

**Table S3.** Genetic polymorphisms in 12 transporters and their in vitro consequences. Non-synonymous and untranslated region (UTR) polymorphisms with known in vitro functions are described in this table.

Transporter	Amino Acid Change	Polymorphism (rsID)	Ref > Alt	Allele Frequency AFR (African)	Allele Frequency AMR (Ad Mixed American)	Allele Frequency EAS (East Asian)	Allele Frequency EUR (European)	Allele Frequency SAS (South Asian)	Allele frequency (Cohort)	In Vitro Effects (Expression)	In Vitro Effects (Uptake)	Substrates	In vitro system	References (PMID)
SLC22A1	Ser14Phe	rs34447885	C > T	0.017	0.004	0	0.001	0	1000 genomes	similar expression as reference	substrate-specific changes in uptake: reduced uptake of MPP+, TEA+, Morphine, Metformin, Tropisetron, Debrisoquine, Tyramine, Monocrotaline, increased uptake of MPP+	MPP+, TEA+, ASP+, Morphine, Metformin, Tropisetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline	Oocytes, HEK293	26157489*, 12719534*
SLC22A1	Ser29Leu	rs375175439	C > T	0	0.000148	0.00011595	0.0000268	0.0000324	gnomADe	reduced cell surface expression	substrate-specific reduction of uptake: MPP+, TEA+, ASP+, Morphine, Metformin, Tropisetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline	MPP+, TEA+, ASP+, Morphine, Metformin, Tropisetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline	HEK293	26157489
SLC22A1	Arg61Cys	rs12208357	C > T	0.004	0.02	0	0.063	0.02	1000 genomes	reduced cell surface expression	substrate-specific reduction of uptake: MPP+, TEA+, ASP+, Morphine, Metformin, Tropisetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline	MPP+, TEA+, ASP+, Morphine, Metformin, Tropisetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline	Oocytes, HEK293	26157489, 12719534, 17476361
SLC22A1	Leu85Phe	rs35546288	C > T	0.005	0	0	0	0	1000 genomes	ND	similar uptake as reference	MPP+	Oocytes	12719534*
SLC22A1	Cys88Arg	rs55918055	T > C	0	0	0	0.003	0	1000 genomes	reduced cell surface expression	substrate-specific reduction of uptake: MPP+, TEA+, ASP+, Morphine, Metformin, Tropisetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline*	MPP+, TEA+, ASP+, Morphine, Metformin, Tropisetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline	HEK293	26157489*, 20639304
SLC22A1	Gln97Lys	rs772259161	C > T	0	0	0	0.0000904	0	1000 genomes	similar expression as reference	substrate-specific reduction of uptake: Metformin	Metformin	HEK293	20639304
SLC22A1	Pro117Leu	rs200684404	C > T	0	0	0.001	0	0	1000 genomes	similar expression as reference	substrate-specific changes: reduced uptake of tropisetron and metformin, increased uptake of morphine	MPP+, TEA+, ASP+, Morphine, Metformin, Tropisetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline	HEK293	26157489, 20639304
SLC22A1	Phe160Leu	rs683369	C > G	0.011	0.108	0.146	0.215	0.172	1000 genomes	ND	substrate-specific reduction in uptake: TEA, Morphine, tropisetron, and tyramine	MPP+, TEA+, ASP+, Morphine, Metformin, Tropisetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline	Oocytes, HEK293	26157489, 12719534
SLC22A1	Ser189Leu	rs34104736	C > T	0	0.001	0	0.001	0	1000 genomes	similar expression as reference	substrate-specific reduction in uptake: MPP, TEA, metformin, tropisetron, O-desmethyl tramadol, tyramine, monocrotaline	MPP+, TEA+, ASP+, Morphine, Metformin, Tropisetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline	HEK293	26157489, 12719534
SLC22A1	Arg206Cys	rs756787089	C > T	0	0	0	0.00004505	0	1000 genomes	reduced cell surface expression	substrate-specific reduction in uptake: MPP+, TEA+, ASP+, Morphine, Metformin, Tropisetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline	MPP+, TEA+, ASP+, Morphine, Metformin, Tropisetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline	HEK293	20639304
SLC22A1	Gly220Val	rs36103319	G > T	0.001	0	0	0	0	1000 genomes	ND	substrate-specific reduction in uptake: MPP+	MPP+	Oocytes, HEK293	26157489, 12719534
SLC22A1	Thr245Met	NA	T > C	0	0	0	Singleton	0	Seitz et al.	similar expression as reference	substrate-specific reduction in uptake: MPP, TEA, ASP, morphine, metformin, tropisetron, O-desmethyl tramadol, tyramine, monocrotaline	MPP+, TEA+, ASP+, Morphine, Metformin, Tropisetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline	HEK293	26157489
SLC22A1	Pro283Leu	rs4646277	C > T	0	0	0.005	0	0	1000 genomes	similar expression as reference	substrate-specific reduction in uptake: MPP, TEA, lamivudine	MPP+, TEA+, Metformin, Lamivudine	Oocytes	17220237, 22415520
SLC22A1	Glu284Lys	NA	G > A	0	0	0	Singleton	0	Seitz et al.	reduced cell surface expression	substrate-specific reduction in uptake: MPP+, TEA+, ASP+, Morphine, Metformin, Tropisetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline	MPP+, TEA+, ASP+, Morphine, Metformin, Tropisetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline	HEK293	26157489
SLC22A1	Pro341Leu	rs2282143	C > T	0.076	0.019	0.126	0.009	0.084	1000 genomes	similar expression as reference	substrate-specific reduction in uptake: MPP, tropisetron, O-desmethyl tramadol, debrisoquine, tyramine, monocrotaline, lamivudine	MPP+, TEA+, ASP+, Morphine, Metformin, Tropisetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline, Lamivudine	Oocytes, HEK293	26157489, 12719534, 22415520
SLC22A1	Arg342His	rs34205214	G > A	0.015	0	0	0.001	0.001	1000 genomes	ND	similar uptake as reference	MPP+, TEA+, ASP+, Morphine, Metformin, Tropisetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline	Oocytes	12719534
SLC22A1	Gly401Ser	rs34130495	G > A	0.003	0.007	0	0.021	0.001	1000 genomes	reduced cell surface expression	substrate-specific reduction in uptake: MPP+, TEA+, ASP+, Morphine, Metformin, Tropisetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline	MPP+, TEA+, ASP+, Morphine, Metformin, Tropisetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline	Oocytes, HEK293	26157489, 12719534, 17476361
