	Customer Ide	Accession	Position	Target Sequence
1	ACAN	NM_007424.2	4861-4960	CAGAACTTTGGTGGAATCTATAACTCAGGCTCCTACTGCTCAAGAAGCTGGAGAAGGACCTTCGGGCATTTTGGAATTCAGTGGTGCCCATTCTGGGACA
2	Acp5	NM_001102405.1	441-540	AACATCCCCTGGTATGTGCTGGCTGGAAACCATGATCACCTTGGCAACGTCTCTGCACAGATTGCATACTCTAAGATCTCCAAGCGCTGGAACTTCCCCA
3	beta actin	NM_007393.1	816-915	CAGGTCATCACTATTTGGCAACGAGCGGTTCCGATGCCCTGAGGCTCTTTTCCAGCCTTCCTTCTTGGGTATGGAATCCTGTGGCATCCATGAAACTACAT
4	Adipoq	NM_009605.4	781-880	GACCACAATGGACTCTATGCAGATAACGTCAACGACTCTACATTTACTGGCTTTCTTCTCTACCATGATACCAACTGACTGCAACTACCCATAGCCCATA
5	Alpl	NM_007431.2	206-305	CTCCAGCGAGGGACGAATCTCAGGGTACACCATGATCTCACCATTTTTAGTACTGGCCATCGGCACCTGCCTTACCAACTCTTTTGTGCCAGAGAAAGAG
6	Atp6v0d2	NM_175406.2	631-730	TCTTACCTTGAGGCATTCTACAAATTCTGCAAGGATCACGGTGATGTCACAGCAGACGTTATGTGTCCCATTCTTGAGTTTGAGGCCGACAGACGCGCTT
7	Atp6v1g1	NM_024173.1	196-295	AGGCCAAAGAAGAAGCCCAGGCTGAAATTGAACAGTACCGCCTGCAGAGGGAGAAGGAGTTCAAGGCCAAGGAAGCGTCGGCATTGGGCTCCCATGGCAG
8	beta 2 microg	NM_009735.3	178-277	CTGAACTGCTACGTAACACAGTTCCACCCGCCTCACATTGAAATCCAAATGCTGAAGAACGGGAAAAAAATTCCTAAAGTAGAGATGTCAGATATGTCCT
9	Bglap	NM_007541.2	252-351	GTGAGCTTAACCCTGCTTGTGACGAGCTATCAGACCAGTATGGCTTGAAGACCGCTCAACAACGCATCTATGGTATCACTATTTAGGACCTGTGCTGCCC
10	Car2	NM_009801.4	438-537	TGCCCAGCATGACCCTGCCCTACAGCCTCTGCTCATATCTTATGATAAAGCTGCGTCCAAGAGCATTGTCAACAACGGCCACTCCTTTAACGTTGAGTTT
11	Casr	NM_013803.2	4361-4460	GCCACATTTAGATCTTAGGATCATAAGTATCACCTCCAAGCACCGGGAAAGGACTGACTCAACCCAACGAGCTGTCTCTGTAACTAATATCAATGTACAT
12	Cd40	NM_011611.2	1426-1525	GCTGCCCAAACCCGGTTACCTGATTTTGATCCCTGGGACTTCATGGTAAAAGGGAGAGAACCAAATCCAGAGGGTTGTCATTTGACCTCCATGTGTGCTC
13	Cd40lg	NM_011616.2	601-700	AGCAGTGGATCTGAGAGAATCTTACTCAAGGCGGCAAATACCCACAGTTCCTCCCAGCTTTGCGAGCAGCAGTCTGTTCACTTGGGCGGAGTGTTTGAAT
14	Cd69	NM_001033122.3	1371-1470	GCAGATTTCAAAGTGCTGGAAAGAAAAGTGCAATACGTGTAGTGGCAATGTCTGTGCAGGACACACCCTGTGGTTTGACCTTGGAATAACTCCAGTCTTG
