

Supplementary information

White-nose syndrome is associated with increased replication of a naturally persisting coronaviruses in bats

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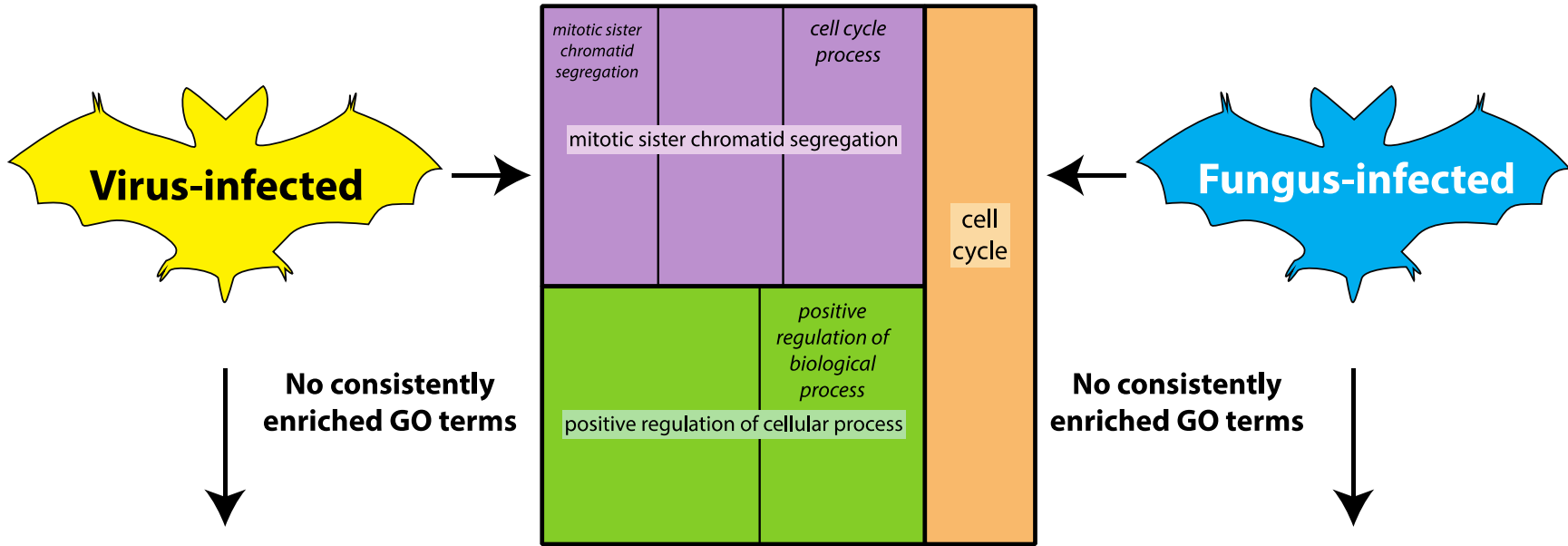
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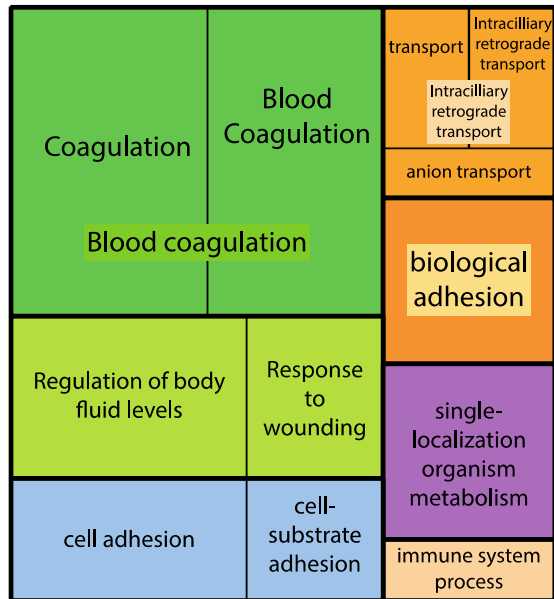
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Supplementary figure 1

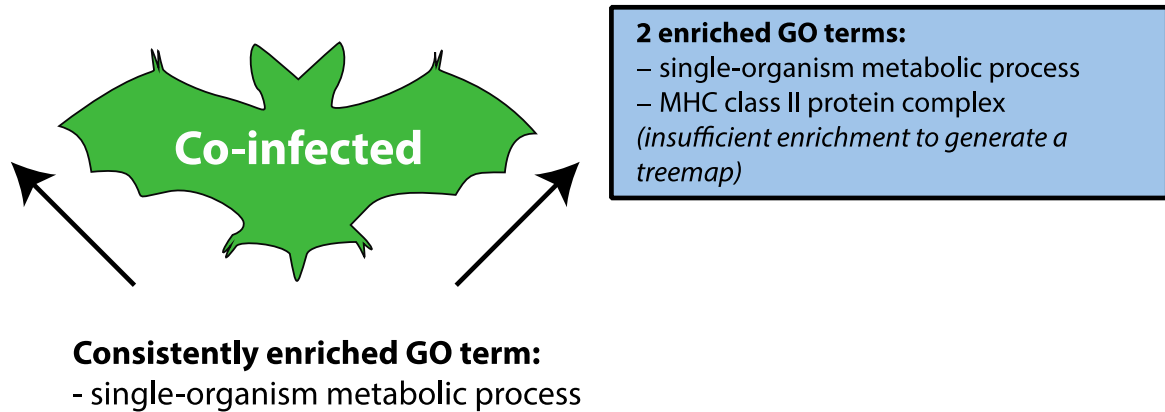
Virus-infected vs fungus-infected (461/9)



Virus-infected vs Co-infected (473/43)



Fungus-infected vs Co-infected (25/2)



List of supplementary tables in the Dataset file:

Table S1. Read statistics of RNA-Seq samples.

Table S2. Differentially expressed genes determined by DESeq2 for the Negative (mock-infected) vs. MylCoV comparison.

Table S3. Differentially expressed genes determined by DESeq2 for the Negative (mock-infected) vs. *P. destructans* comparison.

Table S4. Differentially expressed genes determined by DESeq2 for the Negative (mock-infected) vs. Coinfected comparison.

Table S5. Differentially expressed genes determined by DESeq2 for the MylCoV vs. *P. destructans* comparison.

Table S6. Differentially expressed genes determined by DESeq2 for the Coinfected vs. MylCoV comparison.

Table S7. Differentially expressed genes determined by DESeq2 for the Coinfected vs. *P. destructans* comparison.

Table S8. Gene Ontology Enrichment Analysis (g:GOST) summary using DESeq2 determined differentially expressed genes (>2 fold change, FDR<0.05).

Table S9. Details of primers used for PCR