Suppl. Fig. 3B
Phylogenetic tree of the SLC21 family constructed from the alignment of Suppl. Fig. 3A. The tree was constructed by the maximum-likelihood method using MOLPHY ProtML (Adachi and Hasegawa 1996).
Bootstrap probabilities were calculated with 1000 samplings. Sequence abbreviations are shown in the legend of Suppl. Fig. 3A. Branch lengths are drawn to scale.