15	Col10a1	NM_009925.4	1851-1950	TAAGATCCCAGGCATATACTATTTCTCCTACCACGTGCATGTGAAAGGGACTCACGTTTGGGTAGGCCTGTATAAGAACGGCACGCCTACGATGTACACG
16	Col14a1	NM_181277.3	785-884	GAGGTTCAACTTCAGGCTTGTGCGCAATTTCTTGGAAAACCTGGTCACAGCGTTCAACGTGGGCTCAGAAAAGACAAGAATCGGCTTGGCACAGTACAGT
17	Col15a1	NM_009928.3	449-548	TCTCAGGTTCACCTGGACCTCACAGTGCTCATTGGTGTCCCATTACCCTCGTCTGTGTCCTTTACCACCGGCTATGGCGGTTTCCCGGCTTACAGCTTTG
18	Col1a1	NM_007742.3	216-315	CAATGGTGAGACGTGGAAACCCGAGGTATGCTTGATCTGTATCTGCCACAATGGCACGGCTGTGTGCGATGACGTGCAATGCAATGAAGAACTGGACTGT
19	Col2a1	NM_001113515.2	4347-4446	ACACACTGGTAAGTGGGGCAAGACCGTCATCGAGTACCGATCACAGAAGACCTCCCGCCTTCCCATTATTGACATCGCACCCATGGACATTGGAGGGGCT
20	Comp	NM_016685.2	515-614	TGGGACTGACCTTCGCTAAGTCCAACAAACAAGTTTGCACGGATATTAATGAGTGTGAGACCGGGCAGCACAATTGCGTTCCCAACTCCGTGTGCGTCAA
21	C-Fms	NM_001037859.1	3656-3755	CCACCACTCTTGACCTTCACTCTGTCTATAGTCCCGCCTCATCCTGGATCTTGTACTGAGCGGCAGCTAAAAGTGTTCTACCCAGTGCCCTGTCACTCTA
22	Ctsk	NM_007802.4	1201-1300	GCGCTCCTGAGAGGGACGCAGCGATGCTAACTAAGATTGTTTCATTTCTCCTCTCGTTGGTGCTTCCAGTGACAACTCTACTTCCCTTCTCTCTGCCCAG
23	Dkk1	NM_010051.3	56-155	GCCAGCCGCCGTGCAAAGTGACCTCTCTTTTCCTGACCTTTGCCTGTTTGCGTCCTTCGGAGATGATGGTTGTGTGTGCAGCGGCAGCTGTCCGGTTCTT
24	Dmp1	NM_016779.2	121-220	AAGACTGTCATTCTCCTTGTGTTCCTTTGGGGGCTGTCCTGTGCTCTCCCAGTTGCCAGATACCACAATACTGAATCTGAAAGCTCTGAAGAGAGGACGG
25	Fgf23	NM_022657.4	419-518	TCTCCACGGCAACATTTTTGGATCGCTTCACTTCAGCCCAGAGAATTGCAAGTTCCGGCCAGTGGACGCTGGAGAATGGCTATGACGTCTACTTGTCGCAG
26	Foxo1	NM_019739.2	2531-2630	TTTCCTCAGACTTGGCAACAGCGGCAGCACTTTCCTGTGCAGGATGTTTGCCCAGCGTCCGCAGGTTTTGTGCTCCTGTAGATAAGGACTGTGCCATTGG
27	Foxp3	NM_054039.2	195-294	TGCCTTCAGACGAGACTTGGAAGACAGTCACATCTCAGCAGCTCCTCTGCCGTTATCCAGCCTGCCTCTGACAAGAACCCAATGCCCAACCCTAGGCCAG
28	Fzd1	NM_021457.3	3447-3546	TCTAGTATCTGGAACTTGCTCTGGGTCTGGTCATCATCATGGAAAGAGCAAGCAAGCTTTGTGGGTTGGGAGAGGCTAAAGAGAGAGGTTATAAAACATTA
