

TECHNICAL CONSIDERATIONS WHEN DESIGNING A GENE EXPRESSION PANEL FOR RENAL TRANSPLANT DIAGNOSIS

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Supplemental Table S5: Nanostring Custom Codeset of 219 selected genes

Gene Identifier	Accession	Position	Target Sequence
ACTB	NM_001101.2	1011-1110	TGCAGAAGGAGATCACTGCCCTGGCACCCAGCACAATGAAGATCAAGATCATTGCTCCT CCTGAGCGCAAGTACTCCGTGTGGATCGGCGGCTCCATCCT
ADAMDEC1	NM_014479.2	907-1006	TTGACAACTTCCTGAGATGGCACAGTTCTAACCTGGGGAAAAAGATCCACGACCATGCT CAGCTTCTCAGCGGGATTAGCTTCAACAATCGACGTGTGGG
ADB15	NM_080928.3	1029-1128	AAATGGTTTTGATGTCAACACTCTACTTGCTGACCACATTTCCCAGAGCTATGACGATGA GAGGAAGACTGCGCTGTATTTTGGCGTTTCTAATAATGAC
AIM2	NM_004833.1	608-707	ACGTGCTGCACCAAAAGTCTCTCCTCATGTTAAGCCTGAACAGAAACAGATGGTGGCCC AGCAGGAATCTATCAGAGAAGGGTTTCAGAAGCGCTGTTTG
AKT1 (PKB-alpha)	NM_001014432.1	1276-1375	GGACGGGCACATTAAGATCACAGACTTCGGGCTGTGCAAGGAGGGGATCAAGGACGGT GCCACCATGAAGACCTTTTGCGGCACACCTGAGTACCTGGCC
AKT2 (PKB-beta)	NM_001626.4	700-799	AGGAGATGGAAGTGGCGGTCTAGCAAGGCACGGGCTAAAGTGACCATGAATGACTTCGA CTATCTCAAACCTCCTTGGCAAGGGAACCTTTGGCAAAGTCAT
AKT3 (PKB-gamma)	NM_005465.4	288-387	GCCAGTTAATGAAAACAGAACGACCAAAGCCAAACACATTTATAATCAGATGTCTCCAGT GGACTACTGTTATAGAGAGAACATTTTCATGTAGATACTCC
ANKRD22	NM_144590.2	58-157	ACTGGCAGAGCAAATATGACTCAGAAACCGGCTCCTCAGGGTTGTAACATTAGATGATA CAGGCTTGGGTTCGTTACACATGACACCAAGTGCCTTTGTTTC
AOAH	NM_001637.3	1304-1403	CTCTGGTGCTACAGGATTTCTGGACTCCACTGTTGGAATTAAGAAAAATCTATTTACCTT CGCTTATGGAAGAAAGAACCACTGTAATCACAGGGACTAC
AP-1/JUN	NM_002228.3	141-240	ACACAGCCAGCCAGGTCGGCAGTATAGTCCGAACTGCAAATCTTATTTTCTTTTCA CCTTCTCTCTAACTGCCAGAGCTAGCGCCTGTGGCTCCC
APOBEC3A	NM_145699.3	32-131	CAGCAGCTTCCAGGTTGCTCTGATGATATATTAAGGCTCCTGAATCCTAAGAGAATGTTG GTGAAGATCTTAACACCACGCCTTGAGCAAGTCGCAAGAG
APOL1	NM_003661.3	821-920	CCGCTTTGACCGGGATTACCAGCAGTACCATGGACTACGGAAAGAAGTGGTGGACACAA GCCAAGCCACGACCTGGTCATCAAAAGCCTTGACAAATT
APOL2	NM_030882.2	881-980	GCAACTTGACCAAAGCGGCACCAATGTAGCAAAGGTGATGAAGGAGTTTGTGGGTGG GAACACACCCAATGTTCTTACCTTAGTTGACAATTGGTACCA

BASP1	NM_006317.3	1161-1260	GATCCGCGTCTGAAAGTGCAGTACATCGTTTGTACCTGAAACTGCCGCCACATGCACTC CTCCACCGCTGAGAGTTGAATAGCTTTTCTTCTGCAATGGG
BCL2	NM_000657.2	6-105	GTGAAGCAGAAGTCTGGGAATCGATCTGGAAATCCTCCTAATTTTTACTCCCTCTCCCCG CGACTCCTGATTCAATTGGGAAGTTTCAAATCAGCTATAAC
BLNK	NM_013314.2	931-1030	ACACCACTGAAGACAACCTCCAGTTGCCTCTCAACAGAATGCTTCAAGTGTTTGTGAAGAA AAACCTATACCTGCTGAACGCCACCGAGGGTCAAGTCACA
BTK	NM_000061.1	571-670	TGATCTGGTTCAGAAATATCACCCTTGCTTCTGGATCGATGGGCAGTATCTCTGCTGCTC TCAGACAGCCAAAAATGCTATGGGCTGCCAAATTTTGGAG
BTLA	NM_181780.2	306-405	ACACTCCATCTTAGCAGGAGATCCCTTTGAACTAGAATGCCCTGTGAAATACTGTGCTAA CAGGCCTCATGTGACTTGGTGCAAGCTCAATGGAACAACA
CAV1	NM_001753.3	435-534	AACCGCGACCCTAAACACCTCAACGATGACGTGGTCAAGATTGACTTTGAAGATGTGATT GCAGAACCAAGGGACACACAGTTTTGACGGCATTGGA
CCL2	NM_002982.3	1-100	GAGGAACCGAGAGGCTGAGACTAACCCAGAAACATCCAATTCTCAAACCTGAAGCTCGCA CTCTCGCCTCCAGCATGAAAGTCTCTGCCGCCCTTCTGTGC
CCL3	NM_002983.2	682-781	CTGTGTAGGCAGTCATGGCACCAAGCCACCAGACTGACAAATGTGTATCGGATGCTTT TGTTCAAGGCTGTGATCGGCCTGGGGAATAATAAAGATGC
CCL4	NM_002984.2	202-301	GAAGCTTCCTCGCAACTTTGTGGTAGATTACTATGAGACCAGCAGCCTCTGCTCCCAGC CAGCTGTGGTATTCCAAACCAAAAGAAGCAAGCAAGTCTGT
CCL5	NM_002985.2	281-380	AGTGTGTGCCAACCCAGAGAAGAAATGGGTTTCGGGAGTACATCAACTCTTTGGAGATGA GCTAGGATGGAGAGTCCTTGAACCTGAACTTACACAAATTT
CCR5	NM_000579.1	2731-2830	TAGGAACATACTTCAGCTCACACATGAGATCTAGGTGAGGATTGATTACCTAGTAGTCAT TTCATGGGTTGTTGGGAGGATTCTATGAGGCAACCACAGG
CD160	NM_007053.3	723-822	AACAAAGACAACACCTTGAGTTCAGCCATAATGAAGGCACTCTCAGTTCAGGCTTCCTAC AAGAAAAGGTCTGGGTAATGCTGGTCACCAGCCTTGTGGC
CD25	NM_000417.1	1001-1100	CTTGGAAGAAGCCGGGAACAGACAACAGAAGTCATGAAGCCCAAGTGAAATCAAAGGT GCTAAATGGTCGCCCAGGAGACATCCGTTGTGCTTGCCTGC
