

Supplementary Figures

Marek's Disease Virus Infection Induces Widespread Differential Chromatin Marks in inbred chicken lines

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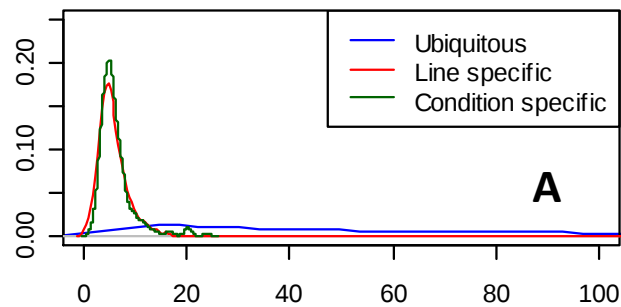
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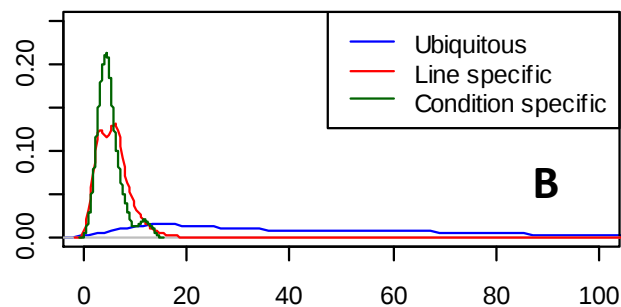
Figure S1: Peak length distributions in different classes of SERs. Probability densities of peak lengths for ubiquitous, line-specific and condition specific SERs. Line-specific and condition-specific SERs predominantly correspond to low enrichment regions for both H3K4me3 (a-d) and H3K27me3 (e-h). 63_inf: line 6₃ infected, 63_non: line 6₃ control, 72_inf: line 7₂ infected, 72_non: line 7₂ control.

H3K4me3

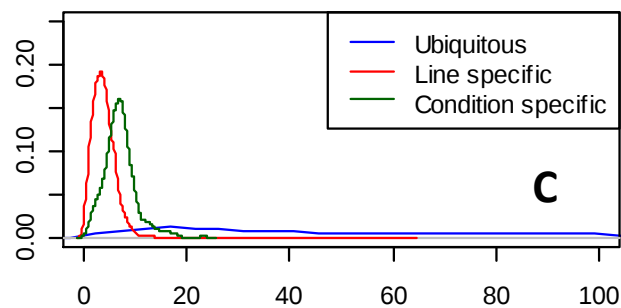
63_inf



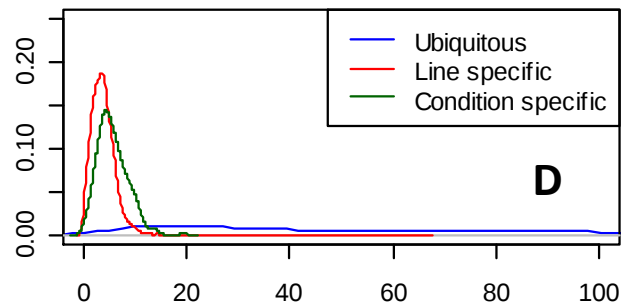
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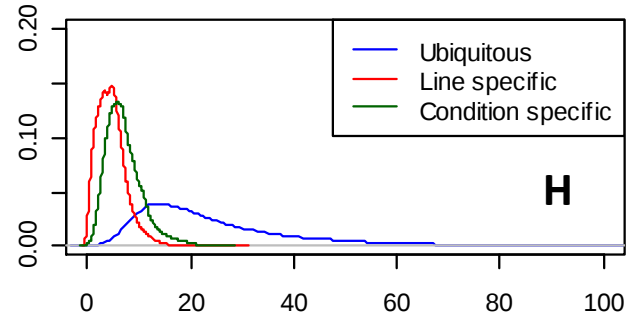
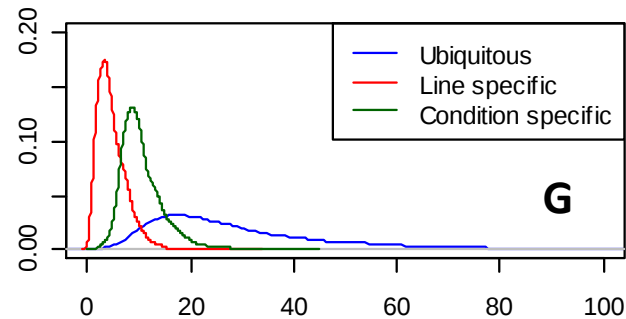
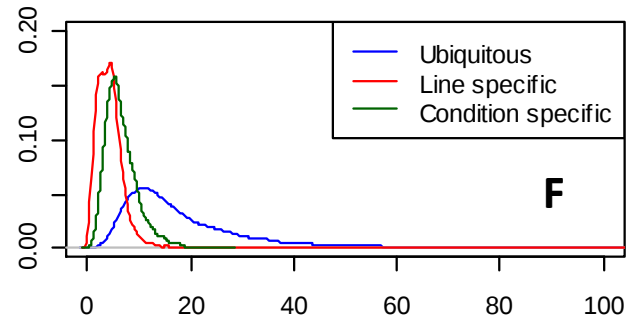
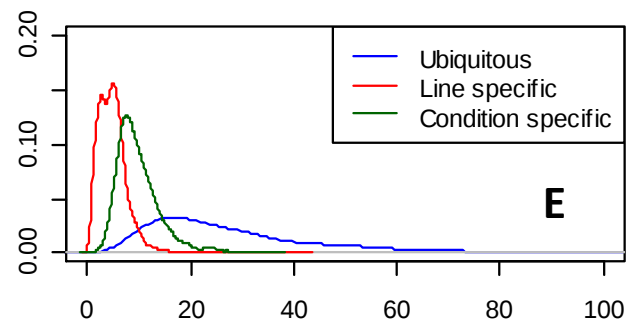
72_inf