29	Gapdh	NM_001001303.1	891-990	AGGTTGTCTCCTGCGACTTCAACAGCAACTCCCACTCTTCCACCTTCGATGCCGGGGCTGGCATTGCTCTCAATGACAACTTTGTCAAGCTCATTTCCTG
30	Gja1	NM_010288.3	1451-1550	CTGGGGTGTTCATTTCGTTCCCGTGGAGGTGGTACTCAACAACCTCAGTAATGAGGCGTAGAAAACAAAGACATTACAATATCTAGGTTCCTTGGGGGGT
31	Prgn	NM_008175.4	1293-1392	AGATCTTGAAGAGTGATACACCTTGTGATGACTTCACTAGGTGTCCTACAAACAATACCTGCTGCAAACTCAATTCTGGGGACTGGGGCTGCTGTCCCAT
32	Hif1a	NM_010431.2	1295-1394	ACCATGATATGTTTACTAAAGGACAAGTCACCACAGGACAGTACAGGATGCTTGCCAAAAGAGGTGGATATGTCTGGGTTGAAACTCAAGCAACTGTCAT
33	Ibsp (sialopro	NM_008318.3	115-214	GGAATGGCCTGTGCTTTCTCGATGAAAAATTTCCATCGAAGAATCAAAGCAGAGGATTCTGAAGAAAACGGGGTCTTTAAGTACCGGCCACGCTACTTTC
34	Ifng	NM_008337.1	96-195	CTAGCTCTGAGACAATGAACGCTACACACTGCATCTTGGCTTTGCAGCTCTTCCTCATGGCTGTTTCTGCTGGTGCACTCATTCCATGGTGTGCACGTCATT
35	Igf1	NM_001111274.1	419-518	GGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAGACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTG
36	Igf1r	NM_010513.2	3391-3490	CGTATGAGAACTTCATGCATCTGATCATTGCTCTGCCGGTTGCCATCCTGCTGATCGTTGGGGGGCTGGTTATCATGCTGTATGTCTTCCATAGAAAGAG
37	Il10	NM_010548.1	986-1085	GGGCCCTTTGCTATGGTGTCCTTTCAATTGCTCTCATCCCTGAGTTCAGAGCTCCTAAGAGAGTTGTGAAGAAACTCATGGGTCTTGGGAAGAGAAACCA
38	Il11ra1	NM_010549.3	23-122	GGGTCCCACAACTCAGTGGAGCGGGAGACAGTTCTTAGCCTGTAGGAGGAAGTCTTGGAGGCCATGGGCACTCAGTCACTGTGATTATCAAGATGAGCAG
39	Il15	NM_008357.2	855-954	CTTGCAAACAGCACTCTGTCTTCTAACAAGAATGTAGCAGAATCTGGCTGCAAGGAATGTGAGGAGCTGGAGGAGAAAACCTTCACAGAGTTTTTGCAAA
40	Il17a	NM_010552.3	206-305	ACCTCAAAGTCTTTAACTCCCTTGGCGCAAAAGTGAGCTCCAGAAGGCCCTCAGACTACCTCAACCGTTCCACGTCACCCTGGACTCTCCACCGCAATGA
41	Il1a	NM_010554.4	226-325	ACCTCTGAAACGTCAAAGATGTCCAACTTCACCTTCAAGGAGAGCCGGGTGACAGTATCTCCAAGCAACGTCAAGCAACGGGAAGATTCTGAAGAAGAGACGGC
42	Il1b	NM_008361.3	1121-1220	GTTGATTCAAGGGGACATTAGGCAGCACTCTCTAGAACAGAACCTAGCTGTCAACGTGTGGGGGATGAATTGGTCATAGCCCGCACTGAGGTCTTTCATT
