**S4 Table 4. SNPs Chosen for TaqMan® SNP Genotyping Assay Genotyping.**

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| DMET™ Probe | SNP | Gene | chr:coora | Strand | Genomicb | Proteomicb | CEU MAFc | PKFAM MAF | TaqMan® Assay |
| AM\_12370 | rs1884725 | *XDH* | 2:31425290 | Minus | c.3030T>C | p.Phe1010= | 0.229 | 0.198 | C\_\_\_3279863\_30 |
| AM\_13323 | rs3856650 | *CHST13* | 11:12779888 | Plus | c.97+3926T>A |  | 0.398 | 0.412 | C\_\_\_1935611\_10  |
| N/A | rs17329885d | *SLCO1B1* | 12:21219832 | Plus | c.359+922T>C |  | 0.190 | N/A | C\_\_33090816\_10 |
| AM\_10496 | rs2306283 | *SLCO1B1* | 12:21221005 | Plus | c.388A>G | p.Asn130Asp | 0.398 | 0.404 | C\_\_\_1901697\_20 |
| AM\_10659 | rs2297322 | *SLC15A1* | 13:98174182 | Minus | c.350G>A | p.Ser117Asn | 0.093 | 0.103 | AHMSVVN |
| AM\_11147 | rs2292954 | *SPG7* | 16:88140624 | Plus | c.1507A>G | p.Thr503Ala | 0.153 | 0.197 | C\_\_\_3224490\_30 |
| AM\_11279 | rs1805041 | *CYP4F3* | 19:15624691 | Plus | c.1044G>A | p.Pro348= | 0.259 | 0.232 | C\_\_\_7496795\_10 |
| AM\_11280 | rs1805042 | *CYP4F3* | 19:15624721 | Plus | c.1074G>A | p.Val358= | 0.297 | 0.359 | C\_\_\_7496796\_10 |
| AM\_11325 | rs1064349 | *CHST8* | 19:38956194 | Plus | c.\*386G>A |  | 0.093 | 0.111 | C\_\_\_7613022\_20 |
| N/A | rs28399435f | *CYP2A6* | 19:46048086 | Minus | c.86G>A | p.Ser29Asn | 0.017 | N/A | C\_\_30634234\_10  |
| AM\_11358 | rs1137115 | *CYP2A6* | 19:46048121 | Minus | c.51A>Ge | p.Val17= | 0.246 | 0.214 | C\_\_26681694\_20 |
| AM\_11364 | rs4803381 | *CYP2A6* | 19:46049184 | Minus | c.-1013A>Ge |  | 0.280 | 0.367 | AHMSY6C |
| N/A | rs2835272d | *CBR1* | 21:36374789 | Plus | 3’ flank, T>C |  | 0.106 | N/A | C\_\_\_2440219\_1\_ |
| AM\_12257 | rs28371725 | *CYP2D6* | 22:40853749 | Minus | c.985+39G>A |  | 0.085 | 0.094 | C\_\_34816116\_20 |
| AM\_12261 | rs16947 | *CYP2D6* | 22:40853887 | Minus | c.886C>T | p.Arg296Cys | 0.297 | 0.318 | C\_\_27102425\_10 |
| AM\_12291 | rs1080985 | *CYP2D6* | 22:40858326 | Minus | c.-1589G>C |  | 0.212 | 0.224 | C\_\_32407252\_30 |

aFrom NCBI36/hg18. bHGVS annotation from dbSNP. cFrom Affymetrix DMET™ Plus annotation, mean count N=59, including proxies, except rs17329885 and rs2835272, from dbSNP. drs17329885 is a proxy for rs11045819 (*r*2=1, CEU). rs2835272 is a proxy for rs2835265 (*r*2=1, CEU). e”A” is minor allele. Reference genome sequence has “T” on + strand, i.e., the minor allele is the genome sequence reference. fOne *CYP2A6* SNP not interrogated by the DMET™ Plus array underwent genotyping, but failed quality control.