SLC22A1	Met408Val	rs628031	A > G	0.731	0.784	0.741	0.586	0.61	1000 genomes	ND	similar uptake as reference	MPP+, TEA+, ASP+, Morphine, Metformin, Tropisetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline	Oocytes, HEK293	26157489, 12719534
SLC22A1	Gly414Ala	rs72552762	G > C	0	0	0	0	0.002	1000 genomes	ND	substrate-specific reduction in uptake: MPP+, TEA+, ASP+, Morphine, Metformin, Tropisetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline	MPP+, TEA+, ASP+, Morphine, Metformin, Tropisetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline	Oocytes, HEK293	26157489**
SLC22A1	Met420DEL	rs202220802	ATG > - (inframe deletion)	0.045	0.288	0.005	0.184	0.145	1000 genomes	similar expression as reference	substrate-specific reduction in uptake: MPP, TEA, ASP, morphine, metformin, tropisetron, O-desmethyl tramadol, tyramine, monocrotaline	MPP+, TEA+, ASP+, Morphine, Metformin, Tropisetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline	Oocytes, HEK293	26157489, 12719534
SLC22A1	Met440Ile	rs35956182	G > A	0	0.001	0	0.012	0	1000 genomes	ND	similar uptake as reference	MPP+	Oocytes	12719534
SLC22A1	Ile449Thr	rs183240019	T > C	0	0	0.002	0	0	1000 genomes	similar expression as reference	substrate-specific reduction in uptake: TEA, metformin, tropisetron, debrisoquine, tyramine, monocrotaline	MPP+, TEA+, ASP+, Morphine, Metformin, Tropisetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline	HEK293	26157489

SLC22A1	Val461Ile	rs34295611	G > A	0.011	0	0	0	0	1000 genomes	ND	similar uptake as reference	MPP+	Oocytes	12719534
SLC22A1	Gly465Arg	rs34059508	G > A	0	0.019	0	0.02	0	1000 genomes	reduced cell surface expression	substrate-specific reduction in uptake: MPP+, TEA+, ASP+, Morphine, Metformin, Tropicsetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline	MPP+, TEA+, ASP+, Morphine, Metformin, Tropicsetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline	Oocytes, HEK293	26157489, 12719534, 17476361
SLC22A1	Arg488Met	rs35270274	G > T	0.034	0	0	0.001	0	gnomADe	ND	substrate-specific reduction in uptake: ASP and debrisoquine	MPP+, TEA+, ASP+, Morphine, Metformin, Tropicsetron, O-desmethyl tramadol, Debrisoquine, Tyramine, Monocrotaline	HEK293	26157489**

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SLC22A2	Met165Ile	rs8177507	C > T	0.003	0	0	0	0	1000 genomes	ND	substrate-specific reduction in uptake: MPP+	MPP+	Oocytes	12142729
SLC22A2	Thr199Ile	rs201919874	G > A	0	0	0.001	0	0	1000 genomes	similar expression as reference	substrate-specific reduction in uptake: MPP+ and metformin	MPP+, TEA+, Metformin, Lamivudine	Oocytes	18728938; 22415520
SLC22A2	Thre201Met	rs145450955	G > A	0	0	0.007	0	0	1000 genomes	similar expression as reference	substrate-specific reduction in uptake: MPP+ and metformin	MPP+, TEA+, Metformin, Lamivudine	Oocytes	18728938; 22415520
SLC22A2	Ala270Ser	rs316019	C > A	0.185	0.092	0.136	0.11	0.134	1000 genomes	increased cell surface expression	substrate-specific reduction in uptake: MPP+ and metformin	MPP+, TEA+, Metformin, Lamivudine	Oocytes	12142729; 18728938; 22415520
SLC22A2	Arg400Cys	rs8177516	C > T	0.013	0	0	0.001	0	1000 genomes	ND	substrate-specific reduction in uptake: MPP+, Metformin, Phenformin, Procainamide, Quinidine	MPP+, Metformin, Phenformin, Procainamide, Quinidine	Oocytes	12142729
SLC22A2	Lys432Gln	rs8177517	T > G	0.039	0.001	0	0	0	1000 genomes	ND	substrate-specific reduction in uptake: MPP+, Metformin, Phenformin, Procainamide, Quinidine	MPP+, Metformin, Phenformin, Procainamide, Quinidine	Oocytes	12142729

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SLC22A6	Arg50His	rs11568626	C > T	0.07	0.001	0	0	0	1000 genomes	ND	substrate-specific reduction in uptake: adefovir, cidofovir and tenofovir	Oocytes	PAH, adefovir, cidofovir, tenofovir, methotrexate, ochratoxin A	15914676, 15864112
SLC22A6	Pro104Leu	rs11568627	G > A	0	0.003	0	0.005	0	1000 genomes	ND	similar uptake as reference	Oocytes	PAH, methotrexate, ochratoxin A	15864112
SLC22A6	Ile226Thr	rs11568623	A > T	0.001	0	0	0	0	gnomADe	ND	similar uptake as reference	Oocytes	PAH, methotrexate, ochratoxin A	15864112
SLC22A6	Ala256Val	rs11568624	G > A	0.0001	0.00009	0	0.00013	0	gnomADe	ND	similar uptake as reference	Oocytes	PAH, methotrexate, ochratoxin A	15864112
SLC22A6	Arg293Trp	rs45607933	G > A	0.002	2.20E-04	6.10E-05	4.80E-05	0	gnomADe	ND	similar uptake as reference	Oocytes	PAH, methotrexate, ochratoxin A	15864112
SLC22A6	Lys525Ile	NA	A > T	Singleton	0	0	0	0	Bleasby et al. (15914676)	ND	similar uptake as reference	Oocytes	PAH, adefovir, cidofovir, and tenofovir	15914676
SLC22A6	Arg454Gln	rs11568634	C > T	1.30E-04	0	0	0	0.0004	gnomADe	ND	substrate-specific reduction in uptake: PAH, methotrexate, ochratoxin A	Oocytes	PAH, methotrexate, ochratoxin A	15864112

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SLC22A8	Phe129Leu	rs11568479	G > T	0	5.96E-05	0	0	0	gnomADe	ND	Similar to reference	HEK293 cells	Esterone sulfate, cimetidine	16291576
SLC22A8	Arg149Ser	rs45566039	G > A	0	4.00E-05	0	1.00E-05	0	gnomADe	ND	Substrate-specific reduction in uptake: Esterone sulfate, cimetidine	HEK293	Esterone sulfate, cimetidine	16291576
SLC22A8	Gln239STOP	rs11568496	G > A	0	0	1.16E-04	0	0	gnomADe	ND	Substrate-specific reduction in uptake: Esterone sulfate, cimetidine	HEK293	Esterone sulfate, cimetidine	16291576
SLC22A8	Ile260Arg	rs11568493	A > C	0	0	0.008	0	0	PMT	ND	Substrate-specific reduction in uptake: Esterone sulfate, cimetidine	HEK293	Esterone sulfate, cimetidine	16291576