43	Cd25	NM_008367.2	326-425	AAGGAATTGGTCTATATGCGTTGCTTAGGAAACTCCTGGAGCAGCAACTGCCAGTGCACCAGCAACTCCCATGACGAACAATCCAGAAAGCAAGTTACAGCTC
44	Il4	NM_021283.1	346-445	TGCTTGAAGAAGAACTCTAGTGTTCTCATGGAGCTGCAGAGACTCTTTCGGGCTTTTCGATGCCTGGATTCATCGATAAGCTGCACCATGAATGAGTCCA
45	Il6	NM_031168.1	41-140	CTCTCTGCAAGAGACTTCCATCCAGTTGCCTTCTTGGGACTGATGCTGGTGACAACCACGGCCTTCCCTACTTCACAAGTCCGGAGAGGGAGACTTCACAG
46	Il6ra	NM_010559.2	2826-2925	CACCTCACTGCCACCTTGGCCTTCCTTGCTTTACGTTTGACTGAGTGGCCTCAGATGCTTTCCCCTGGGGCTTTGAGGAATCCAGTGATGTTAGTGGTCA
47	Lef1	NM_001276403.1	1327-1426	CTGCCCACTGAGCGGCACTGCCTCCGGTCTCTGTGCGATCCTCCAGCATCTTCTGTGCTGACCTGTCACCCTTCCGCAAGGACAGACAGGACCTTGGCTG
48	Lrp1	NM_008512.2	1311-1410	GAGCAGATGGCAATCGACTGGCTGACGGGAAACTTCTACTTTGTCGACGACATTGACGACAGGATCTTTGTCTGTAACCGAAACGGGGACACCTGTGTCA
49	Lrp5	NM_008513.3	1681-1780	ATGCCAAAACTGATAAAATCGAGGTGATCAACATAGATGGGACAAAGCGGAAGACCCTGCTTGAGGACAAGCTCCCACATATTTTTGGGTTCACACTGCT
50	Lrp6	NM_008514.3	3316-3415	GCTACCAATGTCATTGATGTGACGAGATTAGATGGACGATCAGTTGGAGTGGTTCTAAAAGGCGAGCAAGACAGACCTCGAGCCATTGTGGTAAACCCCG
51	Mepe	NM_053172.1	323-422	CAGGAGAAGAGACCTCAGAGTGTTCTAAGCGTAATTCCAGCAGATGTCAATGATGCTAAAGTCTCCTTAAAAGACATAAAGAATCAAGAGAGTTATCTGC
52	Mmp10	NM_019471.2	1051-1150	CAGACTTAGATGCTGCCTATGAGGCTCACAACAGGGACAGTGTTCTGATTTTTAAAGGAAGTCAGTTCTGGGCAGTCCGAGGAAATGAAGTCCAAGCAGG
53	Mmp12	NM_008605.3	593-692	AAGGTGGTACACTAGCCCATGCTTTTTATCCTGGACCTGGTATTCAAGGAGATGCACATTTTGATGAGGCAGAAACGTGGACTAAAAGTTTTCAAGGCAC
54	Mmp13	NM_008607.2	203-302	GGGAATCCTGAAGAAGTCTACAGTGACCTCCACAGTTGACAGGCTCCGAGAAATGCAATCTTTCTTTGGCTTAGAGGTGACTGGCAAACTTGATGATCCC
55	Mmp14	NM_008608.3	555-654	AGTTTGGGACTGAGATCAAGGCCAATGTTCGGAGGAAGCGCTATGCCATTCAGGGCCTCAAGTGCTTGTTGGCAGGATGGAGTGACTTTCTGCATTCAGAATTA
56	Mmp2	NM_008610.2	2377-2476	AGTTAACCAGCCTTCTCCTTCACCTGGTGACTTCAGATTTAAGAGGGTGGCTTCTTTTTGTGCCCAAAGAAAGGTGCTGACTGTACCCTCCCGGGTGCTG
