Supplemental Materials - Report Template Descriptions

File 1 *CYP2D6* Genotyping Method and Data Templates

This template provides a standardized way of reporting all pertinent information including method(s) and/or platform(s) utilized, which SNVs were tested and how CNVs were detected for *CYP2D6* genotype determination. This table can be published in a revised form in a manuscript methods section, or as supplemental table.

The first tab in the spreadsheet labeled 'methods' allows the user to describe the methods used in a semi-structured way.

The second tab in the spreadsheet 'labeled '*CYP2D6* SNVs tested_template' contains a comprehensive list of many SNVs routinely tested by many platforms or methods, it does, however, not represent a complete list of SNVs known to occur in *CYP2D6*. Also, a SNV may occur in allele(s) other than those listed. The third tab labeled '*CYP2D6* SNVs tested_examples' provides examples of how data may be provided. In column G it is indicated whether a SNV was tested (yes/no); rows for SNVs not tested were left blank in this example but may be removed or hidden; rows may be added for SNVs not listed. Columns I-N provide examples of how to present genotype data for individual subjects; genotype calls for each subject are provided at the bottom of each column. Users are encouraged to provide results for individual subjects in their study. Alternatively, as exemplified in columns O-Q, data may also be summarized 'by genotype', i.e. the genotype call and the number of subjects with that call is provided in the column header and SNVs tested are as indicated.

The fourth tab in the spreadsheet labeled '*CYP2D6* allele freq_template' provides a template to report allele frequencies. If the Activity Score system is used to translate genotype to phenotype, values used for AS calculation can be reported here. The fifth tab labeled '*CYP2D6* allele freq examples' provides a fictional dataset to exemplify how data may be provided.

Please provide data on tabs labeled '*CYP2D6* SNVs tested_template' and 'CYP2D6 allele freq_template' and remove respective example tabs before publishing.

File 2 *CYP2D6* Genotype to Phenotype Translation Template

This template provides a standardized way of reporting how *CYP2D6* genotype was translated into phenotype (G2P, genotype to phenotype). Although CPIC-recommends translating genotype into phenotype using the consensus method jointly developed by the CPIC, the DPWG and a panel of experts (48), not every investigator is utilizing this method. It is imperative, however, that the method of how genotype is translated (i.e. which genotypes were classified into which phenotype group) is provided in detail. Please enter data into the first tab labeled '*CYP2D6* G2P translation_template' (G2P, genotype to phenotype). The second tab labeled '*CYP2D6* G2P translation_examples' provides a data set to exemplify how data may be presented. In this example, genotypes are sorted by their assigned Activity Score and respective phenotype assignments (UM, NM, IM, and PM) per CPIC recommendations. The template is also configured to provide genotype frequencies. The table can be revised as needed to accommodate the genotypes detected in a study.

This table can be published in a revised form in a manuscript methods section, or as supplemental table. Please remove the 'example tab' before publishing.