Table S1. Primers used: Sequences, amplicon sizes, and efficiencies

Gene	***Forward sequence***	***Reverse sequence***	***Amplicon (bp)***	***Efficiency (%)***
ADAMTS4	CTACAACCATCGCACGGA	GCCTGGCAGGTGAGTT	108	88
ADAMTS5	TCTTCCATCCTAACCAGCATTG	GGTGGCATCATAAGTCTGTCC	165	98
ADAMTSL3	CCAAGGACCCAAGGCATCGT	TCTGACACACCTGCTTTCTTCTCTG	134	96
ADORA2A	CGTGGTCCCTATGAACTAC	CCGCCAGGAAGATGC	101	100
ANGPTL7	GCTGTCACTTGGCTCTG	AGTCCTTCTCCTGCTTCTTG	193	94
APOE	GGTGCAGACGCTGTCTGACCA	CCTCCAACTCCGCCTTGTAGG	122	90
AQP4	CGACATGGTTCTCATCTCCCTTTG	GAAGACAGACTTGGCGATGCT	148	94
BCO2	GCCCATTGTCCTATTCTTCAGCCAGT	TGCCGAAAGCCACAGCCATAGA	181	95
BMP2	GGACACCAGGTTAGTGAATCAGAACA	TGCTTCTCTTCCAAATGAGCCACT	135	97
BMP4	AAAGTCGCCGAGATTC	ATTGTGCTCTTGCTAGG	134	86
CABP5	AAATGCGAGATGCCTTCAAAGA	CTGCCTCCTGGACAACCT	138	96
CAMP	GAGGATGAGGACCCAGAC	TCTCCAACCCGTTCTTCTT	118	98
CDC42	CCCGTGACCTGAAGGCTGTC	ACACACCTGCGACTCTTCTTGGG	130	98
CHAT	AGGCACTGACTTTCGTGAGAG	CGGTCTGGGCTCGGATG	99	96
CHRNA7	GTACTTCGCCAGCATCAT	ACACCAGTTCAGCAGGA	133	95
CILP	GCCTTCTGTGACGACCAGTC	GTAGGGCTGAGGGACACCAATA	132	97
COL12A1	CAGGTGTCCCGATCAAAGAG	GCCTGGTGGAATGGTGG	95	97
COL6A6	ATCAGCCACATCAATCAAGAG	GATGAGGATGAGGAACTTCTT	195	94
CYP26B1	GCACTACCTGGACTGTGTCA	CGCTGTGTCGTGGGTATCTC	157	95
CYR61	TGGAACCTCGCATTCTGTATAACC	GCCACAAGGTCGCACTTCAC	176	97
DCN	CTGCGTGCCCATGAGAACGAGATC	GGTATCAGCAATGCGGATGTACGAAAGC	168	96
DRD2	CACGCACATCCTGAACATACA	GTTGAAGGTGGTGTAGATGATGG	118	91
EGF	GGAGACGCCAGATAGAATAACG	GACGATGTGCTCACCGAA	193	95
EGR1	TCCCTGACTACCTGTTTCC	AGTGGAGTGAGCGAAGG	112	90
EPHA1	GCCTCCTGGACAACTTC	CACATCACAATCCCAAAGC	136	94
FAM180A	AGACATTCGTCGCCTGAGT	CTTCTGATACCCGTGGGACAA	130	94
FGFR1	CCTGGAGGTCATCATCTACTGC	AGAGTTCATGGAAGCACTGGAG	196	99
FMOD	TCCTGCTGGACCTGAG	TTGTTGGTGAGGCTGTTAT	172	96
GFRA1	CGGCAAGGAGACCAACTT	TTGTAGAGCGACTTCTGCTTC	96	96
GRM5	GCATCGCCCACTCTTACAAA	CCATCAGCAGACCTCTCACT	144	93
HIF1A	ACTGGTTGCATCTCCGTCTCCTACTCA	TCCTGCTCTGTTTGGTGAGGCTGTC	109	94
IGF2	TGGCATTGTTGAAGAGTGTTG	GAAGCACGGTCGGAGAG	113	100
IGF2R	GTACTCTGACGGAGACCTCACC	TGATTGCACTCAAAGTTTATGACACTCA	96	102
IL1B	CAAGGAAGAAGATGGAGAAGCGATT	GGCAGGTAGCTTGGTGAAGTC	182	97
INSR	AACGAGGCGTCGGTCATG	ATCATCTCTTGCAGGGTAGGG	194	92
LTBP1	GGACGAGTGCCTGGAACC	TGCTTGTGGTCTGGAGTTGG	111	103
LTF	GGCTCCAAGTCACGCTGT	GGGCAGTCAACACCGTTTCTT	105	97
MEST	CAAAGATGGAGGTGTGCTGTC	ACTGTAAGAGACTGTCGATGACTAAG	179	94