CD274	NM_014143.3	50-149	AGTTCCCGAGGCTCCGCACCAGCCGCGCTTCTGTCCGCCTGCAGGGCATTCCAGAAA GATGAGGATATTTGCTGTCTTTATATTCATGACCTACTGGCA
CD28	NM_001243078.1	2066-2165	GCTGCTCCTGTACCTTGGAGGTCCATTCACATGGGAAAGTATTTTGAATGTGTCTTTTG AAGAGAGCATCAGAGTTCTTAAGGGACTGGGTAAGGCCTG
CD34	NM_001025109.1	1581-1680	AGGTAACTCCTGTCTTTACACATTCGGCTCCCTGGAGCCAGACTCTGGTCTTCTTTGG GTAAACGTGTGACGGGGGAAAGCCAAGGTCTGGAGAAGCT
CD3D	NM_000732.4	111-210	TATCTACTGGATGAGTTCCGCTGGGAGATGGAACATAGCACGTTTCTCTCTGGCCTGGT ACTGGCTACCCTTCTCTCGCAAGTGAGCCCCTTCAAGATAC
CD4	NM_000616.4	976-1075	TGGCAGGCGGAGAGGGCTTCCTCCTCCAAGTCTTGGATCACCTTTGACCTGAAGAACAA GGAAGTGTCTGTAAAACGGGTTACCCAGGACCCTAAGCTCC
CD55	NM_000574.3	1130-1229	CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAA CCTACCACAGTAAATGTTCCAACCTACAGAAGTCTACCAAC

CD59	NM_000611.4	731-830	GACTTGAAGTAGATTGCATGCTTCCTCCTTTGCTCTTGGGAAGACCAGCTTTGCAGTGAC AGCTTGAGTGGGTTCTCTGCAGCCCTCAGATTATTTTCC
CD6	NM_001254751.1	1723-1822	AACCCTGGACACTGCATTACAGACCCGCCATCCCTGGGCCCTCAGTATCACCCGAGGA GCAACAGTGAGTCGAGCACCTCTTCAGGGGAGGATTACTGCA
CD7	NM_006137.6	441-540	CCTACACCTGCCAGGCCATCACGGAGGTCAATGTCTACGGCTCCGGCACCCCTGGTCCT GGTGACAGAGGAACAGTCCCAAGGATGGCACAGATGCTCGGA
CD72	NM_001782.2	453-552	CCGCCATCTGCCTGGGAGTGCGCTATCTGCAGGTGTCTCAGCAGCTCCAGCAGACGAA CAGGGTTCTGGAAGTCACTAACAGCAGCCTGAGGCAGCAGCT
CD74	NM_001025159.1	965-1064	TTCAGCCCCCAGCCCCTCCCCATCTCCCACCCTGTACCTCATCCCATGAGACCCTGGT GCCTGGCTCTTTCGTCACCCTTGACAAAGACAAACCAAGTC
CD84	NM_001184879.1	29-128	TCTGCTAGAACAGTGCCGTGCTTTTCCACAGAAGGTTAGACCCTGAAAGAGATGGCTCA GCACCACCTATGGATCTTGCTCCTTTGCCTGCAAACCTGGC
CD86	NM_175862.3	1266-1365	CCAGCTCTGCTCCGTATGCCAAGAGGAGACTTTAATTCTCTTACTGCTTCTTTTCACTTCA GAGCACACTTATGGGCCAAGCCCAGCTTAATGGCTCATG
CD8A	NM_001768.5	1321-1420	GCTCAGGGCTCTTTCCTCCACACCATTAGGTCTTTCTTTCCGAGGCCCTGTCTCAGG GTGAGGTGCTTGAGTCTCCAACGGCAAGGGAACAAGTACTT
CD8B	NM_172099.2	440-539	TCAGCTGAGTGTGGTTGATTTCCCTCCCACCACTGCCAGCCCACCAAGAAGTCCACCC TCAAGAAGAGAGTGTGCCGTTACCCAGGCCAGAGACCCAG
CD96	NM_005816.4	429-528	TCACTTGTGACTTTCACAGAACTCCTGAGAATGGGTCAAATGGACTCTGCACTTAAGG AATATGTCTTGTTTCAGTCAGTGGAAGGTACGAGTGTATGC
CDH13	NM_001220488.1	211-310	CTCCTCAAAGCCTGGCTCCCACGGAAAATATGCTCAGTGCAGCCGCGTGCATGAATGAA AACGCCGCCGGGCGCTTCTAGTCGGACAAAATGCAGCCGAG
CDH5	NM_001795.3	3406-3505	TCTCCCCTTCTCTGCCTCACCTGGTCGCCAATCCATGCTCTCTTTCTTTTCTGTCTACT CCTTATCCCTTGTTTTAGAGGAACCCAAGATGTGGCCTT
CETP	NM_000078.2	663-762	AGAGATCAACGTCATCTCTAACATCATGGCCGATTTTGTCAGACAAGGGCTGCCAGCA TCCTTTCAGATGGAGACATTGGGGTGGACATTTCCCTGACA
CHCHD10	NM_213720.1	369-468	CTGCAGATGGGGCCCTGCGCCTACGAGATCAGGCAGTTCCTGGACTGTTCCACCACTC AGAGTGACCTGTCCCTGTGTGAGGGCTTCAGCGAGGCCCTGA
COL13A1	NM_080798.3	1658-1757	CAAGGGCTCCAAGGGGAGAACCAGGGAAAGGAGAGATGGTGGATTACAATGGAAACATC AATGAGGCTCTCCAGGAGATCCGGACGCTGGCCTTGATGGGG
COL1A1	NM_000088.3	5211-5310	CAGAAACATCGGATTTGGGGAACGCGTGTCAATCCCTTGTCGCCGAGGGCTGGGCGGG AGAGACTGTTCTGTTCTTGTGTAACGTGTTGCTGAAAGAC
COL4A3	NM_000091.4	1085-1184	CTGGAAGTGAGGGAGTCAAGGGCAACAGGGGTTCCCTGGGTAAATGGGTGAAGATGG CATTAAAGGGACAGAAAGGGGACATTGGCCCTCCAGGATTTCCG
COL4A4	NM_000092.4	761-860	TATATGGGAGTGGAAAGAAATACATTGGTCCTTGTTGGAGGAAGAGATTGCTCTGTTTGC CACTGTGTTCTGAAAAGGGGTCTCGGGGTCCACCAGGACC
COL4A5	NM_000495.4	1715-1814	GTGACACTTGCTTCAACTGCATTGGAAGTGGTATTTAGGGCCTCCAGGTCAACCTGGT TTGCCAGGTCTCCAGGTCTCCAGGATCTCTTGTTTTCCC

CPA3	NM_001870.2	221-320	ACCCACCACGTAGCTGCTAATATGATGGTGGATTTCCGAGTTAGTGAGAAGGAATCCCA AGCCATCCAGTCTGCCTTGGATCAAAATAAAATGCACTATG
CTLA-4	NM_005214.3	406-505	AGTCTGTGCGGCAACCTACATGATGGGGAATGAGTTGACCTTCCTAGATGATTCCATCT GCACGGGCACCTCCAGTGGAATCAAGTGAACCTCACTATC
