

Supplementary Figure S1. Linkage disequilibrium plot for the HapMap CHB (Han Chinese from Beijing, China, n=84) reference dataset single-nucleotide polymorphisms (SNPs) (genotypes downloaded from the International HapMap Project website; HapMap3, release 2; chr1:165663570..165742500) in *CD247*. This plot was obtained with Haploview 4.2 using the pairwise R-square color scheme in a grey scale.

*Significant *P*-value, obtained for the Asian cohort in our study, under the additive model and adjusted for the first three principal components and gender ($P_{\text{adj}} < 0.05$); **Significant *P*-value, obtained for the Asian cohort in our study, overpassing Bonferroni correction ($P_{\text{adj}} < 0.0017$); ■Significant *P*-value obtained in the Asian population GWAS [19] ($P < 0.05$); ■■The most significant *P*-value in *CD247* obtained in the Asian population GWAS [19] ($P = 8.70\text{E-}05$). SNP ID from our study is indicated for the highlighted SNPs, when there is no correspondence with our SNPs then SNP rs is indicated.