

CDR_SBD_Mouse (627 genes)

Customer Iden	Accession	Position	Target Sequence
Abcb1a	NM_011076.1	2601-2700	AAGGGGCTACAGGGTCTAGGCTTGCTGTGATTTCCAGAACATAGCAATCTTGGGACAGGAATCATATATCCCTAATCTATGGCTGGCAACTAACACT
Abcf1	NM_013854.1	876-975	GAGGTGTCTTCCCGCCAGGCAATGTTAGAAAAATGCATCTGACATTAGTTGGAAAAGTTACAGCATCTCCGCCACGGCAAGGAGCTATTTCGTCATATGCTG
Acan	NM_007424.2	4861-4960	CAGAACCTTTGGTGAATCTATAACTCAGGCTCCTACTGCTCAAGAAGCTGGAGAAGGACCTTCGGGCATTTTGAATTTCAGTGGTGCCCACTTCGGGACA
Aco2	NM_080633.2	768-867	GGTTGGACCTCACCAAATGATGTGATCCTGAAAAGTGGCAGGTATCCTCACGGTGAAGAGTGGCACAGGTGCTATTGTGGAATACCACGGACCCGGTGTGCG
Acp5	NM_001102405.1	441-540	AACATCCCCTGGTATGTGCTGGCTGAAAACCATGATCACCTTGGCAACGCTCTGACACAGATTGCATACTAAGATCTCCAAGCGCTGGAACCTCCCCA
Acta1	NM_001272041.1	172-271	CTGAAACTAGACACCATGTGCGACGAGACGAGACCCTGCTTGTGTGTGACAACGGCTCTGGCCTGGTAAAAGCTGGCTTGGCCGGGGATGATGCC
Asma	NM_007392.2	46-145	GGAAACCTGAGACGCTGCTCCAGCTATGTGTAAGAGGAAGACAGCACAGCCCTGGTGTGCGACAATGGCTCTGGGCTCTGTAAGGCCGGCTTCGCTGGT
Bact	NM_007393.3	72-171	AGTTCCGCAATGGATGACGATATCGCTGCGCTGCTGTCGACAACGGCTCCGGCATGTGCAAAGCCGGCTTCGCGGGCAGCATGCTCCCGGGCTGTATT
Actn3	NM_013456.2	353-452	TTCCACAAAAATCGCCAATGTCAATAAAGCCCTAGACTTCATTGCGACAAAGGAGTTAAGCTAGTGTCCATCGTGCTGAAAGAAATTTGACGGGAACC
Acvr1	NM_007394.3	2256-2355	TCTGGGCATTAAGACAGTGGCTCTCTGCGTATCTTTGCGGGTCTCCTAGACACTCCCCACGGGAAGCTCAAGGAGGCGGTGAATTTCGTAATCAGCAATA
Acvr2b	NM_007397.2	771-870	CTTCCCACTTCAGGACAAGCAGTCGTGGCAGAGTGAACGGGAAATCTTCAGCACACCCGGCATGAAGCACGAAAACCTTGTTCAGTTCATTGCTGCCGAG
Admts5	NM_011782.2	2721-2820	CCCACCAATGGTAAATCTTTTCGCATGAGCAGTGTGAAGCAAATAAGGCTATCAGTCTGATGCAAAGGAGTCAAACATTTGTAGAATGGGTTCCC
Adcy10	NM_173029.3	3947-4046	AAAATGACTTCAGATCATCAAGGCTTACCTGGACTTTCCCTGTACCACCTCGCTGGCTACCAGGCGTGTGGTTCAAATATGAAATACTGGTCAAT
Adipoq	NM_009605.4	781-880	GACCAACATGGACTCTATGAGATAACGTCACGACTCTACATTTACTGGCTTCTTCTCTACCATGATACCAACTGACTGCAACTACCCATAGCCATA
Adnp2	NM_175028.1	1867-1966	CCAGCCGGTGAGAGCTGGAACGTCACAAAACACTACTTTCTTACTTACGGCTCTATTCTCAGACAGCTCATTCTACTGGGAAACAGGTGAATGGAATC
Adora1	NM_001008533.3	1604-1703	AAGTGTGAGTTGAGAAAGTTATCAGCATGAGTACATGGTCTACTTCAACTTCTCGTCTGGTGTGCTCCGCCATTGCTCCTCATGTGTTCTATCTACC
Adora2a	NM_009630.2	2307-2406	ACTATGAAAGGCGGGTGCCAGAGTGTGGGCTCACGCTCAGGATTGAGTTAGAGACATCAAGTCAATGACCCCGAGCTGGATAGTTCAGAGCTGCCCTG
Adora2b	NM_007413.4	1095-1194	CTACTCTCAGTCTGGCTTATGACCTAGGCTCTGGCCTTTGGAGAAGGAGGCTTAAATAAAACAATGGGACTAGACACAACCTGCGCATCCACTGTG
Adora3	NM_009631.4	574-673	GGTACACCTTTGGCATTGCTGTGAGCCTGCAAGTCAAGATGCACTTCTATGCTGCTTTTTCATGCTGTGCTGTGCTGATCTTACCCATGCTTCC
Adrb2	NM_007420.2	681-780	GATTGTATCTGGCCTTACTCCTTTTTGCTATCCAGATGCACTGTGACCGTGCCACCACAAGAAAGCTATCGATTGTTACACCGAGGAGACTTGCTGT
Ager	NM_007425.2	362-461	CAACTACCGAGTCCGAGTCTACAGATTCTGGGAAGCCAGAAATTTGGATCCTGCTGAACTCACAGCCAGTGTCCCTAATAAGGTGGGGACATGT
Agrn	NM_021604.3	7156-7255	TAGAGCAAATACTGACTGAACTGAAGCATCCATCTGCTTCTCATTCCCTGTCTTTAAGTCCAGCACATTGGGAGACAACTAAGCAAATCTGGGATG
Akt1	NM_001165894.1	899-998	GCCATGAAGATCTCAAGAAAGGAGTCACTCGCCAAAGGATGAGTGTGCCACAGCTTACTGAGAACCCGTCTCTGCGAACTGAGGACTCCGATCCCTCC
Akt2	NM_001110208.1	2505-2604	CCGCTCGGCCCTTTGGATGGCTCCGTTCTGCTGCTGGGCGAGGGAAGCCAACCTTGGCTGTACACATCTCACACCAAGACAGTATTGGGCCCTTG
Alcam	NM_009655.1	2606-2705	ATTTATCTTAAACCAAGTGGGGAGGTGACCAAGCAGATTGGCGATACCCTGCTGTGTCATGCACAATATCTGCAAGTAGGAACCGGACTGTGGTGTG
Alox12	NM_007440.4	1231-1330	CTCCTCGTTCCACATCCGTTACTACTATGAAATTAACACGCGAAGCCGGACCCAGCTCATCTCAGATGGAGGAATATTTGATCAGGTAGTGAGCACAG
Alox15	NM_009660.3	816-915	CAGCTGGATGAGGAGCTCAAGAAAGGCACTGTTTGAAGCGGATTTCTCCTCTGGATGGATCAAGGCCAATGTCATCTTTGTAGTCAGAGTACC
Alox5	NM_009662.2	1976-2075	TTGAGCCAGTTTCAAGAAAATGAGCTGTTTCTAGGCATGTACCCAGAGAGCATTTTATTGAGAAGCCAGTGAAGGAAGCCATGATCCGATTCCGCAAGA
Alpl	NM_007431.3	1456-1555	ACGGACAAGAACCCCTTCCGGCCATCTATATGGTAACGGCCCTGGCTACAAGTGGTGGACGGTGAACGGGAAAATGTCTCATGGTAGATTACGCTC
Ank1	NR_102385.2	2985-3084	TCCAAGGATCCCTTGTGTACACCTGAGACCGTTGTGATCCGATCTGAAGATCAGGAACAAGCATCTAAAGAATATGATGAGGATTCCCTCATTCCAG
Anpep	NM_008486.2	1716-1815	ATCATGGACCGCTGGATTCTACAGATGGGCTTCCCGTTACTCTGTGAACACCAATACAGGAGAATCTCCAGAAACACTTCTCCTGGATTCCAAGT
Anxa3	NM_013470.2	1230-1329	CGCTCAAATCTCTGCACACTGCTTTCATGCAGCACTCTAAAGTGCAAAGCAAGTGAAGACAGAACCTGTCTGCTGATAGGCATTGGCATCGTTCAAGT
Anxa5	NM_009673.2	1596-1695	CCTTAGCGGTGAAATTGTGAACCTTTGAAATGCTGTCAATCAAGCTTACTGCTTAGCAGACCTGCAAAATATGATGGTAGTATCCAAAACATTGGCG
App	NM_007471.2	512-611	GTGAGCGACGCCCTTCTGTGCCGACAAGTGCAAGTCTCACCCAGGAGCGGATGATGTTGTGAGACCATCTTCACTGGCACACCGTCGCCAAAG
Ar	NM_013476.3	2216-2315	CATGGGTTGGCGGTCTTCACTAATGTCAACTCCAGGATGCTCTACTTTGACCTGACTTGGTTTTCAATGAGTACCCGATGCACAAGTCTCGGATGTAC
Ascl2	NM_008554.2	346-445	GCCTGAGGCCCGTGAAGGTGCAACGTCACCTTCCACCGCACCCGGTTCCTCGGAGCACTTTCTGTGCCGACCCAGAACTCGTAGCAGGGGCCAG
Atf4	NM_009716.2	813-912	CAAGGAGATGCTCCTTTCCGGACAGATTGGATGTTGGAGAAGATGGATGCAAGAGTTTGACTTCGATGCTGTGTTTGAAGTGGTGTGACTGGAAACC
Atg7	NM_028835.1	856-955	TGCAGGGAGCTAGAGACGTGACACATAGCATCATCTTTGAAGTGAACCTTCCAGAAATGGCATTAGCCAGATTGCTCAAAGCTGTTGGCTGGGAGAA
Fsp1	NM_178628.5	1511-1610	GAGGTTTGTGGTGTGATAAACCATTTTTGGCCCTAACGACCTGCAAGCAAGCACCTGCAGCTAAAGAAAGAAATCTGTGAAGTTATCCGAGCGGTGA
Atp2a1	NM_007504.2	381-480	GGTTTGAGGAAGGCGAAGAAACCGTCACTGCCTTTGTGGAACCTTTGTCACTTCTTGTATCCTCATTGCCAACGCCATTGTGGGGTTTGGCAGGAACG
Atp5a1	NM_007505.2	1761-1860	GGGCTTATCTTGACAACTGGAGCCAGCAAGTACACAAGTTTGAGAATGCTTCTGTCTCAGTTATCAGCCAGCACCATCCCTTTGGGCAATAT
Atp5b	NM_016774.3	1306-1405	AGGACTACAAATCTCCAGGACATCTTCCGATCTTGGGTTGGATGAACTTCTGAGGAAGATAAATTGACTGTGCCGGGCAAGAAAGATACAGCG
Atp5c1	NM_020615.4	53-152	TGAGCTCCCGCGACGCGCACTGAGTCCCGTCTGCCGACCTTCAAGGCTCCACCATTTCTCGCGGCGAGCGTTGTGCGGCTGTGCGCCTGCGCGTG
Atp5d	NM_025313.2	77-176	CTCCTGAAGGCCGCTCGCTTGCACAGTGTGTCGCGCCGCGAAGCTAGAGTCCACTGACTTTCCGCCACCATGTTGCCCGCTCACTGCTTCTG
Atp5e	NM_025983.3	187-286	AAGACCGAGTTCAAAGCGAACGCTGAGAAGACTTCCGGCAGCAGCATAAAAATTTGAAAGTCTGAAAGAAAGGAGTAGCTGAATCTGAAGCCTGAAGTGC
Atp5g1	NM_007506.6	378-477	CATCTCAAGCAGCAGCTCTTCTCCTATGCAATCTGGGTTGGCTTCTGAGGCGGACTTCTGTGTTGATGGTGCCTTCTCACTCTTCTT
Atp5g3	NM_175015.2	173-272	ATATAGACCAATTTCTGCATCAGTGTATCTCGGCCAGAGACTAGGACTGGAGAGGGCTCTACAGTTTTAATGGGGCCAGAATGGTGTGTGTCAGCTG
Atp5h	NM_027862.1	179-278	AAACCACCTGCGATTGACTGGGCTTACTACAGGGCAATGTGGCAAGCCTGGCTTGTGGATGATTTGAAAAGAAAGTATAATGCCCTGAAGATTCTG
Atp5j	NM_016755.2	356-455	GAGGATCTTCAGGCTCTCTGTCTTCCGTCAGCAGTCTGTGCTATTTGAAGAGGAACATTGGTGTACAGCTGTGGCCTTAAATGAAGAACTTGAT
Atp5j2	NM_020582.2	10-109	GGGGTGTGTCGCCCTTCCAGCAGCTTTGCGCGCGCTGGAGTCTGCGGACACCAGGACTTCAAGATGGCGTCACTGTGCCGTGAAGGAGAAGAA

Atp5k	NM_007507.3	227-326	AGCTCAAGATGACAGCATTCTCAAGTGAGGCGTCAGCGAGCTTGCTTTTCTAGTCGTTGAGAACGAATAAAGCTTCATTGTGTGATGCTGAAAAAA
Atp5o	NM_138597.2	517-616	CCTCTAGATGACGCTGTTCTCTGAGTTAAAGACGCTGCTGAAGAGCTTCTGAGTCCAAACCAAACTGAAACTGGAGATCAAGACTGACCCGTCAA
Atp5f1	NM_009725.3	705-804	CTGAATATGGAGGAAAAGTGCCTCTGGGCTGATTCTGAGGAATTTTCCAGTTCCTTACCTAAGACTGGTGAACAGACCTTATGTGCTTGGAAAC
Atp6v0d2	NM_175406.2	631-730	TCCTACCTTGAGGCATTCTACAAATTCTGCAAGATCACGCTGATGTACACAGCAGACGTTATGTGCCATTCTTGAGTTTGAGGCCGACAGACGCGCTT
Atp6v1g1	NM_024173.1	196-295	AGGCCAAAGAAGAAGCCAGGCTGAAATGAACATACCCGCTGAGAGGGAGAAGGAGTTCAAGGCCAAGGAAGCTGCGGCATTGGCTCCCATGCGCAG
Atp6v1h	XM_006495434.2	1297-1396	TGGAAAACCTGGTGAGAGTGTCCAGGACTTAGCTCATTGTGAAATACAGTTCAGAACTTAAATCTGGAAGATTGGAATGGACCCCTGTACCAAGTC
Atxn1l	NM_001080930.1	3091-3190	GAGAGAGAGAGAGAAGCCCTTGGGTTTGAATAAGGACTGCTTGCAGGAACCCAGTCGGGACTGTGGAGAAAAGATTTGACTGATAGATGTTGG
Axin2	NM_015732.4	1121-1220	ACCGCGAGTGTGAGATCCAGGAAACAGCTGAAAACGGATTGAGTCTTCAAGAGAAGCGACCCAGTCAATCTTATCACGTAGTTCGGCTATGTCT
B2m	NM_009735.3	178-277	CTGAACCTGCTACGTAACACAGTCCACCCCGCTCACATTGAAATCCAAATGCTGAAGAACCGGAAAAAAATCCTAAAGTAGAGATGCAGATATGTCT
Bcl2	NM_009741.3	1845-1944	GGCCTTCTTGAGTTGGTGGGTCATGTGTGTGGAGAGCGTCAACAGGGAGATGTCAACCCTGGTGGACAACATCGCCCTGTGGATGACTGAGTACCTG
Bdnf	NM_007540.4	3261-3360	AGTCCCCTGTACTTTACCCTTGGGGTTAGAAGTCAAGTTGGAAGCCTGAATGAATGGACCCAATGAGAAGTGTAAAGCCCATTTCCCTAGTCAG
Bglap	NM_007541.3	119-218	CCAAGCCCAGCGCCCTGAGTCTGACAAAGCCTTATGTCCAAGCAGGAGGGCAATAAGGTAGTGAACAGACTCCGGCGCTACCTTGGAGCCTCAGTCCC
Bmp1	NM_009755.2	1712-1811	GATGACATCAAAAGCACATCCAGTCGGCTCTGCTCAAGTTCGCTCTGACGGGTCCTTAAACAAAGCTGGCTTCGCAGTCAACTTTTCAAAGAGGTGG
Bmp2	NM_007553.2	886-985	GAGGATTAGCAGGCTTTTGCACCAAGATGAACACAGCTGGTACAGATAAAGGCCATTGTAGTGACTTTTGACATGATGGAAAAGGACATCCGCTCCAC
Bmp3	NM_173404.2	1656-1755	AGTAGGAACAAAAGAACAGAGGAAAGGGTCCCATCAGAAGGGACAGACGCTGCAATTTGATGAGCAGACCTGAAGAAGGCAAGGCGAAAGCAGTGGG
Bmp4	NM_007554.2	1501-1600	AGACCTAGTCAACTCTGTTAATCTAGTATCCCTAAGGCTGTGTGTCCTCAAGCTGAACCTGAGTGCATTTCCATGTTGACTGGATGAGTATGACAA
Bmp5	NM_007555.3	166-265	CACTAAGACCATAAAAAGATGTTCAAGTTACTAGGCTGCCGACAAATCTAATCCAACCAAGGTGCAGATCAGCGTAGATCTGTGATTGACAGC
Bmp6	NM_007556.2	2266-2365	TCAGCAGGCTCTGTGGAGGTCCCTCTGCTACTGTGTAGTTACGTGTTTTGTGTTGACTCTCGGTGGTGTGAGAATGTACTAATCTCTGCAAGACAA
Bmp7	NM_007557.2	691-790	GGTTTGTCTTCCAAGATCCCCGAGGGCGAAGCGGTGACCCGAGCGAATTCAGGATCTATAAGGACTACATCCGGGAGCGATTTGACAAACGAGACCTT
Bmp8a	NM_001256019.1	2085-2184	GACTGATCCTTGGCCATCTCAGCCCAATGGCAAATTCGGATCTGAAAGCTCAAGAGCTGGAATTCAAAGTAGATGATCTGGGCTCTCGCACCTT
Bmpr1a	NM_009758.4	1791-1890	CCAGTGACCCATCTATGAGGACATGCGTGTGGTGTGTGTAAGCTGCTGCGGCCAATCGTGTCTAACCCCTGGAACAGCGAATGTGACTTCCGAGC
Bmpr1b	NM_007560.3	2751-2850	AGGAGCAGCAGATACATGGCTTGTCTTCTATGTGCATAAGAACCATCACAGCAGCCAGGAAAGAAGTGTGCACGGCACAGTTTGTATAGATATGTA
Bmpr2	NM_007561.3	506-605	TTGATAGTCGCTTATGTTTTGGATACAGAATGTTGACAGGAGACCGGAAACAGGGTCTTACAGCATGAACATGATGGAGGCGGAGCAGCAGAGCCCT
Bnip2	NM_001008238.3	1077-1176	TCAAAGTTCAGTCAGAAGATCAGATACGCTTTAACTTGGCCGAGCTGGCAGAGCTTTCCTTCCATGGAGTATGTCCGATACCAGAGTGCATCAAAACAAG
Bsg	NM_009768.2	971-1070	AGCACTGAAGCCAATGGCAAGTATGGTGGTATCCAGCTGAGAACTGAGAACTGACCCATGACCAACTGACGCAACTTGGAGTAAATGTTACCTGTCACAGC
Calca	NM_007587.2	222-321	CTCCAGGCAGTGCCTTTGAGGTCAATCTTGAAGCAGCCAGGCATGGCCACTCTCAGTGAAGAAGAAGTTCGCTGCTGGCTGCACTGGTGCAGGACT
Calcr	NM_001042725.1	806-905	CCTGGCTCTTGTGGGTCACTCCTTGTGATTGCTGCTTGGTTGCTTCCATGCTGATCTTCTGGATTTTCAAGAACCTTAGCTGCCAGAGGGTGACCTTG
