Michigan Genomics Initiative Data Freeze 4 Pharmacogene Star Allele and Activity Phenotype Inferences

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1 Data Description

The star allele nomenclature system is used to summarize variants into alleles for genes that interact with pharmaceuticals (pharmacogenes). Star alleles may be associated with inferred pharmacogene activity levels, which often follow consensus terms of ultrarapid, rapid, normal, intermediate, and poor metabolizer for enzymes and increased, normal, decreased, and poor function for transporters [1].

Pharmacogene star allele and activity phenotype inferences are available for 60,215 genotyped MGI participants in Data Freeze 4. These inferences cover 369 distinct star alleles across 51 pharmacogenes affecting drug response, including polymorphic enzymes (i.e., CYP2C9, UGT1A4, TPMT), and transporters (i.e., SLCO1B1).

Table S1 lists star alleles that are inferred for each pharmacogene available with this release in addition to highlighting star alleles that are not possible to infer due to missing genotype data in Freeze 4 (see section 4). The frequency of inferred activity phenotypes observed in participants included with Data Freeze 4 are listed in Table S2. The frequency of inferred star allele diplotypes observed in Data Freeze 4 and the activity phenotype assigned to each of these diplotypes are given in Table S3.

These data are available in a tab delimited format containing a row for each participant and columns for the inferred star allele diplotype, candidate star allele haplotypes, the core variants used to define each star allele (in build 38 coordinates), and the inferred activity phenotype. Most pharmacogene activity phenotypes in the available data follow Clinical Pharmacogenetics Implementation Consortium (CPIC) standardized pharmacogenetic terms [1].

To access these data, please apply through our ticketing system (submit a "Custom Data Request" in JIRA): https://doctrjira.med.umich.edu/. You will need to submit an IRB application through IRBMED to access these data, which you can apply for in eResearch Regulatory Management: https://its.umich.edu/academics-research/research/eresearch. For further assistance, please contact the Research Scientific Facilitators at phdatahelp@umich.edu, who can guide you through the data request process.

Gene	# Samples Compared	# Concordant Haplotypes	# Compared Haplotypes	Haplotype Concordance Rate [%]
CYP1A2	27	41	41	100
CYP2B6	11	13	13	100
CYP2D6	24	32	36	88.89
CYP2C19	16	18	19	94.74
CYP2C9	10	11	11	100
CYP3A4	3	3	3	100
UGT1A4	5	5	5	100
UGT2B15	21	28	28	100
TPMT	5	5	5	100

Table 1: Star allele haplotype concordance. Concordance rate between star allele haplotypes called by a commercial pharmacogenomic test platform and star allele haplotypes inferred as the main allele by Stargazer.

2 Data Production

Production and quality control of genotype data for participants of the MGI was described previously [2]. We used Stargazer v 1.1.5 to infer star allele diplotypes for each participant using single nucleotide variants and indels imputed from the Trans-Omics for Precision Medicine r2 panel with Rsq > 0.3 and MAF > 0.01% [3, 4].

For UGT1A1, TPMT, SLCO1B1, NUDT15, CYP3A5, CYP2D6, CYP2C9, CYP2C19, and CYP2B6 we translated inferred participant star allele diplotypes to inferred activity phenotypes based on PharmGKB "Diplotype-Phenotype Tables" that we accessed from https://www.pharmgkb.org/page/pgxGeneRef on 7/1/2021. We used PyPGx v 0.1.37 to infer participant activity phenotypes whenever PharmGKB-based diplotype to phenotype mappings were not available [5].

3 Data Quality Evaluation

3.1 Haplotype Concordance

For a small subset of MGI participants we evaluated concordance between star allele inferences made by Stargazer and star allele calls made by commercially available pharmacogenomics tests for CYP1A2, CYP2B6, CYP2D6, CYP2C19, CYP2C9, CYP3A4, UGT1A4, UGT2B15, and TPMT.

We found the mean star allele haplotype concordance rate across 9 evaluated pharmacogenes to be 98.18% with rates ranging from 88.89% to 100% (Table 1). We note that discordant haplotypes for CYP2D6 include calls made by the commercial test for 1 gene deletion (*5) and 1 duplication (*1xN). We do not currently consider copy number variation when inferring star alleles for MGI participants. For a detailed description of our haplotype concordance evaluation see subsection 5.1.

3.2 Activity Phenotype Frequency

We compared the frequency of inferred activity phenotypes in 44,861 European ancestry MGI participants of Data Freeze 4 that were unrelated to the 2nd degree to those estimated for Europeans by PharmGKB for UGT1A1, TPMT, NUDT15, CYP3A5, CYP2D6, CYP2C9, CYP2C19, and CYP2B6 (Figure 1, Table 2) [6]. When
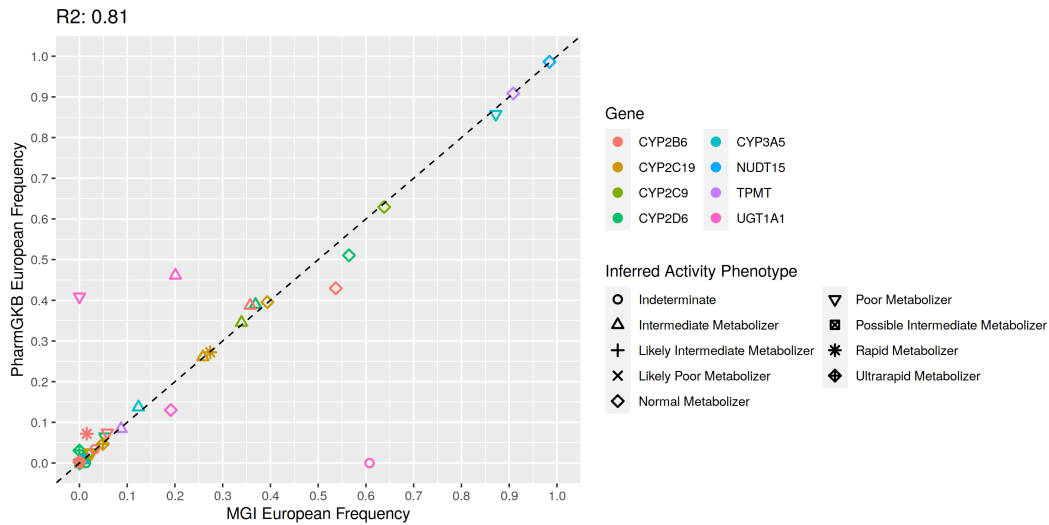
Figure 1: Comparison of pharmacogene activity phenotype frequency in MGI and PharmGKB. Comparison of frequency of inferred activity phenotypes in 44,861 unrelated European ancestry MGI participants of Data Freeze 4 to that estimated for Europeans by PharmGKB. R2, square of the Pearson correlation coefficient between inferred frequency observed in Data Freeze 4 and frequency estimated by PharmGKB across all 8 pharmacogenes compared here.

considering all 8 of these pharmacogenes, the square of the Pearson correlation coefficient between the frequency of activity phenotypes that were inferred in participants of Data Freeze 4 and estimated by PharmGKB was .81.

Notable is the relative low frequency of inferred UGT1A1 poor and intermediate metabolizers in Data Freeze 4 participants when compared to PharmGKB estimates. This is primarily driven by heterozygote and homozygous UGT1A1 *79 inferences in Data Freeze 4 which are inferred as indeterminate metabolizers by PyPGx. Consistent with PyPGx, the UGT Nomenclature Committee currently recognizes UGT1A1 *79, but does not assign a known enzyme activity level [7]. The UGT1A1 resource from PharmGKB that we used in this evaluation estimated activity phenotype frequency using only those UGT1A1 star alleles found in the CPIC guidance for Atazanavir, which includes *6, *27, *28, *37, *38, and *80, but not UGT1A1 *79 [7, 8].

Also notable is the relative low frequency of inferred CYP2D6 poor metabolizers and lack of CYP2D6 ultrarapid metabolizers in Data Freeze 4 when compared to PharmGKB estimates (Table 2). Inferred activity phenotype frequencies of CYP2D6 in Data Freeze 4 are likely to be affected by copy number variation [9].

4 Limitations of These Data

MGI genetic data may be missing core variants that define some star alleles, which may sometimes result in incorrectly inferred star alleles and activity phenotypes. We inferred star alleles for participants included in Data Freeze 4 using genotype data imputed from an array, which constrains the set of star alleles that are inferrable in MGI to only those star alleles defined by core variants that were all imputed in MGI data with Rsq > 0.3 and a MAF > 0.01%. For example CYP2B6 *4 (rs2279343) has an estimated frequency of 0.04 in Europeans, but is not contained in the genetic data used to infer star alleles in Data Freeze 4 [10]. Thus, no participant in Data Freeze 4 will be inferred to carry CYP2B6 *4, although true carriers of this star allele may exist in the MGI cohort.

Star alleles that are defined by duplications, deletions, or gene fusions are currently not inferred for MGI participants. Pharmacogenes that are characterized by extensive structural variation, such as CYP2D6, may result in incorrect star allele and activity phenotype inferences in MGI participants. Using this MGI service

3

Gene	Activity Phenotype	MGI EUR Frequency	PharmGKB EUR Frequency
CYP2B6	Ultrarapid Metabolizer	0.000111	0.003011
CYP2B6	Rapid Metabolizer	0.015225	0.071921
CYP2B6	Indeterminate	0.032055	0.034129
CYP2B6	Poor Metabolizer	0.058313	0.074285
CYP2B6	Intermediate Metabolizer	0.357482	0.387153
CYP2B6	Normal Metabolizer	0.536814	0.429502
CYP2C19	Likely Poor Metabolizer	0.000045	0.000203
CYP2C19	Likely Intermediate Metabolizer	0.000134	0.001117
CYP2C19	Indeterminate	0.000178	0.000009
CYP2C19	Poor Metabolizer	0.024676	0.023722
CYP2C19	Ultrarapid Metabolizer	0.049130	0.046821
CYP2C19	Intermediate Metabolizer	0.258376	0.260389
CYP2C19	Rapid Metabolizer	0.273890	0.272180
CYP2C19	Normal Metabolizer	0.393571	0.395558
CYP2C9	Indeterminate	0.000736	0.000000
CYP2C9	Poor Metabolizer	0.021466	0.025604
CYP2C9	Intermediate Metabolizer	0.339449	0.345150
CYP2C9	Normal Metabolizer	0.638350	0.629246
CYP2D6	Ultrarapid Metabolizer	0.000000	0.030752
CYP2D6	Indeterminate	0.013687	0.000000
CYP2D6	Poor Metabolizer	0.053075	0.064662
CYP2D6	Intermediate Metabolizer	0.368806	0.389469
CYP2D6	Normal Metabolizer	0.564432	0.510496
CYP3A5	Possible Intermediate Metabolizer	0.000000	0.000000
CYP3A5	Indeterminate	0.000000	0.000000
CYP3A5	Normal Metabolizer	0.004436	0.005491
CYP3A5	Intermediate Metabolizer	0.123604	0.137225
CYP3A5	Poor Metabolizer	0.871960	0.857283
NUDT15	Possible Intermediate Metabolizer	0.000000	0.000023
NUDT15	Poor Metabolizer	0.000067	0.000015
NUDT15	Indeterminate	0.005484	0.006049
NUDT15	Intermediate Metabolizer	0.010009	0.007605
NUDT15	Normal Metabolizer	0.984441	0.986308
TPMT	Possible Intermediate Metabolizer	0.000089	0.000244
TPMT	Indeterminate	0.001672	0.005269
TPMT	Poor Metabolizer	0.002363	0.001950
TPMT	Intermediate Metabolizer	0.087336	0.084179
TPMT	Normal Metabolizer	0.908540	0.908359
UGT1A1	Poor Metabolizer	0.000022	0.408677
UGT1A1	Normal Metabolizer	0.191369	0.130120
UGT1A1	Intermediate Metabolizer	0.201043	0.461203
UGT1A1	Indeterminate	0.607566	0.000000

Table 2: Pharmacogene activity phenotype frequency in MGI and PharmGKB. The frequency of inferred activity phenotypes in 44,861 unrelated European ancestry MGI participants and the estimated frequency of activity phenotypes in Europeans by PharmGKB. EUR, European.

to analyze star alleles for pharmacogenes where structural variation is not uncommon may require careful consideration.

Star allele and activity phenotype inferences for any given MGI Data Freeze may become outdated over time as these inferences are updated only upon release of a new Data Freeze.

We offer resources for investigators to examine the quality of these inferences on a per-allele and per-gene basis. Tables S1, S2, and S3, summarize the frequency of inferred star allele haplotypes, activity phenotypes, and diplotypes that we observe in MGI participants included in Data Freeze 4, respectively. Together these tables may inform on how well inferences are made for a given star allele or pharmacogene activity phenotype of interest.

References

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[5] Sbslee/pypgx: A Python package for pharmacogenomics research. https://github.com/sbslee/pypgx.

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[7] https://www.pharmacogenomics.pha.ulaval.ca/wp-content/uploads/2015/04/Exon2-51.htm.

[8] CPIC® Guideline for Atazanavir and UGT1A1. https://cpicpgx.org/guidelines/guideline-for-atazanavir-and-ugt1a1/.

[9] Del Tredici, A. L. *et al.* Frequency of CYP2D6 Alleles Including Structural Variants in the United States. *Frontiers in Pharmacology* **9** (2018).

[10] Gene-specific Information Tables for CYP2B6. https://www.pharmgkb.org/page/cyp2b6RefMaterials.

5 Supplementary Notes

5.1 Haplotype Concordance Evaluation Approach

We evaluated haplotype star allele concordance rate as the percentage of star allele haplotypes that were the same when called by a commercial pharmacogenomic test platform and inferred by Stargazer. To limit ambiguous comparisons, we evaluated only haplotypes where either Stargazer or the commercial test reported a non-reference star allele.

We considered so-called "sub-alleles" (star alleles that share core variants) concordant when missing data would prevent a perfect match between the Stargazer inference and commercial test. For example, the commercial test for CYP2B6 probes both *6 (rs2279343, rs3745274) and *9 (rs3745274). Freeze 4 contains data for the variant rs3745274, but is missing data for rs2279343, thus only CYP2B6 *9 may be inferred in Freeze 4 as some data needed to infer CYP2B6 *6 are missing. In this example, we would consider a CYP2B6 *9 inference by Stargazer concordant with a CYP2B6 *6 call by the commercial test.

For each haplotype, Stargazer reports a main star allele inference in addition to candidate star allele inferences that are also compatible with the participant's genotypes. We first evaluated haplotype concordance by only comparing between the commercial test call and the main star allele inference made by Stargazer (results in Table 1).

In a second, less stringent evaluation we considered haplotypes concordant if either the main or any candidate star allele haplotype inferred by Stargazer matched the commercial test result (Table S4).

6   Supplementary Tables

Gene	Allele	Core (build 38)	Inferred in MGI	Rsq	MAF
CYP4F2	*2	chr19:15897578:A>C	True	0.996917	0.17206
CYP4F2	*3	chr19:15879621:C>T	True	0.999863	0.277503
CFTR	*S1	chr7:117559591:TCTT>T	False		
CFTR	*S10	chr7:117614699:G>C	True	0.98958	0.00046
CFTR	*S11	chr7:117642528:G>A	True	0.964163	0.000853
CFTR	*S12	chr7:117590409:A>G	False		
CFTR	*S13	chr7:117534363:G>A	False		
CFTR	*S14	chr7:117509035:G>A	False		
CFTR	*S15	chr7:117594930:G>T	False		
CFTR	*S16	chr7:117611595:T>G	True	0.969053	0.000833
CFTR	*S17	chr7:117611663:T>A	False		
CFTR	*S18	chr7:117611646:G>A	True	0.949573	0.000283
CFTR	*S19	chr7:117642451:G>A	False		
CFTR	*S2	chr7:117602868:G>A	True	0.660953	0.000137
CFTR	*S20	chr7:117664770:G>A	False		
CFTR	*S21	chr7:117534318:G>A	False		
CFTR	*S22	chr7:117587806:G>A	True	0.99024	0.00041
CFTR	*S23	chr7:117587805:G>A	False		
CFTR	*S24	chr7:117509123:G>A	False		
CFTR	*S25	chr7:117611620:A>C	False		
CFTR	*S26	chr7:117535285:T>G	True	0.981547	0.00017
CFTR	*S27	chr7:117509069:C>T	False		
CFTR	*S28	chr7:117611650:G>A	False		
CFTR	*S29	chr7:117611649:C>T	False		
CFTR	*S3	chr7:117611555:A>G	True	0.762507	0.000103
CFTR	*S30	chr7:117530974:C>T	True	0.95518	0.00016
CFTR	*S31	chr7:117530975:G>A	True	0.992223	0.002187
CFTR	*S32	chr7:117540270:G>A	False		
CFTR	*S33	chr7:117540285:G>A	False		
CFTR	*S34	chr7:117509089:C>T	True	0.977667	0.00098
CFTR	*S35	chr7:117642472:G>A	False		
CFTR	*S36	chr7:117642483:T>C	False		
CFTR	*S37	chr7:117587800:G>A	False		
CFTR	*S38	chr7:117587799:A>C	False		

Gene	Allele	Core (build 38)	Inferred in MGI	Rsq	MAF
CFTR	*S39	chr7:117587801:T>G	False		
CFTR	*S4	chr7:117639961:C>T	True	0.55294	0.000197
CFTR	*S40	chr7:117603708:C>T	False		
CFTR	*S41	chr7:117606695:C>T	False		
CFTR	*S42	chr7:117627662:CT>C	False		
CFTR	*S43	chr7:117664769:G>A	False		
CFTR	*S44	chr7:117540284:C>T	False		
CFTR	*S5	chr7:117534366:G>T	False		
CFTR	*S6	chr7:117611640:G>A	False		
CFTR	*S7	chr7:117548795:C>A	False		
CFTR	*S8	chr7:117530955:C>A	False		
CFTR	*S9	chr7:117530953:G>C	False		
CYP2C8	*10	chr10:95042890:C>A	False		
CYP2C8	*11	chr10:95045951:C>A	False		
CYP2C8	*12	chr10:95037216:TCAA>T	False		
CYP2C8	*13	chr10:95058485:A>C	False		
CYP2C8	*14	chr10:95058442:C>G	False		
CYP2C8	*2	chr10:95058349:T>A	True	0.99918	0.012853
CYP2C8	*3	chr10:95067273:C>T,chr10:95038...	True	0.99576	0.104477
CYP2C8	*4	chr10:95058362:G>C	True	0.997563	0.047323
CYP2C8	*5	chr10:95067213:GT>G	False		
CYP2C8	*6	chr10:95064931:C>T	False		
CYP2C8	*7	chr10:95064886:G>A	True	0.97242	0.000293
CYP2C8	*8	chr10:95064886:G>C	False		
CYP2C8	*9	chr10:95058414:T>C	False		
CYP1A2	*10	chr15:74750240:G>C	False		
CYP1A2	*11	chr15:74750296:C>A	False		
CYP1A2	*12	chr15:74750372:A>T	False		
CYP1A2	*13	chr15:74751252:G>A	True	0.99393	0.00037
CYP1A2	*14	chr15:74754850:C>T	True	0.988123	0.00033
CYP1A2	*15	chr15:74749863:C>G	False		
CYP1A2	*16	chr15:74752211:G>A	False		
CYP1A2	*17	chr15:74753201:C>T,chr15:74749...	False	0.987067	0.300963
CYP1A2	*18	chr15:74753206:A>C	False		
CYP1A2	*19	chr15:74755066:G>A	False		
CYP1A2	*1C	chr15:74745879:G>A	True	0.984633	0.045863
CYP1A2	*1F	chr15:74749576:C>A	True	0.987067	0.300963
CYP1A2	*1K	chr15:74749000:T>G,chr15:74749...	True	0.897093	0.00258
CYP1A2	*1L	chr15:74745879:G>A,chr15:74747...	True	0.984633	0.045863
CYP1A2	*2	chr15:74749801:C>G	False		
CYP1A2	*20	chr15:74754843:G>A	True	0.966907	0.000173
CYP1A2	*21	chr15:74755022:C>A	False		
CYP1A2	*3	chr15:74751854:G>A	True	0.99806	0.00013
CYP1A2	*4	chr15:74752237:A>T	False		
CYP1A2	*5	chr15:74753234:G>A	False		
CYP1A2	*6	chr15:74754828:C>T	True	0.989377	0.000983
CYP1A2	*7	chr15:74753271:G>A	True	0.99215	0.00011
CYP1A2	*8	chr15:74754904:G>A	False		
CYP1A2	*9	chr15:74749986:C>T	False		
CYP26A1	*2	chr10:93074881:C>A	True	0.995633	0.003103
CYP26A1	*3	chr10:93074922:C>A	False		
CYP26A1	*4	chr10:93076616:T>C	False		
CYP26A1	*S1	chr10:93074387:G>C	False		
IFNL3	*S1	chr19:39248147:C>T	True	0.997353	0.330793

Gene	Allele	Core (build 38)	Inferred in MGI	Rsq	MAF
IFNL3	*S2	chr19:39252525:T>G	True	0.996653	0.186237
IFNL3	*S3	chr19:39241143:A>G	True	0.997377	0.31514
CYP3A7	*1B	chr7:99735407:G>A	True	0.901087	0.003603
CYP3A7	*1C	chr7:99735363:A>C,chr7:9973535...	False		
CYP3A7	*1D	chr7:99735184:C>T	True	0.994307	0.005877
CYP3A7	*1E	chr7:99735142:C>T	True	0.998573	0.007883
CYP3A7	*2	chr7:99709062:G>C	True	0.996453	0.12617
CYP3A7	*3	chr7:99731082:C>CA	False		
VKORC1	*2	chr16:31092475:A>G,chr16:31093...	True	0.99513	0.37086
VKORC1	*3	chr16:31091000:C>T	True	0.999887	0.3841
VKORC1	*4	chr16:31094032:G>A	True	0.999933	0.211977
VKORC1	*A41S	chr16:31094609:C>A	False		
VKORC1	*L128R	chr16:31091243:A>C	False		
VKORC1	*R58G	chr16:31094558:T>C	False		
VKORC1	*V29L	chr16:31094645:C>A	False		
VKORC1	*V45A	chr16:31094596:A>G	False		
VKORC1	*V66M	chr16:31093399:C>T	False		
CYP2S1	*2	chr19:41203611:C>T	True	0.97124	0.00037
CYP2S1	*3	chr19:41206370:C>T	True	0.78135	0.022583
CYP2S1	*4	chr19:41194548:G>A	False		
CYP2S1	*5	chr19:41198743:T>G	False		
UGT1A4	*2	chr2:233718890:C>A	True	0.989387	0.05002
UGT1A4	*3A	chr2:233718962:T>G,chr2:233718...	True	0.97805	0.092403
UGT1A4	*3B	chr2:233718962:T>G	True	0.97805	0.092403
UGT1A4	*4	chr2:233718851:C>T	True	0.931017	0.00334
UGT1A4	*5	chr2:233718946:CA>C	False		
UGT1A4	*6	chr2:233718993:CG>C	False		
UGT1A4	*7	chr2:233719268:T>C,chr2:233718...	False	0.97805	0.064623
UGT1A4	*8	chr2:233719688:G>T	False		
UGT1A4	*S3	chr2:233719112:C>T	True	0.434863	0.000103
TPMT	*10	chr6:18139027:C>G	False		
TPMT	*11	chr6:18139689:C>T	False		
TPMT	*12	chr6:18139710:G>A	True	0.726793	0.00031
TPMT	*13	chr6:18149045:T>A	False		
TPMT	*14	chr6:18149127:T>C	False		
TPMT	*15	chr6:18133890:C>T	False		
TPMT	*16	chr6:18138969:C>T	False		
TPMT	*17	chr6:18149004:G>C	False		
TPMT	*18	chr6:18147845:C>T	False		
TPMT	*19	chr6:18143597:T>G	False		
TPMT	*2	chr6:18143724:C>G	True	0.94199	0.00177
TPMT	*20	chr6:18130694:T>C	False		
TPMT	*21	chr6:18147851:G>C	False		
TPMT	*22	chr6:18138969:C>G	False		
TPMT	*23	chr6:18133884:G>C	False		
TPMT	*24	chr6:18133847:C>A	True	0.997347	0.001673
TPMT	*25	chr6:18130772:A>G	False		
TPMT	*26	chr6:18132136:A>G	False		
TPMT	*27	chr6:18143643:A>C	False		
TPMT	*28	chr6:18143613:C>G	False		
TPMT	*29	chr6:18149126:A>G	False		
TPMT	*30	chr6:18149022:C>T	False		
TPMT	*31	chr6:18132147:A>G	False		
TPMT	*32	chr6:18143622:C>T	False		