57	Mmp3	NM_010809.1	1576-1675	TCTTTGTGAAAGGAAGTGCTTTGTTCAGCATGTGCTATGGCAGAACCAAACAGGAGCTATGGATGACACCAGTCAACGTCAAGTTGTCAAAGGATGTTCA
58	Mmp8	NM_008611.4	233-332	CTACAACTTACCAAGCAATCAATTCCGGTCTTCGAGGAATGCCACGATGGTTGCAGAGAAGCTTAAAGAGATGCAGCGCTTCTTCAGCTTAGCAGAGACT
59	Mmp9	NM_013599.2	1571-1670	CCTCTACAGAGTCTTTGAGTCCGGCAGACAATCCTTGCAATGTGGATGTTTTTGATGCTATTGCTGGGCAGTTCCAGGGCGCTCTGCATTTCTTCAAGGACGG
60	Myod1	NM_010866.2	1201-1300	TGGGGATGGTGTCCCTGGTTCTTCACGCCCAAAAGATGAAGCTTAAATGACACTCTTCCCAACTGTCCTTTCGAAGCCGTTCTTCCAGAGGGAAGGGAAG
61	Nanog	NM_028016.2	1083-1182	GCCTTGGAATTATCCTGAACTACTCTGTCACCAGGTGAAATATGAGACTTACGCAACATCTGGGCTTAAAGTCAGGGCAAAGCCAGGTTCCTTC
62	Nes	NM_016701.3	2717-2816	GCAGAGAATTGTGAAACCTCTAGAAAAAGTGAGCCAGGTCTCCCTCGAATCTCTCGAAAAAGAGAATGTGCAGTCACCAAGGTATCTGGAAGAAGATGAC
63	Ngf	NM_001112698.1	631-730	CAAGGAGGTGACAGTGCTGGCCGAGGTGAACATTAACAACAGTGTATTCAGACAGTACTTTTTTGAGACCAAGTGCCGAGCCTCCAATCCTGTTGAGAGT
64	Ngfr	NM_033217.3	1996-2095	AACAGGGAGATCAATTGTAGGCTGACACACTCCTTTCTGAATGAGGGCGTCAAGTGCTTGTTGGCAGGGATGGAGTGACTTTCAGGGAAACATCTGGAAA
65	NLRP3	NM_145827.3	509-608	ACGTGTACATCACATTCCTCTATGGTATGCCAGGAGGACAGCCTTGAAGAAGAGTGGATGGGTTTGCTGGGATATCTCTCCCGCATCTCCATTTGTAAAA
66	Nog	NM_008711.2	896-995	GATCAAAGGGCTGGAGTTCTCCGAGGGCTTGGCCCAAGGCAAGAAACAGCGCCTGAGCAAGAAGCTGAGGAGGAAGTTACAGATGTGGCTGTGGTCACAG
67	Oscar	NM_175632.3	205-304	CTCATCCTGCTGCAGTTGTGACTCCTGGGATCAACGTGACCTTGACTTGCCGCGCACCTCAATCTGCCTGGCGGTTTGCACTCTTCAAAAGTGGCCTTGT
68	Pax3	NM_001159520.1	732-831	GAAGAAAATTGAGGAATACAAAAGAGAGAACCCGGGCATGTTTAGCTGTGGAAATCAGAGACAAATTGCTCAAGGACGCTGTCTGTGATCGGAACACTGTG
69	Pax7	NM_011039.2	3681-3780	CAACATTCCAACGCTTGGACCAATCATAATGATCTGCCCGTGAGGGTAACCGCAACTAGAGACCTGCTTGGGAGAAAACAAAATGACTTCTCATTCCATG
70	Pdgfa	NM_008808.3	806-905	TGTGCGTGGCGTGTGACATTCCTGAACATACTATGTATGGTGCTTCATTGCCAATGTGCGTGCGGTCTTTGTTCTCCTCCGTGAAAAACTGTGTCCGAGG
71	Pdgfrb	NM_008809.1	1186-1285	CTCAAGGACAACCGTACCTTGGGTGACTCCGGCGCTGGCGAGTTAGTTTTGTCTACTCGCAACATGTCTGAGACCCGGTACGTGTCAGAACTGATCCTGG
