

Supplementary Figures

Figure S1. PCA plots of all samples (A), and without the outlier sample (B).

Figure S2. Heatmap of the distribution of all samples (A), and without the outlier simple (B).

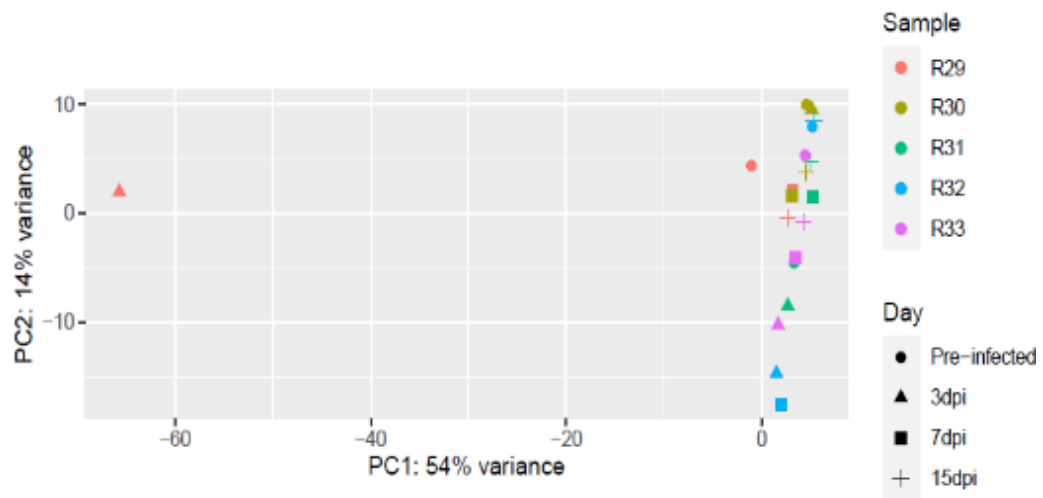
Figure S3. Volcano graphs of the statistically significant Differentially Expressed Genes (SDEGs), indicated by red dots, between symptomatic and asymptomatic animals ($\text{padj} < 0,05$) five days pre-infection, three, seven and fifteen days post-infection (A), and among symptomatic cattle ($\text{padj} < 0.05$) over time (B).

Figure S4. Venn diagram of the shared numbers of the Significant Differentially Expressed Genes (SDEGs) between symptomatic vs. asymptomatic animals five days pre-infection, three, seven and fifteen days post-infection (A), and among symptomatic cattle overtime (B).

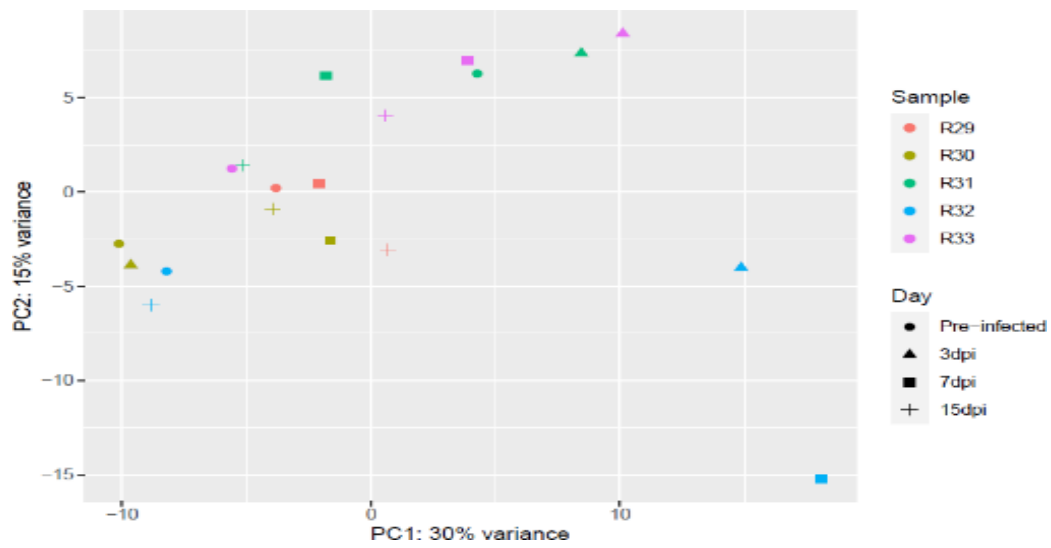
Figure S5. Gene Ontology (GO) enrichment test ($\text{padj} < 0,05$) for the symptomatic vs. asymptomatic contrasts (A) and symptomatic cattle over time (B).

Figure S6. KEGG pathway enrichment test ($\text{padj} < 0.05$) for the symptomatic vs. asymptomatic contrasts (A) and symptomatic cattle over time (B).

Figure S7. The KEGG view on the cytokine-cytokine receptor interaction pathway (bta04060) enriched on 7 days post-infection among symptomatic cattle ($\text{padj} < 0.05$).

