

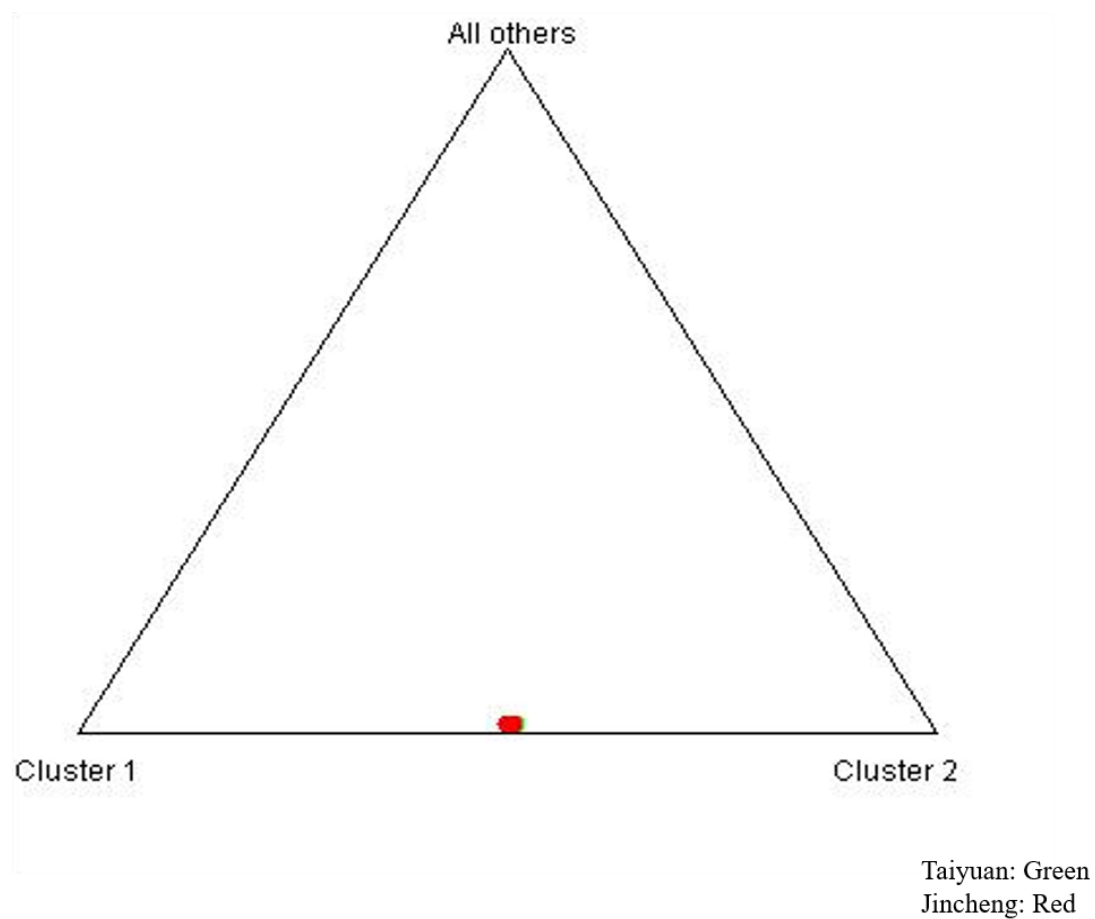
Supplementary Data

Figure S1. Clustering results of AIMs of Chinese Han population. Each color represents collection site for a sample. Red: Taiyuan; Green: Jincheng.

Figure S2. The LD structures for *CHRNA5/A3/B4* in the Chinese sample were drawn with Haploview (v. 4.2),⁴⁵ and haplotype blocks were defined according to Gabriel *et al.*⁴⁶ The arrow above the figure represents the gene transcription direction from 5' to 3'.

Figure S3. The LD structures for *CHRNA7*, *CHRNA4*, and *CHRNA2* in the Chinese sample were drawn by Haploview (v. 4.2),⁴⁵ and haplotype blocks were defined according to Gabriel *et al.*⁴⁶ The arrow above the figure represents the gene transcription direction from 5' to 3'.

