###### Title: Data archive 3 - Summary of T-genes regulated by each eQTL from our SNP-based PLS analysis by population.

**Description:** This Excel file provides a table that summarized the T-genes regulated by each eQTL from our SNP-based PLS analysis by population. The table consists of 3 components and each row represents an eQTL. The first component provides the “SNP ID (Probe\_Set)”, “Gene symbol”, and “Gene ID”: each eQTL is named by the SNP probe set. The gene symbol and Entrez gene ID of the gene where an eQTL was located are provided. The second component provides the “data availability” of the SNPs: “1” indicates that the data is available and “NA” indicates it is not available in the g-eQTL mapping. The third component provides the names of T-genes regulated by eQTL through a cis- or trans-regulatory mechanism according population. For each population, the first column records whether a cis-acting regulation occurred in an S-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 T-genes regulated by an eQTL. Each T-gene is named by its gene symbol followed by an Entrez gene ID, and multiple T-genes are separated by commas.