATTTGCACACCTCACCATCAATGCTGCCAGCATCCCATCGGGTTCCATAAAGTCACTCTGTCCTCTTGGTAC
Tnfsf12	NM_011614.3	TCAAAGGCAGCCAGAGCTTGTTACATGTTTTCCATTCCACAGACGTATCCTTGCTCTTCTTTAACA TCCCATCCCACCACAACCTATCCACCTCACTAGC
Tnfsf13	NM_023517.2	AAAAAGATATATGTTAGGTGCCTCGATATGCATGCCATTCATCCTCCCCATTCTCCTATACACTTCCGAGCTGGGCACTGAGCTTTACGCCTTAAATCAC
Tnfsf13b	NM_033622.1	TCTGCAAAGACCCTGCCACCACCGTGCCTCTGTTTTGCTCCGAGAAAGGAGAAGATATGAAAGTGGGATATGATCCCATCACTCCGCAGAAGGAGGAGG
Tnfsf14	NM_019418.2	CAGGAAGAAAGAATCAAGCTGGGGTATTTATGCTTCTGATGCAAACACTGAGATTTGGCTTTCTGGGTTTTGAGCTGGAGGCAAGAAACCTTCCAGAG
Tnfsf15	NM_177371.3	AAGACTCACAAGCCCCGAGTTGCAGTTACTTTTCTGAAGCAACATAGTATGTTAATGGAATGGCCA GAACTCTACTCTTGGCACATGGCACTGAATTTGAT
Tnfsf18	NM_183391.3	GCACAGTGAGAACATGGGTAGATGAACCCTAAGACTCTTACCTCAATTCAGAACTCGCAAGGAGTTAAGTGAGTGGGGTCTTCATTAGACCATTACATG
Tnfsf4	NM_009452.2	CCAGATGTGAGGATGGGCAACTATTCATCAGCTCATACAAGAATGAGTATCAAACCTATGGAGGTGCAGAACAATTCCGTTGTCATCAAGTGCGATGGGCT
Tnfsf8	NM_009403.2	ATCCAGGATGCAGGGGAAAATCCTTCTTGAACAGAGCTGGGTACAGAACCGAATCAGATGAGGAGAGATAAGGTGTGATGTGGGACAGACTATATAAAG
Tollip	NM_023764.3	CTCAGCATCACTGTGGTACAGGCAAAATTGGCAAAGAATTATGGCATGACTCGTATGGACCCTTACTGCCGTCTGCGTCTGGGCTATGCTGTTTATGAAA
Tpsab1	NM_031187.4	GGCTGGGGTAACATCGACAATGGTGTAACCTGCCGCCACCATTTCTTTGAAGGAGGTGCAAGTTCCCATTATAGAAAACCACCTTTGTGACTTGAAGT
Traf2	NM_009422.2	GGCCTTTTAATCAGAAGGTAACATTGATGTTGCTGGACCATAACAACCGGGAGCATGTGATCGACGCATTCAGGCCCGATGTAACCTCGTCTCTCTTCCA
Traf3	NM_001048206.1	GGTTGGGGTCAGTGCAGACAGCTGCAGACTGTTCTAAAGTTCCGTTCTTATCTCTGATGGCACACCTCTCGTGTTTCAGTTCTATTACCCAAAAAACAAAG
Traf6	NM_009424.2	GTGCTGTGTCCATGGCATATGAAGAGAAAGAGATCCATGATCAAAGCTGTCCTCTGGCAAATATCATCTGTGAATACTGTGGTACAATCCTCATCAGAGA
Trem1	NM_021406.5	GTGGCTCCTGTGCTTTCTTAGGACACACTGGCATTGCTTGTTTCCACCTCTTTGGGTGGGAAAA GGATGGTAGATCCATTCTTCTACTTCAGCAGTG
Trem2	NM_031254.2	GAATCAAGAGACCTCCTTCCCACCCACCTCCATTCTTCTCCTCCTGGCCTGCGTTCTCCTGAGCAAGTTTCTTGACAGCCAGCATCCTCTGGGCTGTGGCC
Trp53	NM_011640.1	CCCTCTCTGAGTAGTGGTTCCTGGCCCAAGTTGGGGAATAGGTTGATAGTTGTCAGGTCTCTGCTGGCCAGCGAAATTCTATCCAGCCAGTTGTTGGAC
Twist1	NM_011658.2	AATGGACAGTCTAGAGACTCTGGAGCTGGATAACTAAAAATAAATCTATATGACAAAGATTTTCATGGAAATTAGAAGAGCAGAGACCAATTCACAAGA
Txk	NM_001122754.1	TTACCAGCCACATCTGGTTTTAGCTATGAAAAGTGGGAGATAGATCCATCAGAGTTGGCTTTTGTCAAGGAGATCGGAAGTGGTCAGTTTGGGGTTGTCC
Txnip	NM_023719.1	CCTGAGTGCTGCGATCAAAGGCCAGCTTGTTATTGCTTTGAGGCTTTCTCCCAACGCACAGAC TTGTGTAATTCTAACACTAATCCTGTGAAGGGTT

Tyk2	NM_001205312.1	ACAAGTGCTTGTTGCTGTGCCTCTGTTCCAGGCTGAGGCCCTGTCCTTTGTGGCCCTGGTCGATG GCTATTTCCGCTTGACTGCTGACTCCAGCCACTA
Ubc	NM_019639.4	AAGACCATCACCTGGACGTCGAGCCCAGTGTTACCACCAAGAAGGTCAAACAGGAAGACAGAC GTACCTTCTCACCACAGTATCTAAAAAGAGCCCTC
Ulbp1	NM_029975.2	GGCAACTGGACCCAACCTGGATCATGAATTCGAGAAGTTTATAGAAATGTGCAAGGAAGACAAGG TTTTAGCTGCCTTTTTAAAGAAGACTACAGAGGGCG
Usp18	NM_011909.2	GGCTGACTTTGGTCATTACTGTGCCTACATCCGGAATCCCGTGGATGGAAAGTGGTTCTGCTCAA TGACTCACATGTTTGTGGGTACCTGGAAGGAT
Usp9y	NM_148943.2	TGGACAACCTCAGCCTTCTTTCCAACAGAACCAGATCTCATCTGATTCTTCCAATGAGACTTCT CCAACAACCTCCTCCATATGAACAAGGCCAAGGT
Vcam1	NM_011693.2	GGTTTTGAGGATGAACACTCTTACCTGTGCGCTGTGACCTGTCTGCAAAGGACACTGGAAAAGAG AACCAGGTGGAGGTCTACTATTCCCTGAAGATC
Vegfa	NM_001025250.3	TCTCTCTCTCCAGATCGGTGACAGTCACTAGCTTGTCTGAGAAGATATTTAATTTTGCTAACACT CAGCTCTGCCCTCCCTTGCCCCACCACACATT
Vegfc	NM_009506.2	TACAGAAAACACACAGAAGTGCTTCCTTAAGGGAAGAAGTTCACCATCAAACATGCAGTTGTT ACAGAAGACCGTGTGCGAATCGACTGAAGCATTGT
Vhl	NM_009507.3	GGCTTTGTAGTGTTTAAGAATAAACATGCAAAGTGCCACTGCGTCTGCCCTTTGTAGAGCACTCAC CCGAGGGAGGAAGACGTTTTTCAGTTTTGCTTCT
Vim	NM_011701.4	CAGCGCTCCTACGATTACAGCCACCGCGCCCTCATTCCCTTGTGTCAGTTTTTCCAGCCGCAGCAA GCCAGCCCACCTTCGAAGCCATGTCTACCAGGT
Vwf	NM_011708.3	GTCAGCATCTACGGCGCTATCATGTATGAAGTCAGGTTTACCCATCTTGCCACATCCTCACATAC ACGCCACAAAACAACGAGTTCCAACCTGCAGCTTA
Xaf1	NM_001037713.3	CTCCACTTCATGCTCCACGAGGCCCACTGCCTGCGCTTCATAGTCCTTTGCCCAGAATGTGAAGAG CCCATCCCAGAGTCAAAGATGAAAGAGCACATGG
Xbp1	NM_013842.2	CCTCTAGTTTTAGAGATCCCCTCTGAGACAGAGAGTCAAACCTAACGTGGTAGTGAAAATTGAGGA AGCACCTCTAAGCTCTTCAGAAGAGGATCACCTG
Xcl1	NM_008510.1	AGAGAGTAGCTGTGTGAACTTACAAACCCAGCGGCTGCCAGTTCAAAAAATCAAGACCTATATCA TCTGGGAGGGGGCCATGAGAGCTGTAATTTTTGTC
Xcr1	NM_011798.4	CTGTCTACTGCCTGTGTTGATCTCAGCACAAATGGAGTTGGTTTCTAGGTGACTTCTTCTGCAAGTTC TTCAACATGATCTTCGGCATCAGCCTCTACAGC
Ythdf2	NM_145393.4	GGACAGTCTACTCAAAGCTCTGGATATAGTAGCAATTACGCTTATGCACCCAGCTCCTTAGGTGGA GCCATGATTGATGGACAGTCAGCTTTTGCCAATG
Yy1	NM_009537.3	CGGTCACCATGTGGTCCTCGGATGAAAAAAGATATTGACCATGAAACAGTGGTTGAAGAGCA GATCATTGGAGAGAACTCACCTCCTGATTATTCTGA
Zap70	NM_009539.2	TACGAGAGTCCCTACAGCGACCCTGAGGAACTCAAAGACAAGAAGCTCTTCTGAAGCGAGAGA ATCTCCTCGTGGCGGACATCGAGCTTGCTGTGGCA
Zbp1	NM_021394.2	CGCCAAGGCTCTGGGAATGACGACAGCCAAAGAAGTGAACCCACTCCTGTATTCCATGAGAAATA AGCACCTTCTGAGCTATGACGGACAGACGTGGAAG
Zfp13	NM_011747.2	TCTGCAGACAGTCAAAGCATCGCGGCTACTGAGAACGAGGAGAAATCCCATGAGGTCCCAGGTA ATGTGCAACACTGTGGAGACATGCTCTCTGGACAGG
Internal Reference Genes		
Abcf1	NM_013854.1	GAGGTGTCTTCCCGCCAGGCAATGTTAGAAAATGCATCTGACATTAAGTTGGAAAAGTTCAGCAT CTCCGCCACGGAAGGAGCTATTGTCATGCTG
Alas1	NM_020559.2	ACTAGGAATATTTCTGGAACGAGCAAGTTCACGTAGAACTGGAGCAGGCACTGGCCGACCTCCA CGGCAAAGATGCGGCGCTCTGTTCTTCTCTGTT
Edc3	NM_153799.3	CTTTATAGTTGCCCTCCTCAGGTGTATAGTTGGAACCTAGTGGCCTGTCTCAAACATGCCAAAATG AGCCAGTTCTAGATGACAGTAGTGGGATTACAGC
Eef1g	NM_026007.4	GGCAAGGTTCCAGCATTTGAGGGTGATGATGGATTCTGTGTGTTTGAGAGCAATGCCATTGCCTA TTATGTAAGCAATGAGGAGCTGCGAGGAAGTACGC
Eif2b4	NM_001127355.1	AGTACTGGTCTGCTGTGAAACGTACAAGTTCTGTGAACGTGTGCAGACTGATGCCTTTGTCTCCAA CGAGCTAGATGATCCCGATGATCTGCAGTGTAAG

G6pdx	NM_008062.2	ACATTCTAGTTCCTGGGCTTGACCGCCATTTTGTCTATGCTGCTGCCACTGCCACCACCAGTAAACCCAGCTACATTCTCAAATACCAGGCATTTAA
Gusb	NM_010368.1	AATACGTGGTTCGGAGAGCTCATCTGGAATTCGCCGACTTCATGACGAACCAGTCACCGCTGAGAGTAATCGGAAACAAGAAGGGGATCTTCACTCGCCA
Hdac3	NM_010411.2	ATGAAACCTCATCGCCTGGCATTGACTCATAGCCTAGTCCTGCATTATGGTCTCTATAAGAAGATGATCGTCTTCAAGCCTTACCAGGCCTCCCAGCATG
Hprt	NM_013556.2	ATGACTGTAGATTTTATCAGACTGAAGAGCTACTGTAATGATCAGTCAACGGGGGACATAAAAGTTATTGGTGGAGATGATCTCTCAACTTTAACTGGAA
Nubp1	NM_011955.2	TGGAGATACACAGTTGCTCTTCTGGACATCGATATCTGTGGGCCATCGATTCCCAAGATCATGGGCTTAGAAGGAGAGCAGGTTACCAGAGCGGCTCC
Oaz1	NM_008753.4	CCCTGTGCCCTCTCCTGGGTTAGTCCACATGTCGTGATTGTGCAGAATAAACGCTCACTCCATTAGCGGGGTGCTTCTTCGAGCTGAATGCTGTGTTTGT
Polr1b	NM_009086.2	TGCCTTTCACTGAGAGTGGCATGATGCCGGACATTCTGTTTAATCCTCACGGGTTTCCCTCCCGTATGACCATAGGTATGTTAATCGAGAGCATGGCTGG
Polr2a	NM_009089.2	GTGAATCGTATTCTCAATGATGCTCGAGACAAAAGTGGCTCCTCTGCACAGAAATCCCTCTCTGAATATAACAACCTCAAGTCTATGGTGGTGTCTGGAG
Ppia	NM_008907.1	CCAAGACTGAATGGCTGGATGGCAAGCATGTGGTCTTTGGGAAGGTGAAAGAAGGCATGAACATTGTGGAAGCCATGGAGCGTTTTGGGTCCAGGAATGG
Rpl19	NM_009078.2	GCCTCTAGTGTCTCCGCTGCGGGAAAAAGAAGGTCTGGTTGGATCCCAATGAGACCAATGAAATCGCCAATGCCAACTCCCGTCAGCAGATCAGGAAGC
Sap130	NM_172965.2	TAAATCCGAAGTGCATGTGTCTATAGCCACTCCAGTTACAGTGTCTTGGAGACCATATCCAATCAAATGCCGAACAGCCTACCGTTGCTGTCCCTCCG
Sdha	NM_023281.1	CTTGCGAGCTGCATTTGGCCTTTCTGAGGCAGGGTTTAATACTGCATGCCTTACAAAGCTCTTTCCTACCCGATCACATACTGTTGCAGCACAGGGAGGT
Sf3a3	NM_029157.3	ACAATTTTAGAGCAGCAACGGCGCTATCATGAGGAGAAGGAACGGCTTATGGATGTTATGGCCAAGAGATGCTTACGAAGAAGTCCACGCTTCGGGACC
Tbp	NM_013684.3	GTGGCGGGTATCTGCTGGCGTTTTGGCTAGGTTTCTGCGGTGCGTCATTTTCTCCGCAGTGCCCAGCATCACTATTTTCATGGTGTGTGAAGATAACCCA
Tubb5	NM_011655.4	ATTGGAAGTGTCTTCCCTGTATTGGTTCTCCTTTCTCGGAGAGATGGGGGTGGGGGTGCGGCAAGGTCTTGGTCTTGGTCTCTGAACACTCCCAATTCC

Supplemental Table 2. Statistically significant, differentially expressed genes from PBMC of human AML or MDS patients comparing post-AZA treatment, responsive samples compared to matched, pre-treatment samples.