SLC22A8	Arg277Trp	rs11568492	G > A	6.54E-05	8.97E-06	5.80E-05	0	0	gnomADe	ND	Substrate-specific reduction in uptake: esterone sulfate	HEK293	Esterone sulfate, cimetidine	16291576
SLC22A8	Val281Ala	rs45438191	A > G	0.065	0.006	0.008	0.001	0	1000 genomes	ND	similar uptake as reference	HEK293	Esterone sulfate, cimetidine	16291576
SLC22A8	Ile305Phe	rs11568482	T > A	0	0.006	0.06	0	0.003	1000 genomes	decreased cell surface expression	Substrate-specific reduction in uptake: esterone sulfate and cefotaxime	HEK293	Esterone sulfate, cimetidine, cefotaxime	16291576; 23649425
SLC22A8	Ala310Val	rs11568481	G > A	0	0.001	0	0	0.002	1000 genomes	ND	similar uptake as reference	HEK293	Esterone sulfate, cimetidine	16291576
SLC22A8	Ala399Ser	rs11568497	C > A	0	0	0	0	0.02	1000 genomes	ND	similar uptake as reference	HEK293	Esterone sulfate, cimetidine	16291576
SLC22A8	Val448Ile	rs11568486	C > T	0.001	0.015	0	0.004	0.005	1000 genomes	ND	similar uptake as reference	HEK293	Esterone sulfate, cimetidine	16291576

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SLC47A1	g.-1975C>A	rs2453579	C > A	0.697	0.301	0.322	0.432	0.294	1000 genomes	increased luciferase activity	ND	HCT-116	NA	23558289
SLC47A1	g.-66T>C	rs2252281	T > C	0.412	0.269	0.214	0.407	0.167	1000 genomes	decreased luciferase activity and mRNA	ND	HCT-116, ACHN, HepG2, HeLa	NA	19745787
SLC47A1	g.-53C>G	rs78572621	C > G	0.00012	0.001	0	0.001	NA	gnomAD	decreased luciferase activity and mRNA	ND	HCT-116, ACHN, HepG2, HeLa	NA	19745787
SLC47A1	ACCCACTGCC	rs76654011	GTACCCACTG CCGGCCTCC GCG > -	0.059	0.008	0	0.007	NA	PMT	decreased luciferase activity and mRNA	ND	HCT-116, ACHN, HepG2, HeLa	NA	19745787
SLC47A1	g.-44C>T	rs111427955	C > T	0.009	0.004	0.003	0.003	0.001	1000 genomes	decreased luciferase activity and mRNA	ND	HCT-116, ACHN, HepG2, HeLa	NA	19745787
SLC47A1	g.-27_-26insGTACCA CTGCCGGCC TCCGCG	rs76164274	-> GTACCCACTG CCGGCCTCC GCG	0.037	0.068	0.044	0.059	NA	PMT	decreased luciferase activity and mRNA	ND	HCT-116, ACHN, HepG2, HeLa	NA	19745787
SLC47A1	Val10Leu	rs555657341	G > T	0	0	0.002	0	0	1000 genomes	similar expression as reference	similar uptake as reference	HEK293	TEA, Metformin	19158817
SLC47A1	Gly64Asp	rs77630697	G > A	0	0	0.002	0	0	1000 genomes	reduced cell surface expression	substrate-specific reduction in uptake: Paraquat, metformin, TEA, Oxaliplatin	HEK293	Paraquat, metformin, TEA, Oxaliplatin	19172157
SLC47A1	Leu125Phe	rs77474263	C > T	0	0.063	0.004	0.002	0	1000 genomes	similar expression as reference	substrate-specific reduction in uptake: paraquat, metformin, TEA	HEK293	Paraquat, metformin, TEA, Oxaliplatin	19172157
SLC47A1	Thr159Met	rs35646404	C > T	0	0.001	0	0	0	1000 genomes	similar expression as reference	substrate-specific reduction in uptake: metformin, TEA	HEK293	Metformin, TEA	20053795
SLC47A1	Ala310Val	rs104806857	C>T	0	0	0.022	0	0	Kajiwara et. al. (Japanese cohort)	similar expression as reference	substrate-specific reduction in uptake: metformin, TEA	HEK293	Metformin, TEA	19158817
SLC47A1	Asp328Ala	rs149774861	A > C	0	0	0.002	0	0	1000 genomes	reduced cell surface expression	substrate-specific reduction in uptake: metformin, TEA	HEK293	Metformin, TEA	19158817
SLC47A1	Val338Ile	rs35790011	G > A	0.076	0.006	0	0	0	1000 genomes	similar expression as reference	substrate-specific reduction in uptake: metformin and TEA	HEK293	Paraquat, metformin, TEA, Oxaliplatin	19172157, 20053795
SLC47A1	Asn474Ser	ss104806858	A>G	0	0	0.006	0	0	Kajiwara et. al. (Japanese cohort)	similar expression as reference	substrate-specific reduction in uptake: TEA	HEK293	TEA, Metformin	19158817
SLC47A1	Val480Met	rs76645859	G > A	0	0	0.001	0	0	1000 genomes	reduced cell surface expression	substrate-specific reduction in uptake: Paraquat, metformin, TEA, Oxaliplatin	HEK293	Paraquat, metformin, TEA, Oxaliplatin	19172157
SLC47A1	Cys497Phe	rs35395280	G > T	0.023	0.007	0	0	0	1000 genomes	similar expression as reference	similar uptake as reference	HEK293	Metformin, TEA	20053795
SLC47A1	Gln519His	rs78700676	G > C	0.000458	0	0	0	0	gnomAD	ND	similar uptake as reference	HEK293	Paraquat, metformin, TEA, Oxaliplatin	19172157

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SLC47A2	NA	rs146770799	C>G	0.01	0	0	0	0	1000 Genomes	no change in luciferase activity	ND	HCT-116	ND	21956618
SLC47A2	NA	rs12943590	G>A	0.18	0.32	0.45	0.27	0.4	1000 Genomes	increased luciferase activity	ND	HCT-116	ND	21956618
SLC47A2	NA	rs139938875	G>A	0.0001147	0.001193	0	0	0	gnomAD	no change in luciferase activity	ND	HCT-116	ND	21956618
SLC47A2	NA	rs146491112	C>T	0	0.00004634	0.0008366	0.00009	0.0001211	gnomAD	no change in luciferase activity	ND	HCT-116	ND	21956618
SLC47A2	Lys64Asn	ss104806859	G > T	0	0	0.006	0	0	Kajiwara et. al., Japanese population	decreased cell surface expression	substrate-specific reduction in uptake: TEA, Metformin	HEK293	TEA, Metformin	21457222, 19158817
SLC47A2	Pro162Leu	rs146901447	G>A	0.031	0.001	0	0	0	1000 Genomes	decreased cell surface expression	substrate-specific reduction in uptake: TEA, Metformin, Amiloride, Trospium	HEK293	TEA, Metformin, Amiloride, Trospium	21956618
SLC47A2	Gly211Val	rs562968062	C>A	0	0	0.001	0	0	1000 Genomes	decreased cell surface expression	substrate-specific reduction in uptake: TEA, Metformin	HEK293	TEA, Metformin	21457222, 19158817
SLC47A2	Gly393Arg	rs34399035	C>T	0	0.006	0	0.007	0.01	1000 Genomes	decreased cell surface expression	substrate-specific reduction in uptake: TEA, Metformin, Amiloride, Trospium	HEK293	TEA, Metformin, Amiloride, Trospium	21956618
SLC47A2	Thr505Ile	rs113679066	G>A	0.0001627	0	0	0	0	gnomADe	ND	similar uptake as reference	HEK293	TEA, Metformin, Amiloride, Trospium	21956618
SLC47A2	Ala525Thr	rs113234335	C > T	0	0.00006	0	0.00007	0	gnomADe	ND	similar uptake as reference	HEK293	TEA, Metformin, Amiloride, Trospium	21956618

