

Lyle et al. Supplementary Table 2

Gene	[F], nM	[R], nM	[P], nM	E	Forward primer	Reverse primer	Probe
Actb	300	300	250	0.95	CTAAGGCCAACCGTGAAAAGAT	CACAGCCTGGATGGCTACGT	TTGAGACCTTCAACACCCCAGCCATG
Adamts1	900	900	250	1.03	TTTGCAAGCCGCCCTTCA	TCGTGCGGCATGTTAAACAC	CACAGCCCACGAATTGGGCCA
Adamts5	900	900	250	0.98	AAGAGGGCCATATACCGTTCCT	CACTGCTCATGGCGAAAAGA	AGTGTTACACCCTGCCACCCAATGGTA
Ankrd3	300	300	250	0.97	TGTCTTTTGAGCGGGAAGCTT	CCACTAGCTTCTTCTTGATGTC	AACAGGCGACCTGGGCCCCA
App	900	900	250	1.02	CCGTGGCACCTTTTGG	GGGCGGGCGTCAACA	ACTCTGTGCCAGCAATACCGAAAATGAAG
Atp5o	300	300	250	1.01	AGCTTGTAAGGCCCCCTGTT	AGAGTACAGGGCGGTTGCAT	GCGGCCTTCGATGCCGTAGACCT
B3galt5	300	300	250	0.97	TGCGCTTTTCAGAAAATTGTG	TCCAGTGCTTGCCAGTAAGTGA	CATGCCATTTTATGAAGCCCCAGGACC
Bace2	300	300	250	1.05	GTCGCTCCTCCGGATCA	AATTGAAACGAGCTCCCATCA	CATTCTCCACAGCTCTACATTAGCCC
Bach1	300	300	250	1.01	CTGAGACGGACACGGAAGGT	GGGCATTGAATGGCAGCTT	ACCTCACAGTCCTGCTCCCTGGCA
C21orf11	300	300	250	0.99	TCCTGCTGTTTCATGGTGACT	GGCTTCTATGGCATCCTTTGC	TGAGCCTTCAGTTTGAACTTCCATCATCAT
C21orf18	300	300	250	0.95	ACGGCTCTCAAGTTGCTGTGT	GGAGATGACTTCGCCAAGGA	AAGCCGAGCGCTTCACATCCTGG
C21orf25	300	300	250	0.99	ACCCACGCAGGTCAAAGAAG	GGGAGGGCAGGGTTCCT	TCAGAGTCTACAGTGCCCTTCCTCCACTG
c21orf4	300	300	250	1.01	CACGTGCGGTGTGTTTTCC	CGCACCTGGGCATTGG	CGCTGGCCTTCTTCATGATAAATGCTGT
c21orf45	300	300	250	0.99	TTGTTCTGCCTCAGCGTTGA	CTTCTGACACGATTGCTTCTCA	CCGTTGAAAGTTACACCTTAGGGTCC
C21orf5	300	300	250	0.99	AATCGAGAAGCGTTGAGAAAC	GCCGAGCGAAGAGATGAGAT	TGCCCATTGCTGGAGGACTCAA
C21orf51	300	300	250	1.01	GGCCCGCCATGAACGT	GGTTTTTGCCGCCAGGAT	TCTTGAACACGTGCCCCTGCTGCT
C21orf59	900	900	250	0.97	GAAGAACACAAGCAGCTGATGCT	GGAGTCATCGTCATTCTCTCCA	TCTACCACAGAAGACAGGAGGAGCTCAAGAAA
C21orf6	300	300	250	1.01	TGTGAGCCTGGACCTCTCTGA	CAGGACTGTAGGATATTTAAAGGGAAGA	TGCAAGACAAAGAAAACGTCAACCACTGCT
C21orf62	300	300	250	1.03	TGCTGGCGGAGAGTTTGG	TGGACTGGTGTTCCTGTTTC	TAAGGAGGTGACCTACAATGGACTGGCTCA