CTSS	NM_004079.3	686-785	ATGACAACGGCTTTCCAGTACATCATTGATAACAAGGGCATCGACTCAGACGCTTCCTAT CCCTACAAAGCCATGGATCAGAAATGTCAATATGACTCAA
CX3CL1	NM_002996.3	1217-1316	CCCCGGAGCTGTGGTAGTAATTCATATGTCCTGGTGCCCGTGTGAACTCCTCTGGCCTG TGTCTAGTTGTTTGATTGAGACAGCTGCCTGGGATCCCTCA
CX3CR1	NM_001337.3	1041-1140	GGGCGCTCAGTCCACGTTGATTTCTCCTCATCTGAATCACAAAGGAGCAGGCATGGAAG TGTTCTGAGCAGCAATTTTACTTACCACACGAGTGATGGAG
CXCL1	NM_001511.1	743-842	TATGTTAATATTTCTGAGGAGCCTGCAACATGCCAGCCACTGTGATAGAGGCTGGCGGA TCCAAGCAAATGGCCAATGAGATCATTGTGAAGGCAGGGGA
CXCL10	NM_001565.2	462-561	GCCATAATTGTTCTTAGTTTGCAGTTACACTAAAAGGTGACCAATGATGGTCACCAAATC AGCTGCTACTACTCCTGTAGGAAGGTTAATGTTTCATCATC
CXCL11	NM_005409.4	283-382	TTCAAAAGAGGACGCTGTCTTTGCATAGGCCCTGGGGTAAAAGCAGTGAAAGTGGCAGA TATTGAGAAAGCCTCCATAATGTACCCAAGTAACAACCTGTG
CXCL13	NM_006419.2	211-310	AGACGCTTCATTGATCGAATTCAAATCTTGCCCCGTGGGAATGGTTGTCCAAGAAAAGAA ATCATAGTCTGGAAGAAGAACAAGTCAATTGTGTGTGTGG
CXCL9	NM_002416.1	1976-2075	CACCATCTCCCATGAAGAAAGGGAACGGTGAAGTACTAAGCGCTAGAGGAAGCAGCCA AGTCGGTTAGTGGAAGCATGATTGGTGCCAGTTAGCCTCTG
CXCR1	NM_000634.2	1951-2050	GCAGCCACCAGTCCATTGGGCAGGCAGATGTTCTAATAAAGCTTCTGTTCCGTGCTTG TCCCTGTGGAAGTATCTTGGTTGTGACAGAGTCAAGGGTGT
CXCR6	NM_006564.1	96-195	TTACCATGAAGACTATGGGTTTCAGCAGTTTCAATGACAGCAGCCAGGAGGAGCATCAAG ACTTCTGCAGTTCAGCAAGGTCTTTCTGCCCTGCATGTAC
CYP4F11	NM_021187.3	3201-3300	TCATAGCCTAAGGGATGTTGCATCGCTAAACCCTGTTGACTTCTCTAATCTCTTCTGTAG CTGATCTCCTTCCCTTGCTACACTCGGTTACTCTGGCCTT
DARC	NM_002036.2	961-1060	CCCTGGATGAATATCCTGTGGGCCTGGTTTATTTTCTGGTGGCCTCATGGGGTGGTTCT AGGACTGGATTTCTGTTGAGGTCCAAGCTGTTGCTGTTGT
DDX50	NM_024045.1	1186-1285	CTACTGTGGAACATTTGGCCATCCAGTGTCATTGGTCTCAGAGGCCAGCAGTTATTGGA GATGTCCTTCAAGTCTACAGTGGGTCTGAAGGGAGGGCTAT
DUSP2	NM_004418.3	1236-1335	CTGGCCCTCATTGCGGGTCGGGAACCAAGGGTGTGTCTGCTCTTCCCTCCCCATCCTC TGGCAGAAATCAGCTAGACGCTATACCGTGGACTCTCCCTG
ECSCR	NM_001077693.3	169-268	TAGCTCTCAGGGAGGCCTTGGCGGTCTAAGTCTGACCACAGAGCCAGTTTCTTCCAACC CAGGATACATCCCTTCCCTCAGAGGCTAACAGGCCAAGCCAT
EHD3	NM_014600.2	2327-2426	CATATCTTGACATTGCTCTGTAGGTGAGAGAGGACCATGACGCCCATGTTTGCAGCTGA TACTTGTGTTGGGCACACCTCCAAGTTCTCGGGATTAGAAGG
EVA1C	NM_058187.3	1155-1254	GTGAAAAAATACCTCACTGTGACCTACGCATGTGTTCCCAAGAACATACTCACAGCGATT GATCCAGCCATTGCTAATCTAAACCTTCTTTGAAGCAGA

EZH2	NM_001203247.1	1122-1221	ACACAGAAACAGCTCTAGACAACAAACCTTGTGGACCACAGTGTTACCAGCATTGAG GGAGCAAAGGAGTTTGCTGCTGCTCTCACCGCTGAGCGGAT
FAM26F	NM_001010919.1	901-1000	AGGGCCAGTACTACAGCATGTTGCACAAATATGTCAACAGAAAAGAGAAGACTCACAGT ATCAGGTCTACTGAAGGAGATACGGTGATTCTGTTCTTGG
FCGR1B	NM_001017986.3	499-598	ATTCTAACCTCACCATTTCTGAAAACCAACATAAGTCACAATGGCACCTACCATTGCTCAG GCATGGGAAAGCATCGCTACACATCAGCAGGAATATCACA
FCGR3A	NM_000569.6	1645-1744	AAATCATGAGGGTGACGTAGAATTGAGTCTTCCAGGGGACTCTATCAGAACTGGACCAT CTCCAAGTATATAACGATGAGTCCTCTTAATGCTAGGAGTA
FGD2	NM_173558.3	1120-1219	TCTAACACCCTGCTCCGTGAGGGCCCGGTCTCAAGATCTCCTTCCGCCGCAACGACC CCATGGAGCGCTACCTTTTCTTGTTCAACAACATGCTGCTCT
FGFBP2	NM_031950.3	952-1051	CTTTCTGGAGTTTGCAGAGTTCAGCAATATGATAGGGAACAGGTGCTGATGGGCCCAAG AGTGACAAGCATACACAACACTACTTATTATCTGTAGAAGTTT
FJX1	NM_014344.3	2377-2476	TCATTCCTGACCTCTTGTCATTTTGGCCTGAAGGCTACAAATTCAGGGTCAGCTGTATGC ACTAAGTCAAATAATGAATTTCTTCCTCCCTCTCGCAACC
FoxP3	NM_014009.3	1231-1330	GGGCCATCCTGGAGGCTCCAGAGAAGCAGCGGACACTCAATGAGATCTACCACTGGTT CACACGCATGTTTGCCTTCTTCAGAAACCATCCTGCCACCTG
GAPDH	NM_001256799.1	387-486	GAACGGGAAGCTTGTCAATGGAAATCCCATCACCATCTTCCAGGAGCGAGATCCCT CCAAAATCAAGTGGGGCGATGCTGGCGCTGAGTACGTCGTG
GATA3	NM_001002295.1	1692-1791	GTGCATGACTCACTGGAGGACTTCCCCAAGAACAGCTCGTTTAACCCGGCCGCCCTCTC CAGACACATGTCCTCCCTGAGCCACATCTCGCCCTTCAGCC
GBP5	NM_052942.3	1956-2055	ATTACAGACTGACCAGGCTCTCACAGAGACGGAAAAAAGAAGAAAGAGGCACAAGTGA AAGCAGAAGCTGAAAAGGCTGAAGCGCAAAGGTTGGCGGCG