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SLCO1B1	Arg57Gln	rs61760182	G > A	0	0	0	0.001	0	1000 genomes	ND	Substrate-specific reduction in uptake: estrone sulfate, cerivastatin	HEK293	esterone sulfate, cerivastatin	23652407
SLCO1B1	Phe73Leu	rs56101265	T > C	0	0.02	ND	ND	ND	11477075	Reduced cell surface expression	Substrate-specific reduction in uptake: estrone sulfate, 17β-estradiol 17β-D-glucuronide, rifampin, rosuvastatin	HeLa	estrone sulfate, 17β-estradiol 17β-D-glucuronide, rifampin, rosuvastatin	11477075**, 12490595, 16697742
SLCO1B1	Val82Ala	rs56061388	T > C	0	0.02	ND	ND	ND	11477075	Reduced cell surface expression	Substrate-specific reduction in uptake: rifampin and rosuvastatin	HeLa	estrone sulfate, 17β-estradiol 17β-D-glucuronide, rifampin, rosuvastatin	11477075**, 12490595**, 16697742**
SLCO1B1	Asn130Asp	rs2306283	A > G	0.82	0.4	0.76	0.55	0.47	1000 genomes	Similar expression as reference	Substrate-specific reduction in uptake: C-tau and rifampin	MDCKII, HeLa, oocytes, HEK293	17β-estradiol 17β-D-glucuronide, estrone sulfate, cerivastatin, rosuvastatin, pravastatin, atorvastatin, cholesterol, simvastatin, cholytaurine, BSP, rifampin, SN-38, atrasentan	15564882, 11477075, 12196548, 12490595, 15608127, 16697742, 16513443
SLCO1B1	Arg152Lys	NA	G > A	ND	ND	0.007	ND	ND	12130747	Similar expression as reference	Substrate-specific reduction in uptake: estradiol and rosuvastatin	HeLa, HEK293	estrone sulfate, 17β-estradiol 17β-D-glucuronide, rifampin, rosuvastatin	11477075**, 12130747**, 12490595**, 16697742**
SLCO1B1	Pro155Thr	rs11045819	C > A	0.06	0.14	0.003	0.03	0.1	1000 genomes	Increased mRNA levels, similar expression as reference	Substrate-specific reduction in uptake: C-tau	MDCKII, HeLa	esterone sulfate, cerivastatin, cholytaurine, BSP, rifampin, rosuvastatin	23652407, 12196548, 11477075, 12196548, 12490595, 16697742
SLCO1B1	Glu156Gly	rs72559745	A > G	0	0.02	ND	ND	ND	11477075	Reduced cell surface expression	Substrate-specific reduction of uptake: rifampin and rosuvastatin	HeLa	estrone sulfate, 17β-estradiol 17β-D-glucuronide, rifampin, rosuvastatin	11477075**, 12490595**, 16697742**
SLCO1B1	Val174Ala	rs4149056	T > C	0.01	0.16	0.12	0.04	0.13	1000 genomes	Reduced cell surface expression	Substrate-specific reduction in uptake: estrone sulfate (study dependent), estradiol (study dependent), rifampin, rosuvastatin, and atrasentan	HeLa, HEK293, oocytes	17β-estradiol 17β-D-glucuronide, pravastatin, atorvastatin, cerivastatin, estrone sulfate, repaglinide, rosuvastatin, rifampin, SN-38, atrasentan	15564882, 23652407, 15970799, 11477075, 12130747, 12490595, 15608127, 16697742, 16513443
SLCO1B1	Leu193Arg	rs72559746	T > G	ND	singleton	ND	ND	ND	12196548	Reduced cell surface expression, increased mRNA	No uptake activity	MDCKII	17β-estradiol 17β-D-glucuronide, cholytaurine, BSP	12196548, 12490595
SLCO1B1	Asp241Asn	NA	G > A	ND	ND	0.007	ND	ND	12130747	Similar expression as reference	Substrate-specific reduction in uptake: estradiol and rosuvastatin	HeLa, HEK293	estrone sulfate, 17β-estradiol 17β-D-glucuronide, rifampin, rosuvastatin	11477075**, 12130747**, 12490595**, 16697742**
SLCO1B1	Pro336Arg	rs72559747	C > G	0	0	0.004	0	0	1000 genomes	ND	Similar uptake as reference	HeLa, HEK293	Pravastatin, atorvastatin, cerivastatin	15970799
SLCO1B1	Thr345Met	rs61760243	C > T	0.00007	0.0001	0.0002	0.00003	0.0005	gnomADe	Similar expression as reference	Substrate-specific reduction in uptake: estrone sulfate	HEK293	esterone sulfate, cerivastatin	23652407
SLCO1B1	Ile353Thr	rs55901008	T > C	0	0.000009	0	0	0.00006	gnomADe	Reduced cell surface expression	Substrate-specific reduction in uptake: estradiol-17β-Glucuronide, estrone-3-sulfate, and rifampin	HeLa	estrone sulfate, 17β-estradiol 17β-D-glucuronide, rifampin, rosuvastatin	21245207, 11477075, 12490595, 16697742
SLCO1B1	Asn432Asp	rs56387224	A > G	0	0.01	0	ND	ND	77075, 21245	Similar expression as reference	Substrate-specific reduction in uptake: estradiol, rosuvastatin, and rifampin	HeLa	estrone sulfate, 17β-estradiol 17β-D-glucuronide, rifampin, rosuvastatin	21245207, 11477075, 12490595, 16697742
SLCO1B1	Asp462Gly	rs72559748	A > G	0	0.01	0	ND	ND	77075, 21245	Similar expression as reference	Similar uptake as reference	HeLa	estrone sulfate, 17β-estradiol 17β-D-glucuronide, rifampin, rosuvastatin	21245207, 11477075, 12490595, 16697742
SLCO1B1	Gly488Ala	rs59502379	A > C	0.04	0	0	0	0.003	1000 genomes	Reduced cell surface expression	Substrate-specific reduction in uptake: estradiol-17β-Glucuronide, estrone-3-sulfate, rosuvastatin, rifampin, atrasentan	HeLa	estrone sulfate, 17β-estradiol 17β-D-glucuronide, rifampin, rosuvastatin, atrasentan	11477075, 12490595, 16697742**, 16513443**
SLCO1B1	Leu543Trp	rs72661137	T > G	0	0	0.002	0	0	1000 genomes	Similar expression as reference	Substrate-specific reduction in uptake: estradiol-17β-Glucuronide, estrone-3-sulfate, pravastatin	HEK293	estradiol-17β-Glucuronide, estrone-3-sulfate, pravastatin	19238167
SLCO1B1	Leu643Phe	rs34671512	A > C	0.07	0.05	0.005	0.05	0.04	1000 genomes	Similar expression as reference	Similar uptake as reference	HEK293	BSP, estrone sulfate, 17β-estradiol 17β-D-glucuronide, Pravastatin, Taurocholic Acid	17989996
SLCO1B1	Asp655Gly	rs56199088	A > G	0	0.02	0	ND	ND	77075, 21245	Similar expression as reference	Substrate-specific reduction in uptake: estrone sulfate	HeLa	estrone sulfate, 17β-estradiol 17β-D-glucuronide, rifampin, rosuvastatin	21245207, 11477075, 12490595, 16697742
SLCO1B1	Glu667Gly	rs55737008	A > G	0.34	0.02	0	ND	ND	77075, 21245	Similar expression as reference	Substrate-specific reduction in uptake: rifampin	HeLa	estrone sulfate, 17β-estradiol 17β-D-glucuronide, rifampin, rosuvastatin	21245207, 11477075, 12490595, 16697742