C21orf61	300	300	250	0.97	TGGCGTTATCGTCAGCAACTC	ACAGCAGAGCGGCTCTCTCT	CCGCGTTCGCTTACATTCGAG
C21orf63	900	900	250	1.03	CCAGTTCGCATCGCGTTTA	ACCAAAGGAATGGCATCTTCA	CCTCAATGATGCCCCAGATGATACACCA
Caf1a	300	300	250	0.96	CATCCATTACCATACCTGAGTGA	GTGGAGGAAATGGCCAAGAA	CCCATCGCTGGACCAGGAAA
Cbr1	300	300	250	0.96	CAAGGAGCTGCTCCCTCTAATAAA	GCCCTGAGACTCACCATGCT	GACACATTCACCACTCTGCCTTGGGG
Cbr3	900	900	250	0.99	GGGACTTAACGTGCTGGTCAA	GTCGAAGGGTGTTGGGTCAT	CATTCTAAAGGCGATGCCCGCGTT
Cbs	900	900	250	0.99	GCACCTGTGGTCAACGAGTCT	CAGCAGGGATGACAGCATGT	CCCGAGGGTCACCATCCCTAGGATG
Cct8	300	300	250	1.01	GGCTAAACAAATCACATCATATGGA	CAAACGCTTCAGCAAACCTCTTAA	GCATACTGTTCAAGCCCAGGACAGCTCT
Cldn14	300	300	250	1.02	GAATGACGTGGTGCAGAATTTT	CCTGGCCGATTTCAAACTTC	TAACCCGCTGCTGCCAGTGG

Cldn17	300	300	250	0.99	GCGCGTGCCCTCATGT	ATGCCAATAATGAGAGCAACCA	GGCAAGAGCCACAGCCACA
Cldn8	300	300	250	0.96	AGGGATTGTTCAAATGCTATTTTG	GGGTTTGTGTCTCTTTGGGTTA	AAATGACAATGAAAATGCTCTTCTCTCCCTCATATAT
Crfb4	300	300	250	1.01	TTCGGAGTGGGTCAATGTCA	TGCATCTCAGGAGGTCCAATG	CTTCTGCCCGTGGAAGACACCA
Cryz11	300	300	250	0.99	TGGAGAAGTTATCAGCTGGTGTTTT	TGGAAACCTTTGCCTCATACAGT	AGGCCTCTGCTCGATGAGCCCA
Cstb	300	300	250	0.96	AAAGCCATATCCTTCAAGAGACAGA	CGCATTTATCTCCACCAACATC	CTGGCACCAACCTCTTCATCAAGG
Dapk3	900	900	250	0.97	CTGACCCTCCCATCCCG	CCGTCTCGCGCCTG	CACCTTGATCCAGGAATGCTCCAGGC
Dncl1	300	300	250	1.04	CCGCACCTTCCCTAGGAGCT	TTTGATCACCGCCTTCCG	CTGGCCTCTGCTCCACGGTAACCA
Dnmt3l	300	300	250	1.04	CCCCTAGGCAGCTCTTGTA	CTGCAGGATCCGGTGGA	CGTGTCGCCGGCTGGTACATGTTT
Donson	300	300	250	1.01	AAGAAATTGGCCATAAGAAGAAAGTT	TCCTCTTCATCTTCGCTACTGACT	TCCTCCTCAGATTCCAGGCTTGGGTCT
Dscam	300	300	250	0.97	GGACAAGGAGAGCGACAGCTA	GAGACCATGCTGCTTCTTGCT	AGCGTCAGCCCATCACAAGACACAGA
Dscr1	300	300	250	0.98	GCCACCCCCGTCATAAATT	GGTCTGTGCGTGCATGCA	CGATCTTTTATATGCCATCTCCAAGCTGGG
Dscr2	300	300	250	0.95	CTTCCAGGAGCTTGAAATGCTT	CATTTGTGGTCATCAACTTCTTCAG	TGAAGAACATTCTCTGAAAGCACAGAAAT