Camk2g	NM_001039138.1	2526-2625	TTCTCTTGGTTTTCTGACATAACAAGGAGAGATCCAGAAGTCTGTTGGCCAGGGCTCCTTTTGCACCTTTTGGCAGTGTGTTGTGCTGATCTGGACC
Capn2	NM_009794.3	2125-2224	TTGGTCCGCTGGAAACGCTATTCAAGATATTCAGCAGCTAGACCCCTGAGAACAACGAAACGATACAGCTCAACCTTGGCTTCTGCTGGCTGAGTTTTTCAG
Capn3	NM_001109761.1	2081-2180	TTCATCTGCTCTTCGTCAGGCTGGGAAGGATGTTACAGACTTTTAAACGCAATTTGACAAGGATGGCGATGGTATCATCAAACTGAATGTACTGAGTGGC
Car1	NM_001083957.1	445-544	CTGGAATCTGCAAAGTACTCCAGTCTTCTGAAGCCATCTCAAAGGCTGATGGCTGGCAATCCTTGGCGTTTTGATGAAGTTGGTCCAGCCAACCCA
Car2	NM_009801.4	1175-1274	TAGGCTGGGTGATTTGATGCCGACTCGCATCTGGTATTGTAGACCTTTTACTCTCATCCGTTGTGCTTACTAACAAAATGTGAAAAGCAAGACCCAGG
Car3	NM_007606.3	226-325	GACCTGCAGAGTTGTGTTGATGATACTTATGACAGGTTCTATGCTGAGGGGTGTGCTCTCTGACCCCTACCGACTTCGCCAATTCATCTTCACTGG
Casp3	NM_009810.2	631-730	GAGGCTGACTTCTGTATGCTTACTACAGCACCTGTTACTATTTCTGGAGAAATTCAAAGGACGGGTGCTGGTTCATCCAGTCCCTTGGCAGCATGC
Casr	NM_013803.3	1517-1616	GAATTCCTACAGAAAGTCCATCCAGGAAGTCTGCCAATGTTTTGCCAAAGAGTTTTTGGGAAGAAACATTTAATGGCCACTGCAAGACGGCGCAA
Casr_var	NM_013803.3	2347-2446	GACTGAGCCCTTTGGAATCGCTCTCACTCTCTTTCGCGTGTGGGCATTTTCTGACCGCTTTGTGCTGGGCGTCTTCATCAAGTTCGAAACACGCCCC
Cast	NM_009817.1	1821-1920	ATTTCTGAAGTAGTTTCTCAGACACCTGCTCCAAGCACCCATGCAGCAGTCCACTGCTGCACTGAGCAGAAAAGACAAGAACTTATGATGCTGCTTGG
Cav1	NM_007616.3	1921-2020	AACCAAACTGAGGAATTTCACTGTGTACCTGAGTCTCCAGAAAGTGCCTGCTGGACACCCAAAAGCCTTTTACTTCCCAGCTCACATTACAGCTC
Cav3	NM_007617.3	1009-1108	CCTTAAGAGGCAGCTAGCGCAAGGCTTGGCTTCCAGTACTGTAATAGCCAGTCTTCTAGAGGTGTGACTCGTCTCCTCATGCTAGGGGGGAGCAAGCA
Ccl2	NM_011333.3	416-515	TCTTCAGCACCTTGAATGTGAAGTTGACCCGTAATCTGAAGCTAATGCATCCACTACCTTTTCCACAACCACCTCAAGCACTTCTGTAGGAGTGACCA
Ccl3	NM_011337.1	61-160	TCTGTCACTGCTCAACATCATGAAGTCTCCACCCTGCTTGGCTGCTTCTCTGTACCATGACACTCTGCAACCAAGTCTTCTCAGCGCCATATGG
Ccl5	NM_013653.1	166-265	CCTCGTGCCACGTCGAAGGATTTTCTACACCAGCAGCAAGTGTCCAATCTTGCAGTGTGTTGCTCACTGGAAGGAACCCCAAGTGTGTGCCAAC
Ccl7	NM_013654.3	142-241	CAACCAGATGGGCCAATGCATCCATGCTGTATGTCAGAAACAAAAGATCCCAAGAGGAATCTCAAGAGCTACAGAAGGATCACCAGTAGTCGGT
Ccl8	NM_021443.2	151-250	ACCTGCTCTTTCATGTTAAAGCTGAAGATCCCTTCCGCTGCTGAAAAGCTACAGAGAAATCAACAATATCCAGTGCCCCATGAAAGCTGTGGTTTT
Cyr61	NM_010516.1	805-904	CTTCTGTCTTTGGACCGAACCGGAGTCTTTTCAACCCTCTGCACGCCATGGCCAGAAATGCATCGTTCAGACCACGTTCTGCTCCAGTGTCTCCA
CD274	NM_021893.2	516-615	TGAACTAATATGTACGCGCGAGGTTATCCAGAAGCTGAGGTAATCTGACAAAACAGTGACCAACCCGTGAGTGGGAAGAGAAGGTCCACACTTCC
Cd34	NM_001111059.1	561-660	CTGATTATTCCGCTAATAATAGCAGCTTTGAGATGACATCACCCACCGGCAATATGCTTACACATCATCTTCTGCTCCGAGTGCCATTAAGGGAGAAT
Cd36	NM_007643.3	1521-1620	GGGACCATTTGGTATGAAAAAGCAGAAATGTCAAACACAAGTACTGGGAAAATCAAGCTCCTTGGCATGTAGAGATGGCTTACTTGGGATTTGGAG
Cd40	NM_011611.2	1426-1525	GCTGCCAAAACCCGTTACTGATTTTGCATCTTCCCTTCCGCTGCTGAAAAGCTACAGAGAAATCCAGAGGTTGTCAATTTGACCTTCCATGTGGCTC
Cdh11	NM_009866.4	1516-1615	TTGAAACAAAAGAGCTTATAGCTTGAAGATAGAGCCGCAATGTTACATTGATCCGAAGTTCATCAGCAATGGACCTTCAAGGACACTGTGACCGT
Cdh15	NM_007662.2	1415-1514	GAGTGTGAGCCCTGCTTACCCTTTTTGAAGGACGGCTGTACAGACCATCATCTAGCCCTGACAAATGCCATCTCTAGCACAGCCACAGGCAC
Cdh2	NM_007664.4	2862-2961	TGATCCTTGTCTCATGTTTGTGGTATGGATGAAACGGCGGGATAAAGAGCGCCAAGCCAAGCAGCTTTAATTGACCCAGAAGATGATGTAAGAGATAA
P21/Cdkn1a	NM_007669.4	1671-1770	AATACCGTGGGTGCAAAGCACTAGTGGGTGACTCCAGCCCCAACATCCCTGTTCTGTAACATCCTGGTCTGGAAGTCTACCTTAGCCCCGAC

P16/Cdkn2a	NM_001040654.1	567-666	CCAAATCCCAAGAGCAGAGCTAAATCCGGCCTCAGCCCGCCTTTTCTTCTAGCTTCACTTCTAGCGATGCTAGCGTGTCTAGCATGTGGCTTTAAAAA
Chr	NM_009893.2	583-682	CGAGTCTCTTTCTGCGCTCAAGTTTACGCTTCTGTCTCTACCAGCGGCTGACCGTCCCAGCAGGGTTCGTTTACAGATCCCACAGGCAACATCC
Chst11/C4st	NM_021439.2	2895-2994	GGTTGACATTTGAGCCACATCCCATGACAGCCAGTGTCCGGGTACGTAGCAGATGCTGTACATAGTTCTGATGATAAGGGAGCTGGTAGGCTGTAAATT
Cln7	NM_011930.3	1206-1305	GTCTTCATCGCCATGGGTGTGGTGGGTGGCATTCTGGAGCTGTGTTCAATGCCTGAATTAAGTCTGCTAACCCATGTTTCGAATCAGGTACATCCACCGGC
Cnr2	NM_009924.3	2651-2750	TCCCAAGACAAGTCTGTGCATCAAAGCTGCTGCAAATTAATCGCTGTTGGGAGGATCAGGGGAAAGTGCATTGCCACGCTTAGTGATTTAG
Col10a1	NM_009925.4	733-172	GAAAAATGCTGCCTCAAATCCCTTCTGCTGCTAAATGTTCTGACCCGTTGTTACCTGGATGTTTTATGCTGAACGGTACCAACGCCACAGCAATAA
Col14a1	NM_181277.4	1341-1440	CTACAGAGCTGATCACTTCTGAAGTCACTGCCAGGAGCTTTATGTTAACTGGACTCAGTCCCAGGAAAAGTGGAAAAATACAGAGTTGTGTATTATCC
Col15a1	NM_009928.3	859-958	TGCTCTTTTCTGACTGTGAGGAACAGAGCCAAGTCCGTTCCAGCGATGCTGCTGGCCTTTGACCTTTGAGCCCAGTCCGGGATCTTTGTGGCAAT
Col1a1	NM_007742.3	134-233	TCTTAGGGGCCACTGCGCTCTGACGCATGGCCAAGAAGACATCCCTGAAGTCACTGATACACAATGGCTAAGGGTCCCAATGGTGAGACGTGGAA
Col2a1	NM_031163.3	3917-4016	GAGAGAAGGGCCCGACCCCATGCAGTACATGCGGGCCGACGAGGCGAGCAGTACCTTGAGACAGCAGCAGTGGAGGTGGACGCTACACTCAAGTCACT
Comp	NM_016685.2	2234-2333	ACCGTTGCAATGATACAATCCCTGAGACTACGAGAGTCAACCGCTGCGAGAGTCTAGGGACCAGTGGGGTCCCGCTGCCTGATGGACTGTGGTGGCAC
Comt	NM_007744.3	626-725	AAAGGCCAAATCATGGATGCACTGATTGCGGAGTACAGGCCCTCGTGGTGTGGAGCTAGGAGCTTATTGTGGTACTCAGCCGTGCGAATGGCCCGCC
Cox10	NM_178379.3	717-816	TTTTTGAGGTGCGGTTGCGACTCAAACATGAATGAAACAAGAAGCAGGCCTCTGGTTGAGGCGAGATAAGCCATTGTAGCCGTGCTTTTCCACCTG
Cox15	NM_144874.4	579-678	CTTGCAATACCTCTGCTGCTACTTTTGGAGAAAGGGTTGGCTCAACCGTGGCATGAAAGGACGTGTTCTCGCCCTCTGTGGCTTAGTCTGTTTTCC
Cox4i1	NM_009941.2	71-170	TTGGCTTCCAGAGCGCTGAGCCTGATTGGCAAGAGAGCCATTACTTCCGTTGCTTCCGAGCAGTGGGAGTGTGTAAGAGTGAAGACTATGCTT
Cox4i2	NM_053091.2	381-480	TCTTCTTCTTATTGGATTACGGCTCTGCTGATTTGGTGGCAGCGAGTCTATGTGTTCCCTAAGAAGTTGTACCCCTGACGGAAGACGGAAGCCCA
Cox5a	NM_007747.2	283-382	GCCTGGGAATTGCGTAAAGGGATGAATACACTTGTGGCTATGATCTGGTCTGAGCCAAAATCATTGATGCTGCATTGCGAGCATGTAGACGGTTAA
Cox5b	NM_009942.2	333-432	ATCTAGTCCGTCATCAGCAACAGAGAAATAGTGGCTGCATCTGTAAGAGGACAACCTGTACTGTATCTGGTTTTGGCTGCACAAGGGCGAGAGTCA
Cox6a2	NM_009943.2	468-567	GGTGTGGAAGTTTTGTCTCTGCTCTTTGGGAACAGCATGTTGGAAGGCTGGGCGAGGCTCTTGGGCGAGTTGGTATCTGGGTTCCAGTTATTTTTT
Cox6b1	NM_025628.3	349-448	CTCTCTGTTCTTTGCTTTTCCCGGATGAAAAGGGGACCTCAGCATGATGGTCTTACCCTGGACCCCTGAATCATGATGCTCAACTACTAAT
Cox6c	NM_053071.2	2-101	CGCTTGAATACTTTTGGACTCTTAGGCCACCGTCCGCGGTTCCCTCAGACTCTTGGCATTGCGTGTGCTGCGAAGGCTCCGTTTTCCGAGAAC
Cox7a1	NM_009944.3	98-197	CTTTTAGCTCATCTACCAGAAGCCACTTAGAAAACCGTGTGGCAGAGAAGCAGAAGCTCTCCAGGCCACAATGACCTCCAGTACACTTGAAGGCGG
Cox7a2	NM_009945.3	420-519	TGGCTGATTTCCCAAGAAGCAGAACAATGTCGTATCCAGTCTTCAAGTGGTTCAAGTTTCAACAGCTCGATGACCAGGAATCTGATGAGTAACT
Cox7b	NM_025379.2	691-790	AGCTGTTTTAGGAGCCACTGGGTCAATGGCCATATAGGTTATGTTACTGCCTTCACTCGTGGTTATATTTGGAATTGCCATTAGCTCCCTCTGCT
Creb1	NM_001037726.1	2735-2834	TTCTGCTGGACAGTCCACAGATTCCAGAGGCTTTCAAAGGCTTAAAGTTTATGCTTTTCTGCTGAGCTGTGGGAAGGAGTACAGCAATAAAG
Crtap	NM_019922.2	623-722	TCTCTGAAGCATCCAGATGACGAGATGATGAAGAGAAACATGGAGTATTATAAGAGCTTGCCTGGAGCCGAGGACCACATTAAGACTTGGAAACCAAG
Cs	NM_026444.3	1915-2014	GATGCCAGCTGTGTCCAACTAGGGCCTTTCCCAATGTACACAACACCTCTACCTAGCAAGATCTCTTGGTTAGCTGGAGACGCTTTGGCACTTTT
Csf1	NM_001113530.1	834-933	TCCAGCTGCTGGAGAAGATCAAGAACTCTTAAATGAAACAAAGAATCTCCTTGAAGGACTGGAACATTTTTACCAAGAAGCTCAACAACAGCTTTGC
C-Fms	NM_001037859.2	1893-1992	GTACAAGCAGAAGCGAAGTACCAGTGCCTGGAAGATCATCGAGAGATACGAAGGCAATAGCTACACCTTATTGACCTACTCAGTTGCCCTACAAT
Csf2	NM_009969.4	733-832	CTGAATCCAGCTTCTCAGACTGCTGCTTTGTGCTCGTAATGAGCCAGGAACCTTGGAAATTTCTGCTTAAAGGGACCAAGAGATGTGGCACAGCCACA
Csf3	NM_009971.1	831-930	TTGTTCTCTGCTTAGAGCAGAGAGAGAAGGCTCTGTGCTCTCTGTTGGAGGCCAGGGAAGGAGATGGGTAATACCAAGTATTGATTCTGCTGCTGC
Ctnna1	NM_009818.1	156-255	GTTGGAGCCTCTTTTACACAGGTTACAACCTGTAAACACCAATAGTAAAGGGCCGCTAATAAAAAGAGAGGCGGTTCTAAGAAGGCCATGTTTTG
Ctsk	NM_007802.3	1-100	AGCCACGCTTCTATCCGAAAAGAGCCTAGCGAAGCAGATTCTCAACAGCAGGATGTGGGTGTTCAAGTTTCTGCTGCTACCCATGGTGAGCTTTGCTCTG
Cxcl1	NM_008176.1	561-660	TGCTAGTAGAAGGGTTGTGCGAAAAGAGTGCAGAGAGATAGTATTAGTATTATGTTTGTATGATTAGGGTGAGGACATGTGTGGGAGCTGTGT
Cxcl12	NM_021704.3	260-359	CTGAAAATCCTCAACACTCCAAGCTGCGCCTTCAGATTGTTGACCGCTGAAGAACAACAACAGACAAGTGTGCTTGAACCCGAAATTAAGTGGATCC
Cxcl15	NM_011339.2	420-519	AGAGAATATTTCCCTTTCCAATTCGGGAGACCTCTAGACACTTTGCTGATTAGCTCACAACAGTGATAGGAATTTTCTACGGGACTCCAGTGAAGTCAAG
Cyc1	NM_025567.2	961-1060	AGCGGCATAAGTGTGCTAGTCTGAAGAGTGCAGAAAGCTGCTTATCGGCCACCAAGTGAACCTGTTCAAGTATCTGCTTGCATCTGCCAGAACAGCTC
Cycs	NM_007808.4	2511-2610	CCTGTGAGATGCGAAAAGGGGACAGTCTGTGACTGATTTACAAGTCAAGGAGTGGGACCACTAGCTGATCTGCTTGTCTTATGTTGCTTTGTAG
Cyp19a1	NM_007810.3	1181-1280	TGACGTAAATTGACGGCTACCCGGTTAAAAAGGGAACATAACATCATTCTGAACATCGGAAGAATGCACAGGCTCGAGTACTTCCCTAAGCCCAATGAATTT
D2hgdh	NM_178882.3	293-392	AGCGATATCCGGTGCAACGGCTGCCGTTTTCTACTGTGTCGAGGAGGACCTGGCTGCATTTGAATGCATACCTGGCAGAGTTATCACAGATCCAGA
Dag1	NM_010017.3	611-710	CCACCGTGGTTGGCATTCCAGACGGTACGGCTGTTGTCGGCGCTCATTTCAGTGAGCATTCCAACGATTTAATTGCCTCCAGTGGGAGATCATCAA
Dbp	NM_016974.3	976-1075	AGGTGCTAATGACCTTTGAACCTGATCCCGCTGATCTCGCCCTGCAAGCATTCCAGGCCATGAGACTTTTACCCCTCGGAGACACCGCTTCTCAGAGGA
Ddr2	NM_022563.2	596-695	TGCTTGTAGTGAACAGTAACCTTATGATGATTCTGAAGGACTTGGAGCCACCATCGTCCGAGATTTGTTCCGCTTATCCAGTCACTGACCACTC
Dkl1	NM_010051.3	716-815	ACTGTGCGCAGGGCTGTGTTGTGCAAGACACTTCTGGTCAAGACTCTGTAACCTGTGCTTAAAGAAAGGTCAGAGTGTGCACCAACAACAAGGAAAGG
Dlat	NM_145614.4	2047-2146	CTCAGGCATGATTCTGGCAATCGGTGCTTCAAGGATAAACTGATCCAGCAGATAAATGAGAAAAGGCTTTGATGTGGCTAGTGTGATGTCGGTTACTACT
Dlx5	NM_010056.2	1017-1116	CACCCGCTGGCACTGGCCTCCGGGACGCTTTATTAGATGGGCTACTTCTCTTCTCAGTTTTGGGACTACAGTGTGCTGGTTAGAAAATCAGAAAAG
Dmd	NM_007868.5	10046-10145	CCTGAGATTGAAGCTGCTCTTCTTCACTGACTGGATGCGCTGGAACCCAGTCTATGGTGTGGCTGCCCTCTTGCACAGAGTGGCTGCTGCTGAAACTG
Dmp1	NM_016779.2	1611-1710	CTGACAGGACGGTACTAGCATTAGCTTGTCTAAGAAATGGCTCTACAGGACGGAGTCTTGGGGCTCCAGAGTAGAGAGTTCACTATACTATAATTT
Dmpk	NM_001190490.1	353-452	TGATTTGAGACTTTAGCTGTTGTGCAAGACTTCTGGTCCAGAGTGGGCGTTCAGCGAGGTGCTGTTGGAAGATGAAACAGACGCGGCAAGTGTATCCATGAAATTATG
Dnm1/Drp1	NM_001025947.1	2076-2175	GGTTAATCATGTGAAGATACTCTCAGAGTGAAGTGGTAGGCGAGCTGTATAAGTATCCTTATTAGATGACCTTCTGACTGAATCCGAGGACATGGCC
Duxf3	XR_001779775.1	3786-3885	AAAGAAGAATGTGTGAAGGCATAACCTGTCAAGAAAAGATCATCTGGGAATACAGTGAGTGTGAAACATCTTATCCAAGCTTGAACACAGC
Dysf	NM_001077694.2	1175-1274	GATCCAGAAGGAAAATAGCCACTCTTCAATGAGACTCTTTCTTCAACGATTTGACTCTCCCTTGGAGCTGTTTGTGAGCCCATCTTATCACCGGTG
