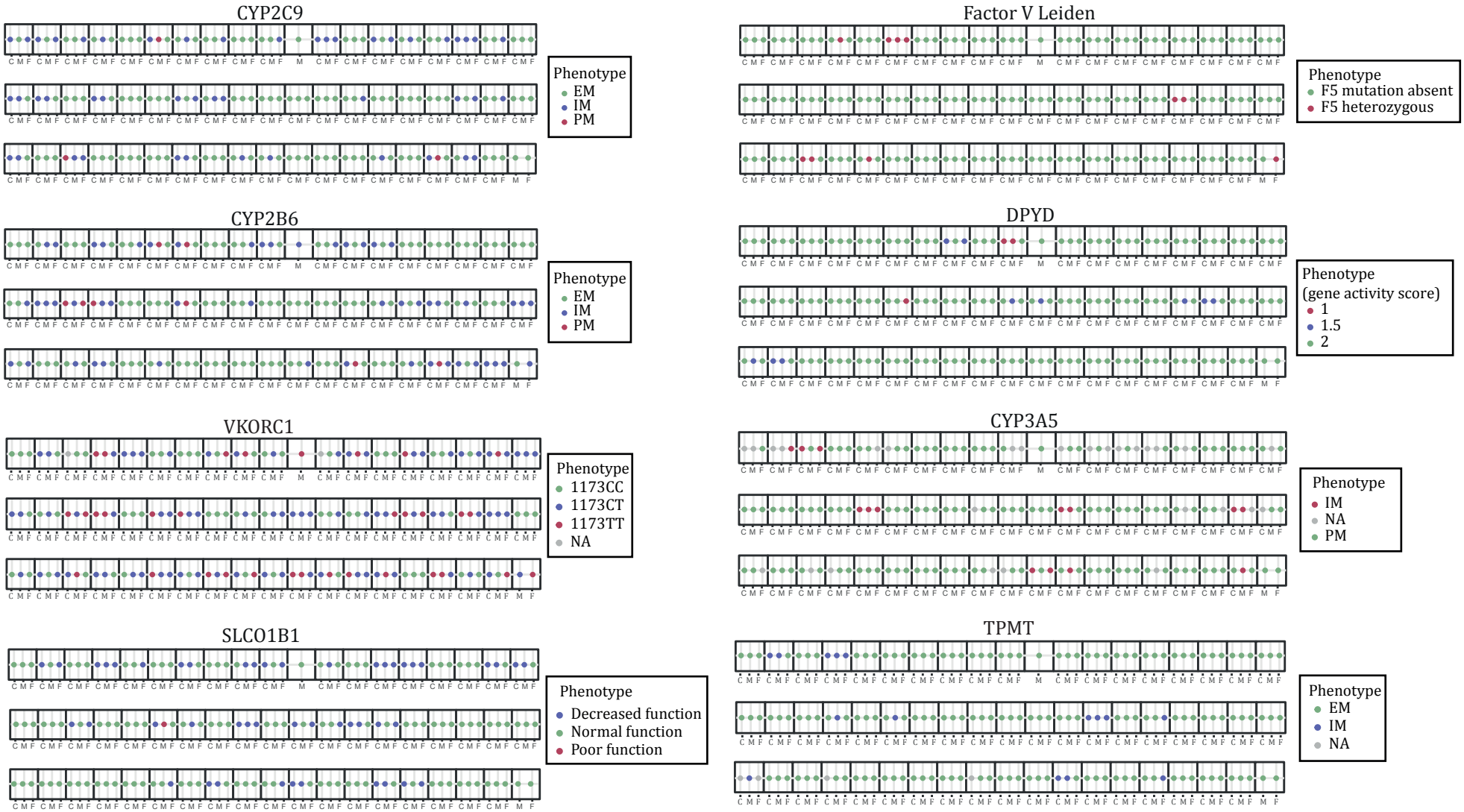

Figure S2: Phenotypes per gene split out per family. Phenotypes are based on the variant panel from the Ubiquitous pharmacogenomics consortium, 42 variants in 11 genes were investigated. No results for *UGT1A1* and for *CYP2C19* could be obtained. *CYP2D6* was excluded from this analysis due to the inability to call phenotypes for all inividuals. In the absence of copy number data, only diplotypes consisting of two null-alleles were assigned a phenotype (N=11) leading to incomplete data for the child-parent trios.
Each cluster represents one child-parent trio and their phenotypes.
C: Child, M: Mother, F: father, PM: Poor Metabolizer, IM: Intermediate Metabolizer, EM: Extensive Metabolizer, F5: factor V Leiden.