Gene	Allele	Core (build 38)	Inferred in MGI	Rsq	MAF
TPMT	*33	chr6:18138970:G>A	True	0.961067	0.000187
TPMT	*34	chr6:18143718:G>A	False		
TPMT	*35	chr6:18147856:A>G	False		
TPMT	*36	chr6:18132163:C>T	False		
TPMT	*37	chr6:18130758:A>T	False		
TPMT	*38	chr6:18133870:A>G	False		
TPMT	*39	chr6:18147838:G>A	False		
TPMT	*3A	chr6:18138997:C>T,chr6:1813068...	True	0.99943	0.036743
TPMT	*3B	chr6:18138997:C>T	True	0.99943	0.036743
TPMT	*3C	chr6:18130687:T>C	True	0.999923	0.0443
TPMT	*4	chr6:18130781:C>T	False		
TPMT	*40	chr6:18130729:C>T	True	0.376383	0.000153
TPMT	*41	chr6:18130687:T>G	False		
TPMT	*5	chr6:18147910:A>G	False		
TPMT	*6	chr6:18133845:T>A	False		
TPMT	*7	chr6:18130725:A>C	False		
TPMT	*8	chr6:18130762:C>T	True	0.98287	0.00139
TPMT	*9	chr6:18143606:T>G	True	0.957597	0.000393
CYP1B1	*11	chr2:38075218:C>G	False		
CYP1B1	*12	chr2:38075207:C>T	True	0.591627	0.000343
CYP1B1	*13	chr2:38074887:C>CA	False		
CYP1B1	*14	chr2:38074548:C>A	False		
CYP1B1	*15	chr2:38074520:C>CG	False		
CYP1B1	*17	chr2:38071277:TTCTGCCTGCACTC>T	True	0.732813	0.00027
CYP1B1	*18	chr2:38071261:C>A	False		
CYP1B1	*19	chr2:38071218:G>A	False		
CYP1B1	*2	chr2:38075034:C>A,chr2:3807524...	True	0.97586	0.302363
CYP1B1	*20	chr2:38071195:C>T	True	0.998383	0.000397
CYP1B1	*21	chr2:38071185:C>T	False		
CYP1B1	*22	chr2:38071147:TGGCATGAGG>TGGCA...	False		
CYP1B1	*23	chr2:38071044:G>A	False		
CYP1B1	*25	chr2:38070949:G>A	False		
CYP1B1	*26	chr2:38070926:AGAAAGTTCTTCGCCA...	False		
CYP1B1	*3	chr2:38071060:G>C	True	0.999783	0.440447
CYP1B1	*4	chr2:38070996:T>C	True	0.997633	0.171917
CYP1B1	*5	chr2:38071060:G>C,chr2:3807524...	True	0.978767	0.302363
CYP1B1	*6	chr2:38075034:C>A,chr2:3807106...	True	0.97586	0.302363
CYP1B1	*7	chr2:38075034:C>A,chr2:3807102...	True	0.97586	0.004273
CYP1B1	*8	chr2:38071033:C>G,chr2:3807106...	False	0.999783	0.440447
CYP1B1	*S1	chr2:38070963:G>GA	False		
CYP1B1	*S2	chr2:38074417:G>GAT	False		
CYP1B1	*S3	chr2:38071261:C>T	False		
CYP2C19	*10	chr10:94781858:C>T	True	0.96751	0.00023
CYP2C19	*11	chr10:94775507:G>A	True	0.856097	0.00532
CYP2C19	*12	chr10:94852914:A>C	False		
CYP2C19	*13	chr10:94849995:C>T	True	0.99148	0.001093
CYP2C19	*14	chr10:94762755:T>C	False		
CYP2C19	*15	chr10:94762760:A>C	True	0.974907	0.001653
CYP2C19	*16	chr10:94852765:C>T	False		
CYP2C19	*17	chr10:94761900:C>T	True	0.996617	0.21174
CYP2C19	*18	chr10:94842861:G>A	True	0.70564	0.000113
CYP2C19	*19	chr10:94762856:A>G	False		
CYP2C19	*2	chr10:94781859:G>A,chr10:94775...	True	0.99735	0.15471
CYP2C19	*22	chr10:94780574:G>C	True	0.99142	0.00015

Gene	Allele	Core (build 38)	Inferred in MGI	Rsq	MAF
CYP2C19	*23	chr10:94775160:G>C	False		
CYP2C19	*24	chr10:94842879:G>A	False		
CYP2C19	*25	chr10:94852785:C>G	False		
CYP2C19	*26	chr10:94781944:G>A	False		
CYP2C19	*28	chr10:94762760:A>C,chr10:94842...	False	0.974907	0.001653
CYP2C19	*29	chr10:94762788:A>T	False		
CYP2C19	*3	chr10:94780653:G>A	True	0.999883	0.0017
CYP2C19	*30	chr10:94775106:C>T	True	0.971257	0.000233
CYP2C19	*31	chr10:94775121:C>T	False		
CYP2C19	*32	chr10:94775185:A>G	False		
CYP2C19	*33	chr10:94780579:G>A	False		
CYP2C19	*34	chr10:94762715:T>C,chr10:94762...	False	0.61787	0.00011
CYP2C19	*35	chr10:94775367:A>G	True	0.99735	0.155693
CYP2C19	*4	chr10:94762706:A>G	True	0.72909	0.002677
CYP2C19	*5	chr10:94852738:C>T	False		
CYP2C19	*6	chr10:94775453:G>A	True	0.69201	0.00039
CYP2C19	*7	chr10:94781999:T>A	False		
CYP2C19	*8	chr10:94775416:T>C	True	0.99849	0.002553
CYP2C19	*9	chr10:94775489:G>A	True	0.952383	0.00098
CYP19A1	*2	chr15:51242798:A>G	True	0.988997	0.000853
CYP19A1	*3	chr15:51222375:G>A	True	0.998373	0.034337
CYP19A1	*4	chr15:51215771:G>A	True	0.998947	0.04859
CYP19A1	*5	chr15:51212492:A>G	False		
CYP4B1	*2	chr1:46815074:GAT>G	True	0.995433	0.13701
CYP4B1	*3	chr1:46813503:C>T	True	0.999737	0.135593
CYP4B1	*4	chr1:46815158:A>G	True	0.993113	0.012437
CYP4B1	*5	chr1:46815187:G>A	True	0.999867	0.165543
CYP4B1	*6	chr1:46815227:G>A,chr1:4681350...	False	0.999737	0.135593
NAT1	*10	chr8:18223142:A>C,chr8:1822313...	True	0.97203	0.263137
NAT1	*11	chr8:18223126:TAATAATAAA>T,chr...	False	0.999953	0.026113
NAT1	*14	chr8:18222607:G>A	True	0.99829	0.016693
NAT1	*15	chr8:18222606:C>T	True	0.996353	0.002817
NAT1	*16	chr8:18223142:A>C,chr8:1822313...	False	0.999857	0.28449
NAT1	*17	chr8:18222237:C>T	True	0.994747	0.005627
NAT1	*18	chr8:18223110:CAAA>C	False		
NAT1	*19	chr8:18222144:C>T	False		
NAT1	*20	chr8:18222449:T>C	True	0.85455	0.00024
NAT1	*21	chr8:18222660:A>G	False		
NAT1	*22	chr8:18222799:A>T	True	0.99915	0.003183
NAT1	*23	chr8:18222824:T>C	True	0.997117	0.001217
NAT1	*24	chr8:18222828:G>A	False		
NAT1	*25	chr8:18222834:A>G	False		
NAT1	*26	chr8:18223111:A>AAAT	False		
NAT1	*27	chr8:18222068:T>G,chr8:1822282...	True	0.997117	0.001217
NAT1	*28	chr8:18223129:TAATAAA>T	False		
NAT1	*29	chr8:18223072:TT>T,chr8:182231...	False	0.97203	0.263137
NAT1	*3	chr8:18223142:A>C	True	0.999857	0.28449
NAT1	*30	chr8:18222492:G>A	True	1.0	0.026113
NAT1	*5	chr8:18222544:GGG>CCC,chr8:182...	False		
CYP2A6	*10	chr19:40843827:C>A,chr19:40843...	False		0.00074
CYP2A6	*11	chr19:40847036:A>G	True	0.748887	0.000127
CYP2A6	*13	chr19:40850414:C>T,chr19:40850...	False	0.88185	0.071693
CYP2A6	*14	chr19:40850341:C>T	True	0.88224	0.0376
CYP2A6	*15	chr19:40848293:T>C,chr19:40850...	False	0.88185	0.071693

Gene	Allele	Core (build 38)	Inferred in MGI	Rsq	MAF
CYP2A6	*16	chr19:40848266:G>T	False		
CYP2A6	*17	chr19:40845362:C>T	True	0.9872	0.00683
CYP2A6	*18	chr19:40844759:T>A	True	0.836987	0.014217
CYP2A6	*19	chr19:40844759:T>A,chr19:40843...	False	0.836987	0.014217
CYP2A6	*2	chr19:40848628:A>T	True	0.882597	0.02452
CYP2A6	*20	chr19:40848284:CTT>C	True	0.87701	0.00074
CYP2A6	*21	chr19:40843854:T>C	True	0.8916	0.01197
CYP2A6	*22	chr19:40848633:G>C,chr19:40848...	False		
CYP2A6	*23	chr19:40848266:G>A	True	0.867053	0.001083
CYP2A6	*24	chr19:40849833:C>G,chr19:40843...	False	0.739087	0.0008
CYP2A6	*25	chr19:40848755:A>G	True	0.900243	0.000943
CYP2A6	*26	chr19:40848716:A>C,chr19:40848...	True	0.900243	0.0003
CYP2A6	*27	chr19:40848263:TGC>TA	False		
CYP2A6	*28	chr19:40844682:T>C,chr19:40844...	True	0.861143	0.001687
CYP2A6	*31	chr19:40850411:T>G	False		
CYP2A6	*35	chr19:40843969:T>A	False		
CYP2A6	*36	chr19:40843969:T>A,chr19:40843...	False		
CYP2A6	*37	chr19:40843969:T>A,chr19:40843...	False		0.00074
CYP2A6	*38	chr19:40845404:A>G	True	0.799157	0.000143
CYP2A6	*39	chr19:40849959:C>T	False		
CYP2A6	*40	chr19:40848660:G>C	False		
CYP2A6	*41	chr19:40846912:C>T	True	0.83462	0.00015
CYP2A6	*42	chr19:40846903:A>G	True	0.805857	0.00012
CYP2A6	*43	chr19:40846021:G>A	False		
CYP2A6	*44	chr19:40844682:T>C,chr19:40844...	False	0.861143	0.001687
CYP2A6	*45	chr19:40843896:A>G	False		
CYP2A6	*6	chr19:40848724:C>T	False		
CYP2A6	*7	chr19:40843869:A>G	False		
CYP2A6	*8	chr19:40843827:C>A	True		0.00074
CYP2A6	*9	chr19:40850474:A>C	True	0.88185	0.071693
CYP2A6	*S4	chr19:40843969:T>A,chr19:40850...	False	0.88185	0.071693
CYP2A6	*S5	chr19:40844759:T>A,chr19:40850...	True	0.836987	0.014217
CYP2A6	*S7	chr19:40849860:G>A	False		
CYP17A1	*S1	chr10:102830742:C>T	False		
CYP17A1	*S10	chr10:102830979:A>C	False		
CYP17A1	*S11	chr10:102830982:C>T	False		
CYP17A1	*S12	chr10:102830983:G>A	False		
CYP17A1	*S13	chr10:102831525:G>C	False		
CYP17A1	*S14	chr10:102831535:A>G	False		
CYP17A1	*S15	chr10:102832532:T>A	False		
CYP17A1	*S16	chr10:102832533:G>C	False		
CYP17A1	*S17	chr10:102832533:G>T	False		
CYP17A1	*S18	chr10:102832565:C>T	False		
CYP17A1	*S19	chr10:102832566:G>A	False		
CYP17A1	*S2	chr10:102830743:G>A	False		
CYP17A1	*S20	chr10:102832577:C>T	False		
CYP17A1	*S21	chr10:102832587:C>T	False		
CYP17A1	*S22	chr10:102832596:GGAG>G	False		
CYP17A1	*S23	chr10:102832610:C>T	False		
CYP17A1	*S24	chr10:102832611:G>A	False		
CYP17A1	*S25	chr10:102832626:G>T	False		
CYP17A1	*S26	chr10:102832655:A>G	False		
CYP17A1	*S27	chr10:102832656:TCTC>T	False		
CYP17A1	*S28	chr10:102832665:A>C	False		

Gene	Allele	Core (build 38)	Inferred in MGI	Rsq	MAF
CYP17A1	*S29	chr10:102833048:T>C	False		
CYP17A1	*S3	chr10:102830761:TGAAAGAGTC>T	False		
CYP17A1	*S30	chr10:102834850:A>T	False		
CYP17A1	*S31	chr10:102834918:A>T	False		
CYP17A1	*S32	chr10:102834922:T>C	False		
CYP17A1	*S33	chr10:102834930:G>T	False		
CYP17A1	*S34	chr10:102835316:C>T	False		
CYP17A1	*S35	chr10:102835343:T>A	False		
CYP17A1	*S36	chr10:102835350:A>C	False		
CYP17A1	*S37	chr10:102835353:C>CGAT	False		
CYP17A1	*S38	chr10:102835359:C>T	False		
CYP17A1	*S39	chr10:102835374:A>C	False		
CYP17A1	*S4	chr10:102730530:A>G	False		
CYP17A1	*S40	chr10:102835374:A>G	False		
CYP17A1	*S41	chr10:102835374:A>T	False		
CYP17A1	*S42	chr10:102837076:G>A	False		
CYP17A1	*S43	chr10:102837084:A>C	False		
CYP17A1	*S44	chr10:102837093:C>T	False		
CYP17A1	*S45	chr10:102837171:T>G	False		
CYP17A1	*S46	chr10:102837199:TGAA>T	False		
CYP17A1	*S47	chr10:102837258:G>A	False		
CYP17A1	*S5	chr10:102830871:A>G	False		
CYP17A1	*S6	chr10:102830910:C>T	False		
CYP17A1	*S7	chr10:102830911:G>A	False		
CYP17A1	*S8	chr10:102830928:G>A	False		
CYP17A1	*S9	chr10:102830946:G>A	False		
CYP2W1	*2	chr7:985219:G>A	True	0.998333	0.064897
CYP2W1	*3	chr7:983384:A>C	False		
CYP2W1	*4	chr7:988643:G>A	True	0.97625	0.00199
CYP2W1	*5	chr7:988643:G>A,chr7:988795:G>...	False	0.97625	0.00199
CYP2W1	*6	chr7:988812:C>T	True	0.98577	0.18969
XPC	*S1	chr3:14145949:G>T	True	0.999847	0.395493
XPC	*S2	chr3:14158387:G>A	True	0.99949	0.234297
CYP3A5	*2	chr7:99652613:G>T	True	0.998313	0.004943
CYP3A5	*3	chr7:99672916:T>C	True	0.96955	0.121937
CYP3A5	*4	chr7:99665237:T>C	False		
CYP3A5	*5	chr7:99666950:A>G	True	0.984137	0.00016
CYP3A5	*6	chr7:99665212:C>T	True	0.999923	0.00932
CYP3A5	*7	chr7:99652770:T>TA	True	0.987523	0.007013
CYP3A5	*8	chr7:99676198:G>A	False		
CYP3A5	*9	chr7:99660516:C>T	False		
CYP1A1	*10	chr15:74720599:G>A	True	0.95681	0.000167
CYP1A1	*11	chr15:74720553:G>C	True	0.95555	0.00014
CYP1A1	*12	chr15:74722914:C>G	True	0.707827	0.00012
CYP1A1	*13	chr15:74722964:C>T	True	0.995077	0.003477
CYP1A1	*2A	chr15:74719300:A>G	True	0.988863	0.127143
CYP1A1	*2B	chr15:74720644:T>C,chr15:74719...	True	0.988863	0.04744
CYP1A1	*2C	chr15:74720644:T>C	True	0.998917	0.04744
CYP1A1	*3	chr15:74719894:A>G	False		
CYP1A1	*4	chr15:74720646:G>T	True	0.99858	0.04098
CYP1A1	*5	chr15:74720638:G>T	True	0.935113	0.00693
CYP1A1	*6	chr15:74721463:C>A	False		
CYP1A1	*7	chr15:74720752:C>CA	False		
CYP1A1	*8	chr15:74720685:A>T	False		

Gene	Allele	Core (build 38)	Inferred in MGI	Rsq	MAF
CYP1A1	*9	chr15:74720638:G>A	False		
CYP1A1	*S1	chr15:74721236:G>A	False		
SLC15A2	*2	chr3:121929321:G>A,chr3:121924...	True	0.99742	0.453973
SLC15A2	*S1	chr3:121911667:G>A	False		
SLC22A2	*2	chr6:160258368:C>A	True	0.993363	0.39072
SLC22A2	*3	chr6:160224800:C>T	True	0.999813	0.239923
SLC22A2	*4	chr6:160242437:A>G	True	0.682123	0.001213
SLC22A2	*5	chr6:160256651:A>G	False		
SLC22A2	*6	chr6:160249250:A>C	True	0.999677	0.10493
SLC22A2	*7	chr6:160243653:G>A	True	0.991787	0.00096
SLC22A2	*8	chr6:160250552:G>A	True		0.000113
SLC22A2	*K432Q	chr6:160242388:T>G	True	0.998043	0.002097
NAT2	*10	chr8:18400502:G>A	False		
NAT2	*11	chr8:18400484:C>T	True	0.999737	0.40936
NAT2	*12	chr8:18400806:G>A	True	0.99986	0.416643
NAT2	*13	chr8:18400285:C>T	True	0.986517	0.32401
NAT2	*14	chr8:18400194:G>A	True	0.997107	0.0061
NAT2	*17	chr8:18400437:A>C	False		
NAT2	*18	chr8:18400848:A>C	False		
NAT2	*19	chr8:18400193:C>T	False		
NAT2	*20	chr8:18400603:A>G	False		
NAT2	*21	chr8:18400461:C>T	False		
NAT2	*22	chr8:18400612:G>T	True	0.99707	0.000683
NAT2	*23	chr8:18400073:T>A	True	0.87407	0.000113
NAT2	*24	chr8:18400406:C>G	True	0.997623	0.000773
NAT2	*25	chr8:18400668:T>G	False		
NAT2	*5	chr8:18400344:T>C	True	0.982917	0.423633
NAT2	*6	chr8:18400593:G>A	True	0.999877	0.284647
NAT2	*7	chr8:18400860:G>A	True	0.999437	0.030997
CYP2E1	*2	chr10:133528530:G>A	False		
CYP2E1	*3	chr10:133537760:G>A	True	0.982513	0.002193
CYP2E1	*4	chr10:133532171:G>A	True	0.995737	0.035913
CYP2E1	*5	chr10:133526101:G>C,chr10:1335...	True	0.963173	0.032213
CYP2E1	*6	chr10:133535369:T>A	False		
CYP2E1	*7	chr10:133527063:A>T	False		
CYP2C9	*10	chr10:94949280:A>G	False		
CYP2C9	*11	chr10:94981224:C>T	True	0.998073	0.003347
CYP2C9	*12	chr10:94989020:C>T	True	0.995873	0.00242
CYP2C9	*13	chr10:94941958:T>C	False		
CYP2C9	*14	chr10:94942234:G>A	True	0.51945	0.000247
CYP2C9	*15	chr10:94947782:C>A	False		
CYP2C9	*16	chr10:94972179:A>G	False		
CYP2C9	*17	chr10:94981365:C>T	False		
CYP2C9	*18	chr10:94986073:A>C,chr10:94981...	False	0.998183	0.063027
CYP2C9	*19	chr10:94988917:G>C	False		
CYP2C9	*2	chr10:94942290:C>T	True	0.99671	0.117043
CYP2C9	*20	chr10:94941897:G>C	False		
CYP2C9	*21	chr10:94938771:C>T	True	0.6173	0.000163
CYP2C9	*22	chr10:94938803:A>G	False		
CYP2C9	*23	chr10:94941915:G>A	False		
CYP2C9	*24	chr10:94981281:G>A	False		
CYP2C9	*25	chr10:94942212:AAGAAATGGAA>A	False		
CYP2C9	*26	chr10:94942249:C>G	False		
CYP2C9	*27	chr10:94942309:G>T	False		

Gene	Allele	Core (build 38)	Inferred in MGI	Rsq	MAF
CYP2C9	*28	chr10:94947938:A>T	False		
CYP2C9	*29	chr10:94972119:C>A	True	0.999583	0.000287
CYP2C9	*3	chr10:94981296:A>C	True	0.998183	0.063027
CYP2C9	*30	chr10:94988984:G>A	False		
CYP2C9	*31	chr10:94981201:T>C	False		
CYP2C9	*32	chr10:94989023:G>T	False		
CYP2C9	*33	chr10:94942255:G>A	False		
CYP2C9	*34	chr10:94981225:G>A	False		
CYP2C9	*35	chr10:94942234:G>A,chr10:94942...	True	0.51945	0.000247
CYP2C9	*36	chr10:94938683:A>G	True	0.73268	0.000483
CYP2C9	*37	chr10:94938828:A>G	False		
CYP2C9	*38	chr10:94941976:G>C	False		
CYP2C9	*39	chr10:94941982:G>T	False		
CYP2C9	*4	chr10:94981297:T>C	False		
CYP2C9	*40	chr10:94942018:T>C	False		
CYP2C9	*41	chr10:94942216:A>G	False		
CYP2C9	*42	chr10:94942231:G>A	False		
CYP2C9	*43	chr10:94942230:C>T	False		
CYP2C9	*44	chr10:94942249:C>T	True	0.458357	0.0001
CYP2C9	*45	chr10:94942254:C>T	True	0.500577	0.00024
CYP2C9	*46	chr10:94942305:G>A	False		
CYP2C9	*47	chr10:94947785:C>T	False		
CYP2C9	*48	chr10:94947917:T>C	False		
CYP2C9	*49	chr10:94949129:A>G	False		
CYP2C9	*5	chr10:94981301:C>G	True	0.992103	0.000847
CYP2C9	*50	chr10:94949144:C>T	False		
CYP2C9	*51	chr10:94972134:A>G	False		
CYP2C9	*52	chr10:94972180:C>G	False		
CYP2C9	*53	chr10:94972233:C>T	False		
CYP2C9	*54	chr10:94981250:C>A	False		
CYP2C9	*55	chr10:94981302:C>A	False		
CYP2C9	*56	chr10:94986042:A>G	False		
CYP2C9	*57	chr10:94947907:A>C	False		
CYP2C9	*58	chr10:94981230:C>A	False		
CYP2C9	*59	chr10:94988855:A>T	False		
CYP2C9	*6	chr10:94949281:GA>G	True	0.994717	0.00077
CYP2C9	*60	chr10:94988955:T>C	False		
CYP2C9	*61	chr10:94942290:C>T,chr10:94988...	False	0.99671	0.117043
CYP2C9	*62	chr10:94942233:C>T	False		
CYP2C9	*7	chr10:94938737:C>A	False		
CYP2C9	*8	chr10:94942309:G>A	True	0.981077	0.00404
CYP2C9	*9	chr10:94949217:A>G	True	0.999373	0.004953
CYP2C9	*S1	chr10:94981368:A>T	False		
CYP2C9	*S2	chr10:94981191:C>T	False		
UGT2B7	*2	chr4:69098620:T>C	True	0.995973	0.492207
UGT2B7	*3	chr4:69096731:G>T	True	0.987687	0.003983
UGT2B7	*4	chr4:69108204:G>A	False		
CYP2A13	*10	chr19:41088545:G>A,chr19:41091...	False	0.955293	0.023393
CYP2A13	*2	chr19:41088545:G>A,chr19:41091...	True	0.955293	0.023393
CYP2A13	*3	chr19:41090100:G>GCCA,chr19:41...	True	0.91523	0.000427
CYP2A13	*4	chr19:41089050:G>A	False		
CYP2A13	*5	chr19:41095814:T>A	False		
CYP2A13	*6	chr19:41095936:C>T	True	0.834713	0.000207
CYP2A13	*7	chr19:41089049:C>T	True	0.68635	0.007963