72_inf



H3K27me3



Reads

Reads

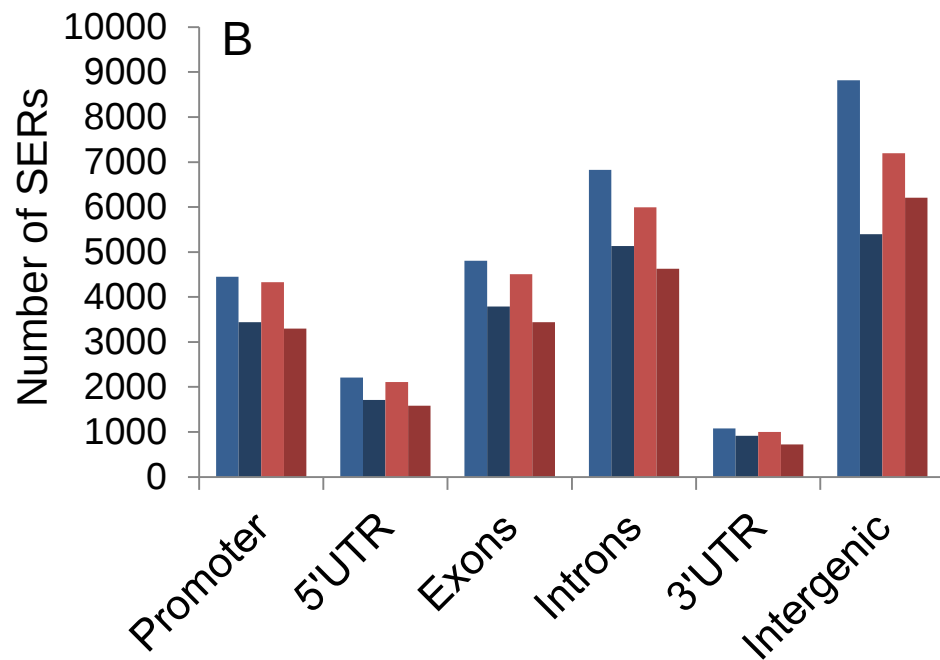
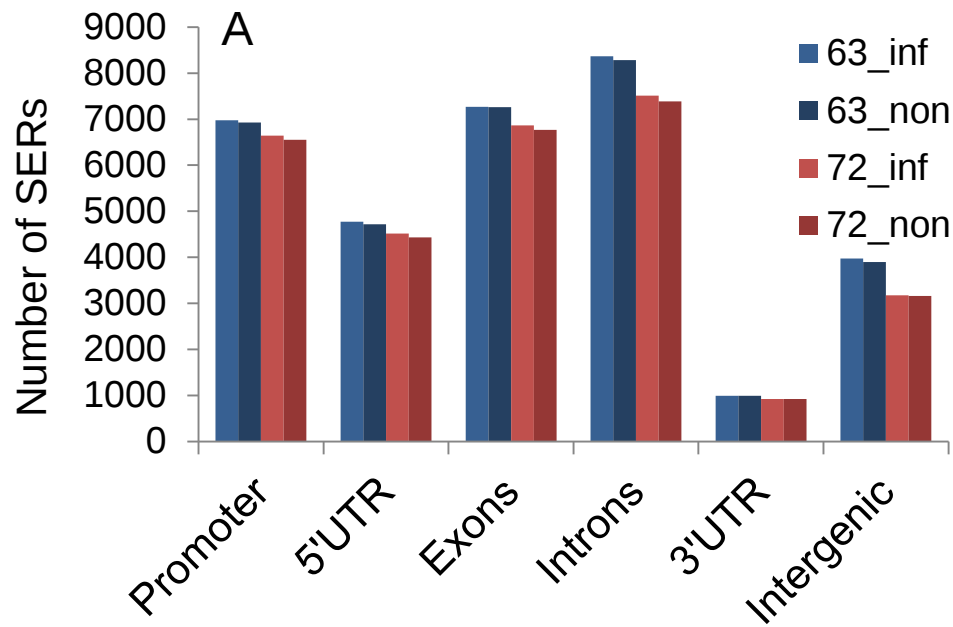


