

Table SI. OATP4A1 variants. Allele frequencies of rs34419428 (R70Q) and rs1047099 (V78I) in different ethnic groups.

A, Variant rs34419428 (<https://www.ncbi.nlm.nih.gov/snp/rs34419428>; coding sequence variant, missense variant)

Molecule type	Sequence change	Amino acid change	Allele frequency
<i>SLCO4A1</i> transcript	NM_016354.4: c.209G>A	R [CGG]>Q [CAG]	-
OATP4A1 protein	NP_057438.4: p.R70Q		-
Population	-	-	-
Overall	-	-	0.021-0.058
European (mixed)	-	-	0.047
East-Asian (mixed)	-	-	0.002
Africa (LWK, ESN)	-	-	0.033
Tokyo, Japan (JPT)	-	-	0.0

B, Variant rs1047099 (<https://www.ncbi.nlm.nih.gov/snp/rs1047099>; coding sequence variant, missense variant)

Molecule type	Sequence change	Amino acid change	Allele frequency
<i>SLCO4A1</i> transcript	NM_016354.4: c.232G>A	V [GTC]>I [ATC]	-
OATP4A1 protein	NP_057438.4: p.V78I		-
Population	-	-	-
Overall	-	-	0.149-0.311
European (mixed)	-	-	0.290
East-Asian (mixed)	-	-	0.168
Africa (LWK, ESN)	-	-	0.0
Asia (JPT)	-	-	0.178

The OATP4A1 minor alleles rs1047099 and rs34419428 are detectable in European and East-Asians populations. The rs1047099 variant is not present in the African populations Luhya (Webuye, Kenya, LWK) and Esan (Nigeria, ESN). The rs34419428 variant was not observed in the Japanese population of Tokyo (JPT). OATP4A1, solute carrier organic anion transporter family member 4A1.

Table SII. OATP4A1 variants rs34419428 (R70Q) and rs1047099 (V78I) in populations of different ethnic origin.

A, European population (mixed) ^a		
SNP	Mutation	Statistics (n=1006)
G_G: 0.710	Wt	D'=1.0
G_A: 0.244	V78I	R ² =0.1198
A_A: 0.047	V78I/R70Q	$\chi^2=120.557$
A_G: 0.0	R70Q	P<0.0001
B, East-Asian population (mixed) ^b		
SNP	Mutation	Statistics (n=1008)
G_G: 0.838	Wt	D'=0.3993
G_A: 0.167	V78I	R ² =0.0016
A_A: 0.001	V78I/R70Q	$\chi^2=1.5861$
A_G: 0.001	R70Q	P<0.2079
C, Africa (LWK, ESN)		
SNP	Mutation	Statistics (n=396)
G_G: 0.967	Wt	n.a.
A_G: 0.033	R70Q	
A_A: 0.0	V78I/R70Q	
G_A: 0.0	V78I	
D, Asia (JPT)		
SNP	Mutation	Statistics (n=208)
G_G: 0.822	Wt	n.a.
G_A: 0.178	V78I	
A_A: 0.0	V78I/R70Q	
A_G: 0.0	R70Q	

^aThe rs34419428 allele is non-randomly associated with the rs1047099 allele. The two alleles are in linkage disequilibrium. ^bThe rs34419428 (A) allele and the rs1047099(A) allele are in linkage equilibrium (they are randomly associated). Statistical differences for the random association of the two alleles in the different populations are given. Wt, wild-type; n.a., not applicable.