

Figure Captions

Figure S1. Heat map representation of DEGs.

Figure S2. The Gene Ontology (GO) enrichment analysis of DEGs in the comparisons of S vs CK (A), SL vs. S (B), SL vs. CK (C), and L vs. CK (D). The dot size and the dot color indicate the number of DEGs of the pathway and q value, respectively.

Figure S3. KEGG pathway enrichment analysis of the annotated DEGs in the comparisons of S vs CK, SL vs. S, SL vs. CK, and L vs. CK.

Figure S4. (A) and (B) Soft threshold in scale independence and mean connectivity, respectively.

Figure S5. Evolutionary relationships of sulfate transporters (SULTRs) polypeptides from *Arabidopsis*, *Zea mays* L., rice (*Oryza sativa* L.), and tomato (*Solanum lycopersicum* L.). The MEGA4 software package (<http://www.megasoftware.net/mega4/mega.html>) was used for phylogenetic analysis. The scale bar indicates the number of amino acid substitution per site. The proposed SULTR protein designations for a tomato sulfate transporter were shown in red.