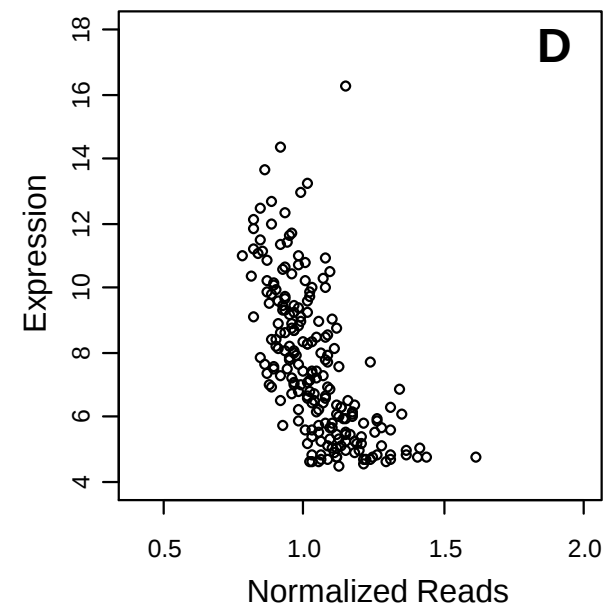
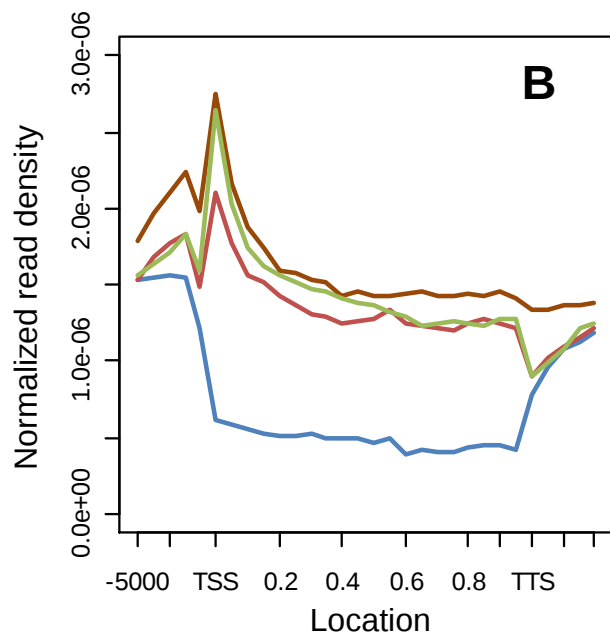
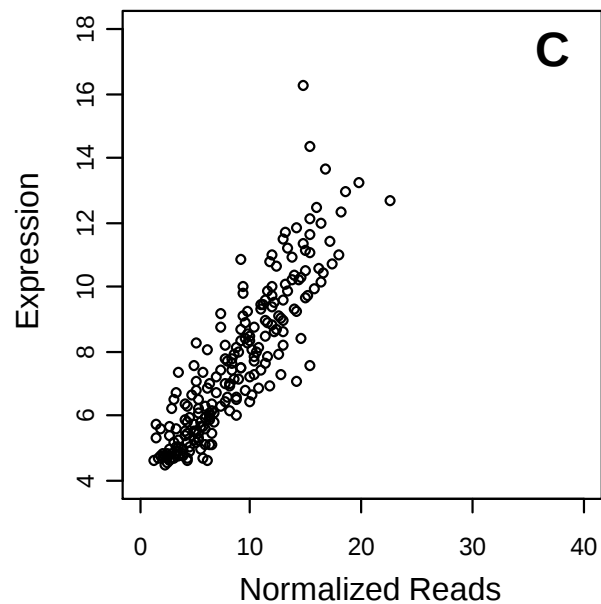
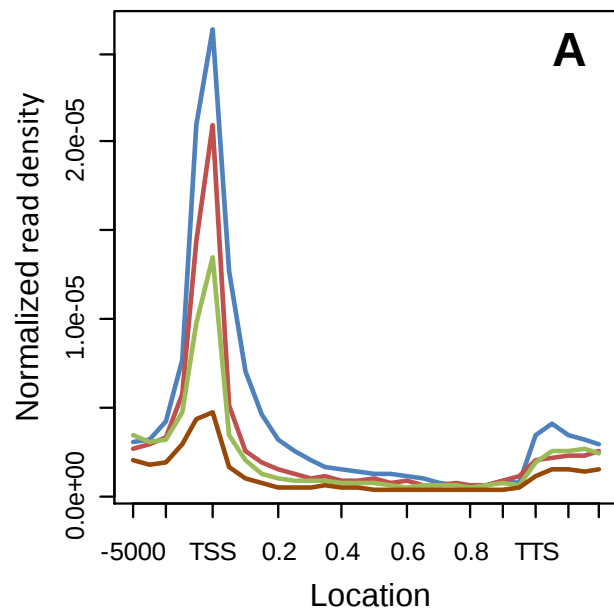
Figure S2. Distribution of SERs over different genomic elements

