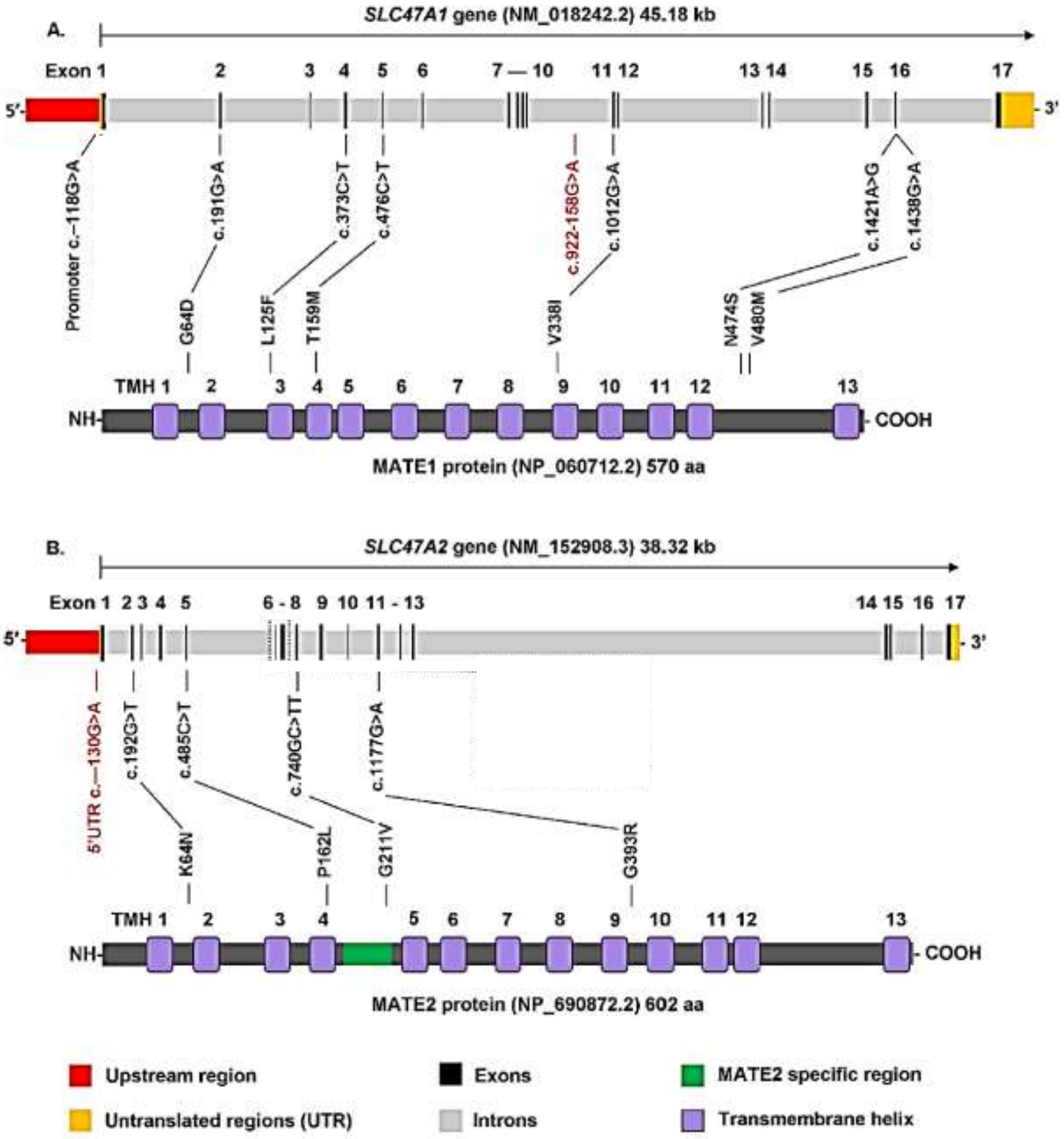

Figure S1. Schematic representation of the gene sequences and the primary protein structure of MATE1 (A) and MATE2 (B). Exons (numbered from 1 to 17) and introns of both genes and arrangement of transmembrane helices (TMH) (numbered from 1 to 13) of encoded proteins are depicted. The studied SNPs (Intronic c.922-158G>A for *SLC47A1* and 5'UTR c.-130G>A for *SLC47A2*) are indicated in red. [Adapted from: Staud F, Cerveny L, Ahmadimoghaddam D, Ceckova M. Multidrug and toxin extrusion proteins (MATE/SLC47); role in pharmacokinetics. *Int J Biochem Cell Biol* **2013**; 45: 2007–11]

Table S1. Comparison of the allele frequencies of SNP rs2289669 (*SLC47A1*) between South Indian population with other ethnic populations

Population	**Allele frequency (%)**		***P****
	A	**G**	
South Indians	53.4	46.6	**Ref.**
African-Americans	10.4	89.6	**<0.001**
Caucasians/ European Americans	44.2	55.8	**0.258**
Chinese Americans	46.4	53.6	**0.396**
Japanese	37.6	62.4	**0.046**
Mexican Americans	49.0	51.0	**0.671**

Fisher's exact test was performed. *$P < 0.05$ was considered statistically significant.

Table S2. Comparison of the allele frequencies of SNP rs12943590 (*SLC47A2*) between South Indian population with other ethnic populations

Population	**Allele frequency (%)**		***P****
	A	**G**	
South Indians	47.5	52.5	**Ref.**
African-Americans	27.7	72.3	**<0.001**
Caucasians/ European Americans	26.2	73.8	**0.002**
Chinese Americans	48.5	51.5	**1.112**
Koreans	45.8	54.2	**0.887**
Mexican Americans	34.1	65.9	**0.061**

Fisher's exact test was performed. **P* < 0.05 was considered statistically significant.