

**SBD\_Mouse\_2 (94 genes)**

Customer	Iden	Accession	Position	Target Sequence
ACAN		NM_007424.2	4861-4960	CAGAACITTTGGTGGAACTATAACTCAGGCTCCTACTGCTCAAGAAGCTGGAGAAGGACCTTCGGGCATTTTGAATTTCAGTGGTGCCATTCTGGGACA
Acp5		NM_001102405.1	441-540	AACATCCCCTGGTATGTGCTGGCTGGAACCATGATCACCTTGGCAACGCTCTGACAGATTGCATACTCTAAGATCTCCAAGCGCTGGAACCTCCCA
beta actin		NM_007393.1	816-915	CAGGTCACTACTATTGGCAACGAGCGGTTCCGATGCCCTGAGGCTCTTTTCCAGCCTTCTCTTGGGTATGGAATCCTGTGGCATCCATGAAACTACAT
Adipoq		NM_009605.4	781-880	GACCACAATGGACTCTATGCAGATAACGTCACGACTCTACATTTACTGGCTTTCTTCTACCATGATACCAACTGACTGCAACTACCCATAGCCCAT
Alpl		NM_007431.2	206-305	CTCCAGCGAGGGACGAATCTCAGGGTACACCATGATCTCACATTTTTAGTACTGGCCATCGGCACCTGCTTACCAACTCTTTTGTCCAGAGAAAGAG
beta 2 microgl		NM_009735.3	178-277	CTGAACTGCTACGTAACACAGTTCCACCCGCTCACATTTGAAATCCAATGCTGAAGAACGGGAAAAAATTCCTAAAGTAGAGATGTCAGATATGTCCT
Bglap		NM_007541.2	252-351	GTGAGCTTAACCTGCTTGTGACGAGCTATCAGACCAGTATGGCTTGAAGACCGCTACAACGCATCTATGGTATCACTATTTAGGACCTGTGCTGCC
Car2		NM_009801.4	438-537	TGCCCAGCATGACCTGCCCTACAGCCTCTGCTCATATCTTATGATAAAGCTGCGTCCAAGAGCATTGTCAACAACGGCCACTCCTTAAAGTTGAGTTT
Casr		NM_013803.2	4361-4460	GCCACATTTAGATCTTAGGATCATAGATACCTCCAAGCACCGGAAAGACTGACTCAACCCAACGAGCTGTCTGTAACTAATATCAATGTACAT
Col10a1		NM_009925.4	1851-1950	TAAGATCCCAGGCATATACTATTTCTCTACCAGTGCATGTGAAAGGGACTCACGTTTGGGTAGGCCTGTATAAGAACGGCCACTACGATGTACACG
Col14a1		NM_181277.3	785-884	GAGGTTCAACTTCAGGCTTGTGCGCAATTTCTGGAAAACTGGTACAGCGTTCAACGTGGGCTCAGAAAAGACAAGAACTCCGCTTGCCACATGACAGT
Col15a1		NM_009928.3	449-548	TCTCAGTTCACTGGACTCACAGTGTCTATTGGTGTCCCATTACCTCGTCTGTGTCCTTACCCGGCTATGGCGGTTCCCGGCTTACAGCTTTG
Col1a1		NM_007742.3	216-315	CAATGGTGAGACGTGGAACCCGAGGTATGCTTGTATCTGTATCTGCCAATGGCACGGCTGTGTGCGATGACGTGCAATGCAATGAAGAAGTGGACTGT
Col2a1		NM_001113515.2	4347-4446	ACACACTGGTAAGTGGGGCAAGACCGTATCGAGTACCGATCACAGAAGACCTCCGCTTCCATTATTGACATCGACCCATGGACATTGGAGGGGCT
Comp		NM_016685.2	515-614	TGGGACTGACCTTCGCTAAGTCCAACAAACAAGTTTGACGGATATTAATGAGTGTGAGACCGGGCAGCACAATTGCGTTCCTCAACTCCGTGTGCGTCAA