72	E11/Pdpn/Gp	NM_010329.2	1626-1725	ATAGAAGATATTTCCAGTCTTCGTGACACGGGGACTCAGTGTTGCTGGGACAGAGCTGTAGTGTCTTGGTCGTCTGTGTTGGTACCCAATACAGTGTAGA
73	Phex	NM_011077.2	2581-2680	TCTTCCTGAGTTATGCTCATGTAAGGTGCAATTCCTATAGACCAGAAGCTGCCAGAGAACAAGTGCAAATTGGTGCTCACAGTCCTCCACAATTTAGGGT
74	Pparg	NM_011146.1	1061-1160	ACCAAGTGACTCTGCTCAAGTATGGTGTCCATGAGATCATCTACACGATGCTGGCCTCCCTGATGAATAAAGATGGAGTCCTCATCTCAGAGGGCCAAGG
75	Prx1	NM_175686.3	106-205	TCTGCCCTCCCAGGGGTCTCCAATTTTCTTGTATTCCCTACAAAGCCTCCTCTCCATGCCAGCCTGTGCCTTTTGAAGTGCCAGAGAGCTTCTTGATCCA
76	Ptgs2	NM_011198.3	676-775	CCATCAGTTTTTCAAGACAGATCATAAGCGAGGACCTGGGTTCACCCGAGGACTGGGCCATGGAGTGGACTTAAATCACATTTATGGTGAAACTCTGGAC
77	Pth1r	NM_001083936.1	397-496	CGATGTCTTTACCAAAGAGGAACAGATTTTCCTGCTGCACCGTGCCAGGCGCAATGTGACAAGCTGCTCAAGGAAGTTCTGCACACAGCAGCCAACATA
78	Pthlh	NM_008970.3	791-890	AAAAACCACCCCGTGCGGTTTGGGTCAGACGATGAGGGCAGATACCTAACTCAGGAAACCAACAAGGTGGAGACGTACAAAGAACAGCCACTCAAGACAC
79	Ptn	NM_008973.2	1689-1788	CGCCGAGTGCAAACAGACCATGAAGACTCAGAGATGTAAGATCCCTTGCAACTGGAAGAAGCAGTTTGGAGCTGAGTGCAAGTACCAGTTCCAGGCTTGG
80	Rora	NM_013646.1	1046-1145	GTGTCAAAATGATCAAATTGTGCTTCTAAAAGCAGGCTCGCTAGAGGTGGTGTTTATTAGGATGTGCCGTGCCTTTGACTCTCAGAACAACACCGTGTAC
81	Rorc	NM_011281.2	649-748	GGGGCCTCCTGCCACCTTGAGTATAGTCCAGAACGAGGCAAAGCTGAAGGCAGAGACAGCATCTATAGCACTGACGGCCAACTTACTCTTGGAAGATGTG
82	Rpl19	NM_009078.1	21-120	GAAGAGGCTTGCCTCTAGTGTCCTCCGCTGCGGGAAAAAGAAGGTCTGGTTGGATCCCAATGAGACCAATGAAATCGCCAATGCCAACTCCCGTCAGCAG
83	Runx2	NM_009820.5	1117-1216	TCCTATGACCAGTCTTACCCCTCCTATCTGAGCCAGATGACATCCCCATCCATCCACTCCACCACGCCGCTGTCTTCCACACGGGGCACCGGGCTACCTG
84	Serpine1	NM_008871.2	1823-1922	AGGGGCAACGGATAGACAGATCAAATGGTGGGCCAATAGCGAGCCTTCTCCCTGCTCCCTCCCTTGACACAGCTTGCTTATGTTATTTCAGAGTGTAGGT
85	serpine2	NM_009255.2	1211-1310	GGCAGCAACAACTGCAATCCTAATTGCAAGGTCATCACCTCCCTGGTTTATAGTAGACAGGCCTTTCCTGTTTTCCATCCGACACAATCCCACAGGTGCC
