**Table S4. Comparative *CYP2D6* data for samples with copy number data indicating one copy of the gene, providing consensus genotype, and previous and new predicted enzyme phenotypes**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **TaqMan CNV data** | **PScan CNV data** | **IonS5**  | **IonS5**  | **AmpliChip** | **Luminex (genomic) RUO** | **PScan** | **Ion S5** | **Consensus genotype** | **Activity Score Consensus** | **Previous Phenotype** | **New Phenotype** |
| **I2** | **I 6** | **E9** | **5’** | **E9** | **3’** | **gene** | **E9** |
| 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | *\*4xN/\*5* | *\*4/\*5* | *\*4/\*5* | *\*4/\*5* | *\*4/\*5* | 0 | PM | PM |
| 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | *\*5/\*35* | *\*5/\*35* | *\*5/\*35* | *\*5/\*35* | *\*5/\*35* | 1 | NM | IM |
| 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | *\*2/\*2* | *\*2/\*5* | *\*2/\*5* | *\*2.001/\*5* | *\*2/\*5* | 1 | NM | IM |
| 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | *\*5/\*10* | *\*5/\*10* | *\*5/\*10* | *\*5/\*10* | *\*5/\*10* | 0.25 | IM | IM |
| 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | *\*1/\*4* | *\*1/\*5* | *\*1/\*5* | *\*1/\*5* | *\*1/\*5* | 1 | NM | IM |
| 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | *\*5/\*41* | *\*5/\*41* | *\*5/\*41* | *\*5/\*41* | *\*5/\*41* | 0.5 | IM | IM |
| 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | *\*1/\*2xN* | *\*1/\*5* | *\*1/\*5* | *\*1/\*5* | *\*1/\*5* | 1 | UM | IM |
| 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | *\*2/\*4* | *\*2/\*5* | *\*2/\*5* | *\*2.001/\*5* | *\*2/\*5* | 1 | NM | IM |
| 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | *\*3/\*5* | *\*3/\*5* | *\*3.001/\*5* | *\*3/\*5* | *\*3/\*5* | 0 | PM | PM |
| 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | *\*5/\*35* | *\*5/\*35* | *\*5/\*35* | *\*5/\*35* | *\*5/\*35* | 1 | NM | IM |
| 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | *\*4/\*35* | *\*3/\*5* | *\*3.001/\*5* | *\*3/\*5* | *\*3/\*5* | 0 | NM | PM |
| 1 |  1 | 1 | 1 | 1 | 1 | 1 | 1 | *\*5/\*41* | *\*5/\*41* | *\*5/\*41* | *\*5/\*41* | *\*5/\*41* | 0.5 | IM | IM |
| 1 | 1 | 1 |  |  |  |  |  | *\*4/\*5* | *\*4/\*5* |  | *NA* | *\*4/\*5* | 0 |  |  |

PScan = PharmacoScan, I2 = intron 2, I6 = intron 6, E9 = exon 9, 5’ = 5’ flanking region, 3’ = 3’ flanking region

Red font denotes adjustments in data owing to new genotypic data

Blue font denotes adjustments in data owing to revised phenotypic definitions based on activity score1

References

1. Caudle K.E., *et al*. Standardizing CYP2D6 Genotype to Phenotype Translation: Consensus Recommendations from the Clinical Pharmacogenetics Implementation Consortium and Dutch Pharmacogenetics Working Group. *Clin Transl Sci.* **13**, 116-124 (2020).