C-Fms		NM_001037859.1	3656-3755	CCACCCTCTTGACCTTCACTCTGTCTATAGTCCCGCTCATCTGGATCTTGTACTGAGCGGAGCTAAAAGTGTCTACCCAGTGCCTGTCACTCTA
Ctsk		NM_007802.4	1201-1300	GCGTCTGAGAGGGACGCGATGCTAACTAAGATTTCTTCTTCTCTGTTGGTCTCCAGTGACAACCTACTTCCCTTCTCTGCCCCAG
Dkk1		NM_010051.3	56-155	GCCAGCCCGTGCAAAGTGACCTCTTTTCTGACCTTGGCTGTTGCGTCTCCGAGATGATGTTGTGTGTGAGCGGAGCTGTCCGTTCTT
Dmp1		NM_016779.2	121-220	AAGACTGTCACTTCTCTTGTGTTCCCTTGGGGGCTGTCTGTGCTCTCCAGTTGCCAGATACCACAATACTGAATCTGAAAGCTCTGAAGAGAGGACGG
Fgf23		NM_022657.4	419-518	TCTCCACGGCAACATTTTGGATCGCTTCACTTCAGCCAGAGAAATGCAAGTCCGCCAGTGGACGCTGGAGAATGGCTATGACGTTACTGTGCGCAG
Foxo1		NM_019739.2	2531-2630	TTTCTCAGACTTGGCAACAGCGGACACTTTCCTGTGAGGATGTTTGCAGCGTCCGAGGTTTTGTGCTCTGTAGATAAAGACTGTGCCATTGG
Fzd1		NM_021457.3	3447-3546	TCTAGTATCTGGAACCTGCTCTGGGTCTGGTTCATCATGGAAGAGCAGCAAGCTTGTGGGTTGGGAGAGGGTAAAGAGAGAGGTTATAAAACATTA
Gapdh		NM_001001303.1	891-990	AGGTTGTCTCCTGCGACTTCAACAGCACTCCACTCTCCACCTTCGATCCGGGGGCTGGCATTGCTCAATGACAACCTTTGTAAGCTCATTTCTCTG
Prgn		NM_008175.4	1293-1392	AGATCTTGAAGAGTGATACACCTTGTGATGACTTCACTAGGTGCTTCCACAAACAATCTGCTGCCAACTCAATTCTGGGGACTGGGGCTGCTGCCAT
Hif1a		NM_010431.2	1295-1394	ACCATGATATGTTACTAAAGGACAAGTACCACAGGACAGTACAGGATGCTTCCAAAAGAGGTGGATATGCTGGGTTGAAACTCAAGCAACTGTCAT
lbsp (sialoprot		NM_008318.3	115-214	GGAAATGGCTGTCTTCTCGATGAAAAATTTCCATCGAAGAATCAAAGCAGAGGATTCTGAAGAAAACGGGGTCTTAAAGTACCGGCCACGCTACTTTC
Igf1		NM_001111274.1	419-518	GGGCTTTTACTTCAACAAGCCACAGGCTATGGCTCCAGCATTGCGAGGGCACCTCAGACAGGCATTGTGGATGAGTGTGCTCCGGAGCTGTGATCTG
Igf1r		NM_010513.2	3391-3490	CGTATGAGAACCTCATGCATCTGATCATTGCTCTGCCGTTGCCATCTGCTGATCGTTGGGGGGCTGGTTATCATGCTGTATGCTTCCATAGAAAAGAG
Il10		NM_010548.1	986-1085	GGGCCCTTTGCTATGGTGTCTTTCAATTGCTCTCATCCCTGAGTTCAGAGCTCCTAAGAGAGTTGTGAAGAACTCATGGGCTTTGGGAAGAGAAAACCA
Il11ra1		NM_010549.3	23-122	GGGTCCCACAACCTGAGGAGCGGGAGACAGTTCTTAGCCTGTAGGAGGAAGTCTGGAGGCCATGGCCACTCAGTCACTGTGATTATCAAGATGAGCAG
Il15		NM_008357.2	855-954	CTTGCAAACAGCACTCTGCTTCTAACAAAGATGTAGCAGAATCTGGCTGCAAGGAATGTGAGGAGCTGGAGGAGAAAACCTTACAGAGTTTTTGCAA
