Supplemental Table S5. Predicted metabolizer phenotypes based on *CYP2C19* genotype and predicted average frequencies

	Predicted Metabolizer Phenotype (Average Multi-Ethnic Frequency[1])								
Allele	***1***	***2***	***3***	***4***	***5***	***6***	***7***	***8***	***17***
1	EM (35-50%)	IM (17-35%)	IM (1-11%)	IM (<1%)	IM (<1%)	IM (<1%)	IM (<1%)	IM (<1%)	UM (3-27%)
2		PM (2-8%)	PM (0-5%)	PM (<1%)	PM (<1%)	PM (<1%)	PM (<1%)	PM (<1%)	IM[2] (1-6%)
3			PM (<1%)	PM (<1%)	PM (<1%)	PM (<1%)	PM (<1%)	PM (<1%)	IM[2] (<1%)
4				PM (<1%)	PM (<1%)	PM (<1%)	PM (<1%)	PM (<1%)	IM[2] (<1%)
5					PM (<1%)	PM (<1%)	PM (<1%)	PM (<1%)	IM[2] (<1%)
6						PM (<1%)	PM (<1%)	PM (<1%)	IM[2] (<1%)
7							PM (<1%)	PM (<1%)	IM[2] (<1%)
8								PM (<1%)	IM[2] (<1%)
17									UM (1-5%)

EM: extensive metabolizer; IM: intermediate metabolizer; PM: poor metabolizer; UM: ultrarapid metabolizer.

[1] Frequencies of predicted metabolizer phenotypes were determined using the allele frequencies from **Supplemental Tables S3** and **S4** and the Hardy-Weinberg equation.

[2] The predicted metabolizer phenotype for these genotypes are provisional classifications. The currently available evidence indicates that the **17* gain-of-function allele is unable to completely compensate for the **2* loss-of-function allele (106); however, this data has not been consistently replicated and is therefore a provisional classification.