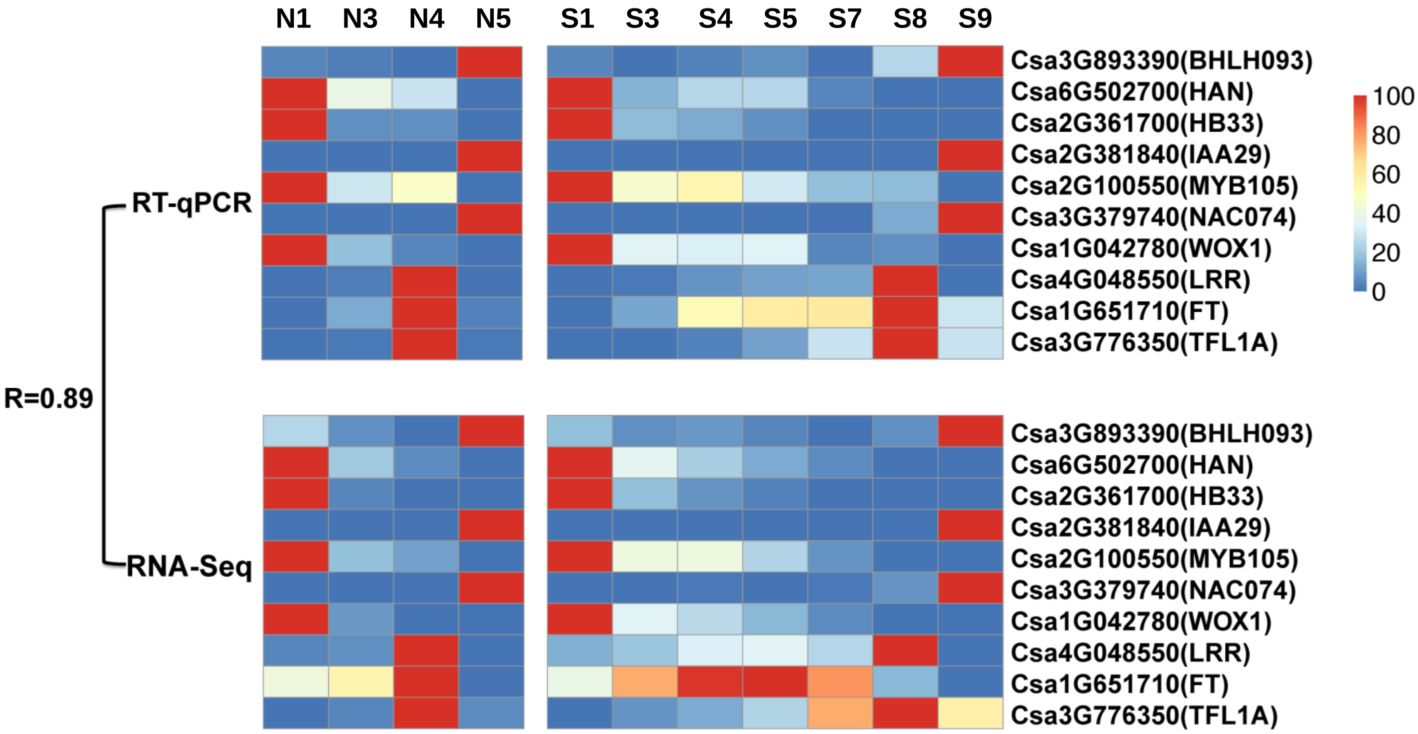

Supplemental Figure S1. Real-time qRT-PCR analysis of selected genes in corollas at different stages in the normal ovary and super ovary.

Transcript levels of ten selected genes were detected by qRT-PCR in the 11 samples of normal ovary and super ovary. Heat map showed the mean value of transcript levels detected in three biological replicates. For each gene, the highest transcript level was set to 100, and transcript levels in other samples were calculated as the relative value to the highest. Relative transcript levels as detected by qRT-PCR (top) or by RNA-Seq (bottom) were shown by color scales. R, correlation coefficient value between RNA-seq data and qRT-PCR data.