Il17a		NM_010552.3	206-305	ACCTCAAAGTCTTTAACTCCCTGGCGCAAAGTGTAGCTCCAGAAGGCCCTCAGACTACCTCAACCGTCCACGTCACCTGGACTCTCCACCGCAATGA
Il1a		NM_010554.4	226-325	ACCTCTGAAACGTCAAAGATGTCAACTTCACTTCAAGGAGAGCGGGTGACAGTATCAGCAACGTCGAAAGCAACGGGAAAGATTCTGAAGAAGAGACGGC
Il1b		NM_008361.3	1121-1220	GTTGATTCAAGGGGACATTAGGCAGCACTCTAGAACAGAACCTAGCTGTCAACGTTGGGGGATGAATTTGTCATAGCCCGCACTGAGGCTTTTCATT
Il6		NM_031168.1	41-140	CTCTCTGCAAGAGACTCCATCCAGTTGCCTTCTGGGACTGATGCTGGTGACAACCAACCGCCCTTCCCTACTTCAAGTCCGGAGAGGAGACTTCACAG
Il6ra		NM_010559.2	2826-2925	CACCTCACTGCAACTGGCCTTCTTCTTACCTTACCTGACTGATGGCTCAGATGCTTCCCTGAGGCTTTCCTTGGGCTTTGAGGAATGATGTAGGTCA
Lrp1		NM_008512.2	1311-1410	GAGCAGATGGCAATCGACTGGCTGACGGGAAACTTCACTTTGTCGACGACATTGACGACAGGATCTTGTCTGTAACCGAAACGGGGACACTGTGTCA
Lrp5		NM_008513.3	1681-1780	ATGCCAAAAGTATAAAATCGAGGTGATCAACATAGATGGGACAAAAGCGGAAAGACCCTGCTGAGGACAAGCTCCACATATTTTTGGGTTCACTGCT
Lrp6		NM_008514.3	3316-3415	GCTACCAATGTCAATTGATGTGACGAGATTAGATGGACGATCAGTTGGAGTGGTCTAAAAGGCGAGCAGACAGACCTCGAGCCATTGTGGTAAACCCCG
Mepe		NM_053172.1	323-422	CAGGAGAAAGAGACTCAGAGTGTCTAAGCGTAATCCAGCAGATGTCAATGATGCTAAAGTCTCCTTAAAAGACATAAAGAATCAAGAGAGTTATCTGC
Mmp10		NM_019471.2	1051-1150	CAGACTTAGATGCTGCCTATGAGGCTCACAAACGAGACGATTTCTGATTTTTAAAGGAAGTCACTTCTGGGCAGTCCGAGGAAATGAAGTCAAAGCAGG
Mmp12		NM_008605.3	593-692	AAGTGGTACACTGACCTGCTTTTCTTCCAGCTGGTATTCAGGAGATGCACATTTTGTAGGAGCAAGGACTGGACTAAAAGTTTTCAAGGCAC
Mmp13		NM_008607.2	203-302	GGGAATCCTGAAGAAGTCTACAGTGCACCTTCCACAGTTGACAGGTTCCGAGAAATGCAATCTTCTTGGCTTGTAGAGGTGACTGGCAAACCTGATGTC
Mmp14		NM_008608.3	555-654	AGTTTTGGGACTGAGATCAAGGCCAATGTTCCGAGGAAGCGCTATGCCATTGAGGCTCAAGTGGCAGCATAATGAGATCACTTTCTGATTGAGAAATTA
Mmp2		NM_008610.2	2377-2476	AGTTAACCAGCTTCTCTTCACTGTTGACTTCAGATTTAAGAGGGTGGCTTCTTTTGTGCCAAAGAAAGGTGCTGACTGTACCTCCCGGGTGTGCTG
Mmp3		NM_010809.1	1576-1675	TCTTTGTGAAAGGAAAGTCTTTGTTGACGATGTGCTATGGCAGAACCAACAGGAGCTATGGATGACACCAGTCAACGTCAGTTGTCAAAGGATGTTCA