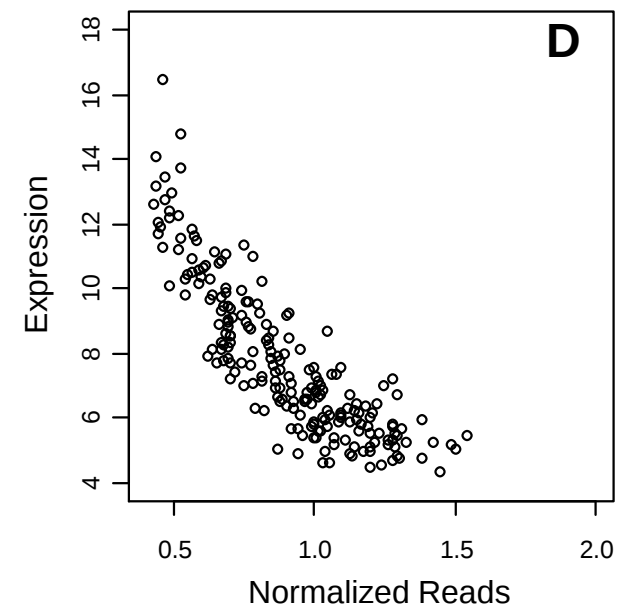
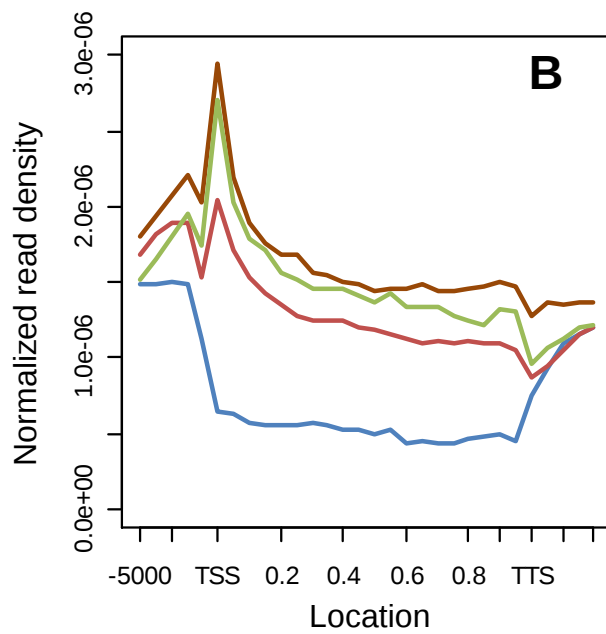
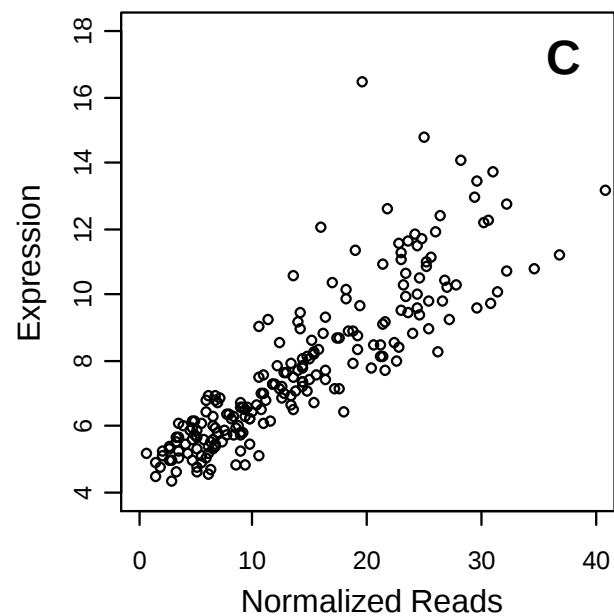
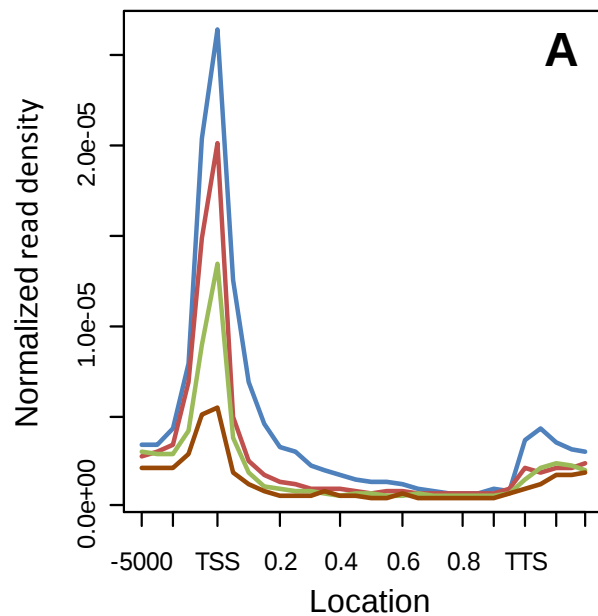
(a) H3K4me3 and (b) H3K27me3 SERs separated by samples. 63_inf: line 6₃ infected, 63_non: line 6₃ control, 72_inf: line 7₂ infected, 72_non: line 7₂ control.

Figures S3-5: Relationship between gene expression and histone marks.

Plots of histone modifications around the gene body (a & b) in genes