86	Sost	NM_024449.4	976-1075	ACGAAAGACCTGGGACTGGTTATGGACGTACAGTGAAGATCTACTCCTTCCACCCAAATGTAAAGCCTGCGGTCGGGCTAGATAGGGTTTCTGACCCTGACCT
87	Sox2	NM_011443.3	1593-1692	TTCTTTTTGGGGGACTATTTTTGTACAGAGAAAACCTGAGGGCGGCGGGGAGGGCGGGGGAATCGGACCATGTATAGATCTGGAGGAAAAAAACTACGCA
88	Sox4	NM_009238.2	2636-2735	TTTTTCTGCAATGAAGACAGAAAGAAGGCTCTGGGGTGATGCGTTTGGCATTTGTGTTGAGCTTAGGGGAGCATTGGCATGGAGAAACTCCACGCTGGCG
89	Sox9	NM_011448.4	3541-3640	ACAAATGAGAGGTTTCAGATGCAGTGAGGAGCACTGAGTCCTTTGACAGTCATTTTCAGCCATAGACCTTTGGGTCTGCCTGGACTGTATGTGGATGTGTGC
90	Sparc	NM_009242.4	175-274	CTCCAAGAGGCTTCCTGCTGCTCGCCTCTAAACCCCTCCACATTCCTGCAGCCCTTCAGACCGCCAGAACTCTTCTGCCGCCTGCCTGCCTGCCTGCCTG
91	Spp1	NM_009263.3	421-520	TGAATCTGACGAATCTCACCATTCGGATGAGTCTGATGAGACCGTCACTGCTAGTACACAAGCAGACATTTCACTCCAATCGTCCCTACAGTCGATGTC
92	Tcf4	NM_013685.1	3046-3145	AATTACCGGATATTGAATAGGGGAAGCCCGGCTGCCCTCGTAACAAAACCAGCAAACGTCCTGATGGCAACGAAGTGATGACATTAGCCATTCCTTAGGG
93	Tgfb1	NM_011577.1	1471-1570	GGAGTTGTACGGCAGTGGCTGAACCAAGGAAGCAGGAATACAGGGCTTTCGATTCAGCGCTCACTGCTCTTGTGACAGCAAAGATAACAAACTCCACGTGG
94	Tgfbr1	NM_009370.2	4426-4525	TCAGAAGTAGTGGCCAGCTGTGTCTCTAGTAGGACAGTAAAGGCATGAAGCTCAGCCTGTAATCCTGCTACTACAGTAGTACTCCAGAAGTGCCTTGAGG
95	Tgfbr2	NM_009371.3	450-549	TCCATCCACCTAAGTGTGTAATAGGACCATCCACTGAAACATTTTAACAGTGATGTCATGGCCAGCGACAATGGCGGTGCGGTCAAGCTTCCACAGC
96	Timp1	NM_011593.2	437-536	AAGCCTCTGTGGATATGCCCACAAGTCCCAGAACCGCAGTGAAGAGTTTCTCATCACGGGCCGCCTAAGGAACGGAAATTTGCACATCAGTGCCTGCAGC
97	Tnf	NM_013693.2	515-614	TGGATCTCAAAGACAACCAACTAGTGGTGCCAGCCGATGGGTTGTACCTTGTCTACTCCCAGGTTCTCTTCAAGGGACAAGGCTGCCCCGACTACGTGCT
98	Tnfrsf11a	NM_009399.3	693-792	ATCTCTGTGGTAGTAGTGGCTGCCATCATCTTCGGCGTTTACTACAGGAAGGGAGGGGAAAGCGCTGACAGCTAATTTGTGGAATTGGGTCAATGATGCTT
99	Tnfrsf11b	NM_008764.3	36-135	CCGGAGTGTCCCAAAGCCCCACCACTAGCTCCCAAGGTTCCTAAAAAGGAACAAGGTTTGTCCAGACAGAGACTAATAGATCAAAGGCAGGGCATACTTC
