

**S1 Table. Primer pairs used in this study for gene expression analysis by RT-qPCR**

<b>Name</b>	<b>Primer sequence (5'-3')</b>	<b>Size of amplicon (bp)</b>	<b>Amplification efficiency</b>
CHRNA5_v1	F: AGATGGAACCCTGATGACTATGGT R: AAACGTCCATCTGCATTATCAAAC	104	1.87
CHRNA5_v2	F: GGAAACTGAGAGTGGTAGTGGA R: CTTCAACAACCTCACGGACA	122	1.95
CHRNA5_v3	F: CATCAGGTGTTGAAGATTGGAAAT R: AAAAAGCCCAAGAGATCCAACAAT	101	1.92
CHRNA5_iso2*	F: TGGAGAATGGGAGATTGTGAGTGCA R: CCAATCTTCAACAACCAGCAACAGC	78	1.97
CHRNA5_iso3*	F: TGGAGAATGGGAGATTGTGAGTGCA R: CCAATCTTCAACAACGGATACCAGC	84	1.96
SDHA	F: TGGGAACAAGAGGGCATCTG R: CCACCACTGCATCAAATTCATG	86	2.01
MAP1B	F: GTTGGAAGGAAAGGCTCAGT R: CTTGCTGTTTCTCATGGGTC	110	1.81
CLDN1	F: CTGTCATTGGGGTTCGATA R: CTGGCATTGACTGGGGTCAT	118	1.88
WDHD1	F: AGCAGCCAAGGACGAGTAA R: CTTCCGGCTTTGGAATCAGAG	192	1.95
ANLN	F: TAAAGCAGGTGATTGTTCCGG R: GTTCTTCATCAACACAGCAG	180	1.97
BIRC5	F: GTTGCGCTTTCTTTCTGTC R: TCTCCGAGTTTCTCAAAT	141	1.92
CDKN1A	F: GTCACTGTCTTGACCCTTGTC R: CGGCGTTTGGAGTGGTAGAA	129	1.82
GPNMB	F: TGCTGACTGTGAGACGAACC R: ACACCAAGAGGGAGATCACAG	204	1.92
GJA1	F: TCTGAGTGCCTGAACTTGCC R: CCCTCCAGCAGTTGAGTAGG	171	2
GADD45A	F: TCTCGGCTGGAGAGCAGAAGAC R: AGCTTGCCGCTTCGTACAC	121	1.96
BAX	F: GGGTTGTCGCCCTTTTCTAC R: CTGGAGACAGGGACATCAGT	198	2.09
BCL2	F: TGAAGTGGGGGAGGATTGTG R: CGTACAGTTCCACAAAGGCA	183	2.04
FAS	F: AATAAACTGCACCCGACCC R: AGAAGACAAAGCCACCCCAA	192	2.06
CCND1	F: CTGCGAAGTGGAACCATCC R: GCACTTCTGTTCTCGCAGA	199	1.97
CCNE2	F: GTAGCTGGTCTGGCGAGGTTT R: GGGCTGCTGCTTAGCTTGTA	83	2.08
CHEK1	F: TGGTCACAGGAGAGAAGGCA R: CAGATAAACCAACCCTGCCA	151	1.72