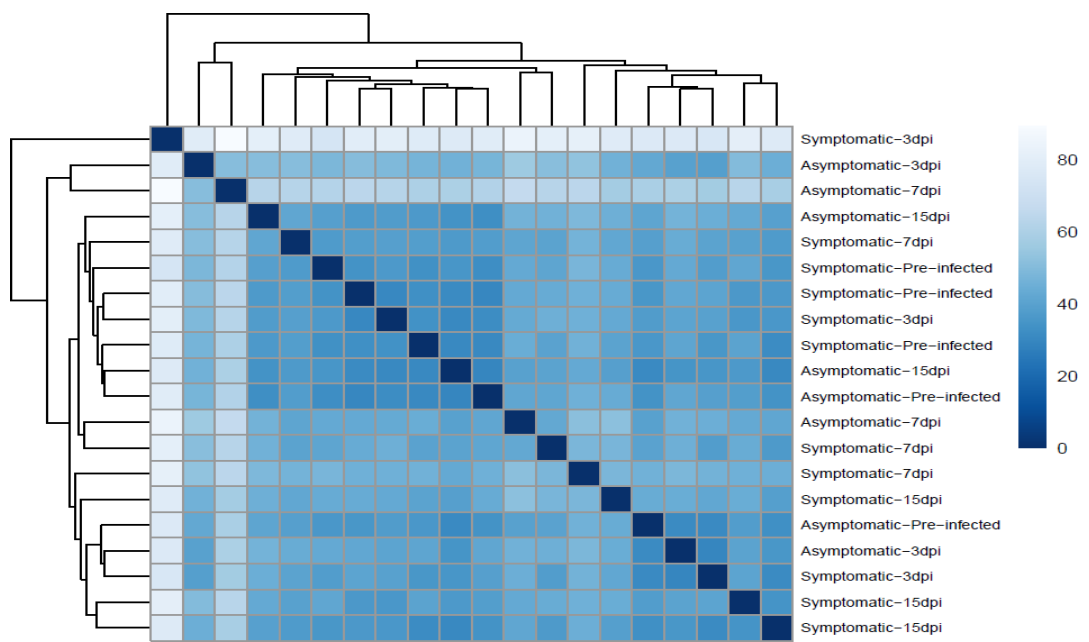


A

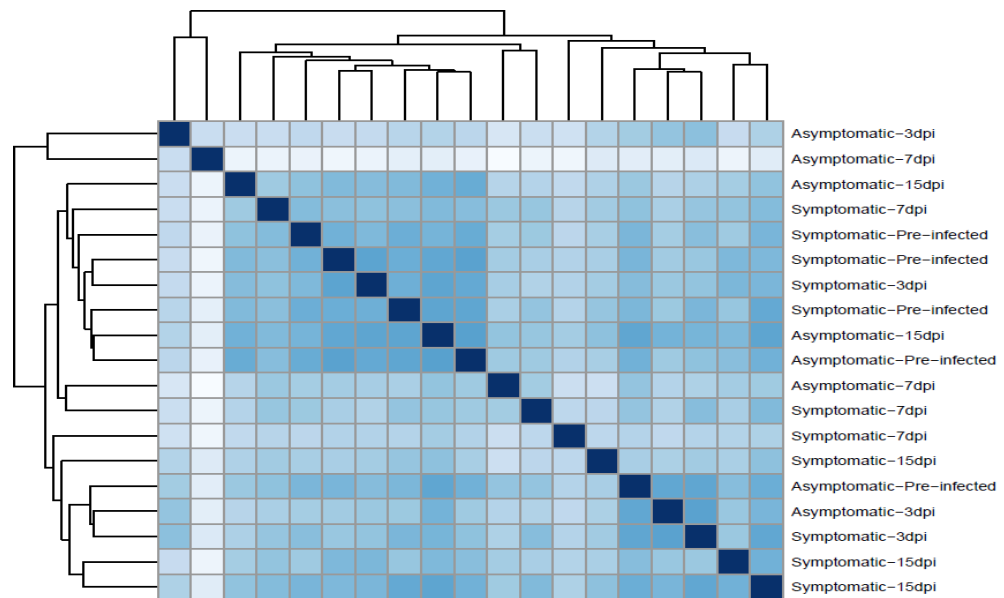


B

Figure S1. PCA plot of all samples (A), and without the outlier sample (B).



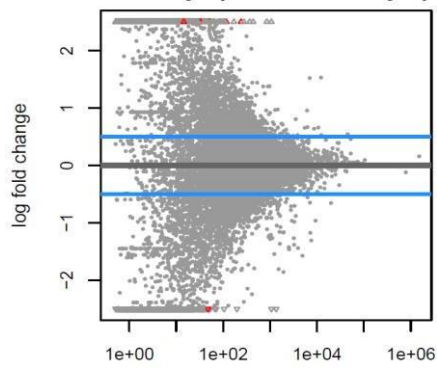
A



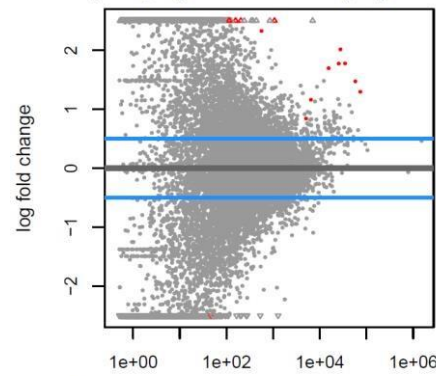
B

Figure S2. Heatmap of the distribution of all samples (A), and without the outlier simple (B).