Gene	Allele	Core (build 38)	Inferred in MGI	Rsq	MAF
CYP2A13	*8	chr19:41090177:C>G	True	0.91523	0.007723
CYP2A13	*9	chr19:41093765:G>T	False		
UGT2B15	*2	chr4:68670366:A>C	True	0.999323	0.48984
UGT2B15	*3	chr4:68670362:A>G	False		
UGT2B15	*4	chr4:68647129:T>G	True	0.964053	0.407643
UGT2B15	*5	chr4:68670366:A>C,chr4:6864712...	True	0.964053	0.407643
UGT2B15	*6	chr4:68655133:G>A	True	0.893983	0.002243
UGT2B15	*7	chr4:68655133:G>A,chr4:6864712...	True	0.893983	0.002243
UGT2B15	*S2	chr4:68647145:G>A	True	0.83201	0.000823
SLCO1B1	*10	chr12:21239077:A>G	False		
SLCO1B1	*11	chr12:21239113:A>G	False		
SLCO1B1	*12	chr12:21239077:A>G,chr12:21172...	False		
SLCO1B1	*13	chr12:21174595:T>C,chr12:21239...	False		
SLCO1B1	*14	chr12:21176879:C>A,chr12:21176...	True	0.99959	0.147233
SLCO1B1	*15	chr12:21178615:T>C,chr12:21176...	True	0.99959	0.14882
SLCO1B1	*16	chr12:21176868:A>G	True	0.979803	0.000123
SLCO1B1	*17	chr12:21130388:G>A,chr12:21178...	True	0.986317	0.06002
SLCO1B1	*18	chr12:21178672:T>G,chr12:21176...	False	0.99959	0.144363
SLCO1B1	*19	chr12:21239042:A>C,chr12:21178...	True	0.9993	0.052853
SLCO1B1	*1B	chr12:21176804:A>G	True	0.99959	0.43857
SLCO1B1	*2	chr12:21172782:T>C	False		
SLCO1B1	*20	chr12:21239042:A>C,chr12:21178...	True	0.9993	0.052853
SLCO1B1	*21	chr12:21130388:G>A,chr12:21178...	True	0.986317	0.06002
SLCO1B1	*22	chr12:21239042:A>C	True	0.9993	0.052853
SLCO1B1	*23	chr12:21172776:G>A	True	0.49382	0.0001
SLCO1B1	*24	chr12:21196951:A>G,chr12:21176...	True	0.99959	0.002687
SLCO1B1	*25	chr12:21196976:G>A,chr12:21176...	True	0.996623	0.000223
SLCO1B1	*26	chr12:21202664:G>A	True	0.950627	0.00013
SLCO1B1	*27	chr12:21202555:C>G,chr12:21176...	True	0.99919	0.00345
SLCO1B1	*28	chr12:21196976:G>A,chr12:21196...	True	0.996623	0.000223
SLCO1B1	*29	chr12:21239158:C>T,chr12:21176...	False	0.99959	0.43857
SLCO1B1	*3	chr12:21174595:T>C,chr12:21176...	False		
SLCO1B1	*30	chr12:21178957:A>G,chr12:21176...	True	0.987213	0.00075
SLCO1B1	*31	chr12:21176804:A>G,chr12:21205...	True	0.99649	0.002353
SLCO1B1	*32	chr12:21176879:C>A,chr12:21196...	True	0.99959	0.002687
SLCO1B1	*33	chr12:21196951:A>G,chr12:21196...	False	0.996623	0.000223
SLCO1B1	*34	chr12:21239145:C>T	False		
SLCO1B1	*35	chr12:21239042:A>C,chr12:21176...	True	0.9993	0.052853
SLCO1B1	*36	chr12:21202553:T>G	False		
SLCO1B1	*4	chr12:21176879:C>A	True	0.99998	0.147233
SLCO1B1	*5	chr12:21178615:T>C	True	0.999717	0.14882
SLCO1B1	*6	chr12:21200595:T>C	False		
SLCO1B1	*7	chr12:21202649:A>G	True		0.000137
SLCO1B1	*8	chr12:21205921:A>G	False		
SLCO1B1	*9	chr12:21205999:G>C	True	0.99649	0.002353
SLCO1B1	*S1	chr12:21196975:C>T	True	0.611597	0.0001
SLCO1B1	*S2	chr12:21176898:G>T	True	0.991173	0.001947
SLCO1B1	*S4	chr12:21222355:C>T	True		0.001593
ABCB1	*2	chr7:87550285:A>G,chr7:8750932...	True	0.992033	0.425033
SLCO1B3	*S1	chr12:20862826:G>A	True	0.99997	0.177153
POR	*10	chr7:75985688:C>T,chr7:7598595...	False	0.99974	0.278973
POR	*11	chr7:75979557:C>T	True	0.722897	0.000213
POR	*12	chr7:75980396:A>G	False		
POR	*13	chr7:75980430:A>G	False		

Gene	Allele	Core (build 38)	Inferred in MGI	Rsq	MAF
POR	*14	chr7:75982279:A>G	False		
POR	*15	chr7:75985184:T>C	False		
POR	*16	chr7:75985795:G>A	False		
POR	*17	chr7:75985947:T>C	False		
POR	*18	chr7:75986189:C>T	False		
POR	*19	chr7:75986374:TTCT>T	False		
POR	*2	chr7:75985179:G>A	False		
POR	*20	chr7:75981111:C>CTACGTGGACAAGC	False		
POR	*21	chr7:75985731:C>CTGCCCATGTTCGT...	False		
POR	*22	chr7:75985799:T>TCCTTCAAGGCCAC...	False		
POR	*23	chr7:75985801:G>GC	False		
POR	*24	chr7:75985157:C>CGAGC	False		
POR	*25	chr7:75954139:G>C	False		
POR	*26	chr7:75985067:C>A	False		
POR	*27	chr7:75985983:T>C	True	0.98939	0.001153
POR	*28	chr7:75985688:C>T	True	0.99974	0.278973
POR	*29	chr7:75981102:G>C	True	0.952377	0.000397
POR	*3	chr7:75981607:G>A	False		
POR	*30	chr7:75985148:C>A	False		
POR	*31	chr7:75981132:C>T	False		
POR	*32	chr7:75985195:C>CATCGCC,chr7:7...	False	0.99974	0.278973
POR	*33	chr7:75985688:C>T,chr7:7598617...	False	0.99974	0.278973
POR	*34	chr7:75985986:A>G	False		
POR	*35	chr7:75985991:G>C	False		
POR	*36	chr7:75985688:C>T,chr7:7598155...	True	0.9929	0.003567
POR	*37	chr7:75986234:G>A,chr7:7598568...	True	0.988337	0.001343
POR	*38	chr7:75954134:AG>A	False		
POR	*39	chr7:75985844:AG>A	False		
POR	*4	chr7:75985655:T>A	False		
POR	*40	chr7:75983831:CGTC>C,chr7:7598...	False	0.99974	0.278973
POR	*42	chr7:75984947:G>A	True	0.616613	0.000173
POR	*43	chr7:75986413:G>A	False		
POR	*44	chr7:75979517:T>C	False		
POR	*45	chr7:75980462:G>A	True	0.97737	0.000703
POR	*46	chr7:75981102:G>A	True	0.76735	0.00019
POR	*47	chr7:75983820:G>A	False		
POR	*48	chr7:75984903:A>C	False		
POR	*5	chr7:75983548:G>C	True	0.97672	0.000287
POR	*6	chr7:75985959:G>A	False		
POR	*7	chr7:75986165:G>T	False		
POR	*8	chr7:75981072:T>G	False		
POR	*9	chr7:75985138:C>CC	False		
NUDT15	*10	chr13:48037748:T>C	False		
NUDT15	*11	chr13:48037885:G>A	False		
NUDT15	*12	chr13:48037902:C>G	False		
NUDT15	*13	chr13:48041103:T>TG	False		
NUDT15	*14	chr13:48037825:C>CGCGG	True	0.767747	0.000127
NUDT15	*15	chr13:48045771:T>A	True	0.948077	0.000113
NUDT15	*16	chr13:48037834:C>T	False		
NUDT15	*17	chr13:48041113:G>T	False		
NUDT15	*18	chr13:48040977:GA>G	False		
NUDT15	*19	chr13:48037749:G>C	False		
NUDT15	*2	chr13:48045719:C>T,chr13:48037...	True	0.903357	0.004987
NUDT15	*3	chr13:48045719:C>T	True	0.99772	0.007197

Gene	Allele	Core (build 38)	Inferred in MGI	Rsq	MAF
NUDT15	*4	chr13:48045720:G>A	True	0.987237	0.00054
NUDT15	*5	chr13:48037798:G>A	True	0.976153	0.000347
NUDT15	*6	chr13:48037782:A>AGGAGTC	True	0.903357	0.004987
NUDT15	*7	chr13:48037847:G>C	False		
NUDT15	*8	chr13:48037849:A>G	False		
NUDT15	*9	chr13:48037782:AGGAGTC>A	True	0.67556	0.00207
CYP3A43	*1B	chr7:99861633:C>T	True	0.997273	0.100533
CYP3A43	*2A	chr7:99836454:TA>T	True	0.991517	0.053213
CYP3A43	*2B	chr7:99836454:TA>T,chr7:998599...	True	0.991517	0.053213
CYP3A43	*3	chr7:99859982:C>G	True	0.9994	0.07141
CYP3A43	*S1	chr7:99855666:T>A	False		
CYP2F1	*2	chr19:41116202:G>GC	True	0.985433	0.20071
CYP2F1	*3	chr19:41122109:G>C,chr19:41121...	False	0.94875	0.066723
CYP2F1	*4	chr19:41121963:G>A,chr19:41116...	True	0.967627	0.048853
CYP2F1	*5	chr19:41125512:T>C	False		
CYP2F1	*6	chr19:41116576:G>C	True	0.993763	0.013967
CYP2J2	*10	chr1:59915967:G>A	False		
CYP2J2	*2	chr1:59912258:T>C	False		
CYP2J2	*3	chr1:59912213:G>A	False		
CYP2J2	*4	chr1:59911717:A>T	False		
CYP2J2	*5	chr1:59905038:C>T	True	0.963883	0.000217
CYP2J2	*6	chr1:59901085:T>A	False		
CYP2J2	*7	chr1:59926822:C>A	True	0.988913	0.071737
CYP2J2	*8	chr1:59907855:C>T	False		
CYP2J2	*9	chr1:59905010:G>A	True	0.58438	0.0001
CYP2B6	*10	chr19:40991369:C>T,chr19:40991...	True	0.876373	0.004807
CYP2B6	*11	chr19:40991441:A>G	True	0.994453	0.003403
CYP2B6	*12	chr19:41004125:G>A	True	0.844627	0.000193
CYP2B6	*13	chr19:41009358:A>G,chr19:41004...	False	0.8069	0.003937
CYP2B6	*14	chr19:41004381:G>A	True	0.89335	0.00427
CYP2B6	*15	chr19:41012693:T>A	True	0.993763	0.00701
CYP2B6	*16	chr19:41009358:A>G,chr19:41012...	False	0.993783	0.00469
CYP2B6	*17	chr19:40991389:CCG>C,chr19:409...	False	0.954567	0.001723
CYP2B6	*18	chr19:41012316:T>C	True	0.993783	0.00469
CYP2B6	*19	chr19:41009358:A>G,chr19:41006...	False	0.948507	0.000297
CYP2B6	*2	chr19:40991369:C>T	True	0.98509	0.05179
CYP2B6	*20	chr19:41006936:G>T,chr19:41006...	False	0.976347	0.25168
CYP2B6	*21	chr19:41012803:C>A	False		
CYP2B6	*22	chr19:40991224:T>C	True	0.966687	0.011547
CYP2B6	*23	chr19:41016726:A>G	False		
CYP2B6	*24	chr19:41016778:G>A	False		
CYP2B6	*25	chr19:41016805:A>T	False		
CYP2B6	*26	chr19:41009358:A>G,chr19:41006...	False	0.976347	0.25168
CYP2B6	*27	chr19:41007013:T>C	False		
CYP2B6	*28	chr19:41012465:C>T,chr19:41010...	False	0.886233	0.00015
CYP2B6	*3	chr19:41009350:C>A	True	0.987527	0.002257
CYP2B6	*31	chr19:41010108:C>A	False		
CYP2B6	*32	chr19:41012740:G>A	False		
CYP2B6	*33	chr19:41016810:C>A	False		
CYP2B6	*34	chr19:41009358:A>G,chr19:41016...	False	0.966687	0.011547
CYP2B6	*35	chr19:41010006:G>C,chr19:41007...	False	0.966687	0.011547
CYP2B6	*36	chr19:41009358:A>G,chr19:41006...	False	0.966687	0.011547
CYP2B6	*37	chr19:41009358:A>G,chr19:41006...	False	0.976347	0.25168
CYP2B6	*38	chr19:41009358:A>G,chr19:41004...	False	0.976347	0.25168

Gene	Allele	Core (build 38)	Inferred in MGI	Rsq	MAF
CYP2B6	*4	chr19:41009358:A>G	False		
CYP2B6	*5	chr19:41016810:C>T	True	0.897577	0.110763
CYP2B6	*6	chr19:41009358:A>G,chr19:41006...	False	0.976347	0.25168
CYP2B6	*7	chr19:41009358:A>G,chr19:41016...	False	0.897577	0.110763
CYP2B6	*8	chr19:41004377:A>G	True	0.8069	0.003937
CYP2B6	*9	chr19:41006936:G>T	True	0.976347	0.25168
CYP2B6	*S1	chr19:40991427:GA>G	False		
PTGIS	*1D	chr20:49568117:C>CGCGGGGCTG	False		
PTGIS	*1E	chr20:49568117:C>CGCGGGGCTGGCG...	False		
PTGIS	*1G	chr20:49568117:C>CGCGGGGCTGGCG...	False		
PTGIS	*1J	chr20:49568117:C>CGCGGGGCTGGCG...	False		
PTGIS	*2	chr20:49550151:G>A	False		
PTGIS	*3	chr20:49547864:A>T	True	0.986483	0.00206
PTGIS	*4	chr20:49513151:G>T	False		
PTGIS	*5	chr20:49511047:C>T	True	0.660113	0.000247
PTGIS	*6	chr20:49514311:C>A	False		
CYP4A11	*S1	chr1:46932824:A>G	True	0.99097	0.1532
CYP4A11	*S2	chr1:46934207:T>C	False		
SLCO2B1	*S1	chr11:75162709:GCACAGAAAA>G	True	0.968277	0.019563
SLCO2B1	*S464F	chr11:75196537:C>T	True	0.994913	0.049637
SULT1A1	*2	chr16:28606193:C>T	False		
SULT1A1	*3	chr16:28606164:C>T	True	0.579647	0.02866
CACNA1S	*S1	chr1:201091993:G>A	False		
CACNA1S	*S2	chr1:201060815:C>T	False		
CACNA1S	*S3	chr1:201043296:CT>C	False		
CACNA1S	*S4	chr1:201060659:T>C	False		
CYP4A22	*10	chr1:47142113:G>A,chr1:4714381...	True	0.960757	0.08985
CYP4A22	*11	chr1:47141609:C>T,chr1:4714381...	True	0.960757	0.087667
CYP4A22	*12	chr1:47142113:G>A,chr1:4714160...	True	0.960757	0.216043
CYP4A22	*13	chr1:47142113:G>A,chr1:4714160...	True	0.960757	0.08985
CYP4A22	*14	chr1:47142113:G>A,chr1:4714160...	True	0.960757	0.087667
CYP4A22	*15	chr1:47142113:G>A,chr1:4714160...	True	0.960757	0.087667
CYP4A22	*2	chr1:47137516:C>T,chr1:4714381...	True	0.960757	0.00182
CYP4A22	*3	chr1:47144551:TG>T	False		
CYP4A22	*4	chr1:47142113:G>A,chr1:4714381...	True	0.960757	0.217817
CYP4A22	*5	chr1:47143817:T>C,chr1:4714217...	True	0.960757	0.37093
CYP4A22	*6	chr1:47143817:T>C,chr1:4714592...	True	0.960757	0.242107
CYP4A22	*7	chr1:47148762:C>T,chr1:4714381...	True	0.960757	0.08985
CYP4A22	*8	chr1:47144393:A>C,chr1:4714381...	True	0.960757	0.087667
CYP4A22	*9	chr1:47143817:T>C,chr1:4714592...	True	0.960757	0.226717
CYP3A4	*10	chr7:99769769:C>G	True	0.65387	0.003843
CYP3A4	*11	chr7:99762206:G>A	True	0.918983	0.000243
CYP3A4	*12	chr7:99762177:G>A	True	0.975923	0.000253
CYP3A4	*13	chr7:99762047:G>A	True	0.99802	0.000223
CYP3A4	*14	chr7:99784038:A>G	False		
CYP3A4	*15	chr7:99769804:C>T	True	0.95794	0.002213
CYP3A4	*16	chr7:99768470:G>C	False		
CYP3A4	*17	chr7:99768458:A>G	False		
CYP3A4	*18	chr7:99764003:A>G	True	0.97076	0.00038
CYP3A4	*19	chr7:99760836:G>A	False		
CYP3A4	*1B	chr7:99784473:C>T	True	0.875387	0.08328
CYP3A4	*2	chr7:99768360:A>G	True	0.990553	0.000207
CYP3A4	*20	chr7:99758183:G>GT	False		
CYP3A4	*21	chr7:99763925:T>C	False		

Gene	Allele	Core (build 38)	Inferred in MGI	Rsq	MAF
CYP3A4	*22	chr7:99768693:G>A	True	0.77027	0.04471
CYP3A4	*23	chr7:99758352:T>C,chr7:9976832...	True	0.86114	0.00026
CYP3A4	*24	chr7:99758352:T>C,chr7:9976832...	False	0.888297	0.080047
CYP3A4	*26	chr7:99766440:G>A	False		
CYP3A4	*3	chr7:99760901:A>G	True	0.722053	0.00595
CYP3A4	*4	chr7:99770202:T>C	False		
CYP3A4	*5	chr7:99768371:G>C	False		
CYP3A4	*6	chr7:99766411:G>GT	False		
CYP3A4	*7	chr7:99778079:C>T	True	0.587513	0.001117
CYP3A4	*8	chr7:99770165:C>T	True	0.877387	0.000123
CYP3A4	*9	chr7:99769781:C>T	False		
CYP3A4	*S1	chr7:99763949:C>T	False		
DPYD	*10	chr1:97079071:C>A	False		
DPYD	*11	chr1:97593343:C>A	False		
DPYD	*12	chr1:97573943:C>A	False		
DPYD	*13	chr1:97515787:A>C	True	0.96638	0.000483
DPYD	*2	chr1:97450058:C>T	True	0.99157	0.004353
DPYD	*3	chr1:97450065:TG>T	False		
DPYD	*4	chr1:97515865:C>T	True	0.99306	0.018317
DPYD	*5	chr1:97515839:T>C	True	0.999627	0.19468
DPYD	*6	chr1:97305364:C>T	True	0.99816	0.046817
DPYD	*7	chr1:97740414:AATGA>A	False		
DPYD	*8	chr1:97691776:G>A	False		
DPYD	*9A	chr1:97883329:A>G	True	0.99983	0.232237
DPYD	*9B	chr1:97883329:A>G,chr1:9709859...	False	0.99983	0.232237
DPYD	*S1	chr1:97450117:C>A	False		
DPYD	*S10	chr1:97679300:T>C	True	0.983093	0.097077
DPYD	*S11	chr1:97515687:G>A	True	0.979	0.1869
DPYD	*S12	chr1:97515686:T>C	True	0.951397	0.416153
DPYD	*S13	chr1:97883368:G>C	False		
DPYD	*S14	chr1:97883353:G>A	False		
DPYD	*S15	chr1:97740400:C>T	False		
DPYD	*S16	chr1:97721650:T>C	False		
DPYD	*S17	chr1:97721542:T>C	True	0.896707	0.000213
DPYD	*S18	chr1:97699533:C>T	False		
DPYD	*S19	chr1:97699430:T>G	False		
DPYD	*S2	chr1:97082391:T>A	True	0.996373	0.005023
DPYD	*S20	chr1:97699399:T>C	False		
DPYD	*S21	chr1:97679170:T>C	True	0.99538	0.007963
DPYD	*S22	chr1:97595149:T>C	True	0.81416	0.000147
DPYD	*S23	chr1:97595088:A>G	False		
DPYD	*S24	chr1:97595083:G>A	False		
DPYD	*S25	chr1:97593379:C>T	False		
DPYD	*S26	chr1:97593322:C>T	False		
DPYD	*S27	chr1:97593289:G>A	False		
DPYD	*S28	chr1:97593238:T>C	False		
DPYD	*S29	chr1:97573918:C>A	False		
DPYD	*S3	chr1:97699535:T>C	True	0.999683	0.09155
DPYD	*S30	chr1:97573919:G>A	False		
DPYD	*S31	chr1:97573839:A>T	False		
DPYD	*S32	chr1:97573821:C>A	False		
DPYD	*S33	chr1:97573805:C>T	False		
DPYD	*S34	chr1:97573785:A>C	False		
DPYD	*S35	chr1:97549735:G>A	True	0.956423	0.000167

Gene	Allele	Core (build 38)	Inferred in MGI	Rsq	MAF
DPYD	*S36	chr1:97549726:G>C	False		
DPYD	*S37	chr1:97549681:G>T	False		
DPYD	*S38	chr1:97549609:G>A	False		
DPYD	*S39	chr1:97549600:T>C	False		
DPYD	*S4	chr1:97573985:A>G	True	0.961233	0.10405
DPYD	*S40	chr1:97549565:C>T	False		
DPYD	*S41	chr1:97515923:C>T	False		
DPYD	*S42	chr1:97515889:G>C	False		
DPYD	*S43	chr1:97515851:C>T	True	0.946913	0.00016
DPYD	*S44	chr1:97515784:C>A	False		
DPYD	*S45	chr1:97450189:C>T	False		
DPYD	*S46	chr1:97450190:G>A	False		
DPYD	*S47	chr1:97450187:C>T	False		
DPYD	*S48	chr1:97450168:A>G	False		
DPYD	*S49	chr1:97450059:G>C	False		
DPYD	*S5	chr1:97573863:C>T,chr1:9757989...	True	0.989497	0.019123
DPYD	*S50	chr1:97382461:T>G	True	0.95151	0.000107
DPYD	*S51	chr1:97373629:C>A	False		
DPYD	*S52	chr1:97373598:C>T	False		
DPYD	*S53	chr1:97306195:C>T	True	0.864577	0.000113
DPYD	*S54	chr1:97305372:G>A	False		
DPYD	*S55	chr1:97305363:A>C	True	0.978867	0.000153
DPYD	*S56	chr1:97305279:G>A	False		
DPYD	*S57	chr1:97234991:G>T	True	0.967667	0.000117
DPYD	*S58	chr1:97234958:G>T	False		
DPYD	*S59	chr1:97193209:C>T	False		
DPYD	*S6	chr1:97699474:T>C	True	0.996137	0.001437
DPYD	*S60	chr1:97193109:T>C	False		
DPYD	*S61	chr1:97098632:T>G	False		
DPYD	*S62	chr1:97098616:C>A	False		
DPYD	*S63	chr1:97098599:G>A	False		
DPYD	*S64	chr1:97082365:T>C	True	0.381453	0.00016
DPYD	*S65	chr1:97079139:T>C	False		
DPYD	*S66	chr1:97079133:T>A	False		
DPYD	*S67	chr1:97079121:T>C	False		
DPYD	*S68	chr1:97079076:A>C	False		
DPYD	*S69	chr1:97079077:G>A	False		
DPYD	*S7	chr1:97883352:C>T	False		
DPYD	*S70	chr1:97079005:C>T	False		
DPYD	*S71	chr1:97078993:C>G	False		
DPYD	*S72	chr1:97078987:G>T	True	0.99644	0.002713
DPYD	*S73	chr1:97699506:C>T	True	0.821927	0.000153
DPYD	*S74	chr1:97549713:G>A	True	0.98662	0.001607
DPYD	*S8	chr1:97573881:C>T	True	0.99444	0.00497
DPYD	*S9	chr1:97450068:A>G	True	0.994273	0.04524
RYR1	*S1	chr19:38440802:T>C	False		
RYR1	*S10	chr19:38451842:C>T	False		
RYR1	*S11	chr19:38451850:C>G	False		
RYR1	*S12	chr19:38455359:A>C	False		
RYR1	*S13	chr19:38455463:G>A	False		
RYR1	*S14	chr19:38455471:C>T	False		
RYR1	*S15	chr19:38455472:G>A	True	0.98161	0.000143
RYR1	*S16	chr19:38455528:C>T	False		
RYR1	*S17	chr19:38457545:C>T	False		

