Table S1. Primers used for *CLCN6* Sanger sequencing

	Forward		Reverse		Predicted PCR sizes
exon 1	5'- AGCCACTCCTGGTCTCAGTC	-3'	5'- GTAGACGCTTCGAGAGCCC	-3'	365
exon 2	5'- TTTAGAAGCTAGCCACTGATTTC	-3'	5'- AATCATAATGCTTCGGCCTG	-3'	228
exon 3	5'- TCCACACGTTGAGTAGCAGG	-3'	5'- TGCCTGTATCGCATGAAAAG	-3'	286
exon 4	5'- GCCAAGATGTATTTCTTCCCC	-3'	5'- ACCAGGCCAGGGCTTTC	-3'	210
exon 5	5'- GATGCCTTCAAGAGGAGCAC	-3'	5'- GAATAGCTAATAAGCGGCCC	-3'	269
exon 6	5'- CTGCACCCTCTCAAGTGATG	-3'	5'- AACAAGAGGCCACTTTCTGC	-3'	304
exon 7	5'- CCAGATTGTTGAGGGTAAGCC	-3'	5'- GGCCCTGCAGTCCAAATC	-3'	294
exon 8	5'- TTCAGTTGTCACGAGGAAGG	-3'	5'- ATTTGGCCCAGTGTAACCAG	-3'	234
exon 9	5'- AGTCCTAGGCTGCCCCTG	-3'	5'- GGGATACTGCCAGGCTAGAG	-3'	270
exon 10	5'- CAGAAACCACCTTTTGGGG	-3'	5'- GTACCGAGTAAGGGACACCC	-3'	267
exon 11	5'- AGGAGGAAGGGTTGGGAG	-3'	5'- CTGCTCATTTCTCTCTGGTCC	-3'	270
exon 12	5'- CTCTTGCTTCTGTCTTCTCTTC	-3'	5'- CTCCTCGGGAGAGATGGCG	-3'	333
exon 13	5'- CTGCTGTGAATGCTGTTTGGAG	-3'	5'- GGAAGGATGAACCCAACATATC	-3'	350
exon 14	5'- TGGACCCGGCTGGAGACATC	-3'	5'- ACACCAATCACCCACGATTG	-3'	273
exon 15/16	5'- GGAACTGGTATGGGGTGTGG	-3'	5'- GTCCATTTGGCCACCTGAAAC	-3'	713
exon 17	5'- CTGTCAGGCTCAGGGCCAC	-3'	5'- GTTACTGTTTCCTACCCTAATAAC	-3'	262
exon 18	5'- AGGGCTGGAGAGCCAGCAC	-3'	5'- GATGAGAACAGTGCCAACTTCC	-3'	400
exon 19	5'- CATTTGAACCACCAGCCTGAG	-3'	5'- GAAACTCAGGAGCCACCTCAC	-3'	415
exon 20	5'- GGCTCAGATGTTGTGAGGTGG	-3'	5'- CCTATGGCACTGTTCACGGC	-3'	375
exon 21/22	5'- TGGGCATATTCAGGCATCAAGG	-3'	5'- ACGGAAGCCGAGCAGGGTTC	-3'	573
exon 23	5'- TCAAGCTGTGTCTGGCTGTGC	-3'	5'- GTGTCCGATGACTCCCGGC	-3'	355

All primers are designed in the flanking intronic regions with at least 50 bp distance from exon/intron boundaries.