Transporter	Amino Acid Change	Polymorphism (rsID)	Ref > Alt	Allele Frequency AFR (African)	Allele Frequency EUR (European)	Allele Frequency EAS (East Asian)	Allele Frequency SAS (South Asian)	Allele Frequency AMR (Ad Mixed American)	Allele frequency (Cohort)	In Vitro Effects (Expression)	In Vitro Effects (Uptake)	In Vitro Expression System	Substrates	References (PMID)
SLCO1B3	Ser112Ala	rs4149117	T > G	0.64	0.14	0.3	0.09	0.16	1000 Genomes	Similar expression as reference	Substrate-specific reduction in uptake: MPAG	HeLa, MDCKII, oocytes, HEK293	cholecystokinin-8, bile acids, bromosulfophthalein, taurocholate, mycophenolic acid-7-O-glucuronide, paclitaxel, carboplatin	21278621, 15226676, 17412826, 19890249**, 26641474
SLCO1B3	Thr147Ala	rs57585902	A > G	0.04	0	0	0	0.003	1000 Genomes	Increased cell surface expression	Similar uptake as reference	HeLa	cholecystokinin-8	21278621
SLCO1B3	Met233Ile	rs7311358	G > A	0.64	0.14	0.3	0.09	0.16	1000 Genomes	Similar expression as reference	Substrate-specific reduction in uptake: CCK8, MPAG, paclitaxel, carboplatin and rosuvastatin	HeLa, MDCKII, HEK293, oocytes	cholecystokinin-8, atorvastatin, rosuvastatin, bile acids, bromosulfophthalein, paclitaxel, carboplatin, taurocholate, mycophenolic acid-7-O-glucuronide	21278621, 15226676, 17412826, 19890249**, 26641474
SLCO1B3	Gly256Ala	rs60140950	G > C	0.01	0.17	0.003	0.07	0.11	1000 Genomes	Reduced cell surface expression	Similar uptake as reference	HeLa	cholecystokinin-8	21278621
SLCO1B3	His520Pro	rs559692629	A > C	0	0	0.001	0	0	1000 Genomes	Reduced cell surface expression	Substrate-specific reduction in uptake: CCK8 and rosuvastatin	HeLa	cholecystokinin-8, atorvastatin, rosuvastatin	21278621
SLCO1B3	Gly522Cys	rs72559743	G > T	ND	0.019	ND	ND	ND	15226676	Reduced cell surface expression	Substrate-specific reduction in uptake: bile acids	MDCKII	bile acids, bromosulfophthalein	15226676
SLCO1B3	Val560Ala	rs12299012	T > C	0.02	0	0	0	0.004	1000 Genomes	Reduced cell surface expression	Substrate-specific reduction in uptake: CCK8 and rosuvastatin	HeLa	cholecystokinin-8, atorvastatin, rosuvastatin	21278621

Transporter	Amino Acid Change	Polymorphism (rsID)	Ref > Alt	Allele Frequency AFR (African)	Allele Frequency EUR (European)	Allele Frequency EAS (East Asian)	Allele Frequency SAS (South Asian)	Allele Frequency AMR (Ad Mixed American)	Allele frequency (Cohort)	In Vitro Effects (Expression)	In Vitro Effects (Uptake)	In Vitro Expression System	Substrates	References (PMID)
SLCO2B1	Arg312Gln	rs12422149	G > A	0.092	0.095	0.32	0.263	0.365	1000 Genomes	Similar expression as reference	Similar uptake as reference	HEK293	estrone-3-sulfate	12130747
SLCO2B1	Ser486Phe	rs2306168	C > T	0.374	0.02	0.261	0.059	0.098	1000 Genomes	Similar expression as reference	Similar uptake as reference	HEK293	estrone-3-sulfate	12130747
SLCO2B1	Thr392Ile	rs1621378	C > T	0	0	0.0001	0	0	gnomAD	Similar expression as reference	Similar uptake as reference	HEK293	estrone-3-sulfate	12130747, 10873595

Transporter	Amino Acid Change	Polymorphism (rsID)	Ref > Alt	Allele Frequency AFR (African)	Allele Frequency EUR (European)	Allele Frequency EAS (East Asian)	Allele Frequency SAS (South Asian)	Allele Frequency AMR (Ad Mixed American)	Allele frequency (Cohort)	In Vitro Effects (Expression)	In Vitro Effects (Uptake)	In Vitro Expression System	Substrates	References (PMID)	
ABCB1	Asn21Asp	rs9282564	A > G	0.018	0.11	0.0004	0.026	0.027	ExAC	decreased cell surface expression	substrate-specific reduction in efflux: verapamil	HeLa, Sf9, HEK293T	Bodipy-FL-Verapamil, Daunorubicin, Bodipy-FL-Vinblastine, Calcein AM, Bodipy-FL-Prazosin, Bisantrene, Bodipy-FL-Paclitaxel, Bodipy-FL-Forskolin, Verapamil	12065748, 15499164, 18287207	
ABCB1	Asn44Ser	rs1202183	A > G	0	0	0.0001	0	0	ExAC	similar expression as reference	substrate-specific increase in efflux: verapamil	Sf9	Verapamil	15499164	
ABCB1	Phe103Leu	NA	T > C	ND	0.012	ND	ND	ND	10716719	decreased cell surface expression	substrate-specific reduction in efflux: verapamil	HeLa, Sf9	Bodipy-FL-Verapamil, Daunorubicin, Bodipy-FL-Vinblastine, Calcein AM, Bodipy-FL-Prazosin, Bisantrene, Bodipy-FL-Paclitaxel, Bodipy-FL-Forskolin, verapamil	12065748, 15499164	
ABCB1	Asn183Ser	rs60419673	A > G	0	0	0	0.01	0	1000 genomes	ND	substrate-specific increase in K <sub>m</sub> : Verapamil	Sf9	Verapamil	16259577	
ABCB1	Gly185Val	rs1128501	G > T	ND	ND	ND	ND	ND	ND	decreased cell surface expression	substrate-specific increase in efflux: verapamil	Sf9	Verapamil	15499164	
ABCB1	Gly191Arg	NA	G > A	ND	064 (Leukem)	ND	ND	ND	18723777	similar expression as reference	substrate-specific reduction in efflux: daunorubicin, vinblastine, vincristine, paclitaxel, etoposide	HEK293	rhodamine 123, doxorubicin, daunorubicin, vinblastine, vincristine, paclitaxel, etoposide	18723777	
ABCB1	Ser400Asn	rs2229109	G > A	0.003	0.03	0	0.009	0.024	1000 genomes	similar expression as reference	substrate-specific increase in efflux: doxorubicin, vinblastine, vincristine, paclitaxel, rhodamine 123; decreased Km and Vmax of verapamil	HeLa, HEK293, Sf9, HEK293T	Bodipy-FL-Verapamil, Daunorubicin, Bodipy-FL-Vinblastine, Calcein AM, Bodipy-FL-Prazosin, Bisantrene, Bodipy-FL-Paclitaxel, Bodipy-FL-Forskolin, doxorubicin, vinblastine, vincristine, paclitaxel, rhodamine 123, verapamil	12065748, 16917872, 15499164, 16259577, 18287207, 20138191	
ABCB1	Ser400Ile	NA	G > T	ND	0.023	ND	ND	ND	16917872	similar expression as reference	substrate-specific reduction in efflux: doxorubicin, substrate-specific induced cellular sensitivity: doxorubicin, vinblastine, vincristine, paclitaxel	HEK293	Rhodamine 123, doxorubicin, vinblastine, vincristine, paclitaxel	16917872	