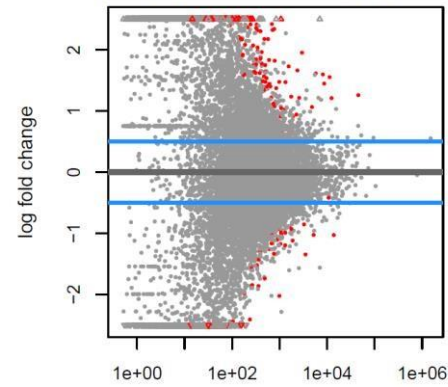
Pre-infected: Symptomatic vs Asymptomatic



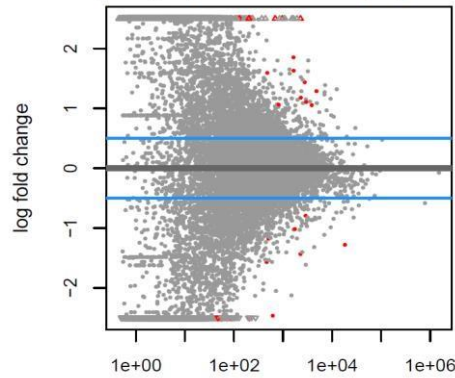
3dpi: Symptomatic vs Asymptomatic



7dpi: Symptomatic vs Asymptomatic

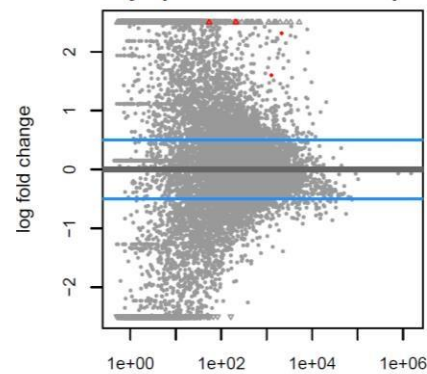


15dpi: Symptomatic vs Asymptomatic

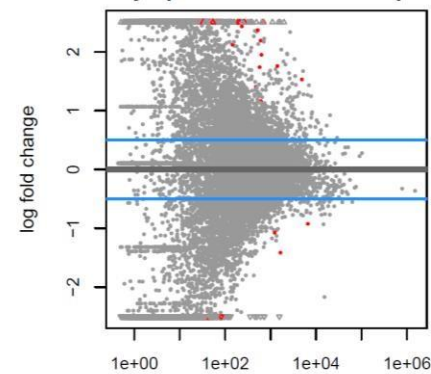


A

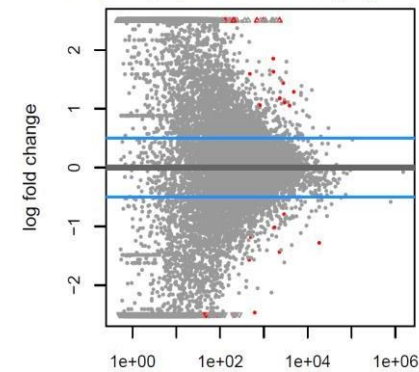
Symptomatic: DE after 3dpi



Symptomatic: DE after 7dpi

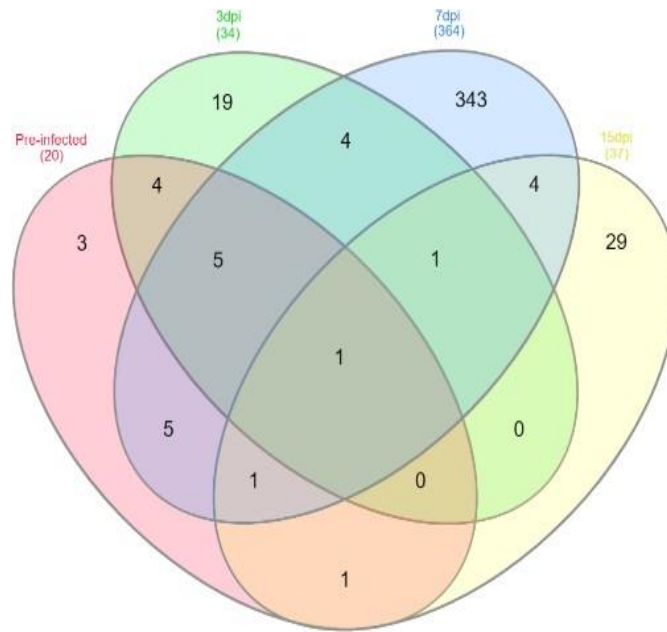


15dpi: Symptomatic vs Asymptomatic

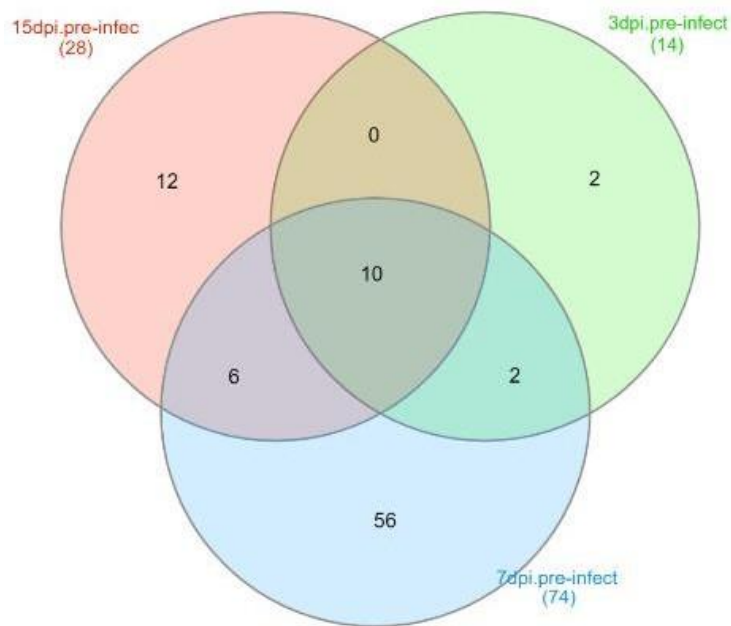


B

Figure S3. Volcano graphs of the statistically Significant Differentially Expressed Genes (SDEGs), indicated by Red dots, between symptomatic and asymptomatic animals ($\text{padj} < 0.05$) five days pre-infection, three, seven and fifteen days post-infection (A), and among symptomatic cattle ($\text{padj} < 0.05$) overtime (B).