Gene	Allele	Core (build 38)	Inferred in MGI	Rsq	MAF
RYR1	*S18	chr19:38457546:G>T	False		
RYR1	*S19	chr19:38494564:C>T	False		
RYR1	*S2	chr19:38440829:C>T	False		
RYR1	*S20	chr19:38494565:G>A	False		
RYR1	*S21	chr19:38494579:G>A	False		
RYR1	*S22	chr19:38496283:C>G	False		
RYR1	*S23	chr19:38496283:C>T	False		
RYR1	*S24	chr19:38499223:G>A	False		
RYR1	*S25	chr19:38499645:GGAG>G	False		
RYR1	*S26	chr19:38499655:G>A	False		
RYR1	*S27	chr19:38499670:C>T	False		
RYR1	*S28	chr19:38499731:G>C	False		
RYR1	*S29	chr19:38499975:G>A	False		
RYR1	*S3	chr19:38444211:C>T	False		
RYR1	*S30	chr19:38499993:G>A	False		
RYR1	*S31	chr19:38499997:G>A	False		
RYR1	*S32	chr19:38500636:C>T	False		
RYR1	*S33	chr19:38500642:C>T	False		
RYR1	*S34	chr19:38500643:G>A	False		
RYR1	*S35	chr19:38500654:C>T	False		
RYR1	*S36	chr19:38500655:G>A	False		
RYR1	*S37	chr19:38500898:C>T	False		
RYR1	*S38	chr19:38500898:C>G	False		
RYR1	*S39	chr19:38500899:G>A	False		
RYR1	*S4	chr19:38444212:G>T	False		
RYR1	*S40	chr19:38512321:G>A	False		
RYR1	*S41	chr19:38543832:G>T	False		
RYR1	*S42	chr19:38580004:A>G	False		
RYR1	*S43	chr19:38580094:C>T	False		
RYR1	*S44	chr19:38580114:C>T	False		
RYR1	*S45	chr19:38580370:C>G	False		
RYR1	*S46	chr19:38580403:G>A	False		
RYR1	*S47	chr19:38580440:G>A	False		
RYR1	*S48	chr19:38584989:T>C	False		
RYR1	*S5	chr19:38446710:G>C	False		
RYR1	*S6	chr19:38446710:G>A	False		
RYR1	*S7	chr19:38448673:C>T	False		
RYR1	*S8	chr19:38448712:G>A	False		
RYR1	*S9	chr19:38448712:G>C	False		
UGT1A1	*10	chr2:233767873:C>T	False		
UGT1A1	*100	chr2:233760863:C>G	False		
UGT1A1	*101	chr2:233767912:T>C	False		
UGT1A1	*102	chr2:233760388:C>A	False		
UGT1A1	*103	chr2:233768342:C>T	False		
UGT1A1	*106	chr2:233772390:C>A	False		
UGT1A1	*107	chr2:233760405:T>C	False		
UGT1A1	*109	chr2:233760841:A>C	False		
UGT1A1	*11	chr2:233767092:G>A	False		
UGT1A1	*110	chr2:233760288:A>G	False		
UGT1A1	*113	chr2:233772434:G>C	False		
UGT1A1	*12	chr2:233760811:T>A	False		
UGT1A1	*13	chr2:233760797:CTTC>C	False		
UGT1A1	*14	chr2:233761113:G>C	False		
UGT1A1	*15	chr2:233760816:T>C	False		

Gene	Allele	Core (build 38)	Inferred in MGI	Rsq	MAF
UGT1A1	*16	chr2:233767922:A>G	False		
UGT1A1	*17	chr2:233768278:C>G	False		
UGT1A1	*18	chr2:233768336:G>C	False		
UGT1A1	*19	chr2:233767857:G>A	False		
UGT1A1	*2	chr2:233767045:CTACATTAATGCTT>...	False		
UGT1A1	*20	chr2:233768237:G>A	False		
UGT1A1	*21	chr2:233768355:A>AG	False		
UGT1A1	*22	chr2:233767044:C>T	False		
UGT1A1	*23	chr2:233768417:A>G	False		
UGT1A1	*24	chr2:233772266:A>T	False		
UGT1A1	*25	chr2:233761127:C>A	False		
UGT1A1	*26	chr2:233767141:TG>T	False		
UGT1A1	*27	chr2:233760973:C>A	True	0.972803	0.000547
UGT1A1	*28	chr2:233760233:CAT>CATAT	False		
UGT1A1	*29	chr2:233768234:C>G	False		
UGT1A1	*3	chr2:233768259:C>T	False		
UGT1A1	*30	chr2:233760331:T>G	False		
UGT1A1	*31	chr2:233768295:C>G	False		
UGT1A1	*32	chr2:233767858:C>T	False		
UGT1A1	*33	chr2:233767050:T>C	False		
UGT1A1	*34	chr2:233767097:A>G	False		
UGT1A1	*35	chr2:233768427:T>C	False		
UGT1A1	*36	chr2:233760233:CAT>C	False		
UGT1A1	*37	chr2:233760233:CAT>CATATAT	False		
UGT1A1	*38	chr2:233768333:A>G	False		
UGT1A1	*39	chr2:233772266:A>T,chr2:233768...	False		
UGT1A1	*4	chr2:233767921:C>T	False		
UGT1A1	*40	chr2:233767044:C>T,chr2:233768...	False		
UGT1A1	*41	chr2:233760407:GCT>G	False		
UGT1A1	*42	chr2:233772345:A>C	False		
UGT1A1	*43	chr2:233760985:T>G	False		
UGT1A1	*44	chr2:233760402:C>G	False		
UGT1A1	*45	chr2:233760509:C>A	False		
UGT1A1	*46	chr2:233760803:GC>G	False		
UGT1A1	*47	chr2:233761008:GAG>G	False		
UGT1A1	*48	chr2:233760961:T>G,chr2:233761...	False	0.983033	0.000593
UGT1A1	*49	chr2:233767893:CA>C	False		
UGT1A1	*5	chr2:233767160:C>T	False		
UGT1A1	*50	chr2:233768353:TA>T	False		
UGT1A1	*51	chr2:233768262:A>G	False		
UGT1A1	*52	chr2:233768265:G>T	False		
UGT1A1	*53	chr2:233772405:G>A	False		
UGT1A1	*54	chr2:233772406:G>A	False		
UGT1A1	*55	chr2:233772444:T>A	False		
UGT1A1	*56	chr2:233767033:G>A	False		
UGT1A1	*57	chr2:233767937:G>T	False		
UGT1A1	*58	chr2:233760432:C>T	False		
UGT1A1	*59	chr2:233768320:TG>T	False		
UGT1A1	*6	chr2:233760498:G>A	True	0.991757	0.005657
UGT1A1	*60	chr2:233757013:T>G	True	0.989183	0.46944
UGT1A1	*61	chr2:233767937:G>A	False		
UGT1A1	*62	chr2:233760534:T>C	False		
UGT1A1	*63	chr2:233768226:C>T	True	0.951357	0.000387
UGT1A1	*69	chr2:233760763:T>C	False		

Gene	Allele	Core (build 38)	Inferred in MGI	Rsq	MAF
UGT1A1	*7	chr2:233772413:T>G	True	0.79949	0.0001
UGT1A1	*70	chr2:233767131:C>G	False		
UGT1A1	*71	chr2:233767133:A>G	True	0.749763	0.000133
UGT1A1	*72	chr2:233767927:G>A	False		
UGT1A1	*75	chr2:233772555:A>C	False		
UGT1A1	*79	chr2:233772999:G>C	True	0.999723	0.23986
UGT1A1	*8	chr2:233760912:C>T	False		
UGT1A1	*80	chr2:233759924:C>T	True	0.999937	0.33328
UGT1A1	*81	chr2:233760224:G>C	True	0.86824	0.000927
UGT1A1	*9	chr2:233767161:A>G	False		
UGT1A1	*94	chr2:233772338:T>C	False		
UGT1A1	*95	chr2:233767859:G>A	False		
UGT1A1	*96	chr2:233767859:G>T	False		
UGT1A1	*97	chr2:233768319:G>T	False		
UGT1A1	*98	chr2:233768294:C>T	False		
GSTM1	*3	chr1:109690516:G>C	False		
TBXAS1	*2	chr7:139872324:G>A	True	0.995237	0.002077
TBXAS1	*3	chr7:139953397:C>A	True	0.996033	0.00719
TBXAS1	*4	chr7:139957679:A>G	True	0.995543	0.000513
TBXAS1	*5	chr7:139962165:C>G	True	0.989003	0.007547
TBXAS1	*6	chr7:140015742:C>G	True	0.884767	0.002057
TBXAS1	*7	chr7:140015841:G>A	True	0.993133	0.019157
TBXAS1	*8	chr7:140015845:C>A	True	0.997613	0.020353
TBXAS1	*9	chr7:140017700:G>A	True	0.63542	0.00152
GSTP1	*2	chr11:67585218:A>G	True	0.998993	0.343983
GSTP1	*3	chr11:67585218:A>G,chr11:67586...	True	0.998993	0.077213
GSTP1	*4	chr11:67586108:C>T	True	0.999097	0.077213
CYP2D6	*10	chr22:42130692:G>A	True	0.96428	0.216287
CYP2D6	*100	chr22:42127962:TG>T	False		
CYP2D6	*101	chr22:42127845:GCACATCCGGATGTA...	False		
CYP2D6	*102	chr22:42126611:C>G,chr22:42129...	False	0.959667	0.346377
CYP2D6	*103	chr22:42126611:C>G,chr22:42129...	False	0.959667	0.346377
CYP2D6	*104	chr22:42126611:C>G,chr22:42127...	False	0.954087	0.31085
CYP2D6	*105	chr22:42126611:C>G,chr22:42127...	False	0.954087	0.31085
CYP2D6	*106	chr22:42126914:C>T	True	0.8852	0.000827
CYP2D6	*107	chr22:42129132:C>T	True	0.944747	0.006907
CYP2D6	*108	chr22:42127556:T>C,chr22:42127...	False		
CYP2D6	*109	chr22:42131751:C>G,chr22:42127...	True	0.79737	0.000757
CYP2D6	*11	chr22:42129910:C>G	True	0.560523	0.00015
CYP2D6	*110	chr22:42126735:C>T	False		
CYP2D6	*111	chr22:42126611:C>G,chr22:42129...	False	0.959667	0.346377
CYP2D6	*112	chr22:42126605:G>A	False		
CYP2D6	*113	chr22:42126752:C>T	False		
CYP2D6	*114	chr22:42129033:C>T,chr22:42130...	False	0.96428	0.216287
CYP2D6	*115	chr22:42127973:T>C,chr22:42128...	True	0.690883	0.000233
CYP2D6	*116	chr22:42127631:C>G	True	0.9596	0.000567
CYP2D6	*117	chr22:42126611:C>G,chr22:42127...	True	0.695177	0.0012
CYP2D6	*118	chr22:42127899:T>C	False		
CYP2D6	*119	chr22:42127803:C>T,chr22:42132...	False	0.9553	0.093033
CYP2D6	*12	chr22:42130668:C>T	False		
CYP2D6	*120	chr22:42130727:AG>A	False		
CYP2D6	*121	chr22:42126611:C>G,chr22:42129...	False	0.959667	0.346377
CYP2D6	*122	chr22:42127512:C>T	False		
CYP2D6	*123	chr22:42127922:A>G,chr22:42127...	False	0.970447	0.093033

Gene	Allele	Core (build 38)	Inferred in MGI	Rsq	MAF
CYP2D6	*124	chr22:42126981:G>GGA	False		
CYP2D6	*125	chr22:42126611:C>G,chr22:42127...	False	0.959667	0.346377
CYP2D6	*126	chr22:42126611:C>G,chr22:42127...	True	0.777843	0.00011
CYP2D6	*127	chr22:42127556:T>C,chr22:42127...	False		
CYP2D6	*128	chr22:42126611:C>G,chr22:42127...	False	0.959667	0.346377
CYP2D6	*129	chr22:42126611:C>G,chr22:42129...	False	0.959667	0.346377
CYP2D6	*130	chr22:42128879:A>G	False		
CYP2D6	*131	chr22:42128325:A>G	False		
CYP2D6	*132	chr22:42126611:C>G,chr22:42127...	True	0.690883	0.000233
CYP2D6	*133	chr22:42126611:C>G,chr22:42127...	False	0.959667	0.346377
CYP2D6	*134	chr22:42127589:C>T	False		
CYP2D6	*135	chr22:42126611:C>G,chr22:42126...	False	0.959667	0.346377
CYP2D6	*136	chr22:42126611:C>G,chr22:42126...	False	0.959667	0.346377
CYP2D6	*137	chr22:42126578:C>T	False		
CYP2D6	*138	chr22:42127803:C>T,chr22:42126...	True	0.578227	0.000103
CYP2D6	*14	chr22:42129033:C>T	False		
CYP2D6	*15	chr22:42130654:C>CA	False		
CYP2D6	*17	chr22:42129770:G>A	True	0.953547	0.01443
CYP2D6	*18	chr22:42126656:C>CCAGTGGGCA	False		
CYP2D6	*19	chr22:42128248:CAGTT>C	False		
CYP2D6	*2	chr22:42126611:C>G,chr22:42127...	True	0.959667	0.346377
CYP2D6	*20	chr22:42128818:T>TC	False		
CYP2D6	*21	chr22:42128211:C>CG	False		
CYP2D6	*22	chr22:42130710:G>A	True	0.84947	0.00243
CYP2D6	*23	chr22:42129836:G>A	False		
CYP2D6	*24	chr22:42127938:T>G	False		
CYP2D6	*25	chr22:42127593:G>C	False		
CYP2D6	*26	chr22:42127514:A>G	False		
CYP2D6	*27	chr22:42126938:C>T	False		
CYP2D6	*28	chr22:42126611:C>G,chr22:42127...	True	0.94925	0.0027
CYP2D6	*29	chr22:42126611:C>G,chr22:42127...	True	0.944747	0.006527
CYP2D6	*3	chr22:42128241:CT>C	True	0.872347	0.01532
CYP2D6	*30	chr22:42128927:T>TGGGGCGAAA	False		
CYP2D6	*31	chr22:42126749:C>T	True	0.711427	0.000197
CYP2D6	*32	chr22:42126938:C>T,chr22:42127...	False	0.970447	0.093033
CYP2D6	*33	chr22:42128308:C>A	True	0.876623	0.011423
CYP2D6	*34	chr22:42127941:G>A	True	0.965797	0.346377
CYP2D6	*35	chr22:42126611:C>G,chr22:42127...	True	0.92998	0.055633
CYP2D6	*37	chr22:42128848:C>T,chr22:42130...	False	0.96428	0.216287
CYP2D6	*38	chr22:42128198:CTCAG>C	False		
CYP2D6	*39	chr22:42126611:C>G,chr22:42129...	True	0.954087	0.436763
CYP2D6	*4	chr22:42128945:C>T	True	0.95985	0.184487
CYP2D6	*40	chr22:42128927:T>TGGGGCGAAAGGG...	False	0.953547	0.01443
CYP2D6	*41	chr22:42127803:C>T	True	0.970447	0.093033
CYP2D6	*42	chr22:42127530:G>GCA	False		
CYP2D6	*43	chr22:42130715:C>T	True	0.83753	0.001713
CYP2D6	*44	chr22:42127841:C>G	False		
CYP2D6	*45	chr22:42126611:C>G,chr22:42127...	True	0.922683	0.003433
CYP2D6	*46	chr22:42126611:C>G,chr22:42130...	True	0.83753	0.001713
CYP2D6	*47	chr22:42130692:G>A,chr22:42130...	False	0.96428	0.216287
CYP2D6	*48	chr22:42129821:G>A	False		
CYP2D6	*49	chr22:42126611:C>G,chr22:42130...	True	0.591197	0.00046
CYP2D6	*50	chr22:42129071:T>G	False		
CYP2D6	*51	chr22:42127619:T>G	False		

Gene	Allele	Core (build 38)	Inferred in MGI	Rsq	MAF
CYP2D6	*52	chr22:42126611:C>G,chr22:42126...	False	0.8852	0.000827
CYP2D6	*53	chr22:42129174:C>A,chr22:42129...	True	0.417493	0.00022
CYP2D6	*54	chr22:42130692:G>A,chr22:42128...	False	0.96428	0.216287
CYP2D6	*55	chr22:42126956:T>G	False		
CYP2D6	*56	chr22:42127590:G>A	False		
CYP2D6	*58	chr22:42126611:C>G,chr22:42127...	False	0.953547	0.01443
CYP2D6	*59	chr22:42127852:C>T	True	0.852953	0.003657
CYP2D6	*6	chr22:42129083:CA>C	True	0.766197	0.010767
CYP2D6	*60	chr22:42128903:T>TTA	False		
CYP2D6	*62	chr22:42126747:G>A	False		
CYP2D6	*64	chr22:42126611:C>G,chr22:42126...	False	0.953547	0.01443
CYP2D6	*65	chr22:42126611:C>G,chr22:42127...	True	0.954087	0.216287
CYP2D6	*69	chr22:42130692:G>A,chr22:42127...	True	0.96428	0.093033
CYP2D6	*7	chr22:42127856:T>G	True	0.655807	0.00045
CYP2D6	*70	chr22:42126611:C>G,chr22:42129...	False	0.944747	0.006527
CYP2D6	*71	chr22:42130667:C>T	False		
CYP2D6	*72	chr22:42130692:G>A,chr22:42127...	False	0.96428	0.216287
CYP2D6	*73	chr22:42129780:C>T	False		
CYP2D6	*74	chr22:42129819:G>T,chr22:42127...	False	0.963403	0.175003
CYP2D6	*75	chr22:42126746:C>T	False		
CYP2D6	*8	chr22:42129033:C>A	False		
CYP2D6	*81	chr22:42128212:G>A	False		
CYP2D6	*82	chr22:42129757:A>G,chr22:42129...	False	0.963393	0.175003
CYP2D6	*84	chr22:42128217:G>T	True	0.828003	0.000203
CYP2D6	*85	chr22:42126611:C>G,chr22:42127...	False	0.954087	0.3372
CYP2D6	*86	chr22:42128181:A>T,chr22:42128...	False	0.616497	0.000367
CYP2D6	*87	chr22:42126611:C>G,chr22:42129...	False	0.954087	0.040537
CYP2D6	*88	chr22:42126611:C>G,chr22:42130...	False	0.954087	0.3372
CYP2D6	*89	chr22:42129113:A>G	False		
CYP2D6	*9	chr22:42128173:CCTT>C	True	0.832513	0.02518
CYP2D6	*90	chr22:42129098:T>C	False		
CYP2D6	*91	chr22:42129056:C>G,chr22:42127...	False	0.970447	0.093033
CYP2D6	*92	chr22:42128795:AG>A	False		
CYP2D6	*93	chr22:42128272:T>G	False		
CYP2D6	*94	chr22:42126611:C>G,chr22:42127...	False	0.954087	0.040537
CYP2D6	*95	chr22:42126611:C>G,chr22:42127...	False	0.954087	0.040537
CYP2D6	*96	chr22:42126896:G>A	False		
CYP2D6	*97	chr22:42126697:G>T	False		
CYP2D6	*98	chr22:42126681:G>C	False		
CYP2D6	*99	chr22:42129827:C>G,chr22:42130...	False	0.96428	0.216287
CYP2R1	*2	chr11:14885847:A>G	True	0.97447	0.000273

Table S1: Star alleles that are inferred in Data Freeze 4. Some star alleles will not be inferrable in MGI if one or more core variants that define the allele are not contained in the freeze genetic data. Also given is the lowest Rsq (estimated imputation value) and lowest minor allele frequency (MAF) in Data Freeze 4 among all core variants that define each respective star allele. Here MAF is estimated among all 60,215 participants in Data Freeze 4.