Mmp8		NM_008611.4	233-332	CTACAACCTACCAAGCAATCAATTCGGTCTTCGAGGAATGCCAGATGGTTGCGAGAGAAGCTTAAAGAGATGCAGCGCTTCTCAGCTTAGCAGAGACT

Mmp9	NM_013599.2	1571-1670	CCCTACAGAGTCTTTGAGTCCGGCAGACAATCCTTGCAATGTGGATGTTTTTATGCTATTGCTGAGATCCAGGGCGTCTGCATTTCTCAAGGACGG
Myod1	NM_010866.2	1201-1300	TGGGGATGGTGTCCCTGTTCTTCCAGCCCAAAAGATGAAGCTTAAATGACACTCTCCCAACTGCTTTTGAAGCCGTTCTTCCAGAGGGAAAGGAAAG
Nanog	NM_028016.2	1083-1182	GCCTTGAATTATTCCTGAACACTCTGTGACTCCACCAGGTGAAATATGAGACTTACGCAACATCTGGGCTTAAAGTCAGGGCAAAGCCAGGTTCTTCC
Nes	NM_016701.3	2717-2816	GCAGAGAATTGTGAAACCTCTAGAAAAAGTGAGCCAGGTCTCCCTGCAATCTCTGAAAAAGAGAATGTGCAGTACCAAGGTATCTGGAAGAAGATGAC
Ngf	NM_001112698.1	631-730	CAAGGAGGTGACAGTGTGGCCGAGGTGAACATTAAACAACAGTGATTAGACAGTACTTTTTGAGACCAAGTCCGAGCCTCCAATCCTGTTGAGAGT
Ngfr	NM_033217.3	1996-2095	AACAGGGAGATCAATTGTAGGCTGACACACTCCTTTCTGAATGAGGGCGTCAAGTGCTTGTGGCAGGGATGGAGTGACTTTCAGGGAACATCTGAAAA
NLRP3	NM_145827.3	509-608	ACGTGTACATCACATTCCTATGGTATGCCAGGAGACAGCCTTGAAGAAGAGTGGATGGGTTTGTGGGATATCTCCCGCATCTCCATTTGTAATA
Nog	NM_008711.2	896-995	GATCAAAGGGCTGGAGTCTCCGAGGGCTTGGCCAAAGGCAAGAAACAGCGCTGAGCAAGAAGCTGAGGAGGAAGTTACAGATGTGGCTGTGGTCCACAG
Oscar	NM_175632.3	205-304	CTCATCTGCTGCAGTTGTACTCCTGGGATCAACGTGACCTTGACTTCCGCGCACCTCAATCTGCTGCGGTTTGCCTCTTCAAAGTGGCCTTGT
Pax3	NM_001159520.1	732-831	GAAGAAAATTGAGGAATACAAAAGAGAGAACCAGGCGATGTTAGCTGGGAAATCAGAGACAAATTGCTCAAGGACGCTGTCTGTGATCGGAACACTGTG
Pax7	NM_011039.2	3681-3780	CAACATTCACACGCTTGGACCAATCATAATGATCTGCCGTGAGGGTAACCGCAACTAGAGACCTGCTTGGGAGAAAAACAAATGACTTCTCATTCCATG
Pdgfa	NM_008808.3	806-905	TGTGCGTGGCGTGTGACATTCCTGAACATACTATGTATGGTGCTTATTGCCAATGTGCGTGGCTTGTCTCTCCGTGAAAAACTGTGTCCGAGG
Pdgfrb	NM_008809.1	1186-1285	CTCAAGGACAACCTGACTGGTGACTCCGCGCTGGCGAGTTAGTTTTGTCTACTCGCAACATGTCTGAGACCCGCTAGCTGTGAGAACTGATCCTGG
E11/Pdpn/Gp3	NM_010329.2	1626-1725	ATAGAAGATATTTCCAGTCTTCGTGACACGGGGACTCAGTGTGCTGGGACAGAGCTGTAGTGTCTTGGTCTGTGTGGTACCCAATACAGTGTAGA
Phex	NM_011077.2	2581-2680	TCTTCTGAGTTATGCTCATGTAAGGTGCAATTCCTATAGACCAGAAGCTGCCAGAGAAACAGTCAAATTGGTGCTCACAGTCTCCCAATTTAGGGT