GIMAP5	NM_018384.3	1277-1376	ATCTCTGGACCCTGGAGCACTTCTAATGTATCACCCCATGGAGTCATTGTTCTAATAATC ACCAATTCAAGACTCAGATCCTCGTGGTCTATGGAGCATGC
GNG11	NM_004126.3	431-530	GAAAATGCCTGCCCTTCACATCGAAGATTTGCCAGAGAAGGAAAAACTGAAAATGGAAG TTGAGCAGCTTCGCAAAGAAGTGAAGTTGCAGAGACAACAA
GNLY	NM_012483.2	881-980	TGCCGGCTCCTCGCTTCCTCGATCCAGAATCCACTCTCCAGTCTCCCTCCCCTGACTCC CTCTGCTGTCCTCCCCTCTCACGAGAATAAAGTGTCAGCA
GUSB	NM_000181.3	1900-1999	CCGATTTTCATGACTGAACAGTCACCGACGAGAGTGCTGGGGAATAAAAAGGGGATCTTC ACTCGGCAGAGACAACCAAAAAGTGCAGCGTTCCTTTTGCG
GZMB	NM_004131.3	541-640	ACACTACAAGAGGTGAAGATGACAGTGCAGGAAGATCGAAAGTGCGAATCTGACTTACG CCATTATTACGACAGTACCATTGAGTTGTGCGTGGGGGACC
HAVCR1	NM_001099414.1	969-1068	GGGAATGACACCGTGACAGAGTCTTCAGATGGCCTTTGGAATAACAATCAAACCTCAACT GTTCTAGAACATAGTCTACTGACGGCCAATACCACTAAAG
HDAC3	NM_003883.3	353-452	TGTTTCCCGGGGCTCTTTGAGTTCTGCTCGCGTTACACAGGCGCATCTCTGCAAGGAGCA ACCCAGCTGAACAACAAGATCTGTGATATTGCCATTAACTG
HPRT1	NM_000194.1	241-340	TGTGATGAAGGAGATGGGAGGCCATCACATTGTAGCCCTCTGTGTGCTCAAGGGGGGC TATAAATTCCTTGCTGACCTGCTGGATTACATCAAAGCACTG

ICAM1	NM_000201.2	2254-2353	AAATACTGAAACTTGCTGCCTATTGGGTATGCTGAGGCCCCACAGACTTACAGAAGAAG TGGCCCTCCATAGACATGTGTAGCATCAAAACACAAAGGCC
ICAM2	NM_000873.3	416-515	ACCTCTCTAGATAAGATTCTGCTGGACGAACAGGCTCAGTGGAACATTACTTGGTCTCA AACATCTCCCATGACACGGTCTCCAATGCCACTTCACCT
ICOS	NM_012092.2	641-740	AACTCTGGCACCCAGGCATGAAGCACGTTGGCCAGTTTTCTCAACTTGAAGTGCAAGA TTCTCTTATTTCCGGGACCACGGAGAGTCTGACTTAACTAC
IDO1	NM_002164.3	51-150	CTATTATAAGATGCTCTGAAAACCTCTTCAGACACTGAGGGGCACCAGAGGAGCAGACTA CAAGAATGGCACACGCTATGGAAAACCTCCTGGACAATCAGT
IFI27	NM_005532.3	391-490	TCACTGGGAGCAACTGGACTCTCCGGATTGACCAAGTTCATCCTGGGCTCCATTGGGTC TGCCATTGCGGCTGTCATTGCGAGGTTCTACTAGCTCCCTG
IFI30	NM_006332.3	386-485	CAGGAACAAAATGTCAGTGGCAGGTGGGAGTTCAAGTGCCAGCATGGAGAAGAGGAGT GCAAATTCAACAAGGTGGAGGCCTGCGTGTTGGATGAACTTG
IFNG	NM_000619.2	971-1070	ATACTATCCAGTTACTGCCGGTTTGAAAATATGCCTGCAATCTGAGCCAGTGCTTTAATG GCATGTCAGACAGAACTTGAATGTGTCAGGTGACCCTGAT
IKZF3	NM_183232.2	1177-1276	ATGTGTATCGGTGTGACCACTGCCGCGTCTCTTCTGGACTATGTGATGTTACGATTCC ACATGGGCTGCCACGGCTTCCGTGACCCTTTCGAGTGTA
IL-1b	NM_000576.2	841-940	GGGACCAAAGGCGGCCAGGATATAACTGACTTCACCATGCAATTTGTGTCTTCCTAAAG AGAGCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAA
IL-6	NM_000600.3	365-464	GGCACTGGCAGAAAACAACCTGAACCTTCCAAAGATGGCTGAAAAAGATGGATGCTTCC AATCTGGATTCAATGAGGAGACTTGCTGTGTAATAATCATC
IL12RB1	NM_005535.1	977-1076	AAGATGCCCTATCTCTCGGGTGCTGCCTACAACGTGGCTGTCATCTCCTCGAACCAATTT GGTCCTGGCCTGAACCAGACGTGGCACATTCTGCGGACA
IL18BP	NM_001039659.1	1046-1145	CACAGCCTCCTTATAATGCCTCCTCCTGCCATTCTCTCTCCACCTATCCATTAGCCT TCCTAACGTCCTACTCCTCACACTGCTCTACTGCTCAGAA
IL1RL1	NM_016232.4	701-800	CCTCTTGAGTGGTTTAAGAATTGTCAGGCTCTTCAAGGATCAAGGTACAGGGCGCACAA GTCATTTTTGGTCATTGATAATGTGATGACTGAGGACGCAG
IL21R	NM_181078.1	2730-2829	GGGCCACTCGGGGGGGTTTCCAGGCTTAAATCAGTCCGTTTTCGTCTCTTGAAACAGC TCCCCACCAACCAAGATTTCTTTTTCTAACTTCTGCTACTA
IL23A	NM_016584.2	412-511	CAGGGACAACAGTCAGTTCTGCTTGCAAAGGATCCACCAGGGTCTGATTTTTTATGAGAA GCTGCTAGGATCGGATATTTTACAGGGGAGCCTTCTCTG
IL8	NM_000584.2	26-125	ACAGCAGAGCACACAAGCTTCTAGGACAAGAGCCAGGAAGAAACCACCGGAAGGAACC ATCTCACTGTGTGTAAACATGACTTCCAAGCTGGCCGTGGCT
IMD52 (LAT)	NM_001014987.1	1291-1390	TGTGTAATAGAATAAAGGCCTGCGTGTGTCTGTGTTGAGCGTGCGTCTGTGTGTGCCTG TGTGCGAGTCTGAGTCAGAGATTTGGAGATGTCTCTGTGTG
INPP5D	NM_005541.3	4076-4175	ATAATGGCCACATGGATCGAACACTCATGATGTGCCAAGTGCTGTGCTAAGTGCTTTAC GAACATTGTCATATCAGGATGACCTCGAGAGCTGAGGCTC
ITGB6	NM_000888.3	1091-1190	AACATTCTCCAGCTGATCATCTCAGCTTATGAAGAACTGCGGTCTGAGGTGGAAGTGA AGTATTAGGAGACACTGAAGGACTCAACTTGTCATTTACAG

KAAG1	NM_181337.3	19-118	AACATGCAGGGGGTGGGAGCAGGGTCACAAAAGTGAGTGTGTCAATTCTACTTGGAAT GAAAGGTTGAAATAATTTAAACAGTACGGGAAATGCAGAGC