Efnb1	NM_010110.4	1148-1247	ATTACTACATTACATCAACGTCCAATGGGAGCTTGGAGGACTGGAGAACCAGGAGGAGTGTGTGTCGCCCGCACTATGAAGATCGTTATGAAGGT

Efnb2	NM_010111.5	310-409	CTGGTACTATACCCACAGATAGGAGACAAATTGGATATTATTTGCCCAAAGTGGACTCTAAAAGTGGCCAGTATGAATATTATAAAGTTTATATGG
Egf	NM_010113.3	1887-1986	AAGTTCTGCTCAGCCGGCAGATGGGAATGTTTTGCTTGGATTATGACCTGTGGAAAGCAAGATATATTTGACAGACAGCCCTGAAGTGGATAGA
Egfr	NM_207655.2	1336-1435	TGCTACAAACATCAAACACTTCAAATACTGCACTGCCATCAGCGGGGACCTTACATCCTGCCAGTGGCCTTTAAGGGGATTCTTTCACGCGCACTCT
Egr1	NM_007913.5	516-615	CGGCAGCAGCGCCTTCAATCCTCAAGGGGAGCCGAGCGAACAACCTATGAGCACGTGACCACAGAGTCTTTTCTGACATCGCTCTGAATAATGAGAAAG
Egr2	NM_010118.2	1786-1885	CAGCTCTGTCCACCTTCTCAGCGACGGCCTTCCGAAAACCTTAGCCCAATTAAGGGAGTTGACTGCACTCCAAGAAATGGGGGAGCAAAAAGAGGGCT
Emcn	NM_001163522.1	231-330	CAAAGATGTTCAAGTACTCTATTCCAACCCGAGCAAACCTTCCACAACAAAGCCCTGTGCAAAATACCAGGCATCGTGTCAGTCAAGTCAACTAAC
Emp1	NM_010128.4	1081-1180	AGTTCGTAGTGGTGTTCAGGTCTTAGCAAGAGCAGATATTGCTCTATGCTGAGGCTAAGTCTGGAAGCCACTTTGTCCTGTGACCTAAAAACAACATC
Eng	NM_001146350.1	575-674	ATTTTCCGGGAATGCTGTCACATCTGGAGCTGACTCTTCCAGCATCAAGCAAATGGCACGGAGACCCAGGAGGTGTTCTGGTCTCGTTCGAAACAA
Enpp1	NM_008813.3	1646-1745	GTGGAAAGTGGATTCATGGCTCTGACAACCTGTTTTCAAACATGCAAGCTCTTTTATTGGCTATGGACCTGCCTTCAAGCATGGTGTGAAGTGGACT
Hif2a	NM_010137.3	1444-1543	ATGTGCTGAGTGAGATCGAGAAGAACGACGTGGTGTCTCCATGGACCAGCCGAATCCCTGTTCAAGCCACCTGATGGCCATGAACAGCATCTTTGA
Epha2	NM_010139.2	1706-1805	AGGATCTGCCAACATGGCGGTGATCGGCGGTGGCTGAGTGTGTTTTGCTTCTGGTACTGGCAGGAGTTGCGCTTTCATCCATCGAAGGAGGAGG
Ephb2	NM_010142.2	1731-1830	CCTCATCGTTGGCTCTCCGCGCGGCTTAGTCTTCTCATCGCTGTGGTCTGTCATTGCCATCGTATGTAACAGACGGGGTTGAGCGTGCCGACTCA
Ephb3	NM_010143.1	2381-2480	GGCAGCGCGGGACTTCTAAGTAGAGGCTTCCATTATGGGTGAGTTGACCATCCCAATAATCCGCTAGAGGGTGTGGTACCAAAAGTCCGTCAGT
Ephb4	NM_010144.6	2241-2340	GCACGGTACCAAGGTCTACATTGATCCTTTACTTACGAAGCCCTAATGAGGCAGTGAGGGAAATTTGCCAAAGAGATCGATGTCTCTATGTCAAGAT
Erbp2	NM_001003817.1	1396-1495	AGATCACAGGTTACCTATACATTTCCAGATGCGCCAGAGACTTCCAAGACCTCAGTGTCTTCCAGAACCTTCGGGTCTTCCGGGACGGATTCTCATGA
Esr1	NM_007956.4	737-836	ACTCGCTACTGTCCGTGTGCAATGACTATGCCCTCTGCTACCATTTAGGGTCTGCTCGAAGGCTGCAAGGCTTTCTTAAAGAGAAGCATCTCAAG
Esr2	NM_010157.3	443-542	TGCTTCTATAAAGTGTAGCCAGTCCATCCTACCCTGGAGCATGGTCCCATCTATATCCCTTCTCTATGTAGAGAGCCGTCACGAATACTCAGCCATG
Esrra	NM_007953.2	1376-1475	AAAGTCTGGCCCTTTCTATGGGTGAAGCTGGAGGGCAAGGTGCCATGCACAAGCTGTTTTGGAAATGCTGAGGCCATGATGACTGAGGCAAG
Etfhdh	NM_025794.2	1711-1810	AAGGATTGTACACCCATTGAGTATCCGAAACCTGATGGACAGATCAGTTTTGACCTCTTATCCTCTGTGGCTTTGAGTGGTACTAATCATGAACATGACC
Ext1	NM_010162.2	1896-1995	TGCTCAGCAAGGATGGGAGTGGCCATTCTCGAAGTCTCGAAGTGAACCAAGTCCGCTCATAGGCGATGAGAGATTGCTATTACAGTACTTCTTAC
Ext2	NM_010163.3	1404-1503	GCATACTTCCAGTCCATTAAAGCATTGCCCCGCCACCTACAGATCATCAATGACAGATCTATCCATATGCAAGCCATCTCCTATGAAGAGTGGAAATG
Fasl	NM_010177.3	646-745	CATTTAACAGGGAACCCCACTCAAGTCCATCCCTCTGGAATGGGAAGACATATGGAACCGCTCTGATCTCTGGAGTGAAGTATAAGAAAGTGGCC
Fbn1	NM_007993.2	4806-4905	CTCCCGTAGTTACACATGCGGATTGCTCCGATTTTGAGCTGAATCCAACCTGCTGCGGCTGTGTCGATACTCGCTCTGAAACTGCTATCTGGATAT
Fbn2	NM_010181.2	9011-9110	CTTCTGATTGAGCTTCCGAAATGTTACCCCTCGCAGGGAAGGATAATTTAGACTCTGTATGGCCAAAGATTTGAGTGCAAAGGCAAACATAGTTACTG
Fbxo32	NM_026346.2	1826-1925	AAATCTCAGCGGCTTGTACCTTATCCTATGAGATGGCAGACCACTGCTACCTCTAAAAGCATAGCGTGTCTGGAACATATCTTATCTGGGAG
Fgf1	NM_010197.3	681-780	TTTTGGTTGACCTACCATGTTCCCTTGACCATTGGCTGCGCTAACCTCAGGCCACAGACCTGAATTTGTAAGCAGTGTCTTAAAAATAGCCAGTTCA
Fgf10	NM_008002.4	1288-1387	CTTCTCCCATGACGATCCAAACATAGAAGAAAACCTGTTGGTGGATGAGTACAACCAATGACTCTTTGGACAGAAAGAGATGGTATCTCACTGAA
Fgf2	NM_008006.2	288-387	CTCTACTGCAAGAACGGCGGCTTCTTCTGCGCATCCACCCGACGGCCGCTGATGCGTCCGCGAGAAAGAGCGACCCACAGTCAAACCTCAACTCC
Fgf23	NM_022657.3	1247-1346	CTAACAGGTAACCCAGACACTTGGCCTTTATTAGCCGGTCTCTTGCCTAGCATTTTAATCGATCAGTTAGCACGAGGAAAGAGTTCACGCTTGAACAC
Fgf7	NM_008008.4	214-313	TGCAGCAACTGGCCTTGTACGACCTGTTCTATAAGGATATACCTATCAGCTGTGTTCTTGAAGGAGGAATCGTGTATTGGTATCAGAAGCTAAAAGA
Fgf9	NM_013518.3	1071-1170	ATTAGCAGTCCGTCACCTCAGCTCCACTGTTGCCAAACTTTGTCGATGCATATGAATGATGGAAGCTTGGATGAGGACTTGCCTTCTGCACT
Fgfr1	NM_001079908.2	1309-1408	CCCCTCTGCGCTGGTTGAAAATGCAAAAGATTTAAGCCTGACCCAGGAATGGAGGCTACAAGTTTCGCTATGCCACCTGGAGCATCATAATGGATT
Fgfr2	NM_010207.2	3206-3305	CAAATGGGCGACTTCCAGTCAAGTGGATGGCTCCTGAAGCCCTTTTGTAGAGTTTACTACTCATCAGAGCGATGTCTGGTCTCGGGGTGTTAATGTG
Fgfr3	NM_008010.3	3521-3620	TCCAGGGTATTGACCCATTTAAGTTGAACCTTTAACATTTAACAGCGGAAGAGTTTCATGCTGGATTTAGGAAATGCTGAGAAGTGCCTGCTGCCCTCCAC
Fgfr4	NM_008011.2	1666-1765	CTGAAAAGACAATGCCCGACAAGGATTTGGCAGACCTGTTCCGAGATGGAGGTGATGAAGCTAATCGGAAGACAAAGAACATCATCAACTGCTGG
Flt1	NM_010228.3	1551-1650	GAAAAGTCCGTGCTCTCGCTTCAAAGCCACCTCTATCCGCTGGGCGAGCAGACAAGTCTCACTTGCACCGTGATGGCATCCCTCGGCCAAACATCA
Fn1	NM_010233.1	2628-2727	TCCAGACCTACCGTGGACCAAGTGTGATGATCCTCATTGTTGTTCCGGTGAGTAGACCCACAGCACCTATCACAGGATATAGAATTTGCTATTCACT
Fos	NM_010234.2	1331-1430	AGCTGGTGCATTACAGAGAGGAGAAACACGCTTCCCTCGAAGGTTCCCGTCGACCTAGGGAGGACCTTACCTGTTGCTGAAACACACCAGGCTGTGGGC
Fosb	NM_008036.2	2889-2988	TAGCATACTTAAGAGGGGCTGAGTTCACCATCCACTCCATCCAATTCCTTCAAGTCCCAAGACGAGTTCTGTCCCTTCCCTCCAGCTTTCACCTCG
Fosl2	NM_008037.3	165-264	CGGATCATGTACCAGGATTATCCCGGAACTTTGACACCTCGTCCCGGGGCGAGCAGCGCTCTCTGCGCACGCCGAGTCTACTCCAGCGGTGGCGGCG
Foxo1	NM_019739.3	1362-1461	CAGCAACGATGACTTTGATAACTGGAGTACATTTGCTCCTCGAACCGCTCAAATGCTAGTACCATCAGTGGAGACTTTCTCCATCATGACAGAGCAG
Foxo3	NM_019740.2	2222-2321	GATGCTGACGGGTTGGATTTTAACTTTGACTCCCTCATCTCCACACAGAAGCTTGTGGTTTGAATGTGGGAACTTCACTGTGCTAAGCAGGCCTCAT
Follistatin	NM_008046.1	681-780	GGGCAGATCCATTGGATTAGCCTATGAGGGAAAGTGTATCAAAAGTCTGTGAAGATATCCAGTGTGGCGCGGGGAAAAATGCCTATGGGATTCCAAAG
Fut1	NM_001271981.1	1129-1228	AGATTGGTCTGACTCATCAGAAGTCAAGCATCCATGCTCTATGCTTTGGTGTATGCTGTGGTACCCCTGGAGCTGTGGGTACTCATTCAGACTTCG
Fut4	NM_010242.3	1766-1865	GGTTTTGAAAGCCGGTGGGTATGAGATAGTGAAGGATTGTGCCACAGTGGGGTTTTCTTTGGTGGTTGGATTCTCAAACCTGCTGAACCTGGAAA
Fyn	NM_008054.2	1031-1130	TTCTTATCCGCGAGAGCGAAACCCAAAGGTGCTACTCACTTTCCATCCGTGATTTGGGATGATATGAAAGGGACCAGTCAAACATTAATAAATCCG
Fzd1	NM_021457.3	1417-1516	GCCGGGACGCTGGAGCGGGGAAAGTTCTCCTGCCGCGCCCTCAGGGTGCCTCTCACTCAACTACCACTTTCTGGGGGAGAAAGACTGCGGGCGCAC
FZD2	NM_020510.2	2956-3055	CCTGGGATCTTTGGCGCTTCCGTTCCCTCTCTCCCGTAGGCTCTCTCCGCGGTGGGATCCAGGTTAGCTGTTTGTAGATTGGGTTGTGTGTTATG
FZD4	NM_008055.4	1337-1436	CCATTTGAAATGCACAGTCTTATTTCCACATCGCAGCTTGGCTATTTCCCGCAGCTGAAACCTTTGTCATCTTATTAGACTAGTGGATCCGATGTA
FZD5	NM_001042659.1	3631-3730	CGAATCTGCGGCTCCGCCACCTCCTTATCATGTTAAACAGTCTCCTGCTTTTTCTTATTCTCTGGTGGAGAGTGGTATTAGAACCACACCCA
Fzd8	NM_008058.1	811-910	CGCGCTTACCGTCTTCTGGATCGGCTGTGTGCTGCTGCTCTCCACCTCGCCACTGTCTCTACCTTCTCATCGATATGGAGCGCTTTA
Fzd9	NM_010246.1	746-845	GTTTTCTTCCACGGCTTCCAGTGTTCACCTTCTGCTGGAGCCTCACCGTTCAGTACCCAGAGCGCCGATTATCTCTTTCTATGTGCTACAA
Gabbr1a	NM_019439.3	1367-1466	TGCTGTAAAAACCTGAAGCGTCAAGATGCTCGAATCATCGTGGGACTTTTCTATGAGACCGAAGCCCGGAAAGTTTTTGTGAGGTCTATAAGGAACG

Gabbr1_var	NM_019439.3	1704-1803	TGGAGGCTTCCAGGAGGCCACTGGCCTATGATGCTATCTGGCCCTGGCTTTGGCCTTGAACAAGACCTTGGAGGAGGTGGCCGTTCCAGGAGTGCCG
Gad1	NM_008077.4	747-846	AGAGACACCTGAAGTACGGGGTTCGCACAGGTCAACCTCGATTTTTCAACACAGCTCTCTACTGTTTTGGATATCATTGGTTAGCTGGTGAATGGCTGA
Gad2	NM_008078.2	770-869	ATAATTGGGAATTTGGCAGACCAACCGCAAATCTGGAGGAAATTTTGACGCATTGCCAAACAACCTCTAAAATATGCAATTAACAGGGCATCCCCGATA
Gapdh	NM_001001303.1	891-990	AGGTTGTCTCCTCGACTTCAACAGCAACTCCCACTCTTCCACTTCGATGCCGGGGCTGGCATTGCTCTCAATGACAACTTTGTCAAGCTCATTTCCTG
Gdf10	NM_145741.2	1936-2035	TGTTGAGTTCTTGGAGAATCTGGAATTAACCTGTGGTCTGCAATTTGCCATCATCCCTGCCACACTTTTCAAGGCCTAGAATAACGTGTGTCTCA
Gdf15	NM_011819.2	716-815	GCTGACGATGGCGGTGGCGAGTGTCCCACTGTATCGCTCCGCAACACGCATGGCAGATCAAAGCAGCGCTGCATGGCTGCATGACAGAGGTG
Gdf5	NM_008109.1	1711-1810	CGGCTGAGTCTATTAGCATCTCTTCATCGACTCTGCCAACACGTGGTGTATAAACAGTACGAGGACATGGTCTGGAACTTTGTGGCTGCAGGTAGC
Gdf6	NM_013526.1	1855-1954	GCATCTCAGATTGGTTGTTTCTACCTGTGTAAGAAAGTAGGCGCTTTGGTCTTTCTAGCCAAGTCTCAGCTGGCGTCTTACCTCACAGGAAGTATTT
Gdf7	NM_013527.1	224-323	CTGTGCGCCGCTGCGGGTCTGGCTCAGGAACGGCTGGTGGTCCACACCACTTCATGATGTCGCTTACAGGAGCCTGGCGGGGAGGGCTCCGGT
Gja1	NM_010288.3	1451-1550	CTGGGGTGTTCATTTCCGTTCCCGTGGAGGTGGTACTCAACAACCTCAGTAATGAGGCGTAGAAAACAAGACATTACAATATCTAGGTTCTTTGGGGGGT
Gja3	NM_001271623.1	2359-2458	CCACCTCCATGTCAGCCAACCTAATCACTATGAGGATGTCTAGGTAAAAAATTAACCACTGTGAGAATGTACGCTAGATAAAAACCTGGGGTAGGGGATTC
Glce	NM_033320.4	85-184	TTGTGGAATAAGTGTCCAGCGACAAGCAATCCAGTTTCTCGCACTTGAGTAGTGGATTAGAGTGGATTAGAAAAAGATCAGCAGCATCTG
Gli1	NM_010296.2	2280-2379	GAGCCAGAGGTTGAACTTCTGTGATGGCAATGGTCTGAACCCATACATGGATTTTTCTCCACTGATCTCTGGGATATGGGGACCGAGGGGACGG
Gnai1	NM_010305.1	471-570	ACACTATCCAGTCCATCATTGCCATCATTAGAGCCATGGGGAGGTTGAAAATCGACTTCGGAGACTCTGCTCGGGCGGATGATGCTCGCAAACCTTTTCGT
Gnai2	NM_008138.4	972-1071	TCCCTGACCATCTGTTTCCCTGAGTACAGCGGGGCCAACAGTACGACGAGGCAGCCAGCTACATCCAGAGCAAGTTTGGAGTCTAATAAAGCGCAAAG
Gnai3	NM_010306.2	355-454	TTCAATCATACGAGCCATGGGACGGTTGAAGATTGATTTTGGGGAATCTGCAGAGCAGATGATGCCGACAGTTATTTGTTTTAGCTGGGAGTGTCTGAA
Gnaq	NM_008139.5	3081-3180	GAATTTGGCGCTTGAACCTAAGAAAGATTGGACTTATCAAAGTACCCGCTCAGTGTCCGTCAGCATGATTTATGTGACGATCATACTAGGAGGG
Gnas	NM_010309.3	2593-2692	CAGTTCAGAGTGGACTACATCTGAGCGTGATGAACGTGCCGAACCTTGACTCCCACTGAATCTATGAGCATGCCAAGGCTCTGTGGGAGGATGAGG
Gpc6	NM_011821.3	883-982	GAGTTTGAACCTTGTAGAAGAGACAAGCCACTTTGTGAGGACCACTTTGTGTCGAGGCACAAGAAATTTGATGAGTTTTCCGAGAGCTGCTGGAAA
Prgn	NM_008175.4	1293-1392	AGACTTGAAGAGTGATACACCTTGTGACTTCACTAGTTGCTTCAACAACTACTGCTGCAAACTCAATCTGGGGACTGGGAGCTGCTGCCAT
Gtf3a	NM_025652.3	355-454	GGCCTTATCAGAGACTACCATCTGAGCGGCATGCTCTGATTACACCGGGGAAAGCCGTTTTGTTTGTGCAGATGATGGCTGTAATCGCAAAATTCAC
Gusb	NM_010368.1	284-383	CCCTTCCGACTTTATTGGCTGGTGTGGTATGAACGGGAAGCAATCTGCCAGCGGATGGACCAAGATACCGACATGAGAGTGGTGTGAGGATCAA
Hand2	NM_010402.4	141-240	CCCAGCTCCGAGGTGCCCTTCAAGGGCCCAAGATTCTTGTCCGGAGAGGAGAGGATCTTAGAAAATGGATGCGCTGAGACCTCTCTGCAAAGCTCCGAGA
Hat1	NM_026115.4	1271-1370	CGCAGTGTCTCAAGAGTGAAGCCCTTGTCCCCAGAATACCTGCAGATTTCTGTGCATGCTGTGAACCTCTGATACCCTAAAGTTATCTATGTTC