GeneID	padj	pvalue	lfcSE	stat	log2Fold Change	baseMean	Symbol	Description
5196	2.88e-16	2.09e-20	0.73	9.26	6.7220	914.99	PF4	platelet factor 4
81027	2.99e-16	4.35e-20	0.67	9.18	6.1426	954.86	TUBB1	tubulin beta 1 class VI
5473	3.79e-15	8.26e-19	0.79	8.86	7.0157	5007.51	PPBP	pro-platelet basic protein
10398	4.75e-15	1.38e-18	0.71	8.80	6.2499	225.77	MYL9	myosin light chain 9
4603	5.53e-15	2.01e-18	0.55	8.76	4.8364	403.83	MYBL1	MYB proto-oncogene like 1
4512	2.35e-14	1.02e-17	0.52	8.57	4.4742	880614.15	COX1	cytochrome c oxidase subunit I
64919	4.61e-14	2.34e-17	0.66	8.48	5.5624	301.09	BCL11B	BCL11 transcription factor B
9402	1.78e-13	1.04e-16	0.69	8.30	5.7090	491.35	GRAP2	GRB2 related adaptor protein 2
22806	1.61e-12	1.08e-15	0.56	8.02	4.5250	524.4	IKZF3	IKAROS family zinc finger 3
4514	1.61e-12	1.17e-15	0.66	8.01	5.2682	973257	COX3	cytochrome c oxidase subunit III
4579	2.73e-12	2.18e-15	0.67	7.93	5.3151	65989.37	TRNY	tRNA-Tyr
3575	4.61e-12	4.02e-15	0.81	7.85	6.3551	304.01	IL7R	interleukin 7 receptor
4511	9.34e-12	8.82e-15	0.67	7.76	5.1702	72358.19	TRNC	tRNA-Cys
57595	1.61e-11	1.64e-14	0.74	7.68	5.7026	151.43	PDZD4	PDZ domain containing 4
105376333	1.80e-11	1.96e-14	0.60	7.65	4.6184	1825.52	LOC105376333	uncharacterized LOC105376333
3934	6.47e-11	7.51e-14	0.95	7.48	7.1088	364.24	LCN2	lipocalin 2
6374	6.84e-10	8.44e-13	0.83	7.15	5.9436	88.61	CXCL5	C-X-C motif chemokine ligand 5
3932	9.55e-10	1.25e-12	0.72	7.10	5.1383	184.67	LCK	LCK proto-oncogene, Src family tyrosine kinase
83888	9.67e-10	1.35e-12	0.71	7.09	5.0282	242.84	FGFBP2	fibroblast growth factor binding protein 2
4513	9.67e-10	1.40e-12	0.65	7.08	4.5795	474435.28	COX2	cytochrome c oxidase subunit II

7049	2.13e-09	3.40e-12	0.56	6.96	3.8800	348.17	TGFB3	transforming growth factor beta receptor 3
6352	2.13e-09	3.34e-12	0.72	6.96	5.0378	979.12	CCL5	C-C motif chemokine ligand 5
923	3.68e-09	6.15e-12	0.78	6.88	5.3526	96.99	CD6	CD6 molecule
800	3.79e-09	6.60e-12	0.91	6.87	6.2487	138.44	CALD1	caldesmon 1
7535	4.22e-09	7.65e-12	0.54	6.84	3.7253	633.74	ZAP70	zeta chain of T cell receptor associated protein kinase 70
9235	4.44e-09	8.38e-12	0.78	6.83	5.3229	271.94	IL32	interleukin 32
388228	1.55e-08	3.04e-11	0.75	6.64	4.9571	101.06	SBK1	SH3 domain binding kinase 1
5197	1.60e-08	3.24e-11	0.97	6.64	6.4052	65.81	PF4V1	platelet factor 4 variant 1
340205	1.83e-08	3.85e-11	0.93	6.61	6.1137	94.12	TREML1	triggering receptor expressed on myeloid cells like 1
9806	1.85e-08	4.04e-11	0.68	6.60	4.4550	432.84	SPOCK2	SPARC (osteonectin), cwcw and kazal like domains proteoglycan 2
399844	1.85e-08	4.17e-11	0.60	6.60	3.9782	2082.94	LINC01002	long intergenic non-protein coding RNA 1002
4519	1.87e-08	4.34e-11	0.71	6.59	4.6491	612427.62	CYTB	cytochrome b
9047	2.77e-08	6.84e-11	0.66	6.52	4.2718	170.51	SH2D2A	SH2 domain containing 2A
4540	2.77e-08	6.81e-11	0.69	6.52	4.5075	641497.04	ND5	NADH dehydrogenase subunit 5
1667	3.17e-08	8.30e-11	1.06	6.50	6.8993	704.86	DEFA1	defensin alpha 1
728358	3.17e-08	8.30e-11	1.06	6.50	6.8993	704.86	DEFA1B	defensin alpha 1B
83699	3.22e-08	8.64e-11	0.73	6.49	4.7208	173.77	SH3BGR L2	SH3 domain binding glutamate rich protein like 2
5335	3.42e-08	9.45e-11	0.62	6.48	4.0306	203.92	PLCG1	phospholipase C gamma 1
107984360	3.68e-08	1.04e-10	1.01	6.46	6.4975	67.89	LOC107984360	
4538	3.73e-08	1.08e-10	0.69	6.45	4.4463	939275.04	ND4	NADH dehydrogenase subunit 4
3820	4.08e-08	1.21e-10	0.76	6.44	4.8871	124.97	KLRB1	killer cell lectin like receptor B1
10417	5.66e-08	1.77e-10	0.59	6.38	3.7395	430.09	SPON2	spondin 2

915	5.66e-08	1.75e-10	0.93	6.38	5.9533	63.29	CD3D	CD3 delta subunit of T-cell receptor complex
10666	6.27e-08	2.00e-10	0.74	6.36	4.7147	503.28	CD226	CD226 molecule
919	1.05e-07	3.42e-10	0.72	6.28	4.5127	332.77	CD247	CD247 molecule
101928512	1.11e-07	3.71e-10	0.68	6.27	4.2679	127.67	LOC101928512	uncharacterized LOC101928512
8784	1.16e-07	4.05e-10	0.86	6.25	5.3934	129.67	TNFRSF18	TNF receptor superfamily member 18
3001	1.16e-07	4.01e-10	0.82	6.25	5.1487	272.2	GZMA	granzyme A
30009	1.16e-07	4.12e-10	0.69	6.25	4.3091	289.63	TBX21	T-box transcription factor 21
171558	1.48e-07	5.36e-10	1.04	6.21	6.4553	74.34	PTCRA	pre T cell antigen receptor alpha
219670	1.95e-07	7.20e-10	1.12	6.16	6.9115	53.56	ENKUR	enkurin, TRPC channel interacting protein
116987	2.02e-07	7.64e-10	0.78	6.15	4.8038	82.03	AGAP1	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1
84433	2.21e-07	8.51e-10	0.58	6.14	3.5854	494.22	CARD11	caspase recruitment domain family member 11
3702	2.43e-07	9.52e-10	0.80	6.12	4.9201	181.27	ITK	IL2 inducible T cell kinase
7504	2.63e-07	1.05e-09	1.01	6.10	6.1531	72.04	XK	X-linked Kx blood group antigen, Kell and VPS13A binding protein
2815	3.03e-07	1.23e-09	0.98	6.08	5.9768	82.38	GP9	glycoprotein IX platelet
9848	3.25e-07	1.34e-09	0.79	6.06	4.8097	87.75	MFAP3L	microfibril associated protein 3 like
84281	3.62e-07	1.53e-09	0.75	6.04	4.5399	256.17	C2orf88	chromosome 2 open reading frame 88
916	4.20e-07	1.80e-09	0.89	6.01	5.3772	118.84	CD3E	CD3 epsilon subunit of T-cell receptor complex
8631	4.37e-07	1.90e-09	0.67	6.01	4.0193	126.18	SKAP1	src kinase associated phosphoprotein 1
3493	4.44e-07	1.97e-09	0.85	6.00	5.0916	76.01	IGHA1	immunoglobulin heavy constant alpha 1
286	6.56e-07	2.95e-09	0.87	5.93	5.1352	90.7	ANK1	ankyrin 1
55287	7.24e-07	3.31e-09	1.08	5.92	6.4090	57.91	TMEM40	transmembrane protein 40
113219467	7.37e-07	3.42e-09	0.76	5.91	4.5044	76179.7	MIR12136	microRNA 12136

321	7.39e-07	3.49e-09	0.93	5.91	5.4982	147.92	APBA2	amyloid beta precursor protein binding family A member 2
4574	7.85e-07	3.76e-09	0.77	5.89	4.5471	35610.06	TRNS1	tRNA-Ser
2781	8.06e-07	3.92e-09	0.83	5.89	4.8570	70.27	GNAZ	G protein subunit alpha z
53637	8.09e-07	3.99e-09	0.90	5.88	5.3183	170.03	S1PR5	sphingosine-1-phosphate receptor 5
3002	8.70e-07	4.36e-09	0.79	5.87	4.6264	378.29	GZMB	granzyme B
925	8.77e-07	4.57e-09	1.01	5.86	5.9427	145.77	CD8A	CD8a molecule
2017	8.77e-07	4.47e-09	0.84	5.87	4.9530	125.5	CTTN	cortactin
27087	8.77e-07	4.58e-09	0.73	5.86	4.3039	92.01	B3GAT1	beta-1,3-glucuronyltransferase 1
4563	9.39e-07	4.97e-09	0.84	5.85	4.9028	850.27	TRNG	tRNA-Gly
2039	9.40e-07	5.05e-09	0.83	5.85	4.8690	158.75	DMTN	dematin actin binding protein
940	1.01e-06	5.48e-09	1.31	5.83	7.6261	62.42	CD28	CD28 molecule
5551	1.20e-06	6.60e-09	0.64	5.80	3.7325	814.54	PRF1	perforin 1
9580	1.51e-06	8.45e-09	0.90	5.76	5.2089	57.92	SOX13	SRY-box transcription factor 13
3824	1.63e-06	9.33e-09	0.76	5.74	4.3793	701.43	KLRD1	killer cell lectin like receptor D1
4157	1.63e-06	9.32e-09	0.72	5.74	4.1180	107.67	MC1R	melanocortin 1 receptor
23531	2.10e-06	1.22e-08	0.75	5.70	4.2533	356.73	MMD	monocyte to macrophage differentiation associated
10578	2.17e-06	1.28e-08	0.77	5.69	4.3968	2002.81	GNLY	granulysin
3690	2.18e-06	1.30e-08	0.77	5.69	4.3970	947.38	ITGB3	integrin subunit beta 3
4646	2.19e-06	1.32e-08	0.78	5.68	4.4177	83.08	MYO6	myosin VI
4576	2.74e-06	1.67e-08	0.80	5.64	4.5201	2420	TRNT	tRNA-Thr
9651	3.05e-06	1.88e-08	0.68	5.62	3.8051	181.4	PLCH2	phospholipase C eta 2
29094	3.51e-06	2.19e-08	0.84	5.60	4.6699	138.21	LGALSL	galectin like

11321848	3.99e-08	2.52e-08	0.79	5.57	4.4242	1190.1	MIR10396B	microRNA 10396b
917	4.20e-06	2.68e-08	1.26	5.56	7.0159	43.66	CD3G	CD3 gamma subunit of T-cell receptor complex
1731	4.28e-06	2.77e-08	0.62	5.56	3.4521	165.85	SEPTIN1	septin 1
100133331	4.54e-06	2.97e-08	0.59	5.54	3.2556	1856.97	LOC100133331	replaced by ID 100288069
107987001	5.10e-06	3.37e-08	0.75	5.52	4.1566	123.26	FAM27E4	family with sequence similarity 27 member E4
105377384	5.24e-06	3.51e-08	1.78	5.51	9.8185	36.96	LOC105377384	uncharacterized LOC105377384
22885	5.24e-06	3.54e-08	1.02	5.51	5.6055	48.88	ABLIM3	actin binding LIM protein family member 3
2812	5.95e-06	4.06e-08	0.99	5.49	5.4339	165.72	GP1BB	glycoprotein Ib platelet subunit beta
4818	7.21e-06	4.97e-08	0.70	5.45	3.8226	662.86	NKG7	natural killer cell granule protein 7
22981	7.48e-06	5.21e-08	0.98	5.44	5.3075	64.59	NINL	ninein like
28526	8.20e-06	5.78e-08	0.83	5.43	4.4807	165.56	TRDC	T cell receptor delta constant
116173	8.31e-06	5.91e-08	1.19	5.42	6.4650	50.94	CMTM5	CKLF like MARVEL transmembrane domain containing 5
4555	9.49e-06	6.82e-08	0.79	5.40	4.2726	353.74	TRND	tRNA-Asp
51176	9.82e-06	7.13e-08	1.02	5.39	5.4696	100.03	LEF1	lymphoid enhancer binding factor 1
3560	9.90e-06	7.26e-08	0.81	5.38	4.3773	842.89	IL2RB	interleukin 2 receptor subunit beta
100506736	1.00e-05	7.41e-08	0.64	5.38	3.4365	213.79	SLFN12L	schlafen family member 12 like
139105	1.24e-05	9.26e-08	1.42	5.34	7.5958	41.53	BEND2	BEN domain containing 2
100507747	1.41e-05	1.06e-07	0.72	5.32	3.8251	387.43	C13orf46	chromosome 13 open reading frame 46
57121	1.57e-05	1.19e-07	0.90	5.29	4.7810	57.28	LPAR5	lysophosphatidic acid receptor 5
10225	1.69e-05	1.30e-07	0.73	5.28	3.8536	249.02	CD96	CD96 molecule
4318	1.83e-05	1.44e-07	1.00	5.26	5.2383	60.45	MMP9	matrix metalloproteinase 9
128611	1.83e-05	1.44e-07	0.70	5.26	3.6576	276.18	ZNF831	zinc finger protein 831

152789	1.94e-05	1.53e-07	1.01	5.25	5.3183	46.41	JAKMIP1	janus kinase and microtubule interacting protein 1
389813	2.04e-05	1.63e-07	0.79	5.24	4.1191	80.25	AJM1	apical junction component 1 homolog
100132062	2.17e-05	1.75e-07	0.59	5.22	3.0796	1831.83	LOC100132062	uncharacterized LOC100132062
4068	2.35e-05	1.91e-07	0.98	5.21	5.0978	53.69	SH2D1A	SH2 domain containing 1A
10316	2.41e-05	1.99e-07	0.71	5.20	3.7122	101.1	NMUR1	neuromedin U receptor 1
2791	2.41e-05	2.01e-07	0.86	5.20	4.4424	208.83	GNG11	G protein subunit gamma 11
342618	2.41e-05	2.01e-07	0.91	5.20	4.7030	103.18	SLFN14	schlafen family member 14
5159	2.99e-05	2.52e-07	0.76	5.16	3.9102	102.47	PDGFRB	platelet derived growth factor receptor beta
23762	3.02e-05	2.57e-07	0.76	5.15	3.8987	79.18	OSBP2	oxysterol binding protein 2
107987206	3.11e-05	2.68e-07	0.83	5.14	4.2491	3084253.92	LOC107987206	replaced by ID 6029
6029	3.11e-05	2.68e-07	0.83	5.14	4.2491	3084253.42	RN7SL1	RNA component of signal recognition particle 7SL1
4541	3.16e-05	2.75e-07	0.84	5.14	4.3254	185894.86	ND6	NADH dehydrogenase subunit 6
2999	3.16e-05	2.78e-07	0.85	5.14	4.3693	128.86	GZMH	granzyme H
1901	4.07e-05	3.61e-07	0.92	5.09	4.6579	78.89	S1PR1	sphingosine-1-phosphate receptor 1
401124	4.53e-05	4.04e-07	0.89	5.07	4.4885	82.71	DTHD1	death domain containing 1
101927854	5.07e-05	4.56e-07	1.89	5.04	9.5540	31.05	THRB-AS2	THRB antisense RNA 2
105378179	5.99e-05	5.48e-07	0.84	5.01	4.2007	4041673.74	LOC105378179	uncharacterized LOC105378179
378706	5.99e-05	5.48e-07	0.84	5.01	4.2008	4041641.81	RN7SL2	RNA component of signal recognition particle 7SL2
387882	8.09e-05	7.46e-07	1.01	4.95	5.0084	135.94	C12orf75	chromosome 12 open reading frame 75
1236	8.44e-05	7.85e-07	1.26	4.94	6.2013	33.87	CCR7	C-C motif chemokine receptor 7
4508	8.78e-05	8.22e-07	0.85	4.93	4.2116	605386.23	ATP6	ATP synthase F0 subunit 6
6775	9.32e-05	8.80e-07	0.67	4.92	3.2960	190.45	STAT4	signal transducer and activator of transcription 4

4753	9.57e-05	9.10e-07	1.74	4.91	8.5485	40.75	NELL2	neural EGFL like 2
2625	1.03e-04	9.87e-07	0.77	4.89	3.7669	137.39	GATA3	GATA binding protein 3
9214	1.24e-04	1.20e-06	0.82	4.86	3.9582	90.93	FCMR	Fc mu receptor
84886	1.27e-04	1.23e-06	0.75	4.85	3.6446	119.31	C1orf198	chromosome 1 open reading frame 198
347404	1.39e-04	1.37e-06	0.99	4.83	4.8007	48.83	LANCL3	LanC like family member 3
8654	1.45e-04	1.43e-06	0.70	4.82	3.3488	165.13	PDE5A	phosphodiesterase 5A
4568	1.49e-04	1.48e-06	0.94	4.81	4.5051	868.52	TRNL2	tRNA-Leu
2113	1.49e-04	1.50e-06	0.70	4.81	3.3880	955.33	ETS1	ETS proto-oncogene 1, transcription factor
109864279	1.52e-04	1.53e-06	0.83	4.81	3.9706	538366.19	RNA45S N2	RNA, 45S pre-ribosomal N2
114804	1.62e-04	1.64e-06	1.20	4.79	5.7492	36.05	RNF157	ring finger protein 157
100131997	1.67e-04	1.71e-06	0.90	4.78	4.2977	114.65	FAM27E3	family with sequence similarity 27 member E3
2811	1.67e-04	1.72e-06	0.74	4.78	3.5548	200.93	GP1BA	glycoprotein Ib platelet subunit alpha
100008589	2.15e-04	2.23e-06	0.58	4.73	2.7227	1773.16	RNA28S N5	RNA, 28S ribosomal N5
5727	2.75e-04	2.88e-06	0.87	4.68	4.0578	63.79	PTCH1	patched 1
914	3.16e-04	3.33e-06	0.98	4.65	4.5406	154.04	CD2	CD2 molecule
4509	3.46e-04	3.67e-06	0.81	4.63	3.7444	70464.84	ATP8	ATP synthase F0 subunit 8
100233209	3.64e-04	3.88e-06	0.94	4.62	4.3254	57.35	PCED1B-AS1	PCED1B antisense RNA 1
8555	3.67e-04	3.95e-06	1.16	4.61	5.3280	32.12	CDC14B	cell division cycle 14B
109864272	3.78e-04	4.09e-06	0.58	4.61	2.6636	1416.82	RNA28S N4	RNA, 28S ribosomal N4
109864282	4.00e-04	4.36e-06	0.58	4.59	2.6780	1379.87	RNA28S N2	RNA, 28S ribosomal N2
1292	4.05e-04	4.43e-06	1.01	4.59	4.6293	484.55	COL6A2	collagen type VI alpha 2 chain
80739	4.31e-04	4.75e-06	0.91	4.58	4.1749	571.27	MPIG6B	megakaryocyte and platelet inhibitory receptor G6b