Dscr3	300	300	250	0.96	CCAAGTCTGTGACTTCACGAT	TGAAGAATTTGGGAAGTGAAGCT	CCGGAACCTTGCGAACGTCAAAGAG
Dscr5	300	300	250	0.96	CCTCTCCACTTGACTCCATTCAT	GGATGGCATCCTCTTGGTAGTTT	CGATCAGATAACTATGCTAAAAACCAACAGAGGA
Dyrk1a	300	300	250	1.04	ATGAGGTGCATCAGATGAATAAAATAGTG	GCTTTCGGTGCTTGGTCAA	AAGTCTTGGGCATCCCACCTGCTCA
Erg	900	50	250	1.02	TGCCGACATTCTTCTCTCACA	TCAACGTCATCGGAAGTCAGAT	CTCCACTACCTCAGAGAGACTCCCCCTCCA
Ets2	300	300	250	1.01	TCCTCATTGGATCAACAGCAAT	TTTGGTGCCTGCATTCCATA	CATTAGGCTTCAGCATGGAACAGGCTCC
G10	900	900	250	1	TCCCAAAGCAAGCTGGAA	AAGGGTGTGAGCCAGAGCAA	TGGGTGCGATCATCGAGTGCACA
Gabpa	300	300	250	0.97	CCAGCCAAGAGCAACAGATG	GAGGCACTGAGGCTGGAATAA	ATGAGATAGTTACCATTGACCAGCCTGTGCA
Gapdh	300	300	250	1.02	TCCATGACAACCTTGGCATTG	CAGTCTTCTGGGTGGCAGTGA	AAGGGCTCATGACCACAGTCCATGC
Gart	300	300	250	1	TGGGCCCTTCGTCAGAAA	CCTTAAAGGAAGGGAGCAAGGA	ACGGGAAAATGCTCAACATCCACCC
Gcf1	300	300	250	0.95	CTCAGAATACGGAGATGACAGCAT	CCTTTCAGATTCACAAACCACTGTT	AGAAAAGCCCAAAATGTAATCAACTGTTTCCCT
Gdi1	300	300	250	1.01	CTGCATTGGAGCTGTTGGAA	CCATCATCAATGGGCTCATATAAA	CACTGATAGCCACAACTTCTGGTCAATGG
Gnas	300	300	250	1.05	AGAACATCCGCCGTGTCTTC	CCTTCTTAGAGCAGCTCGATTGG	CGTGACATCATCCAGCGCATGCAT
Gpx	300	300	250	0.96	TCGGTTTCCCGTGCAATC	TGAGGGAATTCAGAATCTCTTCATT	TTGCCATTCTCCTGGGTGCCGAA
GusB	300	300	250	0.97	ACGGGATTGTGGTCATCGA	TGACTCGTTGCCAAAACCTCTGA	AGTGTCCCGGTGTGGGCATTGTG
Hlcs	300	300	250	1.03	TGGAGGCAAGTGGGTCTATC	AAATATCGTTGGGCCACTTCA	TCGCAAGTTGATATCCTCATACCCTG
Hmg14	300	300	250	0.97	GGACGCGAAGCCGAAAA	TCGCTCCCCTCTTCCCTTT	CCGCGGGAAAGGATAAAGCATCAGAC
Ifnar	300	300	250	0.96	CATCTTTTGGGAAAAACATTCCA	CTGCAGGTCTTGGAGGTGAA	TACTAAGATAAGCATGGAGAAGGATGGCCCA
Ifnar2	300	300	250	1	CGGATTGGTTATATATGCCTAAAGAC	TGACCCTTCAGGGATTATCCA	CCAATGTCTTGAACCTCCGCCACTTTTAAAC

Ifngr2	300	300	250	0.98	CCTGTCACGAAACAACAGCAA	CCCAACGGAATCAGGATGACT	TGCCTCCGCCAGGCTGCA