Pparg	NM_011146.1	1061-1160	ACCAAGTGACTCTGCTCAAGTATGGTGTCCATGAGATCATCTACAGATGCTGGCCTCCCTGATGAATAAAGATGGAGTCTCATCTCAGAGGGCCAAGG
Prx1	NM_175686.3	106-205	TCTGCCCTCCAGGGGTCTCAATTTTCTGTATTCCCTACAAAGCCTCCTCCATGCCAGCCTGTGCCCTTTGAAGTGCCAGAGAGCTTCTTGATCCA
Pth1r	NM_001083936.1	397-496	CGATGCTTTACCAAAGAGGAACAGATTTTCTGCTGCACCGTGCCAGGCGCAATGTGACAAGCTGCTCAAGGAAGTTCTGCACACAGCAGCCAACATA
Pthlh	NM_008970.3	791-890	AAAAACCACCCCGTGCGGTTTGGGTGAGACGATGAGGGCAGATACTAAGTCACTCAGGAAACCAAGGTGGAGACGTACAAGAACAGCCAATCAAGACAC
Rpl19	NM_009078.1	21-120	GAAGAGGCTTGCCTAGTGTCCCTCCGCTGCGGGAAAAAGAGGTCTGGTTGGATCCCAATGAGACCAATGAAATCGCAATGCCAATCCCGTCCAGCAG
Runx2	NM_009820.5	1117-1216	TCCTATGACCAGTCTTACCCTCTATCTGAGCCAGATGACATCCCATCCATCCACTCCACACGCGCTGTCTTCCACACGGGGCACCCGGTACCTG
serpine2	NM_009255.2	1211-1310	GGCAGCAAACTGCAATCTAATTGCAAGTGCATCACCTCCCTGTTTATAGTAGACAGGCTTTCTGTTTTCCATCCGACACAATCCACAGGTGCC
Sost	NM_024449.4	976-1075	ACGAAAGACCTGGGACTGGTTATGACGTACAGTAAGATCTACTCCTCCACCAAAATGTAAGCCTGCGTGGGCTAGATAGGGTTTCTGACCTGACCT
Sox2	NM_011443.3	1593-1692	TTCTTTTTGGGGACTATTTTTGTACAGAGAAAACCTGAGGGCGGGGGAGGGCGGGGGAATCGGACCATGTATAGATCTGGAGGAAAAAACTACGCA
Sox4	NM_009238.2	2636-2735	TTTTTCTGCAATGAAGACAGAAAGAAGGCTCTGGGGTGTATGCGTTTGGCATTGTGTTGAGCTTAGGGGAGCATTGGCATGGAGAACTCCACGCTGGCG
Sox9	NM_011448.4	3541-3640	ACAAATGAGAGTTTTAGATGACGTGAGGAGCAGTGTCTTGGCAATGTTTTGAGCAGTACTGAGCCTTGGGCTGCTTGGAGTATGTGGATGTGTC
Sparc	NM_009242.4	175-274	CTCCAAGAGGCTTCTGCTGCTGCTCTAAACCCCTCCACATTCTGACGCCCTCAGACCCGAGAACTCTTCTGCGCCTGCTGCTGCTGCTGCTG
Spp1	NM_009263.3	421-520	TGAATCTGACGAATCTCACCATTGCGATGAGTCTGATGAGACCGTCACTGCTAGTACACAAGCAGACACTTTCCTCAATCGTCCCTACAGTCGATGTC
Tgfb1	NM_011577.1	1471-1570	GGAGTTGTACGCGAGTGGCTGAACCAAGGAGACGGAATACAGGGCTTTCGATTGAGCGTCACTGCTCTGTGACAGCAAAGATAACAACTCCACGTTGG
Tgfb1	NM_009370.2	4426-4525	TCAGAAAGTAGTGCCAGCTGTGCTCTAGTAGGACAGTAAAGGCATGAAGTCAAGCCTGTAATCCTGCTACTACAGTAGTACTCCAGAGTGCTTGGAGG
Tgfb2	NM_009371.3	450-549	TCCATCCACTAAGCTGTAATAGGACCATCCACTGAAACATTTAACAGTGTATGTCATGGCCAGCACAATGGCGGTGGGTCAGCTTCCACAGC
