

Table S2. RT-PCR and qPCR primers used in this investigation.

Gene	Forward Primer (RT-PCR and qPCR)			Reverse Primer (RT-PCR)			RT-PCR product			Reverse Primer (qPCR)			qPCR product	
	Sequence	Tm		Sequence	Tm		length, bp			Sequence	Tm		length, bp	
BAD	CAGTGACCTTCGCTCCACAT	60.04		CATTTGGTAGTGAGCACGGC	59.55		359			GACTCCGGATCTCCACAGC	59.56		101	
BAX	GTGATGGACGGGTCCGGG	62.16		GTCCATGTCCAGCCCATGA	60.03		429			CACCTCGCTCAGCTTCTTGGT	60.32		170	
BCL2	CCTTTGTGAACTGTACGGC	59.13		CCGGCCAAACAACATGGAAG	59.5		521			CCGTACAGTTCACAAAGGC	59.13		78	
BCL2L1	GTTCAGACCAACCCTAGTCC	60.04		GGCCCTTCTAGTCAGCCCTA	60.4		303			CTCTGGGCGCATCTGTCTTGG	60.11		86	
BID	CATGGACCGTAGCATCCCTC	59.97		ACAGCTGTGACCACATCGAG	60.04		353			TCCCTGTTCCGGTCTCTCC	60.3		90	
CCNA1	GCTGCTAACTGCAAAATGGC	60.46		TGCTTTGGGTCTGTGCCTTA	59.52		436			CACAGTCAGGGAGTGCTTTCT	59.93		122	
CCND1	AACTACTGGACCGCTTCTCT	60.54		CATGGAGGGCGGATTGGAAA	60.4		360			CAGGGGATGGTCTCCTTCA	60.62		111	
CCND2	GCAGAAGACATCCAAACCCT	59.67		AGCGAGCTCACTTCTCTCATC	59.54		528			GGAAGACCTCTTCTTCGCACT	59.73		92	
CCND3	CCTGGATCGCTACCTGTCTT	58.88		GCGGGTACATGGCAAAGGTA	60.39		347			GTTTTTCGATGGTCAGGGGC	59.47		119	
CCNE1	TCACAGGGAGACCTTTTACTTGG	59.93		ATTTGCTGGGGATACTGCGG	60.47		339			ACAGCGTGGTCGGTGTAGAT	61.25		130	
CDH1	GAAACAGCAAGGGCTTGA	59.59		TCACGTGCTCAAAATCCTCCCT	61.94		362			TGGGGGCTTCATTACATCC	60.03		146	
CDK2	CTGCATCTTTGCTGAGATGGTGA	61.18		TGAGTCCAAATAGCCCAAGGC	60.34		414			AGAAGTAACCTCTGGCCACAC	59.65		127	
CDK4	GTGTACAAGGCCGTGATCC	60.74		AGGCCTCTTAGAAACTGGCG	59.75		326			TCTCACACTCTTGAGGGCCA	60.47		85	
CDK6	ACACCTTGTGGCTTATGG	59.96		GCCTGGATTACCCACTCCAC	60.11		303			GCGGTTTCTTGGAGAAGCA	60.89		119	
CDKN1A	CTCAAATCGTCCAGCGACT	60.11		CCTGCCCTCGAGAGGTTTAC	59.82		344			TGCTGACTCCTTGTTCGCG	59.97		87	
CDKN1B	GCTGAGGAACTGACGTGGAG	60.39		CAAAACTCCCAAGCACCTCG	59.41		433			TCAAACCCCTCCCCAAAATTGC	59.89		107	
CREB1	TGAACGAAAGCAGTGACGGA	59.9		ATGGCAGGTGCTGAAGTCTC	60.04		496			ACAGCTGCATCTCCACTCTG	59.75		94	
CTNNB1	GTACGGAGCCCTTCACATC	60.18		TCCATACCCAAAGGCATCTCTG	59.15		478			GCAGCTGCACAAAACAATGGA	59.97		90	
E2F3	CTTACACCGACTCAGGGAG	60.11		TACCATTGGGTGAGGCACAT	59		490			GCAGCTGCACAAAACAATGGA	59.97		144	
EGF	TTTCTGTGGCTTCCCTTGG	60.18		GTGCAGGACCCACACAAGTA	59.89		352			GCCCTGGGCGATCTTTTACT	60.03		104	
EGFR	AATGCGTGGACAAAGTGCAAC	59.97		GCGATGGACGGGATCTTAGG	60.04		340			ATGTTCATGGCTGAGGCAG	60.4		106	
FGFR1	GCCAGACAACCTGCCTTAT	60.03		AGACACTGTTACCTGTCTGCG	60		389			CACGTATACTCCCTGCGTC	59.97		121	
