###### Title: Data archive 1 - Summary of the regulatory S-genes (g-eQTL) for each T-gene from our gene-based PLS analysis according to population.

Description: This Excel file provides a table that summarizes the regulatory S-genes (g-eQTL) for each T-gene from our gene-based PLS analysis by population. The table consists of 3 components and each row represents a T-gene. The first component provides “T-gene name”: each gene is named by its gene symbol followed by an Entrez gene ID. For example, the gene symbol and gene ID of the first gene in this table are 2’-PDE and 201626. The second component provides the “data availability” of a gene expression and SNP: “1” indicates the data is available and “NA” indicates the data is not available in the g-eQTL mapping. The third component provides the g-eQTL names that regulated T-genes through a cis- or trans-regulatory mechanism according to population. For each population, the first column records if a cis-acting regulation was occurred in the T-gene (“1” indicates a cis-acting relation was identified and “NA” indicates there was no cis-acting relation). The second column summarizes all the trans-acting S-genes that regulate a T-gene. Each S-gene is named by its gene symbol followed by an Entrez gene ID, and multiple S-genes are separated by commas.