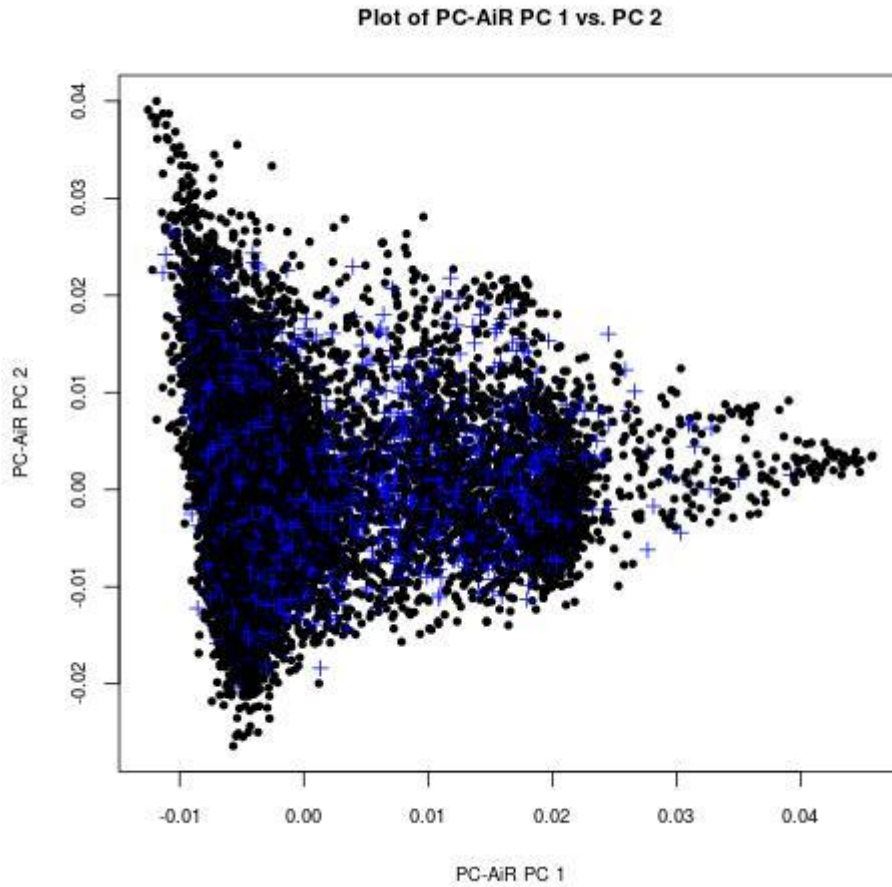
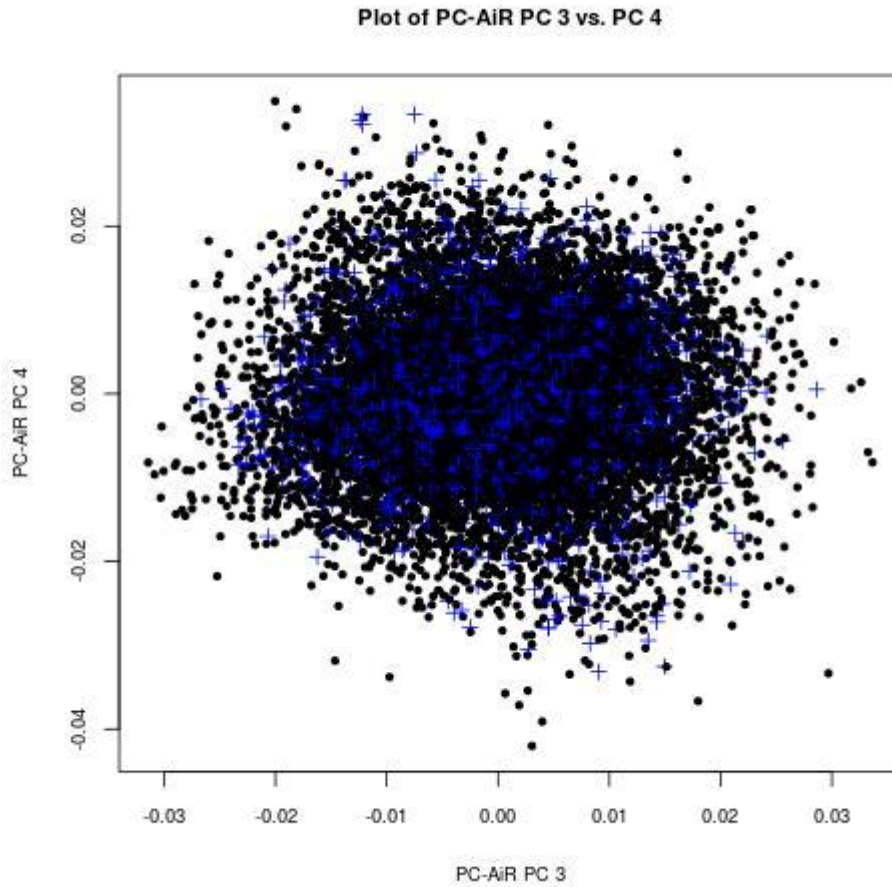


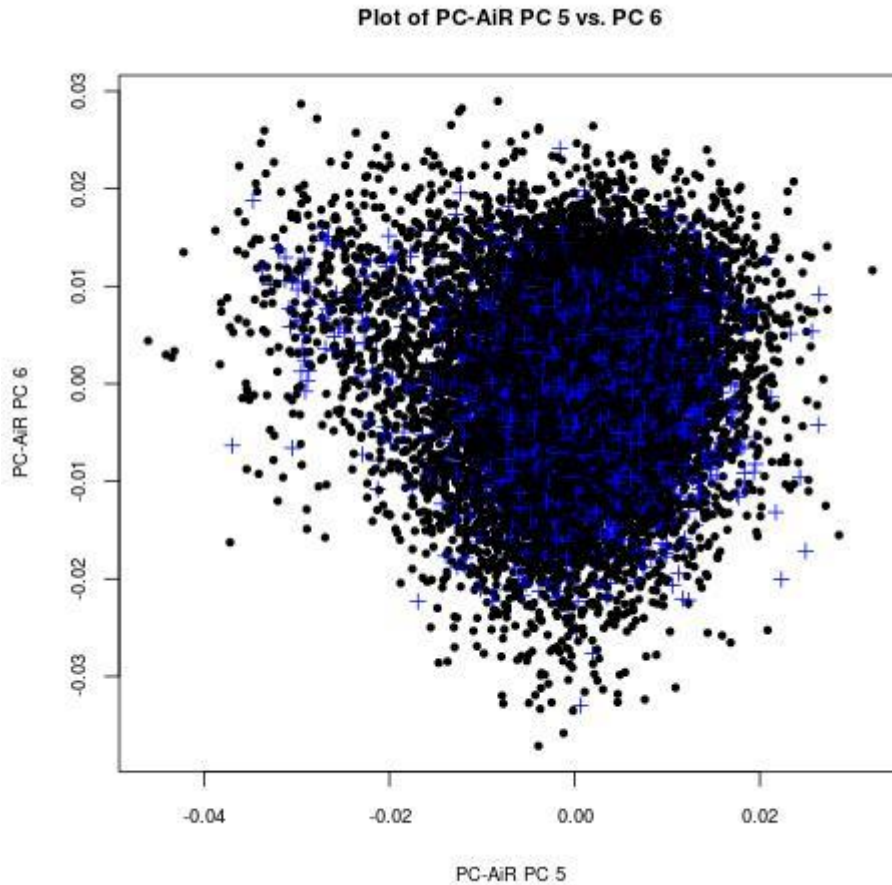
Supplementary Fig. S1. Relatedness Estimation. The scatter plot of estimated kinship coefficients against estimated probabilities of sharing zero alleles that are identical by descent, $k(0)$, for each pair of subjects by using PC-Relate.



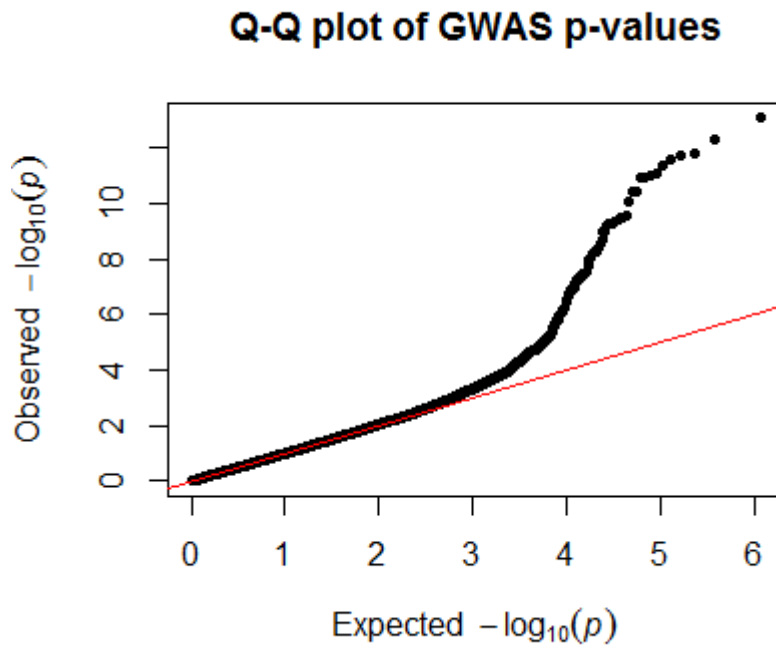
Supplementary Fig. S2. Population Structure Inference: Scatter plots of principal components 1 and 2 by using PC-AiR. Each point in one of these plots represents an individual in the sample. These plots visualize population structure in the sample and identify clusters of individuals with similar ancestry. Principal component values were plotted as black dots and blue pluses for individuals in the “unrelated subset” and “related subsets”, respectively.



