

ESM Fig. 1. Multidimensional scaling analysis (MDS) plot showing the first two principal components, based on genotype data of 11 populations from HapMap (African ancestry in Southwest USA (ASW), Utah residents with Northern and Western European ancestry from the CEPH collection (CEU), Han Chinese in Beijing, China (CHB), Chinese in Metropolitan Denver, Colorado (CHD), Gujarati Indians in Houston, Texas (GIH), Japanese in Tokyo, Japan (JPT), Luhya in Webuye, Kenya (LWK), Mexican ancestry in Los Angeles, California (MEX), Maasai in Kinyawa, Kenya (MKK), Tuscan in Italy (TSI) and Yoruban in Ibadan, Nigeria (YRI)), as well as the 3 case-controls cohorts (Hong Kong GWAS 1 (HK1), Hong Kong GWAS 2 (HK2) and Shanghai GWAS (SH)) in the stage 1 genome scan of the present study.

