



**Supplementary Figure 2. Novel variant statistics.** **a**, Number of novel SNPs that were not identified in elsewhere. Public databases include Kaviar, gnomAD (2.1.1 release), and dbSNP150. **b**, Distribution of novel SNP per population. Novel SNPs found in multiple and all populations were included in 'Shared' and 'All', respectively. **c**, Distribution of novel SNPs based on RefSeq gene definition.