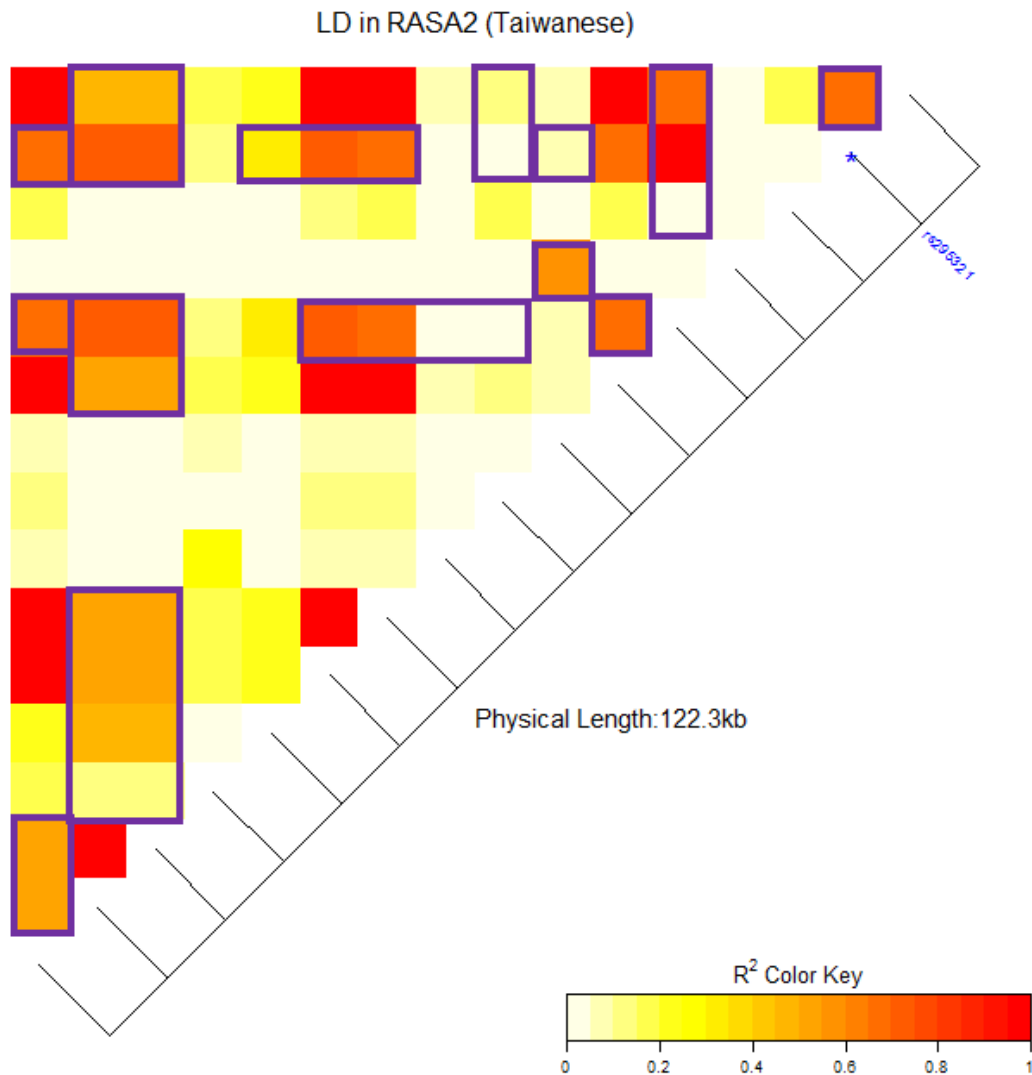
Supplementary Fig. S3. Population Structure Inference: Scatter plots of principal components 3 and 4 by using PC-AiR. Each point in one of these plots represents an individual in the sample. These plots visualize population structure in the sample and identify clusters of individuals with similar ancestry. Principal component values were plotted as black dots and blue pluses for individuals in the “unrelated subset” and “related subsets”, respectively.



