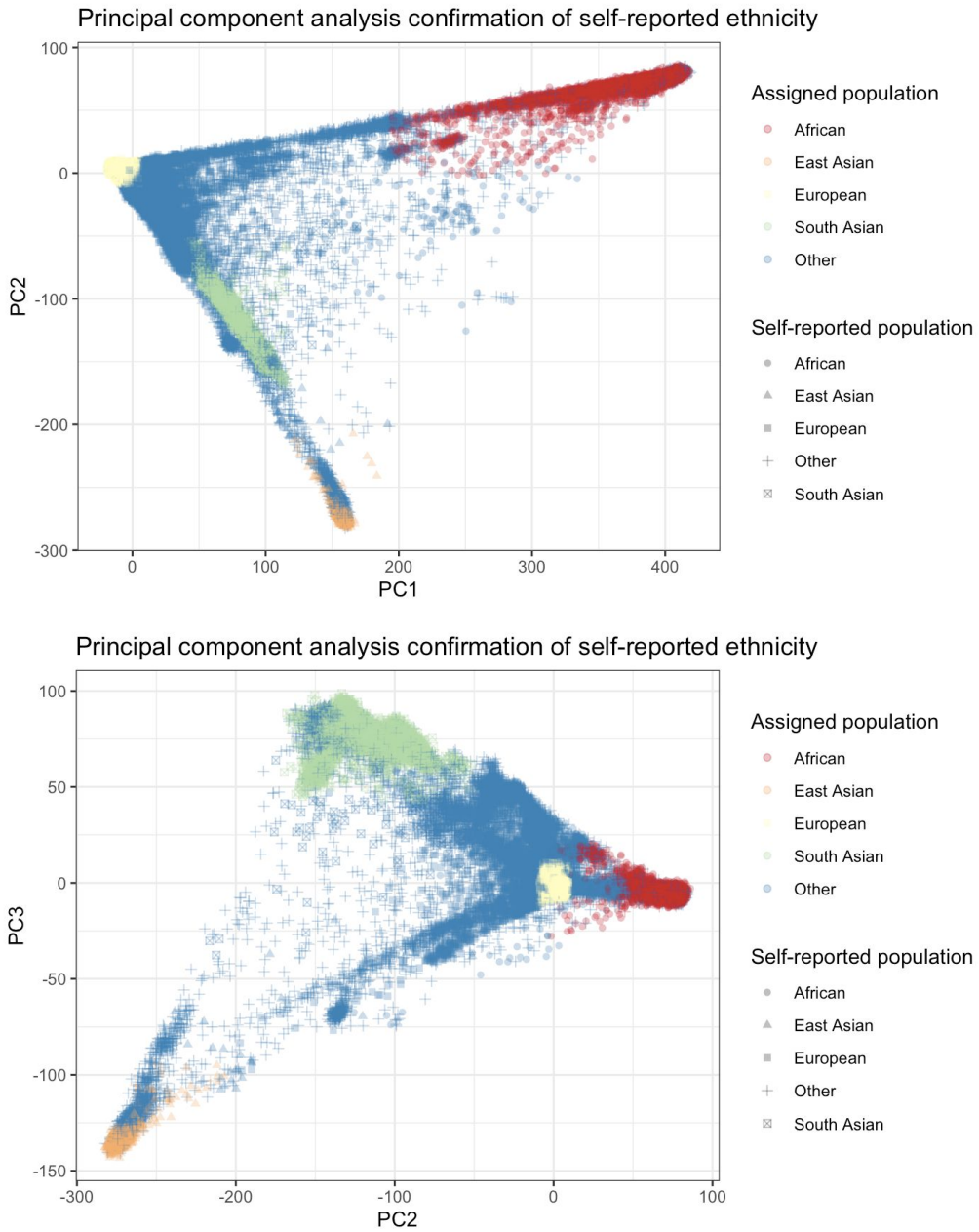

Supplementary Figure 1. Principal component confirmation of self-reported ethnicity. Ethnicity was confirmed using the first three principal components from PCA performed on genotype data. Genetic ancestry was assigned to each subject if they were within three standard deviations of the mean for the three principal components of their self-reported ethnicity. Any subject who's self-reported ethnicity did not match their genetic ancestry was marked as other.