Figure S4. Associations between genotype data of risk-nominating variants and extent of methylation in blood of 72 Chinese Han participants tested for *cis*-mQTLs. Distribution of the values at the methylation sites is presented for individuals carrying zero, one, and two minor alleles. Only the marginally significant *cis*-mQTLs are shown for each variant ($p < 4.7 \times 10^{-4}$).

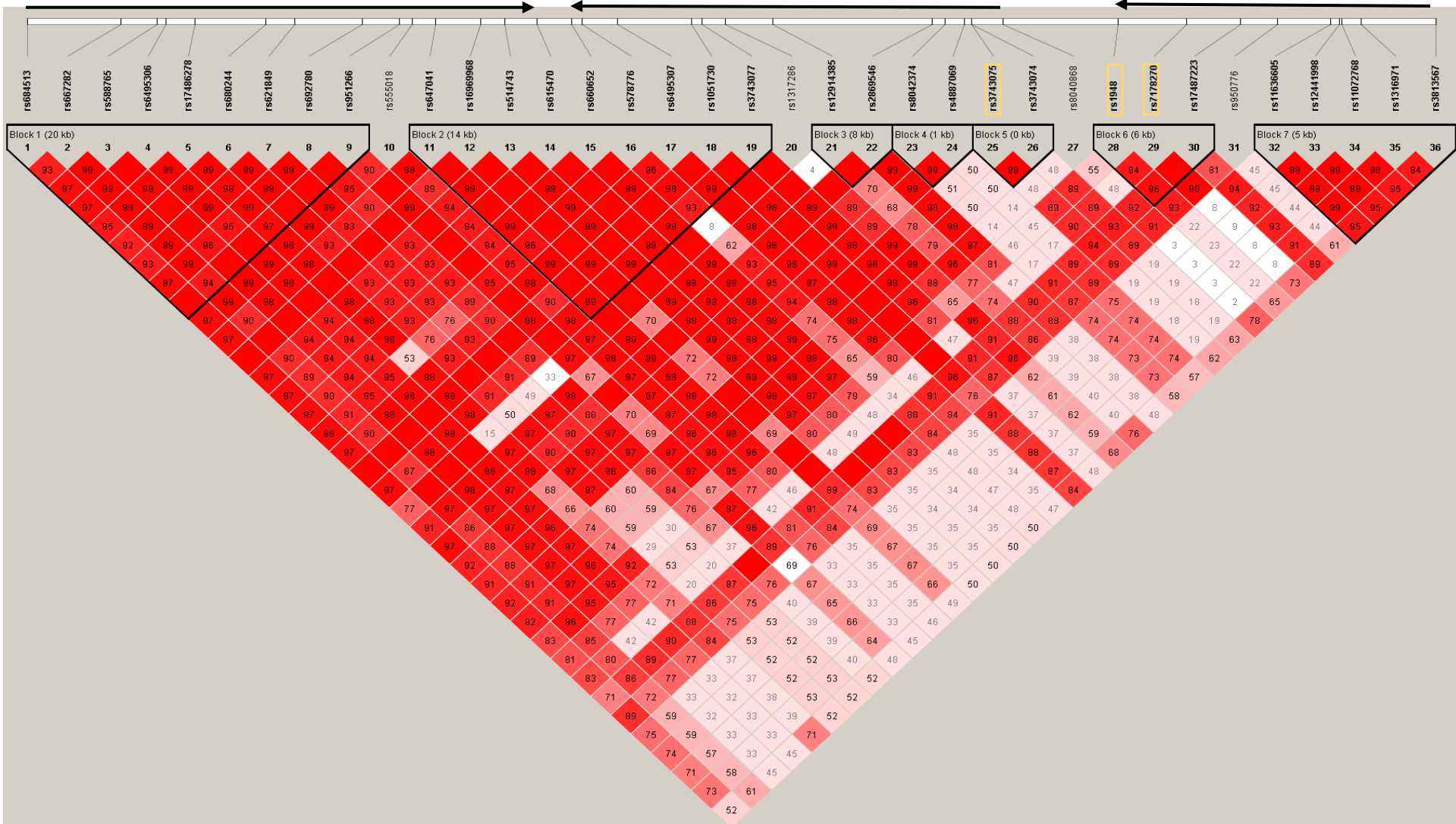


Supplementary Figure S1

CHRNA5

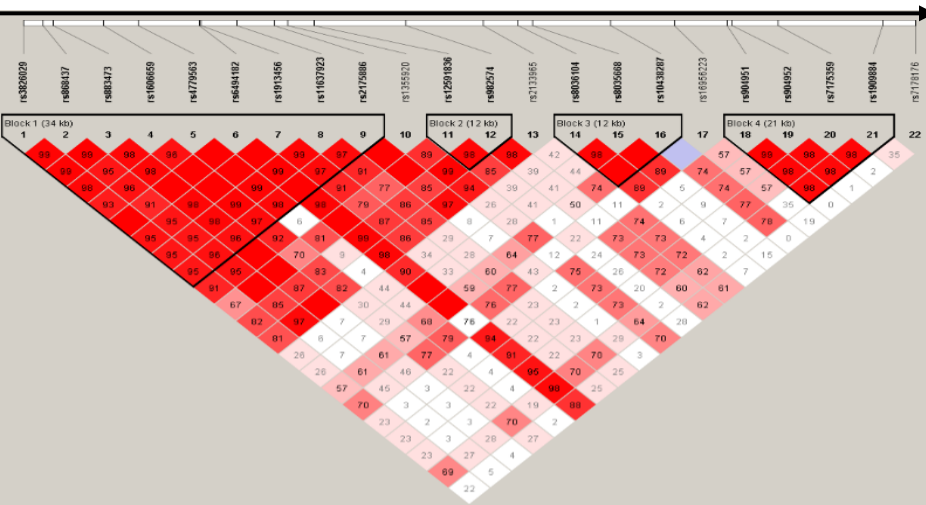
