

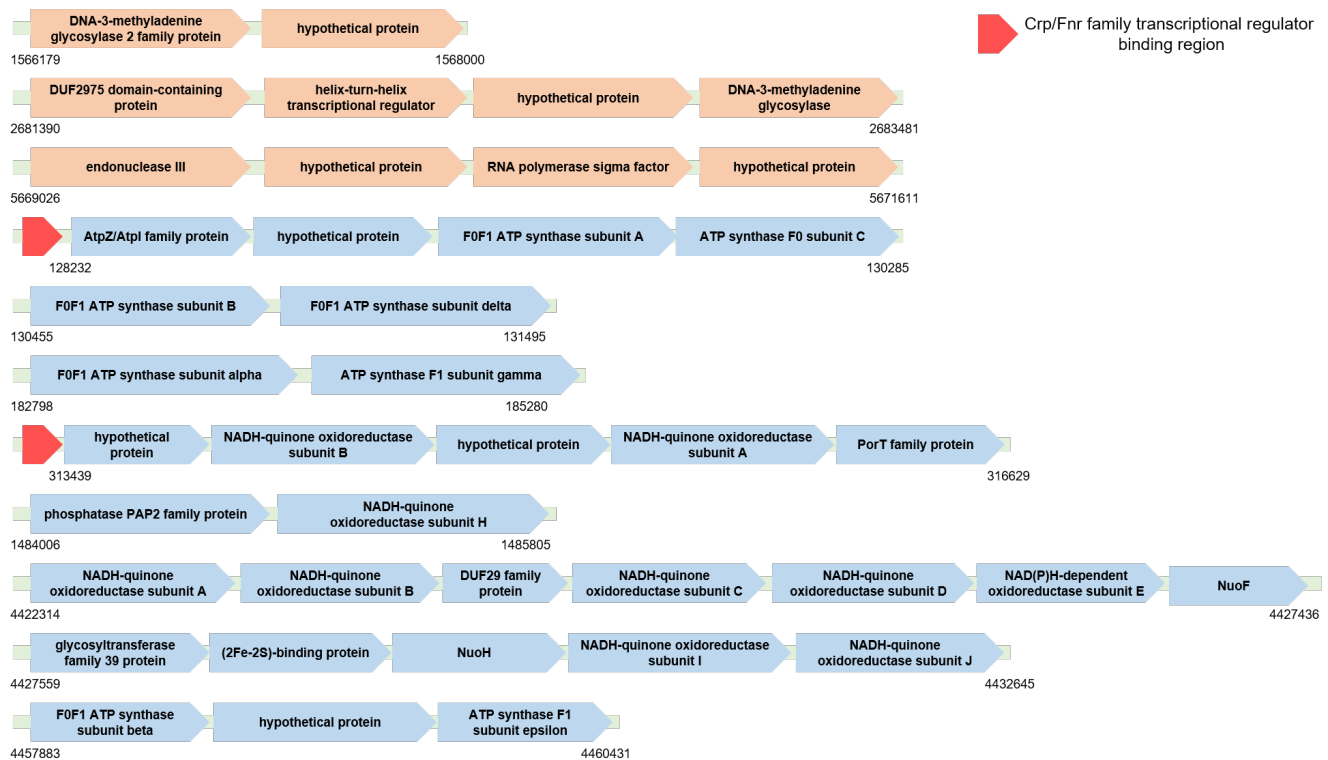


Figure S1. Visualization of operons involved in the early response and including DNA repair and oxidative phosphorylation-related genes. Top three operons contains Base excision repair-related genes. The other eight operons contains Oxidative phosphorylation-related genes. The numbers below each operon indicate the start and end positions of the operon. Red colored marker indicates the binding region of Crp/Fnr family transcriptional regulator.