having high, medium, low and no activity. We also compared epigenetic marks with transcriptional levels: H3K4me3 shows positive correlation with gene expression levels (c) while H3K27me3 exhibits a negative relationship (d).

S3: Line 6₃ control, **S4:** Line 7₂ control, **S5:** Line 7₂ infected.





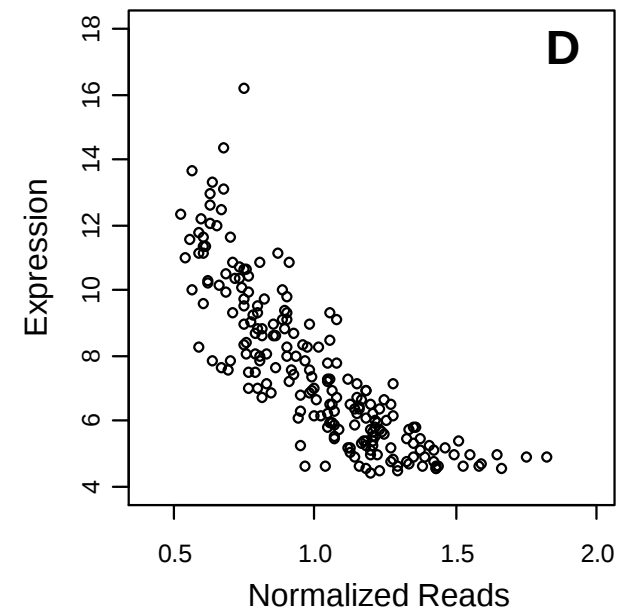
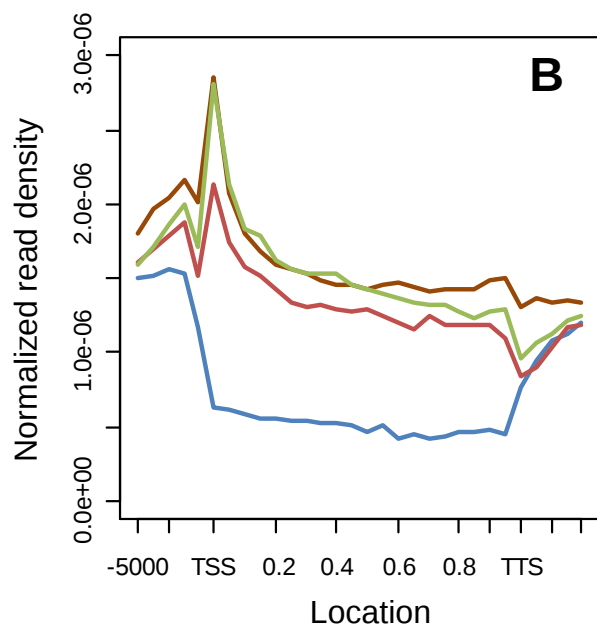
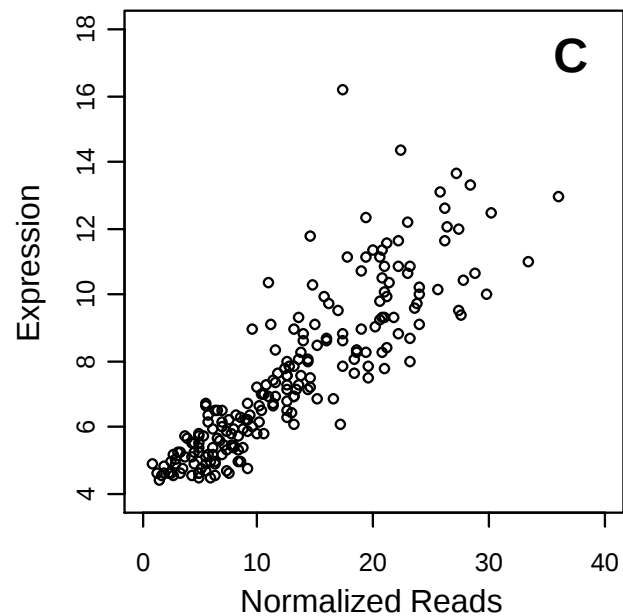
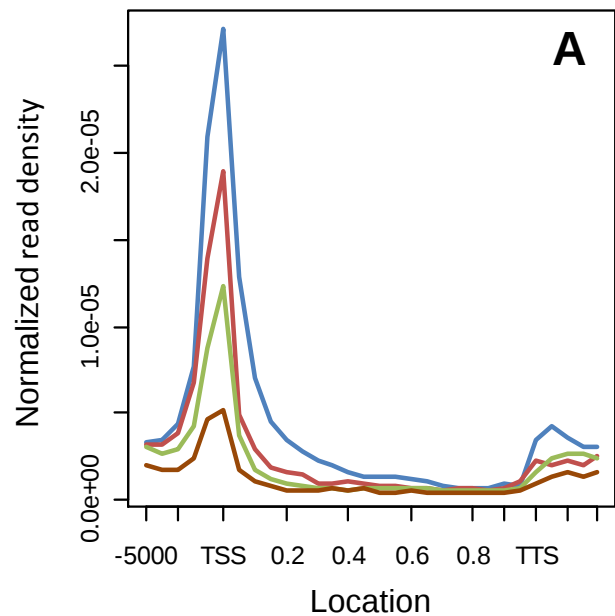