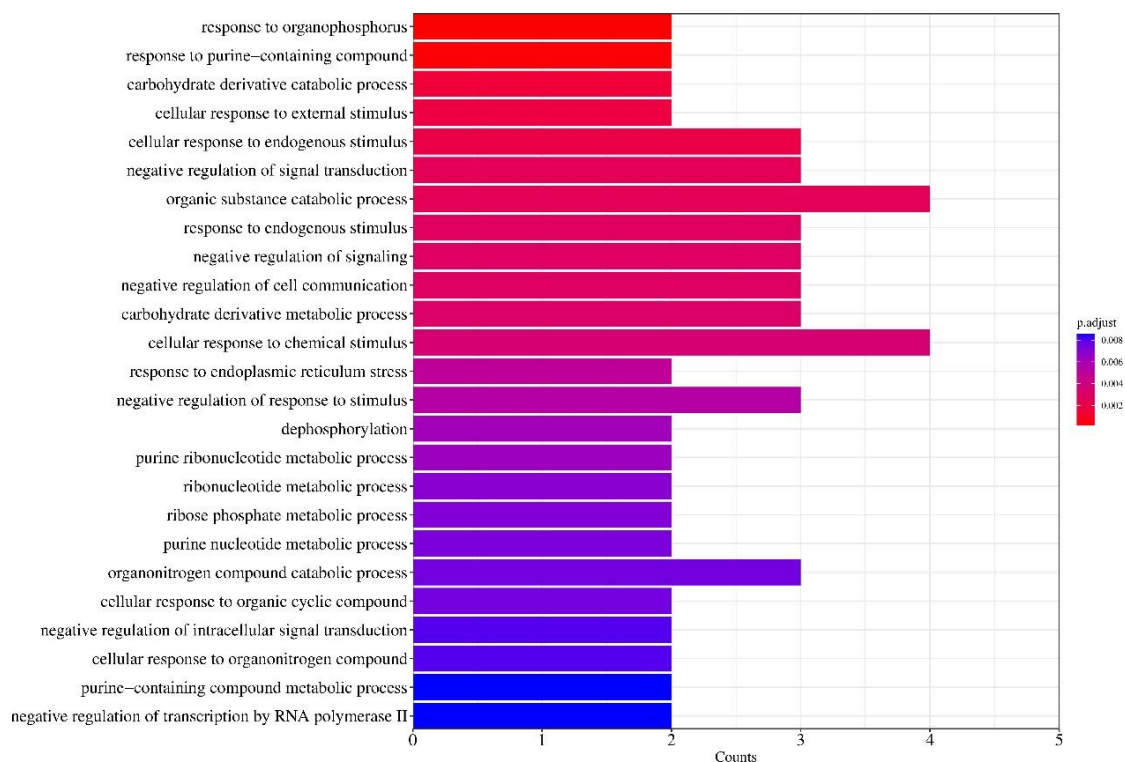


A

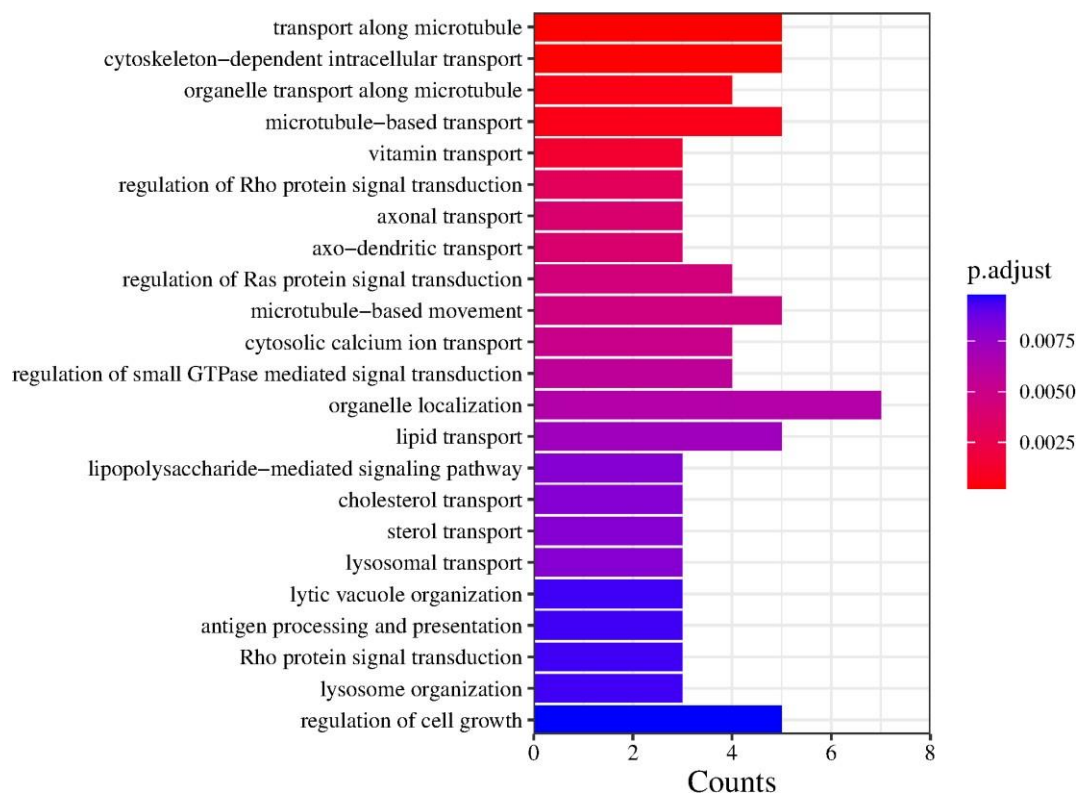


B

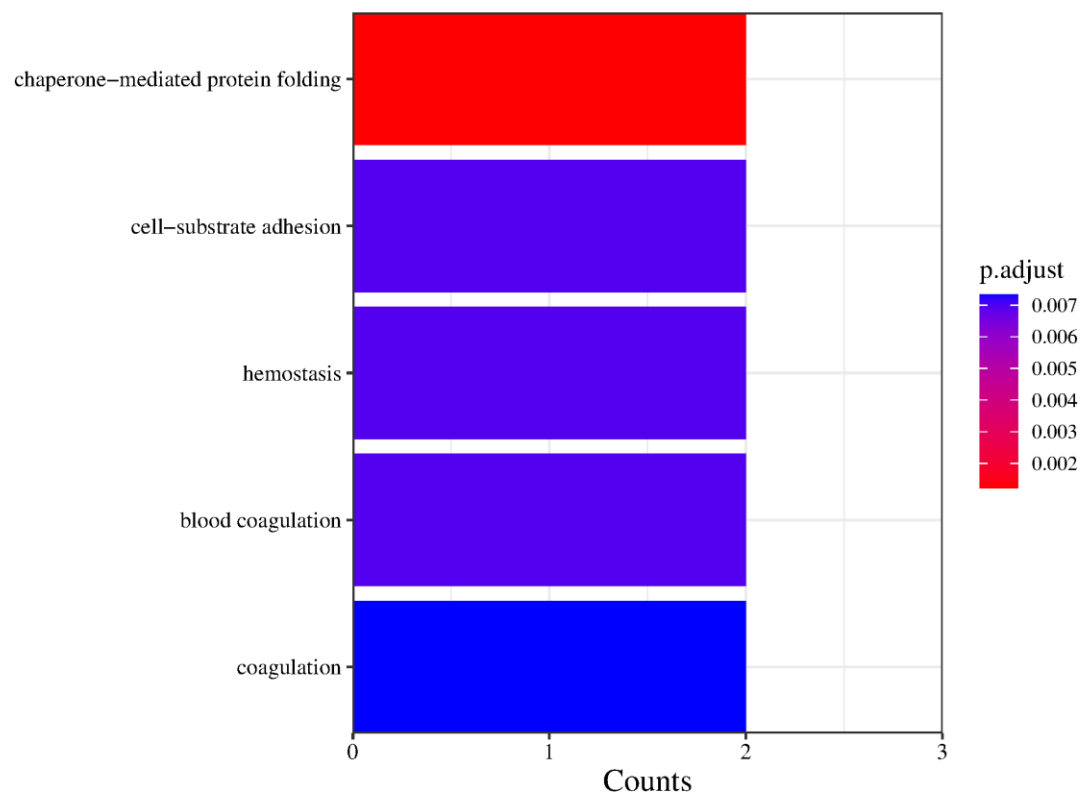