Gene	Activity Phenotype	Frequency
CYP2W1	Indeterminate	0.445387
CYP2W1	Normal Metabolizer	0.554613
CYP3A5	Poor metabolizer	0.000720
CYP3A5	Normal Metabolizer	0.020171

Gene	Activity Phenotype	Frequency
CYP3A5	Intermediate Metabolizer	0.163622
CYP3A5	Poor Metabolizer	0.815487
NAT2	Indeterminate	0.000016
NAT2	Normal Function	0.065747
NAT2	Decreased Function	0.934237
CYP1A1	Poor Metabolizer	0.000016
CYP1A1	Intermediate Metabolizer	0.011542
CYP1A1	Indeterminate	0.307666
CYP1A1	Normal Metabolizer	0.680775
IFNL3	No Function	0.101910
IFNL3	Decreased Function	0.426529
IFNL3	Normal Function	0.471561
UGT2B7	Normal Function	0.242896
UGT2B7	Indeterminate	0.757104
UGT1A1	Poor Metabolizer	0.000544
UGT1A1	Normal Metabolizer	0.185730
UGT1A1	Intermediate Metabolizer	0.236605
UGT1A1	Indeterminate	0.577121
CYP2F1	Poor Metabolizer	0.044391
CYP2F1	Indeterminate	0.121520
CYP2F1	Intermediate Metabolizer	0.290810
CYP2F1	Normal Metabolizer	0.543279
CYP3A43	Poor Metabolizer	0.005219
CYP3A43	Intermediate Metabolizer	0.082299
CYP3A43	Indeterminate	0.240607
CYP3A43	Normal Metabolizer	0.671875
CYP1B1	Intermediate Metabolizer	0.000208
CYP1B1	Normal Metabolizer	0.020459
CYP1B1	Indeterminate	0.979333
CYP2R1	Indeterminate	0.000512
CYP2R1	Normal Metabolizer	0.999488
TBXAS1	Indeterminate	0.021483
TBXAS1	Decreased Function	0.053596
TBXAS1	Normal Function	0.924920
CYP2A13	Poor Metabolizer	0.000080
CYP2A13	Intermediate Metabolizer	0.011718
CYP2A13	Indeterminate	0.058015
CYP2A13	Normal Metabolizer	0.930187
CYP2D6	Indeterminate	0.015592
CYP2D6	Poor Metabolizer	0.046825
CYP2D6	Intermediate Metabolizer	0.355067
CYP2D6	Normal Metabolizer	0.582516
CYP2A6	Poor Metabolizer	0.000880
CYP2A6	Intermediate Metabolizer	0.056110
CYP2A6	Indeterminate	0.073591
CYP2A6	Normal Metabolizer	0.869419
UGT2B15	No Function	0.000016
UGT2B15	Decreased Function	0.000528
UGT2B15	Normal Function	0.034594
UGT2B15	Indeterminate	0.964861
CYP3A7	Indeterminate	0.240719
CYP3A7	Normal Metabolizer	0.759281
CYP4A11	Intermediate Metabolizer	0.025822
CYP4A11	Normal Metabolizer	0.974178
CYP2B6	Ultrarapid Metabolizer	0.000224

Gene	Activity Phenotype	Frequency
CYP2B6	Rapid Metabolizer	0.015624
CYP2B6	Indeterminate	0.029536
CYP2B6	Poor Metabolizer	0.070533
CYP2B6	Intermediate Metabolizer	0.369011
CYP2B6	Normal Metabolizer	0.515072
CYP19A1	Intermediate Metabolizer	0.004098
CYP19A1	Indeterminate	0.066915
CYP19A1	Normal Metabolizer	0.928987
SLCO1B3	Normal Function	0.041430
SLCO1B3	Decreased Function	0.271343
SLCO1B3	Poor Function	0.687227
CYP2C19	Indeterminate	0.000416
CYP2C19	Likely Poor Metabolizer	0.000480
CYP2C19	Likely Intermediate Metabolizer	0.001809
CYP2C19	Poor Metabolizer	0.028719
CYP2C19	Ultrarapid Metabolizer	0.046953
CYP2C19	Rapid Metabolizer	0.262026
CYP2C19	Intermediate Metabolizer	0.267469
CYP2C19	Normal Metabolizer	0.392127
CYP4F2	Intermediate Metabolizer	0.080122
CYP4F2	Normal Metabolizer	0.919878
ABCB1	Normal Function	0.398514
ABCB1	Indeterminate	0.601486
SLC22A2	Normal Metabolizer	0.146846
SLC22A2	Indeterminate	0.853154
CYP2E1	Indeterminate	0.062273
CYP2E1	Normal Metabolizer	0.937727
CYP4A22	Normal Metabolizer	0.405526
CYP4A22	Indeterminate	0.594474
CFTR	Indeterminate	0.001249
CFTR	Decreased Function	0.010357
CFTR	Normal Function	0.988394
CYP2C8	Intermediate Metabolizer	0.000432
CYP2C8	Indeterminate	0.301551
CYP2C8	Normal Metabolizer	0.698017
TPMT	Possible Intermediate Metabolizer	0.000448
TPMT	Poor Metabolizer	0.002401
TPMT	Indeterminate	0.006964
TPMT	Intermediate Metabolizer	0.086830
TPMT	Normal Metabolizer	0.903357
RYR1	Increased Function	0.000272
RYR1	Normal Function	0.999728
POR	Indeterminate	0.002689
POR	Decreased Function	0.478156
POR	Normal Function	0.519154
VKORC1	Normal Function	0.008661
VKORC1	Indeterminate	0.991339
SULT1A1	Normal Function	1.000000
NUDT15	Possible Intermediate Metabolizer	0.000128
NUDT15	Poor Metabolizer	0.000352
NUDT15	Indeterminate	0.006820
NUDT15	Intermediate Metabolizer	0.016617
NUDT15	Normal Metabolizer	0.976083
PTGIS	Indeterminate	0.004290
PTGIS	Normal Function	0.995710

Gene	Activity Phenotype	Frequency
XPC	Normal Function	0.157347
XPC	Indeterminate	0.842653
SLCO1B1	Possible Poor Function	0.000368
SLCO1B1	Possible Decreased Function	0.002241
SLCO1B1	Poor Function	0.028799
SLCO1B1	Possible Increased Function	0.055998
SLCO1B1	Indeterminate	0.119711
SLCO1B1	Decreased Function	0.183281
SLCO1B1	Increased Function	0.214097
SLCO1B1	Normal Function	0.395505
SLC15A2	Normal Metabolizer	0.298654
SLC15A2	Indeterminate	0.701346
CYP4B1	Poor Metabolizer	0.020747
CYP4B1	Intermediate Metabolizer	0.189236
CYP4B1	Indeterminate	0.309427
CYP4B1	Normal Metabolizer	0.480590
CYP26A1	Indeterminate	0.006083
CYP26A1	Normal Metabolizer	0.993917
SLCO2B1	Indeterminate	0.126083
SLCO2B1	Normal Function	0.873917
CYP2C9	Indeterminate	0.000977
CYP2C9	Poor Metabolizer	0.020283
CYP2C9	Intermediate Metabolizer	0.326284
CYP2C9	Normal Metabolizer	0.652456
CYP2S1	Indeterminate	0.038356
CYP2S1	Normal Metabolizer	0.961644
CYP3A4	Intermediate Metabolizer	0.001905
CYP3A4	Indeterminate	0.131269
CYP3A4	Normal Metabolizer	0.866826
CYP1A2	Intermediate Metabolizer	0.009157
CYP1A2	Normal Metabolizer	0.168857
CYP1A2	Ultrarapid Metabolizer	0.821986
NAT1	No Function	0.000016
NAT1	Decreased Function	0.042054
NAT1	Indeterminate	0.456097
NAT1	Normal Function	0.501833
UGT1A4	No Function	0.000016
UGT1A4	Indeterminate	0.102806
UGT1A4	Decreased Function	0.165719
UGT1A4	Normal Function	0.731458
GSTP1	Normal Function	0.432853
GSTP1	Indeterminate	0.567147
CYP2J2	Indeterminate	0.137993
CYP2J2	Normal Metabolizer	0.862007
DPYD	Poor Metabolizer	0.000400
DPYD	Intermediate Metabolizer	0.057967
DPYD	Normal Metabolizer	0.941633

Table S2: Frequency of inferred activity phenotypes in Data Freeze 4. Here inferred activity phenotype frequency is estimated among all 60,215 participants in Data Freeze 4.

Gene	Diplotype	Activity Phenotype	Frequency
CYP2W1	*4/*4	Indeterminate	0.000080
CYP2W1	*2/*4	Indeterminate	0.000352
CYP2W1	*4/*6	Indeterminate	0.000928
CYP2W1	*1/*4	Indeterminate	0.002385
CYP2W1	*2/*2	Indeterminate	0.004258
CYP2W1	*2/*6	Indeterminate	0.024621
CYP2W1	*6/*6	Indeterminate	0.039141
CYP2W1	*1/*2	Indeterminate	0.096371
CYP2W1	*1/*6	Indeterminate	0.277250
CYP2W1	*1/*1	Normal Metabolizer	0.554613
CYP3A5	*7/*7	Poor metabolizer	0.000720
CYP3A5	*6/*6	Poor Metabolizer	0.000993
CYP3A5	*6/*7	Poor Metabolizer	0.001473
CYP3A5	*3/*7	Poor Metabolizer	0.005267
CYP3A5	*1/*7	Intermediate Metabolizer	0.005827
CYP3A5	*1/*6	Intermediate Metabolizer	0.007300
CYP3A5	*3/*6	Poor Metabolizer	0.007636
CYP3A5	*1/*1	Normal Metabolizer	0.020171
CYP3A5	*1/*3	Intermediate Metabolizer	0.150495
CYP3A5	*3/*3	Poor Metabolizer	0.800118
NAT2	*1/*11	Normal Function	0.000016
NAT2	*22/*5	Indeterminate	0.000016
NAT2	*11/*12	Normal Function	0.000016
NAT2	*11/*5	Decreased Function	0.000016
NAT2	*11/*6	Decreased Function	0.000032
NAT2	*13/*7	Decreased Function	0.000384
NAT2	*14/*7	Decreased Function	0.000400
NAT2	*14/*14	Decreased Function	0.000656
NAT2	*13/*13	Normal Function	0.000672
NAT2	*12/*12	Normal Function	0.000720
NAT2	*12/*7	Decreased Function	0.000816
NAT2	*13/*14	Decreased Function	0.000896
NAT2	*12/*13	Normal Function	0.001073
NAT2	*12/*14	Decreased Function	0.001121
NAT2	*1/*14	Decreased Function	0.001457
NAT2	*7/*7	Decreased Function	0.001713
NAT2	*1/*13	Normal Function	0.002065
NAT2	*14/*6	Decreased Function	0.002978
NAT2	*13/*6	Decreased Function	0.003090
NAT2	*14/*5	Decreased Function	0.003826
NAT2	*1/*12	Normal Function	0.003986
NAT2	*13/*5	Decreased Function	0.003986
NAT2	*12/*6	Decreased Function	0.005923
NAT2	*12/*5	Decreased Function	0.008228
NAT2	*1/*7	Decreased Function	0.015752
NAT2	*6/*7	Decreased Function	0.016713
NAT2	*5/*7	Decreased Function	0.024109
NAT2	*1/*1	Normal Function	0.057198
NAT2	*6/*6	Decreased Function	0.082540
NAT2	*1/*6	Decreased Function	0.131541
NAT2	*5/*5	Decreased Function	0.189220
NAT2	*1/*5	Decreased Function	0.195543
NAT2	*5/*6	Decreased Function	0.243296
CYP1A1	*10/*2A	Indeterminate	0.000016
CYP1A1	*13/*5	Indeterminate	0.000016

Gene	Diplotype	Activity Phenotype	Frequency
CYP1A1	*5/*5	Poor Metabolizer	0.000016
CYP1A1	*10/*2B	Indeterminate	0.000016
CYP1A1	*13/*4	Indeterminate	0.000032
CYP1A1	*1/*2C	Normal Metabolizer	0.000032
CYP1A1	*1/*10	Indeterminate	0.000272
CYP1A1	*13/*13	Indeterminate	0.000464
CYP1A1	*2B/*5	Indeterminate	0.000464
CYP1A1	*4/*5	Indeterminate	0.000608
CYP1A1	*2A/*5	Indeterminate	0.000880
CYP1A1	*13/*2A	Indeterminate	0.000912
CYP1A1	*13/*2B	Indeterminate	0.001281
CYP1A1	*4/*4	Indeterminate	0.001985
CYP1A1	*1/*13	Indeterminate	0.003602
CYP1A1	*2B/*4	Indeterminate	0.003762
CYP1A1	*2B/*2B	Indeterminate	0.004082
CYP1A1	*2A/*4	Indeterminate	0.005651
CYP1A1	*2A/*2B	Indeterminate	0.008164
CYP1A1	*2A/*2A	Indeterminate	0.008404
CYP1A1	*1/*5	Intermediate Metabolizer	0.011542
CYP1A1	*1/*4	Indeterminate	0.067796
CYP1A1	*1/*2B	Indeterminate	0.072374
CYP1A1	*1/*2A	Indeterminate	0.126883
CYP1A1	*1/*1	Normal Metabolizer	0.680743
IFNL3	*S3/*S3	No Function	0.101910
IFNL3	*1/*S3	Decreased Function	0.426529
IFNL3	*1/*1	Normal Function	0.471561
UGT2B7	*3/*3	Indeterminate	0.000688
UGT2B7	*2/*3	Indeterminate	0.002545
UGT2B7	*1/*3	Indeterminate	0.003698
UGT2B7	*1/*1	Normal Function	0.242896
UGT2B7	*2/*2	Indeterminate	0.261738
UGT2B7	*1/*2	Indeterminate	0.488434
UGT1A1	*60/*7	Intermediate Metabolizer	0.000032
UGT1A1	*6/*7	Intermediate Metabolizer	0.000048
UGT1A1	*7/*79	Indeterminate	0.000080
UGT1A1	*27/*6	Poor Metabolizer	0.000080
UGT1A1	*1/*27	Intermediate Metabolizer	0.000096
UGT1A1	*27/*60	Intermediate Metabolizer	0.000336
UGT1A1	*6/*6	Poor Metabolizer	0.000464
UGT1A1	*27/*79	Indeterminate	0.000544
UGT1A1	*1/*6	Intermediate Metabolizer	0.001345
UGT1A1	*6/*79	Indeterminate	0.004290
UGT1A1	*6/*60	Intermediate Metabolizer	0.004306
UGT1A1	*1/*1	Normal Metabolizer	0.029824
UGT1A1	*1/*79	Indeterminate	0.122993
UGT1A1	*79/*79	Indeterminate	0.130293
UGT1A1	*1/*60	Normal Metabolizer	0.155906
UGT1A1	*60/*60	Intermediate Metabolizer	0.230442
UGT1A1	*60/*79	Indeterminate	0.318920
CYP2F1	*6/*6	Indeterminate	0.000336
CYP2F1	*4/*6	Indeterminate	0.001425
CYP2F1	*4/*4	Indeterminate	0.002561
CYP2F1	*2/*6	Indeterminate	0.005123
CYP2F1	*2/*4	Indeterminate	0.020619
CYP2F1	*1/*6	Indeterminate	0.020683

Gene	Diplotype	Activity Phenotype	Frequency
CYP2F1	*2/*2	Poor Metabolizer	0.044391
CYP2F1	*1/*4	Indeterminate	0.070773
CYP2F1	*1/*2	Intermediate Metabolizer	0.290810
CYP2F1	*1/*1	Normal Metabolizer	0.543279
CYP3A43	*2A/*2A	Poor Metabolizer	0.000192
CYP3A43	*2A/*3	Indeterminate	0.001073
CYP3A43	*3/*3	Indeterminate	0.001505
CYP3A43	*1B/*2A	Indeterminate	0.001601
CYP3A43	*2A/*2B	Poor Metabolizer	0.001633
CYP3A43	*2B/*2B	Poor Metabolizer	0.003394
CYP3A43	*2B/*3	Indeterminate	0.004114
CYP3A43	*1B/*3	Indeterminate	0.005155
CYP3A43	*1B/*2B	Indeterminate	0.006932
CYP3A43	*1B/*1B	Indeterminate	0.011590
CYP3A43	*1/*2A	Intermediate Metabolizer	0.017849
CYP3A43	*1/*3	Indeterminate	0.044888
CYP3A43	*1/*2B	Intermediate Metabolizer	0.064450
CYP3A43	*1/*1B	Indeterminate	0.163750
CYP3A43	*1/*1	Normal Metabolizer	0.671875
CYP1B1	*5/*5	Indeterminate	0.000048
CYP1B1	*17/*4	Indeterminate	0.000080
CYP1B1	*1/*17	Intermediate Metabolizer	0.000096
CYP1B1	*17/*3	Indeterminate	0.000112
CYP1B1	*1/*20	Intermediate Metabolizer	0.000112
CYP1B1	*2/*20	Indeterminate	0.000128
CYP1B1	*17/*2	Indeterminate	0.000128
CYP1B1	*7/*7	Indeterminate	0.000144
CYP1B1	*5/*7	Indeterminate	0.000176
CYP1B1	*20/*4	Indeterminate	0.000192
CYP1B1	*4/*5	Indeterminate	0.000224
CYP1B1	*1/*5	Indeterminate	0.000272
CYP1B1	*20/*3	Indeterminate	0.000368
CYP1B1	*1/*7	Indeterminate	0.000432
CYP1B1	*4/*7	Indeterminate	0.000608
CYP1B1	*2/*5	Indeterminate	0.000784
CYP1B1	*5/*6	Indeterminate	0.001345
CYP1B1	*6/*7	Indeterminate	0.001441
CYP1B1	*2/*7	Indeterminate	0.001777
CYP1B1	*1/*6	Indeterminate	0.002081
CYP1B1	*4/*6	Indeterminate	0.002241
CYP1B1	*3/*5	Indeterminate	0.002465
CYP1B1	*3/*7	Indeterminate	0.003666
CYP1B1	*6/*6	Indeterminate	0.004370
CYP1B1	*2/*6	Indeterminate	0.007268
CYP1B1	*3/*6	Indeterminate	0.015384
CYP1B1	*1/*1	Normal Metabolizer	0.020459
CYP1B1	*4/*4	Indeterminate	0.031873
CYP1B1	*1/*4	Indeterminate	0.034082
CYP1B1	*1/*2	Indeterminate	0.059760
CYP1B1	*2/*2	Indeterminate	0.079402
CYP1B1	*1/*3	Indeterminate	0.082075
CYP1B1	*2/*4	Indeterminate	0.096787
CYP1B1	*3/*4	Indeterminate	0.145437
CYP1B1	*3/*3	Indeterminate	0.174764
CYP1B1	*2/*3	Indeterminate	0.229417

Gene	Diplotype	Activity Phenotype	Frequency
CYP2R1	*2/*2	Indeterminate	0.000016
CYP2R1	*1/*2	Indeterminate	0.000496
CYP2R1	*1/*1	Normal Metabolizer	0.999488
TBXAS1	*4/*7	Indeterminate	0.000016
TBXAS1	*2/*3	Indeterminate	0.000016
TBXAS1	*6/*6	Normal Function	0.000016
TBXAS1	*6/*7	Normal Function	0.000016
TBXAS1	*3/*9	Indeterminate	0.000016
TBXAS1	*4/*8	Indeterminate	0.000016
TBXAS1	*8/*9	Indeterminate	0.000064
TBXAS1	*5/*7	Decreased Function	0.000080
TBXAS1	*2/*8	Indeterminate	0.000096
TBXAS1	*2/*7	Indeterminate	0.000096
TBXAS1	*7/*9	Indeterminate	0.000096
TBXAS1	*5/*8	Decreased Function	0.000096
TBXAS1	*3/*3	Indeterminate	0.000128
TBXAS1	*5/*6	Decreased Function	0.000192
TBXAS1	*3/*8	Indeterminate	0.000288
TBXAS1	*3/*7	Indeterminate	0.000368
TBXAS1	*7/*7	Normal Function	0.000416
TBXAS1	*8/*8	Decreased Function	0.000512
TBXAS1	*5/*5	Decreased Function	0.000704
TBXAS1	*7/*8	Decreased Function	0.000864
TBXAS1	*1/*4	Indeterminate	0.000993
TBXAS1	*1/*9	Indeterminate	0.002097
TBXAS1	*1/*6	Normal Function	0.002513
TBXAS1	*1/*2	Indeterminate	0.003906
TBXAS1	*1/*5	Decreased Function	0.012951
TBXAS1	*1/*3	Indeterminate	0.013287
TBXAS1	*1/*7	Normal Function	0.035587
TBXAS1	*1/*8	Decreased Function	0.038196
TBXAS1	*1/*1	Normal Function	0.886372
CYP2A13	*6/*8	Indeterminate	0.000016
CYP2A13	*6/*6	Indeterminate	0.000016
CYP2A13	*7/*8	Indeterminate	0.000048
CYP2A13	*2/*3	Indeterminate	0.000064
CYP2A13	*7/*7	Poor Metabolizer	0.000080
CYP2A13	*2/*7	Indeterminate	0.000176
CYP2A13	*1/*6	Indeterminate	0.000320
CYP2A13	*8/*8	Indeterminate	0.000320
CYP2A13	*1/*3	Indeterminate	0.000768
CYP2A13	*2/*8	Indeterminate	0.001313
CYP2A13	*2/*2	Indeterminate	0.002289
CYP2A13	*1/*7	Intermediate Metabolizer	0.011718
CYP2A13	*1/*8	Indeterminate	0.011942
CYP2A13	*1/*2	Indeterminate	0.040742
CYP2A13	*1/*1	Normal Metabolizer	0.930187
CYP2D6	*106/*35	Indeterminate	0.000016
CYP2D6	*116/*45	Indeterminate	0.000016
CYP2D6	*106/*3	Indeterminate	0.000016
CYP2D6	*35/*69	Intermediate Metabolizer	0.000016
CYP2D6	*117/*28	Indeterminate	0.000016
CYP2D6	*116/*39	Indeterminate	0.000016
CYP2D6	*138/*4	Indeterminate	0.000016
CYP2D6	*117/*6	Indeterminate	0.000016

Gene	Diplotype	Activity Phenotype	Frequency
CYP2D6	*116/*9	Indeterminate	0.000016
CYP2D6	*2/*53	Normal Metabolizer	0.000016
CYP2D6	*17/*34	Normal Metabolizer	0.000016
CYP2D6	*106/*46	Indeterminate	0.000016
CYP2D6	*6/*7	Poor Metabolizer	0.000016
CYP2D6	*11/*41	Intermediate Metabolizer	0.000016
CYP2D6	*3/*7	Poor Metabolizer	0.000016
CYP2D6	*107/*9	Indeterminate	0.000016
CYP2D6	*39/*46	Normal Metabolizer	0.000016
CYP2D6	*10/*7	Intermediate Metabolizer	0.000016
CYP2D6	*4/*53	Intermediate Metabolizer	0.000016
CYP2D6	*10/*84	Indeterminate	0.000016
CYP2D6	*41/*84	Indeterminate	0.000016
CYP2D6	*33/*7	Intermediate Metabolizer	0.000016
CYP2D6	*17/*59	Intermediate Metabolizer	0.000016
CYP2D6	*106/*33	Indeterminate	0.000016
CYP2D6	*39/*39	Normal Metabolizer	0.000016
CYP2D6	*106/*28	Indeterminate	0.000016
CYP2D6	*126/*2	Indeterminate	0.000016
CYP2D6	*33/*43	Indeterminate	0.000016
CYP2D6	*31/*45	Intermediate Metabolizer	0.000016
CYP2D6	*17/*22	Indeterminate	0.000016
CYP2D6	*35/*53	Normal Metabolizer	0.000016
CYP2D6	*29/*7	Intermediate Metabolizer	0.000016
CYP2D6	*45/*59	Normal Metabolizer	0.000016
CYP2D6	*117/*9	Indeterminate	0.000016
CYP2D6	*116/*17	Indeterminate	0.000016
CYP2D6	*31/*41	Intermediate Metabolizer	0.000016
CYP2D6	*107/*2	Indeterminate	0.000016
CYP2D6	*28/*59	Indeterminate	0.000016
CYP2D6	*22/*59	Indeterminate	0.000016
CYP2D6	*107/*4	Indeterminate	0.000016
CYP2D6	*117/*33	Indeterminate	0.000016
CYP2D6	*43/*9	Indeterminate	0.000016
CYP2D6	*11/*39	Intermediate Metabolizer	0.000016
CYP2D6	*116/*33	Indeterminate	0.000032
CYP2D6	*41/*7	Intermediate Metabolizer	0.000032
CYP2D6	*11/*35	Intermediate Metabolizer	0.000032
CYP2D6	*10/*106	Indeterminate	0.000032
CYP2D6	*31/*6	Poor Metabolizer	0.000032
CYP2D6	*33/*45	Normal Metabolizer	0.000032
CYP2D6	*126/*41	Indeterminate	0.000032
CYP2D6	*10/*116	Indeterminate	0.000032
CYP2D6	*10/*11	Intermediate Metabolizer	0.000032
CYP2D6	*10/*34	Normal Metabolizer	0.000032
CYP2D6	*11/*4	Poor Metabolizer	0.000032
CYP2D6	*1/*138	Indeterminate	0.000032
CYP2D6	*3/*43	Indeterminate	0.000032
CYP2D6	*10/*31	Intermediate Metabolizer	0.000032
CYP2D6	*1/*107	Indeterminate	0.000032
CYP2D6	*116/*3	Indeterminate	0.000032
CYP2D6	*126/*4	Indeterminate	0.000032
CYP2D6	*39/*59	Normal Metabolizer	0.000032
CYP2D6	*10/*117	Indeterminate	0.000032
CYP2D6	*28/*6	Indeterminate	0.000048

Gene	Diplotype	Activity Phenotype	Frequency
CYP2D6	*117/*3	Indeterminate	0.000048
CYP2D6	*31/*4	Poor Metabolizer	0.000048
CYP2D6	*1/*34	Normal Metabolizer	0.000048
CYP2D6	*28/*29	Indeterminate	0.000048
CYP2D6	*116/*35	Indeterminate	0.000048
CYP2D6	*10/*59	Intermediate Metabolizer	0.000048
CYP2D6	*2/*31	Intermediate Metabolizer	0.000048
CYP2D6	*35/*46	Normal Metabolizer	0.000048
CYP2D6	*59/*6	Intermediate Metabolizer	0.000048
CYP2D6	*4/*69	Poor Metabolizer	0.000048
CYP2D6	*34/*35	Normal Metabolizer	0.000048
CYP2D6	*3/*45	Intermediate Metabolizer	0.000048
CYP2D6	*10/*22	Indeterminate	0.000048
CYP2D6	*43/*45	Indeterminate	0.000048
CYP2D6	*10/*46	Normal Metabolizer	0.000048
CYP2D6	*4/*46	Intermediate Metabolizer	0.000064
CYP2D6	*28/*33	Indeterminate	0.000064
CYP2D6	*22/*3	Indeterminate	0.000064
CYP2D6	*106/*29	Indeterminate	0.000064
CYP2D6	*29/*6	Intermediate Metabolizer	0.000064
CYP2D6	*2/*34	Normal Metabolizer	0.000064
CYP2D6	*35/*7	Intermediate Metabolizer	0.000064
CYP2D6	*22/*33	Indeterminate	0.000064
CYP2D6	*29/*9	Intermediate Metabolizer	0.000064
CYP2D6	*45/*9	Normal Metabolizer	0.000064
CYP2D6	*34/*41	Normal Metabolizer	0.000064
CYP2D6	*4/*84	Indeterminate	0.000064
CYP2D6	*1/*69	Intermediate Metabolizer	0.000064
CYP2D6	*1/*31	Intermediate Metabolizer	0.000064
CYP2D6	*10/*28	Indeterminate	0.000064
CYP2D6	*31/*35	Intermediate Metabolizer	0.000064
CYP2D6	*28/*3	Indeterminate	0.000064
CYP2D6	*106/*45	Indeterminate	0.000064
CYP2D6	*45/*46	Normal Metabolizer	0.000064
CYP2D6	*17/*28	Indeterminate	0.000080
CYP2D6	*29/*39	Normal Metabolizer	0.000080
CYP2D6	*17/*84	Indeterminate	0.000080
CYP2D6	*1/*84	Indeterminate	0.000080
CYP2D6	*45/*45	Normal Metabolizer	0.000080
CYP2D6	*117/*35	Indeterminate	0.000080
CYP2D6	*34/*4	Intermediate Metabolizer	0.000080
CYP2D6	*106/*41	Indeterminate	0.000080
CYP2D6	*41/*46	Normal Metabolizer	0.000080
CYP2D6	*2/*84	Indeterminate	0.000080
CYP2D6	*1/*11	Intermediate Metabolizer	0.000080
CYP2D6	*3/*59	Intermediate Metabolizer	0.000080
CYP2D6	*39/*45	Normal Metabolizer	0.000096
CYP2D6	*1/*126	Indeterminate	0.000096
CYP2D6	*17/*6	Intermediate Metabolizer	0.000096
CYP2D6	*39/*6	Intermediate Metabolizer	0.000096
CYP2D6	*1/*53	Normal Metabolizer	0.000096
CYP2D6	*33/*59	Normal Metabolizer	0.000096
CYP2D6	*116/*41	Indeterminate	0.000096
CYP2D6	*29/*43	Indeterminate	0.000112
CYP2D6	*2/*7	Intermediate Metabolizer	0.000112