CHRNA3

CHRNA4

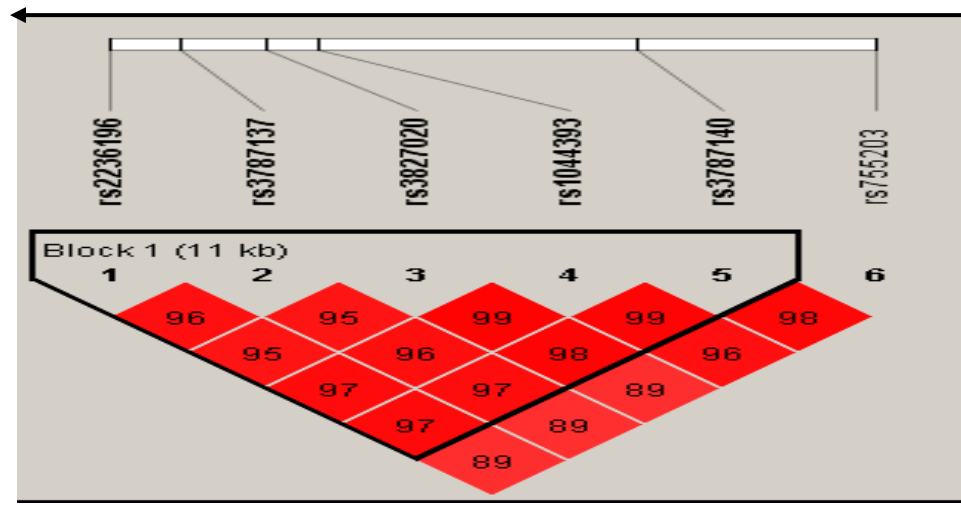


Supplementary Figure S2

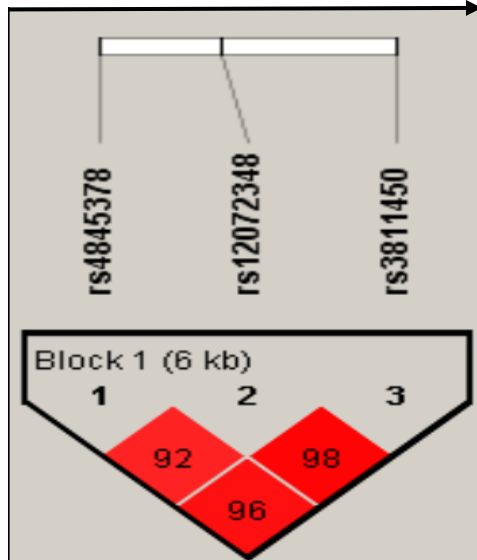
CHRNA7



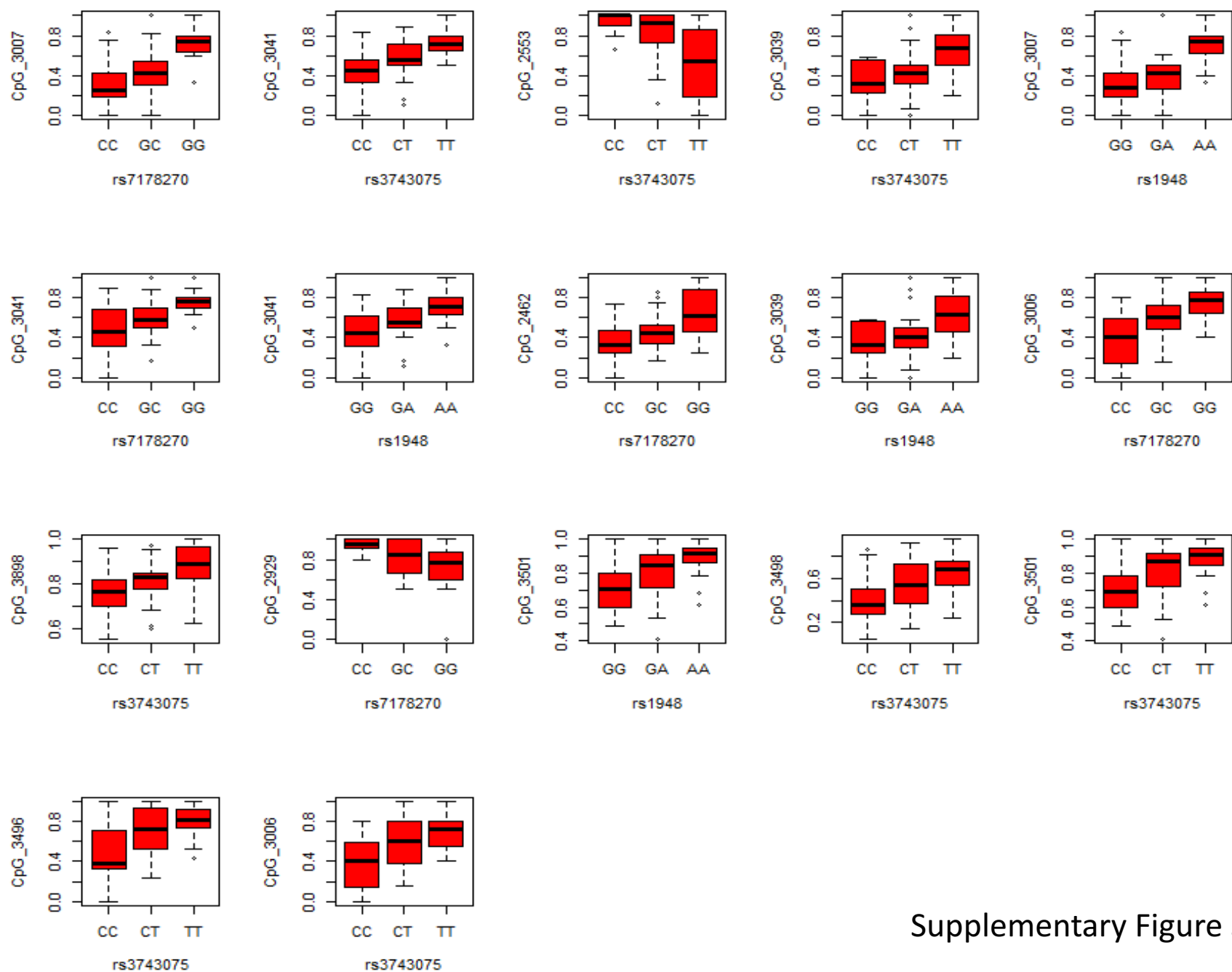
CHRNA4



CHRNA2



Supplementary Figure S3



Supplementary Figure S4