100	Tnfsf11	NM_011613.3	616-715	CCAGCGAGGCAAGCCTGAGGCCCAGCCATTTGCACACCTCACCATCAATGCTCCAGCATCCCATCGGGTTCCCATAAAGTCACTCTGTCCTCTTGGTAC
101	Gilz (TSC22D	NM_010286.3	1061-1160	CTAAGCAGAAGCAACCTCTCTCTTCTTCTCTGTCTTTTCCAGGCAGGGGCAGAGATGGGAGAGATTGAGCCAAATGAGCCTTCTGTTGGTTAATACTGTA
102	Vcam1	NM_011693.2	1441-1540	GGTTTTGAGGATGAACACTCTTACCTGTGCGCTGTGACCTGTCTGCAAAGGACACTGGAAAAGGAGAACCCAGGTGGAGGTCTACTCATTCCCTGAAGATC
103	Vegfa	NM_001025250.3	3016-3115	TCTCTCTCTCCCAGATCGGTGACAGTCACTAGCTTGTCCTGAGAAGATATTTAATTTTGCTAACACTCAGCTCTGCCCTCCCTTGTCCCCACCACACATT
104	Vegfb	NM_011697.3	288-387	GGCTCGCACCCAGGCCCCTGTGTCCCAGTTTGATGGCCCCAGCCACCAGAAGAAAGTGGTGCCATGGATAGAGCGTTTATGCACGTGCCACATGCCAGCCC
105	Wnt1	NM_021279.4	2189-2288	ACCTCACTGCTCCTCTGTTCTGCTCGCCAGTCCTTTTGTTATCCGACCTTTTTTCTCTTTTACCCAGCTTCTCATAGGCGCCCTTGCCCACCGGATCAGT
106	Wnt10a	NM_009518.1	2322-2421	TGACTCTAAGGGCTCCAGACCTCTGCTCCTGTCTTTCACTTAACAGATATTTATTTTTGCGCTCTCTTTGAGACACTCTCTGGGGAAAAAGAAGCTCCGG
107	Wnt10b	NM_011718.1	1751-1850	AGCGCTTCTCTCACCTACAGCTCCCTCGGGCTCAGGTTCTACTTCCTTTTGGCCACTCCTCTTCCTCGAAGGATAATAGC
108	Wnt11	NM_001285792.1	1783-1882	TGGGGCCTGAGTGCCCACATGTTGCCTTCCAGGCTGCTCCAAGAAGTCAGGGCAGGGATGGGTAAGACTGTGCATTTGACCTTTCAAGGCCAGAAAGACC
109	Wnt3a	NM_009522.2	1280-1379	AGATCCTACCTGTGAGGGTCTCATACCTAAGGACCCGGTTTCTGCCTTCAGCCTGGGCTCCTTATTTGGGATCGGGTTCCTTTTTAGGGGAGAAGCTCCT
110	wnt4	NM_009523.1	65-164	TGCGGTCCCTGCGACTCCTCGTCTTCGCCGTGTTCTCGGCCGCCGCGAGCAATTGGCTGTACCTGGCCAAGCTGTCATCGGTGGGCAGCATCTCCGAAGA
111	Wnt5a	NM_009524.2	3021-3120	TGGAGGTACGGTAACTTGATGTGTTTTGATGATATCTCTTGGCCCAGGGAGTCCACAGAGGTGTTGCAGCTGTTTGGTTGTTATCCTCCTGCGTTTAGAC
112	Wnt6	NM_009526.3	1716-1815	CTAGAGGGCCAGGATATGGAAGAAAGTTGGTCCTGGTAGAGTTAGCATTTCAGTCTGAGTCTATCATTCCACCTGTTACCAAGGCATGACGGAGTGAGGG
113	Wnt7b	NM_009528.2	1783-1882	TACAAGGCCTGAGATGGCCGCAGAGGACAGCCAATCTTCCATTCCATTTGGAGACTGTCATGCAAATCAAATGTCCCTTGTGTCAGGCTCCAGGCATGCC