Gene	Diplotype	Activity Phenotype	Frequency
CYP2D6	*29/*46	Normal Metabolizer	0.000112
CYP2D6	*17/*3	Intermediate Metabolizer	0.000112
CYP2D6	*41/*43	Indeterminate	0.000112
CYP2D6	*17/*43	Indeterminate	0.000112
CYP2D6	*17/*33	Normal Metabolizer	0.000128
CYP2D6	*4/*7	Poor Metabolizer	0.000128
CYP2D6	*35/*45	Normal Metabolizer	0.000128
CYP2D6	*117/*41	Indeterminate	0.000128
CYP2D6	*41/*45	Normal Metabolizer	0.000144
CYP2D6	*33/*33	Normal Metabolizer	0.000144
CYP2D6	*3/*39	Intermediate Metabolizer	0.000144
CYP2D6	*2/*46	Normal Metabolizer	0.000160
CYP2D6	*33/*39	Normal Metabolizer	0.000160
CYP2D6	*28/*9	Indeterminate	0.000160
CYP2D6	*22/*9	Indeterminate	0.000160
CYP2D6	*59/*9	Intermediate Metabolizer	0.000176
CYP2D6	*4/*43	Indeterminate	0.000176
CYP2D6	*3/*3	Poor Metabolizer	0.000176
CYP2D6	*39/*9	Normal Metabolizer	0.000192
CYP2D6	*10/*45	Normal Metabolizer	0.000192
CYP2D6	*6/*6	Poor Metabolizer	0.000192
CYP2D6	*106/*4	Indeterminate	0.000208
CYP2D6	*106/*17	Indeterminate	0.000208
CYP2D6	*17/*39	Normal Metabolizer	0.000224
CYP2D6	*17/*9	Intermediate Metabolizer	0.000224
CYP2D6	*29/*35	Normal Metabolizer	0.000224
CYP2D6	*117/*4	Indeterminate	0.000224
CYP2D6	*116/*2	Indeterminate	0.000240
CYP2D6	*106/*2	Indeterminate	0.000240
CYP2D6	*10/*39	Normal Metabolizer	0.000256
CYP2D6	*22/*35	Indeterminate	0.000272
CYP2D6	*17/*46	Normal Metabolizer	0.000288
CYP2D6	*1/*116	Indeterminate	0.000304
CYP2D6	*117/*2	Indeterminate	0.000304
CYP2D6	*3/*33	Intermediate Metabolizer	0.000304
CYP2D6	*116/*4	Indeterminate	0.000304
CYP2D6	*33/*6	Intermediate Metabolizer	0.000304
CYP2D6	*2/*43	Indeterminate	0.000336
CYP2D6	*1/*7	Intermediate Metabolizer	0.000336
CYP2D6	*10/*33	Normal Metabolizer	0.000352
CYP2D6	*29/*41	Intermediate Metabolizer	0.000368
CYP2D6	*28/*35	Indeterminate	0.000368
CYP2D6	*35/*59	Normal Metabolizer	0.000400
CYP2D6	*3/*6	Poor Metabolizer	0.000416
CYP2D6	*29/*45	Normal Metabolizer	0.000416
CYP2D6	*22/*41	Indeterminate	0.000432
CYP2D6	*17/*35	Normal Metabolizer	0.000432
CYP2D6	*35/*39	Normal Metabolizer	0.000448
CYP2D6	*1/*43	Indeterminate	0.000448
CYP2D6	*10/*6	Intermediate Metabolizer	0.000464
CYP2D6	*29/*29	Intermediate Metabolizer	0.000464
CYP2D6	*9/*9	Intermediate Metabolizer	0.000480
CYP2D6	*4/*45	Intermediate Metabolizer	0.000480
CYP2D6	*28/*41	Indeterminate	0.000480
CYP2D6	*10/*3	Intermediate Metabolizer	0.000528

Gene	Diplotype	Activity Phenotype	Frequency
CYP2D6	*10/*29	Intermediate Metabolizer	0.000528
CYP2D6	*1/*106	Indeterminate	0.000528
CYP2D6	*1/*117	Indeterminate	0.000528
CYP2D6	*6/*9	Intermediate Metabolizer	0.000528
CYP2D6	*41/*59	Intermediate Metabolizer	0.000544
CYP2D6	*1/*46	Normal Metabolizer	0.000560
CYP2D6	*33/*9	Normal Metabolizer	0.000560
CYP2D6	*3/*9	Intermediate Metabolizer	0.000672
CYP2D6	*2/*45	Normal Metabolizer	0.000736
CYP2D6	*2/*22	Indeterminate	0.000800
CYP2D6	*17/*45	Normal Metabolizer	0.000848
CYP2D6	*2/*28	Indeterminate	0.000880
CYP2D6	*35/*6	Intermediate Metabolizer	0.000880
CYP2D6	*22/*4	Indeterminate	0.000912
CYP2D6	*10/*9	Intermediate Metabolizer	0.000912
CYP2D6	*29/*4	Intermediate Metabolizer	0.000944
CYP2D6	*28/*4	Indeterminate	0.000993
CYP2D6	*39/*41	Normal Metabolizer	0.001105
CYP2D6	*10/*17	Intermediate Metabolizer	0.001121
CYP2D6	*17/*41	Intermediate Metabolizer	0.001121
CYP2D6	*2/*59	Normal Metabolizer	0.001249
CYP2D6	*4/*59	Intermediate Metabolizer	0.001249
CYP2D6	*1/*45	Normal Metabolizer	0.001329
CYP2D6	*33/*35	Normal Metabolizer	0.001345
CYP2D6	*1/*22	Indeterminate	0.001457
CYP2D6	*2/*39	Normal Metabolizer	0.001505
CYP2D6	*3/*35	Intermediate Metabolizer	0.001649
CYP2D6	*33/*41	Normal Metabolizer	0.001809
CYP2D6	*41/*6	Intermediate Metabolizer	0.001969
CYP2D6	*1/*28	Indeterminate	0.001969
CYP2D6	*17/*17	Intermediate Metabolizer	0.001985
CYP2D6	*2/*29	Normal Metabolizer	0.002065
CYP2D6	*39/*4	Intermediate Metabolizer	0.002129
CYP2D6	*10/*35	Normal Metabolizer	0.002145
CYP2D6	*17/*29	Intermediate Metabolizer	0.002273
CYP2D6	*17/*4	Intermediate Metabolizer	0.002385
CYP2D6	*1/*59	Normal Metabolizer	0.002513
CYP2D6	*35/*9	Normal Metabolizer	0.002625
CYP2D6	*3/*41	Intermediate Metabolizer	0.002737
CYP2D6	*2/*6	Intermediate Metabolizer	0.002898
CYP2D6	*35/*35	Normal Metabolizer	0.003282
CYP2D6	*4/*6	Poor Metabolizer	0.003362
CYP2D6	*2/*33	Normal Metabolizer	0.003378
CYP2D6	*1/*39	Normal Metabolizer	0.003970
CYP2D6	*33/*4	Intermediate Metabolizer	0.004114
CYP2D6	*1/*29	Normal Metabolizer	0.004210
CYP2D6	*10/*41	Intermediate Metabolizer	0.004258
CYP2D6	*41/*9	Intermediate Metabolizer	0.004402
CYP2D6	*2/*3	Intermediate Metabolizer	0.004706
CYP2D6	*17/*2	Normal Metabolizer	0.005267
CYP2D6	*10/*10	Intermediate Metabolizer	0.005347
CYP2D6	*3/*4	Poor Metabolizer	0.005635
CYP2D6	*1/*6	Intermediate Metabolizer	0.006852
CYP2D6	*10/*4	Intermediate Metabolizer	0.007140
CYP2D6	*1/*33	Normal Metabolizer	0.008292

Gene	Diplotype	Activity Phenotype	Frequency
CYP2D6	*2/*9	Normal Metabolizer	0.008533
CYP2D6	*1/*17	Normal Metabolizer	0.008597
CYP2D6	*10/*2	Normal Metabolizer	0.008757
CYP2D6	*4/*9	Intermediate Metabolizer	0.009045
CYP2D6	*41/*41	Intermediate Metabolizer	0.009669
CYP2D6	*35/*41	Normal Metabolizer	0.010149
CYP2D6	*1/*3	Intermediate Metabolizer	0.011030
CYP2D6	*1/*9	Normal Metabolizer	0.017433
CYP2D6	*2/*35	Normal Metabolizer	0.019146
CYP2D6	*1/*10	Normal Metabolizer	0.020267
CYP2D6	*35/*4	Intermediate Metabolizer	0.021595
CYP2D6	*2/*2	Normal Metabolizer	0.027583
CYP2D6	*2/*41	Normal Metabolizer	0.030784
CYP2D6	*4/*41	Intermediate Metabolizer	0.033986
CYP2D6	*4/*4	Poor Metabolizer	0.036723
CYP2D6	*1/*35	Normal Metabolizer	0.042358
CYP2D6	*2/*4	Intermediate Metabolizer	0.061488
CYP2D6	*1/*41	Normal Metabolizer	0.068388
CYP2D6	*1/*2	Normal Metabolizer	0.123121
CYP2D6	*1/*4	Intermediate Metabolizer	0.139049
CYP2D6	*1/*1	Normal Metabolizer	0.143036
CYP2A6	*14/*28	Indeterminate	0.000016
CYP2A6	*21/*28	Indeterminate	0.000016
CYP2A6	*20/*20	Poor Metabolizer	0.000016
CYP2A6	*42/*9	Indeterminate	0.000016
CYP2A6	*14/*27	Indeterminate	0.000016
CYP2A6	*27/*28	Indeterminate	0.000016
CYP2A6	*2/*8	Intermediate Metabolizer	0.000016
CYP2A6	*18/*27	Intermediate Metabolizer	0.000016
CYP2A6	*2/*41	Poor Metabolizer	0.000016
CYP2A6	*18/*8	Normal Metabolizer	0.000016
CYP2A6	*20/*28	Indeterminate	0.000016
CYP2A6	*41/*41	Poor Metabolizer	0.000016
CYP2A6	*28/*41	Indeterminate	0.000016
CYP2A6	*14/*8	Indeterminate	0.000016
CYP2A6	*25/*9	Indeterminate	0.000016
CYP2A6	*23/*23	Intermediate Metabolizer	0.000032
CYP2A6	*41/*9	Intermediate Metabolizer	0.000032
CYP2A6	*17/*41	Intermediate Metabolizer	0.000032
CYP2A6	*23/*28	Indeterminate	0.000032
CYP2A6	*20/*27	Poor Metabolizer	0.000032
CYP2A6	*17/*27	Intermediate Metabolizer	0.000032
CYP2A6	*18/*26	Intermediate Metabolizer	0.000032
CYP2A6	*17/*21	Intermediate Metabolizer	0.000048
CYP2A6	*2/*28	Indeterminate	0.000048
CYP2A6	*11/*9	Intermediate Metabolizer	0.000048
CYP2A6	*38/*9	Indeterminate	0.000048
CYP2A6	*2/*23	Intermediate Metabolizer	0.000048
CYP2A6	*26/*9	Intermediate Metabolizer	0.000064
CYP2A6	*17/*25	Indeterminate	0.000064
CYP2A6	*27/*9	Intermediate Metabolizer	0.000080
CYP2A6	*17/*2	Intermediate Metabolizer	0.000080
CYP2A6	*17/*18	Intermediate Metabolizer	0.000080
CYP2A6	*17/*26	Intermediate Metabolizer	0.000112
CYP2A6	*1/*41	Intermediate Metabolizer	0.000128

Gene	Diplotype	Activity Phenotype	Frequency
CYP2A6	*28/*9	Indeterminate	0.000128
CYP2A6	*20/*9	Intermediate Metabolizer	0.000144
CYP2A6	*17/*28	Indeterminate	0.000144
CYP2A6	*8/*9	Normal Metabolizer	0.000160
CYP2A6	*18/*21	Intermediate Metabolizer	0.000160
CYP2A6	*14/*17	Indeterminate	0.000160
CYP2A6	*18/*18	Intermediate Metabolizer	0.000176
CYP2A6	*17/*20	Intermediate Metabolizer	0.000176
CYP2A6	*1/*11	Normal Metabolizer	0.000176
CYP2A6	*23/*9	Intermediate Metabolizer	0.000176
CYP2A6	*1/*38	Indeterminate	0.000176
CYP2A6	*1/*42	Indeterminate	0.000176
CYP2A6	*17/*23	Intermediate Metabolizer	0.000192
CYP2A6	*21/*21	Intermediate Metabolizer	0.000272
CYP2A6	*1/*26	Normal Metabolizer	0.000336
CYP2A6	*17/*17	Intermediate Metabolizer	0.000336
CYP2A6	*1/*25	Indeterminate	0.000336
CYP2A6	*1/*27	Intermediate Metabolizer	0.000592
CYP2A6	*2/*21	Intermediate Metabolizer	0.000672
CYP2A6	*18/*2	Intermediate Metabolizer	0.000704
CYP2A6	*2/*2	Poor Metabolizer	0.000800
CYP2A6	*14/*21	Indeterminate	0.000880
CYP2A6	*14/*18	Indeterminate	0.000896
CYP2A6	*1/*20	Intermediate Metabolizer	0.000961
CYP2A6	*17/*9	Intermediate Metabolizer	0.001057
CYP2A6	*1/*8	Normal Metabolizer	0.001137
CYP2A6	*14/*14	Indeterminate	0.001425
CYP2A6	*1/*23	Normal Metabolizer	0.001441
CYP2A6	*21/*9	Intermediate Metabolizer	0.001441
CYP2A6	*18/*9	Intermediate Metabolizer	0.001537
CYP2A6	*14/*2	Indeterminate	0.001985
CYP2A6	*1/*28	Indeterminate	0.002641
CYP2A6	*2/*9	Intermediate Metabolizer	0.003170
CYP2A6	*14/*9	Indeterminate	0.004706
CYP2A6	*9/*9	Intermediate Metabolizer	0.005267
CYP2A6	*1/*17	Normal Metabolizer	0.010774
CYP2A6	*1/*21	Normal Metabolizer	0.018826
CYP2A6	*1/*18	Normal Metabolizer	0.019370
CYP2A6	*1/*2	Intermediate Metabolizer	0.038196
CYP2A6	*1/*14	Indeterminate	0.059599
CYP2A6	*1/*9	Normal Metabolizer	0.110602
CYP2A6	*1/*1	Normal Metabolizer	0.706581
UGT2B15	*5/*6	Indeterminate	0.000016
UGT2B15	*S2/*S2	No Function	0.000016
UGT2B15	*4/*6	Indeterminate	0.000016
UGT2B15	*1/*6	Indeterminate	0.000096
UGT2B15	*5/*S2	Indeterminate	0.000192
UGT2B15	*2/*S2	Indeterminate	0.000384
UGT2B15	*4/*S2	Indeterminate	0.000384
UGT2B15	*1/*S2	Decreased Function	0.000528
UGT2B15	*1/*1	Normal Function	0.034594
UGT2B15	*2/*2	Indeterminate	0.057630
UGT2B15	*1/*5	Indeterminate	0.072454
UGT2B15	*5/*5	Indeterminate	0.075448
UGT2B15	*1/*2	Indeterminate	0.081707

Gene	Diplotype	Activity Phenotype	Frequency
UGT2B15	*1/*4	Indeterminate	0.089103
UGT2B15	*4/*4	Indeterminate	0.116654
UGT2B15	*2/*5	Indeterminate	0.129268
UGT2B15	*2/*4	Indeterminate	0.156739
UGT2B15	*4/*5	Indeterminate	0.184770
CYP3A7	*1D/*1E	Indeterminate	0.000016
CYP3A7	*1B/*1E	Indeterminate	0.000016
CYP3A7	*1B/*1B	Indeterminate	0.000016
CYP3A7	*1B/*1D	Indeterminate	0.000064
CYP3A7	*1D/*1D	Indeterminate	0.000080
CYP3A7	*1B/*2	Indeterminate	0.000688
CYP3A7	*1E/*1E	Indeterminate	0.000704
CYP3A7	*1D/*2	Indeterminate	0.001425
CYP3A7	*1E/*2	Indeterminate	0.005443
CYP3A7	*1/*1B	Indeterminate	0.006515
CYP3A7	*1/*1E	Indeterminate	0.008693
CYP3A7	*1/*1D	Indeterminate	0.009941
CYP3A7	*2/*2	Indeterminate	0.022044
CYP3A7	*1/*2	Indeterminate	0.185074
CYP3A7	*1/*1	Normal Metabolizer	0.759281
CYP4A11	*S1/*S1	Intermediate Metabolizer	0.025822
CYP4A11	*1/*S1	Normal Metabolizer	0.254614
CYP4A11	*1/*1	Normal Metabolizer	0.719564
CYP2B6	*18/*8	Poor Metabolizer	0.000016
CYP2B6	*10/*11	Indeterminate	0.000016
CYP2B6	*14/*5	Indeterminate	0.000016
CYP2B6	*10/*18	Indeterminate	0.000016
CYP2B6	*10/*15	Indeterminate	0.000016
CYP2B6	*8/*8	Poor Metabolizer	0.000016
CYP2B6	*12/*12	Poor Metabolizer	0.000016
CYP2B6	*3/*9	Indeterminate	0.000032
CYP2B6	*11/*11	Indeterminate	0.000032
CYP2B6	*12/*2	Intermediate Metabolizer	0.000032
CYP2B6	*11/*15	Indeterminate	0.000032
CYP2B6	*15/*8	Indeterminate	0.000048
CYP2B6	*15/*15	Indeterminate	0.000048
CYP2B6	*10/*10	Indeterminate	0.000048
CYP2B6	*10/*8	Indeterminate	0.000064
CYP2B6	*12/*5	Intermediate Metabolizer	0.000064
CYP2B6	*11/*8	Indeterminate	0.000064
CYP2B6	*12/*9	Poor Metabolizer	0.000080
CYP2B6	*22/*8	Intermediate Metabolizer	0.000080
CYP2B6	*18/*5	Intermediate Metabolizer	0.000128
CYP2B6	*1/*3	Indeterminate	0.000128
CYP2B6	*11/*22	Indeterminate	0.000128
CYP2B6	*10/*22	Indeterminate	0.000160
CYP2B6	*1/*12	Intermediate Metabolizer	0.000160
CYP2B6	*15/*22	Indeterminate	0.000208
CYP2B6	*18/*22	Intermediate Metabolizer	0.000224
CYP2B6	*22/*22	Ultrarapid Metabolizer	0.000224
CYP2B6	*2/*8	Intermediate Metabolizer	0.000256
CYP2B6	*18/*18	Poor Metabolizer	0.000320
CYP2B6	*11/*2	Indeterminate	0.000336
CYP2B6	*18/*2	Intermediate Metabolizer	0.000352
CYP2B6	*10/*2	Indeterminate	0.000368

Gene	Diplotype	Activity Phenotype	Frequency
CYP2B6	*15/*2	Indeterminate	0.000656
CYP2B6	*11/*5	Indeterminate	0.000656
CYP2B6	*5/*8	Intermediate Metabolizer	0.000720
CYP2B6	*2/*22	Rapid Metabolizer	0.000784
CYP2B6	*10/*5	Indeterminate	0.000993
CYP2B6	*11/*9	Indeterminate	0.001649
CYP2B6	*8/*9	Poor Metabolizer	0.001665
CYP2B6	*15/*5	Indeterminate	0.001681
CYP2B6	*10/*9	Indeterminate	0.002081
CYP2B6	*2/*2	Normal Metabolizer	0.002337
CYP2B6	*22/*5	Rapid Metabolizer	0.002401
CYP2B6	*15/*9	Indeterminate	0.003234
CYP2B6	*18/*9	Poor Metabolizer	0.003570
CYP2B6	*1/*11	Indeterminate	0.003794
CYP2B6	*1/*8	Intermediate Metabolizer	0.003890
CYP2B6	*1/*18	Intermediate Metabolizer	0.004274
CYP2B6	*1/*10	Indeterminate	0.005171
CYP2B6	*22/*9	Intermediate Metabolizer	0.005747
CYP2B6	*1/*15	Indeterminate	0.007860
CYP2B6	*2/*5	Normal Metabolizer	0.010662
CYP2B6	*1/*22	Rapid Metabolizer	0.012439
CYP2B6	*5/*5	Normal Metabolizer	0.012839
CYP2B6	*2/*9	Intermediate Metabolizer	0.023548
CYP2B6	*5/*9	Intermediate Metabolizer	0.051835
CYP2B6	*1/*2	Normal Metabolizer	0.052700
CYP2B6	*9/*9	Poor Metabolizer	0.064850
CYP2B6	*1/*5	Normal Metabolizer	0.119439
CYP2B6	*1/*9	Intermediate Metabolizer	0.277699
CYP2B6	*1/*1	Normal Metabolizer	0.317095
CYP19A1	*2/*2	Intermediate Metabolizer	0.000016
CYP19A1	*2/*4	Intermediate Metabolizer	0.000208
CYP19A1	*3/*3	Indeterminate	0.001329
CYP19A1	*1/*2	Normal Metabolizer	0.001409
CYP19A1	*3/*4	Indeterminate	0.002625
CYP19A1	*4/*4	Intermediate Metabolizer	0.003874
CYP19A1	*1/*3	Indeterminate	0.062961
CYP19A1	*1/*4	Normal Metabolizer	0.086173
CYP19A1	*1/*1	Normal Metabolizer	0.841404
SLCO1B3	*1/*1	Normal Function	0.041430
SLCO1B3	*1/*S1	Decreased Function	0.271343
SLCO1B3	*S1/*S1	Poor Function	0.687227
CYP2C19	*10/*35	Likely Poor Metabolizer	0.000016
CYP2C19	*2/*22	Poor Metabolizer	0.000016
CYP2C19	*3/*9	Likely Poor Metabolizer	0.000016
CYP2C19	*10/*22	Likely Poor Metabolizer	0.000016
CYP2C19	*30/*9	Indeterminate	0.000016
CYP2C19	*4/*8	Poor Metabolizer	0.000016
CYP2C19	*15/*9	Likely Intermediate Metabolizer	0.000016
CYP2C19	*11/*17	Rapid Metabolizer	0.000016
CYP2C19	*15/*8	Intermediate Metabolizer	0.000016
CYP2C19	*13/*9	Likely Intermediate Metabolizer	0.000016
CYP2C19	*22/*35	Poor Metabolizer	0.000016
CYP2C19	*13/*13	Normal Metabolizer	0.000016
CYP2C19	*13/*22	Intermediate Metabolizer	0.000016
CYP2C19	*18/*2	Intermediate Metabolizer	0.000016