105379857	4.54e-04	5.04e-06	0.84	4.56	3.8449	58.53	LOC105379857	replaced by ID 642819
4638	4.54e-04	5.08e-06	0.91	4.56	4.1321	130.67	MYLK	myosin light chain kinase
6678	4.66e-04	5.24e-06	0.82	4.55	3.7413	360.13	SPARC	secreted protein acidic and cysteine rich
8436	5.11e-04	5.82e-06	0.90	4.53	4.0978	545.74	CAVIN2	caveolae associated protein 2
378707	5.11e-04	5.86e-06	0.76	4.53	3.4260	338691.09	RN7SL3	RNA component of signal recognition particle 7SL3
105372446	5.11e-04	5.86e-06	1.06	4.53	4.7926	39.8	LIM2-AS1	LIM2 and SIGLEC10 antisense RNA 1
106632264	5.16e-04	5.95e-06	0.59	4.53	2.6802	1688.58	RNA28S N1	RNA, 28S ribosomal N1
5730	5.73e-04	6.66e-06	0.85	4.50	3.8484	74.51	PTGDS	prostaglandin D2 synthase
348378	6.02e-04	7.04e-06	1.00	4.49	4.5061	49.36	SHISAL2 A	shisa like 2A
81606	6.29e-04	7.40e-06	0.74	4.48	3.3265	112.26	LBH	LBH regulator of WNT signaling pathway
79616	6.35e-04	7.52e-06	1.03	4.48	4.6155	38.45	CCNJL	cyclin J like
4535	6.37e-04	7.58e-06	0.86	4.48	3.8383	713934.18	ND1	NADH dehydrogenase subunit 1
5577	6.62e-04	7.93e-06	0.77	4.47	3.4346	474.72	PRKAR2 B	protein kinase cAMP-dependent type II regulatory subunit beta
4564	6.70e-04	8.08e-06	0.93	4.46	4.1357	1883.31	TRNH	tRNA-His
107986461	6.71e-04	8.13e-06	1.32	4.46	5.9042	26.15	LOC107986461	uncharacterized LOC107986461
4566	7.44e-04	9.07e-06	0.89	4.44	3.9404	1543.83	TRNK	tRNA-Lys
9886	7.46e-04	9.16e-06	0.78	4.44	3.4675	92.92	RHOBTB 1	Rho related BTB domain containing 1
728262	8.18e-04	1.01e-05	0.59	4.41	2.6184	2010.11	FAM157 A	family with sequence similarity 157 member A
4550	8.18e-04	1.02e-05	0.90	4.41	3.9566	262.81	RNR2	I-rRNA
8530	8.88e-04	1.11e-05	0.71	4.39	3.1021	207.99	CST7	cystatin F
6095	9.03e-04	1.13e-05	0.75	4.39	3.3120	244.43	RORA	RAR related orphan receptor A
85379	9.15e-04	1.16e-05	1.22	4.39	5.3521	27.68	KIAA1671	KIAA1671

54843	9.23e-04	1.17e-05	0.71	4.38	3.1244	141.13	SYTL2	synaptotagmin like 2
28951	9.79e-04	1.25e-05	0.70	4.37	3.0415	101.4	TRIB2	tribbles pseudokinase 2
3003	1.03e-03	1.33e-05	1.34	4.36	5.8517	76.63	GZMK	granzyme K
100500862	1.14e-03	1.47e-05	0.93	4.33	4.0309	11787.95	MIR3648-1	microRNA 3648-1
103504731	1.15e-03	1.49e-05	0.93	4.33	4.0231	23318.02	MIR3648-2	microRNA 3648-2
100289124	1.25e-03	1.64e-05	1.10	4.31	4.7453	54.17	FAM27E2	family with sequence similarity 27 member E2
50852	1.28e-03	1.68e-05	1.82	4.30	7.8346	25.64	TRAT1	T cell receptor associated transmembrane adaptor 1
149628	1.30e-03	1.71e-05	0.74	4.30	3.1719	148.48	PYHIN1	pyrin and HIN domain family member 1
154075	1.30e-03	1.76e-05	0.84	4.29	3.6147	206.39	SAMD3	sterile alpha motif domain containing 3
23224	1.30e-03	1.75e-05	0.68	4.29	2.8986	1317.56	SYNE2	spectrin repeat containing nuclear envelope protein 2
9437	1.30e-03	1.74e-05	0.91	4.30	3.9240	76.34	NCR1	natural cytotoxicity triggering receptor 1
113218501	1.30e-03	1.76e-05	1.04	4.29	4.4554	268.18	MIR10396A	microRNA 10396a
4536	1.36e-03	1.85e-05	0.89	4.28	3.8011	734832.3	ND2	NADH dehydrogenase subunit 2
343413	1.37e-03	1.87e-05	0.81	4.28	3.4488	73.61	FCRL6	Fc receptor like 6
6403	1.46e-03	2.00e-05	0.88	4.27	3.7668	135.52	SELP	selectin P
9254	1.69e-03	2.34e-05	0.88	4.23	3.7231	57.73	CACNA2D2	calcium voltage-gated channel auxiliary subunit alpha2delta 2
8277	1.69e-03	2.34e-05	1.21	4.23	5.1177	51.12	TKTL1	transketolase like 1
6043	1.81e-03	2.53e-05	0.94	4.21	-3.9531	122.45	SNORA63	small nucleolar RNA, H/ACA box 63
9953	1.82e-03	2.55e-05	0.84	4.21	3.5489	94.43	HS3ST3B1	heparan sulfate-glucosamine 3-sulfotransferase 3B1
2920	1.85e-03	2.60e-05	0.64	4.21	-2.6869	371.47	CXCL2	C-X-C motif chemokine ligand 2
28639	1.86e-03	2.63e-05	0.95	4.20	4.0018	55.35	TRBC1	T cell receptor beta constant 1
8807	1.88e-03	2.67e-05	0.69	4.20	2.9035	136.42	IL18RAP	interleukin 18 receptor accessory protein

5583	1.88e-03	2.69e-05	0.60	4.20	2.5272	810.23	PRKCH	protein kinase C eta
100128731	1.91e-03	2.75e-05	0.59	4.19	2.4621	589.79	OST4	oligosaccharyltransferase complex subunit 4, non-catalytic
100130231	1.95e-03	2.81e-05	1.03	4.19	4.3111	108.49	LINC00861	long intergenic non-protein coding RNA 861
666	2.02e-03	2.93e-05	0.94	4.18	3.9099	43.61	BOK	BCL2 family apoptosis regulator BOK
143872	2.09e-03	3.05e-05	1.18	4.17	4.9206	31.45	ARHGAP42	Rho GTPase activating protein 42
1793	2.14e-03	3.14e-05	0.87	4.16	-3.5991	192.46	DOCK1	dedicator of cytokinesis 1
84131	2.33e-03	3.43e-05	0.61	4.14	2.5401	289.46	CEP78	centrosomal protein 78
259215	2.48e-03	3.68e-05	1.24	4.13	5.1340	28.73	LY6G6F	lymphocyte antigen 6 family member G6F
51348	2.48e-03	3.69e-05	0.95	4.13	3.8998	150	KLRF1	killer cell lectin like receptor F1
81563	2.59e-03	3.87e-05	0.72	4.12	2.9448	137.04	C1orf21	chromosome 1 open reading frame 21
105377806	2.68e-03	4.03e-05	0.85	4.11	3.4713	109.15	LOC105377806	
4050	2.77e-03	4.18e-05	0.66	4.10	2.6877	138.21	LTB	lymphotoxin beta
81794	2.98e-03	4.53e-05	0.65	4.08	2.6647	253.96	ADAMTS10	ADAM metalloproteinase with thrombospondin type 1 motif 10
339541	3.11e-03	4.75e-05	1.00	4.07	-4.0516	148.54	ARMH1	armadillo like helical domain containing 1
58486	3.25e-03	4.97e-05	0.72	4.06	-2.9294	120.56	ZBED5	zinc finger BED-type containing 5
3693	3.59e-03	5.52e-05	0.83	4.03	3.3455	79.38	ITGB5	integrin subunit beta 5
8787	3.68e-03	5.69e-05	0.93	4.03	3.7281	42.63	RGS9	regulator of G protein signaling 9
10158	3.90e-03	6.09e-05	1.88	4.01	7.5241	20.9	PDZK1IP1	PDZK1 interacting protein 1
57732	3.90e-03	6.07e-05	0.68	4.01	2.7084	117.73	ZFYVE28	zinc finger FYVE-type containing 28
22914	3.90e-03	6.12e-05	0.94	4.01	3.7704	103.95	KLRK1	killer cell lectin like receptor K1
54796	3.98e-03	6.27e-05	1.01	4.00	4.0214	46.94	BNC2	basonuclin 2
101929531	4.34e-03	6.87e-05	1.33	3.98	5.2740	22.25	LINC01871	long intergenic non-protein coding RNA 1871

79993	4.55e-03	7.23e-05	0.89	3.97	3.5273	135.06	ELOVL7	ELOVL fatty acid elongase 7
93010	4.56e-03	7.29e-05	0.98	3.97	3.9048	37.06	B3GNT7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7
864	4.57e-03	7.32e-05	0.60	3.97	2.3704	1024.65	RUNX3	RUNX family transcription factor 3
4900	4.76e-03	7.67e-05	0.68	3.95	2.6853	1430.52	NRGN	neurogranin
109910382	5.10e-03	8.25e-05	0.55	3.94	2.1542	1042.18	RNA28S N3	RNA, 28S ribosomal N3
105379807	5.44e-03	8.87e-05	1.17	3.92	4.5978	38.71	LOC105379807	uncharacterized LOC105379807
92591	5.44e-03	8.88e-05	0.87	3.92	3.4114	171.51	ASB16	ankyrin repeat and SOCS box containing 16
124602	5.65e-03	9.27e-05	1.11	3.91	4.3402	44.07	KIF19	kinesin family member 19
9289	5.80e-03	9.56e-05	0.68	3.90	2.6365	465.08	ADGRG1	adhesion G protein-coupled receptor G1
117157	5.92e-03	9.81e-05	0.99	3.90	3.8584	117.34	SH2D1B	SH2 domain containing 1B
54758	5.98e-03	9.95e-05	0.57	3.89	2.2291	299.45	KLHDC4	kelch domain containing 4
760	6.08e-03	1.01e-04	0.82	3.89	3.1916	123.83	CA2	carbonic anhydrase 2
3823	6.16e-03	1.03e-04	0.92	3.88	3.5710	59.19	KLRC3	killer cell lectin like receptor C3
5874	6.32e-03	1.06e-04	0.87	3.88	3.3555	240.25	RAB27B	RAB27B, member RAS oncogene family
60509	6.62e-03	1.12e-04	0.61	3.86	2.3535	382.95	AGBL5	AGBL carboxypeptidase 5
4573	6.62e-03	1.12e-04	0.95	3.86	3.6809	306.24	TRNR	tRNA-Arg
2274	6.69e-03	1.14e-04	0.88	3.86	3.4101	48.27	FHL2	four and a half LIM domains 2
11098	6.80e-03	1.16e-04	0.91	3.85	3.5156	51.9	PRSS23	serine protease 23
4569	6.97e-03	1.20e-04	0.89	3.85	3.4226	682.49	TRNM	tRNA-Met
4537	7.23e-03	1.25e-04	0.92	3.84	3.5099	157586.17	ND3	NADH dehydrogenase subunit 3
4539	7.81e-03	1.35e-04	0.93	3.82	3.5386	139355.36	ND4L	NADH dehydrogenase subunit 4L
23043	8.03e-03	1.40e-04	0.56	3.81	2.1283	380.44	TNIK	TRAF2 and NCK interacting kinase

10125	8.03e-03	1.40e-04	0.71	3.81	2.6914	163.54	RASGRP1	RAS guanyl releasing protein 1
26030	8.07e-03	1.42e-04	0.53	3.81	2.0257	470.15	PLEKHG3	pleckstrin homology and RhoGEF domain containing G3
6932	8.10e-03	1.43e-04	0.82	3.80	3.1000	387.11	TCF7	transcription factor 7
9495	8.39e-03	1.49e-04	0.93	3.79	3.5344	48.48	AKAP5	A-kinase anchoring protein 5
107987026	8.62e-03	1.53e-04	0.93	3.79	3.5297	95.78	LOC107987026	uncharacterized LOC107987026
109864271	8.86e-03	1.58e-04	0.90	3.78	3.4098	426294.63	RNA45S N4	RNA, 45S pre-ribosomal N4
10123	9.12e-03	1.64e-04	0.58	3.77	2.1911	1100.53	ARL4C	ADP ribosylation factor like GTPase 4C
100528032	9.52e-03	1.71e-04	0.93	3.76	3.5015	120.66	KLRC4-KLRK1	KLRC4-KLRK1 readthrough
820	1.03e-02	1.87e-04	1.21	3.74	4.5029	32.12	CAMP	cathelicidin antimicrobial peptide
83988	1.03e-02	1.87e-04	0.79	3.74	2.9563	63.94	NCALD	neurocalcin delta
11278	1.07e-02	1.95e-04	0.75	3.73	2.8096	242.64	KLF12	KLF transcription factor 12
57211	1.08e-02	1.97e-04	1.88	3.72	-7.0025	68.04	ADGRG6	adhesion G protein-coupled receptor G6
387509	1.11e-02	2.04e-04	1.05	3.71	3.9001	32.45	GPR153	G protein-coupled receptor 153
4575	1.11e-02	2.04e-04	0.98	3.71	3.6310	1251.35	TRNS2	tRNA-Ser
55930	1.12e-02	2.07e-04	1.82	3.71	-6.7664	65.57	MYO5C	myosin VC
102724646	1.13e-02	2.10e-04	0.71	3.71	2.6310	165.84	LOC102724646	uncharacterized LOC102724646
129049	1.13e-02	2.12e-04	1.47	3.70	5.4433	22.97	SGSM1	small G protein signaling modulator 1
440823	1.25e-02	2.34e-04	0.72	3.68	2.6367	193.92	MIAT	myocardial infarction associated transcript
9124	1.27e-02	2.39e-04	0.80	3.67	2.9344	198.16	PDLIM1	PDZ and LIM domain 1
3674	1.27e-02	2.39e-04	0.85	3.67	3.1086	365.67	ITGA2B	integrin subunit alpha 2b
84879	1.31e-02	2.49e-04	1.64	3.66	-5.9959	37.54	MFSD2A	MFSD2 lysolipid transporter A, lysophospholipid
23345	1.31e-02	2.49e-04	0.53	3.66	1.9435	2229.53	SYNE1	spectrin repeat containing nuclear envelope protein 1

105376626	1.32e-02	2.52e-04	1.92	3.66	-7.0378	27.27	LOC105376626	uncharacterized LOC105376626
54438	1.33e-02	2.55e-04	0.56	3.66	2.0469	310.53	GFOD1	glucose-fructose oxidoreductase domain containing 1
2696	1.35e-02	2.59e-04	1.16	3.65	4.2418	26.77	GIPR	gastric inhibitory polypeptide receptor
55655	1.35e-02	2.61e-04	1.06	3.65	3.8808	45.33	NLRP2	NLR family pyrin domain containing 2
54855	1.41e-02	2.74e-04	1.11	3.64	4.0208	282.75	TENT5C	terminal nucleotidyltransferase 5C
161882	1.43e-02	2.79e-04	0.65	3.63	2.3771	129.01	ZFPM1	zinc finger protein, FOG family member 1
26051	1.52e-02	2.97e-04	0.60	3.62	2.1631	192.26	PPP1R16B	protein phosphatase 1 regulatory subunit 16B
112268284	1.52e-02	2.97e-04	0.73	3.62	2.6257	547.02	LOC112268284	
28638	1.55e-02	3.06e-04	0.90	3.61	3.2520	98.06	TRBC2	T cell receptor beta constant 2
3039	1.61e-02	3.18e-04	2.13	3.60	7.6657	3003.76	HBA1	hemoglobin subunit alpha 1
8542	1.62e-02	3.21e-04	0.76	3.60	2.7336	760.21	APOL1	apolipoprotein L1
122416	1.75e-02	3.49e-04	0.76	3.58	2.7136	105.46	ANKRD9	ankyrin repeat domain 9
23336	1.75e-02	3.50e-04	1.06	3.57	3.7834	31.75	SYNM	synemin
3004	1.75e-02	3.49e-04	1.19	3.58	4.2615	31.8	GZMM	granzyme M
4571	1.80e-02	3.62e-04	0.89	3.57	3.1609	5876.29	TRNP	tRNA-Pro
284	1.84e-02	3.71e-04	1.34	3.56	-4.7648	124.32	ANGPT1	angiopoietin 1
106633800	1.85e-02	3.75e-04	0.80	3.56	-2.8334	164.61	SNORD133	small nucleolar RNA, C/D box 133
59352	1.86e-02	3.78e-04	1.10	3.55	3.9145	51.9	LGR6	leucine rich repeat containing G protein-coupled receptor 6
7293	1.89e-02	3.85e-04	0.99	3.55	3.5203	57.36	TNFRSF4	TNF receptor superfamily member 4
9053	1.93e-02	3.96e-04	1.52	3.54	-5.3839	75.24	MAP7	microtubule associated protein 7
3494	1.93e-02	3.96e-04	1.22	3.54	4.3330	30.15	IGHA2	immunoglobulin heavy constant alpha 2 (A2m marker)
3738	1.96e-02	4.03e-04	0.59	3.54	2.0960	401.84	KCNA3	potassium voltage-gated channel subfamily A member 3

