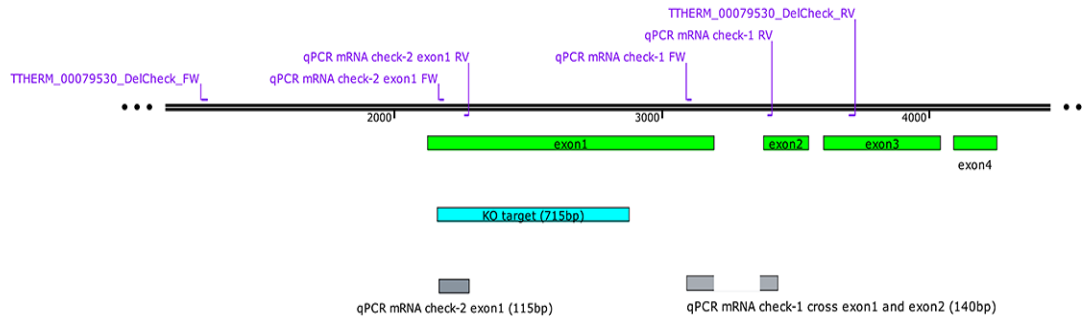


(I) Supplementary materials

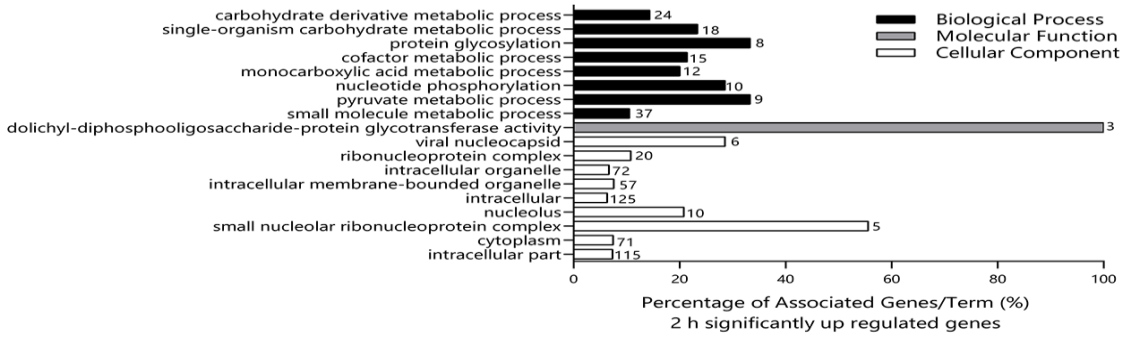
Supplementary tables (Table S1-S6) were in the format of MS Excel forms and uploaded separately.



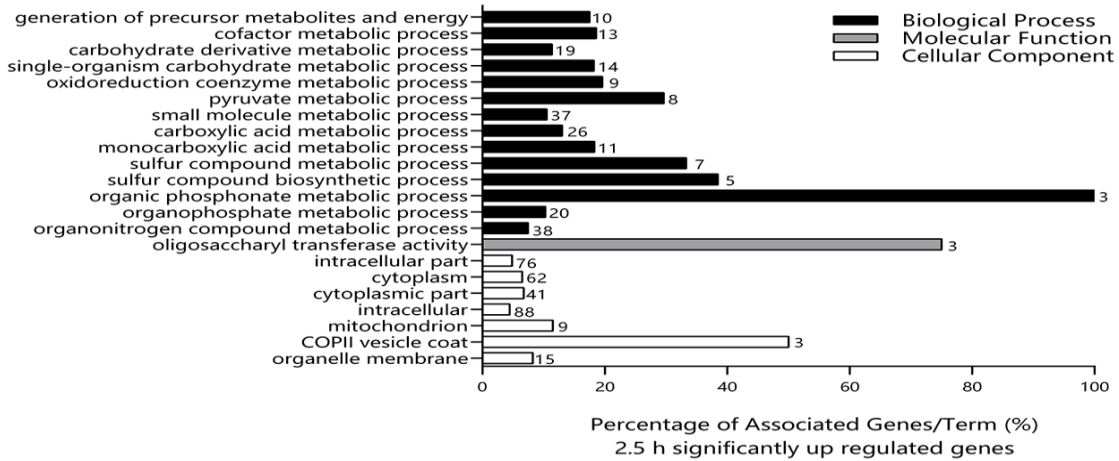
Supplementary Figure 1

Primer sets in UTR and CDS of THERM_00079530 (CYC2): KO target 715bp: Knock-out target sequence was 715bp long in exon1 in CDS of THERM_00079530. THERM_00079530_DelCheck_FW and THERM_00079530_DelCheck_RV were primers for whole cell extract PCR (**Figure 1B**). qPCR mRNA check-1 FW and qPCR mRNA check-1 RV were primers for RT-qPCR product across exon1 and exon2 of CYC2 CDS and qPCR mRNA check-2 exon1 FW and qPCR mRNA check-2 exon1 RV were primers for RT-qPCR product in exon1.

