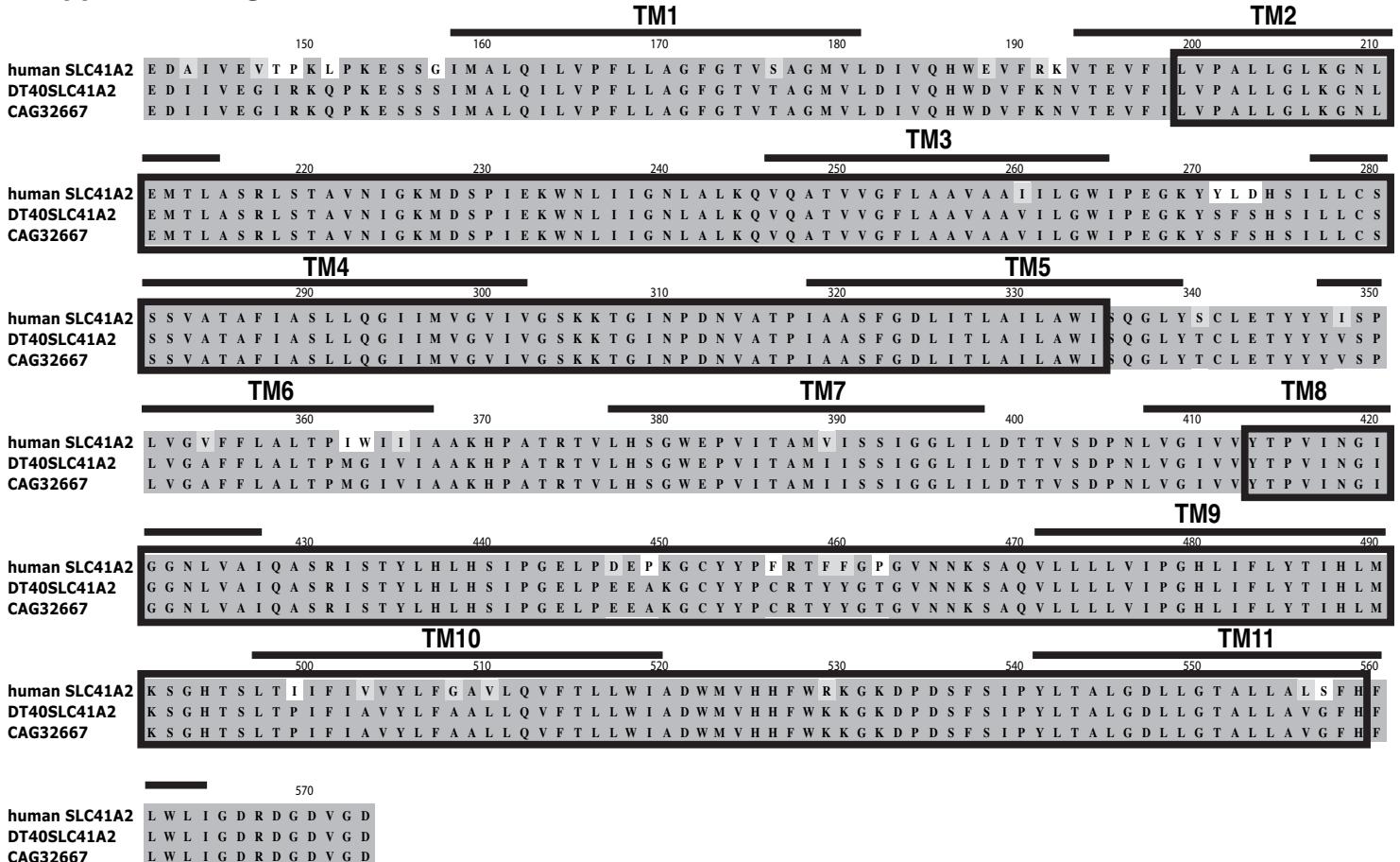


Supplemental figure.1



Supplemental Figure 1: Human and Chicken SLC41A2 sequences. ClustalW alignment of the MgtE domain regions of human SLC41A2 (top), a SLC41A2 sequence obtained by direct sequence analysis of an RT-PCR reaction from DT40 RNA (middle), and the closest homologous chicken sequence in Genbank-CAG32667/XP_425486 (a predicted protein sequence from genomic sequence data). In the alignment, dark grey shading represents identity and light gray shading represents similarity. Bold lines on the top indicate the location of the proposed 11 TM spans. Grey boxes indicate the most highly conserved portions of the MgtE domains (D1 and D2), each of which contains 4 TM spans. Both D1 and D2 are preceded by a TM span which are not highly homologous to each other but are presumably a part of a functional five TM span MgtE domain, as predicted by hydrophobicity analyses of prokaryotic MgtE proteins. The 6th TM span is clearly distinct from those observed in prokaryotic MgtE proteins, and its existence outside of the MgtE domains is further supported by the likely need to maintain a similar topology of the two MgtE domains.