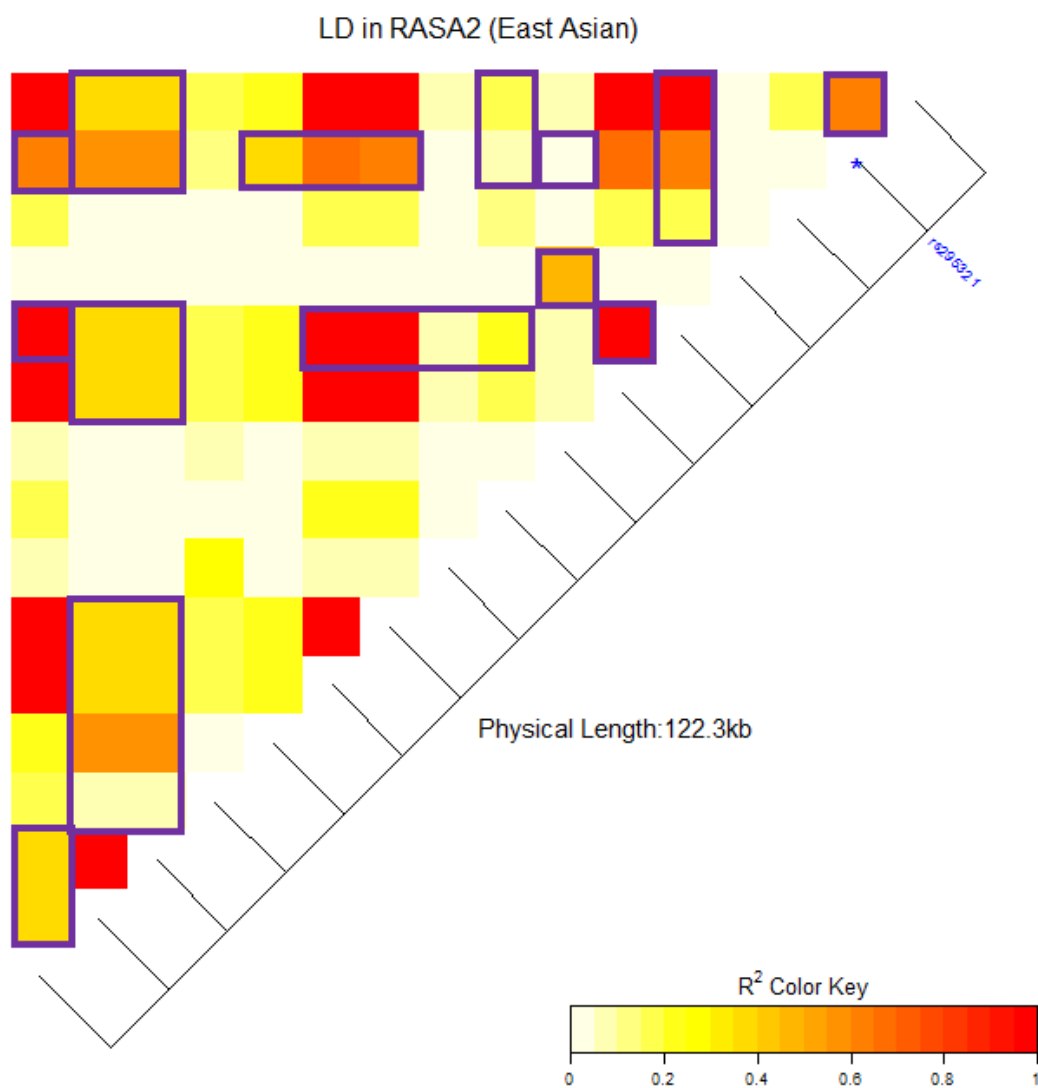
Supplementary Fig. S4. Population Structure Inference: Scatter plots of principal components 5 and 6 by using PC-AiR. Each point in one of these plots represents an individual in the sample. These plots visualize population structure in the sample and identify clusters of individuals with similar ancestry. Principal component values were plotted as black dots and blue pluses for individuals in the “unrelated subset” and “related subsets”, respectively.