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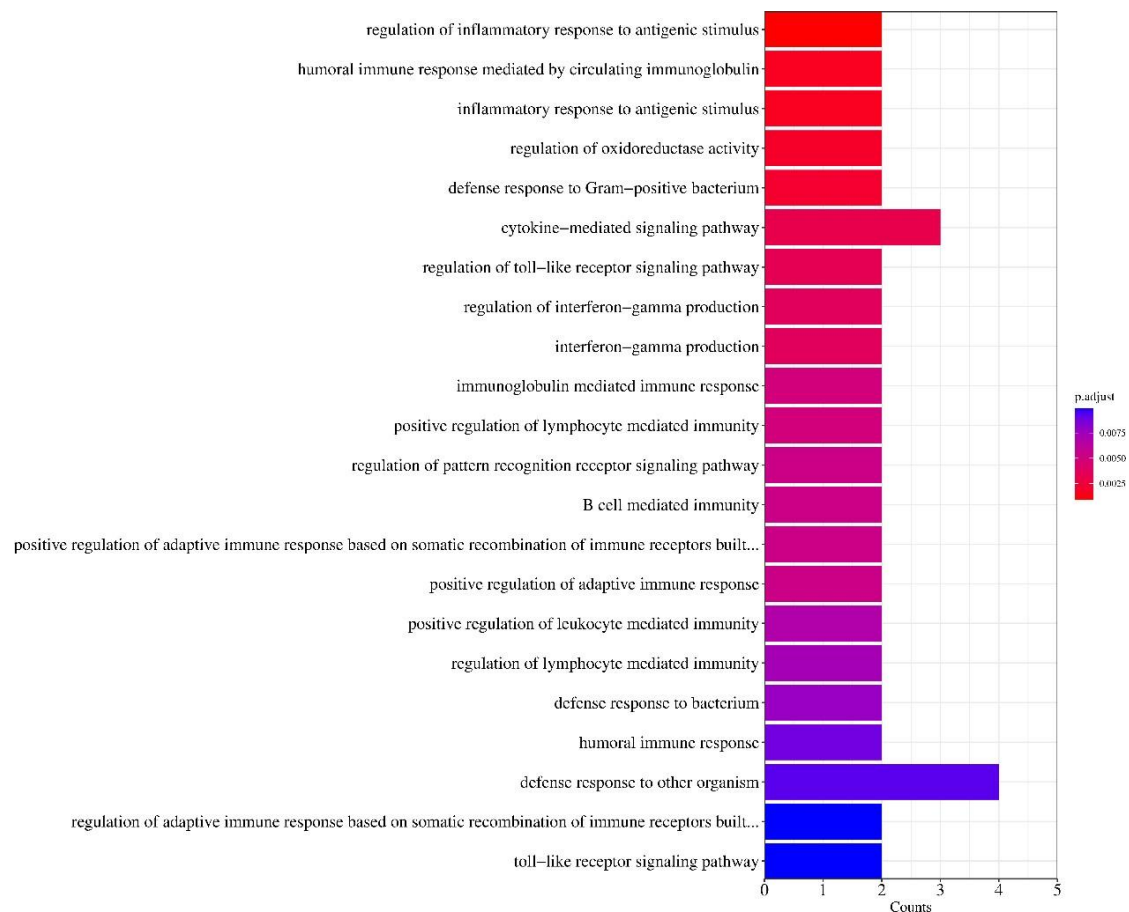
A1