KLF4	NM_004235.4	1981-2080	CGAGCATTTTCCAGGTCGGACCACCTCGCCTTACACATGAAGAGGCATTTTTAAATCCCA GACAGTGGATATGACCCACACTGCCAGAAGAGAATTCAGT
KLH13	NM_001168303.1	421-520	TCTCATCCCATTTGCAGTCTTCCAAGGCAGGACCTACACGCATCTTTACCAGCAATACCC ACAGTTCTGTGGTGTTACAGGGCTTTGACCAGCTTCGACT
KLRF1	NM_016523.2	102-201	AGTCAAAGAAAAGGAGTTCTGCCCAAACATCTCAACTTACATTTAAAGATTATTCAGTGAC GTTGCACTGGTATAAAATCTTACTGGAATATCTGGAAC
LAG3	NM_002286.5	1736-1835	CTTTTGGTGACTGGAGCCTTTGGCTTTACCTTTGGAGAAGACAGTGGCGACCAAGACG ATTTTCTGCCTTAGAGCAAGGGATTACCCCTCCGCAGGCTC
LAIR1	NM_002287.3	1196-1295	GCACCTGAGGGTAGAAAGTCACTCTAGGAAAAGCCTGAAGCAGCCATTTGGAAGGCTTC CTGTTGGATTCTCTTCATCTAGAAAGCCAGCCAGGCAGCT
LAP3	NM_015907.2	451-550	GTGCTAGTTGGCCTCGGCAAAAAGGCAGCTGGAATCGACGAACAGGAAAACCTGGCATG AAGGCAAAGAAAACATCAGAGCTGCTGTTGCAGCGGGGTGCA
LCN2	NM_005564.3	326-425	AATGTCACCTCCGTCCTGTTTAGGAAAAAGAAGTGTGACTACTGGATCAGGACTTTTGT CCAGGTTGCCAGCCCGGCGAGTTCACGCTGGGCAACATTA
LCP2	NM_005565.3	1828-1927	ATGAACCGTCCTCCTGCCTCTGTTGCCAACACGAGATCAATCAGCCTTGGTCAATGGAC AAACACTTAGGACTGAACTGAACCCCTCCCATGAACACAA
LDHA	NM_001165414.1	1691-1790	AACTTCCTGGCTCCTTCACTGAACATGCCTAGTCCAACATTTTTTCCAGTGAGTCACAT CCTGGGATCCAGTGTATAAATCCAATATCATGTCTTGTGC
LTF	NM_002343.2	591-690	TTCCCCAACCTGTGTGCGCTGTGTGCGGGGACAGGGGAAAACAAATGTGCCTTCTCCTC CCAGGAACCGTACTTCAGCTACTCTGGTGCCTTCAAGTGTC
MALL	NM_005434.3	606-705	ACAAGTACATGCCACGATTGTTTCTGAGAACTGCTGGACCCAAGAATTTACTACATTAA TTCGGCAGCCTCGTTCTTCGCTTCATCGCCACGCTGCTC
MAPK1 (ERK)	NM_138957.2	431-530	ACTGCCAGAGAACCCTGAGGGAGATAAAAATCTTACTGCGCTTCAGACATGAGAACATC ATTGGAATCAATGACATTATTCGAGCACCAACCATCGAGCA
MAPK11 (p38 b)	NM_002751.6	419-518	CACCCTGATGGGCGCCGACCTGAACAACATCGTCAAGTGCCAGGCGCTGAGCGACGAG CACGTTCAATTCTGGTTTACCAGCTGCTGCGCGGGCTGAAG
MAPK12 / ERK6 (p38-g)	NM_002969.3	426-525	TATTCACCTCTGATGAGACCCTGGATGACTTCACGGACTTTTACCTGGTGATGCCGTTCA TGGGCACCGACCTGGGCAAGCTCATGAAACATGAGAAGCT
MAPK13 /SAPK4 (p38-s)	NM_002754.3	1051-1150	CGGAGGCCAGCAGCCGTTTGATGATTCTTAGAACACGAGAACTCACAGTGGATGAA TGGAAGCAGCATCTACAAGGAGATTGTGAACTTCAGCCC
MAPK14 (p38-a)	NM_001315.2	793-892	GGTGACCCATCTCATGGGGGCAGATCTGAACAACATTGTGAAATGTCAGAAGCTTACAG ATGACCATGTTTCAGTTCTTATCTACCAAATTCTCCGAGGT
MAPK8 (JNK)	NM_002750.2	946-1045	TCTCTGTAGATGAAGCTCTCCAACACCCGTACATCAATGTCTGGTATGATCCTTCTGAAG CAGAAGCTCCACCACCAAAGATCCCTGACAAGCAGTTAGA

MEGF11	NM_032445.2	5096-5195	ACCTCAGTATTTTCAGGGCAGCAAGTGTTTGTGAAGCAAGGATGAGCAGCATGAAGATGT CAGATCAGCAAGGAGAACTTCAACTCAATCCCAGGTTTTTC
MEOX1	NM_001040002.1	1711-1810	TCCTCCATGGGATGGATTTAAGCTCTTGCTGTGTGTTCTACAAATGCTGTTATTGTGGGA GGAAATGCTAGGTTTTTGTGTGTGGACTGCCCAGACCTCA
MET	NM_001127500.1	1926-2025	GGCTGACCATATGTGGCTGGGACTTTGGATTTCTGGAGGAATAATAAATTTGATTTAAAGA AAACTAGAGTTCTCCTTGAAATGAGAGCTGCACCTTGAC
MMRN1	NM_007351.2	3271-3370	GCAGACATCCTTTTACTGGTGACAACTGCACTATCAAGCTTGTGGAAGAAAATGCTTTAG CTCCAGATTTTTTCCAAAGGATCTTACAGATATGCACCCAT
MS4A6A	NM_152852.2	147-246	GAACAGACTTGCCTAACAAACAGGAACTTGTATGTCTCGAAGTGGAATTCACACATAAG GCTCCATGACTCCTGAACTCTCACAAATATTAGTTGGCTC
MS4A7	NM_206939.1	717-816	TCACTGTGCTGGAGCTCTTATTAGCTGCATACAGTTCTGTCTTTTGGTGGAACAGCTCT ACTCCAACAACCCTGGGAGTTCATTTTCTCGACCCAGTC
MYB	NM_001130173.1	184-283	CCGCGCCCGCCGCGCCATGGCCCGAAGACCCCGGCACAGCATATATAGCAGTGACGA GGATGATGAGGACTTTGAGATGTGTGACCATGACTATGATGGG
MYBL1	NM_001080416.3	1031-1130	TTCAACACAAACCTTGTGCAGCTATGGATCATATGCAAACCCAGAATCAGTTTTACATAC CTGTTTCAGATCCCTGGGTATCAGTATGTGTACCTGAAGG
NAFTC1	NM_172389.1	1985-2084	CGAATTCTCTGGTGGTTGAGATCCCGCCATTTCTGGAATCAGAGGATAACCAGCCCCGTT CACGTCAGTTTCTACGTCTGCAACGGGAAGAGAAAGCGAAG
NAFTC2	NM_012340.3	1816-1915	GACGGACATTGGAAGAAAGAACACGCGGGTGAGACTGGTTTTCCGAGTTCACATCCCAG AGTCCAGTGGCAGAATCGTCTCTTTACAGACTGCATCTAAC
