

Fig. S1. *Slc16a6* evolutionary history inferred using the maximum parsimony (MP) method. The bootstrap consensus tree inferred from 1000 replicates is taken to represent the evolutionary history of the taxa. The MP tree was obtained using the Close-Neighbor-Interchange algorithm in MEGA5 using alignments generated by CLUSTALW. GenBank and Ensembl accession numbers of amino acid sequences are as follows. Branch Slc26a6.A: sea bream (*Sparus aurata*, this study translated FM155691.1), cod (*Gadus morhua*, ENSGMOP00000018827), Gulf toadfish (*Opsanus beta*, ABQ01444.1), Nile tilapia (*Oreochromis niloticus*, ENSONIP00000015691), medaka (*Orzyas latipes*, ENSORLP00000011505), stickleback (*Gasterosteus aculeatus*, ENSGACP00000002987), green pufferfish (*Tetraodon nigroviridis*, ENSTNIP00000008886), torafugu (*Takifugu rubripes*, ENSTRUP00000007745), mefugu A (*Takifugu obscurus*, BAE75796.1). Branch Slc26a6.B: stickleback (*Gasterosteus aculeatus*, ENSGACP00000007629), Nile tilapia (*Oreochromis niloticus*, ENSONIP00000002151), medaka (*Orzyas latipes*, ENSORLP000000003731), cod (*Gadus morhua*, ENSGMOP00000002315), torafugu (*Takifugu rubripes*, ENSTRUP00000007000), mefugu B (*Takifugu obscurus*, BAE75797.1). Branch Slc26a6.C: cod (*Gadus morhua*, ENSGMOP00000010092), Nile tilapia (*Oreochromis niloticus*, ENSONIP00000002151), medaka (*Orzyas latipes*, ENSORLP00000002390), stickleback (*Gasterosteus aculeatus*, ENSGACP00000001974), green pufferfish (*Tetraodon nigroviridis*, ENSTRUP00000038102), mefugu C (*Takifugu obscurus*, BAE75798.1).