Hdac1	NM_008228.2	471-570	TACGTCAATGACATCGTGGCCATCCTGGAACCTGTAAGTACCAAGTACCCAGAGGCTCTATATTGACATTGACATTACCAGTGGCGGCTGGGTGAAG
Hdac4	NM_207225.1	2801-2900	AGACGCTGAGTACTTGGCAGCCTCAGAACGGTGGTTATGCCTATCGCAAATGAGTTTGGCCAGATGTGGTACTGGTGCATCGGGCTTCGATGCTGTG
Hdac5	NM_010412.3	2123-2222	GGAGGAAGAGGAGGACTGCATTGAGTCAAGGATGAGGATGGCGAGAGTGGTCTGATGAAGGCCCTGACTTGAAGAGTCCAGTGTCTGGTTACAAAAAG
Hgf	NM_010427.5	484-583	AATAGTATGTCAGAGTGGAGTGAIAAAAGGGTTTTGGCCATGAATTTGACCTCTATGAAAACAAGACTATATTAGAAGTGCATCTTTGGTAAAGGAGGCA
Hif1a	NM_010431.1	2336-2435	AGCTCATCAAAGGAGCCTTAAGCTGTCTGCCACTTTGAATCAAAGAAATACTGTTCTGAGGAAGAATTAACCCAAAGACAATAGCTTCGAGAATGCT
Hif3a	NM_001162950.1	2751-2850	CAGCGACTTCCCTCACTCCACAGACCTATAATCTGTGATCTTGAATACTGACTCCCACTTACTGTTTGTAGACTGTGCAACTTCTAGCCTTCCCTG
Hk1	NM_001146100.1	757-856	CATGGAGAAAAGGAGATCAAGGACAAGAAATACCCGTTGGATTACGTTTTCTTCCGTCGCCACAATCAAATAAGACGAGGCCGCTACTGATCAGC
Hk2	NM_013820.3	4405-4504	TTTTAAAGTCAATCAGATCGTTGGAGCAGACCACATGAAGCATCGAGAGAACTCGACCAACCTCAGGGGCGTCTCGGGGTGTTGTACATTTATTTGC
Hmga2	NM_010441.2	3566-3665	ACAGTGGCTTATAAATATCAGATTCTCATTCCGGTCTTGGATGGGCCTTACAGAAACCTCATTTTGGCCAGCTCAAAAAACTGAAGCAGCTTCTCGT
Hmgb1	NM_010439.3	1575-1674	GTGGACTATTAGGATCAAGCAATCGAACGCTGTCTCTTGAAGGACTAGAAAAGTACCTTCAATCCTTACACGAGGACTCTCCTTTAACCCCAT
Hmox1	NM_010442.2	611-710	CTGGGAGGGGCTGGCTTTTTTACCTTCCCGAACATCGACAGCCCAACAGTTCAACACAGCTCTATCGTGCAGAAATGAACCTCTGGAGATGACACC
Hnf1a	NM_009327.1	2696-2795	GCCATCTGTTCCCTGGATGTGCTTCTGATGCCAGCCTGGCACTGCATCCTAGAAAAGGCCATTTAGGGCTCGGGTGTGCATCCCTGTTCTTAG
Hoxa7	NM_010455.2	61-160	GCTTTTATTGTTCTCTAAAGAACTGGGGTTCACAATGAGCTACAGCACCAGGCTCTGAGATTACTCTCTGCTCTAATCCAGCTCAAAACTGTTA
Hprt	NM_013556.2	31-130	TGCTGAGGCGGCGAGGAGCGTGGGCTTACTCACTGCTTTCCGGAGCGGTAGCACCTCTCCGCGGCTTCTCTCAGACCCGCTTTTGGCCGGA
Hs2st1	NM_011828.3	3536-3635	TGAGAGTTCCCACTAACTTTAGGTAGTTAAGGCGAGCACTAGAACAATACTGGGACTTTCCCTAAAAGTCTCTCAAAAAGACCAGGTAATGAGTCA
Hs6st1	NM_015818.2	2149-2248	CACTGAAACATTTATACAAGGCTTGTGTGCCAATGTTCTACCATAACAGCAACTCTTCTATCCCGTGAATAAAGCATCCCTGGCTGGGATATAGG
Hs6st2	NM_001077202.1	1431-1530	GCGCAAGACCCAGTACCTGTTGAGAAGACCTTCAACATGAACCTTATCTGCGGTTTACCAGTATAATACCAGTGGCCCTAGTGTGAGATCAAT
Hs6st3	NM_015820.3	125-224	TCACTGCGCGCTGAGAACGGACCATGGATGAAGGTTCAACAAGTGGCTGTGACGCGGTGCTCACTCTCTCTCGTGTGCATGATACCGATA
Hsd11b1	NM_008288.2	111-210	CAGGTCCCTGTTTGGCAGTTATGAAAAATACCTCTCCGATCTGGTGTCTTCTGGCTACTACTACTATTCTACAATGAAGAGTTCAGACC
lbsp	NM_008318.3	115-214	GGAATGGCCTGTGCTTCTCGATGAAAAATTTCCATCGAAGAAATCAAAGCAGAGGCTGCTTCTGAAGAAAACGGGCTTTTAAAGTACCGGCCAGCTCTTCT
Icam1	NM_010493.2	2196-2295	CACATGGGTGAGGGTCTTCTACTGGTCCAGGATGCTTTCTCATAAGGGTCGACTTTTTTACCAGTACATAAACACTATGTGGACTGGCAGTGGTTC
ldh3a	NM_029573.2	1081-1180	TGTCGTAGAGTCAAAGACTTAGATTAGCACTCTGCTGGTGGATTTGCTGCAGTCAATCACTCAAAGGATACCCTGTAATCCTCTTGGAGGGG
ldh3b	NM_130884.4	272-371	AAGGAGCATCATCTGAGCGAGGTGAGAATATGGCTTCTGAGGAGAAAGTGGAGCAGGTGCTGAGTTCATGAAGGAGAACAAGTTGCCATCATTGGAA
ldh3g	NM_008323.1	187-286	GCTAAGTATGTTGGCGGCATACAGTACTATGATCCAGGGGATGGCATCGGCCAGACTCATGTTGCATGTAAGTCTGATTAGCAGCATGATG
lfng	NM_008337.1	96-195	AGCTCTGAGACAATGAACGCTACACGCTTGGCTTGGCTTCTCTCTGAGTCTTCTGCTGTTTCTGCTGTTACTGCCAGCCAGCATGTTGAAAG
lgf1	NM_001111274.1	4096-4195	AAAAAGGCGCGTGGCCCTTGGACTCCTTCTCTTGAATGTCAATGTGAATGTGGCATGCTGTGTACATGAACCACTCTCATACCTATGGC
lgf1r	NM_010513.2	4936-5035	TTACCCGAACCTTAACTGACATGGCCCTGCAAACTTAAATGACAACACTTAAATGACAACAGGACACTCGAGAAATGAGTCTCTCGTTCTCTGCTT
lgfbp3	NM_008343.2	1646-1745	ATGTTCTAGGGCACTCTGGGAGCCATAAGGACAAGGATAAGGACCTTTCTTGTGAGGATCTTCTGATGACTTGGCCAGCAGAAAAGCCCCAAGTGG
lgfbp4	NM_010517.3	1341-1440	AACATACTATGTCCAGCTTTAGTTTTCCAGCCGGGGAAGCCTCGTTGTGATTTCTCCGATTGTAGAATGTGACGAGGTGTTCTCAACTCAAGCCCCAC

Igfbp5	NM_010518.2	2771-2870	CTTCCAACCCGAGAAAGTAACGTCTCACACCACACACATAAACCTGCCAGATCCATCTGTAACCCACTGGCCTGCCAGACCTTTTTTCCCATCTG
Ihh	NM_010544.2	536-635	GGTGGGCGCCGCGGAGGCCGCTCGCAAGCTCGTGCCTCTTGCTACAAGCAGTTCAGCCCCAAGCTGCCGAGAAGACCTGGCGCCAGCGGGCCG
Ikbkb	NM_010546.2	499-598	CTTACCCTGCTGAGTGACATCGCATCGCTCTTAGATACCTTACGAAAACAGAATCATCCATCGAGACCTGAAGCCAGAAAACATCGTTCTGCAGCAAG
Il10	NM_010548.2	251-350	GACAACTACTGCTAACCGACTCCTTAATG CAGGACTTTAAGGGTTACTTGGTTGCCAAGCCTTATCGGAAATGATCCAGTTTTACCTGGTAGAAGTGA
Il11ra1	NM_010549.3	732-831	CCTACTGGATGTGAGATTACAGAGCATCTTGCCTCTGATCCACCCCAAGGACTGCGGGTGAATCCGTACTCTGGTTACCCGAGACGCCATCGATGCCAGC
Il15	NM_001254747.1	287-386	GAATCCACTGTGACATGGCCCTCTGCTCTTCAAAGCACTGCTCTTCAAGTCTGTGCTGTGAGTGCCTTAAGAACAACAGAAAACCTGTGACAG
Il17a	NM_010552.3	66-165	AGGGAGAGCTTACTGTGTCTGTATGCTTTGCTGCTGCTGAGCTGGCGCTACAGTGAAGGCAGCAGCGATCATCCCTCAAAGCTCAGCGTGTCCA
Il1a	NM_010554.4	513-612	CAAACACTATCTCAGCACCCTGGTAAATGACCTGCAACAGGAAGTAAAATTTGACATGTATGCTACTCGTGGGAGGAGACGACTCTAAATATCCT
Il1b	NM_008361.3	109-208	TTGACAGTGATGAGAATGACTGTTCTTTGAAGTTGACGGACCCCAAAGATGAAGGGCTGCTTCAAACCTTTGACCTGGGCTGCTCTGATGAGAGCAT
Il6	NM_031168.1	201-300	ATGTTCTCGGAAATCGTGAATGAGAAAAGAGTTGCAATGGCAATTCTGATTGTATGAACAACGATGATGCACCTGCAGAAAAACAATCTGAAACT
Il6ra	NM_010559.2	2826-2925	CACCTCACTGCCACTTGGCCTTCTTGTCTTACGTTTTGACTGAGTGGCCTCAGATGCTTTCCCTGGGCTTTGAGGAATCCAGTGATGTTAGTGGTCA
Inhba	NM_008380.1	751-850	GGAAATGGGCTTAAAGGGGAGAGGAGTGAAGTGTGCTATCAGAGAAAGTAGTTGATGCTCGGAAGAGTACCTGGCACATCTTCCAGTGTCCAGCAGC
Irf1	NM_008390.1	366-465	TGTTCCGGAGCTGGGCCATTACACAGGCCGATACAAGCAGGAGAAAAGAGCCAGATCCAAGACATGGAAGGCAAACCTCCGTTGTGCCATGAACCTC
Irx6	NM_022428.2	619-718	TGAAGACGCCCTGCTATGGCCTTTTACCTTTTGGACACCCGATGGCAGCACATCCAGTTTCTGTGTCTGCAAGTCCAGTGCACCTTGTCTGCGAAA
Itda1	NM_001033228.3	2551-2650	ATTGAAGTCAAAGAAGACTCAGTTTACAGGCTGATCTGCAGTACCGTTCACCTTGATTCTGCTGAGGCAGATATCAGGAGCTTTTTTCTGGAAT
Itda11	NM_176922.5	1027-1126	TTTCTAAATGAAATCAAATACATCGCCAGCCACTGACGACAAGCACTTCTCAACGTACAGATGAGCGGCCCTGAAGGACATTTGTTGATGCCCTTG
Itda2	NM_008396.2	1861-1960	ATTTCAAATGGTACCAGGGTACCATTGACACCAAGTACTCCAGAAAATCCTGGGTCCAATGGAGCCTTTAGGAGACATCTCCAGTCTTTTGGAAAGT
Itda3	NM_013565.2	1066-1165	AAGGACTGGGATTTATCTGAATATAGCTACAGGGGCTCAGAGGAGCAAGGAAACCTTATATTGGTACACGGTGCAGGTAGCAACGCCATCCTACATC
Itda5	NM_001314041.1	2623-2722	CCTCAGCAAGAACCTGAACAACTCACAAGCAACCGTGGTCTCTTCCACTCTGCTGGTGAAGGCTCAAGCCCAGTCTCCCTAATGGTGTCTCCAAGCT
Itda6	NM_008397.3	911-1010	CAGTGGGCTGTAGTTTTGTAAAAAGAGACACTCCGCGACTCTCTCCCTGAGTATATATTTGACGGAGAAGCCCTGGCTTCCGTTGTTGGCTAT
Itdam	NM_001082960.1	3026-3125	ATCCCTGTTCAGATCAAATGTCACGGTATGGGATCATCCCAAGTCTTCTCCGAACTCTCAAGTCCCTGTCACTGAGCAAAATCCCCC
Itdav	NM_008402.2	3146-3245	CAAGGAGAACCAGAACCTTCTATTGCTGAAGTCACTGCTTCTTAAATCATAGAATTCCCTACAAGAACCTGCCGATCGAGGATCTCTTCAAC
Itdax	NM_021334.2	328-427	GGGCTGTCCCTTGCTGCTGCCACCAACCTTCTGGCTTGGCTTGTGCTCTACTGTGCACCACACATGAGAGAGAATATATACTGTACAGGGCTC
Itdb1	NM_010578.1	1856-1955	CTGTGATAGGTTACTTGGCTTAAATTTGTGGAGGCAATGGCGTGTGCAGGTGTCGTGTTTGTGAATGCTATCCAATTACACTGGCAGTGATGTACTGT
Itdb3	NM_016780.2	2596-2695	TGGAAATGATCTCTGTGTGTAACCTGAGAGTGTGGGAAATGTGAATTAATAAATTTGATGTGTCTCACAGGACAGCTCCAGTCCAGCC
Jag1	NM_013822.2	2156-2255	AAAATGGCTGAAAGGAAAGACTTCCATTCCCGTGACAGCCAGTGTGACGAAGCCACGTGTAATAATGGTGGTACCTGCTATGATGAAGTGGACACGTT
Jak1	NM_146145.2	4081-4180	CATAGCAAAGACTGTGCGCTGGCATAATTGATCTCAGATAAAAACCTGTGGACTTGGCTGACACTCTCCCTGCCCTGAAATCTCAATGCTATTCAGT
Jun	NM_010591.2	2213-2312	CGCGACCAGAACGATGGACTTTTCTGTTAACTTACCAAGAAGCTGATGGACCTAACATTCGATCTCATTGATTAAGGGGGGGTGGGAGGGGTTACA
Jund	NM_010592.5	1637-1736	ATCATCCAGTCCAACGGCTGTGTGACCACTACCCGACCAGTACGCAGTTCCTCTACCCGAAGGTGGCAGCTAGCGAGGAGCAGGATTCGCCGAAGGCT
Kat2b	NM_020005.3	3031-3130	CTTCCACAATAGCGCTGCTGCTACTCCTAAGGAAGGACTTTTTATAAGCTCTGGGGCTTTGATCATTCTGTCTACTATTACAGACTTGAGAGTGCA
Kdm1b	NM_172262.3	2035-2134	CCACGACAGATGGTATGGGGCATTCTGCACAAAAGGTGTTAGTCACTGTGCCATTGGCCACTACAGAGAGGTGCCATCCAGTTTAAATCCACCATTGTC
Kdm5a	XR_377436.1	2315-2414	ATGCAGAACAAATGCTTAGTACCCTATCCACTAGAAGACCTTCCATCTCTGCTTATGGTGTCAAAGTGAGAGCAAACTCCTATGACACTTGGGTC
Kdr	NM_010612.2	996-1095	TTAAATTTACAGCGAGAACAGAGCTCAATGTGGGGCTTGATTTCACTGGCACTTCCACCTTCAAAGTCTCATATAAGAAGATTGTAACCCGGGATG
Kitl	NM_013598.1	281-380	CTGCGGAAATCCTGTGACTGATAATGTAAGAACATACAAAACCTGTGGCAAATCTTCAAATGACTATATGATAACCTCAACTATGTCGCCGGGATG
Klf4	NM_010637.3	2398-2497	GACTGGAAAGTTTGTGGATATCAGGGTATACACTAAATCAGTGAGCTTGGGGGAGGGAAGACCAAGGATCCCTTGAATTGTTCGATGATGCAATA
Lama1	NM_008480.2	1303-1402	TCTGAGTTCTGTCTGATCAAGGATGACCGCATGCCGATTTAGCCAATGGAAGTGGCCAGGTGAGTGTCCATGTAGGAAAGGTTATGCTGGAGATAAA
Lck	NM_010693.2	1181-1280	TCGGGCATCAAGTTGAATGTCAACAAACTTTTGGACATGGCAGCCAGATTGCAGAGGGCATGGCCTTCAAGAACAGAAATACATACATCGGGACC
Lcn2	NM_008491.1	191-290	GCAGGCAATGCGGTCCAGAAAAAACAGAAGGCAGCTTACGATGTACAGCACCATCTATGAGCTACAAGAACAAATAGCTACAATGTCACTCCATCC
Ldha	NM_010699.2	1355-1454	CTGCAGCTTCGATTACCCTGTGAGCCTGCTGCACTTGTGCTGCCCTGACCAAAACATGCCTAGGCCGACGAGTCCAGTTAAGTCGTATAACCTGGCTCC
Ldhd	NM_008492.2	1139-1238	TGTGACCATGAACCTTTAGTCTTCCAGCATGATGTAGGTACAGTTTCTTCTTCCCTGACATGTGATGAGCTCACAGATCAAAGCCAGGCTTGT
Lef1	NM_010703.3	1338-1437	ATAATGATGCCAATATGAACAGCGACCCGTACATGTCAAATGGTCCCTTCTCCACCATCCGAGGACATCAAATAAGTGGCCGTGGTGCAGCCCT
Lep	NM_008493.3	1116-1215	CCTATTGATGGTCTGCCAAGGCAAACCTAATTTTGTAGTACTGGAAGGAAGTGGGATCTTCAAACAAGAGTCTATGACAGGTAGCGCTCAAGCTT
Lrg5	NM_010195.2	2124-2223	CTGGCTGCCGTGGATGCATTCACTTTTGGCCGTTTTGCTCAGCACGGTGGTGGTGGGAAGACGGAATCGGCTGCCAAATCGTTGGCTTCTGTCCATTT
Lrg6	NM_001033409.3	404-503	CGTCTTCCGAGGAGCTGCGGCTCAGGGAACCCACTCTCACACATCCCGGACAGGCATTTCTGCTCCACAGCCTCAAATTTCAAAATCTAATGCTCAGA
Lif	NM_008501.2	3436-3535	ACATCTTTCACCTGGAAGCATTGACTTCCACCGAGCATAGTAGGTAGTGTGCTGGACCAGAGAAAAGGGATGGGGCATTTTGCAGTTTATCCAGAGAG
Kin28a	NM_145833.1	2741-2840	AAGACCCATGTGAAAATCTGAAGAAGCCAGGAACCTCATTCTTCTGTCCCTAACTCAGTGAAGAGTTTGGTTGGTGGTTTTGAGACAGGGCCTC
Lmna	NM_001002011.2	1612-1711	CCAGTCCATGGCAACTGGCAGATCAGGCGTCAGAATGGTGACGATCCTTTGATGACCTATCGCTTCCACCCGAAGTTCACCTAAAGGCTGGGAGGTTG
Lox	NM_010728.2	2301-2400	GATACTTGTGCTATTCATCCACGCTGCTTAGCTTTTCTGTGGCAGAAATGCTAATGTGACAATCAGCACATCCCATTTGTAGGTTTCACGGCAT
Lox1	NM_010729.2	2031-2130	ACATTTCTGGAGCTGACTTCAACCAAGCTGGTGAAGTACTCAACACTCACAGGTGCTGCTACGTTTCTACAACAACCTGAAAATCTAATGCAAGTC
Lox2	NM_033325.2	3701-3800	TTCCACTTGGCGCTGTGCTTCCAACTCCACCAACAATAACCCATTCAGTTCTGTTCTCTAAAAGCGCTCTAGGGCTTCTGGACCCAAAGTCTAAGT