Gene	Diplotype	Activity Phenotype	Frequency
CYP2C19	*1/*11	Normal Metabolizer	0.000016
CYP2C19	*35/*8	Poor Metabolizer	0.000016
CYP2C19	*35/*9	Likely Poor Metabolizer	0.000016
CYP2C19	*8/*8	Poor Metabolizer	0.000032
CYP2C19	*22/*9	Likely Poor Metabolizer	0.000032
CYP2C19	*15/*35	Intermediate Metabolizer	0.000032
CYP2C19	*35/*35	Poor Metabolizer	0.000048
CYP2C19	*17/*18	Rapid Metabolizer	0.000048
CYP2C19	*13/*35	Intermediate Metabolizer	0.000048
CYP2C19	*17/*30	Indeterminate	0.000064
CYP2C19	*3/*3	Poor Metabolizer	0.000080
CYP2C19	*17/*22	Intermediate Metabolizer	0.000080
CYP2C19	*10/*2	Likely Poor Metabolizer	0.000080
CYP2C19	*17/*6	Intermediate Metabolizer	0.000096
CYP2C19	*2/*30	Indeterminate	0.000096
CYP2C19	*1/*18	Normal Metabolizer	0.000096
CYP2C19	*13/*15	Normal Metabolizer	0.000096
CYP2C19	*10/*17	Likely Intermediate Metabolizer	0.000112
CYP2C19	*2/*6	Poor Metabolizer	0.000112
CYP2C19	*1/*22	Intermediate Metabolizer	0.000144
CYP2C19	*1/*10	Likely Intermediate Metabolizer	0.000240
CYP2C19	*1/*30	Indeterminate	0.000240
CYP2C19	*17/*3	Intermediate Metabolizer	0.000256
CYP2C19	*2/*9	Likely Poor Metabolizer	0.000304
CYP2C19	*1/*6	Intermediate Metabolizer	0.000368
CYP2C19	*17/*9	Likely Intermediate Metabolizer	0.000400
CYP2C19	*13/*2	Intermediate Metabolizer	0.000464
CYP2C19	*2/*35	Poor Metabolizer	0.000480
CYP2C19	*15/*2	Intermediate Metabolizer	0.000496
CYP2C19	*2/*4	Poor Metabolizer	0.000496
CYP2C19	*13/*17	Rapid Metabolizer	0.000496
CYP2C19	*15/*17	Rapid Metabolizer	0.000624
CYP2C19	*17/*35	Intermediate Metabolizer	0.000640
CYP2C19	*2/*8	Poor Metabolizer	0.000656
CYP2C19	*17/*4	Intermediate Metabolizer	0.000832
CYP2C19	*2/*3	Poor Metabolizer	0.000848
CYP2C19	*1/*13	Normal Metabolizer	0.000993
CYP2C19	*17/*8	Intermediate Metabolizer	0.001009
CYP2C19	*1/*9	Likely Intermediate Metabolizer	0.001025
CYP2C19	*1/*15	Normal Metabolizer	0.001489
CYP2C19	*1/*35	Intermediate Metabolizer	0.001681
CYP2C19	*1/*3	Intermediate Metabolizer	0.002097
CYP2C19	*1/*4	Intermediate Metabolizer	0.002625
CYP2C19	*1/*8	Intermediate Metabolizer	0.003330
CYP2C19	*2/*2	Poor Metabolizer	0.025902
CYP2C19	*17/*17	Ultrarapid Metabolizer	0.046953
CYP2C19	*17/*2	Intermediate Metabolizer	0.064034
CYP2C19	*1/*2	Intermediate Metabolizer	0.189188
CYP2C19	*1/*17	Rapid Metabolizer	0.260842
CYP2C19	*1/*1	Normal Metabolizer	0.389422
CYP4F2	*2/*2	Normal Metabolizer	0.002337
CYP4F2	*2/*3	Normal Metabolizer	0.003970
CYP4F2	*1/*2	Normal Metabolizer	0.019530
CYP4F2	*3/*3	Intermediate Metabolizer	0.080122
CYP4F2	*1/*3	Normal Metabolizer	0.390654

Gene	Diplotype	Activity Phenotype	Frequency
CYP4F2	*1/*1	Normal Metabolizer	0.503386
ABCB1	*2/*2	Indeterminate	0.147422
ABCB1	*1/*1	Normal Function	0.398514
ABCB1	*1/*2	Indeterminate	0.454064
SLC22A2	*7/*7	Indeterminate	0.000016
SLC22A2	*7/*K432Q	Indeterminate	0.000016
SLC22A2	*6/*6	Indeterminate	0.000016
SLC22A2	*6/*K432Q	Indeterminate	0.000016
SLC22A2	*1/*8	Indeterminate	0.000016
SLC22A2	*4/*4	Indeterminate	0.000032
SLC22A2	*4/*6	Indeterminate	0.000032
SLC22A2	*2/*4	Indeterminate	0.000336
SLC22A2	*3/*4	Indeterminate	0.000528
SLC22A2	*2/*7	Indeterminate	0.000544
SLC22A2	*1/*7	Indeterminate	0.000544
SLC22A2	*3/*7	Indeterminate	0.000720
SLC22A2	*3/*6	Indeterminate	0.000816
SLC22A2	*1/*4	Indeterminate	0.000944
SLC22A2	*2/*K432Q	Indeterminate	0.001105
SLC22A2	*3/*K432Q	Indeterminate	0.001441
SLC22A2	*1/*K432Q	Indeterminate	0.001489
SLC22A2	*1/*6	Indeterminate	0.001601
SLC22A2	*2/*6	Indeterminate	0.001889
SLC22A2	*3/*3	Indeterminate	0.052284
SLC22A2	*1/*1	Normal Metabolizer	0.146846
SLC22A2	*2/*2	Indeterminate	0.158083
SLC22A2	*1/*3	Indeterminate	0.168409
SLC22A2	*2/*3	Indeterminate	0.174268
SLC22A2	*1/*2	Indeterminate	0.288008
CYP2E1	*3/*5	Indeterminate	0.000096
CYP2E1	*3/*4	Normal Metabolizer	0.000096
CYP2E1	*4/*5	Indeterminate	0.001873
CYP2E1	*5/*5	Indeterminate	0.002017
CYP2E1	*4/*4	Normal Metabolizer	0.003602
CYP2E1	*1/*3	Normal Metabolizer	0.004194
CYP2E1	*1/*5	Indeterminate	0.058287
CYP2E1	*1/*4	Normal Metabolizer	0.062193
CYP2E1	*1/*1	Normal Metabolizer	0.867642
CYP4A22	*10/*12	Indeterminate	0.000016
CYP4A22	*10/*5	Indeterminate	0.000016
CYP4A22	*1/*4	Indeterminate	0.000016
CYP4A22	*15/*6	Indeterminate	0.000032
CYP4A22	*1/*10	Indeterminate	0.000048
CYP4A22	*13/*13	Indeterminate	0.000048
CYP4A22	*13/*9	Indeterminate	0.000048
CYP4A22	*13/*15	Indeterminate	0.000096
CYP4A22	*9/*9	Indeterminate	0.000288
CYP4A22	*12/*13	Indeterminate	0.000560
CYP4A22	*13/*5	Indeterminate	0.000720
CYP4A22	*1/*13	Indeterminate	0.001681
CYP4A22	*15/*9	Indeterminate	0.002337
CYP4A22	*12/*9	Indeterminate	0.003170
CYP4A22	*5/*9	Indeterminate	0.003314
CYP4A22	*15/*15	Indeterminate	0.009717
CYP4A22	*1/*9	Indeterminate	0.012230

Gene	Diplotype	Activity Phenotype	Frequency
CYP4A22	*12/*12	Indeterminate	0.017193
CYP4A22	*5/*5	Indeterminate	0.021788
CYP4A22	*12/*15	Indeterminate	0.024013
CYP4A22	*15/*5	Indeterminate	0.025453
CYP4A22	*12/*5	Indeterminate	0.037636
CYP4A22	*1/*15	Indeterminate	0.105432
CYP4A22	*1/*12	Indeterminate	0.154626
CYP4A22	*1/*5	Indeterminate	0.173996
CYP4A22	*1/*1	Normal Metabolizer	0.405526
CFTR	*S18/*S18	Indeterminate	0.000016
CFTR	*S31/*S31	Decreased Function	0.000016
CFTR	*1/*S3	Decreased Function	0.000176
CFTR	*1/*S2	Decreased Function	0.000208
CFTR	*1/*S4	Decreased Function	0.000304
CFTR	*1/*S26	Indeterminate	0.000336
CFTR	*1/*S30	Decreased Function	0.000336
CFTR	*1/*S34	Indeterminate	0.000336
CFTR	*1/*S18	Indeterminate	0.000560
CFTR	*1/*S22	Decreased Function	0.000784
CFTR	*1/*S10	Decreased Function	0.000912
CFTR	*1/*S16	Decreased Function	0.001585
CFTR	*1/*S11	Decreased Function	0.001681
CFTR	*1/*S31	Decreased Function	0.004354
CFTR	*1/*1	Normal Function	0.988394
CYP2C8	*3/*7	Indeterminate	0.000016
CYP2C8	*4/*7	Indeterminate	0.000064
CYP2C8	*1/*7	Intermediate Metabolizer	0.000432
CYP2C8	*2/*4	Indeterminate	0.000656
CYP2C8	*2/*3	Indeterminate	0.001169
CYP2C8	*2/*2	Indeterminate	0.001441
CYP2C8	*4/*4	Indeterminate	0.002545
CYP2C8	*3/*4	Indeterminate	0.010854
CYP2C8	*3/*3	Indeterminate	0.012118
CYP2C8	*1/*2	Indeterminate	0.021051
CYP2C8	*1/*4	Indeterminate	0.077961
CYP2C8	*1/*3	Indeterminate	0.173676
CYP2C8	*1/*1	Normal Metabolizer	0.698017
TPMT	*2/*24	Possible Intermediate Metabolizer	0.000016
TPMT	*12/*3A	Possible Intermediate Metabolizer	0.000016
TPMT	*2/*2	Poor Metabolizer	0.000016
TPMT	*3C/*9	Possible Intermediate Metabolizer	0.000016
TPMT	*33/*3C	Possible Intermediate Metabolizer	0.000032
TPMT	*3A/*9	Possible Intermediate Metabolizer	0.000032
TPMT	*24/*3A	Possible Intermediate Metabolizer	0.000048
TPMT	*3A/*8	Possible Intermediate Metabolizer	0.000048
TPMT	*2/*3C	Poor Metabolizer	0.000048
TPMT	*24/*24	Indeterminate	0.000064
TPMT	*24/*8	Indeterminate	0.000080
TPMT	*1/*40	Indeterminate	0.000096
TPMT	*3C/*8	Possible Intermediate Metabolizer	0.000112
TPMT	*24/*3C	Possible Intermediate Metabolizer	0.000128
TPMT	*2/*3A	Poor Metabolizer	0.000144
TPMT	*3C/*3C	Poor Metabolizer	0.000160
TPMT	*1/*33	Indeterminate	0.000240
TPMT	*3A/*3C	Poor Metabolizer	0.000528

Gene	Diplotype	Activity Phenotype	Frequency
TPMT	*1/*12	Indeterminate	0.000544
TPMT	*1/*9	Indeterminate	0.000736
TPMT	*3A/*3A	Poor Metabolizer	0.001505
TPMT	*1/*8	Indeterminate	0.002241
TPMT	*1/*24	Indeterminate	0.002962
TPMT	*1/*2	Intermediate Metabolizer	0.003314
TPMT	*1/*3C	Intermediate Metabolizer	0.013767
TPMT	*1/*3A	Intermediate Metabolizer	0.069749
TPMT	*1/*1	Normal Metabolizer	0.903357
RYR1	*1/*S15	Increased Function	0.000272
RYR1	*1/*1	Normal Function	0.999728
POR	*28/*46	Indeterminate	0.000064
POR	*28/*42	Indeterminate	0.000080
POR	*11/*28	Decreased Function	0.000096
POR	*28/*29	Indeterminate	0.000112
POR	*28/*5	Decreased Function	0.000128
POR	*1/*42	Indeterminate	0.000192
POR	*1/*46	Indeterminate	0.000272
POR	*1/*11	Decreased Function	0.000272
POR	*28/*45	Indeterminate	0.000368
POR	*1/*5	Decreased Function	0.000432
POR	*27/*28	Decreased Function	0.000464
POR	*1/*29	Indeterminate	0.000624
POR	*1/*45	Indeterminate	0.000977
POR	*1/*27	Decreased Function	0.001761
POR	*28/*28	Decreased Function	0.079498
POR	*1/*28	Decreased Function	0.395505
POR	*1/*1	Normal Function	0.519154
VKORC1	*1/*4	Indeterminate	0.006547
VKORC1	*1/*1	Normal Function	0.008661
VKORC1	*1/*2	Indeterminate	0.011958
VKORC1	*1/*3	Indeterminate	0.028367
VKORC1	*4/*4	Indeterminate	0.047481
VKORC1	*2/*2	Indeterminate	0.147454
VKORC1	*3/*3	Indeterminate	0.150511
VKORC1	*2/*4	Indeterminate	0.161173
VKORC1	*3/*4	Indeterminate	0.162390
VKORC1	*2/*3	Indeterminate	0.275457
SULT1A1	*3/*3	Normal Function	0.004530
SULT1A1	*1/*3	Normal Function	0.028463
SULT1A1	*1/*1	Normal Function	0.967007
NUDT15	*4/*9	Possible Intermediate Metabolizer	0.000016
NUDT15	*6/*6	Indeterminate	0.000016
NUDT15	*9/*9	Poor Metabolizer	0.000032
NUDT15	*2/*5	Possible Intermediate Metabolizer	0.000032
NUDT15	*3/*5	Possible Intermediate Metabolizer	0.000032
NUDT15	*2/*4	Possible Intermediate Metabolizer	0.000048
NUDT15	*3/*3	Poor Metabolizer	0.000080
NUDT15	*2/*3	Poor Metabolizer	0.000112
NUDT15	*1/*15	Indeterminate	0.000128
NUDT15	*2/*2	Poor Metabolizer	0.000128
NUDT15	*1/*14	Intermediate Metabolizer	0.000224
NUDT15	*1/*5	Indeterminate	0.000592
NUDT15	*1/*4	Indeterminate	0.000993
NUDT15	*1/*9	Intermediate Metabolizer	0.002946

Gene	Diplotype	Activity Phenotype	Frequency
NUDT15	*1/*2	Intermediate Metabolizer	0.004114
NUDT15	*1/*6	Indeterminate	0.005091
NUDT15	*1/*3	Intermediate Metabolizer	0.009333
NUDT15	*1/*1	Normal Metabolizer	0.976083
PTGIS	*3/*3	Indeterminate	0.000064
PTGIS	*1/*5	Indeterminate	0.000320
PTGIS	*1/*3	Indeterminate	0.003906
PTGIS	*1/*1	Normal Function	0.995710
XPC	*1/*S2	Indeterminate	0.000016
XPC	*1/*1	Normal Function	0.157347
XPC	*S1/*S1	Indeterminate	0.365825
XPC	*1/*S1	Indeterminate	0.476812
SLCO1B1	*19/*19	Indeterminate	0.000016
SLCO1B1	*22/*S2	Indeterminate	0.000016
SLCO1B1	*1/*S1	Poor Function	0.000016
SLCO1B1	*16/*17	Indeterminate	0.000016
SLCO1B1	*19/*21	Indeterminate	0.000016
SLCO1B1	*19/*23	Indeterminate	0.000016
SLCO1B1	*17/*S2	Poor Function	0.000016
SLCO1B1	*17/*31	Possible Poor Function	0.000016
SLCO1B1	*15/*7	Indeterminate	0.000016
SLCO1B1	*14/*7	Indeterminate	0.000016
SLCO1B1	*1B/*7	Indeterminate	0.000016
SLCO1B1	*15/*23	Possible Poor Function	0.000016
SLCO1B1	*27/*5	Indeterminate	0.000016
SLCO1B1	*14/*28	Indeterminate	0.000016
SLCO1B1	*15/*24	Indeterminate	0.000016
SLCO1B1	*22/*30	Indeterminate	0.000016
SLCO1B1	*21/*30	Indeterminate	0.000016
SLCO1B1	*S2/*S4	Poor Function	0.000016
SLCO1B1	*28/*35	Indeterminate	0.000016
SLCO1B1	*S4/*S4	Poor Function	0.000016
SLCO1B1	*23/*35	Indeterminate	0.000016
SLCO1B1	*1/*23	Decreased Function	0.000016
SLCO1B1	*22/*5	Indeterminate	0.000016
SLCO1B1	*21/*28	Indeterminate	0.000016
SLCO1B1	*21/*31	Indeterminate	0.000016
SLCO1B1	*16/*16	Indeterminate	0.000016
SLCO1B1	*1/*4	Indeterminate	0.000032
SLCO1B1	*31/*S2	Poor Function	0.000032
SLCO1B1	*1B/*9	Possible Decreased Function	0.000032
SLCO1B1	*22/*35	Indeterminate	0.000032
SLCO1B1	*17/*S4	Poor Function	0.000032
SLCO1B1	*24/*27	Indeterminate	0.000032
SLCO1B1	*21/*S4	Indeterminate	0.000032
SLCO1B1	*17/*19	Indeterminate	0.000032
SLCO1B1	*14/*23	Indeterminate	0.000048
SLCO1B1	*24/*S2	Indeterminate	0.000048
SLCO1B1	*30/*S2	Indeterminate	0.000048
SLCO1B1	*24/*31	Indeterminate	0.000048
SLCO1B1	*31/*5	Possible Poor Function	0.000048
SLCO1B1	*21/*S2	Indeterminate	0.000048
SLCO1B1	*30/*35	Indeterminate	0.000064
SLCO1B1	*19/*5	Indeterminate	0.000064
SLCO1B1	*S2/*S2	Poor Function	0.000064

Gene	Diplotype	Activity Phenotype	Frequency
SLCO1B1	*1/*28	Indeterminate	0.000064
SLCO1B1	*17/*22	Indeterminate	0.000064
SLCO1B1	*19/*35	Indeterminate	0.000064
SLCO1B1	*1/*16	Indeterminate	0.000064
SLCO1B1	*14/*22	Indeterminate	0.000064
SLCO1B1	*14/*24	Indeterminate	0.000064
SLCO1B1	*19/*1B	Indeterminate	0.000080
SLCO1B1	*15/*19	Indeterminate	0.000080
SLCO1B1	*15/*30	Indeterminate	0.000080
SLCO1B1	*1/*24	Indeterminate	0.000096
SLCO1B1	*30/*31	Indeterminate	0.000096
SLCO1B1	*1B/*22	Indeterminate	0.000112
SLCO1B1	*5/*S4	Poor Function	0.000112
SLCO1B1	*15/*22	Indeterminate	0.000112
SLCO1B1	*27/*27	Indeterminate	0.000112
SLCO1B1	*1B/*S1	Poor Function	0.000112
SLCO1B1	*27/*S2	Indeterminate	0.000112
SLCO1B1	*1/*7	Indeterminate	0.000112
SLCO1B1	*14/*30	Indeterminate	0.000112
SLCO1B1	*31/*31	Possible Poor Function	0.000112
SLCO1B1	*16/*1B	Indeterminate	0.000128
SLCO1B1	*27/*31	Indeterminate	0.000128
SLCO1B1	*14/*19	Indeterminate	0.000128
SLCO1B1	*15/*S2	Poor Function	0.000144
SLCO1B1	*35/*S4	Decreased Function	0.000144
SLCO1B1	*1B/*28	Indeterminate	0.000160
SLCO1B1	*15/*31	Possible Poor Function	0.000176
SLCO1B1	*27/*30	Indeterminate	0.000176
SLCO1B1	*31/*35	Indeterminate	0.000192
SLCO1B1	*15/*27	Indeterminate	0.000208
SLCO1B1	*35/*S2	Decreased Function	0.000224
SLCO1B1	*1B/*24	Indeterminate	0.000240
SLCO1B1	*21/*21	Indeterminate	0.000256
SLCO1B1	*14/*31	Indeterminate	0.000272
SLCO1B1	*15/*S4	Poor Function	0.000288
SLCO1B1	*1/*30	Indeterminate	0.000304
SLCO1B1	*1B/*S4	Poor Function	0.000320
SLCO1B1	*14/*S2	Decreased Function	0.000352
SLCO1B1	*14/*S4	Decreased Function	0.000464
SLCO1B1	*27/*35	Indeterminate	0.000464
SLCO1B1	*17/*17	Poor Function	0.000464
SLCO1B1	*14/*27	Indeterminate	0.000512
SLCO1B1	*1/*22	Indeterminate	0.000528
SLCO1B1	*1B/*30	Indeterminate	0.000576
SLCO1B1	*1/*19	Indeterminate	0.000656
SLCO1B1	*5/*5	Poor Function	0.000704
SLCO1B1	*17/*21	Indeterminate	0.000752
SLCO1B1	*17/*5	Poor Function	0.000896
SLCO1B1	*1/*S2	Poor Function	0.001041
SLCO1B1	*21/*5	Indeterminate	0.001041
SLCO1B1	*1/*31	Decreased Function	0.001217
SLCO1B1	*1/*27	Indeterminate	0.001489
SLCO1B1	*21/*35	Indeterminate	0.001617
SLCO1B1	*1B/*S2	Poor Function	0.001633
SLCO1B1	*1/*S4	Poor Function	0.001681

Gene	Diplotype	Activity Phenotype	Frequency
SLCO1B1	*17/*35	Indeterminate	0.001761
SLCO1B1	*1B/*31	Possible Decreased Function	0.002209
SLCO1B1	*1B/*21	Indeterminate	0.002481
SLCO1B1	*35/*35	Possible Increased Function	0.002593
SLCO1B1	*1B/*27	Indeterminate	0.002609
SLCO1B1	*35/*5	Indeterminate	0.002785
SLCO1B1	*1B/*5	Decreased Function	0.003378
SLCO1B1	*17/*1B	Decreased Function	0.003538
SLCO1B1	*15/*21	Indeterminate	0.003618
SLCO1B1	*15/*17	Poor Function	0.004258
SLCO1B1	*14/*17	Indeterminate	0.005507
SLCO1B1	*14/*21	Indeterminate	0.005651
SLCO1B1	*15/*5	Poor Function	0.006179
SLCO1B1	*14/*5	Indeterminate	0.008629
SLCO1B1	*1B/*35	Possible Increased Function	0.009253
SLCO1B1	*15/*35	Indeterminate	0.010389
SLCO1B1	*15/*15	Poor Function	0.010774
SLCO1B1	*15/*1B	Decreased Function	0.013287
SLCO1B1	*14/*35	Indeterminate	0.014328
SLCO1B1	*1/*21	Indeterminate	0.018282
SLCO1B1	*1/*17	Decreased Function	0.020027
SLCO1B1	*14/*1B	Possible Increased Function	0.020507
SLCO1B1	*14/*14	Possible Increased Function	0.023644
SLCO1B1	*1B/*1B	Normal Function	0.026030
SLCO1B1	*1/*5	Decreased Function	0.028831
SLCO1B1	*14/*15	Indeterminate	0.031521
SLCO1B1	*1/*35	Increased Function	0.055085
SLCO1B1	*1/*1B	Normal Function	0.075656
SLCO1B1	*1/*15	Decreased Function	0.111803
SLCO1B1	*1/*14	Increased Function	0.159012
SLCO1B1	*1/*1	Normal Function	0.293819
SLC15A2	*2/*2	Indeterminate	0.206877
SLC15A2	*1/*1	Normal Metabolizer	0.298654
SLC15A2	*1/*2	Indeterminate	0.494469
CYP4B1	*4/*4	Indeterminate	0.000208
CYP4B1	*4/*5	Indeterminate	0.000352
CYP4B1	*3/*4	Indeterminate	0.003138
CYP4B1	*2/*4	Indeterminate	0.003314
CYP4B1	*2/*5	Indeterminate	0.003842
CYP4B1	*5/*5	Indeterminate	0.008308
CYP4B1	*3/*5	Indeterminate	0.010245
CYP4B1	*1/*4	Indeterminate	0.017577
CYP4B1	*3/*3	Indeterminate	0.019194
CYP4B1	*2/*2	Poor Metabolizer	0.020747
CYP4B1	*1/*5	Indeterminate	0.024749
CYP4B1	*2/*3	Indeterminate	0.036835
CYP4B1	*1/*3	Indeterminate	0.181664
CYP4B1	*1/*2	Intermediate Metabolizer	0.189236
CYP4B1	*1/*1	Normal Metabolizer	0.480590
CYP26A1	*2/*2	Indeterminate	0.000080
CYP26A1	*1/*2	Indeterminate	0.006003
CYP26A1	*1/*1	Normal Metabolizer	0.993917
SLCO2B1	*S1/*S1	Indeterminate	0.000560
SLCO2B1	*S1/*S464F	Indeterminate	0.001953
SLCO2B1	*S464F/*S464F	Indeterminate	0.007924