Figure S6: H3K4me3 and H3K27me3 marks around *GALR2*. No significant histone marks are observed on *GALR2*

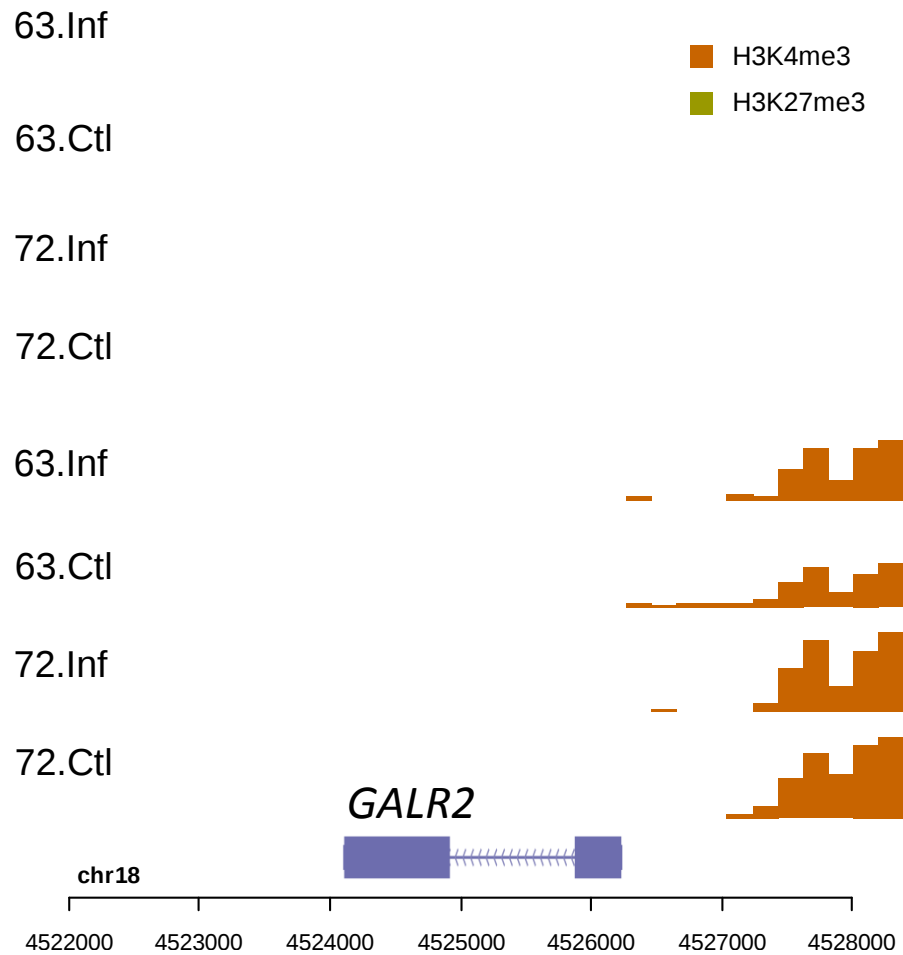
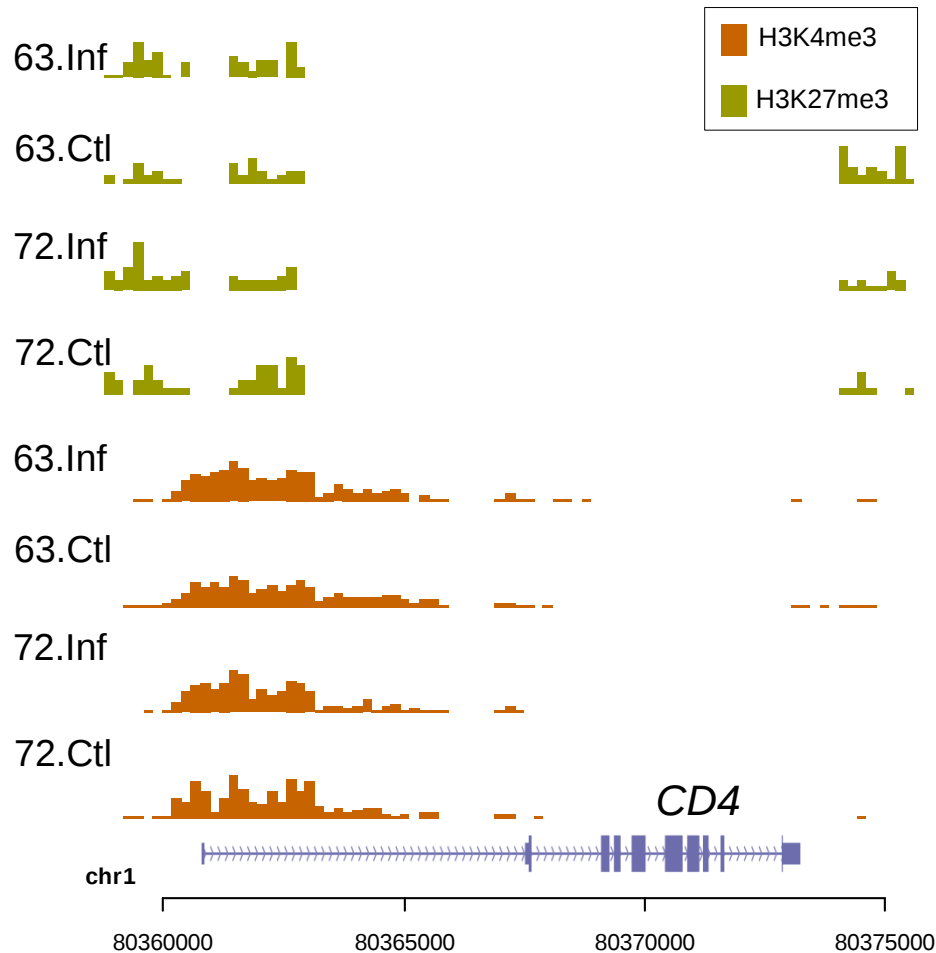


