Supplementary Materials

Effects of Mitochondrial Transplantation on Transcriptomics in a Polymicrobial Sepsis Model

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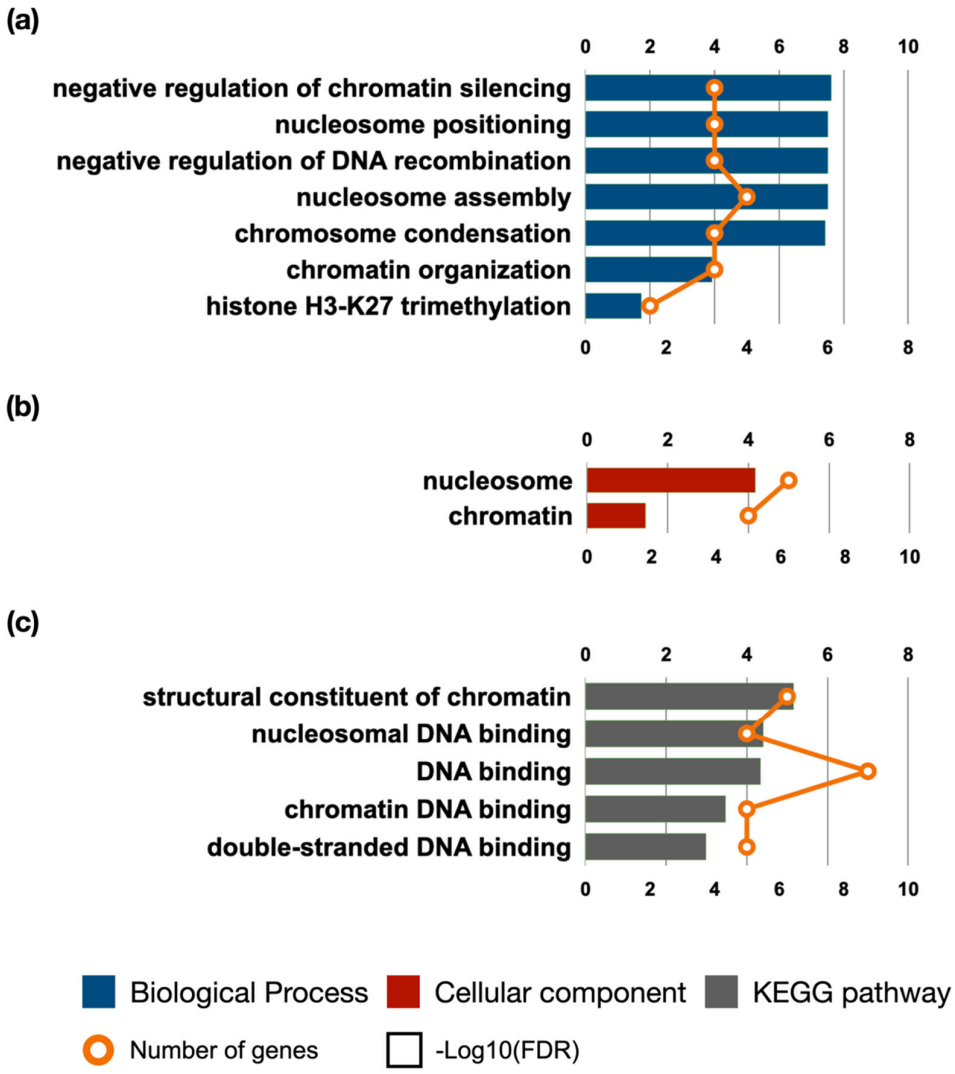

Figure S1. The significantly enriched Gene ontology (GO) biological process (**a**) and cellular component (**b**) categories and KEGG (**c**) pathways of 160 DEGs that were significantly upregulated in SEPSIS versus SEPSIS + MT.