Gene	Diplotype	Activity Phenotype	Frequency
SLCO2B1	*1/*S1	Indeterminate	0.034754
SLCO2B1	*1/*S464F	Indeterminate	0.080891
SLCO2B1	*1/*1	Normal Function	0.873917
CYP2C9	*36/*8	Indeterminate	0.000016
CYP2C9	*3/*36	Indeterminate	0.000016
CYP2C9	*5/*8	Intermediate Metabolizer	0.000016
CYP2C9	*14/*2	Intermediate Metabolizer	0.000016
CYP2C9	*11/*29	Intermediate Metabolizer	0.000016
CYP2C9	*29/*3	Poor Metabolizer	0.000016
CYP2C9	*11/*6	Poor Metabolizer	0.000016
CYP2C9	*11/*5	Intermediate Metabolizer	0.000016
CYP2C9	*5/*6	Poor Metabolizer	0.000032
CYP2C9	*2/*21	Indeterminate	0.000032
CYP2C9	*3/*45	Poor Metabolizer	0.000032
CYP2C9	*36/*9	Indeterminate	0.000032
CYP2C9	*2/*29	Intermediate Metabolizer	0.000048
CYP2C9	*11/*11	Intermediate Metabolizer	0.000048
CYP2C9	*2/*5	Intermediate Metabolizer	0.000064
CYP2C9	*2/*6	Poor Metabolizer	0.000064
CYP2C9	*5/*9	Intermediate Metabolizer	0.000080
CYP2C9	*1/*44	Intermediate Metabolizer	0.000080
CYP2C9	*2/*36	Indeterminate	0.000080
CYP2C9	*6/*9	Intermediate Metabolizer	0.000096
CYP2C9	*6/*8	Poor Metabolizer	0.000128
CYP2C9	*3/*8	Poor Metabolizer	0.000176
CYP2C9	*1/*45	Intermediate Metabolizer	0.000176
CYP2C9	*11/*9	Intermediate Metabolizer	0.000176
CYP2C9	*1/*21	Indeterminate	0.000176
CYP2C9	*8/*8	Intermediate Metabolizer	0.000176
CYP2C9	*3/*9	Intermediate Metabolizer	0.000176
CYP2C9	*11/*8	Intermediate Metabolizer	0.000176
CYP2C9	*1/*14	Intermediate Metabolizer	0.000192
CYP2C9	*12/*3	Poor Metabolizer	0.000240
CYP2C9	*11/*3	Poor Metabolizer	0.000256
CYP2C9	*9/*9	Normal Metabolizer	0.000304
CYP2C9	*2/*8	Intermediate Metabolizer	0.000320
CYP2C9	*2/*9	Intermediate Metabolizer	0.000336
CYP2C9	*8/*9	Intermediate Metabolizer	0.000432
CYP2C9	*1/*29	Intermediate Metabolizer	0.000496
CYP2C9	*11/*2	Intermediate Metabolizer	0.000592
CYP2C9	*1/*36	Indeterminate	0.000624
CYP2C9	*12/*2	Intermediate Metabolizer	0.000640
CYP2C9	*1/*5	Intermediate Metabolizer	0.001169
CYP2C9	*1/*6	Intermediate Metabolizer	0.001233
CYP2C9	*1/*12	Intermediate Metabolizer	0.003970
CYP2C9	*3/*3	Poor Metabolizer	0.004242
CYP2C9	*1/*11	Intermediate Metabolizer	0.005427
CYP2C9	*1/*8	Intermediate Metabolizer	0.006243
CYP2C9	*1/*9	Normal Metabolizer	0.007732
CYP2C9	*2/*3	Poor Metabolizer	0.015080
CYP2C9	*2/*2	Intermediate Metabolizer	0.015128
CYP2C9	*1/*3	Intermediate Metabolizer	0.101334
CYP2C9	*1/*2	Intermediate Metabolizer	0.187411
CYP2C9	*1/*1	Normal Metabolizer	0.644420
CYP2S1	*2/*3	Indeterminate	0.000032

Gene	Diplotype	Activity Phenotype	Frequency
CYP2S1	*3/*3	Indeterminate	0.000432
CYP2S1	*1/*2	Indeterminate	0.000704
CYP2S1	*1/*3	Indeterminate	0.037188
CYP2S1	*1/*1	Normal Metabolizer	0.961644
CYP3A4	*10/*8	Indeterminate	0.000016
CYP3A4	*10/*7	Indeterminate	0.000016
CYP3A4	*7/*7	Indeterminate	0.000016
CYP3A4	*10/*15	Indeterminate	0.000016
CYP3A4	*11/*22	Intermediate Metabolizer	0.000016
CYP3A4	*13/*1B	Indeterminate	0.000016
CYP3A4	*2/*22	Indeterminate	0.000032
CYP3A4	*18/*1B	Indeterminate	0.000032
CYP3A4	*1B/*2	Indeterminate	0.000032
CYP3A4	*1B/*7	Indeterminate	0.000048
CYP3A4	*1B/*8	Indeterminate	0.000048
CYP3A4	*11/*1B	Indeterminate	0.000064
CYP3A4	*1B/*3	Indeterminate	0.000064
CYP3A4	*22/*3	Indeterminate	0.000064
CYP3A4	*1/*23	Indeterminate	0.000112
CYP3A4	*1B/*23	Indeterminate	0.000112
CYP3A4	*22/*7	Indeterminate	0.000112
CYP3A4	*1/*8	Normal Metabolizer	0.000160
CYP3A4	*1/*12	Normal Metabolizer	0.000224
CYP3A4	*10/*1B	Indeterminate	0.000256
CYP3A4	*12/*1B	Indeterminate	0.000288
CYP3A4	*10/*22	Indeterminate	0.000288
CYP3A4	*1/*2	Indeterminate	0.000352
CYP3A4	*1/*11	Normal Metabolizer	0.000384
CYP3A4	*1/*13	Normal Metabolizer	0.000416
CYP3A4	*1/*18	Indeterminate	0.000704
CYP3A4	*1/*7	Indeterminate	0.001345
CYP3A4	*1/*3	Indeterminate	0.001425
CYP3A4	*22/*22	Intermediate Metabolizer	0.001889
CYP3A4	*1B/*22	Indeterminate	0.004210
CYP3A4	*1/*10	Indeterminate	0.005299
CYP3A4	*1B/*1B	Indeterminate	0.026126
CYP3A4	*1/*22	Normal Metabolizer	0.073575
CYP3A4	*1/*1B	Indeterminate	0.090176
CYP3A4	*1/*1	Normal Metabolizer	0.792066
CYP1A2	*1C/*3	Intermediate Metabolizer	0.000016
CYP1A2	*1K/*1K	Intermediate Metabolizer	0.000032
CYP1A2	*1C/*6	Intermediate Metabolizer	0.000032
CYP1A2	*1/*7	Normal Metabolizer	0.000080
CYP1A2	*1/*3	Normal Metabolizer	0.000112
CYP1A2	*1C/*1K	Intermediate Metabolizer	0.000112
CYP1A2	*1F/*7	Normal Metabolizer	0.000128
CYP1A2	*1F/*3	Normal Metabolizer	0.000144
CYP1A2	*1/*6	Intermediate Metabolizer	0.000432
CYP1A2	*1/*1K	Normal Metabolizer	0.001297
CYP1A2	*1F/*6	Normal Metabolizer	0.001473
CYP1A2	*1F/*1K	Normal Metabolizer	0.003090
CYP1A2	*1C/*1C	Intermediate Metabolizer	0.008533
CYP1A2	*1/*1C	Normal Metabolizer	0.029936
CYP1A2	*1C/*1F	Normal Metabolizer	0.043111
CYP1A2	*1/*1	Normal Metabolizer	0.089487

Gene	Diplotype	Activity Phenotype	Frequency
CYP1A2	*1/*1F	Ultrarapid Metabolizer	0.383482
CYP1A2	*1F/*1F	Ultrarapid Metabolizer	0.438504
NAT1	*15/*22	Decreased Function	0.000016
NAT1	*17/*17	Decreased Function	0.000016
NAT1	*15/*15	No Function	0.000016
NAT1	*17/*27	Decreased Function	0.000016
NAT1	*22/*27	Decreased Function	0.000016
NAT1	*1/*30	Indeterminate	0.000016
NAT1	*17/*22	Decreased Function	0.000032
NAT1	*27/*27	Normal Function	0.000032
NAT1	*22/*22	Decreased Function	0.000032
NAT1	*15/*17	Decreased Function	0.000048
NAT1	*27/*3	Indeterminate	0.000064
NAT1	*14/*15	Decreased Function	0.000096
NAT1	*14/*22	Decreased Function	0.000112
NAT1	*22/*3	Indeterminate	0.000160
NAT1	*15/*3	Indeterminate	0.000176
NAT1	*14/*17	Decreased Function	0.000240
NAT1	*17/*3	Indeterminate	0.000272
NAT1	*14/*14	Decreased Function	0.000288
NAT1	*3/*3	Indeterminate	0.000720
NAT1	*14/*3	Indeterminate	0.000896
NAT1	*10/*27	Indeterminate	0.001073
NAT1	*1/*27	Normal Function	0.001169
NAT1	*10/*15	Indeterminate	0.001233
NAT1	*10/*22	Indeterminate	0.001249
NAT1	*10/*17	Indeterminate	0.002593
NAT1	*1/*15	Decreased Function	0.004034
NAT1	*1/*22	Decreased Function	0.004690
NAT1	*10/*14	Indeterminate	0.007172
NAT1	*1/*17	Decreased Function	0.008100
NAT1	*10/*3	Indeterminate	0.012391
NAT1	*1/*14	Decreased Function	0.024317
NAT1	*1/*3	Indeterminate	0.035891
NAT1	*10/*10	Indeterminate	0.065010
NAT1	*1/*10	Indeterminate	0.327181
NAT1	*1/*1	Normal Function	0.500632
UGT1A4	*3B/*3B	Decreased Function	0.000016
UGT1A4	*S3/*S3	No Function	0.000016
UGT1A4	*3B/*4	Indeterminate	0.000016
UGT1A4	*3A/*S3	Decreased Function	0.000016
UGT1A4	*1/*S3	Decreased Function	0.000064
UGT1A4	*4/*4	Indeterminate	0.000112
UGT1A4	*2/*3B	Indeterminate	0.000128
UGT1A4	*2/*4	Indeterminate	0.000176
UGT1A4	*3A/*3B	Decreased Function	0.000304
UGT1A4	*3A/*4	Indeterminate	0.000752
UGT1A4	*1/*3B	Decreased Function	0.002481
UGT1A4	*2/*2	Indeterminate	0.002962
UGT1A4	*1/*4	Indeterminate	0.005107
UGT1A4	*2/*3A	Indeterminate	0.008645
UGT1A4	*3A/*3A	Decreased Function	0.008693
UGT1A4	*1/*2	Indeterminate	0.084909
UGT1A4	*1/*3A	Decreased Function	0.154145
UGT1A4	*1/*1	Normal Function	0.731458

Gene	Diplotype	Activity Phenotype	Frequency
GSTP1	*3/*4	Indeterminate	0.000016
GSTP1	*2/*4	Indeterminate	0.000080
GSTP1	*1/*4	Indeterminate	0.000288
GSTP1	*3/*3	Indeterminate	0.005891
GSTP1	*2/*3	Indeterminate	0.040758
GSTP1	*2/*2	Indeterminate	0.074311
GSTP1	*1/*3	Indeterminate	0.101606
GSTP1	*1/*2	Indeterminate	0.344198
GSTP1	*1/*1	Normal Function	0.432853
CYP2J2	*5/*7	Indeterminate	0.000016
CYP2J2	*7/*9	Indeterminate	0.000032
CYP2J2	*1/*9	Indeterminate	0.000192
CYP2J2	*1/*5	Indeterminate	0.000400
CYP2J2	*7/*7	Indeterminate	0.005811
CYP2J2	*1/*7	Indeterminate	0.131541
CYP2J2	*1/*1	Normal Metabolizer	0.862007
DPYD	*S12/*S21	Normal Metabolizer	0.000016
DPYD	*S10/*S4	Normal Metabolizer	0.000016
DPYD	*9A/*S64	Intermediate Metabolizer	0.000016
DPYD	*4/*S72	Normal Metabolizer	0.000016
DPYD	*9A/*S57	Normal Metabolizer	0.000016
DPYD	*S72/*S74	Normal Metabolizer	0.000016
DPYD	*S10/*S8	Normal Metabolizer	0.000016
DPYD	*S12/*S64	Intermediate Metabolizer	0.000016
DPYD	*1/*S21	Normal Metabolizer	0.000016
DPYD	*S4/*S72	Normal Metabolizer	0.000016
DPYD	*1/*S55	Normal Metabolizer	0.000016
DPYD	*S10/*S6	Intermediate Metabolizer	0.000016
DPYD	*13/*4	Intermediate Metabolizer	0.000016
DPYD	*6/*S8	Normal Metabolizer	0.000016
DPYD	*2/*S10	Intermediate Metabolizer	0.000016
DPYD	*5/*S22	Intermediate Metabolizer	0.000016
DPYD	*S6/*S8	Intermediate Metabolizer	0.000016
DPYD	*S3/*S8	Normal Metabolizer	0.000016
DPYD	*9A/*S50	Normal Metabolizer	0.000016
DPYD	*S5/*S72	Intermediate Metabolizer	0.000016
DPYD	*S5/*S64	Poor Metabolizer	0.000016
DPYD	*2/*S21	Intermediate Metabolizer	0.000016
DPYD	*S12/*S55	Normal Metabolizer	0.000016
DPYD	*9A/*S55	Normal Metabolizer	0.000016
DPYD	*13/*S3	Intermediate Metabolizer	0.000016
DPYD	*S4/*S8	Normal Metabolizer	0.000016
DPYD	*5/*S53	Normal Metabolizer	0.000016
DPYD	*S6/*S72	Intermediate Metabolizer	0.000032
DPYD	*S10/*S3	Normal Metabolizer	0.000032
DPYD	*5/*S57	Normal Metabolizer	0.000032
DPYD	*S12/*S53	Normal Metabolizer	0.000032
DPYD	*S8/*S8	Normal Metabolizer	0.000032
DPYD	*S3/*S6	Intermediate Metabolizer	0.000032
DPYD	*1/*S64	Intermediate Metabolizer	0.000032
DPYD	*2/*2	Poor Metabolizer	0.000032
DPYD	*S6/*S9	Intermediate Metabolizer	0.000032
DPYD	*13/*6	Intermediate Metabolizer	0.000032
DPYD	*S2/*S2	Intermediate Metabolizer	0.000032
DPYD	*4/*S10	Normal Metabolizer	0.000032

Gene	Diplotype	Activity Phenotype	Frequency
DPYD	*S8/*S9	Normal Metabolizer	0.000032
DPYD	*S5/*S6	Intermediate Metabolizer	0.000032
DPYD	*5/*S64	Intermediate Metabolizer	0.000048
DPYD	*S10/*S9	Normal Metabolizer	0.000048
DPYD	*2/*S2	Poor Metabolizer	0.000048
DPYD	*S12/*S57	Normal Metabolizer	0.000048
DPYD	*13/*S5	Poor Metabolizer	0.000048
DPYD	*13/*S4	Intermediate Metabolizer	0.000048
DPYD	*S4/*S6	Intermediate Metabolizer	0.000048
DPYD	*9A/*S22	Intermediate Metabolizer	0.000080
DPYD	*9A/*S74	Normal Metabolizer	0.000080
DPYD	*S12/*S22	Intermediate Metabolizer	0.000080
DPYD	*6/*S6	Intermediate Metabolizer	0.000080
DPYD	*S12/*S74	Normal Metabolizer	0.000080
DPYD	*13/*9A	Intermediate Metabolizer	0.000096
DPYD	*1/*S22	Intermediate Metabolizer	0.000096
DPYD	*S10/*S5	Intermediate Metabolizer	0.000112
DPYD	*2/*S4	Intermediate Metabolizer	0.000128
DPYD	*S2/*S4	Intermediate Metabolizer	0.000144
DPYD	*1/*S72	Normal Metabolizer	0.000144
DPYD	*6/*S10	Normal Metabolizer	0.000144
DPYD	*4/*S2	Intermediate Metabolizer	0.000144
DPYD	*2/*S3	Intermediate Metabolizer	0.000160
DPYD	*13/*5	Intermediate Metabolizer	0.000176
DPYD	*S2/*S5	Intermediate Metabolizer	0.000176
DPYD	*2/*4	Intermediate Metabolizer	0.000224
DPYD	*5/*S72	Normal Metabolizer	0.000224
DPYD	*9A/*S72	Normal Metabolizer	0.000240
DPYD	*S12/*S72	Normal Metabolizer	0.000240
DPYD	*S2/*S3	Intermediate Metabolizer	0.000240
DPYD	*1/*13	Intermediate Metabolizer	0.000240
DPYD	*13/*S12	Intermediate Metabolizer	0.000256
DPYD	*2/*S5	Poor Metabolizer	0.000256
DPYD	*2/*S9	Intermediate Metabolizer	0.000272
DPYD	*S2/*S9	Intermediate Metabolizer	0.000288
DPYD	*6/*S2	Intermediate Metabolizer	0.000288
DPYD	*1/*S6	Intermediate Metabolizer	0.000320
DPYD	*5/*S8	Normal Metabolizer	0.000320
DPYD	*S4/*S4	Normal Metabolizer	0.000352
DPYD	*S9/*S9	Normal Metabolizer	0.000432
DPYD	*S5/*S5	Intermediate Metabolizer	0.000448
DPYD	*2/*6	Intermediate Metabolizer	0.000448
DPYD	*4/*4	Normal Metabolizer	0.000464
DPYD	*4/*S4	Normal Metabolizer	0.000496
DPYD	*4/*S5	Intermediate Metabolizer	0.000496
DPYD	*S4/*S5	Intermediate Metabolizer	0.000496
DPYD	*1/*S8	Normal Metabolizer	0.000496
DPYD	*S3/*S3	Normal Metabolizer	0.000512
DPYD	*S12/*S6	Intermediate Metabolizer	0.000544
DPYD	*5/*S6	Intermediate Metabolizer	0.000560
DPYD	*S12/*S8	Normal Metabolizer	0.000576
DPYD	*5/*S10	Normal Metabolizer	0.000576
DPYD	*S3/*S9	Normal Metabolizer	0.000624
DPYD	*9A/*S10	Normal Metabolizer	0.000640
DPYD	*4/*S9	Normal Metabolizer	0.000704

Gene	Diplotype	Activity Phenotype	Frequency
DPYD	*S3/*S4	Normal Metabolizer	0.000704
DPYD	*S4/*S9	Normal Metabolizer	0.000752
DPYD	*9A/*S8	Normal Metabolizer	0.000784
DPYD	*S5/*S9	Intermediate Metabolizer	0.000832
DPYD	*4/*S3	Normal Metabolizer	0.000848
DPYD	*S10/*S12	Normal Metabolizer	0.000880
DPYD	*S3/*S5	Intermediate Metabolizer	0.000896
DPYD	*9A/*S6	Intermediate Metabolizer	0.001073
DPYD	*1/*S10	Normal Metabolizer	0.001105
DPYD	*6/*S4	Normal Metabolizer	0.001169
DPYD	*2/*9A	Intermediate Metabolizer	0.001457
DPYD	*2/*5	Intermediate Metabolizer	0.001457
DPYD	*4/*6	Normal Metabolizer	0.001489
DPYD	*6/*S9	Normal Metabolizer	0.001537
DPYD	*6/*S5	Intermediate Metabolizer	0.001601
DPYD	*5/*S2	Intermediate Metabolizer	0.001713
DPYD	*9A/*S2	Intermediate Metabolizer	0.001841
DPYD	*6/*6	Normal Metabolizer	0.001857
DPYD	*6/*S3	Normal Metabolizer	0.001905
DPYD	*1/*2	Intermediate Metabolizer	0.001969
DPYD	*2/*S12	Intermediate Metabolizer	0.002113
DPYD	*1/*S2	Intermediate Metabolizer	0.002401
DPYD	*S12/*S2	Intermediate Metabolizer	0.002513
DPYD	*9A/*S4	Normal Metabolizer	0.005443
DPYD	*5/*S4	Normal Metabolizer	0.005875
DPYD	*4/*9A	Normal Metabolizer	0.005939
DPYD	*9A/*S3	Normal Metabolizer	0.006435
DPYD	*9A/*S5	Intermediate Metabolizer	0.006467
DPYD	*5/*S5	Intermediate Metabolizer	0.006627
DPYD	*9A/*S9	Normal Metabolizer	0.006820
DPYD	*1/*S4	Normal Metabolizer	0.006884
DPYD	*4/*5	Normal Metabolizer	0.007188
DPYD	*5/*S3	Normal Metabolizer	0.007268
DPYD	*S12/*S4	Normal Metabolizer	0.007300
DPYD	*5/*S9	Normal Metabolizer	0.008100
DPYD	*1/*S9	Normal Metabolizer	0.008356
DPYD	*1/*4	Normal Metabolizer	0.008436
DPYD	*1/*S5	Intermediate Metabolizer	0.008452
DPYD	*S12/*S5	Intermediate Metabolizer	0.009429
DPYD	*S12/*S9	Normal Metabolizer	0.009445
DPYD	*4/*S12	Normal Metabolizer	0.009445
DPYD	*1/*S3	Normal Metabolizer	0.009605
DPYD	*S12/*S3	Normal Metabolizer	0.009941
DPYD	*6/*9A	Normal Metabolizer	0.013319
DPYD	*5/*6	Normal Metabolizer	0.014632
DPYD	*1/*6	Normal Metabolizer	0.018762
DPYD	*6/*S12	Normal Metabolizer	0.019770
DPYD	*9A/*9A	Normal Metabolizer	0.034898
DPYD	*5/*5	Normal Metabolizer	0.036643
DPYD	*1/*1	Normal Metabolizer	0.057022
DPYD	*S12/*S12	Normal Metabolizer	0.061360
DPYD	*5/*9A	Normal Metabolizer	0.067876
DPYD	*1/*9A	Normal Metabolizer	0.083164
DPYD	*9A/*S12	Normal Metabolizer	0.087838
DPYD	*1/*5	Normal Metabolizer	0.090656

Gene	Diplotype	Activity Phenotype	Frequency
DPYD	*5/*S12	Normal Metabolizer	0.095827
DPYD	*1/*S12	Normal Metabolizer	0.116461

Table S3: Frequency of inferred star allele diplotypes in Data Freeze 4. The frequency of each inferred star allele diplotype among all 60,215 participants in Data Freeze 4 is given in addition to the activity phenotype associated with each diplotype.

Gene	# Samples Compared	# Concordant Haplotypes	# Compared Haplotypes	Haplotype Concordance Rate [%]
CYP1A2	28	44	44	100
CYP2B6	11	13	13	100
CYP2D6	25	33	37	89.19
CYP2C19	16	18	19	94.74
CYP2C9	10	11	11	100
CYP3A4	3	3	3	100
UGT1A4	5	5	5	100
UGT2B15	21	28	28	100
TPMT	5	5	5	100

Table S4: Star allele haplotype concordance allowing candidate allele comparisons. Concordance rate between star allele haplotypes called by a commercial pharmacogenomic test platform and star allele haplotypes inferred as either the main or candidate allele by Stargazer.