

## Supporting information

Figure S1: Data quality control and data filtering. (a, b) Correlation scatter plot of mRNA and mitochondrial RNA in tender leaves and functional leaves. Left picture: The X-axis represents the RNA reads count, the Y-axis represents the percentage of mitochondrial RNA expression. Right picture: The X-axis represents the RNA reads count, the Y-axis represents the quantity of RNA expression. (c, d) QC violin plots of tender leaves and functional leaves. Left picture: Violin plot showing the quantity of mRNA expression; Middle picture: mRNA reads count violin plot; Right picture: Percentage of mitochondrial RNA violin diagram.

Figure S2: Gene ontology (GO) analysis of DEGs in tender leaves.

Figure S3: Gene ontology (GO) analysis of DEGs in functional leaves.

Figure S4: Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis of enriched pathways among DEGs in tender leaves.

Figure S5: Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis of enriched pathways among DEGs in functional leaves.

Figure S6: Top10 marker gene clustering heat map of different cell clusters in tender leaves. On the right, the main body of the heat map; on the left, GO function annotation.

Figure S7: Top10 marker gene clustering heat map of different cell clusters in functional leaves. On the right, the main body of the heat map; on the left, GO function annotation.

Figure S8: Top10 marker gene clustering heat map of different cell clusters in tender leaves. On the right, the main body of the heat map; on the left, KEGG function annotation.

Figure S9: Top10 marker gene clustering heat map of different cell clusters in functional leaves. On the right, the main body of the heat map; on the left, KEGG function annotation.