494470	1.99e-02	4.12e-04	1.00	3.53	3.5138	62.46	RNF165	ring finger protein 165
139065	1.99e-02	4.13e-04	0.94	3.53	-3.3180	76.99	SLITRK4	SLIT and NTRK like family member 4
202020	2.09e-02	4.35e-04	1.92	3.52	-6.7558	22.42	TAPT1-AS1	TAPT1 antisense RNA 1 (head to head)
5521	2.10e-02	4.41e-04	0.94	3.51	3.3171	51.66	PPP2R2B	protein phosphatase 2 regulatory subunit Bbeta
256691	2.10e-02	4.39e-04	1.45	3.52	-5.0834	113.64	MAMDC2	MAM domain containing 2
23348	2.10e-02	4.41e-04	1.01	3.51	3.5339	53.89	DOCK9	dedicator of cytokinesis 9
103021164	2.10e-02	4.43e-04	2.02	3.51	7.0951	15.17	CASC21	cancer susceptibility 21
84002	2.10e-02	4.45e-04	0.98	3.51	-3.4341	150.14	B3GNT5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5
6622	2.15e-02	4.57e-04	0.83	3.50	2.9029	160.64	SNCA	synuclein alpha
2322	2.17e-02	4.65e-04	0.82	3.50	-2.8844	205.22	FLT3	fms related receptor tyrosine kinase 3
3040	2.17e-02	4.62e-04	2.22	3.50	7.7566	3930.13	HBA2	hemoglobin subunit alpha 2
6915	2.17e-02	4.65e-04	1.28	3.50	4.4765	34.89	TBXA2R	thromboxane A2 receptor
100037417	2.35e-02	5.07e-04	0.75	3.48	2.6199	275.03	DDTL	D-dopachrome tautomerase like
5729	2.41e-02	5.22e-04	0.91	3.47	3.1667	65.68	PTGDR	prostaglandin D2 receptor
8809	2.53e-02	5.48e-04	0.98	3.46	3.3904	73.66	IL18R1	interleukin 18 receptor 1
10178	2.64e-02	5.75e-04	0.96	3.44	3.2996	49.23	TENM1	teneurin transmembrane protein 1
105369402	2.65e-02	5.79e-04	1.94	3.44	-6.6822	21.29	LOC105369402	uncharacterized LOC105369402
652966	2.68e-02	5.88e-04	0.93	3.44	-3.2043	118.06	SNORD10	small nucleolar RNA, C/D box 10
10826	2.69e-02	5.92e-04	0.69	3.44	2.3688	210.39	FAXDC2	fatty acid hydroxylase domain containing 2
6080	2.84e-02	6.27e-04	0.74	3.42	-2.5439	587.68	SNORA73A	small nucleolar RNA, H/ACA box 73A
54541	2.89e-02	6.40e-04	0.64	3.41	2.1916	140.83	DDIT4	DNA damage inducible transcript 4
8320	2.95e-02	6.55e-04	1.12	3.41	3.8075	35.91	EOMES	eomesodermin

8425	2.95e-02	6.57e-04	0.67	3.41	2.2964	323.27	LTBP4	latent transforming growth factor beta binding protein 4
8510	2.96e-02	6.64e-04	0.81	3.40	2.7449	81.45	MMP23B	matrix metalloproteinase 23B
55607	2.96e-02	6.62e-04	1.01	3.40	3.4504	32.61	PPP1R9A	protein phosphatase 1 regulatory subunit 9A
4684	3.15e-02	7.09e-04	0.87	3.39	2.9587	221.2	NCAM1	neural cell adhesion molecule 1
158038	3.16e-02	7.13e-04	1.10	3.38	3.7310	27.66	LINGO2	leucine rich repeat and Ig domain containing 2
54797	3.20e-02	7.24e-04	0.80	3.38	2.7041	293.08	MED18	mediator complex subunit 18
54910	3.20e-02	7.27e-04	0.72	3.38	2.4343	114.63	SEMA4C	semaphorin 4C
1668	3.59e-02	8.19e-04	2.06	3.35	6.8952	845.14	DEFA3	defensin alpha 3
100526833	3.65e-02	8.36e-04	1.09	3.34	3.6273	233.04	SEPT5-GP1BB	SEPT5-GP1BB readthrough
4570	3.65e-02	8.37e-04	0.81	3.34	2.6991	4503.41	TRNN	tRNA-Asn
64407	3.70e-02	8.55e-04	0.62	3.33	2.0712	910.06	RGS18	regulator of G protein signaling 18
1116	3.70e-02	8.57e-04	1.17	3.33	3.9016	77.95	CHI3L1	chitinase 3 like 1
4602	3.70e-02	8.54e-04	1.19	3.33	-3.9641	309.63	MYB	MYB proto-oncogene, transcription factor
671	3.79e-02	8.80e-04	0.90	3.33	3.0079	407.29	BPI	bactericidal permeability increasing protein
1521	3.79e-02	8.84e-04	0.74	3.33	2.4454	352.02	CTSW	cathepsin W
5243	3.95e-02	9.24e-04	0.88	3.31	2.9062	82.04	ABCB1	ATP binding cassette subfamily B member 1
8690	3.99e-02	9.36e-04	0.90	3.31	-2.9668	59.6	JRKL	JRK like
256380	4.00e-02	9.40e-04	0.90	3.31	2.9675	105.59	SCML4	Scm polycomb group protein like 4
6232	4.03e-02	9.53e-04	0.59	3.30	1.9478	2438.21	RPS27	ribosomal protein S27
26053	4.03e-02	9.51e-04	0.71	3.30	2.3556	184.35	AUTS2	activator of transcription and developmental regulator AUTS2
23365	4.07e-02	9.67e-04	0.72	3.30	2.3616	246.27	ARHGEF12	Rho guanine nucleotide exchange factor 12
57613	4.09e-02	9.74e-04	1.97	3.30	-6.4960	18.72	FAM234B	family with sequence similarity 234 member B

652965	4.14e-02	9.89e-04	0.76	3.29	-2.5110	441.42	8	SNORA4	small nucleolar RNA, H/ACA box 48
102724364	4.34e-02	1.04e-03	0.60	3.28	1.9821	212.36	4P	SEC22B	SEC22 homolog B4, pseudogene
4145	4.40e-02	1.06e-03	0.79	3.28	2.5723	216.52		MATK	megakaryocyte-associated tyrosine kinase
55759	4.43e-02	1.07e-03	0.91	3.27	-2.9844	63.19		WDR12	WD repeat domain 12
60312	4.52e-02	1.09e-03	1.08	3.27	3.5314	46.95		AFAP1	actin filament associated protein 1
84628	4.63e-02	1.12e-03	0.69	3.26	2.2385	142.89		NTNG2	netrin G2
4549	4.67e-02	1.14e-03	1.11	3.25	3.6065	148.56		RNR1	s-rRNA
100861532	4.68e-02	1.14e-03	0.94	3.25	3.0486	269159.77		RNA45S N5	RNA, 45S pre-ribosomal N5
105379282	4.87e-02	1.20e-03	0.80	3.24	2.5973	156.8		LOC105379282	
4092	4.87e-02	1.19e-03	0.73	3.24	2.3625	169.55		SMAD7	SMAD family member 7
79037	4.95e-02	1.22e-03	0.82	3.23	2.6512	75.01		PVRIG	PVR related immunoglobulin domain containing
144203	4.96e-02	1.23e-03	1.14	3.23	3.6825	26.84		OVOS2	alpha-2-macroglobulin like 1 pseudogene

Supplemental Table 3. Complete Annotations Lists with Accompanying P-values from Gene Ontology Analysis of Genes Differentially Expressed in AZA-treated Compared to Vehicle-treated Mouse Blood.

Gene Ontology Cellular Compartment	p-value	Gene Ontology Molecular Function	p-value	Gene Ontology Biological Process	p-value	PANTHER Pathway	p-value
alphav-beta3 integrin-PKCalpha complex	4.58E-04	fibrinogen binding	6.29E-07	activation of membrane attack complex	2.29E-04	Blood coagulation (P00011)	1.16E-02
plasma membrane	2.34E-02	protein-containing complex binding	4.75E-02	complement activation	1.28E-02	p53 pathway (P00059)	1.93E-02
cell periphery	3.14E-02	collagen V binding	1.14E-03	positive regulation of response to stimulus	1.14E-02	Integrin signalling pathway (P00034)	4.25E-02
alpha9-beta1 integrin-ADAM8 complex	4.58E-04	collagen binding	1.73E-02	positive regulation of biological process	2.20E-03		
integrin alphallb-beta3 complex	6.87E-04	C-X3-C chemokine binding	1.14E-03	regulation of immune system process	4.34E-03		
integrin complex	7.53E-03	chemokine binding	2.35E-05	positive regulation of immune system process	1.20E-03		
plasma membrane signaling receptor complex	4.45E-02	cytokine binding	2.72E-06	positive regulation of adenylate cyclase-inhibiting opioid receptor signaling pathway	2.29E-04		
protein complex involved in cell adhesion	1.34E-02	protein binding	1.69E-02	regulation of adenylate cyclase-inhibiting opioid receptor signaling pathway	2.29E-04		
alphav-beta3 integrin-HMGB1 complex	6.87E-04	neuregulin binding	1.37E-03	regulation of opioid receptor signaling pathway	9.16E-04		
integrin alphav-beta3 complex	6.87E-04	growth factor binding	4.38E-04	regulation of G protein-coupled receptor signaling pathway	3.54E-02		
integrin alpha9-beta1 complex	6.87E-04	vascular endothelial growth factor receptor 2 binding	1.83E-03	positive regulation of opioid receptor signaling pathway	4.58E-04		
alphav-beta3 integrin-IGF-1-IGF1R complex	9.16E-04	vascular endothelial growth factor receptor binding	3.66E-03	positive regulation of G protein-coupled receptor signaling pathway	9.81E-03		
fibrinogen complex	1.37E-03	growth factor receptor binding	3.43E-02	positive regulation of cellular process	2.38E-02		
extracellular space	5.07E-03	complement component C3b binding	2.06E-03	angioblast cell migration	2.29E-04		
extracellular region	1.31E-02	opsonin binding	5.03E-03	cell migration	8.62E-04		
symbiont cell surface	1.60E-03	complement binding	6.40E-03	cell motility	1.70E-03		
other organism part	1.83E-03	insulin-like growth factor I binding	2.97E-03	blood vessel morphogenesis	9.78E-05		
serine-type endopeptidase complex	3.89E-03	insulin-like growth factor binding	4.12E-03	tube morphogenesis	4.24E-04		
serine-type peptidase complex	4.34E-03	fibroblast growth factor binding	1.36E-05	anatomical structure morphogenesis	6.97E-04		
peptidase complex	2.90E-02	fibronectin binding	2.63E-05	developmental process	1.63E-03		
endopeptidase complex	2.22E-02	protein disulfide isomerase activity	4.12E-03	anatomical structure development	1.10E-03		
glycinergic synapse	4.12E-03	intramolecular oxidoreductase activity, transposing S-S bonds	4.12E-03	tube development	1.02E-03		

filopodium membrane	4.34E-03	intramolecular oxidoreductase activity	1.34E-02	multicellular organism development	2.75E-04
filopodium	2.67E-02	isomerase activity	4.23E-02	multicellular organismal process	4.13E-03
platelet alpha granule	4.80E-03	low-density lipoprotein particle binding	4.12E-03	blood vessel development	1.88E-04
cytoplasmic vesicle	8.86E-03	lipoprotein particle binding	6.85E-03	vasculature development	3.17E-06
intracellular vesicle	8.95E-03	protein-lipid complex binding	6.85E-03	system development	3.73E-03
vesicle	1.06E-02	C-C chemokine receptor activity	5.48E-03	circulatory system development	2.41E-05
lamellipodium membrane	5.26E-03	chemokine receptor activity	5.71E-03	negative regulation of nitric oxide mediated signal transduction	4.58E-04
leading edge membrane	4.61E-02	cytokine receptor activity	2.20E-02	regulation of nitric oxide mediated signal transduction	2.52E-03
lamellipodium	4.89E-02	immune receptor activity	3.12E-02	negative regulation of dendritic cell antigen processing and presentation	6.87E-04
microvillus membrane	7.76E-03	G protein-coupled chemoattractant receptor activity	5.71E-03	negative regulation of antigen processing and presentation	1.60E-03
microvillus	2.74E-02	heparan sulfate proteoglycan binding	5.71E-03	regulation of antigen processing and presentation	4.80E-03
sarcoplasmic reticulum	1.84E-02	proteoglycan binding	1.00E-02	regulation of dendritic cell antigen processing and presentation	2.29E-03
sarcoplasm	2.47E-02	sulfur compound binding	1.84E-03	negative regulation of antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	6.87E-04
ruffle membrane	2.31E-02	transforming growth factor beta binding	5.71E-03	regulation of antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	1.14E-03
ruffle	4.39E-02	C-C chemokine binding	5.71E-03	immune complex clearance	6.87E-04
melanosome	2.45E-02	laminin binding	7.31E-03	monocyte aggregation	6.29E-07
pigment granule	2.45E-02	extracellular matrix binding	1.01E-04	leukocyte aggregation	3.81E-06
external side of plasma membrane	1.87E-06	protein kinase C binding	1.39E-02	leukocyte cell-cell adhesion	8.15E-05
cell surface	3.48E-05	enzyme binding	1.07E-02	cell-cell adhesion	1.07E-04
side of membrane	1.16E-05	RNA polymerase binding	1.46E-02	cell adhesion	6.84E-04
focal adhesion	4.47E-02	phosphatidylserine binding	1.62E-02	negative regulation of endothelial cell chemotaxis	9.16E-04
cell-substrate junction	4.78E-02	modified amino acid binding	2.61E-02	regulation of endothelial cell chemotaxis	5.26E-03
		integrin binding	4.94E-04	regulation of locomotion	2.49E-02
		cell adhesion molecule binding	1.99E-03	regulation of response to external stimulus	2.52E-02

heparin binding	6.21E-04	regulation of endothelial cell migration	6.65E-04
glycosaminoglycan binding	1.23E-03	regulation of cell migration	2.05E-02
protease binding	7.33E-04	regulation of cell motility	2.29E-02
extracellular matrix structural constituent	3.21E-02	negative regulation of chemotaxis	1.03E-02
endopeptidase inhibitor activity	4.39E-02	negative regulation of endothelial cell migration	1.30E-02
endopeptidase regulator activity	4.94E-02	regulation of complement activation, alternative pathway	9.16E-04
peptidase inhibitor activity	4.56E-02	regulation of response to stress	3.94E-02
identical protein binding	1.27E-02	regulation of complement activation	5.26E-03
		regulation of humoral immune response	1.14E-02
		regulation of postsynaptic neurotransmitter receptor diffusion trapping	9.16E-04
		regulation of receptor localization to synapse	8.90E-03
		regulation of localization	9.93E-03
		regulation of biological quality	2.07E-03
		regulation of cellular localization	2.44E-02
		negative regulation of long-chain fatty acid import across plasma membrane	9.16E-04
		negative regulation of transmembrane transport	2.96E-02
		negative regulation of transport	5.00E-03
		regulation of transport	5.58E-03
		regulation of transmembrane transport	5.22E-03
		regulation of long-chain fatty acid import across plasma membrane	1.60E-03
		regulation of long-chain fatty acid import into cell	2.06E-03
		regulation of fatty acid transport	9.35E-03
		regulation of lipid transport	5.06E-04
		regulation of lipid localization	7.87E-04
		regulation of organic acid transport	2.40E-02

negative regulation of long-chain fatty acid import into cell	9.16E-04
negative regulation of fatty acid transport	2.29E-03
negative regulation of organic acid transport	6.85E-03
negative regulation of lipid transport	2.35E-05
negative regulation of lipid localization	8.67E-05
mast cell chemotaxis	1.14E-03
leukocyte chemotaxis	3.14E-02
cell chemotaxis	4.85E-02
chemotaxis	2.22E-03
taxis	2.25E-03
response to external stimulus	3.75E-04
locomotion	2.71E-03
response to chemical	5.01E-03
cellular response to chemical stimulus	3.92E-04
cellular response to stimulus	3.87E-02
mast cell migration	1.83E-03
myeloid leukocyte migration	3.19E-02
apolipoprotein A-I-mediated signaling pathway	1.14E-03
negative regulation of low-density lipoprotein receptor activity	1.14E-03
negative regulation of receptor-mediated endocytosis	6.85E-03
negative regulation of endocytosis	1.64E-02
regulation of receptor-mediated endocytosis	3.23E-02
negative regulation of molecular function	1.14E-02
regulation of molecular function	5.79E-03
negative regulation of lipoprotein metabolic process	1.14E-03

negative regulation of protein metabolic process	1.41E-02
regulation of protein metabolic process	7.76E-03
regulation of lipoprotein metabolic process	4.57E-03
regulation of serotonin uptake	1.37E-03
regulation of neurotransmitter uptake	4.80E-03
regulation of neurotransmitter transport	3.01E-02
negative regulation of cGMP-mediated signaling	1.37E-03
regulation of cGMP-mediated signaling	3.43E-03
negative regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis	1.60E-03
negative regulation of endothelial cell proliferation	1.07E-02
negative regulation of epithelial cell proliferation	3.79E-02
regulation of epithelial cell proliferation	7.31E-05
regulation of cell population proliferation	1.91E-04
regulation of endothelial cell proliferation	3.34E-06
regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis	3.89E-03
positive regulation of glomerular mesangial cell proliferation	1.83E-03
positive regulation of cell proliferation involved in kidney development	2.29E-03
positive regulation of cell population proliferation	2.24E-05
regulation of cell proliferation involved in kidney development	3.66E-03
regulation of glomerular mesangial cell proliferation	2.74E-03
negative regulation of plasminogen activation	1.83E-03
negative regulation of protein processing	5.94E-03
regulation of protein processing	1.55E-02
regulation of protein maturation	1.64E-02
regulation of proteolysis	8.14E-03