ABCB1	Arg492Cys	rs754872565	C > T	0.0002	0.00004	0.00006	0	0.00003	gnomADe	ND	study dependent: increased or reduced efflux	Sf9	Verapamil	16259577, 20138191	
ABCB1	Leu662Arg	rs35657960	T > G	0	0	0	0	0.001	1000 genomes	similar expression as reference	substrate-specific increase in efflux: daunorubicin, doxorubicin, valinomycin	Yeast	actinomycin D, valinomycin, daunorubicin, doxorubicin	17352537	
ABCB1	Arg669Cys	rs35023033	C > T	0.01	0	0	0	0	1000 genomes	similar expression as reference	substrate-specific increase in efflux: verapamil, daunorubicin, doxorubicin, actinomycin D, valinomycin	Sf9, yeast	Verapamil, daunorubicin, doxorubicin, actinomycin D, valinomycin, Calcein AM	16259577, 17352537, 18287207, 20138191	
ABCB1	Ile849Met	rs36105130	A > G	0	0.005	0	ND	0	12893986	ND	study dependent: increased or reduced efflux	Sf9	Verapamil	16259577, 20138191	
ABCB1	Ala893Thr	rs2032582	G > A	0.02	0.041	0.4	0.59	0.37	1000 genomes	similar expression as reference	substrate-specific increase in efflux: verapamil	Sf9, HEK293, HEK293T	rhodamine 123, calcein AM, glycine, glutamic acid, dopamine, norepinephrine, epinephrine, GABA, histamine, serotonin, melatonin, verapamil, nifedipine, diltiazem, bepridil, fentanyl, prenylamine, nicarpidine, dexaamethasone, betamethasone, prednisone, cortisone, nicorandil, pinacidil, acetylsalicylic acid, indomethacin, acetaminophen, ibuprofen, naproxen, meprizole, vinblastine, etoposide, actinomycin D, daunorubicin, paclitaxel, methotrexate, doxorubicin, 5-fluorouracil, quinidine, PAH, penicillin G, tracrolimus, novobiocin	16259577, 18408562, 18287207, 20138191	***all studies use ala as the reference but dbSNP lists Ser as the reference,
ABCB1	Ala893Ser	rs2032582	G > T	0.001	0.02	0.13	0.05	0.06	1000 genomes	decreased cell surface expression	substrate-specific changes: decreased efflux of daunorubicin, doxorubicin, verapamil, diltiazem, bepridil, fentanyl, prenylamine, paclitaxel, tracrolimus, nicarpidine, dexaamethasone, betamethasone, prednisone, cortisone; increased efflux of digoxin, acetaminophen, naproxen, ibuprofen, meprizole, novobiocin, actinomycin D	HeLa, GP+E-86, Sf9, Yeast, HEK293, HEK293T	Bodipy-FL-Verapamil, Daunorubicin, Bodipy-FL-Vinblastine, Calcein AM, Bodipy-FL-Prazosin, Bisantrene, Bodipy-FL-Paclitaxel, Bodipy-FL-Forskolin, Digoxin, Daunorubicin, Actinomycin D, Valinomycin, rhodamine 123, glycine, glutamic acid, dopamine, norepinephrine, epinephrine, GABA, histamine, serotonin, melatonin, verapamil, nifedipine, diltiazem, bepridil, fentanyl, prenylamine, nicarpidine, dexaamethasone, betamethasone, prednisone, cortisone, nicorandil, pinacidil, acetylsalicylic acid, indomethacin, acetaminophen, ibuprofen, naproxen, meprizole, vinblastine, etoposide, actinomycin D, daunorubicin, paclitaxel, methotrexate, doxorubicin, 5-fluorouracil, quinidine, PAH, penicillin G, tracrolimus, novobiocin	12065748, 11503014, 15499164, 17352537, 18408562, 18287207, 20138191	***all studies use ala as the reference but dbSNP lists Ser as the reference
ABCB1	Met986Val	rs926081975	A > G	ND	ND	0.025 (Korean)	ND	ND	17225463	similar expression as reference	substrate-specific increase in efflux: verapamil	Sf9	Verapamil	15499164, 16259577, 20138191	
ABCB1	Ala999Thr	rs72552784	G > A	ND	ND	ND	ND	ND	ND	ND	substrate-specific increase in efflux: verapamil	Sf9	Verapamil	16259577	
ABCB1	Pro1051Ala	rs28401798	C > G	0.0017	0	0	0	0	ExAC	ND	similar efflux as reference	Sf9	Verapamil	16259577, 20138191	
ABCB1	Gly1063Ala	rs2707844	G > C	ND	ND	ND	ND	ND	ND	ND	substrate-specific increase in efflux: verapamil	Sf9	Verapamil	16259577, 20138191	
ABCB1	Trp1108Arg	rs35730308	T > C	0.0022	0	0	0	0.00009	ExAC	similar expression as reference	substrate-specific reduction in efflux: valinomycin, doxorubicin, daunorubicin	yeast	doxorubicin, daunorubicin, actinomycin D, valinomycin	17352537	
ABCB1	Ser1141Thr	rs2229107	T > A	0.068	0.00007	0	0.00001	0.0025	ExAC	similar expression as reference	substrate-specific changes: reduced efflux of daunorubicin, increased efflux of valinomycin	Yeast, HEK293T	daunorubicin, doxorubicin, actinomycin D, valinomycin, calcein AM	17352537, 18287207	
ABCB1	Val1251Ile	rs28364274	G > A	0.00048	0.00003	0.003	0	0.029	ExAC	similar expression as reference	substrate-specific increase in efflux: calcein AM	HEK293T	calcein AM	18287207	

Transporter	Amino Acid Change	Polymorphism (rsID)	Ref > Alt	Allele Frequency AFR (African)	Allele Frequency EUR (European)	Allele Frequency EAS (East Asian)	Allele Frequency SAS (South Asian)	Allele Frequency AMR (Ad Mixed American)	Allele frequency (Cohort)	In Vitro Effects (Expression)	In Vitro Effects (Uptake)	In Vitro Expression System	Substrates	References (PMID)
ABCC2	NA	rs369192412	G > -	0.05	0.08	0.37	0.04	0	gnomAD	reduced luciferase activity	ND	HepG2	NA	17502832
ABCC2	NA	rs17222653	G>A	0.002	0	0	0	0	1000 Genomes	no change in luciferase activity	ND	HepG2	NA	22664480
ABCC2	NA	rs1885301	A>G	0.57	0.58	0.75	0.56	0.64	1000 Genomes	no change in luciferase activity	ND	HepG2	NA	17502832
ABCC2	NA	rs17222667	A>G	0.02	0	0	0	0	1000 Genomes	no change in luciferase activity	ND	HepG2	NA	22664480
ABCC2	NA	rs17222646	G>A	0.02	0.003	0	0	0	1000 Genomes	no change in luciferase activity	ND	HepG2	NA	22664480
ABCC2	NA	rs17216128	C>A	0.01	0	0	0	0	1000 Genomes	ND	ND	ND	NA	22664480
ABCC2	NA	rs45593436	G>GG	0.005	0	0	0	NA	PMT	ND	ND	ND	NA	22664480
ABCC2	NA	rs7910642	G>A	0.13	0.08	0.27	0.1	0.14	1000 Genomes	no change in luciferase activity	ND	HepG2	NA	22664480
ABCC2	NA	rs2804402	A>G	0.32	0.4	0.25	0.44	0.36	1000 Genomes	no change in luciferase activity	ND	HepG2	NA	22664480
ABCC2	NA	rs17222533	C>A	0.0002	0	0	0	0	gnomAD	ND	ND	ND	NA	22664480
ABCC2	NA	rs17216135	G>A	0	0	0.004	0	0.001	1000 Genomes	no change in luciferase activity	ND	HepG2	NA	22664480