NAFTC3	NM_004555.2	2191-2290	GTCCTTGAAGTTCCTCCATATCATAACCCAGCAGTTACAGCTGCAGTGCAGGTGCACTTT TATCTTTGCAATGGCAAGAGGAAAAAAGCCAGTCTCAAC
NF-kb 1	NM_003998.2	1676-1775	AGGGTATAGCTTCCCACACTATGGATTTCTACTTATGGTGGGATTACTTTCCATCCTGG AACTACTAAATCTAATGCTGGGATGAAGCATGGAACCATG
NF-kb 1A	NM_020529.1	946-1045	GGATGAGGAGAGCTATGACACAGAGTCAGAGTTCACGGAGTTCACAGAGGACGAGCTG CCCTATGATGACTGTGTGTTTGGAGGCCAGCGTCTGACGTTA
NF-kb 2	NM_001077493.1	1062-1161	TGTGTTCCGGACACCCCCCTATCACAAGATGAAGATTGAGCGGCCTGTAACAGTGTTTC TGCAACTGAAACGCAAGCGAGGAGGGGACGTGTCTGATTCC
NFKBIZ	NM_001005474.1	2031-2130	ATTTGGTTCCCGATGGCCCTGTGGGAGAACAGATCCGACGTATCCTGAAGGGAAAGTCC ATTCAGCAGAGAGCTCCACCGTATTAGCTCCATTAGCTTGG
NKG7	NM_005601.3	633-732	CTGTGGCGGTCCCCGTCTGGCTATGAAACCTTGTGAGCAGAAGGCAAGAGCGGCAAG ATGAGTTTTGAGCGTTGTATTCCAAAGGCCTCATCTGGAGCC
NLRP3	NM_001079821.2	416-515	AGTGGGGTTTCAGATAATGCACGTGTTTCGAATCCCACTGTGATATGCCAGGAAGACAGC ATTGAAGAGGAGTGGATGGGTTTACTGGAGTACCTTTTCGAG
NNMT	NM_006169.2	606-705	GTTCTAAAAGAAGGGCTGAACTGATGGAAGGAATGCTGTTAGCCTGAGACTCAGGAAGA CAACTTCTGCAGGGTCACTCCCTGGCTTCTGGAGGAAAGAG
NPHS1	NM_004646.3	4051-4150	CCAGAGTAGAAACAAGGTGCATCCTGGGGTTGGCTTTAGAACTAACTTCTCCAAAAG GACAGGGCAGATTGTAAACGTCGTCTCAAAAATGAAATGCT

NPHS2	NM_014625.2	1181-1280	CCTTCCAAACCTGTTGAGCCACTAAATCCTAAAAAGAAAGACTCTCCCATGTTATAGGAA GGATGGGGCATAATGTGACTGTAAAGGGGCCTGCCATAGA
OAZ1	NM_004152.2	314-413	GGTGGGCGAGGGAATAGTCAGAGGGATCACAATCTTTCAGCTAACTTATTCTACTCCGA TGATCGGCTGAATGTAACAGAGGAACAACTGTCACGACA
OSMR	NM_003999.2	711-810	CCCTTTGGAATGTGCCACACACTTTGTAAGAATAAAGAGTTTGGTGGACGATGCCAAGTT CCCTGAGCCAAATTTCTGGAGCAACTGGAGTTCTCTGGGAG
P2RX7	NM_002562.5	781-880	ACATCACTTGTACCTTCCACAAGACTCAGAATCCACAGTGTCCCATTTTCCGACTAGGAG ACATCTTCCGAGAAACAGGCGATAATTTTTTCAGATGTGGC
PALMD	NM_017734.4	261-360	GATCTGTGCATCTGCTCGGAGACGCTCCTGACAAGTCGGGAATTTCTCTATTTCTCCACT GGTGCAAAGAGCGGATTTCTCCCTGCTTCTCTTCTGTAC
PDGFB	NM_033016.2	1481-1580	GATTCACCTCTTCTCTGTTTCTTTTCTCTCTACCTCCACCCTGCATTTTCTCTTGT CCTGGCCCTTCAGTCTGCTCCACCAAGGGGCTCTTGAAC
PECAM1	NM_000442.3	1366-1465	ATCTGCACTGCAGGTATTGACAAAAGTGGTCAAGAAAAGCAACACAGTCCAGATAGTCGT ATGTGAAATGCTCTCCCAGCCCAGGATTTCTTATGATGCC
PGM5	XM_024447573.1	264-363	GGCAGCTCGGGCGGTCTGGCAGCGGAGAAGGTGGGTGGGAGAAAACTTTACAGGAAG GCAGAAGCAATCTCTGCCGAGAGAGTCAGCCGAGCGGCCGCGC
PHEX	NM_000444.5	1695-1794	TTAGCAGGCGCTTTTCAATATAGATGGCTGGAATTCTCAAGGGTAATCCAGGGGACCACA ACTTTGCTGCCTCAATGGGACAAATGTGTAACTTTATTGA
(PI3K) gamma	NM_002649.2	2126-2225	AAAACATACCAATTGTTGGCCAGAAGGGAAGTCTGGGATCAAAGTGCTTTGGATGTTGG GTTAACAATGCAGCTCCTGGACTGCAACTTCTCAGATGAAA
Phospholipase A2 G2A	NM_000300.2	716-815	TTCCCTGGAAACCTTCCACCCAGTGCTGAATTTCCCTCTCTCATACCCTCCCTCCCTACC CTAACCAAGTTCCTTGGCCATGCAGAAAGCATCCCTCACC
PKC (D form)	NM_006254.3	2166-2265	ACCATAAACTGGACTCTGCTGGAAAAGCGGAGGTTGGAGCCACCTTTCAGGCCCAAAGT GAAGTCACCCAGAGACTACAGTAACTTTGACCAGGAGTTCC
PLA1A	NM_015900.2	1251-1350	CAACCGAGTTTGGAAAAAAGACCGGACTACCATTATTGGGAAGTTCTGCACTGCCCTTTT GCCTGTCAATGACAGAGAAAAGATGGTCTGCTTACCTGAA
PLAT	NM_000931.2	1335-1434	CAAGGTTACCAACTACCTAGACTGGATTCTGTGACAACATGCGACCGTGACCAGGAACAC CCGACTCCTCAAAGCAAATGAGATCCCGCCTCTTCTTCTT
PLCG2	NM_002661.2	526-625	GCTTGAAAATCTTACACCAGGAAGCGATGAATGCGTCCACGCCACCATTATCGAGAGT TGGCTGAGAAAGCAGATATATTCTGTGGATCAAACCAGAAG
POLR2A	NM_000937.2	3776-3875	TTCCAAGAAGCCAAAGACTCCTTCGCTTACTGTCTTCTGTTGGGCCAGTCCGCTCGAG ATGCTGAGAGAGCCAAGGATATTCTGTGCCGTCTGGAGCAT
PSMB10	NM_002801.2	222-321	ACCATCGCGGGCCTGGTGTTCGAAGACGGGGTCATTCTGGGCGCCGATACGCGAGCCA CTAACGATTTCGGTCGTGGCGGACAAGAGCTGCGAGAAGATCC
PSMB9	NM_002800.4	456-555	TCAGGTATATGGAACCCTGGGAGGAATGCTGACTCGACAGCCTTTTGCCATTGGTGGCT CCGGCAGCACCTTTATCTATGGTTATGTGGATGCAGCATAT