Lox3	NM_013586.4	2085-2184	CGTGGGATGTTGGATCTCTACAGGCATGACATTTGACTGTGAGTGGATCGACATCACAGATGTGAAGCCAGGAAACTACATTTCTCAGGTGTTATCAAC
Lox4	NM_053083.3	4579-4678	TTTCAGAGCAGCCACGCACTCAAACAGCTCCTTATCTTGGAGAGTTCTGTTCTCTGAGAGCAGCAGCCGACTGTGTTCTCCATTAGCTCCTTCA
Lrp1	NM_008512.2	1311-1410	GAGCAGATGGCAATCGACTGCTGACGGGAACTTCTACTTTGTCGACGACATGACGACAGGATCTTGTCTGTAACCGAAACGGGGACACCTGTGTCA

Lrp5	NM_008513.3	1681-1780	ATGCCAAAAGTATAAAATCGAGGTGATCAACATAGATGGGACAAAGCGGAAGACCTGCTTGAGGACAAGCTCCACATATTTTTGGTTTCACTGCT
Lrp6	NM_008514.3	3316-3415	GCTACCAATGTCATTGATGTGACGAGATTAGATGGAGCATAGTTGGAGTGGTCTAAAAGCGAGCAAGACAGACCTCGAGCCATTGGTAAACCCCG
Lta	NM_010735.2	777-876	CCAGCAGTGATTTCTTTGGAGCCTTGCCTGACTGTAGATTCTAAAGAAACCAAGAATTGGATTCCAGGCCTCCATCCTGACCGTTGTTCAAGGGTACAT
Ltbp2	NM_013589.3	6077-6176	GGCATGAGCTCTTTTTGCCACATCTCCATCTTAGACAGTCTGAGCCCTCATCTCAGAGGATGAAGACTAATACTAAGTCTGAGTGGTAAAGAAA
Ly6a	NM_010738.2	207-306	GAGGCAGCAGTTATTGTGGATTCTCAAAACAGGAAAGTAAAGAAACATCTTCTTACCCATCTGCCTCCTAATATTGAAAGTATGGAGATCCCTGGGTA
Ly6e	NM_001164040.1	465-564	TGGCTACCCGTGAACAAGGGCTGCTCCCGACTCTGCCAGTGAATAATCTCAATCTCGGTGCGGTCGGTGAACAGCTCAACAGCTGCTCCAGTCA
Mab21i2	NM_011839.3	1633-1732	GGAAATCCTCACCAATCCCAAAAGCTTGGACAAACTATAGAGTGTCTGCCGACTGCGTGGAAAGCAACATAAATGGGCATGCTCTCCAGAACACACAACA
Map2k1	NM_008927.3	1696-1795	CTTTGTGCTTGGGCTATTTGCTGTTTCATCAACACATGCCAGGCTGAACACAGTGAACCCCTAGTGACCTGGTGGTGGTCTTACTGATGTTTGCA
Map3k7	NM_172688.2	2406-2505	CAATACTAAGTGTAGTCCCACTGTTACTATTAAGGTGAGTGGTGGCAGCTGTGCTTAAAGGAGAGCAAGTTTACTGACTTTCGTGAGGTTGAGCATCGT
Mapk1	NM_011949.3	1211-1310	TGCTGAAGCGCCATCAAGTTTGACATGGAGTTGGACGACTTACTAAGGAGAAGCTCAAAGAACTATTTTTGAAGAGACTGTAGATTCCAGCCAGGA
Mapk14	NM_011951.2	1421-1520	GAAGACCTTCTCATGGGAACTCCAAATACCATCAAGTGCCCTCTTGTGAAAGATTCTTCTATGTGGAAAGGGGTGCATGTATGTGTTAGTGTGTTT
Mapk3	NM_011952.2	826-925	ACCTTAATTGCATCATTAAACATGAAGGCCGAAACTACTGCACTCTGCTCCCTCGAAAACCAAGGTGGCTGGGCCAAGCTCTTCTAAATCTGACTC
Mapk8	NM_016700.3	971-1070	GAAAAAGGCTAAATACGCTGGATATAGCTTTGAGAAACTGTTCCCGATGTGCTTTCCAGCTGACTCAGAGCATAACAACTTAAAGCCAGTCAGG
Mb	NM_001164048.1	669-768	TCTGGGCAGTGTACCTGGAGCCCAGAGGTGCAAAGTGGCCTTCTGCTGCTGCCGGTCTGCTCAGGTCCTAAGTCCAGTCCATTTTCTTCTG
Mcam	NM_023061.2	631-730	CCAGTGGCTGTACACCTTGAAGAGTGTCTGAGTGCACGCTAGTTAAGGAAGACAAAGATGCCAGTTTTACTGTGAACCTCAGTACCCGCTACCCAG
Mdh1	NM_008618.2	56-155	TGCTTTTGCAGGTGCAGAGATCGGCCCTTGCAGTTTCAATAATGTCGAACCAATCAGAGTCTTGTGACTGGAGCAGCTGGTCAAATGTCATATTAC
Mdh2	NM_008617.2	536-635	TCACAGCAGAAGTTTTCAAGAAGCAGGTTGTACAACCCTAACAAGATCTTGGTGTGACAACCTTGACATCGTCCAGAGCAGAACACGTTTGTGGCAGA
Me2	NM_145494.2	711-810	CGTGGCAGTATAACATGCACTATTAAGATCCGTTTTATATGGGCTGTATCAGAAGCGAGATCGTCCAGCTCTATGATGATCTGATGGACGAG
Mef2a	NM_001033713.1	487-586	TCTAATAAGCTGTTTTCAGTACGCTAGCAGTACATGACAAAGTCCCTTCTCAAATCACTGAGTATAACGAGCCTCATGAAAGCAGGACGAACTCGGATA
Mef2b	NM_001045484.1	1092-1191	GACACGTGGCCAGGTAGCGTCCAAGAGTTCCTCCAGCTCCACAGAGTCCCAAGTCCCAAGTCCAGTCCAGTTCCTATACCACCAGGACGACGACGAGGCA
Mef2c	NM_001170537.1	4342-4441	TTCTACTACTAAAGGTATCAATGAAACATGAAGACAGTATTTAGCAGAGAAACCAAGCAAAACCATCTTCAAAACATGCTTACTGTCACATCTGTTT
Mef2d	NM_133665.3	843-942	CACAGTCCCGTGTCCAATCAGAGCTCCATGCAGTTCAGCAATCAAGTAGCTCTGTGCTACTCCTTCCCTGGTGACATCATCCCTACGGACCCACGG
Mepe	NM_053172.2	37-136	CCCGAAGAAGCCAAGCTTCTCTGAAGGTGAATGACGCCAGAGGGCTCATGAAGATGCAGGCTGTGCTGTTGGACTGCTCCTTTCAGTATGACCTGGG
Mettl7a1	NM_027334.3	572-671	CTACTGGAAATTAATCTTGGCAGCAGGTCTGGATCCTGTGCTGTTCTTTTTTGTATGGATGCAATCTGACGAGAGAGAGCTGGAAGACCATTAGAGCA
Mfn1	NM_024200.4	2066-2165	CTGTACCTTTACATGATGACGAGCTGTACTTATGAGCTTATGAGCTGTGAGTGTGACGACCCCTGCGAAAAGAGAGCGTTTAAAGCATGTTGTAAC
Mfn2	NM_133201.3	400-499	ATGTCCTGCTCTTTCTCGATGCAACTCCATCGTACCCTCAAGAAGGATAAGCGACACATGGCTGAAGTGAATGCTTCCCTCAAGCACTTTGTCA
Mgat4c	NM_026243.4	931-1030	AGTCATAGCATCTTGGAAAGAACATACTGGTAACTCTTGAGTCTCTAAACTTGGCTACATTGGTAAACTCTATCTCAGCATCTCCACGCTCTG
Mitf	NM_001178049.1	3187-3286	TACGATTGAATCCTGTGTGGCATAAAGCATACCTTTTCAAGATGAAGTGCTTAAAAATCTCAGCAGTCTTTTTGGACCAGCACTGACTGAACTGTAAC
Mmp10	NM_019471.3	803-902	TTTTCTCAAGATGATAGAGGGCATTCAATCCCTGTATGGAGCCGGTCCCTCCGATGCCACAGTGGTTCCTGTGTTGCTCTCTCAAAGACCTG
Mmp12	NM_008605.3	2347-2446	CTGTGCTCAATTTACATCAGAAAGTGGGTTGATGACTTGTATGCTATGTTGGCTTACAGGACATTAATGGAAGCTTAAAGAGATGCAGCGCTTCTCAGCTTAGCAGAGACT
Mmp13	NM_008607.1	191-290	ACAGTGACCTCCACAGTTGACAGGCTCCGAGAATGCAATCTTTCTTGGCTTAGAGGTGACTGGCAAATGATGATCCACCTTAGACATCATGAGAA
Mmp14	NM_008608.3	555-654	AGTTTGGACTGAGATCAAGGCCAATGTTGGAGGAAAGGCTATGCCATTACAGGCCCTCAAGTGGCAGCATAATGAGATCACTTTCTGCATTCAAGATTA
Mmp2	NM_008610.2	2377-2476	AGTTAAACAGCCTTCTCCTTCACTGGTACTTCAAGTTAAGAGGGTGGCTTCTTTTTGTGCCAAAGAAAGGTGCTGACTGTACCTCCCGGGTGTCTG
Mmp3	NM_010809.1	1576-1675	TCTTTGTGAAAGGAAGTCTTTGTTGACATGTGCTATGGCAGAACCAACAGGAGCTATGATGACACCAGTCAAGTTGCAAAGGATGTTCA
Mmp8	NM_008611.4	233-332	CTAGAACCTTCAAGCAATCAATCCGGTCTCGAAGATGCCAGATGTTTGCAGAGAAGCTTAAAGAGATGCAGCGCTTCTCAGCTTAGCAGAGACT
Mmp9	NM_013599.2	1571-1670	CCTCTACAGAGTCTTGGAGTCCGGCAGACAATCCTTGAATGTGGATGTTTTGATGCTATTGCTGAGATCCAGGGCGCTCTGCATTTCTCAAGGACGG
Mstn	NM_010834.2	666-765	CTGGAATCCGATCTCTGAAACTGACATGAGCCAGGCACTGGTATTTGGCAGAGTATGATGTAAGACAGTGTTCGAAAATGGCTCAAACAGCCTGA
Msx2	NM_013601.2	787-886	CTACCCCTTCCATAGACCTGTGCTCCCATCCCGCTGTGGACTCTATGCCAGCCGGTGGATATGGCATGTACCATCTATCTAAGGAAGACAGGAT
Cox1	ENSMUST00000082402	558-657	ATCCGTACTTATTACAGCCGTACTGCTCTTATTACTACTACCAGTGTAGCCGACGGCATTACTATACTACTAACAGACCCGCAACCTAAACACAACCTTC
Cox2	ENSMUST00000082405	507-606	ACTTAAAATGATGCCATCCAGGCGGACTAAATCAAGCAACAGTAAACATCAAACCCAGCCAGGGTATTCTATGGCCAATGCTGAAAATTTGGGATCT
Cytb	ENSMUST00000082421	403-502	TGAGGACAAATATCATTCTGAGGTGCCACAGTTATTACAACCTCCTATCAGCCATCCCATATATTGGAACAACTAGTCGAATGAATTTGAGGGGCT
Mthfr	NR_027809.1	863-962	GAAGGCTGCACAGAGATAGGCATCTCTGCCCTATCCTGCTGGATCTTCCCTATTCAGGGCTACACTTCCCTTCCGAGCTTGTAAAAGTGTCCAAG
Musk	NM_001037127.2	235-334	GTCTATCACACGCTCTTGAAGTGTAGATGCTTGGTTGAAGAAGTAGCGACTTTCATGTGTGCGTGGAAATCCTACCTCAGCCGAGATTTCTTGGGA
Myc	NM_010849.4	631-730	CCCTCAACGTGAAGTCAACAGGAACTATGACCTCAGACTAACAGCTCCGACAGCTATTTTCACTCTGCGACGAGGAAGAAATTTCTATCACCAGCA
Myf5	NM_008656.5	746-845	CTTTGACAGCATCTACTGCTGATGTATCAAATGCATGTGCTGCAGATAAAAGCTCCGTGTCAGCTTGGATTGCTTGCAGCATTGTTGGATCGGATC
Myf6	NM_008657.2	627-726	CTAAGGAAGGAGGAGCAACGTGGATGCCTCAGCCTCAGCAGTCTTCCAGCGCTTTCTCCATCGTGGACAGTATTTCTCAGAGGAACGCAAACCTCC
Myh1	NM_030679.1	4527-4626	CCGCTCTCTCAGCAGAGCTGTTCAAGATTAAGAATGCTTATGAGGAATCTTTAGACCATCTCGAAACCTTGAAGGGAAGAATAAGAATTTGCAACAG
Myh2	NM_001039545.2	3973-4072	AGAGAGGACGACTGACAGCCAACTCCGTTGAAATTTCCAGGAGCTTGTAGGAAAGGAGCGTGGTATCTCATGATATCAAGGGGAAGCAAGCACTTAC
Myoc	NM_010865.3	1395-1494	CTACTCTCAGCCCTGCAACCGTCAACTACGACTAACAGCTCCGACAGCTTAAGACCCCTACCATCCATCCATCCAGTAATCGCTACCAAGTACAGC
Myod1	NM_010866.2	1201-1300	TGGGGATGGTGTCCCTGTTCTTCCGCCCCAAAGATGAAGCTTAAATGACACTTCCCACTGTCTTTGAAAGCCGTTCTCCAGAGGGAAGGGAAG
Myog	NM_031189.2	617-716	GCGGCTGACCCTACAGACGCCACAATCTGCACTCCCTACGTCATCTGTTGACAGCATACGTTGGAGGATATGCTGTTGCTTCCAGACGAAACCA
Myot	NM_001033621.3	1685-1784	GTGAAACAAGCTTTAAACCTGAAGGAGAATTTGAGCGCTGGCAGCTCAATCCGACTCTACGAAAGTGAAGAATTTAATACTTTGCCACAGGGAA
Nanog	NM_028016.2	381-480	TCCTTGAAGACCTGCCTCTTCAAGGCAGCCCTGATCTTCTACCAGTCCCAACAAAGCTCTCAAGTCTGAGGCTGACAAGGGCCCTGAGGAGGAGG

Ncoa2	XM_017319230.1	379-478	AGCTGGCCGAGCTGATCTTCGCAAACCTTAAATGATATTGACAACCTCAACTTCAAACCTGACAAATGTCCATCTAAAAGAAACTGTGAAGCAGATCCG
Ndst1	NM_008306.5	1768-1867	ATCTGTGCTGGCAGAGCAGATGGCCCTGAACAAGAAAGTTGCTGTGAGCAGCGCATCCCCACAGATATGGGCTATGCGGTGGCGCCCCACCTCCGGT
Ndst2	NM_010811.2	991-1090	ACTCGAACGGAACCTGTGGTCTTTGTGTTTGTGAAAGTGCACTACTACAACCTGGGGCAGGAGATTGTGGCCATCTTGAATCTAGTCGCTTTGTTATA
Ndst3	NM_031186.2	1433-1532	TCTGAAACCAGCTAGATATCGGAGAGGCTTCATTCAAAAAACATCATGGTCTCCCAAGACAAACCTGTGGGCTCTTACCACACAAATTTCTACAAG
Ndst4	NM_022565.2	67-166	ATAGTTCTCATAGCCTTTTGTGTACCCGGTCTGCTCCCTGGGGTAAGGCTCGTGTCCGAGAAGGAAGCTGCATTTAAACGGTGTGCTGAACAGAGGTC
Ndufa1	NM_019443.3	233-332	TTACCAACGGGGCAAGGAAACGAAATGTCGTGTTCAGTACCGTGGATCTGATGGAACCGGATAGACGTATCTCTGGACTCTACTATG
Ndufa10	NM_024197.1	71-170	GCCTCGCGCCGGAGCCAGCGCTGGGACGAATTCATACCAAGTGTGCACTGCAAGCTGAGGTATGGGCTTTGGCCGCACTTCTGGTGATAAGACAA
Ndufa11	NM_027244.1	2339-2438	CCCACCTCTGCTCCATCTACTCAGGGCCAAGGCTCAAGTCTCTGCTCCAGCGGCTGCACCATGTTGTACAGTGCATCTCGTCTGTGTGCC
Ndufa12	NM_025551.3	121-220	AGGGCAAATGATAAAGGATTGACACTGGTGGGAGAAGACAAATATGAAATAAATACTACGAAGACAAACAGCAATTTTTGGCCGCCAGGATGGG
Ndufa13	NM_023312.2	1028-1127	CAGATTCTCCGGGAAAACCTGGAGGAGGAAGCCATCATGAAGATGTGCCAACTGGAAGGTGGGCGAGTCTGTGTTCCATACCACAGTGGGGTGC
Ndufa3	NM_025348.2	16-115	CAAGAACAAAGATGGCCGGGAAATCTCTGCCCTTCAAGAATGCTGGGCGAAGGAGCCGGTGTGGTGGTGTCTTCTCTGTCTGGGGCCCTCGCTATA
Ndufa4	NM_010886.2	115-214	CATCCAGCTTGATTCTCTCTCGTATTTATTGGAGCAGGGGTAAGTGGAGCAGCACTGTATGTGATGCGCTTGGCACTGTTAATCCAGATGTCAGCT
Ndufa4l2	NM_001098789.1	300-399	ACTTCTAAGTCAGAGATCTCCACGTAATCACTCTTTCTGCTCCCTGCCACAGCCCTGGGCGTCTGTCTAGCAGCATCAGTCCAGCTTCTGCTAAAG
Ndufa5	NM_026614.3	365-464	GTGGTGAAAGTGAAGAGGTGATTCTTCAGGCTGAAAAAGAACTAAGTCTGCAAGGAAAATGTTGAAGTGAAGCCATGGGAGCCATTGGTGAAGAGCC
Ndufa6	NM_025987.3	110-209	CCAGTACCTCGGTGAAGCCATTTTTCAGTCGCGACCTGAACGAGGCCAAGCGGAGGTTGCGCGAGCTCTACCGGCTTGGTATCGGAGGTGCCAAGAC
Ndufa8	NM_026703.2	45-144	GCCGTCATGCCGGGATAGTGGAGCTGCCAACTCTGGAAGAGCTGAAAGTGAAGGAGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT
Ndufa9	NM_025358.3	281-380	ATATCGGTGTGATGATATGACATCATGCACCTTCTGCTGATGGGTGACCTGGGCCAGCTTACCTTTCTGGAATGGGATGCACGAGACAAAGATTCTATC
Ndufb10	NM_026684.2	179-278	ACTGGCCCGTACCTCTGTGAGAGAGTTTATTGAACGACAGCATGCCAAGAACCGAACCTACTACTACCACCGACAGTACCGTCAAGTGCAGACATCAC
Ndufb2	NM_026612.3	233-332	CTGGATTCTTGGCGATTTTGGCATGACTCGGATGCTGTGCTGGTCACTTTTATATCCAGATCCTTACAGTGGACAGATGAAGAAGTGGGAATCCCT
Ndufb4	NM_026610.1	198-297	TGCTTGAATTCGCTGGCAATGCAAGATCAGCAAATTTATCTAAATTTACAGGCCCTCCAAGAACTCACTTTTAGAGCTGTGGCAGGGTTTGGG
Ndufb5	NM_025316.2	107-206	GGAAATTTTCTACGCGGACTTTCCGAAGACTGCTGCTCTGCGCACAGTGGCCAGCATGGCAAGAGACTGTTTTCGTCGAAGCTTTCTTATACT
Ndufb6	NM_001033305.2	311-410	CCATACACCATTGTTAGCTCGAAGCCAGGATATTTCCAGGTGATAACAATCTGGAGACTGGAGAAGTAATCCCAATGAGAGATTTTCTGATCAAC