Tnf	NM_013693.2	515-614	TGATCTCAAAGCAACCACTAGTGTGCCAGCGATGGTGTACTCTTCTACTCCAGTCTTCTTCAAGGACAAGGCTGCCACTACGTTGCT
Tnfrsf11a	NM_009399.3	693-792	ATCTCTGTGGTAGTAGTGGCTGCCATCTTCGCGTTTACTACAGGAAAGGAGGAAAGCGCTACAGCTAATTTGGAATTGGGTCAGTATGCTT
Tnfrsf11b	NM_008764.3	36-135	CCGGAGTGTCCCAAAGCCCACTAGCTCCAAGTCTCTAAAAGGAAACAAGGTTTGTCCAGACAGAGACTAATAGATCAAAGGCGAGGGCATACTTC
Tnfsf11	NM_011613.3	616-715	CCAGCGAGGCAAGCCTGAGGCCAGCCATTGACACCTCACCATCAATGCTGCCAGCATCCCATCGGTTCCCATAAAGTCACTCTGTCTTGGTAC
Gilz (TSC2D3)	NM_010286.3	1061-1160	CTAAGCAGAAGCAACTCTCTCTTCTCTGCTTTCCAGGCAAGGGGAGAGATGGGAGAGATTGAGCCAAATGAGCCTTCTGTTGTTAATACTGTA
Vcam1	NM_011693.2	1441-1540	GGTTTTGAGGATGAACACTTACTCTGTGCGCTGTGACCTGCTGCAAAGGACTGGAAGAGAAACCCAGGTGGAGGTCTACTCATTCCCTGAAGATC
Vegfa	NM_001025250.3	3016-3115	TCTCTCTCCAGATCGGTGACACTACTAGTGTCTGAGAAAGATATTAATTTTGTCTAACACTGAGCTGCCCTCCCTTGTCCCAACACACAT
Vegfb	NM_011697.3	288-387	GGCTCGCACCAAGGCCCTGTGCTCCAGTTTGTATGCCAGCCACAGAAAGAGTGGTGCATGGATAGACGTTTATGCACTGCTCCATGCCACATGCCAGCCC
Wnt10a	NM_009518.1	2322-2421	TGACTCTAAGGGCTCCAGACCTCTGCTCTGCTTCTTCACTTAAACAGATATTTATTTTGGCCTCTCTTGGAGACTCTCTGGGAAAAAAGAAGCTCCGG
Wnt10b	NM_011718.1	1751-1850	AGCGTCTTCTACTACAGCTCCCTCGGGCTCAGTTCTACTTCTTTGGATAGGGAGTCTATCTTTGGCCACTCCTCTTCTCGAAGGATAATAGC
Wnt11	NM_001285792.1	1783-1882	TGGGGCCTGAGTGCCACATGTTGCCTTCCAGGCTGCTCAAAGAAGTCAGGGCAGGGATGGGTAAAGACTGTGCATTTGACCTTTCAAGGCCAGAAAGACC
Wnt3a	NM_009522.2	1280-1379	AGATCTACTGTGAGGGTCTACACTAAGGACCCGTTTCTGCTTCCAGCTGGGCTCTATTGGGATCTGGGTTCTTTTAGGGGAGAAGCTCCT
wnt4	NM_009523.1	65-164	TGCGGTCCTGCGACTCTCTGTTGCGCGTGTCTGCGCCGCGGAGCAATTGGCTGTACTTGGCCAAGCTGTATCGGTGGGCGAGCATCCGAAGA
Wnt5a	NM_009524.2	3021-3120	TGGAGGTACGGTAACTTGTATGTTTTGATGATATCTTGGCCAGGGAGTCCACAGAGGTGTGACAGCTGTTGGTTGTTATCTCTCGGTTTAGAC
Wnt6	NM_009526.3	1716-1815	CTAGAGGGCCAGGATATGGAAGAAAGTTGGTCTGGTAGAGTTAGCATTTCAGTCTGATCTATCATTCCACCTGTTACCAAGGCATGACGGAGTGAGGG
Wnt7b	NM_009528.2	1783-1882	TACAAGCCTGAGATGCGCCAGAGGACAGCCAATCTCCATCCATTTGGAGACTGCTATGCAAATCAAATGTCCCTGTGTGAGCTCCAGGCATGCC