A2

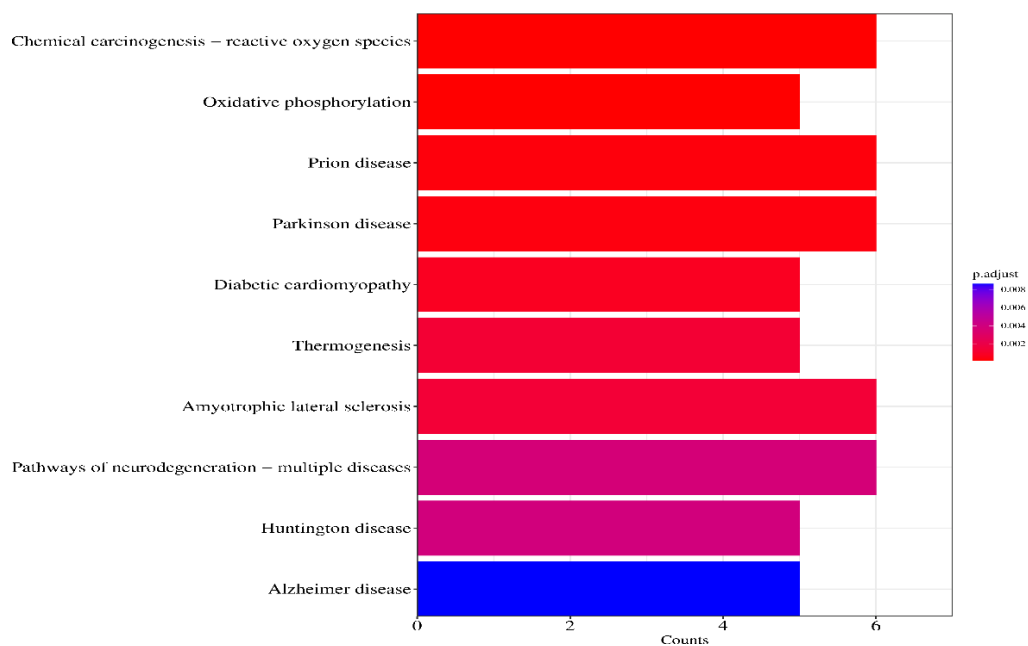


A3

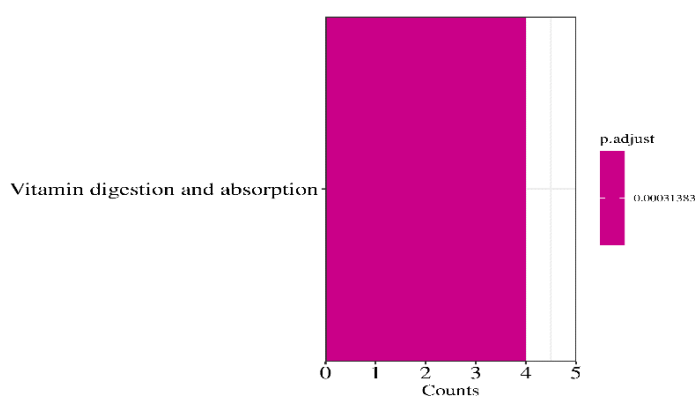


B

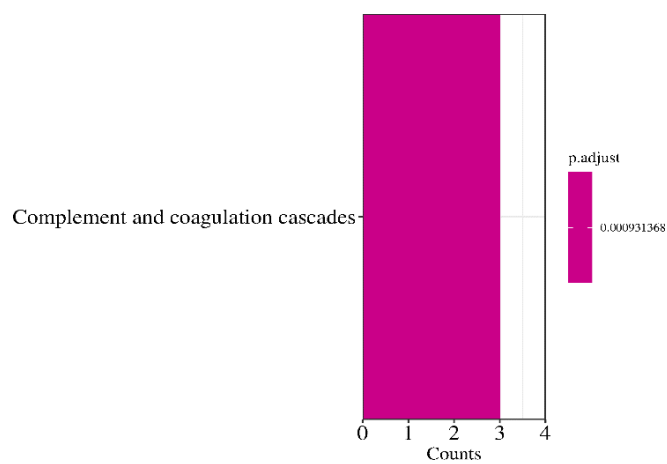
Figure S5. Gene Ontology (GO) enrichment test ($\text{padj} < 0.05$) for the symptomatic vs. asymptomatic contrasts on three, seven, and fifteen days post-infection (A1-A3, respectively) and among symptomatic cattle seven days post-infection vs. pre-infection (B). There was no significantly enriched GO in the symptomatic vs. asymptomatic contrast on pre-infection and among the symptomatic cattle in the post-infection vs. pre-infection contrast on three and fifteen days post-infection.



