

Table. Primers for SYBR green qPCR analysis of mouse heart tissues.

Gene	Forward sequence (5' - 3')	Reverse Sequence (5' - 3')	Amplicon Size (bp)	Target exon(s)
<i>Wnt1</i>	AGGGCGAACGACCGTGT	TCGGTTGCCGTAAGGACG	169	3-4
<i>Wnt2</i>	GACCTGATGTAGACGCAAGGG	TGTAGCTCTCATGTACCACCAT	127	1-2
<i>Wnt2b</i>	ACACGTCCCTGGTGGTACATAG	ATGTCTGGGTAGCGTTGACA	107	1-2
<i>Wnt3</i>	TGTTCCAACTATTGGGGGCG	GGCCAGGGACCACCAAAT	163	1-2
<i>Wnt3a</i>	CTACCCGATCTGGTGGTCCT	ACAGAGAATGGGCTGAGTGC	70	1-2
<i>Wnt4</i>	CGAGCAATTGGCTGTACCTGG	GTTTCTCGCACGTCTCCTCT	72	1-2
<i>Wnt5a</i>	GCTTTGGATTGTCCCCAAG	ATTCCAATGGGCTTCTTCATGG	123	1-2
<i>Wnt5b</i>	GTTCCCTGAATGGCGGCTA	AGAGCTAGTGACCACCAGGA	179	1-2
<i>Wnt6</i>	TTCCAGTTCCGTTTCCGACG	CTGTCTCTCGGATGTCCTGC	85	2-3
<i>Wnt7a</i>	GAGATCAAGCAGAATGCCCG	TTCTCCTCCAGGATCTTCCGA	74	3-4
<i>Wnt7b</i>	CCTAGGAAGGCCAGTGACCA	CACGGATGACAATGCTCTGTAAG	153	1-2
<i>Wnt8a</i>	GCCTATCTGACCTACACCGC	GATGTCTCTCTCGTGGCAGC	155	3-4
<i>Wnt9a</i>	CCTCGTGGGTGTGAAGGTGATA	CTTCATTGGTAGTGCTGCCC	179	3-4
<i>Wnt10a</i>	CATCTTCAGCCGAGGTTTTCG	AGCCTTCAGTTTACCAGAGC	106	2-3
<i>Wnt11</i>	GCAACCTCGCAGGCGG	CAAGGCAAAGAGCAGAGCCT	157	2-3
<i>Fzd1</i>	ACGAGGCTTACCAACAGCAA	CAGGCGATGGCTAGGATCAG	93	1
<i>Fzd2</i>	CCTCAAGGTGCCGTCTATC	CAACACCGACCATGTGAGGA	151	1
<i>Fzd3</i>	GCAGATAGGTGGGCACAGTT	ATAGGGTGAAGGGCTCCAT	150	2-3
<i>Fzd4</i>	TTCGGGGACGAGGAGGAG	ACCGAACAAAGGAAGAACTGC	194	1-2
<i>Fzd5</i>	TGTCGTTAAACTTTCCAGCTCT	CTCCAAGGACAGAACTCTCGGA	113	1-2
<i>Fzd6</i>	CGGAGCCGCAGCAGTT	GGGACCTTCCATCTTGCCA	186	1-2
<i>Fzd7</i>	TACGTGGGCCTGTCTAGTGT	CTTCTCTGTCTTGGTGCCGT	156	1
<i>Fzd8</i>	CCGCCTAGAGAAGGAGGACT	GAGCGAGGTCACTTCCAACA	75	1
<i>Fzd9</i>	CGTCGAGGTGTTCTGGTCTC	GAAGAAACACAACGCGGACC	79	1
<i>Lrp5</i>	TGCTCCCACATCTGTATCGC	AGGTAGGAGGCTCACCAACA	106	17-18
<i>Lrp6</i>	CTGCTGAGAGCGGCC	CCAAACACAAAGTCCACCGC	137	1-2
<i>Vangl2</i>	GGGAAACAGGCGAGTGGTCT	GCAGCTCCCCGCCACT	196	1-2
<i>Ror2</i>	CTTCCCCTCTGAAAGGCTACT	CTTCGTGGCTCTTGACAAC	164	1-2
<i>Dkk1</i>	CTCTTGACAACCTACCAGCCCT	AGCACATAGCGTGCCTCAT	162	1-2
<i>Dkk3</i>	CATAAGCGTGTCAAGTGGAGC	GGAGTCCAAGTGACCGTCG	145	1-2
<i>Dkk4</i>	ACAAAGCAGTAAGGGACAGGA	TCCCTCTCGTAGAACTGGCT	118	3-4
<i>Sfrp1</i>	GCAAGCGAGTTTGCACTGAG	CCGCTTCAGCTCCTTCTTCT	126	2-3
<i>Sfrp2</i>	GCCACAGAGGAAGCTCCCAAG	GACACGCCGTTGAGCTTGTA	194	1-3
<i>Frzb</i>	GCCGTTGTGGAAGTGAAGGA	GCCTTCTACCAAGAGTAACCTGG	174	4-5
<i>Axin2</i>	GGCAACTCAGTAACAGCCCAA	GCTCATGTGAGCCTCCTCTCTTT	139	1-2
<i>Tcf7l2</i>	AATCCACCTCCGCACTTACC	GGCTGACCTTGCTGTGGT	158	5-7

<i>Cacna1c</i>	GACGTGCTGTACTGGGTCAA	CCCGCTAAGAACACCGAGAA	120	7-8
<i>Kcnd2</i>	GCACACTCCACTACCACCTC	CAGAGCCTGGTGCGTCTC	72	1
<i>Kcnj2</i>	ACTTGCTTCGGCTCATTCTCT	CCAGAGAACTTGTCCTGTTGCT	116	1-2
<i>Kcnh2</i>	GTTTGAGGGCCAGAGCCG	TTGCAGTAGATGACAGCGCA	72	1-2
<i>Kcnq1</i>	CAGGGCCGAGTCTACAACCT	AGAACAATGAGGAAGACGGTGA	83	1-2
<i>Hcn1</i>	TGCTGGCGTTATCACCAAGT	CAGCAGGCATATCTCTCCGA	76	6-7
<i>Hcn2</i>	TGAACACCGGTACCAAGGGA	GAAGTTCACAATCTCCTCACGC	88	5-6
<i>Hcn4</i>	TGAGCCACTTCGAGAGGAGA	TGGAAGACCTCGAAACGCAA	129	5-6
<i>Scn5a</i>	TCCCAAGTTGTGTCTGGTGG	GTAAGTGTCTCGGGAGTCTCA	174	17-18
<i>Nppa</i>	CTGATGGATTTCAAGAACCTGCT	TCTCAGAGGTGGGTTGACCT	168	1-2
<i>Nppb</i>	GAGTCCTTCGGTCTCAAGGC	ACTTCAGTGCGTTACAGCCC	141	2-3
<i>Myh6</i>	CTGTCCAAGTTCGCAAGGT	CTCGTCGTGCATCTTCTTGG	129	38-39
<i>Myh7</i>	TTGCTACCCTCAGGTGGCTC	GCCATCGCTGAGTCTTGGATT	120	1-4