FN1	AATGTCGTGGGGAATGGAC	60.03		GTCACTTCTTGGTGGCCGTA	59.97		568			CCCCTCTTCATGACGCTTGT	60.04		114	
HRAS	GCTGACCCTCAGCTGATCC	60.53		AGGCACTCTCCACTCCCTG	60.69		429			CCCCTCAATGACCACCTGCT	60.03		91	
IRS2	CGTCTCGGCCCTTATTGAA	59.82		CAAACTGCCAAACCCGGAC	59.76		457			GGCTCGGTGTGGACGTAAA	60.01		91	
KDR	ACCCACGATCACAGGAAC	59.96		TCCACAGGGATTGCTCCAAC	59.96		876			n/a	n/a		n/a	
KRAS	TGAGATGGCATGGTGAGGTG	59.75		TGTCGCTAATGGATTGGGCA	59.75		606			TGATGTCCTCAAAATCAGAGTCTCT	59.47		98	
MAPK3	GACGGAGTATGTGGCTACGC	60.59		CTTTGGAGTCTGACTTGGGGA	59.3		305			GGAAGATGGCCGGTTAGAG	59.89		134	
MDM2	GCTTCGGAACAAGAGACCCT	59.68		TCCCCTGCCTGATACACAGT	60.25		794			TTTGTGCACCAACAGACTTTAAT	57.41		73	
MMP2	GAACCTCCGTCTGTCCAGG	60.04		ACGACGGCATCCAGGTTATC	59.9		576			GTCAATGTCAAGGAGAGGCC	60.11		70	
PDGFC	CCTGGTTAAACGCTGTGGTG	59.41		ACAGAACCACGCTAGTGGA	58.27		528			CTTTGCTTGGGACACATTGACA	59.64		77	
PDGFRB	GTCTCCAACACTACATGGCCC	60.11		AACCTTCGCCCAACAGTCTC	60.25		596			TTGATCAAAAGTTGCTCGGCAG	59.46		78	
PIK3CA	TGTGAGCCTCCTTGCACAAA	60.11		CTGAAGTACCCAGAAAGTGCT	59.37		324			GGTGAATCGGCCATGTGGT	60.97		129	
PIK3R3	CTCTTCCACCAAGCCACCT	59.89		TGGACACTGGGTACATCAGC	59.39		378			CCATCTGGCATATCCCGCAA	60.25		148	
PTEN	GGAGACTTGGTCTCTCCCT	59.96		ATGCTTTGAATCCAAAACCTTA	57.93		600			n/a	n/a		n/a	
SHC1	GCCAACCCACATGCAATC	60.39		GGGTCTCCTACAGGCAATGT	60.04		440			GCTGTGTCCGGATCCCC	59.43		56	
SMAD4	GGGACCGGATTACCCAGAC	59.82		CTGAGCCATGCCTGACAAAT	60.32		343			GGTCTGCAATCGCATGGTA	60.46		116	
STAT1	TGGTGATCTCCAACGTGACG	60.04		AACCGCATGGAAGTCAGGTT	59.89		527			TCTGAAAAGCTGAGCCCCATCG	60.11		133	
TGFB1	ACCTGCCACAGATCCCTAT	60.03		GAGCAACACGGGTTACAGGTA	59.97		712			AATAACCTAGATGGGCGCGA	58.95		68	
TGFB3	TCGCAGTGCAGTGAGTTTCAT	59.97		ATAGGGGACGTGGGTCTATCA	60.03		355			CCTGGAGAGGAAGAGACCCC	60.69		56	
TGFBR2	AAGTGTCTAGCTGCTTGTA	59.37		TCTGACCTGTATCGGGGAA	59.66		679			TTCTGTTGTACAGGTGGA	59.9		141	
TLR2	GTATCTGCAAGGGCAGCTCA	60.11		TATGCAGCCTCCGGATTGTT	59.45		855			GCTGGCCAAATCAATCAAGACT	58.9		103	
TSC2	GGGTCTGCAGATGAGAACTCC	58.87		CCTCCTTGGTCTGTCTCACAT	63.2		322			ACGTATCGAGCCATCATGTCC	60		101	
VEGFC	GACCTGCCCCACCAATTACA	59.96		CCTTCTGGCGGTTCTGATACAT	60.11		458			CAGCTCCTTGTTTGGTCCAC	59.1		136	
GAPDH	GGTCACCAGGGCTGCTTTTA	60.25		TGTTTCACACCCCATGACGAA	60.5					TTCCCGTTTCTCAGCCTTGAC	60.0		147	
RNA18s	CGTCTGCCCTATCAACTTTC	61.3		n/a	n/a		n/a			TTTTCGTCACTACCTCCCC	61.5		120	
RNA28S	GGGGTGTGGGGTCTCTTCC	64.3		n/a	n/a		n/a			GCGGCCCTCTCTACTCGTC	63.8		182	