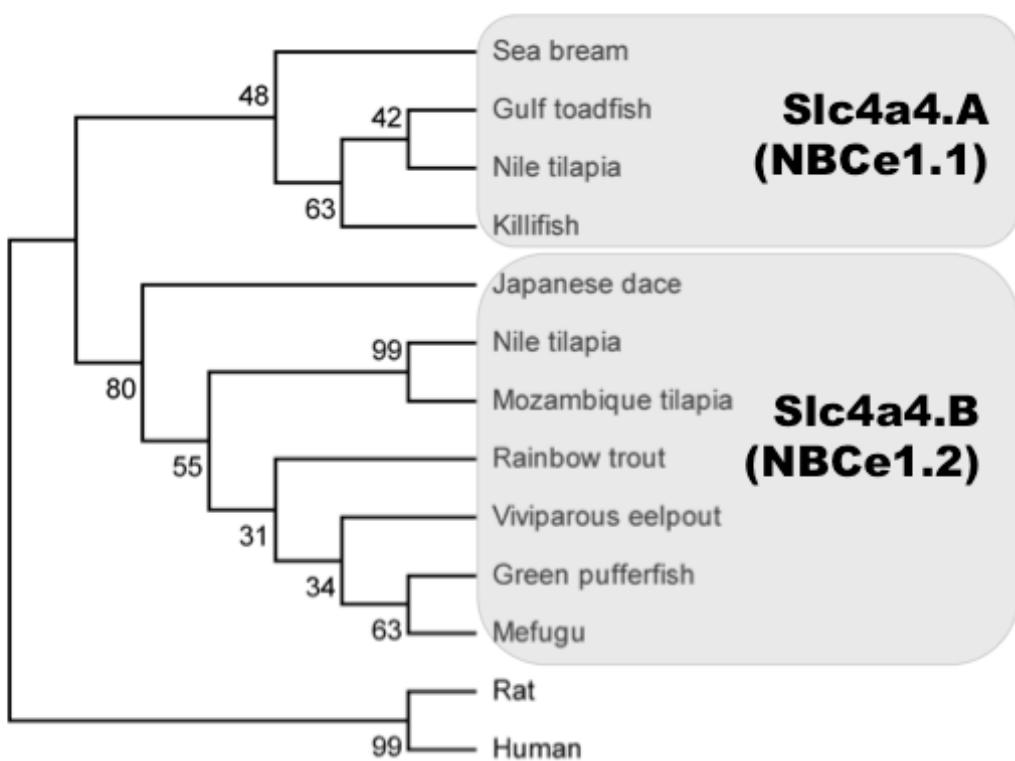


Fig. S2. *Slc4a4* (NB Ce1) evolutionary history inferred using the Maximum Parsimony (MP) method. The bootstrap consensus tree inferred from 1000 replicates is taken to represent the evolutionary history of the taxa. The MP tree was obtained using the Close-Neighbor-Interchange algorithm in MEGA5 using alignments generated by CLUSTALW. GenBank and Ensembl accession numbers of amino acid sequences are as follows. Branch *Slc4a4.A* (NB Ce1.1): sea bream (*Sparus aurata*, this study translated FM157528.1), Gulf toadfish (*Opsanus beta*, ACK37865.1), Nile tilapia (*Oreochromis niloticus*, XP_003444524.1), killifish (*Fundulus heteroclitus*, ACU44673.1). Branch *Slc4a4.B* (NB Ce1.2): Japanese dace (*Tribolodon hakonensis*, BAB83084.1), Nile tilapia (*Oreochromis niloticus*, XP_003449699.1), Mozambique tilapia (*Oreochromis mossambicus*, BAJ49842.1), rainbow trout (*Oncorhynchus mykiss*, NP_001117797.1), viviparous eelpout (*Zoarces viviparous*, ACB46956.1), green pufferfish (*Tetraodon nigroviridis*, CAAE01014533.1), mefugu C (*Takifugu obscurus*, BAG15993.1).

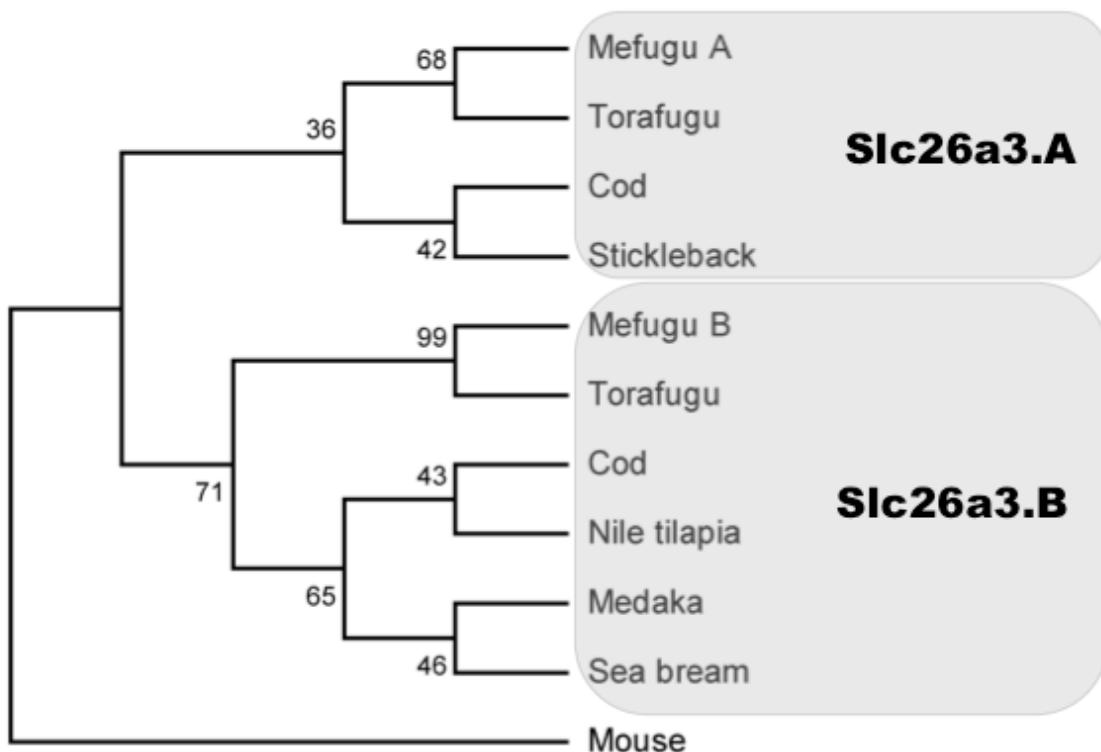


Fig. S3. *Slc26a3* evolutionary history inferred using the Maximum Parsimony (MP) method. The bootstrap consensus tree inferred from 1000 replicates is taken to represent the evolutionary history of the taxa. The MP tree was obtained using the Close-Neighbor-Interchange algorithm in MEGA5 using alignments generated by CLUSTALW. GenBank and Ensembl accession numbers of amino acid sequences are as follows. Branch *Slc26a3.A*: mefugu A (*Takifugu obscurus*, BAE75796.1), torafugu (*Takifugu rubripes*, ENSTRUP00000015967), cod (*Gadus morhua*, ENSGMOP00000014051), stickleback (*Gasterosteus aculeatus*, ENSGACP00000025627). Branch *Slc26a3.B*: mefugu B (*Takifugu obscurus*, BAE75794.1), torafugu (*Takifugu rubripes*, ENSTRUP00000014138), cod (*Gadus morhua*, ENSGMOP00000014075), Nile tilapia (*Oreochromis niloticus*, ENSONIP00000015007), medaka (*Orzyas latipes*, ENSORLP00000015168), sea bream (*Sparus aurata*, this study translated AM973894).