negative regulation of protein maturation	5.94E-03
regulation of plasminogen activation	3.89E-03
engulfment of apoptotic cell	2.06E-03
apoptotic cell clearance	2.49E-05
phagocytosis	4.81E-04
endocytosis	4.98E-03
vesicle-mediated transport	3.12E-02
import into cell	9.15E-03
phagocytosis, engulfment	1.03E-02
plasma membrane invagination	1.23E-02
membrane invagination	1.39E-02
cellular component organization	2.33E-02
cellular component organization or biogenesis	2.62E-02
regulation of complement-dependent cytotoxicity	2.06E-03
regulation of cell killing	3.45E-02
negative regulation of fibrinolysis	2.29E-03
positive regulation of blood coagulation	5.94E-03
positive regulation of coagulation	7.08E-03
regulation of coagulation	1.71E-02
regulation of multicellular organismal process	2.62E-02
positive regulation of multicellular organismal process	5.67E-03
positive regulation of hemostasis	5.94E-03
regulation of hemostasis	1.62E-02
regulation of body fluid levels	4.34E-05
positive regulation of wound healing	1.46E-02

positive regulation of response to wounding	1.84E-02
regulation of response to wounding	3.99E-02
regulation of wound healing	2.99E-02
regulation of blood coagulation	1.57E-02
regulation of fibrinolysis	3.20E-03
negative regulation of macrophage derived foam cell differentiation	2.29E-03
negative regulation of cell differentiation	1.02E-02
regulation of developmental process	1.01E-03
negative regulation of developmental process	9.52E-04
regulation of macrophage derived foam cell differentiation	5.71E-03
retinal pigment epithelium development	2.29E-03
tissue development	6.32E-03
retina development in camera-type eye	4.45E-02
sensory organ development	9.44E-03
animal organ development	2.41E-02
complement activation, alternative pathway	2.52E-03
defense response	3.12E-03
response to stress	3.08E-03
nitric oxide-cGMP-mediated signaling	2.52E-03
nitric oxide mediated signal transduction	5.48E-03
intracellular signaling cassette	1.32E-02
cGMP-mediated signaling	7.53E-03
positive regulation of fibroblast migration	1.26E-05
positive regulation of cell migration	7.39E-03
positive regulation of cell motility	8.11E-03

positive regulation of locomotion	8.53E-03
regulation of fibroblast migration	5.32E-05
cellular response to insulin-like growth factor stimulus	2.97E-03
response to nitrogen compound	2.56E-02
response to oxygen-containing compound	4.73E-03
cellular response to oxygen-containing compound	1.51E-03
cellular response to nitrogen compound	8.79E-03
positive regulation of extrinsic apoptotic signaling pathway via death domain receptors	3.20E-03
positive regulation of extrinsic apoptotic signaling pathway	1.55E-02
regulation of extrinsic apoptotic signaling pathway	3.97E-02
regulation of apoptotic process	3.54E-03
regulation of programmed cell death	3.86E-03
positive regulation of apoptotic signaling pathway	3.81E-02
regulation of extrinsic apoptotic signaling pathway via death domain receptors	1.14E-02
positive regulation of osteoblast proliferation	3.43E-03
regulation of osteoblast proliferation	7.08E-03
blood coagulation, fibrin clot formation	3.43E-03
protein activation cascade	4.34E-03
protein metabolic process	3.19E-02
blood coagulation	3.86E-04
coagulation	3.86E-04
hemostasis	4.03E-04
wound healing	1.71E-03
response to wounding	3.57E-03
negative regulation of sprouting angiogenesis	3.43E-03

negative regulation of angiogenesis	2.65E-02
negative regulation of blood vessel morphogenesis	2.70E-02
regulation of anatomical structure morphogenesis	7.45E-04
negative regulation of vasculature development	2.72E-02
regulation of vasculature development	3.05E-05
regulation of multicellular organismal development	3.50E-03
regulation of angiogenesis	2.86E-05
regulation of sprouting angiogenesis	1.09E-02
retinal rod cell development	3.43E-03
retinal rod cell differentiation	5.71E-03
camera-type eye photoreceptor cell differentiation	9.58E-03
neural retina development	2.11E-02
retina morphogenesis in camera-type eye	1.91E-02
camera-type eye morphogenesis	3.59E-02
eye morphogenesis	4.25E-02
animal organ morphogenesis	2.31E-02
eye photoreceptor cell differentiation	1.43E-02
photoreceptor cell differentiation	1.91E-02
eye photoreceptor cell development	1.00E-02
photoreceptor cell development	1.46E-02
negative regulation of cell migration involved in sprouting angiogenesis	3.89E-03
regulation of cell migration involved in sprouting angiogenesis	9.35E-03
regulation of blood vessel endothelial cell migration	2.29E-02
negative regulation of blood vessel endothelial cell migration	8.44E-03
regulation of trophoblast cell migration	3.89E-03

cellular response to nitric oxide	4.12E-03
response to nitric oxide	5.48E-03
cellular response to reactive nitrogen species	4.57E-03
inflammatory response to wounding	4.12E-03
inflammatory response	1.87E-04
platelet aggregation	2.63E-05
platelet activation	8.15E-05
cell activation	1.26E-02
homotypic cell-cell adhesion	6.66E-05
maintenance of postsynaptic specialization structure	4.12E-03
postsynaptic density organization	8.22E-03
postsynaptic specialization organization	1.00E-02
postsynapse organization	3.12E-02
maintenance of synapse structure	9.58E-03
cell junction maintenance	1.57E-02
cellular component maintenance	1.95E-02
negative regulation of interleukin-12 production	4.34E-03
regulation of interleukin-12 production	1.46E-02
positive regulation of transforming growth factor beta production	4.57E-03
regulation of transforming growth factor beta production	7.76E-03
positive regulation of gene expression	3.15E-02
positive regulation of metabolic process	3.86E-02
positive regulation of macromolecule metabolic process	3.01E-02
negative regulation of fibroblast growth factor receptor signaling pathway	4.57E-03
negative regulation of cellular response to growth factor stimulus	2.47E-02

regulation of fibroblast growth factor receptor signaling pathway	7.99E-03
smooth muscle cell migration	4.57E-03
muscle cell migration	8.44E-03
mitochondrial DNA metabolic process	4.80E-03
mitochondrial genome maintenance	7.76E-03
eosinophil chemotaxis	4.80E-03
eosinophil migration	5.03E-03
granulocyte migration	2.29E-02
granulocyte chemotaxis	1.84E-02
positive regulation of protein export from nucleus	4.80E-03
regulation of protein export from nucleus	9.13E-03
regulation of intracellular protein transport	3.97E-02
regulation of protein localization	2.00E-02
regulation of nucleocytoplasmic transport	3.12E-02
positive regulation of intracellular protein transport	2.52E-02
positive regulation of intracellular transport	3.48E-02
positive regulation of nucleocytoplasmic transport	1.75E-02
growth plate cartilage development	5.03E-03
connective tissue development	1.48E-03
endochondral bone growth	6.85E-03
bone growth	7.99E-03
organ growth	3.12E-02
bone development	1.07E-03
skeletal system development	5.79E-03
cartilage development involved in endochondral bone morphogenesis	8.67E-03

cartilage development	8.12E-04
endochondral bone morphogenesis	1.62E-02
bone morphogenesis	2.58E-02
positive regulation of cell adhesion mediated by integrin	5.26E-03
positive regulation of cell adhesion	5.42E-03
regulation of cell adhesion	1.33E-02
regulation of cell adhesion mediated by integrin	1.12E-02
response to magnesium ion	5.26E-03
positive regulation of endothelial cell apoptotic process	5.48E-03
regulation of endothelial cell apoptotic process	7.14E-05
neutrophil homeostasis	5.71E-03
myeloid cell homeostasis	4.03E-02
leukocyte homeostasis	2.85E-02
positive regulation of macrophage chemotaxis	5.71E-03
positive regulation of leukocyte chemotaxis	2.40E-02
positive regulation of chemotaxis	3.63E-02
positive regulation of leukocyte migration	6.00E-04
regulation of leukocyte migration	1.26E-03
regulation of leukocyte chemotaxis	3.03E-02
positive regulation of macrophage migration	7.08E-03
positive regulation of mononuclear cell migration	2.18E-04
regulation of mononuclear cell migration	4.69E-04
regulation of macrophage migration	1.12E-02
regulation of granulocyte chemotaxis	1.39E-02
regulation of macrophage chemotaxis	7.76E-03

mesodermal cell differentiation	5.94E-03
mesoderm formation	1.68E-02
mesoderm morphogenesis	1.77E-02
mesoderm development	2.79E-02
formation of primary germ layer	2.76E-02
anatomical structure formation involved in morphogenesis	1.06E-03
gastrulation	4.05E-02
positive regulation of bone resorption	6.17E-03
regulation of bone resorption	1.21E-02
regulation of bone remodeling	1.43E-02
regulation of tissue remodeling	1.95E-02
peptide cross-linking	6.17E-03
cellular response to platelet-derived growth factor stimulus	6.40E-03
response to platelet-derived growth factor	7.08E-03
positive regulation of macrophage activation	7.08E-03
regulation of macrophage activation	1.43E-02
behavioral response to pain	7.31E-03
response to pain	1.16E-02
multicellular organismal response to stress	2.56E-02
positive regulation of transforming growth factor beta receptor signaling pathway	7.31E-03
positive regulation of cellular response to transforming growth factor beta stimulus	7.31E-03
regulation of cellular response to transforming growth factor beta stimulus	3.41E-02
regulation of transforming growth factor beta receptor signaling pathway	3.34E-02
positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	2.45E-02
negative regulation of endothelial cell apoptotic process	7.76E-03

negative regulation of apoptotic process	8.52E-04
negative regulation of programmed cell death	9.44E-04
vascular associated smooth muscle cell differentiation	7.76E-03
smooth muscle cell differentiation	1.23E-02
negative regulation of lipid storage	7.99E-03
regulation of lipid storage	1.48E-02
heterotypic cell-cell adhesion	8.44E-03
ventricular system development	8.44E-03
negative regulation of cell-matrix adhesion	8.44E-03
negative regulation of cell-substrate adhesion	1.43E-02
regulation of cell-substrate adhesion	1.10E-03
regulation of cell-matrix adhesion	3.42E-04
positive regulation of T cell migration	8.44E-03
positive regulation of lymphocyte migration	1.03E-02
regulation of lymphocyte migration	1.62E-02
regulation of T cell migration	1.19E-02
regulation of postsynaptic neurotransmitter receptor internalization	8.90E-03
regulation of receptor internalization	2.16E-02
positive regulation of osteoclast differentiation	9.13E-03
regulation of osteoclast differentiation	2.02E-02
regulation of myeloid leukocyte differentiation	3.37E-02
positive regulation of myeloid leukocyte differentiation	1.75E-02
positive regulation of leukocyte differentiation	4.89E-02
positive regulation of hemopoiesis	4.89E-02
positive regulation of developmental process	3.06E-03

positive regulation of myeloid cell differentiation	2.67E-02
negative chemotaxis	9.35E-03
positive regulation of substrate adhesion-dependent cell spreading	9.35E-03
positive regulation of cell-substrate adhesion	4.09E-04
regulation of substrate adhesion-dependent cell spreading	1.34E-02
cell-substrate junction assembly	9.58E-03
cell-substrate junction organization	1.00E-02
cell adhesion mediated by integrin	1.00E-02
response to dietary excess	1.05E-02
energy homeostasis	2.27E-02
substrate adhesion-dependent cell spreading	1.12E-02
cell-substrate adhesion	4.19E-02
positive regulation of G1/S transition of mitotic cell cycle	1.14E-02
regulation of G1/S transition of mitotic cell cycle	3.77E-02
regulation of cell cycle G1/S phase transition	4.39E-02
positive regulation of cell cycle G1/S phase transition	1.48E-02
positive regulation of cell cycle phase transition	2.70E-02
positive regulation of mitotic cell cycle phase transition	2.22E-02
positive regulation of mitotic cell cycle	3.03E-02
determination of adult lifespan	1.14E-02
endocardial cushion development	1.16E-02
positive regulation of endothelial cell proliferation	2.23E-04
positive regulation of epithelial cell proliferation	1.18E-03
regulation of protein tyrosine kinase activity	1.21E-02
regulation of protein kinase activity	4.45E-03

regulation of kinase activity	5.06E-03
regulation of phosphorylation	1.88E-02
regulation of phosphate metabolic process	2.40E-02
regulation of phosphorus metabolic process	2.41E-02
regulation of transferase activity	6.61E-03
regulation of catalytic activity	1.64E-03
regulation of protein phosphorylation	1.68E-02
regulation of protein modification process	2.70E-02
embryo implantation	1.28E-02
female pregnancy	4.63E-02
positive regulation of angiogenesis	5.35E-06
positive regulation of vasculature development	5.63E-06
ERK1 and ERK2 cascade	1.37E-02
MAPK cascade	4.76E-02
positive regulation of smooth muscle cell proliferation	3.06E-04
regulation of smooth muscle cell proliferation	8.12E-04
nucleosome assembly	1.41E-02
protein-DNA complex assembly	3.52E-02
protein-DNA complex organization	3.97E-02
nucleosome organization	1.82E-02
positive regulation of blood vessel endothelial cell migration	1.41E-02
positive regulation of endothelial cell migration	2.72E-04
sprouting angiogenesis	1.43E-02
angiogenesis	2.58E-03
glomerulus development	1.48E-02

nephron development	3.50E-02
symbiont entry into host cell	1.48E-02
symbiont entry into host	1.48E-02
biological process involved in interaction with host	2.47E-02
biological process involved in symbiotic interaction	4.81E-02
viral life cycle	2.70E-02
viral process	3.39E-02
positive regulation of cell-matrix adhesion	1.50E-02
regulation of extracellular matrix organization	1.52E-02
chemokine-mediated signaling pathway	1.57E-02
cellular response to chemokine	1.82E-02
response to chemokine	1.82E-02
response to cytokine	1.82E-02
response to peptide	1.88E-02
activation of protein kinase activity	1.64E-02
positive regulation of protein kinase activity	1.63E-03
positive regulation of protein phosphorylation	7.25E-03
positive regulation of phosphorylation	7.84E-03
positive regulation of phosphate metabolic process	9.41E-03
positive regulation of phosphorus metabolic process	9.41E-03
positive regulation of protein modification process	1.15E-02
positive regulation of protein metabolic process	1.61E-03
positive regulation of kinase activity	1.77E-03
positive regulation of transferase activity	2.38E-03
positive regulation of catalytic activity	3.41E-04

positive regulation of molecular function	1.09E-03
positive regulation of smooth muscle cell migration	1.64E-02
regulation of smooth muscle cell migration	2.47E-02
cellular response to mechanical stimulus	1.71E-02
response to mechanical stimulus	1.19E-03
response to abiotic stimulus	2.79E-02
cellular response to external stimulus	1.75E-02
G1/S transition of mitotic cell cycle	1.73E-02
mitotic cell cycle phase transition	3.19E-02
cell cycle phase transition	3.50E-02
cell cycle G1/S phase transition	1.77E-02
positive regulation of fibroblast proliferation	1.77E-02
regulation of fibroblast proliferation	2.85E-02
positive regulation of reactive oxygen species metabolic process	1.86E-02
regulation of reactive oxygen species metabolic process	3.66E-02
negative regulation of cysteine-type endopeptidase activity	1.91E-02
negative regulation of endopeptidase activity	3.19E-02
regulation of endopeptidase activity	1.65E-03
regulation of peptidase activity	1.99E-03
regulation of hydrolase activity	7.46E-03
negative regulation of peptidase activity	3.54E-02
negative regulation of hydrolase activity	4.81E-02
regulation of cysteine-type endopeptidase activity	8.86E-04
regulation of release of sequestered calcium ion into cytosol	1.91E-02
regulation of sequestering of calcium ion	3.05E-02

regulation of calcium ion transmembrane transport	4.23E-02
organ or tissue specific immune response	1.95E-02
integrin-mediated signaling pathway	1.98E-02
response to activity	1.98E-02
outflow tract morphogenesis	2.00E-02
platelet-derived growth factor receptor signaling pathway	2.02E-02
positive regulation of MAP kinase activity	2.29E-02
positive regulation of protein serine/threonine kinase activity	3.48E-02
regulation of MAP kinase activity	3.57E-02
positive regulation of MAPK cascade	5.60E-03
positive regulation of intracellular signal transduction	2.63E-02
regulation of MAPK cascade	1.07E-02
response to unfolded protein	2.34E-02
response to topologically incorrect protein	2.74E-02
roof of mouth development	2.36E-02
positive regulation of tumor necrosis factor production	2.74E-02
regulation of tumor necrosis factor production	4.45E-02
regulation of tumor necrosis factor superfamily cytokine production	4.52E-02
positive regulation of tumor necrosis factor superfamily cytokine production	2.79E-02
positive regulation of cysteine-type endopeptidase activity	2.94E-02
positive regulation of endopeptidase activity	3.28E-02
positive regulation of peptidase activity	3.50E-02
cell-matrix adhesion	2.99E-02
positive regulation of translation	3.19E-02
mitochondrial gene expression	3.32E-02

response to calcium ion	3.37E-02
response to glucose	3.54E-02
response to hexose	3.68E-02
response to monosaccharide	3.86E-02
response to carbohydrate	4.41E-02
visual perception	3.66E-02
sensory perception of light stimulus	3.74E-02
ATP metabolic process	3.77E-02
purine ribonucleoside triphosphate metabolic process	4.30E-02
purine nucleoside triphosphate metabolic process	4.47E-02
nucleoside triphosphate metabolic process	4.81E-02
ribonucleoside triphosphate metabolic process	4.43E-02
positive regulation of peptidyl-tyrosine phosphorylation	3.79E-02
calcium-mediated signaling	3.83E-02
positive regulation of cytosolic calcium ion concentration	4.43E-02
positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	4.47E-02
neuromuscular process	4.59E-02
cellular response to xenobiotic stimulus	4.81E-02
positive regulation of ERK1 and ERK2 cascade	4.92E-02

Supplemental Table 4. Complete Annotations Lists with Accompanying P-values from Gene Ontology Analysis of Genes Differentially Expressed in Post-AZA treated, Responsive Patient PBMC Compared to Pre-treated matched, PBMC.

