

**Supplementary Data Set: Regional association plots of 183 genome-wide significant loci from trans-ethnic meta-analysis.**

Regional association plots are shown for all genome-wide significant loci from trans-ethnic meta-analysis (n=457,690). The y-axis shows  $-\log_{10}(\text{two-sided nominal p-value})$  from the meta-analysis using inverse variance weighted fixed effect method. Correlation ( $r^2$ ) with the index SNP was estimated based on the 1000 Genomes EUR reference samples. Plots were generated using the stand-alone version 1.3 of LocusZoom (Pruim, R.J. *et al. Bioinformatics* 26, 2336-7, 2010). Genetic positions refer to GRCh37/hg19 coordinates. Zoomed in versions of pages 19, 21, 52, 54, 57, 69, 71, 93, 115, and 119 are appended at the end of the document.

































































































































































































































































































































































































