Table 2. PCR primers for intron detection and radiation-hybrid mapping

Gene	Forward primer (5' to 3')	Reverse primer (5' to 3')	Result*
Detecting introns in zebrafish and mouse claudin genes			
cldn7	GGCTGCTGAAAGCGAGCGATATT	CCTTTCCAGGTCGTGAACAAATGG	4-5 kb instead of 753 bp
cldn10	CCCTTGAATTTTGGATTTCTGAGGTTG	CATCAACGTAACAACAGTTCAGCCTTGT	8 kb instead of 732 bp
cldn11	ACAAGTTTTTGGCCTTGAGGAGCA	TTTCCCAGTGAGTCTCTCACACATGTTC	6-7 kb instead of 835 bp
cldn12	GCTGACTTCAGCCATGTCTTGTCG	CCTTAGACAGCCAATCTCAATCTGTGAGG	2.5 kb instead of 1,055 bp
cldn19	CATGGCGGAGTGGAAGATGTCCT	GCCTGCAGTCAGGTGTGTGTTCA	4 kb instead of 809 bp
cldna	GCTGTCTAATACACCTGCAATTGTTCCA	CCTCCTTGAATGTAGTACTTTTGGTTCCTCA	679 bp
cldnb	GAACCACCAACCAACCAACAAGGA	CCGTAAACATTGTAGAGTCCATTTTCCTGA	723 bp
cldnc	TGAACATTCAACAGGAGAAAGAGACTGGA	CAGCTACAAAACAAATGTCCTCTGAGCTTC	719 bp
cldnd	GTGGAAGGTGACGGCTTTCATTG	ACTAGTCCAGAAAGTCGGTGCGTCA	563 bp
cldne	CACAAGCCCACAAACAAACAAGCA	CTTTGCGATCTCGGCGTAGCTCT	679 bp
cldnf	GTGGCGGGTCACCACCTACATC	CTTTAGACGACGTCCGTCCTTTGTG	653 bp
cldng	AGTTGCAAGCTCATCTGTAGGTC†	TTCAAACAGACATCCTTCAGTCA†	1.7 kb instead of 679 bp‡
cldnh	CGGCTTCAACAAAGACATCTCAACACTT	TGTTCACCCTTTTCATCCGTCTTTG	742 bp
cldni	AATAAAGGATGGGCTCCGCTGGT	GTAATTTTTGCTGGGCGCTGAGG	2 kb instead of 638 bp
cldnj	GTGGTCTCCAGCCCGCTCCT	GGAAATCCAATCATTTTTGTTCAGTCTACG	705 bp
Cldn13	TCAGCAAACAAGAGGCCATCAGC	GGTATCGTTGTTGGCTCCTGAAGGT	617 bp
Radiation-hybrid mapping of zebrafish claudin genes			
cldn7	TGGGTAGAAGTTTGCCCTGT	CCCCTTTGCAAACTCACATT	LG10
cldn10	TTCCCATTTTAACAAGGCTGA	CCGCATCCATGAAAATTGA	LG2
cldn11	CAGCATCCTGCACTAAACCTC	GGATATTAGCGGAGATGTCTCAA	LG24
cldn12	CTCCAAAACCCCTGACGAC	AACCAGACGGAGGGTGG	LG16
cldn19	ACTGACCGCGTCTGAACAC	TGATGAGCCGGTCATTTACA	LG2
cldna	CGGTTGTTGTTTGTTCATGC	GGCACCCTGACATGTTCATT	LG15
cldnb	TGCAGGACTTGAAAAGCAGA	TGACCACGGTACAAAAGAACA	LG21
cldnc	TGGCTCCAAGTACCTATAACAAGA	TCAACTTATATAATGGATTTTGAAACG	LG21
cldnd	CTGGGAGCGTCACTCTTCAT	TTCCTACACAAACAGGAGACGA	LG21
cldne	TTGCTGGAGTTCTGGTGCT	ACGCCCCATCCGATGTA	LG15
cldnf	AAGCTCAATCAACCTCAATTTGT	CAGAATCTTCATTTTTGGGTGA	LG15
cldng	TGCAGCTCTTACCCAAAAGG	TCAATTGATCACTTCATCTCTGC	LG1
cldnh	GAATGGGCTATTCTGCTCCA	CACAAACAAAGCAAACAGCTAAA	LG21
cldni	TTGGTGAGAGTGGAACTGGA	ACACAAGCTCTGTCCCATCC	LG3
cldnj	TCTGGCACTCACAGTGGCTA	GTAAACACACACAAATTAAGTTGAACA	LG15
Radiation-hybrid mapping of zebrafish orthologs of human genes at 7q11.23 near *CLDN3* and *CLDN4*§			
baz1b	GGAAAAGGAAGCAGAAGAGGA	GCGTTCTCCTCAACACCAG	LG18
bcl7b	CAGCAACCAGAGTTCTCTGTCA	GTGGCTGTGGGTCATCAGT	LG10
cyln2	GTCTCCGCGTCACTCTGC	GCAGCAAAAGTTTCTCTCTCAGG	LG5
gtf2ird1	GCATTAGGCCTGGATCACAT	AGGATGCGCTTGAGTTTAGG	LG5
hip1	GGCAGTTCAAACCTTTCTCG	TATCCTCGATCTGAGACTTGC	LG15
wbscr1	TTTATGTTCACTGGATGTTGTATGC	TTGAAATGATTTATTTGGTGTTGC	LG15

* Length of PCR product (top) or linkage group (middle and bottom). A PCR product longer than predicted from the cDNA sequence revealed the presence of at least one intron.

† Annealing temperature of 60°C.

‡ Intron in 5' untranslated region between nucleotides 91 and 92.

§ Primer sequences were based on the following expressed sequence tags from zebrafish: *baz1b,* fb34a12, fc43h10, and fi60d02 (predicted protein sequence 61% identical to human *BAZ1B)*; *bcl7b,* fa96f08 (70% identical to *BCL7B)*; *cyln2,* fc60a01 (62% identical to *CYLN2)*; *gtf2ird1,* fk08g11 (84% identical to *GTF2IRD1)*; *hip1,* fi33d04 and fj87e12 (80% identical to *HIP1)*; *wbscr1,* fe24e08, fe16e08, and fe16e09 (82% identical to *WBSCR1).*