

**Supplementary Table S1.** The effective data volume and quality of sequence reads.

**Supplementary Table S2.** Gene IDs and GO enrichment.

**Supplementary Table S3.** RNAseq filtered data of gene expression profiles and gene annotation.

**Supplementary Table S4.** Differentially Expressed Genes and GO term categorization.

**Supplementary Table S5.** Categories of the first and the second round of gene classification.

**Supplementary Figure S1.** Groups of gene ontology classification.

**Supplementary Figure S2.** Top GO terms extracted from the data.

**Supplementary Figure S3.** Genes classified in top GO terms of the Biological Process category.

**Supplementary Figure S4.** Genes classified in top GO terms of the Cellular Components category.

**Supplementary Figure S5.** Genes classified in top GO terms of the Molecular Function category.

**Supplementary Figure S6.** Red Love 'General' vs. 'Early Fuji' comparison of up- and down-regulation of genes classified in KEGG pathways.