

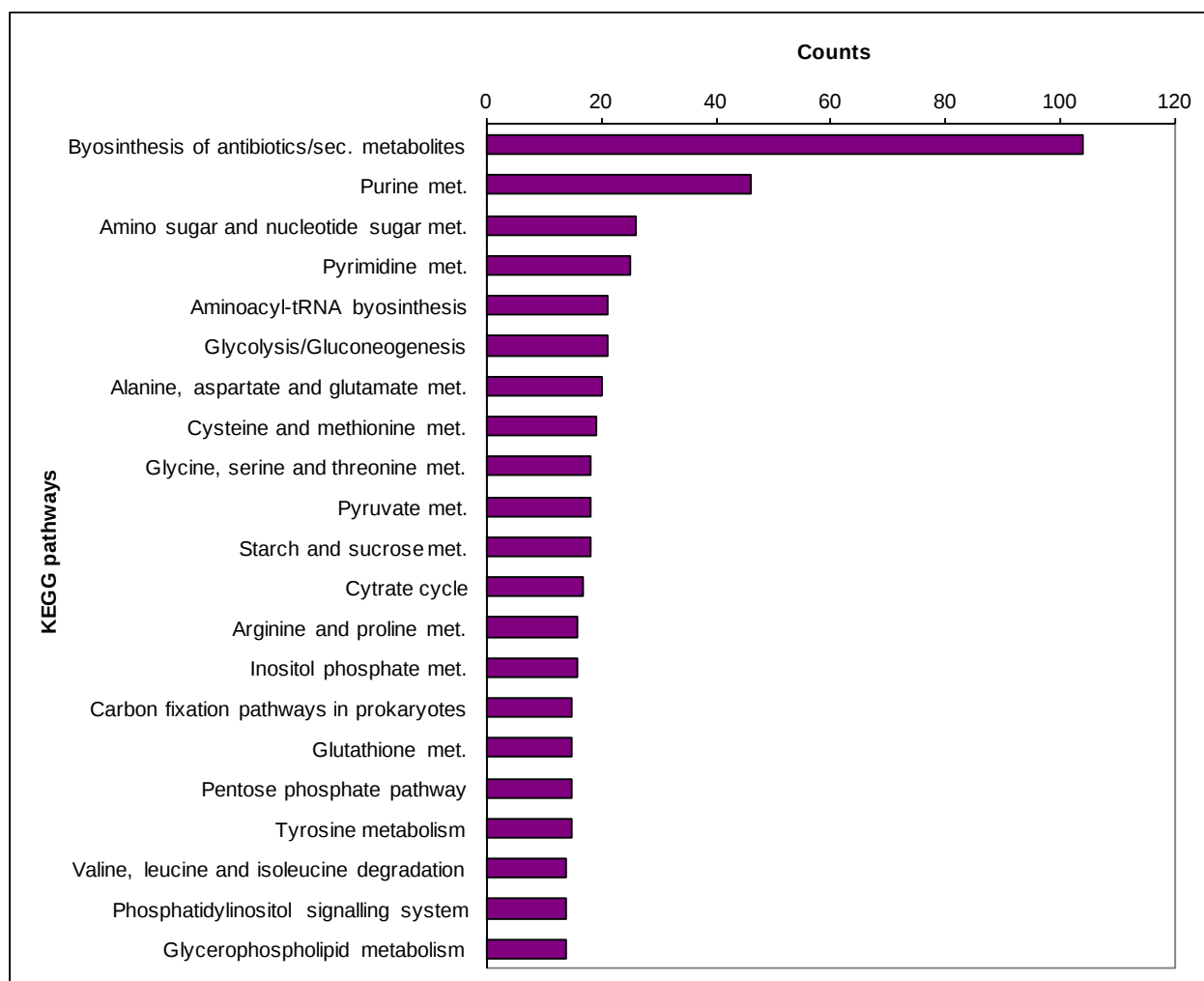


Figure S1. Most represented KEGG pathways in *T. notatus* transcriptome. Transcriptome annotation was performed with Blast2GO. Met. indicates metabolism.

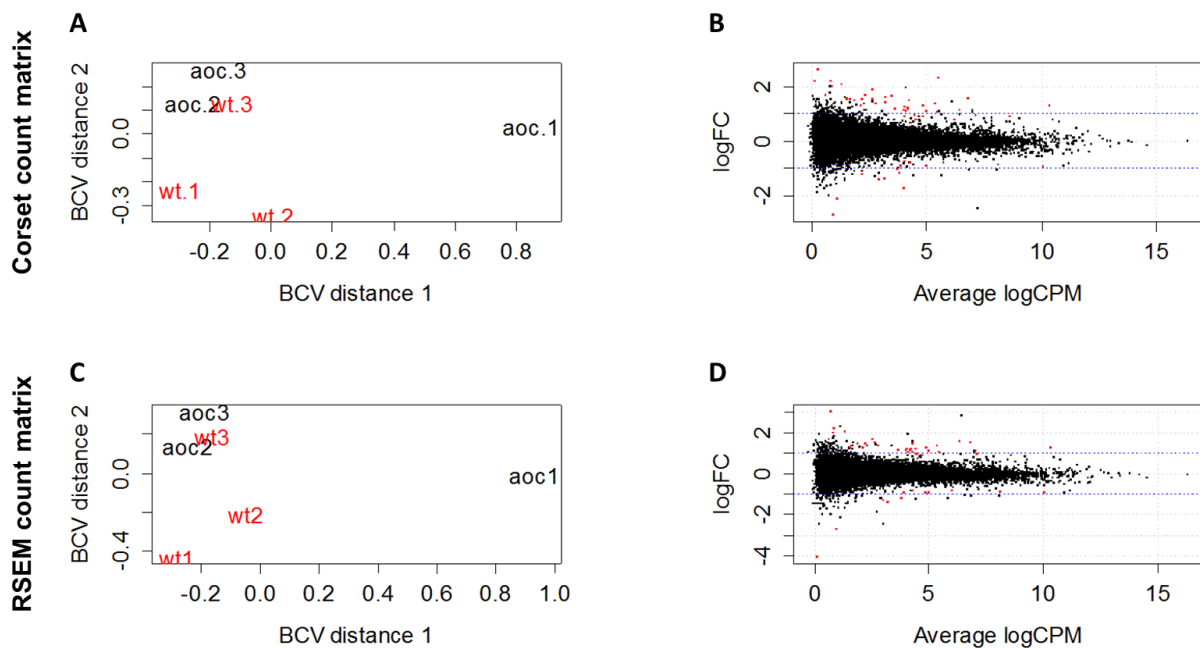


Figure S2. Outcomes of differential expression analysis run in EdgeR using count matrix estimated with Corset or RSEM. A) and C) multidimensional scaling (MDS) plots showing sample relations among replicates and treatments. B) and D) Smearplots showing differentially expressed (DE) genes identified with EdgeR. Red spots highlight DE contigs at FDR < 0.05. Dotted blue lines indicate log fold-change (FC) 1. CPM stands for counts per million.