Ndufb8	NM_026061.2	380-479	CCCTGTGCTCTGGGATGTCATGTGTAACATCTCTCGGCTTTGTGGCTTTCATGTTTTATGTTCTGGTAGGGCAGTGTTCCTTCTACCAGCCT
Ndufb9	NM_023172.3	295-394	TTCTTCGAGAGATGAGTGTACAAGTCCAGAAATGGTCTTAGATTACTGGCATCCCTCTGAGAAAGCAATGTATCTGATTACTTTTCAAGAGA
Ndufc1	NM_025523.1	273-372	AGTCAGCTTACGTGATGATCACAGTCTTCTGATTCACTGAGTGGAGCTGAGAAAAGAGTTACATGCGAATATGAGCAATGAGCAATCCACGTT
Ndufc2	NM_024220.2	270-369	CCCGCGCTTGTCTACATGGGCTTGTGGGCTACTGCACGGGCTGATGGACAACATGCTGCGGATGCGACCGGTGATGAGAGCAGGTTTGCACCCGACG
Ndufs1	NM_001160038.1	553-652	CCTAAAGGATATGTTCCGACAACCTGGCACAGCAGCAAGTAACTTATTGAAATTTTGTGATGGTCACTCTGTATGTTGGAACCCAGGAACCACTGTT
Ndufs2	NM_153064.4	403-502	AAGACCTATCTGCAGGCCCTTCCATACTTTGACCGTTGGACTATGTGTCATGATGTGTAATGAACAGCCCTATTCGATAGCTGTGAGAAAGTTGCTAA
Ndufs3	NM_026688.2	351-450	ATCCCAACGCTGACTTTTCTCAGGGATCACCAATGCACAATTAATCCTTGGCTGACTTGACGGCAGTGGATGTCCCAACTCGGCAGAACCCGTTTTG
Ndufs4	NM_010887.1	71-170	GTAGAGTTCCATGCGAGTTGTGAGACATCCACTTGGAAAGCTGGCAGACACCAAGACTCGGGACACACAGCTTATAACAGTTGATGAGAAACTGGATAT
Ndufs5	NM_001030274.1	111-210	TCAGCTGGACCCGCCATTTATGTTCTAAGCGCAGAACAGCCCTATAAGAACGCCCTCGGTGCCACGCATTTGAAAAGAGTGGATAGAGTGTGCACA
Ndufs6	NM_010888.2	410-509	TGACTCCTATGGAACATCTCCACGCTGGGTGTTCTGTGTGAGGCCACTGCTCTGTAATGGTGTCCCTTGTGTTGAAATAAAGGATGTCCACCATGAAA
Ndufs7	NM_029272.3	328-427	GTGGAGATGATGCACATGGCTGCGCCGCTATGACATGGACCGCTTGGGTGTGGTGTCCGTGCCAGTCCGCGCCAGGCTGATGTGATGATTGTAGCTG
Ndufs8	NM_144870.5	721-820	GCAGCCGCGAACGACAGCTATGACATGCATGACCAAGTGTATCTACTGTGTTTTCTCCAGGAAGCCTGCCCTTGTGATGCCATTGTGGAGGGCCC
Ndufv1	NM_133666.2	1151-1250	GGCAGGCTGCAAGTATTGTTATGATCGCTCGACAGACATTTGAAAGCCATCGCTCTCATTGAGTTCTACAAGCATGAGAGCTGTGGCCAGTGTA
Ndufv2	NM_001278415.1	545-644	TACAATGTATAATCGAAAGCCAGTTGGGAAGTACCATATCCAGGCTGCACTACTACCTTGCATGCTGCGAGATTCTGACAGCATATTGGAGACCTT
Ndufv3	NM_001083891.1	103-202	GCGGTCTCTCTCTCGCGGGGAGACGATCCGGGCGCTGAAGGCTGTGCTCTGGAGGCAAGGGTGTCCCGGGAGAACTGTTTCTGTAGTAGGCG
Neb	NM_010889.1	7143-7242	AAGATTATGTGATGCGGATACACCAGATATTTTGAAGCAAGCAAGAACTTACAGTCAAGAACTCTATAGACTTGGTTGGGAAGAGGGCTC
Nell1	NM_001037906.2	2575-2674	ACCAAAGTCTCCATCAGAGGAAGGCGTTTGGGTTGCCCTTACCCTTCTCATCTTCTGCTGACCTAGTCTAGATGCTCGCAGTACCGTGTATTTCCGGTC
Neo1	NM_001042752.1	6449-6548	TTACTTTCAACAAGATGAGCTCTTGTATGATTGCGGGCGGGGATATGAAAATGCAATGATCTAACTCTGTTGCTCTTCTAGCTGGTACATGACGGC
Nes	NM_016701.3	2717-2816	GCAGAGAATTTGAAAACCTTAGAAAAAGTGAGCCAGTCTCCCTGCAATCTCTGAAAAAGAGAAATGTGCAGTACCAAGGTATCTGGAAGAAGATGAC
Nf1	NM_010897.2	2706-2805	CCCACCTATGGGGCGTGTGAGTGAACGCAAAGGCTCTATGATTTCTGTAATGCTTCTGAAGGGAAATATTGATTCACCTGTGAGCAGATTTATGGACGG
Nfatc1	NM_016791.4	1571-1670	ATCCGTTGCTTCCAGAAAATAACATGCGAGCCATCATCGACTGTGCTGGGATCCTGAAGCTCAGAACTCTGATATTGAGCTGAGGAAAGGGGAGACAG
Nfkb1	NM_008689.2	2126-2225	GTCCTTACACTTACCATCTCCACCTCCAGCTCAGCTTGTGAGGGATCTGGCTGGAAGTACATCTGGTTTGTATCTGATGACATCAACATGAGAA
Ngf	NM_013609.2	281-380	TGAGGTGCATAGCGTAATGTCATGTTTCTACTCTGATCACTGCGTTTTTGTGCGGTACAGGCAGAACCTTACACAGATAGCAATGTCCAGAA
Ngfr	NM_033217.3	904-1003	TTCTGTCTATTGCTCCATCTTGGCTGTGTGGTTGTGGCCCTGTGCGCTATATTGCTTCAAGAGATGGAACAGCTGCAAGCAAAATAAACAGGAGC
NLRP3	NM_145827.3	509-608	ACGTGTACATCACATCTCTATGGTATGCCAGGAGGACAGCCCTGAAGAAAGAGTGGATGGGTTTGTGGGATATCTCCCGCATCTCCATTTGTA
Nog	NM_008711.2	1310-1409	ACCTCAAACCACTTCCACCCTCTAGCGAGGTTTTCAATGAACCTTTTTCTTCTTGGCTACAGAGACCTGGCTTTGTTCTGTATGCACTGT
Nos2	NM_010927.3	3716-3815	CCCTCCCTCCACCTACCAAGTAGATTGTAATTTGGAATCTAAACTTCTCTCTCTCTCCCTCCCTCTCTCCCTTCTCCCTTCTCTCTCT
Nos3	NM_008713.4	3614-3713	ATACCTGGTCTGACAGTCTTCTCCCTCCAGTTCGGGAAAGAGGGATTGTGCACTTCTGTTGCGTTGACCAAGGCTAGCCACCTCTCTGAAGAAT
Notch1	NM_008714.2	1426-1525	TGAGATTGATGTTAATGAGTGCATCTCAAACCATGTGCAAGATGATGCCACTTCTGACCAAGATTGGGAGTTCCAATGCATATGTATGCCAGGTTAT
Npnt	NM_001029836.1	2651-2750	ATGGTGACCTGTATCTATGCTATGACTTAAACAGCAGCAAGAAAACCTGCAAGAGTGTGCGGCTTGGGGTAGTGTATGATGGCTTTGTTCTGTGTC
Npy	NM_023456.2	231-330	GACACTACATCAATCTCATACCAGACAGAGATGGAAGAGATCCAGCCCTGAGACACTGATTTACAGACCTCTAATGAAGGAAAGCAGAAAAACGC

Nr3c1	NM_008173.3	1801-1900	ACCAGGATTGAGAACTACACTGGATGACCAAAATGACCCCTTACAGTACTCATGGATGTTTCTCATGGCATTGGCCCTGGGTTGGAGATCATACAGA
Nt5e	NM_011851.3	1601-1700	AAGCATGACTCTGGTATCAAGATATCAGCGTGGTTTCTGAATACATCTCAAAAATGAAAGTAGTTTACCAGCCGTTGAAAGGCGGATCAAGTTCTCTG
Ntn3	NM_010947.3	4527-4626	GCCAGGCACTCTTAAGTGCTTGTGGAGGGAATAAAGATGCCACTTTTTGAATGCTACATGTCAACTAGTGAAGTACGCAATGTAGTGGCTTTTGGCTG
Ntrk1	NM_001033124.1	1482-1581	ACTCCAGGGCCACATCATGGAGAACCCACAGTACTTCTAGTGATACCTGTGCCATCACATCAAGCGCCAGGACATCATTCTCAAGTGGGAGCTAGGGGAG
Nudt6	NM_153561.2	643-742	ACAGGAGCCCTGGGCGCTTGGGATGTGACAGCATGTACTGGTCTGCCGCTGCAGCTCGTTCCTTCACTTCAACTTCTGCCAGCAGGAATGCTTGA
Ogdh	NM_010956.3	3641-3740	ACTATAGCTGCCAGGATTTGGAGTCAACAGATTTGTGTGAATGAGTGTGTTGAGGAGTATTAGAGACTTTAGCAGTGTGTTAGTGGACCCCTG
Ogdhl	NM_001081130.1	295-394	AGCAGAAGCGGAGTCACTCCAGTTATGTGGAAGAGATGTACTTTGCTGTTGGAAACCCACAGAGCGTTCACAAGTCTGGGACAGCTTTTTTCAGA
Olfm4	NM_001030294.1	1035-1134	TTAATCTATCCCACTCCGAGACTATCGGATTCGCTATGGCCAAGGAGGTGTACAGTAGCATTCAACAACAACCTGTATGTGAATTTGTACAATGGGG
Opa1	NM_001199177.1	2846-2945	CTACCAGAGGCATTTTATAGATTCTGAGCTGGAATGCAATGACGTGTCCTGTTTTGGCGAATACAGCGCATGCTCGCTATCACTGCCAATACATTAAGG
Opa3	NM_207525.3	1899-1998	ATGAGGGGCATAATTAATACGGACCTTCAAACCTGGGCCAGTGATCATTAAACAATAGAGAAATCCGGGCTTGGTAGCTCATATCTGAAATCCAGCACTCT
Oscar	NM_175632.2	1125-1224	CTGGCCGCTGGGATCATAGTTTCACTTACCACACCCAGCAAAAATTTCTAATTCATATTTTAAGGGTAATACCCAGCCCTCAGCCGTGTGTAGAGG
Ostn	NM_198112.2	417-516	GGATTGGTAGAAACCGCTCTCCAGTCCAGAGGCTGATGGATTCTATTGTGCGACTTACTTGTGTGAGATGGCACAGAACTATAGAAGACACTTCAGT
P2rx7	NM_001038839.2	379-478	GGAGAATGTACAGAGGGTGGGGTGACGAAGTTAGGACACAGCATTTTGACACTGCAGACTACACCTTCCCTTTCAGGGGAACCTATTCTTTGTCATG
Pappa	NM_021362.1	3037-3136	CTCTGCTAGAAGATGTAGCCTCATTACTCCACCTCAACAGAAGATTATGACACCGGATCTGAAACTTGGCAGTGTGTACCAGTACCGGATTATCACCAT
Park7	NM_020569.3	335-434	TGCAAAAACGCAAGGACCATACGATGTGGTGTCTTCCAGGAGGAAATCTGGGTGCACAGAATTTATCTGAGTCGCCTATGTGAAGGAGATCTCTCAAG
Pax3	NM_008781.4	851-950	GCCGCATCTGAGAGTAAATTTGAAAAGGAGAAGAGGAGGCGGATCTAGAAAAGAAAGGAAGCAGAAGAAAGCGAGAAAAGGCTAAAACACGACAT
Pax7	NM_011039.2	942-1041	GCCCAGCTGCCACCTACCAGCTGCCGACTCTACCTACCCACCACCACCTCTCCCAAGATGGAGGCGACAGTACACAGGCCCCAGCCCTTCCG
Pdcd1lg2	NM_021396.2	1871-1970	ATTGTTAGGGCACTTGAGGGTGGGCGTCTGGAAGTCTTTCAGGTAGTGTGGGGGAGGGTGTCTCAGAATACATAAAGGTGCTAACTTAAACTGC
Pdgfa	NM_008808.3	806-905	TGTGCGTGGCGTGTGACATTCCTGAACATACTATGTATGGTCTTATTGCCAATGTGCGTGCAGTCTTGTCTCCTCCGTGAAAAACTGTGCCGAGG
Pdgfrb	NM_008809.1	1186-1285	CTCAAGGACAACCGTACTTGGTGACTCCGCGTGGCGAGTTAGATTTTTGCTACTCGCAACTGTCTGAGCCCGGACGTGTGAGAGTATCACTCTGG
Pdha1	NM_008810.2	2181-2280	TGGCTCTGTGTAGAGTGTGGATCTTTAAACAAGAGTGAAGAAGAGGCTATCACTTCACTGCCTTGCACCCCTGAACCTGAGAAAAATGAGCTGTCTTGG
Pdhb	NM_024221.3	1193-1292	CTTCACTGATGTGTACTGCGAGACTGTAGTACATAAAGTAAATGCTGAAGTGACAGCAGGTGTCTGAACTGTAAGAAGTTCAATGTGCTTATGAGTGG
Pdhx	NM_175094.4	2186-2285	AGTTGGGGGAGCAGCTGGTTGTACCTATAACCTCAGCCTTTGAGAGAGATTGAGAAAAGGAGGCCCGCTTTGAGGCTAGCTGGGCTACGCGGTGAGGGC
Pdk1	NM_172665.3	646-745	GATTCATAGTGCATCTCAATTAGAATGCTACTCAACCAGCACTCTTATTGTTCCGGTGGAAAAGGAAGTCCATCTCATGAAAGCAGTATGGAAAG
Pdk2	NM_133667.2	671-770	AAACACATTGGCAGCATGCCCACTGCAGCGTGTCTGATGTGGTGAAGAAGCCCTATGACATGGCTAAGCTCCTGTGTGACAAATGATCGGTTCTGCT
Pdk4	NM_013743.2	1356-1455	AGCGGATGACCGCTGACATTTTACGGGATCAAAGTGGGTCTGTGGCATTGCTGCTTCTGTAATGTGTGGACTCTAGTTTCCGCAAAAACACGCAACAC
Pdp1	NM_001098231.1	121-220	AGTCTGCCACTGTTCTGATGCCATGCCAGCACTCACTGTTTTTCTCTGTCGGTAACTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG
E11/Pdpm	NM_010329.3	541-640	AAGCCTCCCTTAGAGGAAGTGTCCACCTCAGCAACCTCAGACCATGATCAGAGAAACAGAGAGTACAACTGTCAAAAGTGGTGAAGTGAAGTGAAGTGAAG
Pdpr	NM_198308.1	1795-1894	GTACTCTGAGCCACATCGTTACTACTGGCATGCTCAATGAATATGGAGGATACGAAAACGACTGCAGCATCGCAGCCTGACCAACGAGTTCCTTTA
Penk	NM_001002927.2	1011-1110	CGCTTGTCTGAGTCTCTGCCCTCGATGAAGAGGCGAAAATTAATCTGAAAGAAAGTCTCTGAGATAGAGAAAAGATACGGGGCTTTATCGGTTCTGAA
Pfkfb3	NM_133232.2	3786-3885	CTGTCTCAGCCTCTCAAATGTTAGTGTTCGGGTTAATGATGAGCCACCACACACCGCTGGTACTATGGCTTTGTACCTAAATGTGGTTTCTTC
Pfkl	NM_008826.4	2155-2254	AGGCCATGTTGTGGGTGCTGTGAGAAGTACGTGATGTCTACCGTAAAGGCGGGTGTGGTCCAAATGCTCCAGACTCAGCCTGTGTGATCGGCTGCGGAA
Pfkl	NM_019703.2	311-410	GGGACCATCATCGGTAGTGCAGCTGCAAAGCCTTTCGAAGCCGTGAAGGCGCCTGAAAGTGCCTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG
Pgk1	NM_008828.2	37-136	CCGGCATTCTGCAGCTTCAAAGCGCAGCTGCGCGCTGTTCTCTCTCTCATCTCCGGCCTTTGCACCTCAGGTTGTCGCAAAATGTCGCTT
Phex	NM_011077.2	2581-2680	TCTTCTGAGTTATGCTCATGTAAGGTGAATTCATAGACCAGAAGTGCAGAGAAACAGTGAAGTGGTCTCACAGTCCCAAAATTTAGGGT
Phf20	NM_172674.2	1966-2065	CAGCTCCATGGTTCAGATAATGAAACCACAAAGGAAATGAAACCTGTGAGGAGGATAATTTGAGTGAAGTCTCTCCGAGAGCTTTCTTTGGAGTG
Phf6	NM_027642.1	2051-2150	AATGCGCTAAAGGACTTTGGACATCATGCTGAAACAGCTTCTCTCAAGTCCCTGTTGTGTGGAACACTTCACATATGGCCAGCATATATAAGGAG
Phf8	NM_001113354.1	1406-1505	GAGGGAAAAAGTCTCAATGTCATTAGTTTGAATTCCTGATACCAGGCTTCAAACCTCGTGAACACCCAGGATTGTTCCGAAAGTGTGATGGGTTG
Pigs	NM_201406.1	1913-2012	TCAGAAGGTACCTTCTGATCTCCATATCTGGCTCGAAGTGAAGGCTTTGTGTGCTTCACTCTGACAGGGGTACTTTGTCTTGCAGCCTGTGAGC
Pik3ca	NM_008839.1	1256-1355	ACTGTCCGTTGGCCTGGGGAACATAAACTGTTTGATTATACAGACACCCTAGTGTCCGGGAAAAATGGCTTGAATCTGCGCTGTACCGCATGGGTT
Pink1	NM_026880.2	689-788	GGAGCAGGCTCCAGGACTCCACCTTTCCCTTTGCCATCAAGATGATGTGGAATATCTCGGAGGTTCTCCAGCGAAGCCATCTTAAGCAAAATGAGC
Pknox1	NM_016670.3	560-659	TCCTGAACTGGAGAAGGTTAATGAGCTCTGTAAGATTTCTGTAGTGCATGTTGTTCTGAAGACAAAATGAACAGCGAGACCTTTGTGAGTGGG
Plod2	NM_001142916.1	2926-3025	AACCTGAAAGCCTGGGATTCTGACGCTACTGGCTCTATGTAATTAATGATCATTGACCTCTGTGTAGGGCTGTTTTCCAGGAATTAGGAAGAAAAA
Polg	NM_017462.2	2095-2194	CG95GTCACCTCAAGCAATGGCACTGAGCTGGATGGTTTTCTCTACACTCAGACTCATGTTGTTGGGCTACCTAGTGTGGGCGTCCGAGGAT
Polr1b	NM_009086.2	2796-2895	TGCCCTTCACTGAGAGTGGCATGATGCCGACATTCTGTTAATCTCACGGGTTCCCTCCGATGACCATAGGTATGTTAATCGAGAGCATGGCTGG
Postn	NM_015784.2	760-859	GACCTTTCATCATTAGAGCAGCCGATACCTCTGACCTCTGGAGTCCCTGGAAGAGATGTCACTTCACTCTTGTCTCCACCAATGAAGCTT
Pou5f1	NM_013633.2	736-835	AAAGCGAACTAGCATTGAGAACCCTGTGAGGTGGAGTCTGGAGACCATGTTTCTGAAGTGCAGGAAAGCCCTCCCTACAGCAGATCACTCACATGCCAAT