Gene Ontology Cellular Compartment	p-value	Gene Ontology Molecular Function	p-value	Gene Ontology Biological Process	p-value	PANTHER Pathway	p-value
stereocilium coat	8.41E-03	cyanamide hydratase activity	7.03E-05	positive regulation of glutathione peroxidase activity	8.41E-03	Blood coagulation (P00011)	2.01E-06
cellular anatomical structure	1.00E-03	NADP phosphatase activity	8.41E-03	regulation of glutathione peroxidase activity	8.41E-03	T cell activation (P00053)	8.17E-05
glycocalyx	8.41E-03	methanethiol oxidase activity	8.41E-03	regulation of peroxidase activity	1.67E-02	GABA-B receptor II signaling (P05731)	3.86E-02
external encapsulating structure	8.74E-03	oxidoreductase activity	2.24E-02	regulation of catalytic activity	4.45E-02	Dopamine receptor mediated signaling pathway (P05912)	1.28E-02
cell periphery	2.93E-11	high-affinity IgM receptor activity	8.41E-03	biological regulation	4.93E-05	Integrin signalling pathway (P00034)	2.26E-04
secretory dimeric IgA immunoglobulin complex	5.84E-07	IgM receptor activity	8.41E-03	positive regulation of peroxidase activity	1.67E-02	PDGF signaling pathway (P00047)	3.35E-02
secretory IgA immunoglobulin complex	5.77E-06	immune receptor activity	2.01E-03	positive regulation of cellular process	2.78E-05	Inflammation mediated by chemokine and cytokine signaling pathway (P00031)	6.82E-03
polymeric IgA immunoglobulin complex	5.77E-06	signaling receptor activity	3.96E-04	positive regulation of biological process	5.80E-08		
IgA immunoglobulin complex, circulating	5.77E-06	molecular transducer activity	3.96E-04	regulation of biological process	2.68E-05		
immunoglobulin complex, circulating	2.99E-08	transmembrane signaling receptor activity	2.75E-02	regulation of cellular process	4.30E-05		
extracellular space	2.72E-06	chemokine receptor antagonist activity	8.41E-03	positive regulation of catalytic activity	3.17E-02		

extracellular region	4.75E-05	signaling receptor binding	4.77E-09	apoptotic process in bone marrow cell	8.41E-03
immunoglobulin complex	1.46E-03	protein binding	2.57E-06	programmed cell death	2.66E-02
protein-containing complex	2.82E-02	binding	1.94E-05	cell death	3.86E-02
IgA immunoglobulin complex	9.74E-07	thiomorpholine-carboxylate dehydrogenase activity	8.41E-03	cellular process	7.02E-04
dimeric IgA immunoglobulin complex	5.84E-07	CCR4 chemokine receptor binding	8.41E-03	natural killer cell mediated cytotoxicity directed against tumor cell target	8.41E-03
cytolytic granule lumen	7.03E-05	chemokine receptor binding	2.88E-04	natural killer cell mediated immune response to tumor cell	8.41E-03
cytoplasm	6.31E-03	cytokine receptor binding	2.73E-02	immune response to tumor cell	1.44E-03
cytoplasmic vesicle lumen	6.81E-03	G protein-coupled receptor binding	4.20E-05	response to tumor cell	1.72E-02
cytoplasmic vesicle	7.18E-04	NADPH phosphatase activity	8.41E-03	response to biotic stimulus	8.63E-11
intracellular vesicle	1.03E-03	thromboxane A2 receptor activity	8.41E-03	response to stimulus	1.36E-14
vesicle	6.93E-06	thromboxane receptor activity	8.41E-03	immune response	1.93E-13
vesicle lumen	6.93E-03	hemoglobin alpha binding	2.40E-08	immune system process	4.52E-17
cytolytic granule	7.46E-08	hemoglobin binding	2.66E-11	natural killer cell mediated immunity	6.56E-08
cyclin D2-CDK6 complex	8.41E-03	haptoglobin binding	2.66E-11	innate immune response	3.63E-03
monomeric IgA immunoglobulin complex	2.32E-06	pore-forming activity	2.10E-04	defense response to symbiont	2.52E-08
laminin-11 complex	2.10E-04	polymeric immunoglobulin binding	1.67E-02	defense response to other organism	1.56E-08
laminin complex	2.43E-03	immunoglobulin binding	2.00E-02	response to other organism	3.28E-11

basement membrane	9.12E-03	protein-containing complex binding	1.11E-05	biological process involved in interspecies interaction between organisms	4.00E-12
collagen- containing extracellular matrix	2.96E-02	iron ion sequestering activity	1.67E-02	response to external biotic stimulus	3.49E-11
extracellular matrix	2.97E-02	metal ion sequestering activity	4.13E-02	response to external stimulus	1.77E-10
integrin alphaIIb- beta3 complex	2.10E-04	5-aminolevulinate synthase activity	1.67E-02	defense response	1.93E-08
integrin complex	1.27E-04	N- succinyltransferase activity	1.67E-02	response to stress	5.78E-09
plasma membrane signaling receptor complex	2.06E-08	succinyltransferase activity	2.50E-02	lymphocyte mediated immunity	8.03E-11
plasma membrane protein complex	4.37E-06	structural constituent of synapse- associated extracellular matrix	1.67E-02	leukocyte mediated immunity	1.61E-09
membrane protein complex	1.16E-03	structural molecule activity	4.46E-02	immune effector process	1.08E-09
membrane	4.54E-05	HLA-E specific inhibitory MHC class Ib receptor activity	1.67E-02	natural killer cell mediated cytotoxicity	1.14E-06
plasma membrane	7.12E-10	inhibitory MHC class Ib receptor activity	1.67E-02	leukocyte mediated cytotoxicity	1.33E-08
receptor complex	3.80E-06	MHC class Ib receptor activity	1.44E-03	cell killing	2.72E-10
protein complex involved in cell adhesion	5.50E-07	MHC class Ib protein binding, via antigen binding groove	1.67E-02	negative regulation of epithelial cell proliferation involved in lung morphogenesis	8.41E-03
hemoglobin complex	8.42E-13	MHC class Ib protein complex binding	3.32E-02	regulation of epithelial cell proliferation	1.10E-02
haptoglobin- hemoglobin complex	6.61E-11	MHC protein complex binding	3.86E-02	regulation of cell population proliferation	1.85E-03

glycoprotein Ib-IX-V complex	5.77E-06	MHC protein binding	3.48E-04	negative regulation of epithelial cell proliferation	2.86E-02
glycoprotein complex	9.14E-04	enterobactin binding	1.67E-02	negative regulation of cellular process	3.52E-04
platelet-derived growth factor complex	1.67E-02	FBXO family protein binding	1.67E-02	negative regulation of biological process	2.13E-04
gamma-delta T cell receptor complex	1.15E-05	interleukin-7 receptor activity	1.67E-02	metanephric glomerular basement membrane development	8.41E-03
T cell receptor complex	3.31E-04	cytokine receptor activity	4.73E-02	extracellular matrix organization	9.64E-03
caveolar macromolecular signaling complex	1.67E-02	asparagine-tRNA ligase activity	1.67E-02	external encapsulating structure organization	9.99E-03
membrane raft	3.72E-02	oxygen carrier activity	5.29E-10	extracellular structure organization	9.81E-03
membrane microdomain	3.83E-02	molecular carrier activity	2.00E-02	anatomical structure development	2.96E-04
neurofilament cytoskeleton	1.67E-02	C-4 methylsterol oxidase activity	2.50E-02	developmental process	4.50E-04
alpha9-beta1 integrin-ADAM8 complex	1.67E-02	IgM binding	2.50E-02	multicellular organismal process	7.79E-08
interleukin-2 receptor complex	1.67E-02	CD8 receptor binding	2.50E-02	CD8-positive, alpha-beta T cell differentiation involved in immune response	8.41E-03
integrin alphav-beta5 complex	1.67E-02	Fc-gamma receptor I complex binding	2.50E-02	alpha-beta T cell activation	4.32E-09
integrin alpha9-beta1 complex	1.67E-02	immunoglobulin receptor binding	4.19E-07	T cell activation	7.46E-11
cyclin D3-CDK6 complex	1.67E-02	procollagen-lysine 5-dioxygenase activity	2.50E-02	lymphocyte activation	5.91E-12
cyclin D1-CDK6 complex	1.67E-02	peptidyl-lysine 5-dioxygenase activity	3.32E-02	leukocyte activation	2.47E-12
ankyrin-1 complex	3.17E-05	arylesterase activity	1.03E-03	cell activation	1.28E-17
platelet alpha granule membrane	3.71E-09	interleukin-2 binding	2.50E-02	alpha-beta T cell differentiation	6.41E-04

secretory granule membrane	1.94E-02	growth factor binding	1.03E-03	T cell differentiation	6.71E-09
secretory granule	2.38E-04	IgA binding	2.50E-02	lymphocyte differentiation	1.12E-07
secretory vesicle	9.70E-04	V1A vasopressin receptor binding	2.50E-02	mononuclear cell differentiation	4.11E-07
platelet alpha granule	2.85E-10	vasopressin receptor binding	2.50E-02	leukocyte differentiation	3.33E-06
laminin-10 complex	2.50E-02	G protein-coupled serotonin receptor binding	2.50E-02	hemopoiesis	7.98E-10
alpha-beta T cell receptor complex	2.27E-06	interleukin-15 receptor activity	2.50E-02	cell development	4.20E-06
laminin-3 complex	2.50E-02	interleukin-2 receptor activity	2.50E-02	cell differentiation	3.81E-05
laminin-1 complex	2.50E-02	fibrinogen binding	1.44E-03	cellular developmental process	3.86E-05
Fc-gamma receptor III complex	2.50E-02	MHC class I protein complex binding	1.44E-03	alpha-beta T cell differentiation involved in immune response	8.57E-03
Fc receptor complex	4.13E-02	myosin light chain kinase activity	3.32E-02	T cell differentiation involved in immune response	1.06E-02
alphav-beta3 integrin-HMGB1 complex	2.50E-02	acetylcholine receptor activator activity	3.32E-02	T cell activation involved in immune response	4.14E-02
alphav-beta3 integrin-PKCalpha complex	2.50E-02	adenylate cyclase inhibitor activity	3.32E-02	lymphocyte activation involved in immune response	3.49E-02
collagen type V trimer	2.50E-02	cyclase inhibitor activity	4.13E-02	leukocyte activation involved in immune response	3.19E-02
supramolecular fiber	2.31E-02	sphingosine-1-phosphate receptor activity	2.43E-03	cell activation involved in immune response	3.42E-02
supramolecular polymer	2.40E-02	bioactive lipid receptor activity	8.79E-03	alpha-beta T cell activation involved in immune response	8.57E-03
pentameric IgM immunoglobulin complex	2.50E-02	neuregulin binding	4.13E-02	olfactory bulb axon guidance	8.41E-03

IgM immunoglobulin complex, circulating	2.50E-02	C-X3-C chemokine binding	4.13E-02	anatomical structure morphogenesis	3.62E-02
IgM immunoglobulin complex	3.02E-03	chemokine binding	3.13E-02	cell morphogenesis	1.86E-02
integrin alphav-beta3 complex	2.50E-02	receptor signaling protein tyrosine kinase activator activity	4.13E-02	positive regulation of piRNA transcription	8.41E-03
alphav-beta3 integrin-vitronectin complex	2.50E-02	kainate selective glutamate receptor activity	4.13E-02	regulation of piRNA transcription	8.41E-03
spectrin-associated cytoskeleton	4.72E-05	thyroid hormone binding	4.13E-02	positive regulation of metabolic process	1.18E-02
postsynaptic specialization of symmetric synapse	2.50E-02	integrin binding involved in cell-matrix adhesion	4.13E-02	positive regulation of biosynthetic process	2.30E-02
cell junction	8.32E-03	integrin binding	6.68E-05	thromboxane A2 signaling pathway	8.41E-03
IgG immunoglobulin complex	3.25E-06	cell adhesion molecule binding	2.75E-03	signal transduction	4.06E-09
glycinergic synapse	1.44E-03	cell adhesion mediator activity	2.62E-02	cellular response to stimulus	5.53E-08
actin cap	3.32E-02	thrombin-activated receptor activity	4.13E-02	signaling	1.61E-08
cortical actin cytoskeleton	4.64E-03	proteinase-activated receptor activity	4.13E-02	cell communication	1.91E-08
actin cytoskeleton	5.62E-04	pyruvate dehydrogenase (acetyl-transferring) kinase activity	4.13E-02	integrin biosynthetic process	8.41E-03
cortical cytoskeleton	3.91E-06	CXCR3 chemokine receptor binding	4.13E-02	plasma membrane organization	3.96E-02

cell cortex	1.00E-04	CXCR chemokine receptor binding	1.05E-05	cytotoxic T cell differentiation	8.41E-03
alphav-beta3 integrin-IGF-1-IGF1R complex	3.32E-02	oxygen binding	2.45E-07	negative regulation of norepinephrine uptake	8.41E-03
cytolytic granule membrane	3.32E-02	T cell receptor binding	3.68E-03	regulation of norepinephrine uptake	1.67E-02
internode region of axon	3.32E-02	platelet-derived growth factor binding	3.68E-03	positive regulation of mammary stem cell proliferation	8.41E-03
main axon	2.36E-02	lipoteichoic acid binding	4.94E-02	regulation of developmental process	7.15E-05
9+0 motile cilium	4.13E-02	MHC class II protein binding	4.94E-02	regulation of mammary stem cell proliferation	8.41E-03
kainate selective glutamate receptor complex	4.13E-02	BH3 domain binding	4.94E-02	positive regulation of cell population proliferation	3.34E-04
phagocytic vesicle lumen	4.13E-02	CCR1 chemokine receptor binding	4.94E-02	positive regulation of multicellular organismal process	9.95E-04
endocytic vesicle	3.31E-03	nerve growth factor binding	4.94E-02	regulation of multicellular organismal process	4.36E-05
endocytic vesicle lumen	3.13E-05	poly(A)-specific ribonuclease activity	5.16E-03	negative regulation of dopamine uptake involved in synaptic transmission	8.41E-03
PAR polarity complex	4.94E-02	3'-5'-RNA exonuclease activity	3.49E-02	negative regulation of catecholamine uptake involved in synaptic transmission	8.41E-03
IgE immunoglobulin complex	4.94E-02	RNA exonuclease activity, producing 5'-phosphomonoesters	4.05E-02	regulation of neurotransmitter uptake	1.21E-02
IgD immunoglobulin complex	4.94E-02	RNA exonuclease activity	4.45E-02	negative regulation of neurotransmitter uptake	2.50E-02
platelet dense granule membrane	4.94E-02	phospholipase activator activity	5.99E-04	positive regulation of adenylate cyclase-inhibiting opioid receptor signaling pathway	8.41E-03
immunological synapse	1.45E-07	lipase activator activity	1.04E-03	regulation of adenylate cyclase-inhibiting opioid receptor signaling pathway	8.41E-03
protein complex involved in cell-matrix adhesion	8.79E-03	platelet-derived growth factor receptor binding	5.98E-03	regulation of opioid receptor signaling pathway	2.50E-02

blood microparticle	1.98E-11	long-chain fatty acid-CoA ligase activity	6.87E-03	regulation of G protein-coupled receptor signaling pathway	2.29E-03
lamellipodium membrane	1.45E-02	fatty acid-CoA ligase activity	1.86E-02	regulation of response to stimulus	4.79E-06
cell leading edge	3.11E-02	fatty acid ligase activity	1.86E-02	positive regulation of opioid receptor signaling pathway	8.41E-03
lamellipodium	2.87E-02	acid-thiol ligase activity	2.79E-02	positive regulation of G protein-coupled receptor signaling pathway	4.27E-03
platelet alpha granule lumen	2.51E-04	ligase activity, forming carbon-sulfur bonds	4.65E-02	positive regulation of response to stimulus	2.54E-05
filamentous actin	2.46E-02	CoA-ligase activity	2.15E-02	negative regulation of endodeoxyribonuclease activity	8.41E-03
actin filament	3.00E-03	carbonate dehydratase activity	6.87E-03	negative regulation of deoxyribonuclease activity	1.67E-02
stress fiber	7.55E-04	chemokine activity	3.30E-05	regulation of hydrolase activity	4.65E-03
actomyosin	1.03E-03	cytokine activity	3.63E-03	negative regulation of hydrolase activity	2.60E-02
contractile actin filament bundle	7.55E-04	peroxidase activity	7.42E-06	activation of phospholipase D activity	8.41E-03
actin filament bundle	1.19E-03	oxidoreductase activity, acting on peroxide as acceptor	9.12E-06	positive regulation of phospholipase activity	4.39E-03
heterotrimeric G-protein complex	3.49E-02	antioxidant activity	8.17E-05	regulation of phospholipase activity	4.34E-04
cytoplasmic side of plasma membrane	4.33E-04	ankyrin binding	1.09E-02	regulation of lipase activity	2.65E-03
cytoplasmic side of membrane	1.98E-03	MHC class I protein binding	1.09E-02	positive regulation of lipase activity	1.45E-02
side of membrane	1.54E-08	phospholipase binding	1.58E-02	fast-twitch skeletal muscle fiber contraction	8.41E-03
GTPase complex	4.65E-02	spectrin binding	2.00E-02	twitch skeletal muscle contraction	1.67E-02
tertiary granule lumen	1.11E-02	sphingolipid binding	2.30E-02	voluntary skeletal muscle contraction	1.67E-02

