

Supplementary Materials: Functional Response of Microbial Communities in Oil-Contaminated Marine Sediment

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Table S1. Full list processes detected from the intersection of DEGs and the 112 days of oil contamination turquoise module, as well as the IDs for each gene involved in it.

<https://github.com/sbcblab/microbialfunctions>

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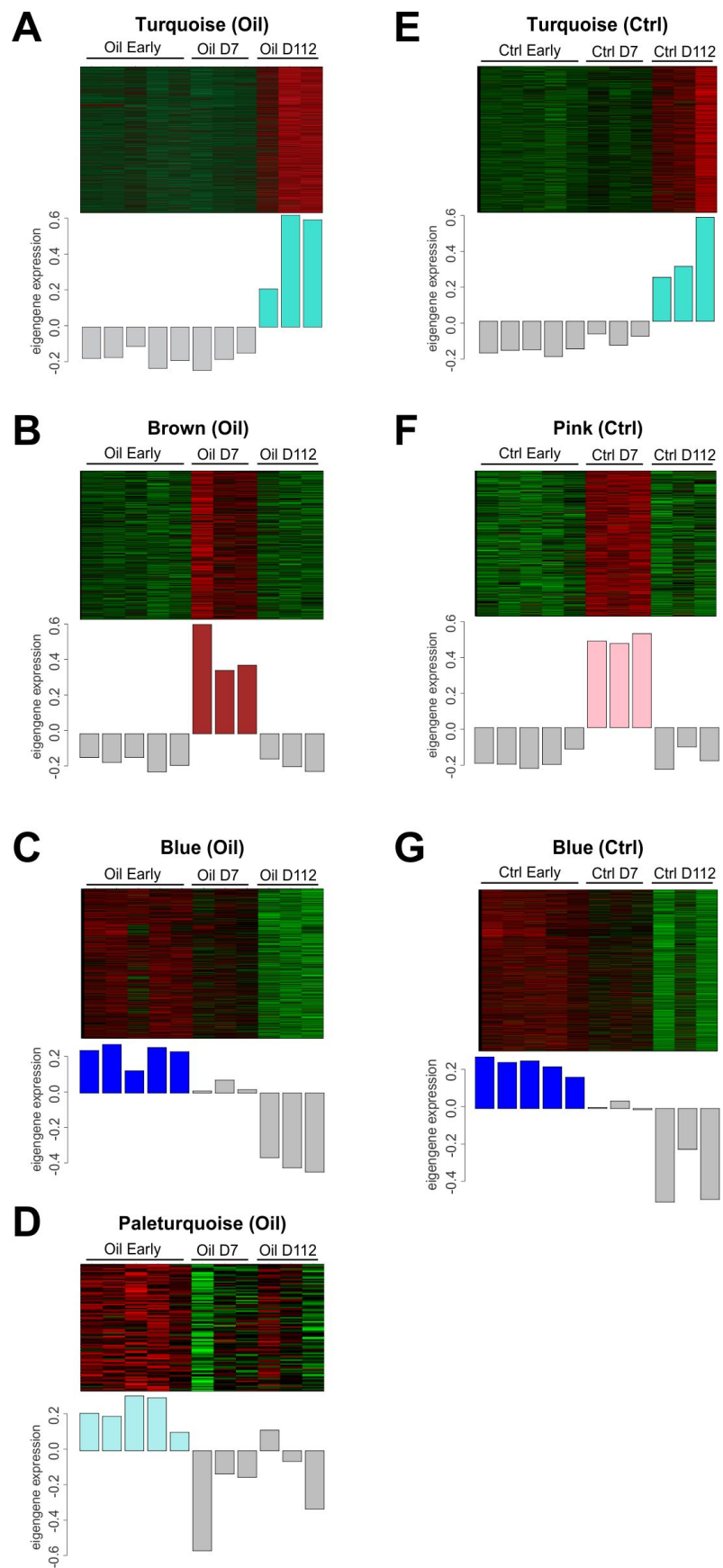


Figure S1. Heatmap (upper panel) corresponding to gene expression and barplot (lower panel) representing eigengene expression of each sample. (A-D) Oil condition. (E-G) Control condition.

