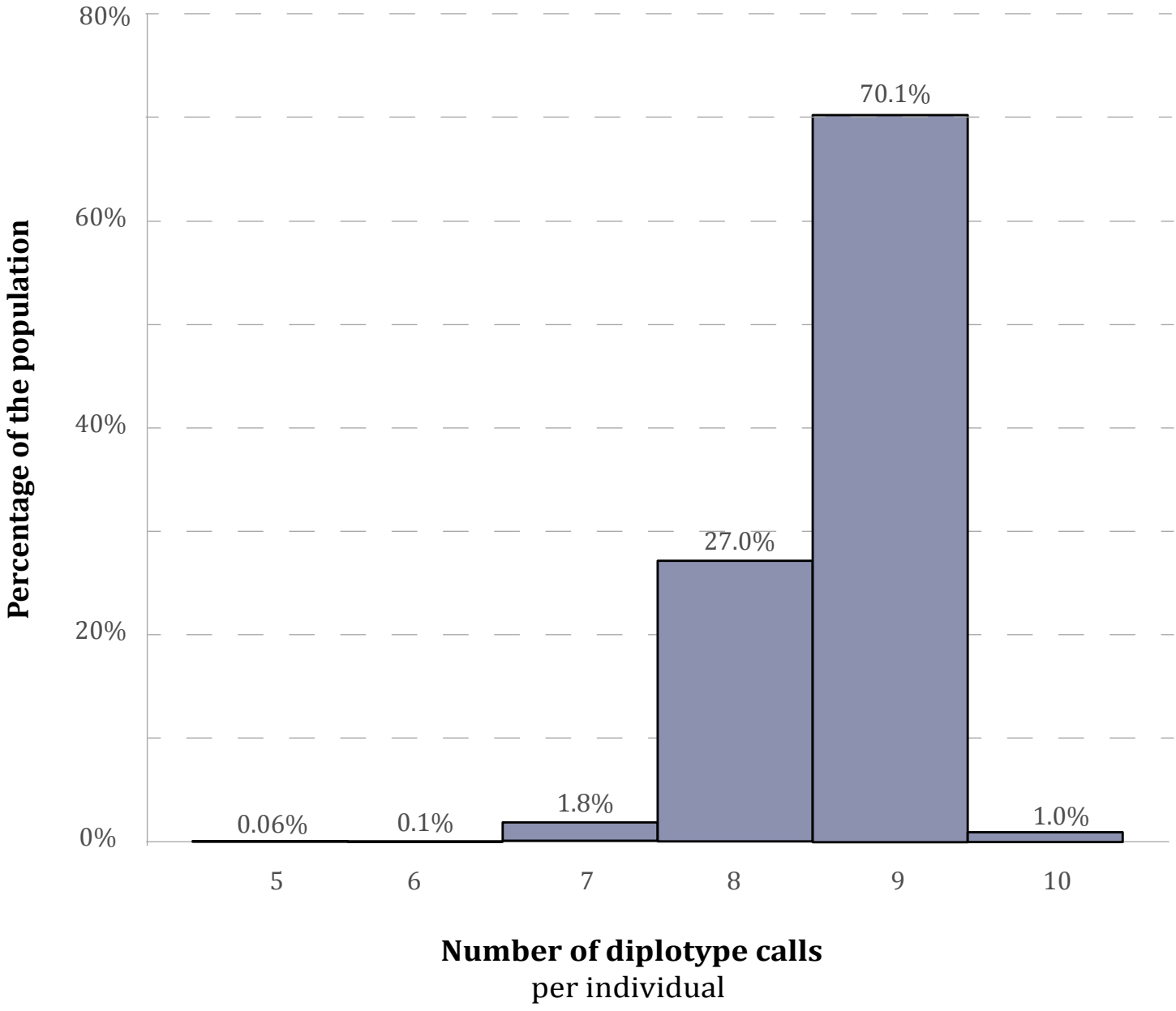

Figure S1: Number of diplotype calls based on SNV data per individual. 11 genes were screened in 1,583 individuals, when there was a lack of coverage for at least one variant a diplotype was not assigned. Copy Number Variants could not be determined and are not included in the diplotype assigment. The majority of individuals had diplotype data for 9 out of 11 genes. No genotype calls for *UGT1A1* were available, only 1% of the diplotypes for *CYP2C19* could be called.