Figure S7: Bivalent domains on some genes are unaffected by virus infection. MDV infection has no effect on the bivalent domains or transcription levels of CD4 and TLR3.

A

Relative Expression

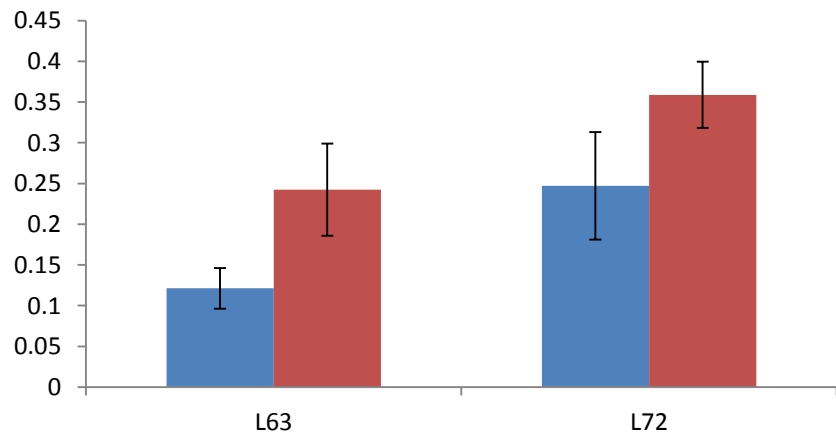
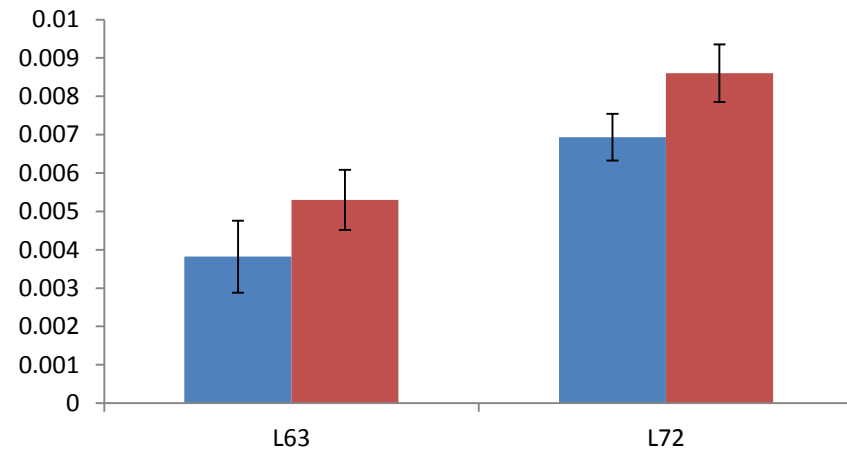
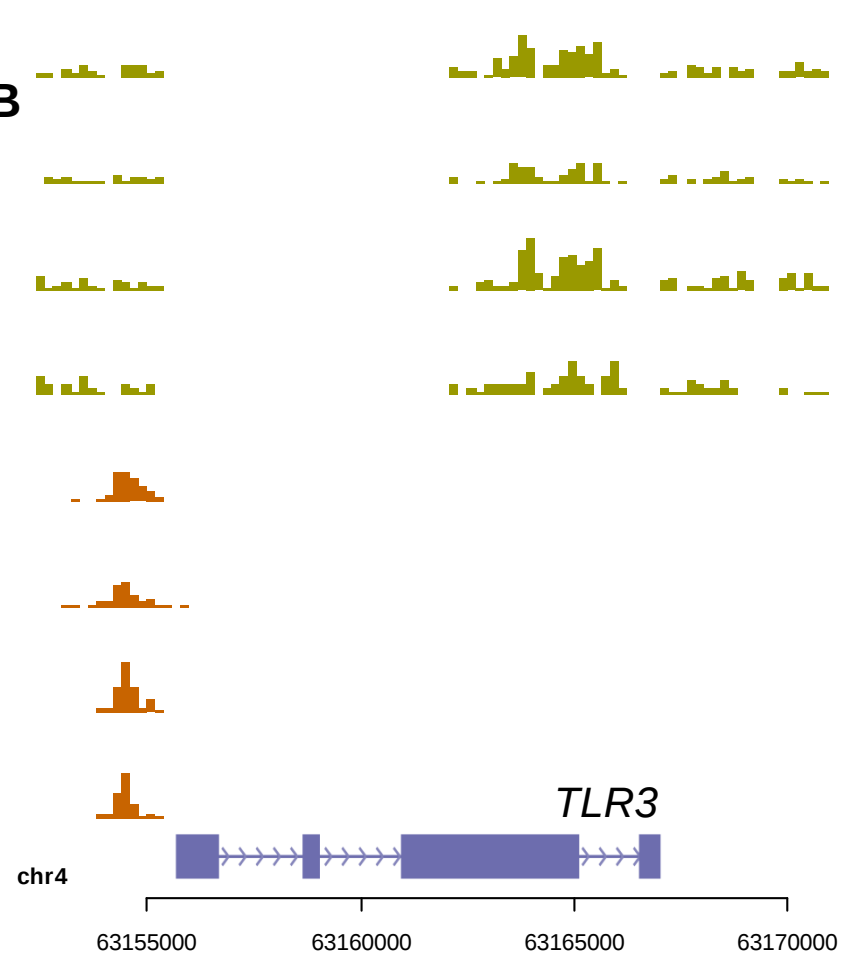
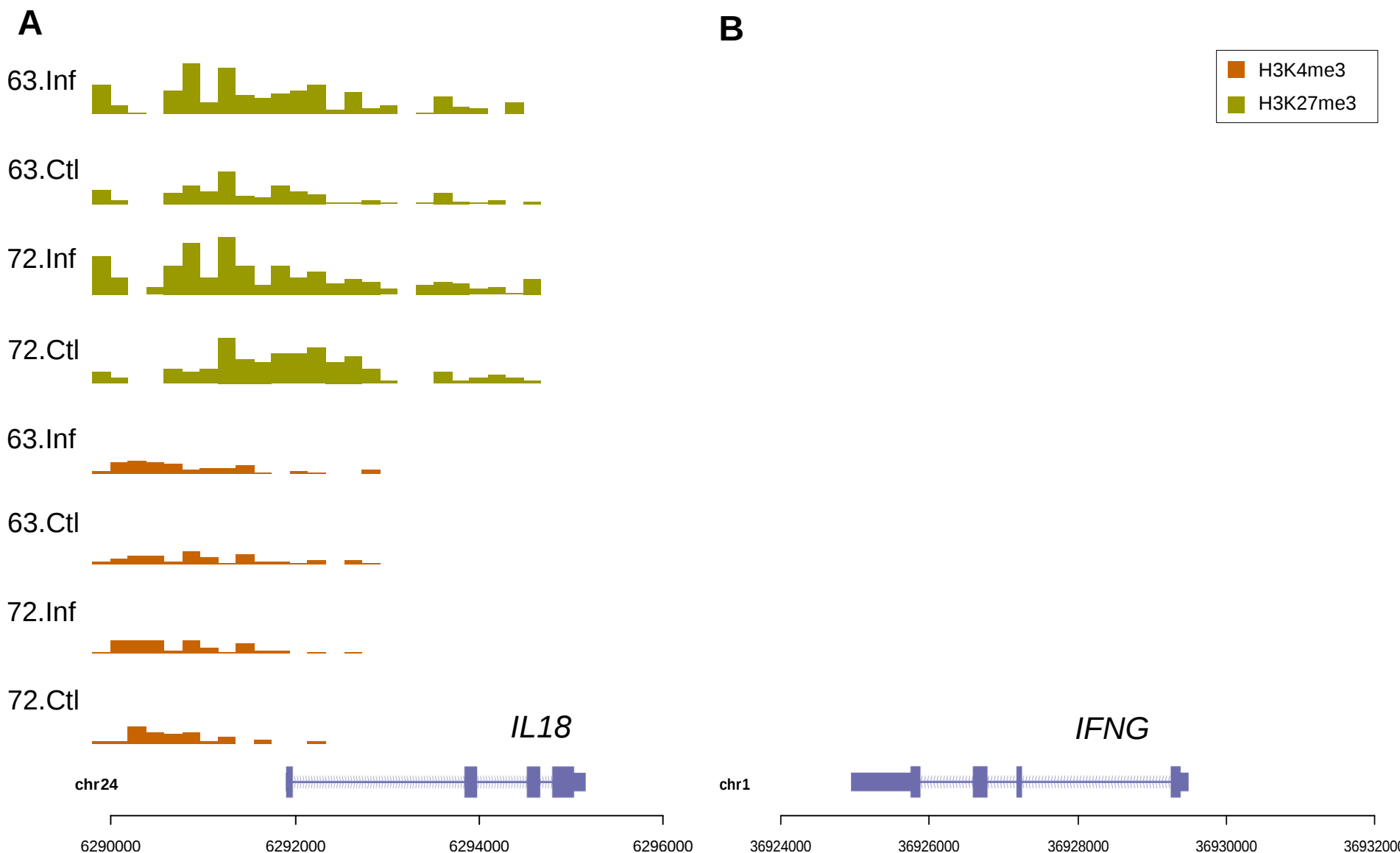
**B**

Figure S8: Epigenetic profiles of host cytokines (a) IL-18 and (b) IFN- γ . IL-18 does not show any notable changes in response to MDV infection while IFN- γ does not show any SER.