external side of plasma membrane	8.24E-09	coreceptor activity	1.73E-03	positive regulation of erythrocyte enucleation	8.41E-03
cell surface	4.42E-08	structural constituent of cytoskeleton	4.53E-05	regulation of cellular component organization	3.45E-02
Z disc	5.36E-03	transcription corepressor binding	8.10E-03	regulation of erythrocyte enucleation	8.41E-03
I band	8.58E-03	extracellular matrix binding	2.45E-03	regulation of cell differentiation	3.74E-04
sarcomere	3.91E-02	protein kinase C binding	9.54E-03	chemokine (C-C motif) ligand 5 signaling pathway	8.41E-03
myofibril	4.56E-03	protein kinase binding	8.76E-04	response to chemical	5.24E-03
contractile muscle fiber	5.66E-03	kinase binding	3.70E-03	cell surface receptor signaling pathway	5.82E-09
acrosomal vesicle	9.06E-03	dynein intermediate chain binding	3.67E-02	positive regulation of somatic stem cell division	8.41E-03
focal adhesion	2.73E-02	collagen binding	3.18E-03	positive regulation of cell division	9.44E-03
cell-substrate junction	3.07E-02	cyclic nucleotide binding	3.86E-02	regulation of cell division	2.15E-02
anchoring junction	1.38E-02	lipopolysaccharide binding	4.45E-02	regulation of somatic stem cell division	8.41E-03
extracellular exosome	3.51E-03	heme binding	2.10E-04	positive regulation of SNARE complex assembly	8.41E-03
extracellular vesicle	5.31E-03	tetrapyrrole binding	3.18E-04	regulation of organelle organization	3.01E-02
extracellular membrane-bounded organelle	5.32E-03	carbohydrate transmembrane transporter activity	4.65E-02	regulation of vesicle fusion	3.49E-02
extracellular organelle	5.32E-03	structural constituent of muscle	4.86E-02	response to antipsychotic drug	8.41E-03
Unclassified	2.01E-03	antigen binding	4.51E-05	lung ciliated cell differentiation	8.41E-03
nuclear protein-containing complex	1.04E-02	SH3 domain binding	2.89E-03	regulation of branching involved in salivary gland morphogenesis by epithelial-mesenchymal signaling	8.41E-03
nucleus	2.56E-03	heparin binding	6.20E-04	epithelial-mesenchymal cell signaling	4.13E-02

glycosaminoglycan binding	2.09E-04	cardiac muscle tissue growth involved in heart morphogenesis	8.41E-03
sulfur compound binding	8.29E-03	growth involved in heart morphogenesis	3.32E-02
iron ion binding	1.95E-03	muscle structure development	1.29E-02
phosphoprotein binding	4.37E-02	pH elevation	8.41E-03
serine-type endopeptidase activity	1.67E-02	regulation of pH	1.23E-02
serine-type peptidase activity	2.42E-02	monoatomic cation homeostasis	4.18E-03
serine hydrolase activity	2.61E-02	monoatomic ion homeostasis	4.82E-03
carbohydrate binding	3.08E-02	homeostatic process	3.55E-02
identical protein binding	1.34E-02	regulation of nuclear migration along microtubule	8.41E-03
Unclassified	1.45E-03	positive regulation of hydrogen peroxide catabolic process	1.67E-02
RNA binding	1.98E-03	positive regulation of hydrogen peroxide metabolic process	4.94E-02
nucleic acid binding	3.65E-03	regulation of hydrogen peroxide catabolic process	3.32E-02
		negative regulation of mesenchymal cell proliferation involved in lung development	1.67E-02
		negative regulation of developmental process	5.06E-03
		regulation of mesenchymal cell proliferation	3.31E-02
		regulation of mesenchymal cell proliferation involved in lung development	1.67E-02
		positive regulation of oocyte development	1.67E-02
		regulation of oocyte development	2.50E-02
		regulation of oogenesis	2.50E-02

metanephric podocyte development	1.67E-02
metanephric podocyte differentiation	1.67E-02
metanephric glomerular epithelial cell differentiation	1.67E-02
metanephric glomerular epithelium development	1.67E-02
metanephric glomerular epithelial cell development	1.67E-02
positive regulation of dipeptide transmembrane transport	1.67E-02
positive regulation of dipeptide transport	1.67E-02
positive regulation of oligopeptide transport	1.67E-02
regulation of oligopeptide transport	1.67E-02
regulation of dipeptide transport	1.67E-02
regulation of dipeptide transmembrane transport	1.67E-02
cytotoxic T cell pyroptotic cell death	1.67E-02
pyroptotic cell death	4.13E-02
pyroptotic inflammatory response	3.13E-02
inflammatory response	3.40E-04
nerve growth factor production	1.67E-02
neurotrophin production	1.67E-02
negative regulation of natural killer cell chemotaxis	1.67E-02
regulation of natural killer cell chemotaxis	1.44E-03

regulation of lymphocyte chemotaxis	1.72E-02
regulation of lymphocyte migration	2.04E-02
regulation of leukocyte migration	1.33E-02
regulation of cell migration	9.32E-03
regulation of cell motility	3.87E-03
regulation of locomotion	3.41E-04
regulation of immune system process	5.33E-09
regulation of chemotaxis	3.19E-02
regulation of response to external stimulus	4.77E-04
negative regulation of lymphocyte chemotaxis	2.50E-02
negative regulation of response to stimulus	1.16E-02
embryonic lung development	1.67E-02
axon extension involved in regeneration	1.67E-02
sprouting of injured axon	1.67E-02
response to wounding	4.37E-08
platelet maturation	1.67E-02
positive regulation of myeloid dendritic cell activation	1.67E-02
positive regulation of leukocyte activation	1.08E-03
positive regulation of immune system process	3.33E-08

positive regulation of cell activation	4.81E-06
regulation of cell activation	4.62E-07
regulation of leukocyte activation	1.21E-04
regulation of myeloid dendritic cell activation	4.13E-02
positive regulation of somatic stem cell population maintenance	1.67E-02
hydroxylysine biosynthetic process	1.67E-02
primary metabolic process	9.21E-03
hydroxylysine metabolic process	1.67E-02
lymphoid lineage cell migration into thymus	1.67E-02
lymphoid lineage cell migration	1.67E-02
cell migration	7.82E-07
cell motility	3.52E-06
regulation of postsynaptic neurotransmitter receptor diffusion trapping	1.67E-02
regulation of biological quality	4.63E-04
nitric oxide transport	4.17E-04
negative regulation of phosphatidylinositol biosynthetic process	1.67E-02
negative regulation of phospholipid biosynthetic process	4.13E-02
negative regulation of phospholipid metabolic process	4.94E-02
regulation of phosphate metabolic process	4.80E-02

	regulation of phosphorus metabolic process	4.82E-02
	regulation of phosphatidylinositol biosynthetic process	4.13E-02
	negative regulation of mitochondrial electron transport, NADH to ubiquinone	1.67E-02
	negative regulation of mitochondrial ATP synthesis coupled electron transport	1.67E-02
	regulation of mitochondrial ATP synthesis coupled electron transport	4.94E-02
	regulation of mitochondrial electron transport, NADH to ubiquinone	4.13E-02
	positive regulation of type III interferon production	1.67E-02
	positive regulation of cytokine production	3.45E-03
	positive regulation of gene expression	7.35E-03
	regulation of type III interferon production	4.13E-02
	dendritic cell apoptotic process	1.67E-02
	oxygen transport	9.19E-10
	gas transport	2.77E-10
	carbon dioxide transport	9.19E-10
	one-carbon compound transport	1.11E-09
	positive regulation of cellular pH reduction	6.91E-04
	regulation of cellular pH reduction	1.90E-03
	regulation of intracellular pH	4.03E-02
	regulation of cellular pH	4.49E-02

intracellular monoatomic cation homeostasis	1.13E-02
intracellular monoatomic ion homeostasis	1.28E-02
blood coagulation, intrinsic pathway	3.17E-05
blood coagulation, fibrin clot formation	8.11E-06
protein activation cascade	1.69E-05
blood coagulation	7.63E-09
coagulation	8.67E-09
hemostasis	1.11E-08
regulation of body fluid levels	9.66E-08
wound healing	2.54E-08
granzyme-mediated programmed cell death signaling pathway	1.52E-06
negative regulation of endodermal cell differentiation	2.50E-02
negative regulation of cell differentiation	1.39E-02
positive regulation of cell-cell adhesion mediated by integrin	1.03E-03
regulation of cell-cell adhesion mediated by integrin	3.68E-03
regulation of cell adhesion mediated by integrin	8.10E-03
regulation of cell adhesion	3.46E-06
regulation of cell-cell adhesion	1.10E-03
positive regulation of cell-cell adhesion	5.33E-04

	positive regulation of cell adhesion	4.29E-06
	positive regulation of cell adhesion mediated by integrin	7.99E-04
	positive regulation of axon guidance	2.50E-02
	positive regulation of respiratory burst	4.72E-05
	regulation of respiratory burst	5.12E-04
	membrane raft polarization	2.50E-02
	membrane raft organization	2.30E-02
	cellular localization	2.19E-03
	maternal aggressive behavior	2.50E-02
	Fc receptor-mediated immune complex endocytosis	2.50E-02
	asparaginyl-tRNA aminoacylation	2.50E-02
	dendritic cell proliferation	2.50E-02
	mononuclear cell proliferation	3.23E-03
	leukocyte proliferation	6.07E-03
	cell population proliferation	9.95E-03
	negative regulation of serotonin uptake	2.50E-02
	regulation of serotonin uptake	4.17E-04
	smooth endoplasmic reticulum calcium ion homeostasis	2.50E-02
	negative regulation of thrombin-activated receptor signaling pathway	2.50E-02

	regulation of thrombin-activated receptor signaling pathway	2.50E-02
	negative regulation of G protein-coupled receptor signaling pathway	1.35E-02
	negative regulation of cell communication	4.91E-02
	establishment or maintenance of actin cytoskeleton polarity	2.50E-02
	cytoskeleton organization	3.56E-03
	actin cytoskeleton organization	7.15E-04
	actin filament-based process	2.12E-03
	positive regulation of metanephric mesenchymal cell migration by platelet-derived growth factor receptor-beta signaling pathway	2.50E-02
	regulation of metanephric mesenchymal cell migration by platelet-derived growth factor receptor-beta signaling pathway	2.50E-02
	cell surface receptor protein tyrosine kinase signaling pathway	2.83E-02
	enzyme-linked receptor protein signaling pathway	4.26E-02
	regulation of metanephric mesenchymal cell migration	3.32E-02
	positive regulation of metanephric mesenchymal cell migration	2.50E-02
	positive regulation of cell migration	2.52E-03
	positive regulation of cell motility	1.28E-03
	positive regulation of locomotion	5.30E-04
	negative regulation of chaperone-mediated autophagy	2.50E-02
	cellular response to water deprivation	2.50E-02

response to water deprivation	4.13E-02
response to oxygen-containing compound	5.74E-03
cellular response to water stimulus	4.94E-02
cellular response to oxygen-containing compound	2.48E-02
cellular response to chemical stimulus	1.57E-03
siderophore transport	2.50E-02
mesodermal to mesenchymal transition involved in gastrulation	2.50E-02
complement-dependent cytotoxicity	2.50E-02
cell differentiation involved in salivary gland development	2.50E-02
positive regulation of platelet activation	3.25E-06
regulation of platelet activation	8.98E-05
striatal medium spiny neuron differentiation	3.32E-02
head development	4.48E-02
principal sensory nucleus of trigeminal nerve development	3.32E-02
trigeminal sensory nucleus development	3.32E-02
club cell differentiation	3.32E-02
aorta smooth muscle tissue morphogenesis	3.32E-02
immunoglobulin transcytosis in epithelial cells	3.32E-02
negative regulation of epithelial cell differentiation involved in kidney development	3.32E-02

T-helper 1 cell lineage commitment	3.32E-02
CD4-positive, alpha-beta T cell activation	4.25E-04
positive T cell selection	2.06E-04
T cell selection	5.06E-05
adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	2.84E-06
adaptive immune response	1.11E-10
establishment of blood-retinal barrier	3.32E-02
negative regulation of T-helper 2 cell cytokine production	3.32E-02
regulation of immune response	3.98E-06
negative regulation of T cell mediated immunity	2.42E-03
negative regulation of lymphocyte mediated immunity	1.74E-02
negative regulation of leukocyte mediated immunity	2.62E-02
regulation of immune effector process	7.90E-03
regulation of leukocyte mediated immunity	3.56E-04
regulation of lymphocyte mediated immunity	4.88E-05
regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	2.87E-02
regulation of adaptive immune response	3.73E-02
negative regulation of adaptive immune response based on somatic recombination of immune	1.54E-02

receptors built from immunoglobulin superfamily domains	
negative regulation of adaptive immune response	1.89E-02
T cell receptor V(D)J recombination	3.32E-02
somatic recombination of T cell receptor gene segments	3.32E-02
immune system development	3.19E-03
somatic diversification of T cell receptor genes	3.32E-02
positive regulation of killing of cells of another organism	3.32E-02
regulation of killing of cells of another organism	4.13E-02
regulation of cell killing	3.81E-05
regulation of programmed cell death	2.66E-02
positive regulation of cell killing	3.08E-04
positive regulation of RNA polymerase II regulatory region sequence-specific DNA binding	3.32E-02
regulation of DNA binding	3.18E-03
regulation of binding	3.08E-02
positive regulation of DNA binding	3.67E-02
regulation of acyl-CoA biosynthetic process	1.90E-03
regulation of sulfur metabolic process	7.80E-03
regulation of ketone metabolic process	2.60E-02
negative regulation of low-density lipoprotein receptor activity	3.32E-02

	negative regulation of glycolytic process through fructose-6-phosphate	3.32E-02
	regulation of glycolytic process through fructose-6-phosphate	3.32E-02
	T cell anergy	3.32E-02
	lymphocyte anergy	3.32E-02
	tolerance induction	1.09E-02
	T cell tolerance induction	4.94E-02
	negative regulation of female receptivity	3.32E-02
	hydrogen peroxide catabolic process	6.48E-08
	hydrogen peroxide metabolic process	9.80E-07
	reactive oxygen species metabolic process	3.81E-05
	CD4-positive, alpha-beta T cell proliferation	2.43E-03
	alpha-beta T cell proliferation	5.98E-03
	T cell proliferation	2.54E-02
	lymphocyte proliferation	1.57E-02
	positive regulation of T cell anergy	4.13E-02
	positive regulation of lymphocyte anergy	4.13E-02
	positive regulation of Fc receptor mediated stimulatory signaling pathway	4.13E-02
	positive regulation of immune response	2.71E-07
	cGMP catabolic process	4.13E-02

cGMP metabolic process	9.84E-03
cyclic purine nucleotide metabolic process	4.65E-02
cyclic nucleotide metabolic process	4.86E-02
regulation of systemic arterial blood pressure by vasopressin	4.13E-02
negative regulation of T cell mediated cytotoxicity	3.02E-03
negative regulation of leukocyte mediated cytotoxicity	2.95E-02
regulation of leukocyte mediated cytotoxicity	1.90E-04
negative regulation of cell killing	3.49E-02
negative regulation of cAMP/PKA signal transduction	4.13E-02
NK T cell differentiation	4.13E-02
positive regulation of dopamine receptor signaling pathway	4.13E-02
negative regulation of MHC class II biosynthetic process	4.13E-02
transposable element silencing by piRNA-mediated heterochromatin formation	4.13E-02
CD27 signaling pathway	4.13E-02
positive regulation of CD4-positive, alpha-beta T cell proliferation	3.02E-03
positive regulation of alpha-beta T cell proliferation	1.72E-02
regulation of T cell proliferation	1.86E-02
regulation of lymphocyte proliferation	1.58E-02
regulation of mononuclear cell proliferation	4.66E-03

regulation of leukocyte proliferation	7.68E-03
regulation of lymphocyte activation	1.37E-03
regulation of T cell activation	1.76E-03
positive regulation of T cell proliferation	1.12E-02
positive regulation of T cell activation	6.29E-03
positive regulation of leukocyte cell-cell adhesion	1.38E-04
regulation of leukocyte cell-cell adhesion	9.57E-05
positive regulation of lymphocyte activation	7.30E-03
positive regulation of lymphocyte proliferation	3.42E-02
positive regulation of mononuclear cell proliferation	8.35E-03
positive regulation of leukocyte proliferation	1.29E-02
regulation of CD4-positive, alpha-beta T cell proliferation	1.45E-02
regulation of CD4-positive, alpha-beta T cell activation	3.39E-02
positive regulation of natural killer cell chemotaxis	4.13E-02
positive regulation of lymphocyte migration	4.86E-02
positive regulation of leukocyte migration	3.96E-02
positive regulation of response to external stimulus	3.35E-03
apolipoprotein A-I-mediated signaling pathway	4.13E-02
nuclear-transcribed mRNA catabolic process, no-go decay	4.13E-02