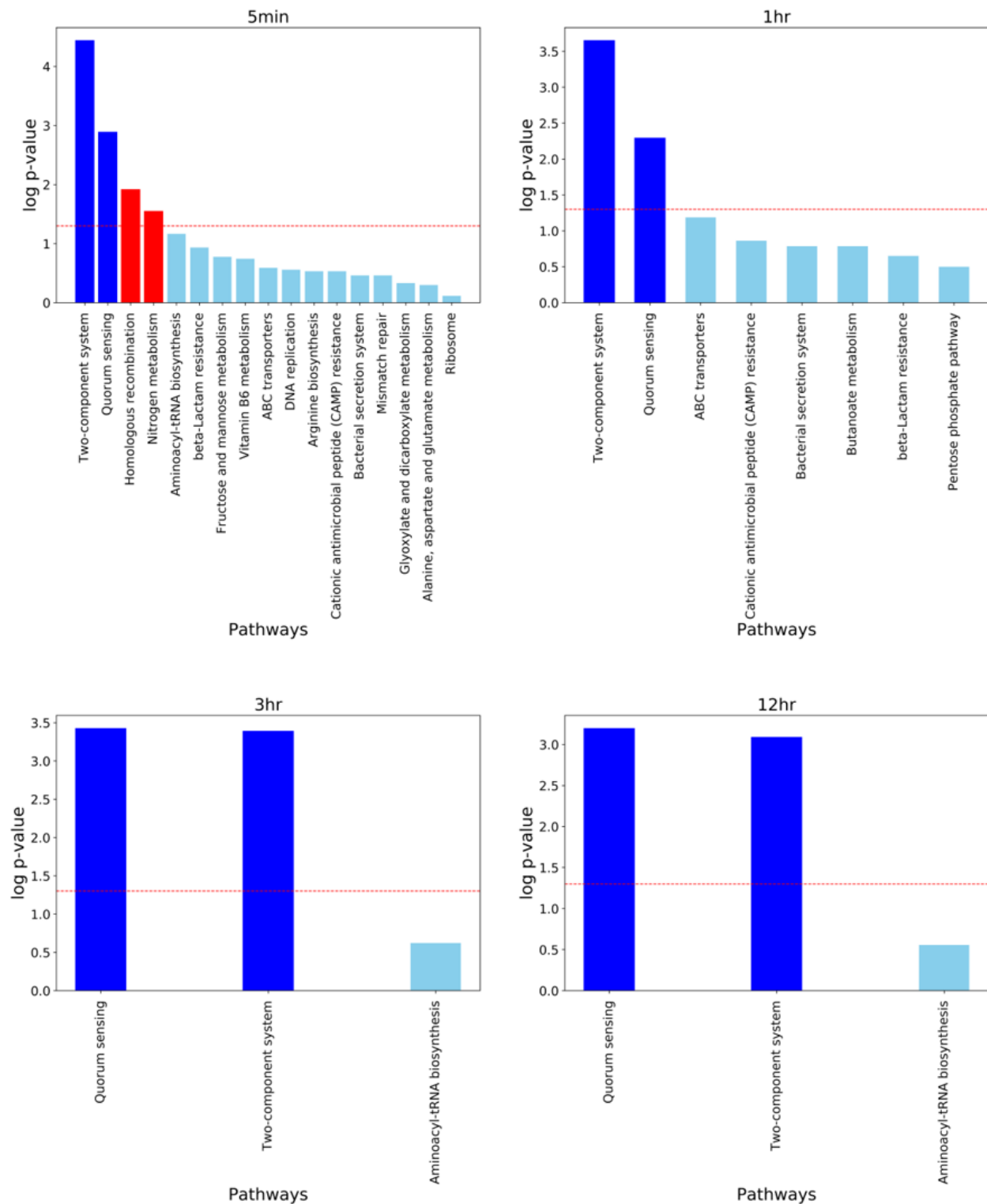


Figure S2. Visualization of pathway enrichment analysis with time-varying transcriptional network modules. Pathway enrichment analysis of genes in early response (5min) module. Red colored bar represents up-regulated terms, blue colored bar represents down-regulated terms, and statistically insignificant terms are colored in light blue.