Pparg	NM_011146.1	1061-1160	ACCAAGTACTCTCAAGTATGGTCCATGAGATCATCTACAGATGCTGGCCTCCCTGATGATAAAGATGGAGTCTCTCATCTCAGAGGGCAAGG
Ppargc1a	NM_008904.2	691-790	CAGAAATCATGGAGCAATAAAGCGAAGGAGCATTTGTCAACAGCAAAAAGCAGTCCCTGCTCAGACTTCTCAAGTATCTCAGCAACCAACGAT
Ppargc1b	NM_133249.2	3011-3110	CCCACATCTGAGGAGTCCCTCCCTCATCTGGGAAAAGCAAGTACGAAGCCATGATTTTGACAGCTTACTGAAAGAGGCCAGCAGAGCCTGCATTGAT
Ppid/Cyp-40	NM_026352.3	1577-1676	GGGTCAACCATGAAGAATGTAATAAAGGTTGAGCAGTACTAGTAAAGTGGGAAACCACTGATGTAAGTGTACGTTTATGTATTAAACGACTATGTG
Ppp3ca	NM_008913.4	1676-1775	AGGGCATGATGGGATTGCTGCATCTCAGCAGTTGGATGTTCTTCCCTGGAAGGTAGCTTGTGCTCTGGGGCCAGGAATTGGATTAGTTTACACTA
Prdm16	NM_027504.3	6816-6915	GCAGGGCAGAGGTTACAGCCAGATTGTTTCCCAATGATACCTTCCATTGTTGCACTGCTCCTCAAATAGAAATTCATTCATCGGGAGGCCACTAGC

Prkaa1	NM_001013367.3	1861-1960	GAATTGAATGAGGATCACTCTGTATCCCGTATTAGTAGGTACACACAGCGTAACACACACAATGGACTGTAGGTCTCAAGCTTACTTGACTTTTGG
Prkab2	NM_182997.2	2127-2226	GCTCACTGGGTGCTCATGCGAGGTTTCCCTACCATTAAAGATGTGTGAGGCAAGAACTACCCTCGGTGTTCCATAACCGTGACAGTATTGCTTTTGCA
Prkag1	NM_016781.2	1510-1609	GAGGCGCGTCCGGTTCTGTGCTGTGCGACGAAAGCAGATGGCTATGTGGAGAGGGCGGTGGGTAGGTAGCCAAGATTAATGCTTTTTGTGGCGAAT
Prkag3	NM_153744.3	1189-1288	GTTCTGGAACAGCTCCTGTCTGACTCGCTGGACATCTTTGTGGACCGACGTGTGTCTGCACTGCCTGTGTCAATGAATCTGGTCAGTCTGTTGGCC
Prkd1	NM_008858.3	3336-3435	GAGCCAGGACCTATCCAGGACACATTGTGTTGGTGTGCTCCATTGACTGTGGTGTGTAAGCAAACCTTTGAGGAGTAGATAATCTGCCGGTGTCT
Prx1	NM_175686.3	106-205	TCTGCCCTCCAGGGTCTCAATTTTTCTGTATTTCCCTCAAAGCTGTCTGATCCAGCCTGTGCCTTTTGAAGTCCAGAGACTCTTGCTGTCCA
Ptgs2	NM_011198.3	676-775	CCATCAGTTTTTCAAGACAGATCATAAGCGAGGACCTGGTTTCCCCGAGGACTGGGCGATGGAGTGGACTTAAATCACATTTATGGTAAACTCTGGAC
Pth1r	NM_001083936.1	397-496	CGATGCTTTTACAAAGAGGAACAGATTTCTGCTGCAACCGTGCAGGCGCAATGTGACAAGCTGCTCAAGGAAGTTCTGCACACAGCAGCCAACATA
Pth2r	NM_139270.2	296-395	CGAGCCTGGGATACAGACTGCTTTTGCCTTGGCAGTTTTGGACATGGCCTGGCTGGAGACTTACCTACATTTGTGGATGGCTGATTCTCAGTAGCTG
Pthlh	NM_008970.3	791-890	AAAAACCACCCGTGGGTTTTGGTGCAGACGATGAGGGCAGATACCTAACTCAGGAAACCAACAAGGTGGAGACGTACAAAGAACAGCCACTCAAGACAC
Ptk2	NM_007982.2	1061-1160	TGTACAGATTTGACAAAGAGTGCTTCAAGTGTGCCCTTGGGTCAAGTTGGATCATTTCTGTGGAATTGGCAATCGGCCAGAAAGAAAGGATCAGTTACCT
Ptprc	NM_011210.3	2321-2420	AGTGGATGTCTATGGTTATGTTGTCAAGCTAAGGCGACAGAGGTGTCTGATGGTGAAGTGGAGGACAGTATATCCTGATTCATCAGGCTTTAGTGGAA
Rac1	NM_009007.2	1046-1145	GCCAAAATACCTTCTGAACCTAAGTTGCGTTGTGCTGAGAACCTAAGCACTAACTCTCTTGAGAGACTTCTGTGTAAGAAGACCGCAGCTTCTGGA
Rhoa	NM_016802.4	1886-1985	CCTGAGGACAGTTATCTTTGGAGGTGGCATAGCCTTTCTCACTGGACTGCAGGGTCTGGCTCTAAGTCAAGTGTCTCTTCTCCACTGTATCCAAAG
Rhot1/Miro1	NM_001163355.1	2116-2215	CAAGAGCTCAACGTTCTGGCTTCCGCGAAGCTTTGGTCTACGGTCTTTGCACTGGTGGCTTGTCTATGTACAGAGCACTACTGAAACAGCGATGATTA
Rpl19	NM_009078.1	21-120	GAAGAGGCTTCCCTAGTGTCTCCGCTGCGGAAAGAAAGGTCGTGGTTGGATCCCAATGAGACCAATGAAATCGCCAATGCCAATCCCGTCAAGCAG
Rplp0	NM_007475.5	1022-1121	AAGGAAGAGTCGGAGGAATCAGATGAGGATATGGATTGGTCTCTTCCACTAATCCCGCAAAGCAACCAAGTCAAGCTGCTTAATTTGAGAAAGATGG
Rps6kb1	NM_001114334.1	534-633	AACATTCTGGAGGAAAGTGAACACCCCTTTCATTGTGGACCTGATTTATGCTTTTCCAGACCGGAGGAAAGCTCTACCTCATCTCGAGTATCTCAGTGGAG
Runx2	NM_009820.5	1117-1216	TCCTATGACCAAGCTTACCCTCTATCTGAGCCAGATGACATCCCACTCCACTCCACCACGCGCTGTCTTCCACACGGGGCACCCGGGCTACCTG
S100a4	NM_011311.2	358-457	AAGATCTCAGATGAAGTGTGGGGTGTAGTTTTGCCAGTGGGGATGTTCCCTGTGGCTGTGAGCATAGTGCCTTACTTGGCTTCTGCACATGTG
S100a6	NM_011313.2	2-101	CAGAGTTTCGAGTCACTGCCAGAAGGAAACTAAACACGGAAATAGAGAAACTTGATGCCCTCTGGCTTGCCTTGGCCGGTTCAGGGC
Satb2	NM_139146.2	1381-1480	CAAGTTAGAGATGAGTTGAAGAGGGCTAGTGTGTCTCAAGCTGTCTTTGCAAGAGTGGCATTCAACCGCACACAGGGATTATTGTGAGAGATACTGCGTA
Scx	NM_198885.2	712-811	AGATCTGCACCTTCTGCTCAGCAACAGAGAAAGTTGAGCAAAGACCGTGACAGAAAGACGGCGATTGCAAGTTAGAAGGAGGAGGGTCCACAGCAGCC
Sdha	NM_023281.1	251-350	TTTGGCAGTGCATTTGGCCTTTCTGAGGCAAGGGTTAATACTGCACTTCAAAGCTTTTCTACCCGATCACATACTGTTGCAGCACAGGGAGGT
Sdhb	NM_023374.3	566-665	CCTTGAGTAACTTCTACGCACAATACAAATGAGCCTTATGAGCCTTATCTGAGAAGAGGATGAGTCCAGGAGGGCAAGCAACAGTATCTGATCCATCGAG
Sdhc	NM_025321.3	326-425	ATGTTTGTGAAGTCCCTGTGTTTGGGGCAACACTGATCTACTCGGCTAAGTTGTGCTTCTCCGCTCATGTACCCTCACTGAATGGGATCCGAC
Sdhd	NM_025848.2	186-285	CAAGCCACCCTCTGGTCCAAGGCTGCATCTCTCACTGGACCAGTGTGAGAGGGTGTGAGTGTCTGCTTGGGCTGATCCCTGCTGGTACTTGAA
Serpib2	NM_001174170.1	716-815	TGGGCTTTATCCTTCCGTTGTAACCTCGCATGAGAGCATACTCTCCAGATGATGTTCTCCATGCAAAGCTGAACATTGGATACATAAAGGACCTGAAG
Serpib5	NM_009257.3	991-1090	TTTCTCTGGAATGTGAGAGACCAAGGGAGTGCCTGTCAAATGTGATTCATAGAGTATGCTTGAATAACCGAAGATGGTGGTGGAGTCCATCGAGGTG
Serpine1	NM_008871.2	1823-1922	AGGGGCAACGGATAGACAGATCAAATGGTGGCCCAATAGCGACCTTCTCCCTGCTCCCTCCCTTGCACACAGCTGCTTATGTTATTTCCAGAGTGAAG
Serpinh1	NM_009825.2	1846-1945	GGAGCCAGATACTATGATACCAAATTCAGGGGTGTACAGCCATTTTGTCTGCCCTGCAAGTTTGTAGTCCAATCTGCCTCAACAGTCAATCAGTGTT
Sfrp1	NM_013834.2	2506-2605	TGCATTCCTCCGGTCATATCTTTGAGGCTAAAGTGCCTATCCGAGGAGATGGTTTCAAAGGCTAACTAATCTGCAGCTTCCCAAGTGCCAGAGGT
Sfrp4	NM_016687.2	896-995	GGAGTGGTTCGAATGAGGTCAACTGTGGTATGATAAAGAGATCTCAAGTCTTTGTACCTATCCCTGCAACACAAGTCCCTCTCATACCAATTC
Sgca	NM_001136080.1	877-976	AGACTCTGACAGATGCTTGGTGACCTTGGTGCCTTTGTTGGTCTGCTGCTTACTCTGTTGCTGGCTTACATCATGTGCTTCCGCGTGAA
Shbg	NM_011367.2	825-924	ATGGCTCAGGACAACCTCTTGTCTTGGAAACAGGAACAATCTTCTGGCTTAACTTCACTTCCAAACCAAAAGCGTGTCTGTCTTCCGAGCGAGA
Shprh	NM_001077707.1	1171-1270	CTGCATCTTATGCGGAGAAATTTACACCTGATGGCTTCAAACCTACTATAATCCATATACAGGCTGCATCATTGAGATTTCCACATGCGGGTC
Sirpb1a	NM_001002898.1	451-550	TGCTAAACCATCTTACCTATGCTCTCCGTCTGAGCCAGAGCTGCTCCCTCAGCAGACAGTACCTTTACATGACAGATCCCATGATTCTTCCGCGG
Sirt1	NM_019812.2	844-943	GGATTCTGACTTCAGATCAAGAGACGGTATCTATGCTGCTTGGCGTGGACTTCCAGACCTCCAGACCTCAAGCCATGTTTGTATTTGAGTATTT
Sirt3	NM_001127351.1	806-905	CCAGCTGTCTGAAGCAGTACAGAAATCAGTGCCCGACTGCTCATCAATCGAGACTGGTGGGGCGTTCGTTCTGAGTCTCGAAGGAAAGATGTGGT
Ski	NM_011385.2	1211-1310	TGATTCGAGACAGCTTCTACTCTCAAGAGCTTTGAGACAGCCGTGGCCCAATGTGGCCTAGCACCAACCCAGCAAAAGGTTGTGAACAGTCC
Slc17a5	NM_172773.2	1421-1520	GGGAATGGCAGACTGCTTCTGTATCGCTGCTGCTATTAACGTGTTGGGGCCATTTTCTCAGCTGTTGCCAAAGGGGAAGTGCAGAGCTGGGCTCT
Slc25a31	NM_178386.3	859-958	AGTTAGAAGACGTATGATGATGAGAGTGGGGAATCTGATCGGCAATATAAAGGAACCATAGACTGCTTCTGAAAATCTACCGTCATGAAGGAGTTCT
Slc25a4	NM_007450.4	855-954	CTGCTGGAGGAAGATTGAAAAGATGAAGGACCAACGCTTTCTCAAAGGTGCTTGGTCCAATGTACTGAGAGGCATGGGTGGTCTTTGTATTGGTA
Slc2a1	NM_011400.3	2191-2290	GGACTCCATTTTGTAGTCTGCCATCTCTGCTTCTTCCAAACCACTCAATTAATCTTTCTTGGCTGAGACCAGTTGGAAGCACTGGAGAGCTGAGG
Slc2a3	NM_011401.4	1191-1290	CTCAGCAGCTCTGGGATCAATGCTGTGTTCTATTACTCAACAGGAATCTTCAAAGACGCGGGTGTCCAGGAACCGATCTATGCCAGATTGGAGCAGG
Slc2a4	NM_009204.2	961-1060	CTGATGTGTCTGACGCACTAGCTGAGCTGAAGGATGAGAAACGGAAGTGGAGAGAGAGCGTCCAATGCTCTTGTCCAGCTCCTGGGAGCCGACCCCA
Slc35a2	NM_153170.3	925-1024	TTCAATTTGAAAGCATCGTGTGGTCTGCTCTGGAAAAACAAGATGAAGGATGCCCGCGCTTCCAAACCTTCTGCTTTGGGGATGTCATCATCACC
Smad1	NM_008539.3	241-340	ACAGAGGGACAGATTTTTACTCTTCCAAACCGCAGACCAAGAACTAAGGAACTATGTAATACTGAAATCTCTGTTGGCTCTGCGCCCAAC
Smad2	NM_010754.4	881-980	TCACAGCTTGGATTTAGTCTGCCATCTCTGCTTCCAAACCACTCAATTAATCTTTCTTGGCTGAGACCAGTTGGAAGCACTGGAGAGCTGAGG
Smad3	NM_016769.3	1846-1945	GTGTATGCCACCTGACTCCTTGTAAATGACAGAGGTCTGGATGTGACAGTCCAAAAGGAAAGTGCCTTTCCATGGCTGGAGTATGGAGTTTACCT
Smad4	NM_008540.2	2886-2985	TCCTAGGGAGAAGTTTTGTATAAAACACTAAAAGCAGTGTCACTCTGCTGCTTCACTGTTCTGCAAGTGGCAGTACTCAACTGAAATAATGAA
Smad5	NM_008541.2	2631-2730	ATACCTTGTCTCTTACCAGACTGTATACAAGACTCGTGCAGTGTAGCCAGTAGAGGCTCTTGGTTGGCCAAAGAAATGAGGCTGTTGGTGAAGTG
Smad9	NM_019483.4	2574-2673	AGCCTTGGGAAAGCTCGAGGCATCTTTGGATCTTATTTATGCATCTCTCAGCCTGGCACCTATGTTAAGTTATTAGCTGGTTACATCAGTGCAGCCTCT

Smarca4	NM_011417.2	3541-3640	CAACGAACCATAAAGTGCTCCTCTTTTGCCAAATGACCTCCCTCATGACCATCATGGAAGACTACTTTGCATACCGTGGCTTCAAATACCTCAGGCTTGA
Smarca5	NM_053124.2	1-100	GAGGAGAAGGCGCGGGAGGCGCTGAGAACCTTCGTTTTCTTTCCCTTCCCTCGGCCCTCCCTCAGAGTCAGCCGCTTCCCTGACCTCC
Smarcad1	NM_007958.1	931-1030	ATGTTTGGTGATGAGGTTGGGACCCAGGAAAGGAAATATCTTCTTCTGAGGAGGATGACGTTAATGATGATCAGTCTGTAAACAGCCGCGAG
Smoc1	NM_001146217.1	2956-3055	TGTTCTTTTGCTGGCTTCTCTCCTCAACCTGCCTTCCCTGGGTTTCCATCTCAGTATCTCTGTAATGATCCACCCTGGTAAACCCTGCTCTATTTTG
Smoc2	NM_022315.2	1811-1910	CAACTCTCACTCCTCGTCCCTCTGTGGAGGGCTGGTTTATTCCCTTGCCTTTCTCTGCCTGCAGTCTCCGTTGGCTTGTCTCCGTCCTGTGATGC
Smurf1	NM_001038627.1	4049-4148	ACTAGTCTCTCAATTCTGCTTCCCTGCCCCAGTGGGCTTCTGTACTCATCTCCTTATGCTTCCGAGGGTCTTCAAACCAGCTCCCTGCCTGACTCTC
Smurf2	NM_025481.1	1020-1119	GGGATCTTAGCAACATCAATTGTGAAGAGCTCGGTCTTTGCTCTGATGGGAGATCCGCAATCCGCAACAGGAAGATTTATTTCTGTTGACCATAA
Snai1	NM_011427.2	911-1010	TCACTGCCAGGACTCCTCCAGCCTTGGTCCGGGACCTGTGGCTCCATGTCTGGACCTGGTCTCTGCTTCTTTGGTGGCCTTTGCCGAGGTG
Snai2	NM_011415.2	816-915	AGACCCACTCTGATGTAAGAAATACCAAGTGCAAAAACTGCTCCAAAACCTTCTCCAGAATGTGCTTCTGCATAAACATGAGGAGTCTGCTGCTGTGT
Snaip	NM_001199151.1	1386-1485	TCGCTGGATGGTGAAGTGAAGCAGAAGCATTGCGGAATTGAGTTGTTCACAGATTTCACAGCCTTATTATTACGAGGTTGCTATGGGCAGGAAAAAG
Socs1	NM_009896.2	1021-1120	CAGCTTGTGCTGGGGCCAGGACCTGAATCCACTCCTACCTCTCCATGTTTACATATCCAGTATCTTTGCACAAACCAGGGTCCGGGAGGGTCTCT
Sod1	NM_011434.1	407-506	TGTGTCCATTGAAGATCGTGTGATCTACTCTCAGGAGAGCATTCCATCATTGGCCGTAACAATGGTGTCCATGAGAAACAAGATGACTTGGGCAAAGGT
Sod2	NM_013671.3	1496-1595	ATAGCTTTGCTCCTGCTTGGAGGAGTCTTATTATGAGAGGAAGTAATTGGTCCCTCGGGTTTTCTATAGGAGACATGCAAAAACAGCTAATCTTGTCT
Sost	NM_024449.6	367-466	CCCGCGCGGCTGCTGCCAACGCCATCGGGCGCGTGAAGTGGTGGCGCCGCAACGACCCGATTTCCGCTGCATCCCGGATCGCTACCGCGCGCAGCGGG
Sox2	NM_011443.3	959-1058	CGCAGCACCCGGGCTCAACGCTCACGGCGCGGCACAGATGCAACCGATGCACCGTACGACGTCAGCGCCCTGCAGTACAACCTCCATGACCAGCTCGCA
Sox4	NM_009238.2	2636-2735	TTTTCTGCAATGAAGACAGAAAGAGGCTCTGGGGTGTGCTGGTGGCATTGTTGAGCTTAGGGAGCATTGGCATGAGAAACTCCAGCTCTGGCG
Sox9	NM_011448.4	3541-3640	ACAAATGAGAGGTTTCAGATGAGTGGAGGAGCACTGAGTCTTTGCAATGTTTTGAGCCATAGACCTTTGGGCTGCTGCTGACTGTATGTGGATGTGTGC
Sp7	NM_130458.3	1786-1885	TCATTAGAACAGAGTTAAGGAGATTGGTGTAGTAACTGGCCGGAGCAGAGTCCAAGAAGGGGAAAGTCCAATGGGGATCTGATCCCAAAGATGG
Spag9	NM_027569.2	2241-2340	AGATGGCGGTTCTGTTGTTGGAGCGAGTATTTTACAAGGATATTGCTGGTTTGGACTGAAGGCAGTAAACAGCGGAGTGGCTCAGAGTAGTTTA