Igsf5	900	900	250	1	CAATGCAGCCTGCAGAACAG	TGGGCCTTCCTCTCCAATACT	TGGATCTGCCTTCCTCTCAGTGAAGA
Itsn	300	300	250	0.98	CCCTCCGAGCAGAGAGCATA	CAGACGCCGCCTTGATTTT	ATGAGAGGACTGCCTGGGTGCA
Kcne1	300	300	250	0.96	ACCAGGTTCCCTTGGCTTCT	AATTGGGCAGGCTCATCCT	ACCCAGGAGTTTGTCTGCATCAGG
Kcne2	300	300	250	0.98	GGCCCGCCATGAACTG	GGTTTTTGCCGCCAGGATAT	TGAACACGTGCCCCTGCTGCTG
Kcnj15	900	900	250	1.02	TGGAGATGCTTCTGAGAAACTTGA	CTTCTCCACCTGGCTACCA	TTCCAAAGGCCATAGCAGAGCCCC
Kcnj6	300	300	250	0.98	ACTGCTGGCCCTCTAAATGC	GAGAGGTGCCCTAAAACTGTCA	TGGCCTTTGTTCCAGGTCCCCC
Kiaa0136	300	300	250	1.01	TAGGATGTCAAGTTAAAGGCAACAA	TTGCTTATTATGAGTTGGCTTAAGGA	ATTACATTCTATAATCCAACCACTCCAACCCCAT
KIAA0539	300	300	250	0.95	TGCCTTGATTCTCTGAATGAAAAG	TCCTTAACATACAGAGACACCAGGAA	AAGAAGCCAAACGAGCTCCTGCAGC
Makv	300	300	250	0.96	TTCTAGTCAAGCCTGTGGCTACTG	AATAGACTCTTCTCCTGGACTTCAC	TGATGACAGATCGGCCGTTCCCA
Mrps6	300	300	250	0.97	GGAGGGTATTTCTGTGGTGATT	CGCCAAGTGTTCCAGTATGTT	CCACAGCACTTGTCGGAGCATA
Mx1	300	300	250	1.01	TGACCCAGCACCTGAAAGC	TGAAGTACTGGATAATCAGAGGGATCT	CCCAATATTCCGTCTGCACTCCTGGTAGTA
Mx2	300	300	250	0.97	AAGACAAATCAAAACCTGGAAGA	ACTTGTAAGGCAGCTCGTACAATT	CAGCTATAGAAATGCTGCACACGGTCACTG
N6amt	300	300	250	0.96	CCTGAAAGCCACAGAAGTAAACAA	TGGCATCAGTCTGAAACCTACTG	TGCCGGCAGCTGAACAATCGC
Nade	900	900	250	1	CGGGAATTGACAGGAGGACTAC	TGGCCATGATGAGATTTTGTTT	GCTATTCTGGGCCTATCCCTTGCGG
Nnp1	300	300	250	1	AGCAGCCCGCACTAAGGAT	GCTCCACAATCGTCTGAAAGATG	CCAGGTTTGCATAAGATCATTGAGA
Olig1	300	300	250	1.01	ACGTCGTAGCGCAGGCTTAT	CGCCCAACTCCGCTTACTT	AAATTCGGTCATTAACGTTCTCATT
Olig2	900	900	250	1.01	CTGCATTACAACGTGGGCTTT	GGGCAGCGCGGAAGA	CTGCGCTGCCTCCTAACCTTCCA
Pcp4	300	300	250	0.96	GAGCGACCAACGAAAAGAC	CGATATCAAATCTTCTTGGACTTTCT	AGACGTCAAGAGATAATGATGGGCAG
Pdxk	300	300	250	1.02	ACAAGCACCCGGACAATCTC	CCTCTGTAGGACGTGCTGCAT	CAGACACGGTTTTCTCACAGGCCACCT
Pfkl	900	900	250	0.99	TGTTGTGGGTGTCTGAGAAGCT	GAGTCTGGAGCATTGGCAAAC	CGTGATGTCTACCGTAAAGGGCGGG
