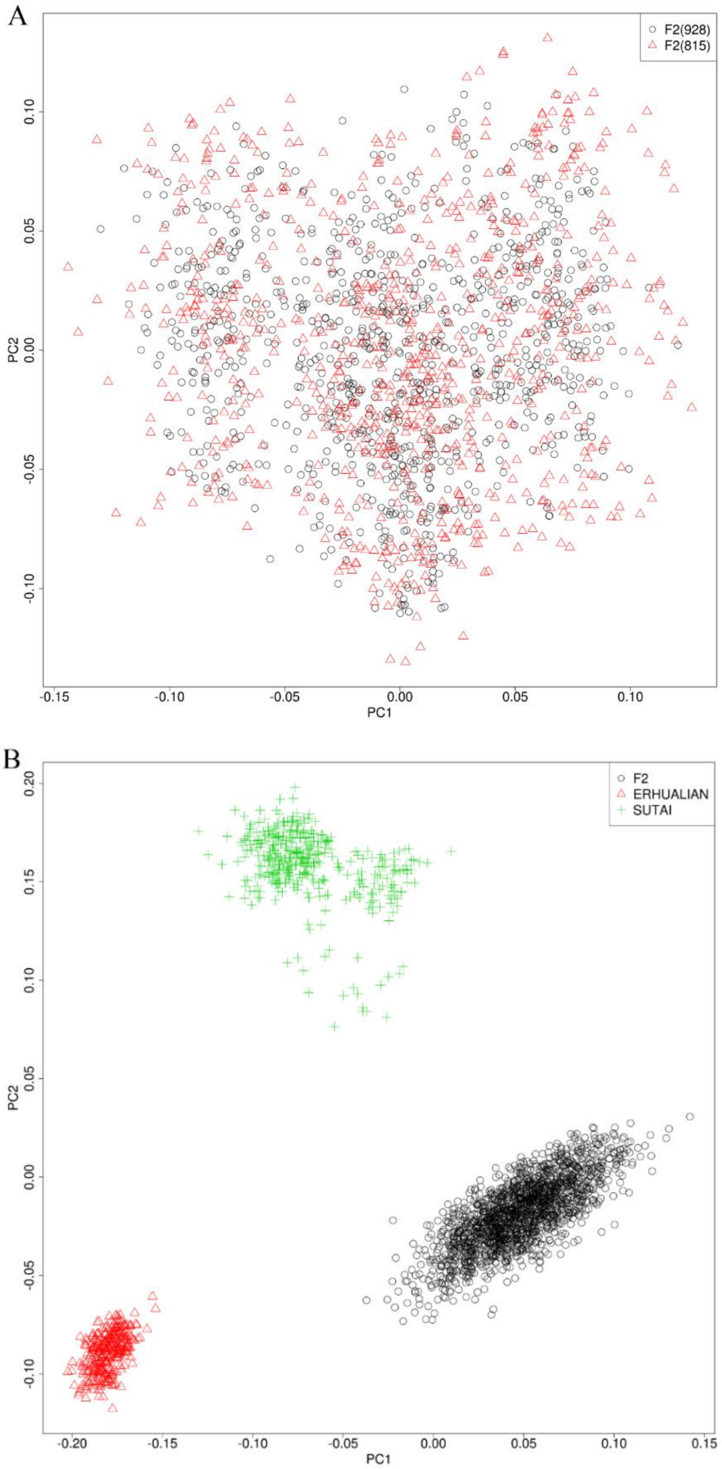
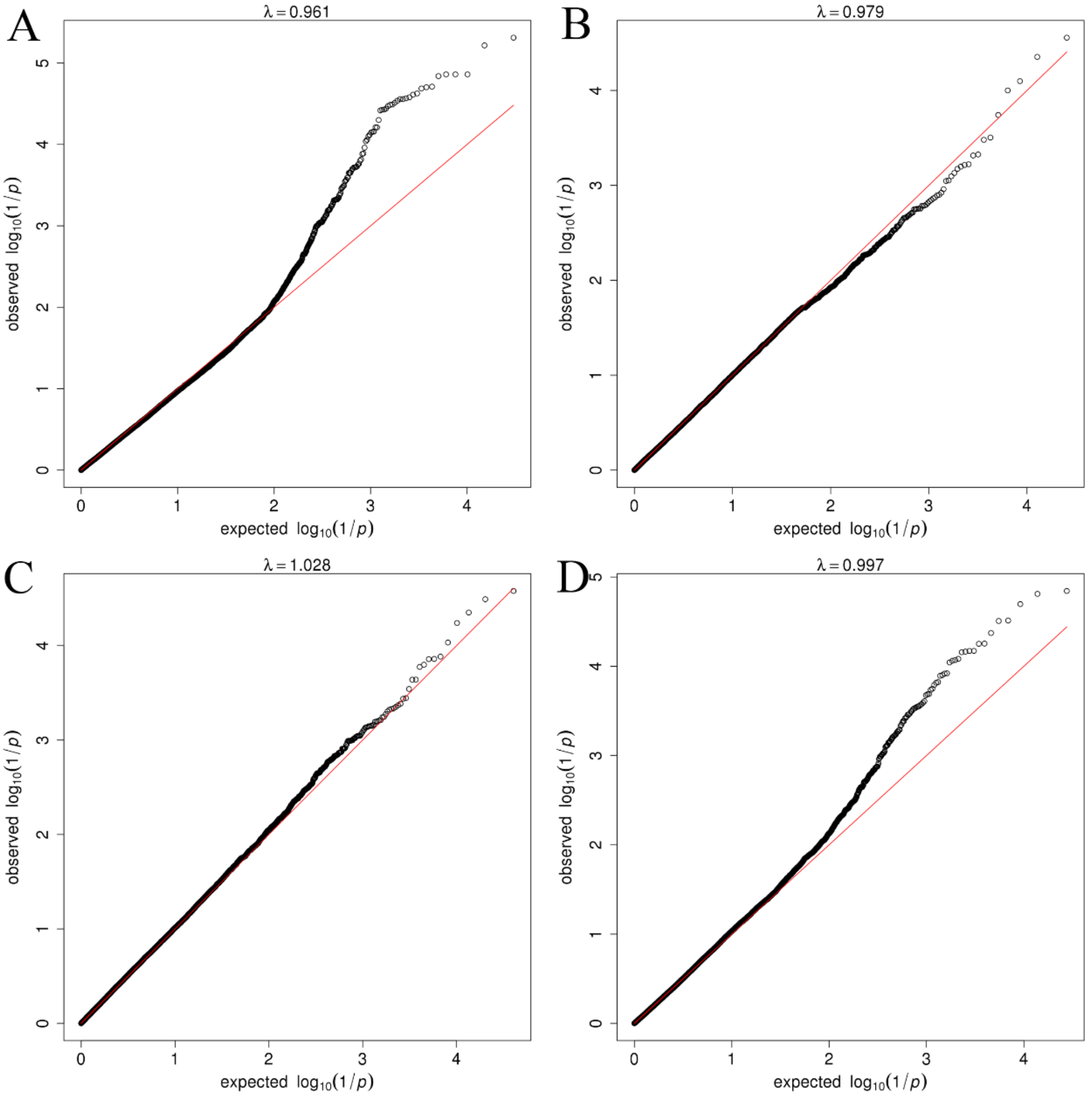


Supplementary Figure 1. Population stratification revealed by principal component analysis (PCA). PCA was conducted on the 928 genotyped F_2 pigs and the 815 F_2 pigs with the imputed data (A), and on the three tested populations including F_2, Erhualian and Sutai pigs (B).



Supplementary Figure 2. The quantile-quantile (Q-Q) plots of SNPs in single-marker GWAS. The Q-Q plots of SNPs for the F_2 resource population (A), Erhualian pigs (B), Sutai pigs (C) and the meta-analysis (D). The observed negative $\log_{10}$ *P*-value versus expected negative $\log_{10}$ *P*-value generated the Q-Q plots.