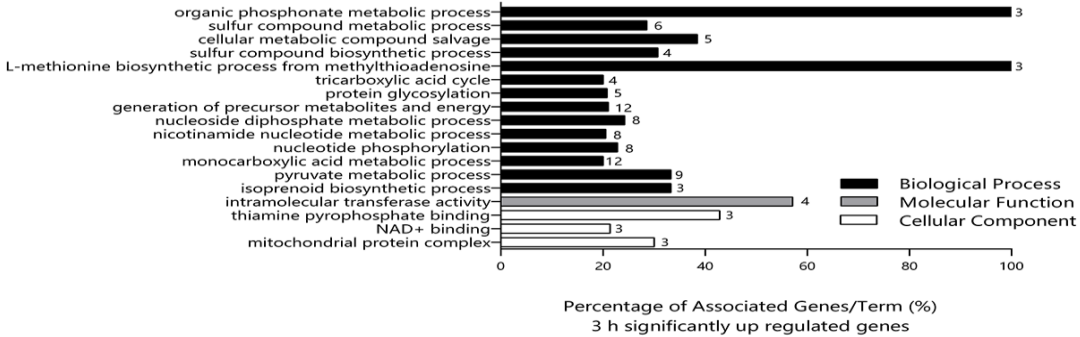
A



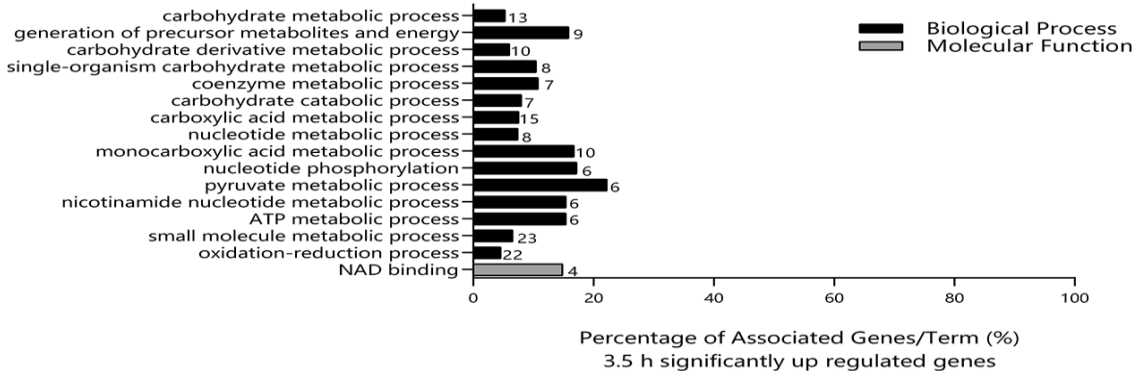
B



C

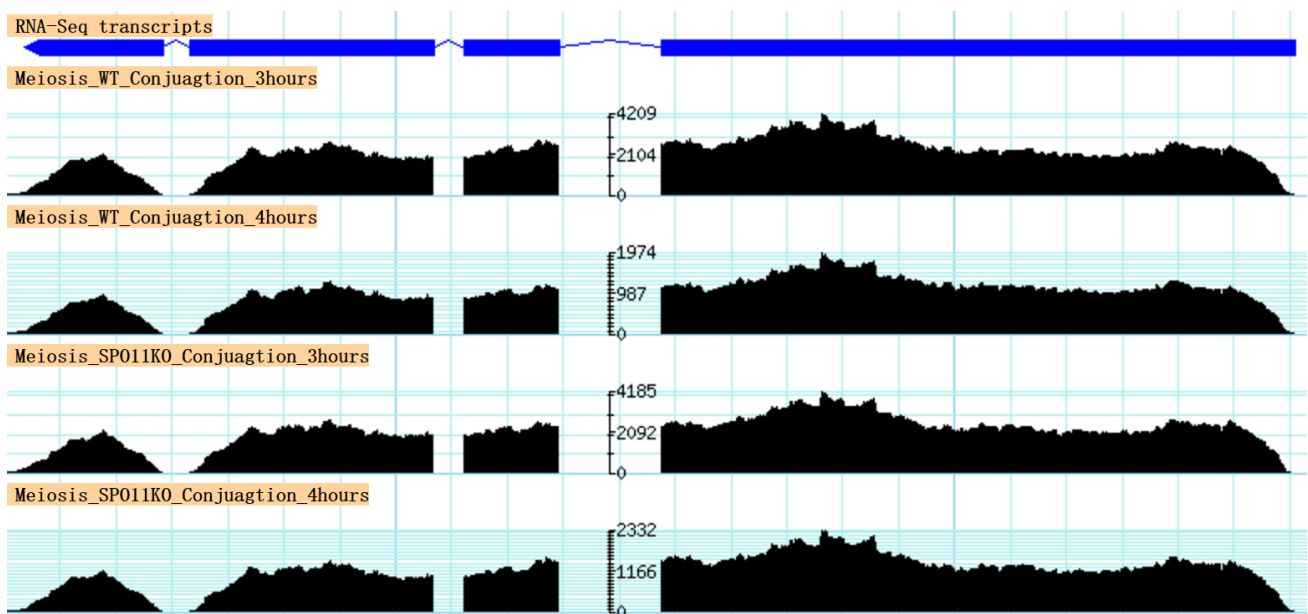


D



Supplementary Figure 2

Gene Ontology (GO) enrichment analysis of up regulated genes: The filtered significantly up regulated genes (Log2 (fold change) >2 and P value <0.05) of each time point were subjected to GO enrichment analysis separately in biological process, molecular biology and cellular function. (A) Percentage of associated genes/term (%) at 2 h. (B) Percentage of associated genes/term (%) at 2.5 h. (C) Percentage of associated genes/term (%) at 3 h. (D) Percentage of associated genes/term (%) at 3.5 h. The length of bars from the each histogram indicates the percentage of associated genes for each term. The number on top of each bar means the number of associated genes.



Supplementary Figure 3

RNA-Seq Data Tracks From TFGD (Tetrahymena Functional Genomics Database). The First track shows the CYC2 gene transcripts locus in genome browser. Other tracks show the transcription profile of CYC2 gene in WT 3 h, WT 4h, SPO11 KO 3 h, SPO11 KO 4 h.