Table S1. *allele defining variants

| dbSNP ID | CYP2D6 Haplotype | Variant Type | Alleles | Functional Consequence | Activity Score |
|---|---|---|---|---|---|
| N/A | *1 | N/A | N/A | N/A | 1 |
| rs35742686 | *3 | Deletion | CT>T | Frameshift Variant | 0 |
| rs3892097 | *4 | SNV | C>T | Splice Variant | 0 |
| rs5030655 | *6 | Deletion | CA>C | Frameshift Variant | 0 |
| rs5030656 | *9 | Deletion | CTTCT>CT | In-frame Deletion | 0.5 |
| rs1065852 | *10 | SNV | G>A / G>C | Missense Variant | 0.25 |
| rs16947 | *17 | SNV | G>A / G>T | Missense Variant | 0.5 |
| rs28371706 | *17 | SNV | G>A / G>C / G>T | Missense Variant | 0.5 |
| rs1058164 | *29 | SNV | G>C | Synonymous Variant | 0.5 |
| rs1135840 | *29 | SNV | C>G / C>T | Missense Variant | 0.5 |
| rs16947 | *29 | SNV | G>A / G>T | Missense Variant | 0.5 |
| rs59421388 | *29 | SNV | C>T | Missense Variant | 0.5 |
| rs61736512 | *29 | SNV | C>T | Missense Variant | 0.5 |
| rs28371725 | *41 | SNV | C>T | Intron Variant | 0.5 |

Note that for *alleles with more than one defining SNP, the non-reference allele must be present for all defining variants and the listed activity score is for the entire haplotype. SNV stands for single nucleotide variant. Activity scores for each *allele were summed over both haplotypes for each participant to produce the total activity score per participant. Ultrarapid metabolizer (UM), normal metabolizer (NM), intermediate metabolizer (IM), and poor metabolizer (PM) were defined by the following combined activity score range, respectively: >2.25, 1.25 <= X <=2.25, 0 <= X <=1.25, and 0.