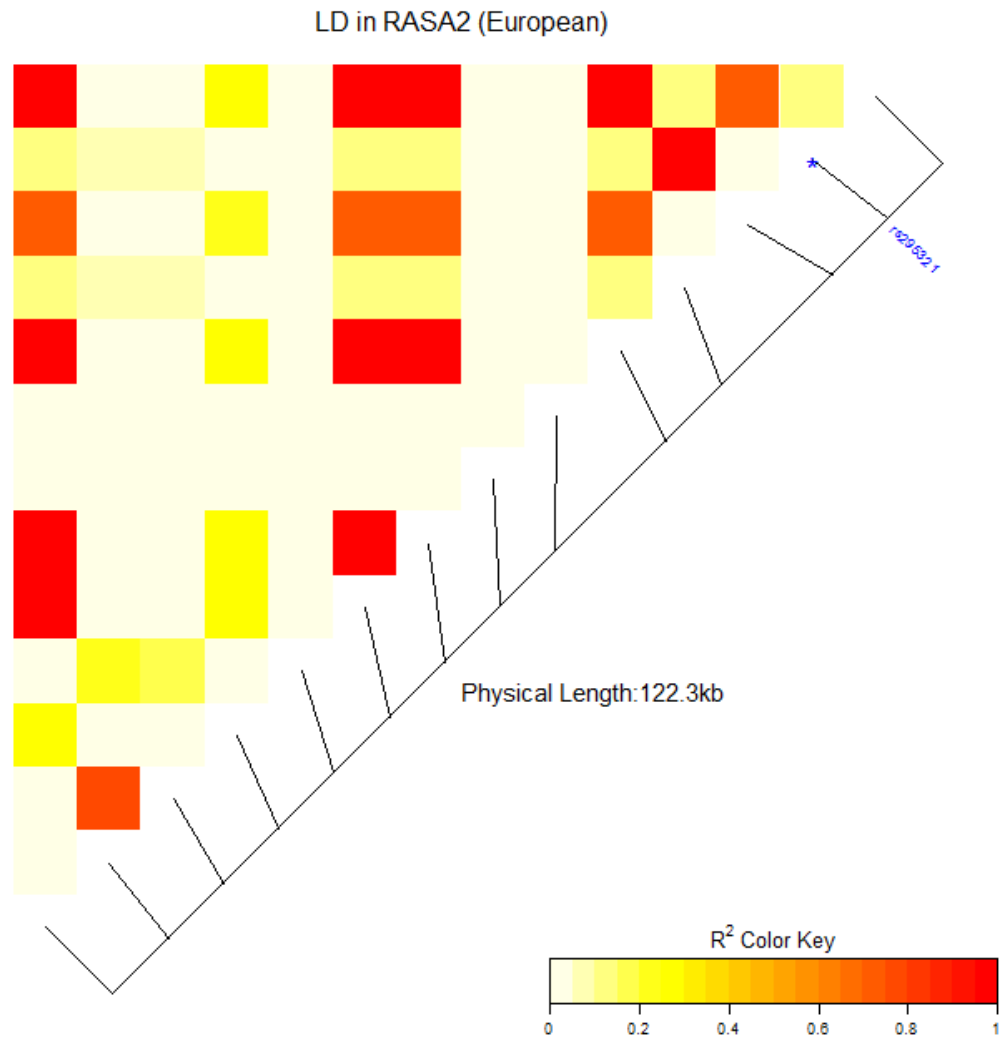
Supplementary Fig. S5. The Q-Q plot of height results. The plot illustrates expected and observed distributions of P-values from the genome-wide association study of height.



Supplementary Fig. S6. Heat map plot for linkage disequilibrium (LD) within the *RASA2* locus using the Taiwanese subjects in the Taiwan Biobank. The genotyped SNPs within the *RASA2* locus in this study were used. The measure of LD is plotted using the squared allelic correlation r^2 . Each colored rectangle shows the correlation r^2 between a pair of SNPs. The novel SNP rs295321, found in this study, is labeled. Distinct LD patterns between the Taiwanese and East Asian populations are highlighted in purple rectangles.



Supplementary Fig. S7. Heat map plot for linkage disequilibrium (LD) within the *RASA2* locus using the East Asian ancestry subjects from the 1000 Genomes Project. The genotyped SNPs within the *RASA2* locus in this study were used. The measure of LD is plotted using the squared allelic correlation r^2 . Each colored rectangle shows the correlation r^2 between a pair of SNPs. The novel SNP rs295321, found in this study, is labeled. Distinct LD patterns between the Taiwanese and East Asian populations are highlighted in purple rectangles.



Supplementary Fig. S8. Heat map plot for linkage disequilibrium (LD) within the *RASA2* locus using the European ancestry subjects from the 1000 Genomes Project. The genotyped SNPs within the *RASA2* locus in this study were used. The measure of LD is plotted using the squared allelic correlation r^2 . Each colored rectangle shows the correlation r^2 between a pair of SNPs. The novel SNP rs295321, found in this study, is labeled.