PSME2	NM_002818.2	316-415	AGAAGAAAGAAGTCCATAAGTGTGGATTTCTCCCTGGGAATGAGAAAGTCCTGTCCCTG CTTGCCCTGTTAAGCCAGAAGTCTGGACTCTCAAAGAGAA

PSTPIP1	NM_001321135.1	849-948	GGCCGTCATGGACCGGGTCCAGAAGAGCAAGCTGTCGCTCTACAAGAAGGCCATGGAG TCCAAGAAGACATACGAGCAGAAGTGCCGGGACGCGGACGAC
PTPN7	NM_001199797.1	589-688	CCTGGACATCCCTGGCCACGCCTCCAAGGACCGATAACAAGACCATCTTGCCAAATCCCC AGAGCCGTGTCTGTCTAGGCCGGGCACAGAGCCAGGAGGAC
RAMP3	NM_005856.2	834-933	TTTCTATGCTGTTTCTTAGCACAGAATCCAGCCTAGCCTTAGCCGCAGTCTAGGCCCTGC TTGGACTAGGACTCCTTGCTTGACCCCATCTCTGGTTCCT
RAPGEF5	NM_012294.3	3421-3520	GCATTTTGCGTACCTCATACAGGCTCCTTGCCACACTATGGAATGACAGCAGCCAGTG CAGGGAGGTTAAGTGACATTTAATGAGTGAAGCACTTAGCA
RARRES1	NM_206963.1	607-706	ATAATCATGGACATATTGATCCCTCTCTGAGACTCATCTGGGATTTGGCTTTCCTTGGA GCTCTTACGTGATGTGGGAAATGACAACACAGGTGTCACA
RARRES3	NM_004585.3	641-740	CTGACCCTCGTGCCCTGTCTCAGGCGTTCTCTAGATCCTTTCCTCTGTTTCCCTCTCTCG CTGGCAAAAGTATGATCTAATTGAAACAAGACTGAAGGAT
RASIP1	NM_017805.2	2469-2568	ACCAGCCAGTGCGAGCTGCACCCTGACCTCGTGTCTCAGACTTTTGGCTACTTGTTCTT CTTCTCCAACGCATCCCTTCTCAACTCGCTGATGGAACGAG
RHOJ	NM_020663.4	231-330	GGGTTTCTTAACCTCACACTGAGAGCGGAAAGGGGGCAGACCCTTTTCATAACTCCCTCAA GTGTGTGTTACCTTTCTTTACCAGCATGGTAAGCAACAGGA
RNF149	NM_173647.3	687-786	GTTGGCACCCGGCATGTACAGGAGTTCATCAGCGGTGAGTCTGTGGTGTGTTGTGGCCAT TGCCTTCATCACCATGATGATTATCTCGTTAGCCTGGCTAA
ROBO4	NM_019055.5	3081-3180	CCTGACTCTCAGATCTCTTCCCAGAGAAGTCAGCTCCACTGTCGATGCCCAAGGCTGG TGCTTCTCCTGTAGATTACTCCTGAACCGTGTCCCTGAGAC
RORgamma	NM_001001523.1	1351-1450	CTCATCAATGCCCATCGGCCAGGGCTCCAAGAGAAAAGGAAAGTAGAACAGCTGCAGTA CAATCTGGAGCTGGCCTTTCATCATCATCTCTGCAAGACTC
RPS6	NM_001010.2	172-271	GAATGGAAGGGTTATGTGGTCCGAATCAGTGGTGGGAACGACAAACAAGGTTTCCCCAT GAAGCAGGGTGTCTTGACCCATGGCCGTGTCCGCTGCTAC
RPS6KB1	NM_003161.2	311-410	GAGAAATTTGAAATCTCAGAACTAGTGTGAACAGAGGGGCCAGAAAAAATCAGACCAGA ATGTTTTGAGCTACTTCGGGTACTTGGTAAAGGGGGCTATG
RXRA	NM_002957.4	5051-5150	TACAAATGTAATTTTATCCCTCATGTATACTTGATATGGCGGGGGGAGGGCTGGGACT GTTTCGTTTCTGCTTCTAGAGATTGAGGTGAAAGCTTCGTC
S1PR1	NM_001400.3	1066-1165	CCTGACGTTCCGCAAGAACATTTCCAAGGCCAGCCGCAGCTCTGAGAAGTCGCTGGCG CTGCTCAAGACCGTAATTATCGTCCTGAGCGTCTTCATCGCC
S1PR5	NM_030760.3	1416-1515	TGCCCTCGTGGAATTGACGTTCTGCTTGGAACACAGAAAAGAACTCGGTGATGAAATA ATGGAGATGATTCCAGTGACAAACGACAGAGATGGTGATGG
SDHA	NM_004168.1	231-330	TGGAGGGGGCAGGCTTGCGAGCTGCATTTGGCCTTTCTGAGGCAGGGTTTAATACAGCAT GTGTTACCAAGCTGTTTCTTACCAGGTACACACTGTTGCA
SELE	NM_000450.2	1506-1605	AATTCACCTACAAGTCCTCTTGTGCCTTCAGCTGTGAGGAGGGATTTGAATTACATGGAT CAACTCAACTTGAGTGCACATCTCAGGGACAATGGACAGA
SERINC5	NM_001174071.2	527-626	CACAATGGCTTTTGGTTCTTTAACTTCTGCTGTTGGGGGCCATGTGCTCAGGAGCTTTC TTCATTCCAGATCAGGACACCTTTCTGAACGCCTGGCGCT

SH2D1A	NM_002351.4	496-595	GCTGTATCACGGTTACATTTATACATACCGAGTGTCCCAGACAGAAACAGGTTCTTGGAGTGCTGAGACAGCACCTGGGGTACATAAAAGATATTTCCGG
SH2D1B	NM_053282.4	546-645	GTTGAAGAGATGAGTAACAGTTCTCACTGATGACCCACTTCTGCAGGCATAGGTCCAGAGCACCAAACCTAGTGGACAATTCAGACTCTCCTGGTTGTG
SHROOM3	NM_020859.3	4705-4804	AGGATGTGCTTTTGGGGCAAGACAGTGGCTTTGGTCTTGTGAAGGATCCATGTTATTTGGCTGGTCTGGATCTAGGTCACTCAGTTGTTTCAGAAAGAGG
SIRPG	NM_001039508.1	132-231	CTTACAGAAGTGGCAGGTGAGGAGGAGCTACAGATGATTCAGCCTGAGAAGCTCCTGTTGGTCACAGTTGGAAAGACAGCCACTCTGCACTGCACTGTGA
SLA	NM_001045556.2	981-1080	GTGTGATTTCTGATGAAGGGGGCTGGTGGAAAGCTATTTCTCTTAGCACTGGTCGAGAGAGTTACATCCCTGGAATATGTGTGGCCAGAGTTTACCATGG
SLAMF8	NM_020125.2	697-796	AGCTGGCGACGGGAGACAACCATGGACTTTGGTATGGAACCACACAGCCTCTTCACAGACGGACAGGTGCTGAGCATTTCCCTGGGACCAGGAGACAGAG
SOD2	NM_000636.2	202-301	TTTGGGGTATCTGGGCTCCAGGCAGAAGCACAGCCTCCCCGACCTGCCCTACGACTACGGCGCCCTGGAACCTCACATCAACGCGCAGATCATGCAGCTG
SOST	NM_025237.2	981-1080	GAGGCAGAAATGGAAGCATTTTCACCGCCCTGGGGTTTTAAGGGAGCGGTGTGGGAGTGGGAAAGTCCAGGGACTGGTTAAGAAAGTTGGATAAGATTCC