negative regulation of lipoprotein metabolic process	4.13E-02
tendon development	4.13E-02
negative regulation of thymocyte apoptotic process	3.02E-03
negative regulation of T cell apoptotic process	5.31E-05
negative regulation of lymphocyte apoptotic process	2.85E-04
regulation of lymphocyte apoptotic process	1.73E-03
regulation of leukocyte apoptotic process	1.08E-03
regulation of apoptotic process	3.64E-02
negative regulation of leukocyte apoptotic process	1.16E-04
negative regulation of apoptotic process	1.23E-02
negative regulation of programmed cell death	1.41E-02
regulation of T cell apoptotic process	4.21E-04
regulation of thymocyte apoptotic process	6.87E-03
negative regulation of urine volume	4.13E-02
renal system process	4.42E-03
positive regulation of receptor binding	4.13E-02
axon midline choice point recognition	4.13E-02
cell recognition	2.93E-02
miRNA-mediated gene silencing by mRNA destabilization	4.13E-02

	gamma-delta T cell activation	2.10E-05
	negative regulation of skeletal muscle cell proliferation	4.13E-02
	salivary gland cavitation	4.13E-02
	tube lumen cavitation	4.13E-02
	wound healing, spreading of epidermal cells	3.02E-04
	wound healing, spreading of cells	2.21E-03
	epiboly involved in wound healing	2.21E-03
	epiboly	2.42E-03
	morphogenesis of an epithelial sheet	1.06E-02
	regulation of basement membrane organization	3.68E-03
	regulation of extracellular matrix organization	1.60E-02
	positive regulation of isotype switching to IgG isotypes	3.68E-03
	positive regulation of isotype switching	2.46E-02
	positive regulation of immune effector process	7.38E-03
	regulation of isotype switching	4.05E-02
	regulation of immunoglobulin mediated immune response	1.54E-02
	regulation of B cell mediated immunity	1.54E-02
	positive regulation of immunoglobulin mediated immune response	5.63E-03
	positive regulation of B cell mediated immunity	5.63E-03

	positive regulation of lymphocyte mediated immunity	1.28E-04
	positive regulation of leukocyte mediated immunity	3.31E-04
	regulation of isotype switching to IgG isotypes	6.87E-03
	megakaryocyte development	3.77E-05
	myeloid cell development	3.67E-07
	myeloid cell differentiation	5.68E-05
	megakaryocyte differentiation	1.11E-04
	negative regulation of megakaryocyte differentiation	4.94E-02
	regulation of hemopoiesis	8.64E-03
	regulation of megakaryocyte differentiation	1.72E-02
	positive regulation of establishment of endothelial barrier	4.94E-02
	positive regulation of endothelial cell development	4.94E-02
	zygotic determination of anterior/posterior axis, embryo	4.94E-02
	response to iron(II) ion	4.94E-02
	positive regulation of integrin-mediated signaling pathway	4.39E-03
	regulation of integrin-mediated signaling pathway	1.21E-02
	endodermal cell fate specification	4.94E-02
	endodermal cell differentiation	6.80E-03
	endoderm formation	1.17E-02

endoderm development	5.29E-03
formation of primary germ layer	1.92E-02
cell fate specification	3.92E-02
negative regulation of transmission of nerve impulse	4.94E-02
negative thymic T cell selection	4.39E-03
negative T cell selection	5.16E-03
thymic T cell selection	6.95E-04
T cell differentiation in thymus	1.77E-05
positive thymic T cell selection	4.39E-03
negative regulation of protein targeting to membrane	4.94E-02
negative regulation of protein localization to membrane	4.45E-02
dopamine uptake involved in synaptic transmission	4.94E-02
catecholamine uptake involved in synaptic transmission	4.94E-02
establishment of localization in cell	2.36E-02
cell dedifferentiation	4.94E-02
dedifferentiation	4.94E-02
thyroid hormone transport	4.39E-03
hemidesmosome assembly	4.94E-02
cell-substrate junction assembly	3.83E-04

cell-substrate junction organization	4.61E-04
cell junction organization	2.95E-02
cell junction assembly	1.44E-02
positive regulation of prostaglandin biosynthetic process	4.94E-02
sperm ejaculation	4.94E-02
negative regulation of cardiac muscle contraction	4.94E-02
regulation of axon diameter	4.94E-02
regulation of anatomical structure size	1.03E-02
hemoglobin biosynthetic process	4.94E-02
hemoglobin metabolic process	9.17E-05
intracellular magnesium ion homeostasis	4.94E-02
response to cycloheximide	4.94E-02
positive regulation of cytoplasmic mRNA processing body assembly	4.94E-02
positive regulation of natural killer cell mediated cytotoxicity directed against tumor cell target	4.94E-02
regulation of natural killer cell mediated cytotoxicity	7.48E-05
regulation of natural killer cell mediated immunity	9.12E-06
regulation of defense response	3.03E-02
regulation of response to stress	9.78E-03
positive regulation of natural killer cell mediated immunity	9.05E-06

positive regulation of innate immune response	4.04E-02
positive regulation of defense response	3.91E-03
positive regulation of natural killer cell mediated cytotoxicity	8.43E-05
positive regulation of leukocyte mediated cytotoxicity	2.45E-03
commitment of neuronal cell to specific neuron type in forebrain	4.94E-02
type II pneumocyte differentiation	4.94E-02
positive regulation of leukocyte tethering or rolling	5.16E-03
regulation of leukocyte tethering or rolling	9.84E-03
regulation of leukocyte adhesion to vascular endothelial cell	2.21E-03
regulation of cellular extravasation	4.65E-02
positive regulation of leukocyte adhesion to vascular endothelial cell	1.04E-03
immunological synapse formation	5.16E-03
negative regulation of peptidyl-threonine phosphorylation	5.16E-03
regulation of peptidyl-threonine phosphorylation	2.79E-02
glomerular filtration	5.99E-04
renal filtration	9.14E-04
commissural neuron axon guidance	5.98E-03
positive regulation of fibroblast migration	5.98E-03
regulation of fibroblast migration	4.05E-02

maintenance of cell polarity	5.98E-03
stress fiber assembly	7.99E-04
contractile actin filament bundle assembly	7.99E-04
actin filament bundle assembly	1.88E-04
actin filament bundle organization	2.34E-04
actin filament organization	9.29E-03
supramolecular fiber organization	1.96E-02
sphingosine-1-phosphate receptor signaling pathway	6.87E-03
sphingolipid mediated signaling pathway	7.80E-03
negative regulation of focal adhesion assembly	7.80E-03
negative regulation of cell-matrix adhesion	3.67E-02
regulation of cell-substrate adhesion	2.51E-03
regulation of cell-matrix adhesion	3.59E-03
negative regulation of cell-substrate junction organization	7.80E-03
negative regulation of cell junction assembly	2.95E-02
B cell receptor signaling pathway	4.87E-07
antigen receptor-mediated signaling pathway	7.56E-11
immune response-activating cell surface receptor signaling pathway	3.84E-10
immune response-regulating cell surface receptor signaling pathway	3.15E-10

immune response-regulating signaling pathway	4.85E-08
immune response-activating signaling pathway	1.98E-08
activation of immune response	2.43E-07
T cell mediated cytotoxicity	8.79E-03
T cell mediated immunity	4.59E-03
acute inflammatory response to antigenic stimulus	9.84E-03
inflammatory response to antigenic stimulus	4.05E-02
regulation of glutamate secretion	9.84E-03
regulation of amino acid transport	4.86E-02
negative regulation of oxidoreductase activity	9.84E-03
complement activation, classical pathway	2.85E-04
humoral immune response mediated by circulating immunoglobulin	2.94E-05
humoral immune response	8.60E-08
immunoglobulin mediated immune response	9.54E-04
B cell mediated immunity	1.12E-03
complement activation	1.26E-03
negative regulation of anoikis	1.09E-02
regulation of anoikis	2.00E-02
positive regulation of T cell receptor signaling pathway	1.09E-02

regulation of T cell receptor signaling pathway	9.54E-03
regulation of antigen receptor-mediated signaling pathway	2.87E-03
positive regulation of antigen receptor-mediated signaling pathway	2.00E-02
response to magnesium ion	1.09E-02
fibrinolysis	1.09E-02
negative regulation of blood coagulation	5.98E-04
negative regulation of coagulation	7.61E-04
regulation of coagulation	4.25E-04
regulation of blood coagulation	2.88E-04
regulation of wound healing	1.28E-04
regulation of response to wounding	5.99E-04
regulation of hemostasis	3.29E-04
negative regulation of hemostasis	6.49E-04
negative regulation of wound healing	2.73E-03
negative regulation of response to wounding	7.59E-03
long-chain fatty-acyl-CoA biosynthetic process	1.09E-02
long-chain fatty-acyl-CoA metabolic process	1.86E-02
fatty-acyl-CoA metabolic process	4.65E-02
fatty-acyl-CoA biosynthetic process	2.30E-02

cellular defense response	6.81E-05
cell adhesion mediated by integrin	4.21E-04
cell adhesion	1.41E-07
erythrocyte development	4.61E-04
erythrocyte differentiation	2.49E-04
erythrocyte homeostasis	4.27E-04
myeloid cell homeostasis	1.34E-03
homeostasis of number of cells	8.41E-04
multicellular organismal-level homeostasis	1.19E-02
T cell costimulation	4.61E-04
lymphocyte costimulation	5.04E-04
neutrophil chemotaxis	8.98E-05
neutrophil migration	2.18E-04
granulocyte migration	1.12E-04
myeloid leukocyte migration	8.17E-04
leukocyte migration	3.73E-05
granulocyte chemotaxis	4.35E-05
leukocyte chemotaxis	1.93E-04
cell chemotaxis	4.13E-04

chemotaxis	3.03E-05
taxis	3.21E-05
locomotion	5.73E-05
nitric oxide biosynthetic process	1.45E-02
nitric oxide metabolic process	2.95E-02
reactive nitrogen species metabolic process	3.31E-02
stimulatory C-type lectin receptor signaling pathway	1.45E-02
cellular response to lectin	1.45E-02
response to lectin	1.45E-02
platelet formation	1.58E-02
platelet morphogenesis	1.86E-02
monocyte chemotaxis	1.72E-02
mononuclear cell migration	1.53E-02
platelet aggregation	7.03E-04
platelet activation	1.99E-07
homotypic cell-cell adhesion	2.32E-03
cell-cell adhesion	2.42E-04
lamellipodium assembly	3.40E-03
lamellipodium organization	5.49E-04

T cell receptor signaling pathway	5.18E-07
positive regulation of positive chemotaxis	2.00E-02
regulation of positive chemotaxis	2.15E-02
natural killer cell activation	2.18E-04
antibacterial humoral response	2.51E-04
antimicrobial humoral response	1.75E-07
defense response to bacterium	6.57E-05
response to bacterium	4.36E-09
positive regulation of interleukin-4 production	2.15E-02
regulation of interleukin-4 production	3.31E-02
defense response to protozoan	2.15E-02
response to protozoan	2.62E-02
negative regulation of miRNA transcription	2.30E-02
negative regulation of miRNA metabolic process	2.62E-02
regulation of miRNA metabolic process	3.70E-02
regulation of miRNA transcription	2.62E-02
killing of cells of another organism	5.12E-06
disruption of cell in another organism	5.12E-06
disruption of anatomical structure in another organism	6.23E-06

release of sequestered calcium ion into cytosol	1.35E-03
negative regulation of sequestering of calcium ion	1.44E-03
regulation of sequestering of calcium ion	8.50E-04
calcium ion transmembrane import into cytosol	8.49E-03
regulation of bone resorption	5.63E-03
regulation of bone remodeling	9.05E-03
regulation of tissue remodeling	2.54E-02
negative regulation of stress fiber assembly	2.46E-02
regulation of actin filament organization	2.69E-02
regulation of actin cytoskeleton organization	2.96E-03
regulation of cytoskeleton organization	1.55E-02
regulation of actin filament-based process	6.25E-03
negative regulation of actin filament bundle assembly	2.95E-02
negative regulation of cytoskeleton organization	1.09E-02
negative regulation of supramolecular fiber organization	1.20E-02
negative regulation of DNA binding	2.46E-02
focal adhesion assembly	2.46E-02
cell-matrix adhesion	1.07E-03
cell-substrate adhesion	9.54E-04

regulation of synaptic vesicle recycling	2.46E-02
cellular oxidant detoxification	1.19E-04
cellular detoxification	4.68E-04
detoxification	1.65E-03
response to toxic substance	1.38E-03
cellular response to toxic substance	7.23E-04
positive regulation of viral genome replication	2.79E-02
regulation of macrophage derived foam cell differentiation	2.79E-02
positive regulation of smooth muscle contraction	2.79E-02
integrin-mediated signaling pathway	1.43E-04
skeletal muscle fiber development	2.95E-02
myotube cell development	3.67E-02
muscle cell differentiation	3.18E-02
striated muscle cell differentiation	3.79E-02
myotube differentiation	4.05E-03
positive regulation of vasoconstriction	2.95E-02
regulation of vasoconstriction	1.96E-02
blood vessel diameter maintenance	3.96E-02
regulation of tube diameter	3.96E-02

regulation of tube size	4.04E-02
positive regulation of blood pressure	3.31E-02
actin filament capping	3.31E-02
negative regulation of actin filament depolymerization	4.05E-02
regulation of actin polymerization or depolymerization	3.88E-02
regulation of actin filament length	4.12E-02
negative regulation of protein polymerization	2.36E-02
regulation of protein polymerization	2.98E-02
regulation of actin filament polymerization	2.60E-02
negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	3.49E-02
negative regulation of extrinsic apoptotic signaling pathway	4.85E-02
negative regulation of signal transduction in absence of ligand	3.49E-02
positive regulation of T cell migration	3.49E-02
very long-chain fatty acid metabolic process	3.49E-02
positive regulation of fibroblast proliferation	1.01E-02
regulation of fibroblast proliferation	3.81E-02
Fc-gamma receptor signaling pathway	3.67E-02
Fc receptor signaling pathway	1.35E-02
positive regulation of interleukin-2 production	3.67E-02

regulation of interleukin-2 production	1.81E-02
nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	3.67E-02
astrocyte development	3.86E-02
astrocyte differentiation	1.96E-02
glial cell differentiation	3.54E-02
negative regulation of intracellular steroid hormone receptor signaling pathway	3.86E-02
positive regulation of establishment of protein localization to mitochondrion	3.86E-02
positive regulation of cell-matrix adhesion	1.17E-02
positive regulation of cell-substrate adhesion	4.27E-03
response to copper ion	4.05E-02
regulation of lamellipodium assembly	4.05E-02
positive regulation of type II interferon production	4.05E-03
regulation of type II interferon production	1.92E-02
heterotypic cell-cell adhesion	4.25E-02
maintenance of blood-brain barrier	4.25E-02
positive regulation of nitric oxide biosynthetic process	4.45E-02
positive regulation of nitric oxide metabolic process	4.65E-02
negative chemotaxis	4.45E-02
spleen development	4.45E-02

hematopoietic or lymphoid organ development	1.08E-02
positive regulation of smooth muscle cell migration	4.45E-02
regulation of smooth muscle cell migration	1.96E-02
antimicrobial humoral immune response mediated by antimicrobial peptide	5.60E-04
regulation of release of cytochrome c from mitochondria	4.65E-02
regulation of substrate adhesion-dependent cell spreading	1.54E-02
Schwann cell development	4.86E-02
positive regulation of wound healing	1.60E-02
positive regulation of response to wounding	2.54E-02
positive regulation of smooth muscle cell proliferation	5.76E-03
regulation of smooth muscle cell proliferation	2.93E-02
cellular response to lipopolysaccharide	2.69E-04
cellular response to molecule of bacterial origin	3.87E-04
response to molecule of bacterial origin	1.56E-04
cellular response to biotic stimulus	8.39E-04
response to lipopolysaccharide	9.47E-05
response to lipid	3.01E-03
cellular response to lipid	1.36E-02
cerebellum development	1.27E-02

metencephalon development	1.72E-02
hindbrain development	1.09E-02
myelination	2.36E-02
axon ensheathment	2.48E-02
ensheathment of neurons	2.48E-02
adenylate cyclase-activating G protein-coupled receptor signaling pathway	1.29E-02
adenylate cyclase-modulating G protein-coupled receptor signaling pathway	1.93E-02
positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	1.98E-02
positive regulation of inflammatory response	4.04E-02
regulation of peptidyl-tyrosine phosphorylation	4.20E-02
regulation of lymphocyte differentiation	3.98E-02
regulation of leukocyte differentiation	2.31E-02
regulation of angiogenesis	3.83E-02
regulation of vasculature development	4.16E-02
positive regulation of phosphorylation	3.03E-02
Unclassified	1.11E-02
protein transport	2.69E-02
establishment of protein localization	2.69E-02
protein localization	2.81E-03

cellular macromolecule localization	2.81E-03
macromolecule localization	5.38E-04
intracellular transport	1.40E-02
protein modification by small protein conjugation	4.81E-02
protein modification by small protein conjugation or removal	2.42E-02
post-translational protein modification	1.10E-02
protein modification process	9.73E-03
macromolecule modification	3.95E-03