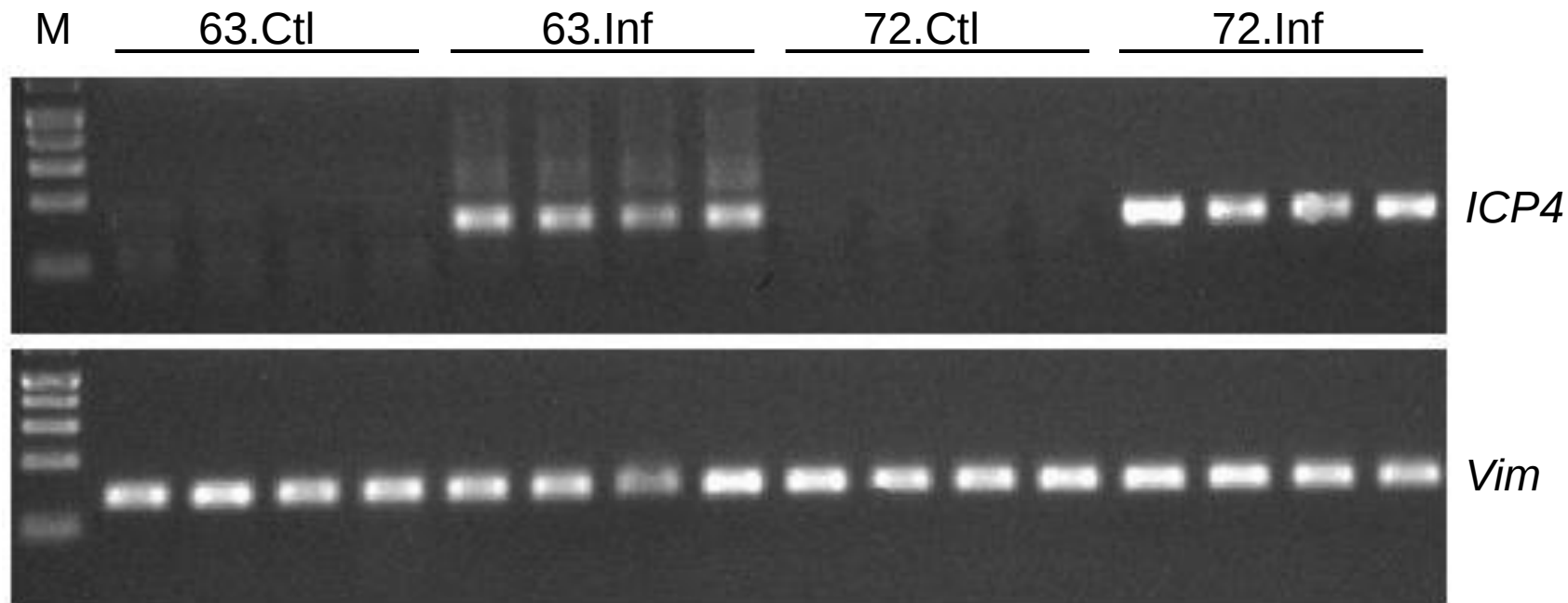
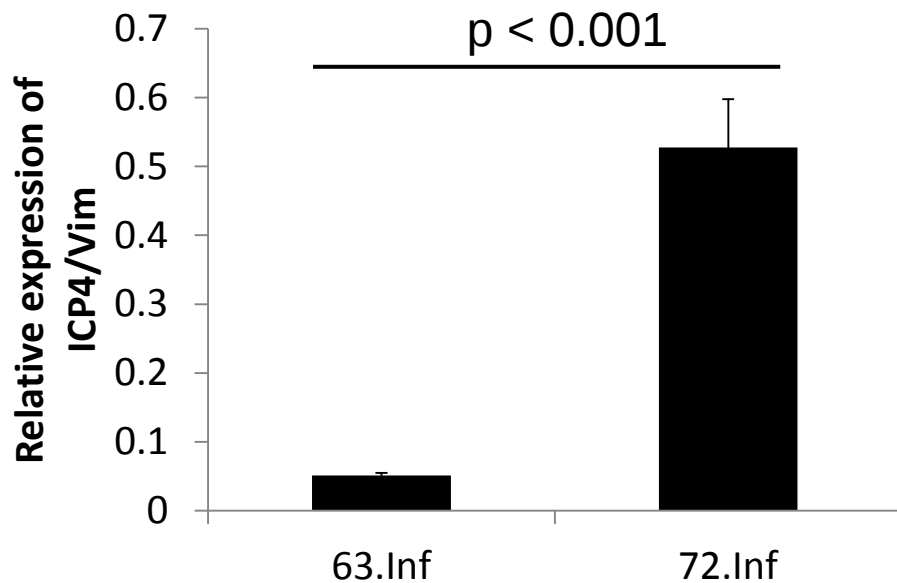
A**B**

Figure S9: Quantification of virus loads in the MDV-challenge experiment using quantitative RT-PCR. The relative virus load is calculated by quantifying viral *ICP4* normalized to the single-copy *Vim* gene (mean $\pm$ SEM, $n = 4$). (a) Only infected birds from the two lines exhibit measurable virus loads, with (b) the susceptible line 7₂ having a significantly higher number of virus particles ($p < 0.001$).