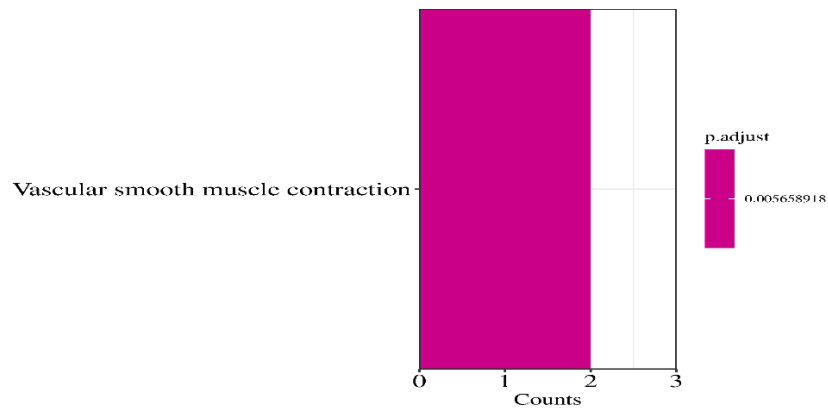
A1



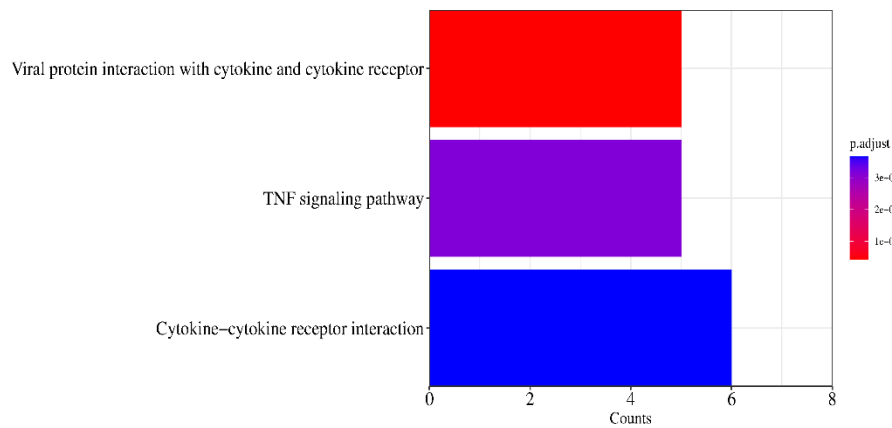
A2



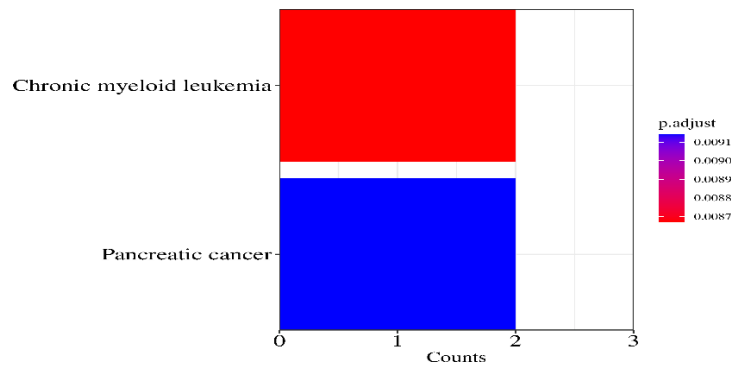
A3



B1



B2



B3

Figure S6. KEGG pathway enrichment test ($p_{adj} < 0.05$) for the symptomatic vs. asymptomatic contrasts (A1 to A3) and among symptomatic cattle over time vs. pre-infection on three, seven and fifteen days post-infection (B1 to B3), respectively. There was no significantly enriched KEGG pathway in the symptomatic vs. asymptomatic contrast on pre-infection.

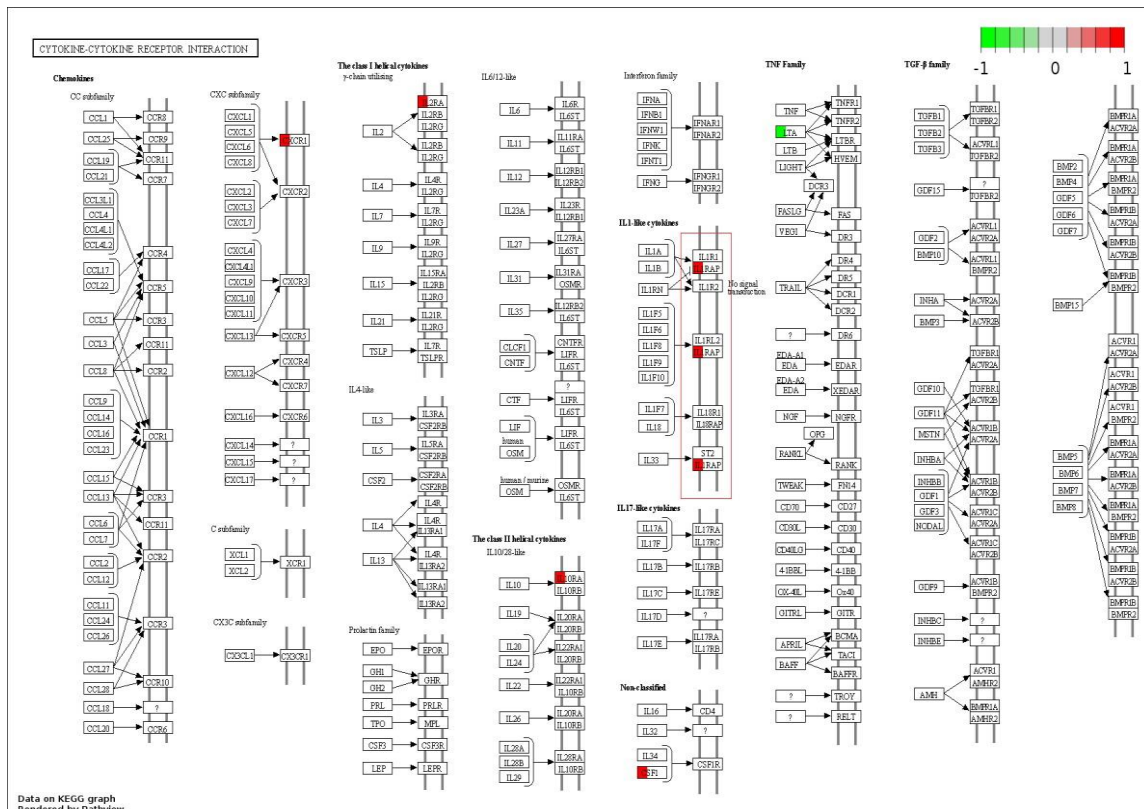


Figure S7. The KEGG view on the cytokine-cytokine receptor interaction pathway (bta04060) enriched seven days post-infection among symptomatic cattle ($p_{adj} < 0.05$). The *IL1RAP* gene has been highlighted in the red box. The up and down-regulated genes have been shown with red and green colors, respectively. The color intensity is proportional to the regulatory activity. Rendered by Pathview Web (Luo & Brouwer 2013; Luo et al. 2017).

1. Luo W. & Brouwer C. (2013) Pathview: an R/Bioconductor package for pathway-based data integration and visualization. *Bioinformatics* 29, 1830-1.
2. Luo W., Pant G., Bhavnasi Y.K., Blanchard S.G., Jr. & Brouwer C. (2017) Pathview Web: user friendly pathway visualization and data integration. *Nucleic Acids Res* 45, W501-w8.