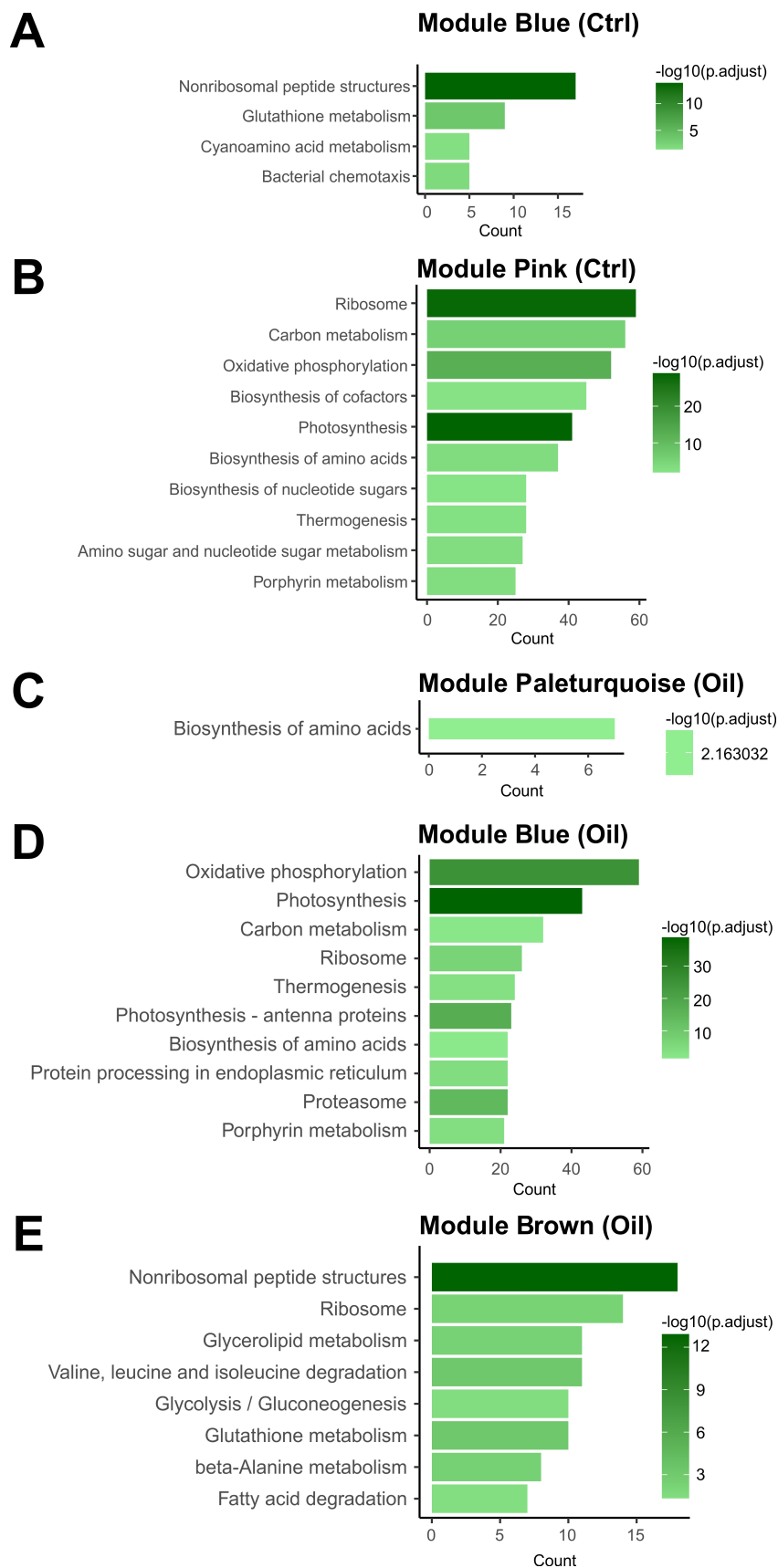


Figure S2. Top 10 enriched biological process of the significant co-expression modules correlated with each time across the experiment. (A-B) Control condition. (C-E) Oil condition.

