



Supplementary Fig. 2. Supplemental observations of differentially expressed genes (DEG) in three transcriptome analyses. *A-D*: Hierarchical clustering heat map and GO enrichment analysis of DEGs in EW_{wis} vs. C_{wis} (d 23), EW_{wis} vs. C_{wis} (d 63), EW_{sd} vs. C_{sd} (d 211), and EW_{sd}+Leu vs. EW_{sd} (d 211). *E*: Quantity statistics of DEGs in each group. *F*: Venn diagram of

the DEGs among EW_{WIS} vs. C_{WIS} (d 23), EW_{WIS} vs. C_{WIS} (d 63), and EW_{SD} vs. C_{SD} (d 211). The GO enrichment analysis was composed of three parts: biological process (BP), cellular component (CC), and GO molecular function (MF).