MMP14	CCCTGGAACCTGGCTACCC	ATAGGTCTTTCCATTGGGCATCC	104	96
MXRA5	GGAAGGAAGGAGTGGATG	GAGGCTGGAAGGTTACA	195	93
NOS1	ACATCACCACGCCACCAA	CCTCCAACACCTCCACGAT	159	94
NOV	CGAACAGACTACAGAGTGGAGTG	GTGATTTCTTGGTGCGGAGACA	191	97
NRG1	CGTGTCCAAGAATGTCATCTCC	TGTGTGCCCATTGCTCCA	145	97
NTS	AATGTGAACAGCCAACCCGAG	AACTCCCAGTGTTGAAAGATCCTG	164	95
NYX	GTGAGCAGGTTCAGCAG	GACAGCGAGGTGTTAGC	101	96
OGN	CTCTCCTTCCTCTACCTGGACCACAAC	CTGAAGATGGATCACGCGCAGACTC	84	96
OPN1LW	ATGGTCACCTGCTGTATC	GGTGGAAGGCGTAGC	232	98
P2RY1	ACGGCAGCATCTTGTTC	GGAGATCGCTACCACCA	146	97
PENK	TCCTTGCCAAGCGATACG	TCTTGCTCATTTCTTCGTCGTT	162	98
PER2	ACGACAACACATACACCGAAT	GCACAGGCGTCTGGATC	100	92
PI15	CCACTGACTCATCCCCGCCAACC	GTTTGCTGCTGGTGGGAACACTTTGC	176	96
PRELP	TTCGGCTGAACTACAACAAGC	GATCTGGGTCCCGTTGATTTTCT	182	99
PTX3	CTGTGTGGGCGGTGGCTTTG	TCCATGTGGCTGAATCTCTGTGACTC	175	94
RASGRF1	GACTCTGACCCAGGAGGA	AGCCTTGTCCGAAGAACTC	185	93
RLBP1	CGTGCCAGGAAGTTCAA	TGAAGAGCATGACCACTC	184	93
RPE65	CACCCAGATGCCTTGGAAGAAGATGA	CTTCACTCAAGTCCTTGGCGTTCAGA	115	99
RXRB	CCTGACCTACTCGTGCC	TACCGCCTCCCTCTTCA	118	91
S100A12	GAGCAAGATGGAAGATCACATGGAGG	TGAGGGTGTTTGGAAGTTCCTTTGTT	134	100
SCUBE3	CCGTCCTCCATTACCACTTAC	CTCGCACGATGTCTTCTACCA	184	95
SERPINH1	ACAAGAACAAGGCAGAC	GCACCAGGAAGATGAAG	186	103
SOSTDC1	GCGGTCCACCAAGTACATCT	ATAGCCTCCTCCGATCCAGTTA	121	97
SST	CCAGACTCCGTCAGTTTCT	CCAGGGCATCGTTCTCA	120	93
TAC1	CGGAGCCCTTCGAGCATCTTCTG	CCCGTTTGCCCATTAATCCAAAGAATTGC	81	96
TGFB2	GCAGAGTTTAGGGTCTTTCGTTTG	CTCGTGAACAGCATCAGTTACATC	189	93
TGFB3	ATCACCATAACCCGCATCTAATCC	CGCACACAGCAGTTCTCCTC	139	90
TGFBI	CCTCGGCACTCATCTCTCC	GCAAATTCTTCATCTTGGCATCG	107	94
THBS1	CTGTCAGAACTCAGTCACCATC	CCACGGAGACCAGCCATC	136	91
THBS2	GAGACCGACTTCAGGAACTTC	CGAAACCCACTGCGATGC	142	100
TIMP2	AGATGGGCTGTGAATGC	CCGTCGCTTCTCTTGAT	151	96
TIMP3	CCGTGTCTATGATGGCAAGATG	ACAAAGCAAGGCAGGTAATAGC	153	99
TNC	AGACGCCAAGACTCGCTACAG	CAGGTTGACACGGTGACAGTTC	184	94
TNMD	GCTGGATGAGAGAGGTTATTGT	TGATGACACGACAGATGACC	137	100
VDR	AACTTGCACGAGGAGGAAC	CTTCTGGATCATCTTGGCATAG	189	93
VIP	AACGAGTGAGCACCAACATCTC	TCTTGACAGCCATTTGTTTCCTAAGG	108	94
VIPR1	TCCACGCTGCTGCTGATTC	CCCACGACCAGCTCAAAGAC	107	99
VIPR2	CCACGCACACCTCCTC	CACTTCCTCTTCAGCTCACT	127	90
ZNF185	GGAGGCGTCTGTACCTACTG	GCAAATCCCACACCTAAAGCAAT	108	97
POLR2A	CTACCAGCCCCAAGTATTC	GGTGAGTAAGTAGGAGACG	106	98