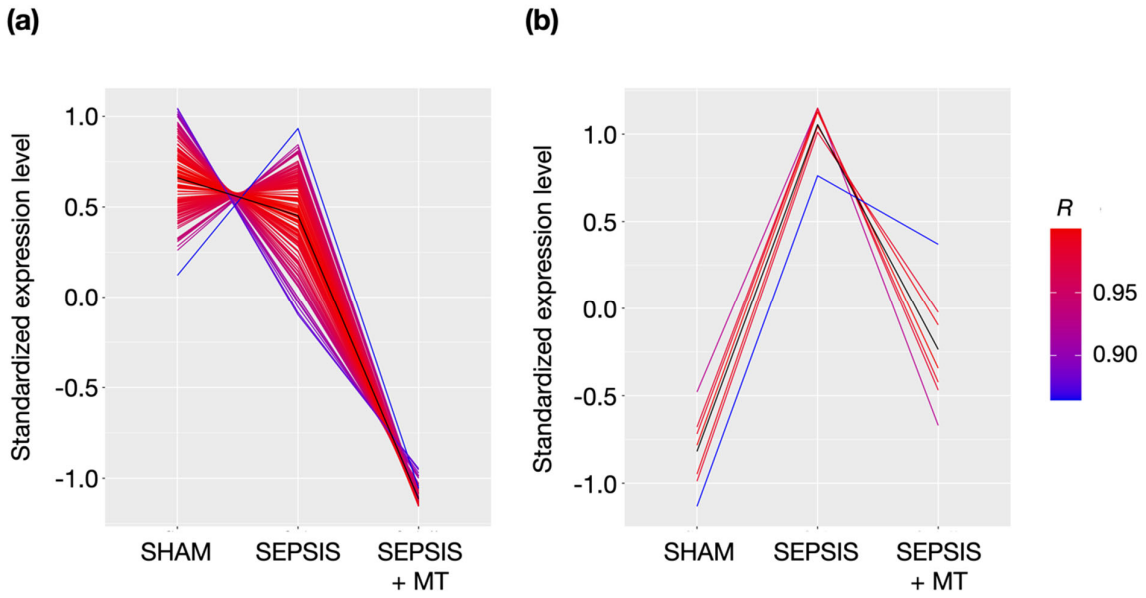

Figure S2. Trajectories of 160 DEGs expression change in three different groups. 153 genes were represented in cluster 1 (**a**) and the others (seven genes) were identified in cluster 2 (**b**). Black and other colored lines represent the centroid of clustered gene expression levels and each their own one, respectively. The gradient scale shows the value of Pearson's correlation coefficients (*R*).

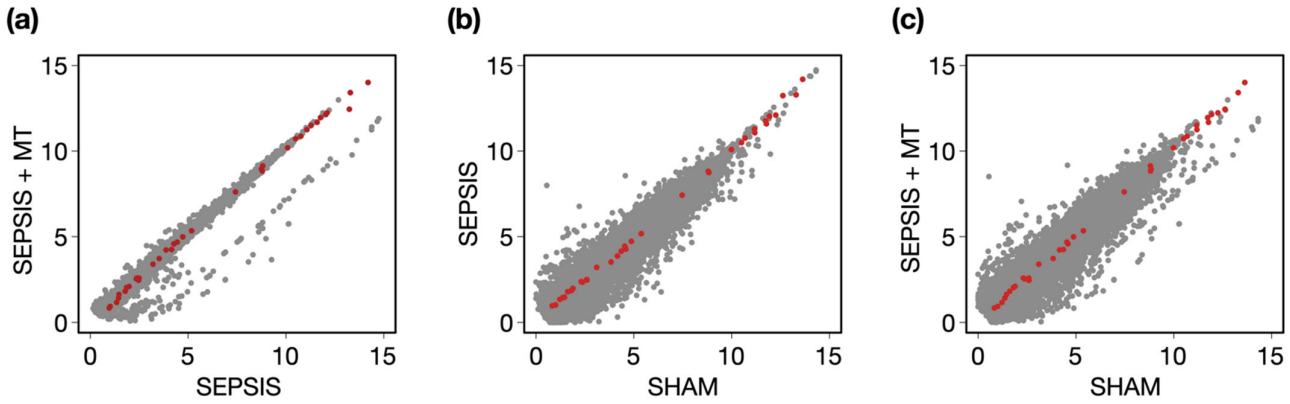

Figure S3. Scatter plots of RNA-seq data between SEPSIS and SEPSIS + MT (**a**), between SEPSIS and SHAM (**b**), and between SEPSIS + MT and SHAM (**c**). Red dot indicates the gene of mitochondrial genome.