Supplementary Table 2. Gene phenotypes leading to non-typical drug response as determined by CPIC

Gene	Non-typical response phenotypes	Reference
CFTR	Ivacaftor non-responsive	[1]
CYP2B6	Intermediate Metabolizer, Poor Metabolizer	[2]
CYP2C19	Intermediate Metabolizer, Poor Metabolizer, Rapid Metabolizer, Ultrarapid Metabolizer	[3–6]
CYP2C9	Intermediate Metabolizer, Poor Metabolizer	[7–9]
CYP2D6	Intermediate Metabolizer, Poor Metabolizer, Ultrarapid Metabolizer*	[3,4,10–13]
CYP3A5	Normal Metabolizer, Intermediate Metabolizer	[14]
CYP4F2	Increased dose phenotype	[7]
DPYD	Intermediate Metabolizer, Poor Metabolizer	[15]
IFNL3	Unfavorable response genotype	[16]
NUDT15	Intermediate Metabolizer, Poor Metabolizer, Possible Intermediate Metabolizer	[17]
SLCO1B1	Poor Function, Decreased Function, Possible Decreased Function	[18]
TPMT	Intermediate Function, Poor Function	[17]
UGT1A1	Poor Metabolizer	[19]
VKORC1	Decreased warfarin dose, possibly decreased warfarin dose	[7]

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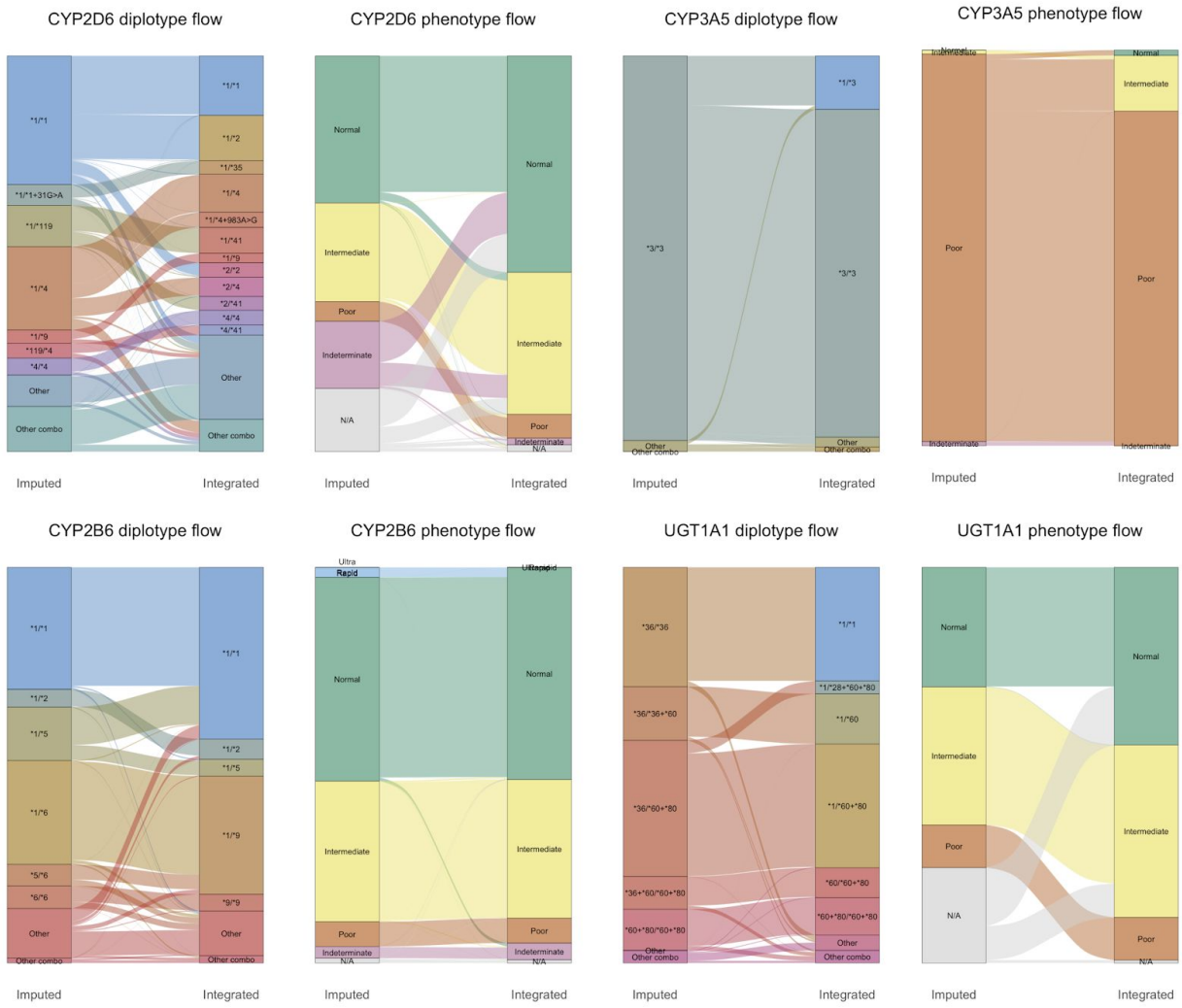

Supplementary Figure 2. Alluvial diagrams of diplotype and phenotype flow between platforms highlight frequent incorrect calls in the imputed data. We show diagrams of the four genes with the lowest concordance between the imputed and integrated callsets (excluding *NUDT15*). Diplotypes occurring with a frequency of less than 3% are grouped into “Other”, and diplotypes containing combination alleles occurring with less than 3% frequency are grouped into “Other combo”.