ABCC2	NA	rs717620	C>T	0.03	0.17	0.22	0.21	0.1	1000 Genomes	increased luciferase activity	ND	HepG2	NA	22664480, 17502832
ABCC2	NA	rs17216156	G>A	0.002	0	0.005	0	0	1000 Genomes	ND	ND	ND	NA	22664480
ABCC2	Phe39Tyr	rs927344	T > A	0.02	0	0	0	0.003	1000 genomes	similar expression as reference	similar efflux as reference	HEK293, Rht14-10	Glutathione-methylfluorescein, glutathione-monochlorobimane	22290738
ABCC2	Asp333Gly	rs17222674	A > G	0.003	0	0	0	0	1000 genomes	similar expression as reference	substrate-specific reduction of efflux: GS-MCB	HEK293, Rht14-10	Glutathione-methylfluorescein, glutathione-monochlorobimane	22290738
ABCC2	Arg353His	rs7080681	G > A	0.05	0.001	0	0	0.003	1000 genomes	similar expression as reference	substrate-specific reduction of efflux: GS-MCB	HEK293, Rht14-10	Glutathione-methylfluorescein, glutathione-monochlorobimane	22290738
ABCC2	Val417Ile	rs2273697	G > A	0.19	0.2	0.1	0.28	0.16	1000 genomes	similar expression as reference	substrate-specific changes in efflux: increased efflux of LTC4 and E217BG, reduced efflux of CDCF	HEK293T, Sf9, LLC-PK1, HEK293	5-6-carboxyfluorescein, Leukotriene C4, Estradiol-3-glucuronide, Estradiol-17-Glucuronide, tauroursodeoxycholic acid, 2,4-dinitrophenyl-S-glutathione, CDCF, Calcein AM	17502832, 21691255, 15180328, 28405913
ABCC2	Thr486Ile	rs17222589	C > T	0	0	0.01	0	0	1000 genomes	similar expression as reference	substrate-specific reduction of efflux: GS-MCB	HEK293, Rht14-10	Glutathione-methylfluorescein, glutathione-monochlorobimane	22290738
ABCC2	Ile670Thr	rs17222632	T > C	0.02	0	0	0	0	1000 genomes	similar expression as reference	similar efflux as reference	HEK293, Rht14-10	glutathione-methylfluorescein, glutathione-monochlorobimane	22290738
ABCC2	Arg768Trp	rs56199535	C > T	0	0.001	0	0	0	1000 genomes	reduced cell surface expression	substrate-specific reduction of efflux: 5-6-carboxyfluorescein	HEK293T, LLC-PK1	5-6-carboxyfluorescein	17502832, 15180328
ABCC2	Ser789Phe	rs56220353	C > T	0	0	0.01	0	0	1000 genomes	reduced cell surface expression	substrate-specific reduction of efflux: CDCF, Calcein AM, Leukotriene C4, Estradiol-3-glucuronide, Estradiol-17-Glucuronide, tauroursodeoxycholic acid, 2,4-dinitrophenyl-S-glutathione	Sf9, LLC-PK1, HEK293	Leukotriene C4, Estradiol-3-glucuronide, Estradiol-17-Glucuronide, tauroursodeoxycholic acid, 2,4-dinitrophenyl-S-glutathione, CDCF, Calcein AM	21691255, 15180328, 28405913
ABCC2	Gly921Ser	rs41318029	G > A	0.001	0.01	0	0.001	0	1000 genomes	similar expression as reference	substrate-specific reduction of efflux: GS-MCB	HEK293, Rht14-10	glutathione-methylfluorescein, glutathione-monochlorobimane	22290738
ABCC2	Ile1036Thr	rs45441199	T > C	0	0.01	0	0	0.001	1000 genomes	similar expression as reference	similar efflux as reference	HEK293, Rht14-10	glutathione-methylfluorescein, glutathione-monochlorobimane	22290738
ABCC2	Arg1174His	rs139188247	G > A	0.002	0.00005	0.0001	0.00006	0.00009	gnomADe	reduced cell surface expression	substrate-specific reduction in efflux: glutathione-methylfluorescein, glutathione-monochlorobimane	HEK293, Rht14-10	glutathione-methylfluorescein, glutathione-monochlorobimane	22290738
ABCC2	Arg1181Leu	rs8187692	G > T	0.12	0.003	0	0	0.009	1000 genomes	reduced cell surface expression	substrate-specific changes; reduced efflux of GS-MCB, increased efflux of GS-MF and Calcein AM	HEK293, Rht14-10	glutathione-methylfluorescein, glutathione-monochlorobimane, Calcein AM, CDCF	22290738, 28405913
ABCC2	Val1188Glu	rs17222723	T > A	0.06	0.07	0	0.02	0.04	1000 genomes	increased cell surface expression	substrate-specific increase in efflux: Calcein AM	HEK293	Calcein AM, CDCF	28405913
ABCC2	Asn1244Lys	rs757141905	T > G	0	0.00002	0.0004	0	0	gnomADe	similar expression as reference	substrate-specific reduction in efflux: glutathione-methylfluorescein, glutathione-monochlorobimane	HEK293, Rht14-10	glutathione-methylfluorescein, glutathione-monochlorobimane	22290738
ABCC2	Pro1291Leu	rs17216317	C > T	0.04	0.001	0	0	0.01	1000 genomes	similar expression as reference	substrate-specific changes; reduced efflux of GS-MCB	HEK293, Rht14-10	glutathione-methylfluorescein, glutathione-monochlorobimane	22290738
ABCC2	Ala1450Thr	NA	G > A	ND	ND	Singleton (Japanese)	ND	ND	Ito et al. (11266082)	reduced cell surface expression	substrate-specific reduction in efflux: LTC4, E2-3G, TUDC	Sf9, LLC-PK1	Leukotriene C4, Estradiol-3-glucuronide, Estradiol-17-Glucuronide, tauroursodeoxycholic acid, 2,4-dinitrophenyl-S-glutathione	21691255, 15180328
ABCC2	Thr1477Met	rs142573385	C > T	0	0	0	0.001	0.001	1000 genomes	reduced cell surface expression	substrate-specific reduction in efflux: E2-3G, increased Km and Vmax of TUDC	Sf9	Leukotriene C4, Estradiol-3-glucuronide, Estradiol-17-Glucuronide, tauroursodeoxycholic acid	21691255
ABCC2	Cys1515Tyr	rs8187710	G > A	0.16	0.07	0	0.02	0.05	1000 genomes	increased cell surface expression	substrate-specific changes: reduced efflux of lopinavir, calcein AM, CDCF; increased efflux of Calcein AM	HEK293	Lopinavir, Calcein AM, carboxyfluorescein diacetate	22027652, 28405913

Transporter	Amino Acid Change	Polymorphism (rsID)	Ref > Alt	Allele Frequency AFR (African)	Allele Frequency EUR (European)	Allele Frequency EAS (East Asian)	Allele Frequency SAS (South Asian)	Allele Frequency AMR (Ad Mixed American)	Allele frequency (Cohort)	In Vitro Effects (Expression)	In Vitro Effects (Uptake)	In Vitro Expression System	Substrates	References (PMID)
ABCG2	Val12Met	rs2231137	G > A	0.06	0.06	0.33	0.15	0.24	1000 genomes	similar expression as reference	similar efflux as reference	PA317, Flp-In-293, SF9 Vesicles	topotecan, mitoxantrone, SN-38, Doxorubicin, Daunorubicin, Vincristine, methotrexate, porphyrin	12479221, 17297656, 16608919
