

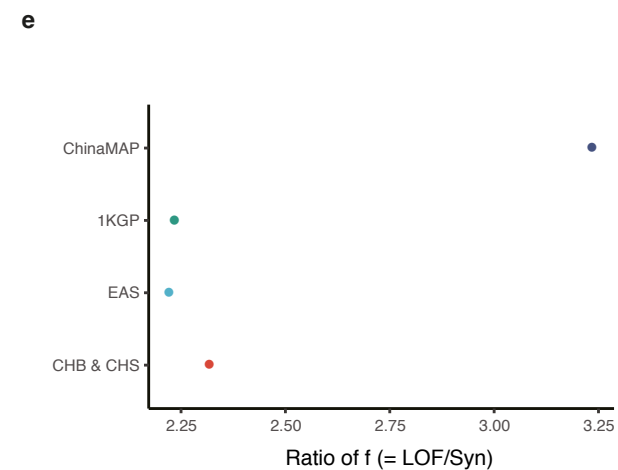
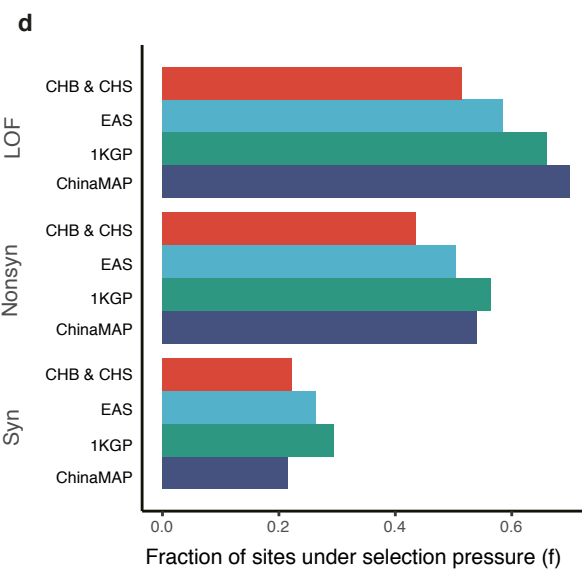
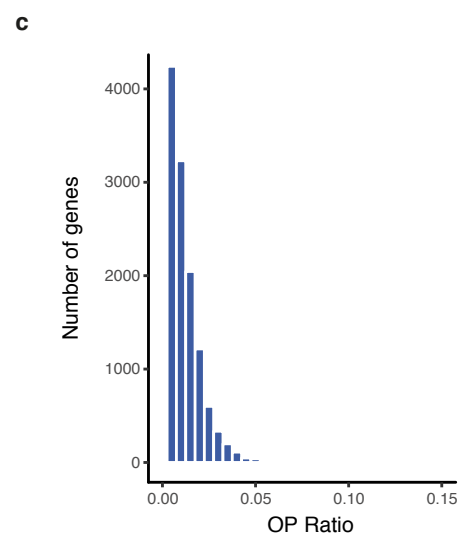
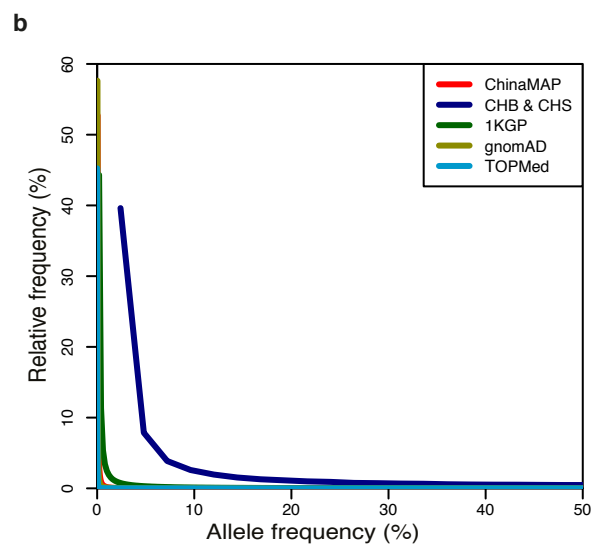
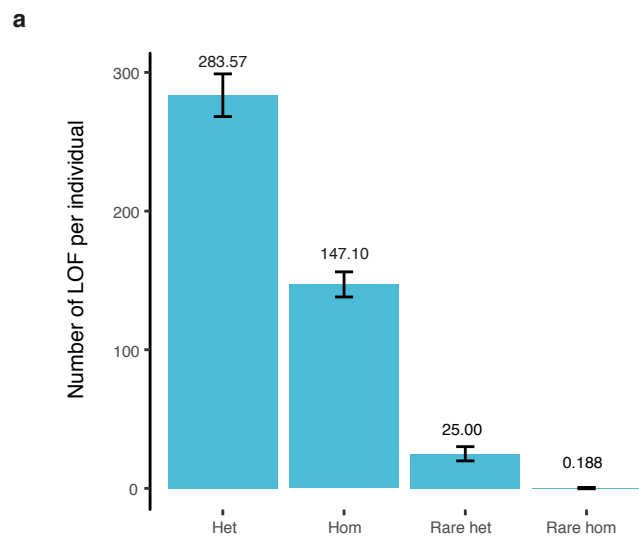


Fig. S4 The functional categories and genomic regions of SNPs. **a** The number of loss-of-function (LOF) variants per individual. Error bars represent standard deviation. Every individual had 284 heterozygous and 147 homozygous LOF variants, of which 25 and 0.188 are rare ($AF < 1\%$) on average. **b** Frequency spectrum for the variants of intergenic regions in the ChinaMAP, CHB & CHS, 1KGP, gnomAD and TOPMed database. **c** The distribution of observed/predicted (OP) ratio. **d** The fraction of sites under selection pressure (f) calculated for LOF, nonsynonymous and synonymous SNPs, separately. **e** The ratio of f between LOF variants and synonymous SNPs in datasets.