Ppia	300	300	250	0.98	AGGGTTCCTCCTTTCACAGAATT	TGCCATTATGGCGGTAAAGTC	TCCAGGATTCATGTGCCAGGGTGG
Rps9	300	300	250	1.03	GACCAGGAGCTAAAGTTGATTGGA	TCTTGGCCAGGGTAAACTTGA	AAACCTCACGTTTGTTCCGGAGTCCATACT
Runx1	300	300	250	1.02	CGAGATTCAACGACCTCAGGTT	AAGACGGTGATGGTCAGAGTGA	GCCTCTACCGCTCCGCCCGA
Sim2	300	300	250	1.02	CCTTCCACCTCCGATATGCA	ACAGCAGCCGGTAGTATTTGGT	CCACCTCTTGCTGGTGAAGGGCC
Slc5a3	300	300	250	1	GCAACCCAGTGGCTTCCAT	GCTGCTTGCCCATTTGGAAT	TCATTGAGAGGCAGAAACACCAGTAGATGCT
Sod1	900	900	250	0.98	GGCCCGCGCGGATGA	CGTCTTTCCAGCAGTCACA	TGCCCAGGTCTCCAACATGCCTCT
Son	300	300	250	0.98	CGGGAAATACAACAGGAGCTTT	TCAATGGGTGGATTTGTTTAC	TCAGCTGGCCTTCACTCCTTCCACTG
Sra4	900	900	250	1.03	CCTGTAACCCAGCCTGTGTCA	GGTGCTGGAGCCCAATTA	TGCTTGGCACTCAAGGAGTTGCACC
Synj1	300	300	250	1.04	GGAGCAGGTGATCTCAAAGCTT	GACACCAGAAATGCCATTTATTTT	TTCAGACTCCTCACCACAGCTGCAGG

Tiam	900	900	250	1.01	TCACTCCATCCTGGTTCTGTCTAC	GCAGGTAATGGGCGGAATG	CACCTTGGAGCTCATTTGCAAGACACATC
Tmprss2	300	300	250	0.96	ACCAGGAATGCTGGATTTTCG	ACCATGGCAGCATTCAACAC	CCACCTATGAGAAAGGGAAGACCTCGGA
Trfr	300	300	250	1	GGAATCCCAGCAGTTTCTTTTG	CAATGCCTCATAGGTATCCAATCTAG	GCCCAAATAAGGATAGTCTGCATCCTCACAAAA
Ttc3	300	300	250	0.95	AGCTAGAACCAAAGGCCAGAAA	TTTCATGGCATATCTCACAGGAA	TTCCATCTGGTGCAGGGACATCATCTT
Usp16	300	300	250	0.99	CCTTCGGTTTGGCTCTGTCTT	GCATGCTGCTCCTGAGAATCT	GCCACAGCCCTGATGGCCACATT
Wdr4	300	300	250	1.05	AGGAGAGCTATGTGGTGCTTCTGT	CTGCTGTCTGCTGGCATCAA	ACGAAGACCACGGGAACGCACTCA
Wdr9	300	300	250	0.95	AGAAGACAGAGGCCTGAAGTACTCA	GAAGAAGATGAAGAGGTAGCTAAGAAATC	CCATTTCACTTCCAAACAGCACAGAACCACT
Wrb	300	300	250	0.98	TGGACGAGTTTGCCAGATACG	GCCTTCACGTGCGTTTTGA	CGTCATCTTGTTGATCTTCCTTCCAGCCT
Znf294	300	300	250	0.97	GTGCAGCAGTGGCGAAACT	AATGCTAAGCCTTCCATGATACTTC	CAGCTGAGCACGTACCTCACTCACCAGA
Znf295	900	900	250	1.01	GCCACCGTTTGCCCTTACT	TGTCCTCATGTTCTGCTTCAG	AGCCTCAGGTTCTTCTCTCCCG
Znf298	300	300	250	0.95	GGTCATGGTCAAGGACTCCTTT	GCGCCTGATCTCCAGGTTAG	GGAGGACCTTGCCCTGCTCAGCA