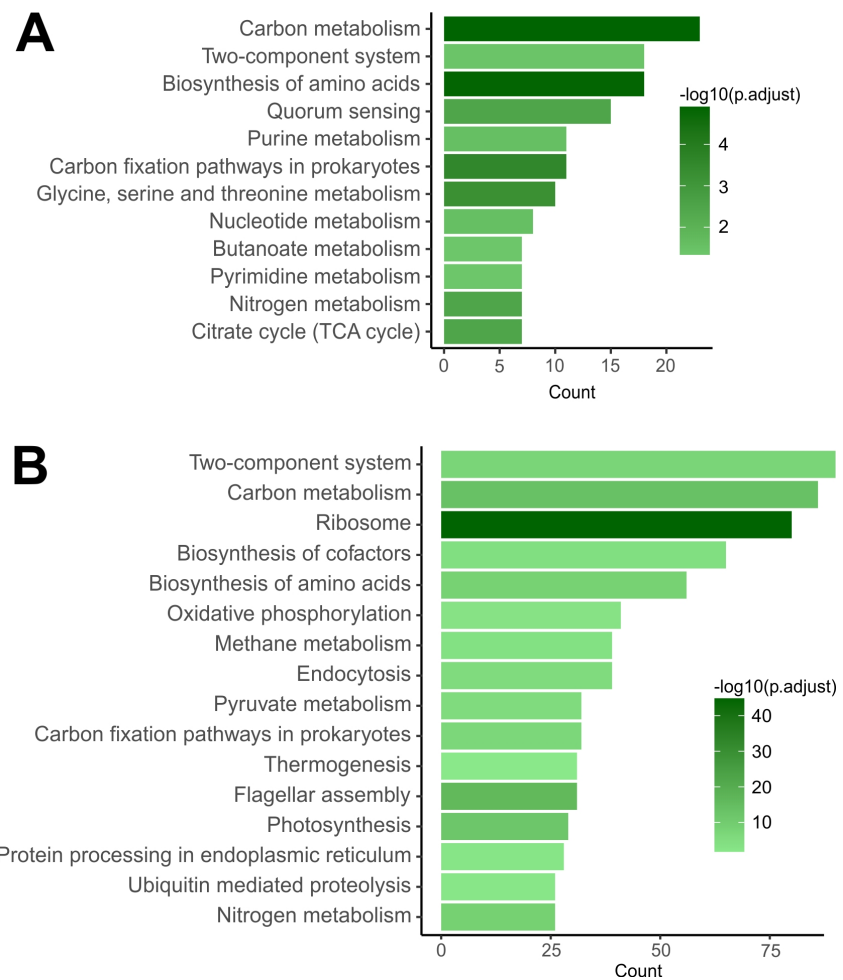


Figure S3. (A) Enrichment analysis from genes exclusively present in the turquoise module after intersection with DEG. (B) Enrichment analysis from DEGs not found in turquoise module from Oil network.

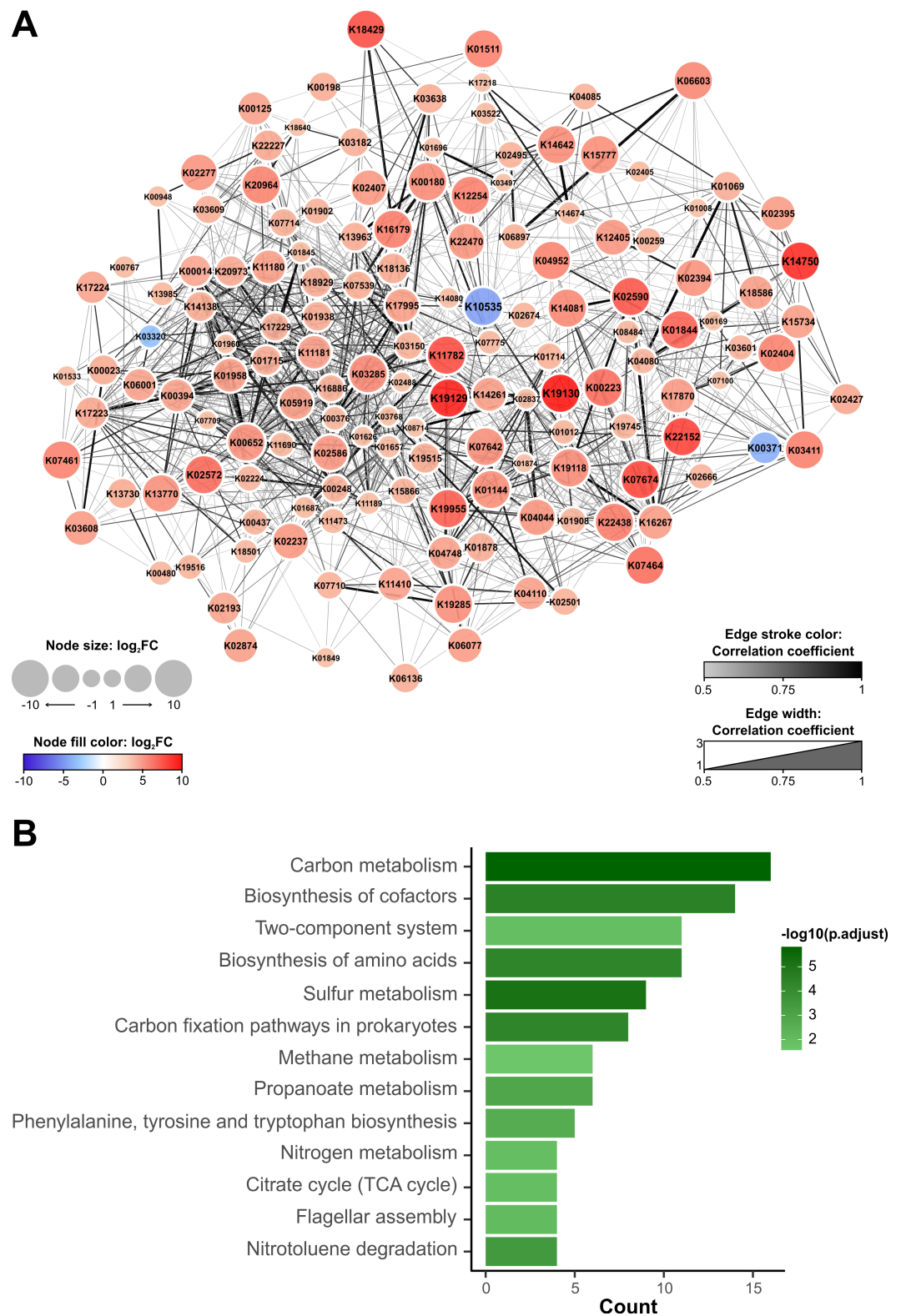


Figure S4. Gene interaction network for the 112 days of oil contamination, and its enriched functions. (A) Interaction network filtered to have only the DEGs, genes from the turquoise module of the 112 days treatment and only the nodes with above average centrality value. (B) Functional enrichment of the genes present in the filtered network.