

Primer	Forward (5' to 3')	Reverse (5' to 3')
<i>BMPR2</i>	GCCACAAATGTCCTGGATGGCA	GAGGGGCGCCACCGCTTAAG
<i>C/EBPb</i>	AACCAACCGCACATGCAGAT	GGCAGAGGGAGAAGCAGAGAGT
<i>CAPNS1</i>	CCCCACGCACACATTA	CGCTATCCATCACGGCCACCAT
<i>CCNE1</i>	TCTTTGTCAGGTGTGGGGA	GAAATGGCCAAAATCGACAG
<i>CDKN2A</i>	GGGTCGGGTGAGAGTGG	GCCGCTTCCTAGAAGACCAG
<i>CEBPA</i>	AACATCGCGGTGCGCAAGAG	TTCGCGGCTCAGCTGTTCCA
<i>CTDSPL</i>	CTGAAGCGGCCACATGTG	CCAGCGGTCTAGGAGGTCA
<i>CyclinA</i>	GCAGAGGCCGAAGACGAGA	TCCAAGGAGGAACGGTGACA
<i>CYP26B1</i>	CACACAGGGCAAGGACTACT	GCATGATGAGTGAGGTGCTG
<i>E2F1</i>	TCTCGGCCAGGTACTGATG	ACCCTGACCTGCTGCTCTT
<i>EIF2C2</i>	ATCTTTGGGGATCGGAAGCC	ATGCGATCCTTGCCCTTCTCC
<i>FGFR3</i>	AGGACGAGGCTGAGGACACA	TGGAGGGAGTGGGGTTGC
<i>FKBP51</i>	TGCAGCGGGAAGAACAATGT	GGGACTCACACACCTTGAAGT
<i>FOXM1</i>	CTCTCAGTGCTGTTGATGGC	GGAGAATTGTCACCTGGAGC
<i>FOXO3</i>	CTTCAAGGATAAGGGCGACA	AGTTCCTCATTCTGGACCC
<i>GAPDH</i>	GAAGGTGAAGGTCGGAGTC	GAAGATGGTGATGGGATTTC
<i>GATA1</i>	CACGACACTGTGGCGGAGAAAT	TTCCAGATGCCTTGCGGTTTCG
<i>GFI</i>	GCTTCAAGAGGTCATCCACACTG	ACCTGGCACTTGTGAGGCTTCT
<i>HIF1A</i>	TCATCCAAGAAGCCCTAACG	TCCATTTTTCGCTTTCTCTGA
<i>HOXA1</i>	CGGAAGTGGAGAAGGAGTTC	TTCACTTGGGTCTCGTTGAG
<i>IGF1R</i>	GGAGAGGAGCAGCTAGAAGG	CCCTTTAGTCCCCGTCACCT
<i>JUN</i>	GTCCTTCTTCTCTTGCGTGG	GGAGACAAGTGGCAGAGTCC
<i>mTOR</i>	CCCTCCATCCACCTCATCAG	ACAGTAGCGAATGTCAGGGT
<i>MPO</i>	GAGCAGGACAAATACCGCACCA	AGAGAAGCCGTCTCATACTCC
<i>MYB</i>	GGGAACAGATGGGCAGAAATCG	GCTGGCTTTTGAAGACTCCTGC
<i>NIPBL</i>	CACCTTACCATCATCAGAGAAGGAC	GATGGAGAGGAAGTTTTGGGCTG
<i>p53</i>	CCCAAGCAATGGATGATTTGA	GGCATTCTGGGAGCTTCATCT
<i>PPP3CA</i>	ATCCACACGAGGTTTTCCAT	GGCAATTGATCCCAAGTTGT
<i>PRDM1</i>	ACGTGTGCCCTTTGGTATGT	GATGGCGGTACTTCGGTTC
<i>PROX1</i>	CAACATCTTTGCCTGCGATA	ACAGGGCTCTGAACATGCAC
<i>Raver2</i>	CCAGTGTCCATAAACCTGTGT	CTCCAGGAGCACAGAAGGAA
<i>RUNX1</i>	CTTCACAAACCCACCGCAAG	CGGGCTTGGTCTGATCATCT
<i>SERPINE1</i>	TTTCAGAGGTGGAGAGAGCC	TTCCACTGGCCGTTGAAGTA
<i>SMAD4</i>	GGTTCCTTCAAGCTGCCCTA	GTCACCTAAGGCACCTGACCC
<i>SMARCA5</i>	GGTCCGAGGATTAACTGGCT	TGAGGCCCAGGAATGTTTCT
<i>SMARCD1</i>	ATCATCCAAGCACTGTGGCA	TGATGATAGGTTCTGGTGGCA
<i>SPI1</i>	TGTTACAGGCGTGCAAAATGG	TGCGTTTGGCGTTGGTATAGA
<i>SPIB</i>	CCAGCAGGAAGTGGTACAGG	ACTTACCGTTGGACAGCCCT
<i>TGFB1</i>	CAACAATTCTGGCGATACCTC	AAAGCCCTCAATTTCCCCTC
<i>THAP2</i>	GCTGTGCCACTACCTACAACA	ACAGGAGGCTTCAAAGTGCT
<i>TRIB2</i>	CACAGGTCTACCCCCATCAC	CCCGATACAAGAAACGCAAT