ABCG2	Gly51Cys	NA	G > T	ND	ND	0.001 (Japanese)	ND	ND	17373578	increased cell surface expression	reduced efflux	SF9 Vesicles	porphyrin, methotrexate	16608919
ABCG2	Gln126Ter	rs72552713	C > T	0	0	0.006	0	0	1000 genomes	Reduced cell surface expression	reduced efflux	SF9 Vesicles	porphyrins, methotrexate	16608919
ABCG2	Gln141Lys	rs2231142	C > A	0.01	0.09	0.29	0.1	0.14	1000 genomes	similar mRNA levels as reference, reduced cell surface expression	substrate-specific reduction in efflux: topotecan, mitoxantrone, SN-38, porphyrins, allopurinol, oxypurinol, glyburide	PA317, Flp-In-293, SF9 Vesicles, HEK293	topotecan, mitoxantrone, SN-38, Doxorubicin, Daunorubicin, Vincristine, Porphyrins, Methotrexate, allopurinol, oxypurinol, glyburide	12479221, 17297656, 16608919, 25676789, 20159988
ABCG2	Thr153Met	rs753759474	C > T	0.00007	0.00008	0.0001	0	0.00003	gnomADe	Reduced cell surface expression	similar efflux as reference	SF9 Vesicles	Porphyrins, Methotrexate	16608919
ABCG2	Gln166Glu	rs1061017	C > G	ND	ND	0.003 (Japanese)	ND	ND	17373578	Reduced cell surface expression	reduced efflux	SF9 Vesicles	Porphyrins, Methotrexate	16608919
ABCG2	Ile206Leu	rs12721643	A > C	0.00007	0.0002	0	0	0.0001	gnomADe	Reduced cell surface expression	reduced efflux	HEK293, SF9 vesicles	Mitoxantrone Phosphobide A, BODIPY-prazosin, topotecan, methotrexate, porphyrins	15743976, 16608919
ABCG2	Phe208Ser	rs1061018	T > C	ND	ND	0.003 (Japanese)	ND	ND	17373578	Similar mRNA levels, but reduced cell surface expression	reduced efflux	Flp-In-293 SF9 Vesicles	SN-38, mitoxantrone, doxorubicin, daunorubicin, vincristine, methotrexate, porphyrins	18237272, 17297656, 16608919
ABCG2	Ser248Pro	NA	T > C	ND	ND	0.005 (Japanese)	ND	ND	17373578	similar expression as reference	substrate-specific reduction in efflux: SN-38, mitoxantrone, doxorubicin, methotrexate, porphyrins	Flp-In-293, SF9 Vesicles	SN-38, mitoxantrone, doxorubicin, daunorubicin, vincristine, methotrexate, porphyrins	17297656, 16608919
ABCG2	Pro269Ser	rs34678167	C > T	0.00007	0	0.002	0	0	gnomADe	similar expression as reference	reduced efflux	SF9 vesicles	Methotrexate, estrone sulfate	17237154
ABCG2	Glu334Ter	rs3201997	G > T	ND	ND	ND	ND	ND	1000 genomes	Reduced cell surface expression	reduced efflux	SF9 vesicles	methotrexate, porphyrins	16608919
ABCG2	Gly406Arg	rs142628079	G > A	0	0	0.001	0	0	1000 genomes	Reduced cell surface expression	reduced efflux	HEK293, SF9 vesicles	Lucifer Yellow, estrone sulfate	28281205
ABCG2	Phe431Leu	NA	T > C	ND	ND	0.008 (Japanese)	ND	ND	18464048	Similar mRNA levels, but reduced cell surface expression	substrate-specific reduction in efflux: Lucifer Yellow, estrone sulfate, SN-38, mitoxantrone, doxorubicin, daunorubicin, methotrexate	HEK293, SF9 vesicles, Flp-In-293	Lucifer Yellow, estrone sulfate, SN-38, mitoxantrone, doxorubicin, daunorubicin, methotrexate, porphyrins, vincristine	28281205, 17297656, 16608919
ABCG2	Ser441Asn	NA	G > T	ND	ND	0.005 (Japanese)	ND	ND	18464048	Similar mRNA levels, but reduced cell surface expression	substrate-specific reduction in efflux: Lucifer Yellow, estrone sulfate, methotrexate, porphyrins	HEK293, SF9 vesicles, Flp-In-293	Lucifer Yellow, estrone sulfate, SN-38, mitoxantrone, doxorubicin, daunorubicin, vincristine, methotrexate, porphyrins	28281205, 18237272, 17297656, 16608919
ABCG2	Pro480Leu	rs202192122	C > T	0.00007	0.0002	0	0	0	gnomADe	Reduced cell surface expression	substrate-specific reduction in efflux: Lucifer Yellow, estrone sulfate	HEK293, SF9 vesicles	Lucifer Yellow, estrone sulfate	28281205
ABCG2	Phe489Leu	rs192169063	T > C	0	0	0.005	0	0	1000 genomes	Similar mRNA levels, but reduced cell surface expression	substrate-specific reduction in efflux: Lucifer Yellow, estrone sulfate, SN-38, mitoxantrone, methotrexate, porphyrins	HEK293, SF9 vesicles, Flp-In-293	Lucifer Yellow, estrone sulfate, SN-38, Mitoxantrone, Doxorubicin, Daunorubicin, Vincristine, methotrexate, porphyrins	28281205, 17297656, 16608919
ABCG2	Met515Arg	rs199806536	T > G	0	0	0	0	0.001	1000 genomes	Reduced cell surface expression	substrate-specific reduction in efflux: Lucifer Yellow, estrone sulfate	HEK293, SF9 vesicles	Lucifer Yellow, estrone sulfate	28281205
ABCG2	Leu525Arg	rs58818712	T > G	ND	ND	ND	ND	ND	1000 genomes	Reduced cell surface expression	substrate-specific reduction in efflux: Lucifer Yellow, estrone sulfate	HEK293, SF9 vesicles	Lucifer Yellow, estrone sulfate	28281205
ABCG2	Ala528Thr	rs45605536	G > A	0	0.007	0.001	0	0.001	1000 genomes	Reduced cell surface expression	substrate-specific reduction in efflux: Lucifer Yellow, estrone sulfate	HEK293, SF9 vesicles	Lucifer Yellow, estrone sulfate	28281205
ABCG2	Thr542Ala	rs35965584	A > G	0.004	0	0	0	0	1000 genomes	Reduced cell surface expression	substrate-specific reduction in efflux: Lucifer Yellow, estrone sulfate	HEK293, SF9 vesicles	Lucifer Yellow, estrone sulfate	28281205
ABCG2	Phe571Ile	rs9282571	T > A	ND	ND	ND	ND	ND	1000 genomes	similar expression as reference	similar efflux as reference	SF9 Vesicles	methotrexate, porphyrins	16608919
ABCG2	Asn590Tyr	rs34264773	A > T	0	0.001	0	0	0.001	1000 genomes	increased cell surface expression	substrate-specific reduction in efflux: Lucifer Yellow, estrone sulfate, SN-38, mitoxantrone, methotrexate	HEK293, SF9 vesicles	Mitoxantrone Phosphobide A, BODIPY-prazosin, topotecan, methotrexate, porphyrins	15743976
ABCG2	Asp620Asn	rs34783571	G > A	0	0.004	0	0.01	0.001	1000 genomes	increased cell surface expression	substrate-specific reduction in efflux: mitoxantrone, methoxyfluride, pheophorbide A, BODIPY-prazosin	HEK293, SF9 vesicles	Mitoxantrone Phosphobide A, BODIPY-prazosin, topotecan, methotrexate, porphyrins	15743976, 16608919