Legend to *CYP2C19* Allelic Variation Summary Table

PubMed® database (1995 to 2014) and Ovid MEDLINE (1995 to 2014) were searched using the following criteria: ((CYP2C19 or 2C19) AND (genotype OR allele OR frequency OR minor allele OR variant OR ethnic OR race OR racial OR ethnicity)) with filter limits set to retrieve "full-text" and "English" literature.

Studies were considered for inclusion if: (1) the ethnicity of the population was clearly indicated; 2) either allele frequencies or alleles for *CYP2C19* genotypes were reported; (3) the method by which *CYP2C19* was genotyped appeared reliable; (4) the sample population consisted of at least 50 individuals; and (5) the study represented publication of novel data (no reviews or meta-analyses). In instances where genotype data from large cohorts of ethnically-diverse individuals were reported, without respect to ethnicity, studies were only considered if one ethnicity was ≥95% of the majority. Multiethnic/heterogeneous populations and populations not fitting into any of the major ethnicities are listed separately.

Worldwide subpopulations and ethnicities were grouped based on the Human Genome Diversity Project-Centre Etude Polymorphism Humain (HGDP-CEPH) (PMID: 16355252, 12493913).

Because the *CYP2C19*17* allele was identified in 2006 (PMID: 16413245), *CYP2C19* studies prior to this date did not include this allele. For many allelic variants, there is only little data available regarding their frequency.

'-' indicates that this allele has not been tested. Healthy subjects and patient cohorts are listed separately or were combined in some instances if 'no difference' was reported.

Allele frequencies were calculated from genotype counts/frequencies in case allele frequencies were not report. In some instances allele frequency calculation errors were detected and are shown corrected (consequently allele frequencies in this table do not always correspond with those in their original publications). Some errors were also discovered in the allele frequency table previously published in the CYP2C19/clopidogrel guideline (PMID: 23698643) and were corrected in this update.

Because *CYP2C19*1* is not genotyped directly, all alleles that are negative for a sequence variation are defaulted to a *CYP2C19*1* assignment. Likewise, sequence variations of alleles that are not tested also default to a *CYP2C19*1* assignment and hence contribute to the frequencies reported for this allele. Therefore, the frequency of **1* depends on the extent of genotyping performed and its frequency may vary considerably among studies. The frequency of **1* was estimated for each major ethnic group and not for each study.

Average, Min and Max indicate the average, minimum and maximum frequencies observed for a given variant allele in a major ethnic group. The frequency of **1* was calculated for the major ethnic groups as following: **1*=100- sum of average of variants (highlighted in blue).

This *CYP2C19* allele frequency summary may not be complete. If you wish to have your paper

and/or data included into this resource, or identify any errors, please contact Andrea Gaedigk, PhD at agaedigk@cmh. This table will be periodically updated to include additional reports and *CYP2C19* allelic variants.

To access the *CYP2C19* allelic variation summary table in excel format please see http://www.pharmgkb.org/download.action?filename=CYP2C19_frequency_table_V1_posted.xlsx

The excel table was last updated December 2014.