SOX7	NM_031439.2	2636-2735	CTGTGAGAATTTGTCTTCCTCACCAGCCAGGTCCTCAGGCAAAGTCCTCAGCCAGTGCTTTAGAGCAACTTCCCGCAAATCAGAACTCACTGTGATTCC
SP140	NM_001005176.2	246-345	GGTTCTTCAGAGAAAACAAGGTGGAGATTGCAAGTGCAATAACAAGGCCATTTCTTTCCTTATGGGCCTCCGAGACCGCTCCTTCATCTCCGAGCAGAT
SPLI	NM_003064.2	331-430	TTTCTGTGAGATGGATGGCCAGTGCAAGCGTGACTTGAAGTGTTGCATGGGCATGTGTGGAAATCCTGCGTTTTCCCTGTGAAAGCTTGATTCTCTGCCA
SPRY4	NM_030964.3	1901-2000	CTCCCTTCCAACCTGCATCAACTAACTCTCGGGGGTGTTCTGCTCACCACACCGTCCTTCGGTTCTTACTGAGTCACAGACTCGCCTGCCCACTACGTGTC
ST5	NM_005418.3	2619-2718	TTTTGCTTCCCTGATGCCAAGGACTGGCTTCTGTGTCAGAGTATAGCAGTGAGACCTTTCTTTTCATGCTGACTGGGGAAGATGGCAGCAGACGCTTTG
ST8SIA4	NM_005668.4	696-795	ATCTACATAGCCTCCTACCTGAAGTTTCACCAATGAAGAATCGCAGGTTTAAGACCTGTGCAGTTGTTGGAAATTCTGGCATTCTGTTAGACAGTGAATG
TAP1	NM_000593.5	2076-2175	GTGGCTGCAGTGGGACAAGAGCCACAGGTATTTGGAAGAAGTCTTCAAGAAAATATTGCTATGGCCTGACCCAGAAGCCAACCTATGGAGGAAATCACAG
TBX21	NM_013351.1	891-990	ACACAGGAGCGCACTGGATGCGCCAGGAAGTTTCATTTGGGAAACTAAAGCTCACAAACAACAAGGGGGCGTCCAACAATGTGACCCAGATGATTGTGCT
TEK	NM_000459.3	1895-1994	CCCGTTAATCACTATGAGGCTTGGCAACATATTCAAGTGACAAATGAGATTGTTACACTCAACTATTTGGAACCTCGGACAGAATATGAACTCTGTGTGC
TGIF1	NM_170695.2	1261-1360	CCGGGATCAGTTTTGGCTCGTCCATCAGTGATCTGCCATACCACTGTGACTGCATTGAAGATGTCCCTTTCTCTCTCTGCCAGTCGGTCGGTGTGGGAC
THBD	NM_000361.2	1247-1346	GTGGAGCCCGTGGACCCGTGCTTCAGAGCCAACCTGCGAGTACCAGTGCCAGCCCCTGAACCAAAGTACCTCTGCGTCTGCGCCGAGGGCTTCGCGC

TIGIT	NM_173799.2	1969-2068	TGGATCTTAGAAGACTTTTATCCTTCCACCATCTCTCTCAGAGGAATGAGCGGGGAGGTT GGATTTACTGGTGACTGATTTTCTTTTCATGGGCCAAGGAA
TM4SF1	NM_014220.2	96-195	AATCGCAGTATTTAAGAGGTAGCAGGAATGGGCTGAGAGTGGTGTTTGCTTTCTCCACC AGAAGGGCACACTTTCATCTAATTTGGGGTATCACTGAGCT
TM4SF18	NM_138786.3	2414-2513	CCCCAGAGTCATGGGCAGCCTATTGTCTTGCTAATGGCCTCTGACTTAGCCTGGAGTAA AACACTGTCCAAACAAGACTGGTGTTTATTCAAGCATAAGA
TNF	NM_000594.2	1011-1110	AGCAACAAGACCACCACTTCGAAACCTGGGATTCAAGGAATGTGTGGCCTGCACAGTGAA GTGCTGGCAACCACTAAGAATTCAAACCTGGGGCCTCCAGAA
TNFSF8	NM_001244.3	400-499	CAGCTATTTCTATTTGACCACAGCCACTCTGGCTCTGTGCCTTGCTTCACGGTGGCCAC TATTATGGTGTTGGTCGTTTCAGAGGACGGACTCCATTCCC
TOX2	NM_001098798.1	785-884	GAAGCCTGTGTGCGCCTACGCACTCTTCTTCAGAGACACTCAGGCCGCCATCAAGGGTC AGAACCCCAGTGCCACTTTCGGTGACGTGTCCAAAATCGTG
TRD	M21624.1	786-885	AGCAACCTTCAAAGAGCTGCCATAAACCCAAAGCCATAGTTCATACCGAGAAGGTGAAC ATGATGTCCCTCACAGTGCTTGGGCTACGAATGCTGTTTGC
TRDV3	ENST0000053588 0.1	288-387	GGATAACAGCAGATCAGAAGGTGCAGATTTTACTCAAGGACGGTTTTCTGTGAAACACAT TCTGACCCAGAAAGCCTTTCCTTGGTGATCTCTCCAGTA
TRIB1	NM_025195.2	3461-3560	CTCGACTGTTGTATCTGTGATACATTATCCGACTAAGGACTCTGGGCTGGCAGGGCCTT CTGCCGGGAAAGCTAGAAACACTAGGTTCTTCTGTACATA
UBB	NM_018955.2	796-895	CACCTGGTCCTGCGCCTGAGGGGTGGCTGTTAATTCTTCAGTCATGGCATTTCGCAGTGC CCAGTGATGGCATTACTCTGCACTATAGCCATTTGCCCAA
VAV1	NM_005428.2	765-864	CCCTGCAACGGTTCCTGAAACCTCAAGACATTGAGATCATCTTTATCAACATTGAGGACC TGCTTCGTGTTCACTACTCACTTCCTAAAGGAGATGAAGGA
VAV2	NM_001134398.1	1616-1715	CACAGTTTCCAGATGTACACGTTTGACAAGACCACCAACTGCAAAGCCTGCAAAATGTTT CTCAGGGGCACCTTCTACCAGGGATACATGTGTACCAAGT
VAV3	NM_001079874.1	353-452	GCAGTCAAGCCTTGCCCATGTGTGCCCAAACCAAGTAGATTATTCTTGCCAACCCTGGTAT GCTGGAGCAATGGAAAGATTGCAAGCAGAGACCGAACTTA
VCAN	NM_004385.3	9916-10015	GCAGGGTGCCCATCTCACAAGCATCCTGTCTCACGAAGAACAATGTTTGTTAATCGTGT GGGCCATGATTATCAGTGGATAGGCCTCAATGACAAGATG
VMP1	NM_030938.3	931-1030	GATGATGAAGAGTATCAGGAATTTGAAGAGATGCTGGAACATGCAGAGTCTGCACAAGA CTTTGCCTCCCGGGGCCAAACTGGCAGTTCAAAAAGTAGTAC
VWF	NM_000552.3	8116-8215	CACCTGCAACCCCTGCCCCCTGGGTACAAGGAAGAAAATAACACAGGTGAATGTTGTG GGAGATGTTTGCCTACGGCTTGCAACATTACGCTAAGAGGA
WNT9A	NM_003395.1	556-655	TCCTGGGCAGACGGTCAAGCAAGGATCTGCGAGCCCGTGTGGACTTCCACAACAACCT CGTGGGTGTGAAGGTGATCAAGGCTGGGGTGGAGACCACCTG