Sparc	NM_009242.4	175-274	CTCAAAGAGCTTCTCTGCTCCTCAACCCCTCCACTTCTGAGGTTCTGACCTTCCAGCCCTCAGACCGCAACTCTTCTGCGGCTGCTCCGCTGCGCTG
Spp1	NM_009263.3	421-520	TGAATCTGACGAACTCACCATTGCGATTGAGTCTGATGAGACGCTCACTGCTAGTACACAAGCAGACACTTTCACTCCAATCGTCCCTACAGCTCGATGC
Stat1	NM_009283.3	1591-1690	ACGCTGGGAACAGAACTAATGAGGGCCTCTCATTGTACCAGAAGAACTTCACTCTTAGCTTTGAAACCCAGTTGTGCCAGCCAGCTTGGTGATTGA
Sucla2	NM_011506.1	956-1055	CATCGGCTCGATGGGAGCATAGGATGTCTAGTAAATGGTGTGGCTTGGCTATGCCCAATGGATATAATAAACTACACGGAGGGACTCCAGCCAAC
Suclg1	NM_019879.3	719-818	CATTACAAGAAGGGAAGAATAGGTATCGTGTCCAGGTCGGTACTCTGACTTATGAAGCAGTTCCAAACAACCCAAGTCGGATTGGGGCAGTCCCTTG
Suclg2	NM_011507.2	331-430	GAGGAGAGGAAAGTGTCTTCAATAGCGGTTTTGAAAGAGGTTGACTTAAAGAAACCCCTAAAGTAGTGGGAGAGTTGGCTCAACAGCATGATTGG
Suz12	NM_199196.1	821-920	TGTCCAATAAGACAAGTCCCTACTGGTAAAAAGCAGGTGCTTTGAACTCTGACCTCAATCAACAAAACCAGGAAATTTCCATCCCTGGCAGTTTCCA
Syk	NM_001198977.1	2065-2164	TGAGGCTTCGCAATTACTACTACGAGCTGGTAACTAACAGCTCCGGCGCCTGCTCCGTGCACACCAGGATCCCAAGCGATCACAGAAATTCATTGAG
Taf2	NM_001081288.1	1907-2006	GGACCTCTAAAGTGACAGTGCAGAGTTAGATGGATCCTTCAACCATACCTTGCATAATGAAGAAAACAGCCTTAAACATGACATACCTGCCACTCCA
Sm22	NM_011526.2	421-520	GTTGACCTCTATGAAGTAAGGATATGGCAGCAGTGCAGAGGACTCAATGGCTTTGGCAGTTTGGCTGTGACCAAAAACAGATGAAACTACCGTGAG
Tbx5	NM_011537.2	1216-1315	AAAGCAGACGAAATAATGGTTCGGTTCAAAGAACACTCGGTTTTGCACCCAGCTCTCCCGGAGACAGCTTTTATCGCTGTACTCTGATCCGATCCGAG
Tcf12	NM_011544.3	3471-3570	CCGCTCTGAGGCTAATTACCTATGGAATCCAAGAGCAATGGTACGGTTCCTTACCCTAGCTTTACTTCTGCTCTTGGTGGTCCGTGGGGGGT
Tcf3	NM_001164147.1	704-803	GAGCGGAATGCTATGCCACTTTGGGAGAGACCCAGTGTGGACCTTGAAGTCCAGGCTGGCTTCTGCCAGGTGAGCTGAGCCTCAGCAGTCCCGGGC
Tcf4	NM_013685.1	3046-3145	AATTACCGGATATTGAATAGGGGAAGCCCGCTGCCCTCGTAACAAAACCAGCAAACGCTCTGATGGCAACGAAAGTATGACATTAGCCATTCTTAGGG
Tert	NM_009354.1	2163-2262	CAGGGTAAGCTGGTGGAGTTGTTGCAATATGATCAGGCACTCGGAGAGCAGTACTGTATCCGCCAGTATGAGTGGTCCGGAGAGATAGCCAAGGCC
Tex9	NM_009359.4	381-480	ATTCAGTGTCAAACCTGAAATATCCTGATGCGCAGACTGCCAACGATGTGGCCATCCACAGCAGATTTCTCAGACTTCTCCCTGCCAAGACGATTAGCAG
Tgfb1	NM_011577.1	1471-1570	GGAGTTGTACGGCAGTGGCTGAACCAAGGAGACGGAATACAGGGCTTTGATTGAGCGTCACTGCTCTTGTGACAGCAAAGATAACAACTCCACGTGG
Tgfb2	NM_009367.1	1686-1785	CCCAAAGCCAGAGTGGCCGAGCAGCGATTGAACGTATCAGATCCTTAAATCCAAAGACTTAAACATCTCCACCCAGCGCTACATCGATAGCAAGTTG
Tgfb3	NM_009368.2	2411-2510	TCATGTAATTAGTTTCTGGCCAGCACTAGCTATCTCAGTCCCTTAGAGATGCTGGACTCAAAGCAGAGGTCAGAATTTGGTTCTCTCATGTATTCCC
Tgfb1	NM_009370.2	4426-4525	TCAGAAGTAGTGGCCAGCTGTCTCTAGTAGGACAGTAAAGGCATGAAGCTCAGCCTGTAATCTGCTACTACAGTAGTACTCAGAAGTGCTTGGAGG
Tgfb2	NM_029575.3	1469-1568	GAGCTAACATCTAGTGAAGAACGACTTACCTGTTGCTGTGACTTCGGGCTGCTTGGCCTGGACCCCTACTCTGTCTGTGGATGACCTGGCC
Tgfb3	NM_011578.3	3615-3714	CACACAACTCAAAGTGCTTAAAGCCAGTTTGTGCTCCTTTCAGGAGAGCGTGAACGTCAGATTTGTGCTGCTGCAACATTCTGTCTCTAA
Tgif1	NM_009372.2	1061-1160	TTTAGTGGATCCAGCTTCTAGTGATTTGCACTCAAACGAGCGGAGAGATGGAGCTTCCAGCCAAACTCACAGCTTAAACCTTTTTTCAAACAAAAC
Thy1	NM_009382.3	426-525	ACTTTTGTGAGCTTCAAGTCTCGGCGCGAATCCCATGAGCTCCAATAAAGTATCAGTGTGTATAGAGACAAGCTGGTCAAGTGTGGCGGCATAAGCCT
Timp1	NM_011593.2	437-536	AAGCCTGTGGATAGCCCAAGTCCCAAGAACCGCAGTGAAGGTTTCTCATCACGGCCCTTAAGGAACCGGAAATTTGCATACAGTGCCTGCAGC
Timp2	NM_011594.3	656-755	TTGCAGGAAAGGCAGAAGGAGATGGCAAGATGCACATTACCCTCTGTGACTTATTGTGCCCTGGGACAGCCTTAGCATCCCCAGAAGAAGAGCCTGAA
Tmem119	NM_146162.2	1551-1650	TGGCTACTTAAGGGTTCCTGCTGGCTGCTTGTACGCTTCTCCTCAAGCTGCTTTCTTATTACCAGGATGCTCACAGCTACAAGTCCAATCTCAC
Tmem64	NM_181401.3	1126-1225	CGCGCTCAAGTGAATTAATGAGCTATTGTAGCTTGTGAGATTGGAACGAAAACCTCTCTGGTTAAAGGCAATCAATCCGATCCAGTGGCTCTTCT
Tnf	NM_013693.2	1132-1231	TCCATTCTGAGTTCTGCAAGGGAGAGTGGTCAGTTGCTCTGTCTCAGAATGAGCTGGATAAGATCTCAGGCCCTTCTACCTTCCAGCTTCCAG
Tnfaip3	NM_009397.2	233-332	GGCTGAACAATCTTCTCAGGCTTTGTATTGAGCAATGCTGGAAAGTGTGAAGATACAGAGAGAAACCGGAAATTTGCATACAGTGCCTGCAGC
Tnfrsf11a	NM_009399.3	3871-3970	ATTGGTGTCTCTTATGTTGGGGTCCATCCCATAGGCAGCTTATAAAACCAATAGCATAAAAGCTTATATTACAGGTGCAGGAAGTGTGCTGGGTAG
Tnfrsf11b	NM_008764.3	685-784	TTCTCAGGTGAGACTTATCGAAAGCACCTGTATAAAACACAGCAACTGCAGCATTGGCTCCTGCTAATTCAGAAAGGAAATGCAACACATGACA
Tnfrsf1b	NM_011610.3	3271-3370	GTGTGTGCTCATGTTGATGTATGTGTGCCAGTGTGTGGAGGCCAGAGTTGGCTTGGGTGTGTTTGTACTCTCAGTACTGAGGCGAGGGCTCT
Tnfrsf11	NM_011613.3	359-458	CTGTACTTTCGAGCGCAGATGGATCCTAACAGAATACAGAAGACAGCACTCACTGCTTTATAGAACTCCTGAGACTCCATGAAAACGAGATTGCGAG

Tnnc1	NM_009393.2	58-157	CAAAGCTGCGGTAGAACAGTTGACAGAGGAGCAGAAGAAATGAGTTC AAGGCTGCCTTTGATATCTTTGCTCTGGGCGGAGGATGGCTGCATCAGCACC
Tnni2	NM_009405.2	167-266	CTGCCCGCCTGACACATCCAGGCTCCATGCTCTGAAGTG CAGGAACCTGCAAACAATGCATGCGAAGATCGACGTGGCTGAAGAGGAGAAATATGAC
Tnnt1	NM_011618.1	223-322	AAGGGGAGCGTGTGGATTTTGTGACATCCACCGAAGCGCATGGAGAAAGACTTACTGGAGCTGCAGACGCTCATCGACGTGCACTTTGAACAGCGGAA
Tnnt3	NM_011620.2	552-651	GACAGCCGGGAAATGAAAAAGAAGATCTTGCCGAAAGGCGCAAGCCTCTGAACATGACCATCTTAGCGATGACAAGCTGAGGGACAAGGCAAAGGAA
Tnp01	NM_001048267.1	2161-2260	GCATGCAGGATAAAATGCCCGAGGTTCCGCGAGGTTCTTTTGCATTGCTAGGTGACCTGACTAAAGCGTGCTCCAGCATGTTAAGCCTTGATAGCTGA
Tob1	NM_009427.2	661-760	TTGGACATTGACGATGTTGCGTGGCAATCTGCCACAGGATTTGAGTGTCTGATCGAACCCGTTTGAGGTTTCTACAGATCGGCGAAAAGGGACCAGTGA
Trim63	NM_001039048.2	1498-1597	ATCACGCCTGGTCATTGTGTGACTGGCGATTGTCAAAAAGTGGGAAGCAAGACAATAGAGATGCCTACTTCTTTCTTGGTGGGAGGGCTGGGT
P53	NM_011640.1	1836-1935	CCCTCTGAGTAGTGGTCTCTGGCCCAAGTTGGGGAATAGGTTGATAGTTGTCAGGTCTCTGCTGGCCAGCGAAATCTATCCAGCCAGTTGTTGGAC
Trpm4	NM_175130.4	1146-1245	AGGAGTTGCTGACGGTCTATTATCAGAAGACGGCTCCGAGGAGTTGAGACTATCGTTTTGAGGGCTCTGTGAAGCCTGTGGGAGCTCTGAGCCCTC
Trpv4	NM_022017.2	1606-1705	GGCTGGCTGGCGAGGTCATCAGCTCTTACAGGAGTCTGTTCTTTACCAGTATCAAAGACTTGTTCCAGGAAGAAATGCCCTGGAGTGAATCTCT
Gilz	NM_010286.3	1061-1160	CTAAGCAGAAGCAACCTCTCTTCTTCTGTCTTTCCAGGCAGGGGAGAGATGGGAGAGATTGAGCCAAATGAGCCTTCTGTTGGTTAACTACTGTA
Tshr	NM_001113404.1	582-681	ATGACTTCGGTCCCTGAAAACGCATTCCAGGGCCTATGCAATGAAACCTTGACCCTGAAACTGTACAACAATGATTTACTTCAGTCCAAGGACATGCTT
Ttn	NM_011652.3	50674-50773	GAAATACACTGTGAAAGGCTTAAAAGAAGGCGATACATATGAGTACCGCGTCAGTCCGTCATATCGTTGGACAAGGCAAGCCATCATTTTGACCAAG
Twist1	NM_011658.2	995-1094	AATGGACAGTCTAGAGACTCTGGAGCTGGATAACTAAAAATAAATCTATATGACAAAGATTTTCATGAAATTAGAAGAGCAGAGACCAAATTCACAAGA
Txnip	NM_023719.1	2341-2440	CCTGAGTGCTGCGATCAAAGGCCAGCTGGTTATTGCTTTTGAGGCTTCCCAACGCACAGACTGTGTAATCTAACACTAATCTGTGAAGGGTT
Ube2g1	NM_025985.4	2381-2480	CAGTACTTGTCACTTGATGCTGTTTGAAGTGGAGAATAGTGTGGCTGCTCCCTGGGGTTTGGATAAATCTTTGGCAGAAGAGGGAATGAAAGGATTC
Ucp3	NM_009464.3	1026-1125	CTGCGTCTGGGAGCTTGAACGTGATGATGTTTGAACATATGAGCAACTGAAGAGGGCCTTAATGAAAGTCCAGGTAAGTGGGAAATCTCCGTTTTGAA
Uqcr10	NM_197979.2	304-403	TAAGGATGAGTTTCAAGTTGCCGTTACCAGCCGCCAGTGTGTGGGCAAGCTATGGCTCCACTGTACAAAACAGACTCACTTCTGCTGTGTTTGAAGTACAG
Uqcr11	NM_025650.2	35-134	GCAGCGGAACGGGGTGACCCTGAGTATTGAGACCCCTGCAGCGATGCTGAGCAGGTTTCTAGGCCCGCTACCCGGAACTGGCCAGAACTGGATTCCCA
Uqcrb	NM_026219.1	193-292	CTGAGGACCTTTATAATGACAGGATGTTTCGAAATTAAGAGAGCCCTGGACCTGACTATGAGGCATCAGATCTTGCCAAAGGATCAGTGGCAAAATATG
Uqcr1	NM_025407.2	1081-1180	TTTGGCCAGAGTTCCAGACCTTCAACATCTCTACTCTGATACTGGCTGTGGCGCACACTTTGCTGTGATGCCATGAGTATCGATGACATGGTCTT
Uqcr2	NM_025899.2	365-464	TTTGACTACCAAAGGAGCTTCTCTTCAAGATAAACCCTGGGATTGAAGCAGTTGGTGGTAAATTAAGTGTACTGCAACAAGGGAAAACATGGCGTAC
Uqcrf1	NM_025710.2	437-536	TGGGTGTTGCTTATGCGGCCAAAATGTGGTCTCCAGTTTGTCCAGCATGAGTCTTCTGCTGACGTAAGTGGCCATGTCGAAGATCGAGATCAAGTT
Uqcrh	NM_025641.3	357-456	AAAACTTGAAGTAAATGTGAGATTGCTCCTCCTCAGCCTGTACTGGGAATCAGGAACAGTTCCTGTGGTTCTGGACGTGGTGTCTGATGGAGTG
Uqcrq	NM_025352.2	299-398	TTTTAGTGTCTCACTGACTCTTCACTCTACCACAAAAGTCAATGTAGACCTACGAAACGTCAGGTGATGGCTAGGGACGTATCTTCAAACCTCATT
Vcam1	NM_011693.2	1441-1540	GGTTTTGAGGATGAACACTCTTACCTGTGCGCTGTGACCTGTCTGCAAAGGACTGGAAAAGAGAACCAGGTGGAGGTACTACTTCCCTGAAGATC
Vdac1	NM_011694.4	563-662	GACGGATGAATCCAGCTTCACTAATGTAATGACGGGACAGAGTTTGGTGGCTCCATTTACCAGAAGGTGAACAAGAAGTTGGAGACTGCTGCAAT
Vdac2	NM_011695.2	289-388	TTTTCAACATCTGGCTCATCTAATACAGACACTGTAAAGTTAGCGGGACCTTGGAGACCAAGTACAATGTTGTGAGTATGGTCTGACTTTACAGAGA
Vdac3	NM_001198998.1	119-218	CTCGGTTGTAGCTATGTGTAACACCAACTATTGCGACCTAGGAAAGGCTGCAAGGATGCTTTAACAAGGGTATGGGTTTGGCATGGTCAAGAT
Vdr	NM_009504.3	2711-2810	GTCCAGTTCTCTGACTCTTCACTCTACCACAAAAGTCAATGTAGACCTACGAAACGTCAGGTGATGGCTAGGGACGTATCTTCAAACCTCATT
Vegfa	NM_001025250.3	3016-3115	TCTCTCTCTCCAGATCGGTGACAGTCACTAGCTTGTCTGAGAAGATATTTAATTTGCTAACACTCAGCTCTGCCCTCCCTGTCCCCACCACACATT
Vegfb	NM_011697.3	288-387	GGCTCGACCCAGGCCCTGTGCTCCAGTTTGTGCCCCAGCCACAGAAGAAAGTGGTGCCATGGATAGACGTTTATGCACGTGCCACATGCCAGCCC
Vwf	NM_011708.3	6355-6454	GTCAGCATCTACGGCGCTATCATGTATGAAGTCAGGTTTACCATCTTGGCCACATCTCACATACAGCCACAAAACAACGAGTTCCAAGTGCAGCTTA
Wnk1	NM_001185020.1	4241-4340	ATCAGATGGCGGACCAACATTTTCTCCCTTTTGGCTAGCATTGCTGGTGTCCAACTGTAGCAGCATCCACACCCGTCAGTATCAGTCCCTATAACAAG
Wnt10a	NM_009518.2	811-910	TCGGAGAACGCTTCTAAGGACTTTCTGACTCCCCGAGAGCCTCACAGAGACATCCATGCTCGAATGAGACTCCACAACAACCGTGTGGCGGGCAGGC
Wnt10b	NM_011718.2	349-448	CGGTCTCGGCTCCGCCCTTAGGCCTCGGGTCTCCTGTTCTTGGCTTTGTCAGTCCGGCTAAGCAATGAGATTCTGGGCTTAACTTCCCGGTG
Wnt11	NM_009519.2	942-1041	CTGCAAGAGCTCCAGGACGTGGCTGCTGACCTCAAGACCCGCTACCTGTGAGCCAGGAGTGTGACACCCGCTATGGGACCCGCAAACACTTGGTGC
Wnt3a	NM_009522.2	1280-1379	AGATCCTACCTGTGAGGTTCTCATACCTAAGGACCCGTTTCTGCTTCAAGCTGGGCTCCTATTTGGGATCTGGGTTCTTTTGGGAGGAGGCTCCT
wnt4	NM_009523.2	1395-1494	TGAGCCTTTGTGTGGCTGCCTCTGACCAAAGGACTTTGTTTATGCCTGCGCTGTCCACATTGACCACTGTTGACTACTCAGTCTTGTCAAGTGTCC
Wnt5a	NM_009524.2	3021-3120	TGGAGGTACGGTAACTTGATGTGTTTTGATGATATCTTTGGCCAGGGAGTCCACAGAGGTGTCAGCTGTTTGGTGTATCTCTCTGCGTTTAGAC
Wnt6	NM_009526.3	545-644	GCAGCAGGACATCCGAGAGACAGCTTTGCTGTTTGCATACCCGAGCTGGTCCAGCCAGCGGTCACTCAAGCCTGTTCCATGGGAGAGCTCCTACAG
Wnt7b	NM_001163634.1	2895-2994	CATTGACCTGGGGAAGGTGACCTTGTGTCCTTGCCTTGCATCCAGCTGTGTGTCCTATCATGTGAGGATGTTCCAAGCCTCTGGGCCACTGGAAAT
Zfhx3	NM_007496.2	15229-15328	GAAGGCAGACAAGTGGCCGTGGTCTGTAGCCATTTCAAAGGCATATGTTTACTACCGTCTCAATTGCTTAGACTGATCTATTGGGGAGTTCACTCCC
Zfp42	NM_009556.3	1113-1212	GCGCTTCCCTGGAATTCAACTTGCACCCATATCCGATCCACACCCGGGAGAGGCGCTTTGTGTCTTTTGTGCTGCGAGAAGAGCTTTATT