

## **Single dose of a VSV-based vaccine rapidly protects macaques from Marburg virus disease**

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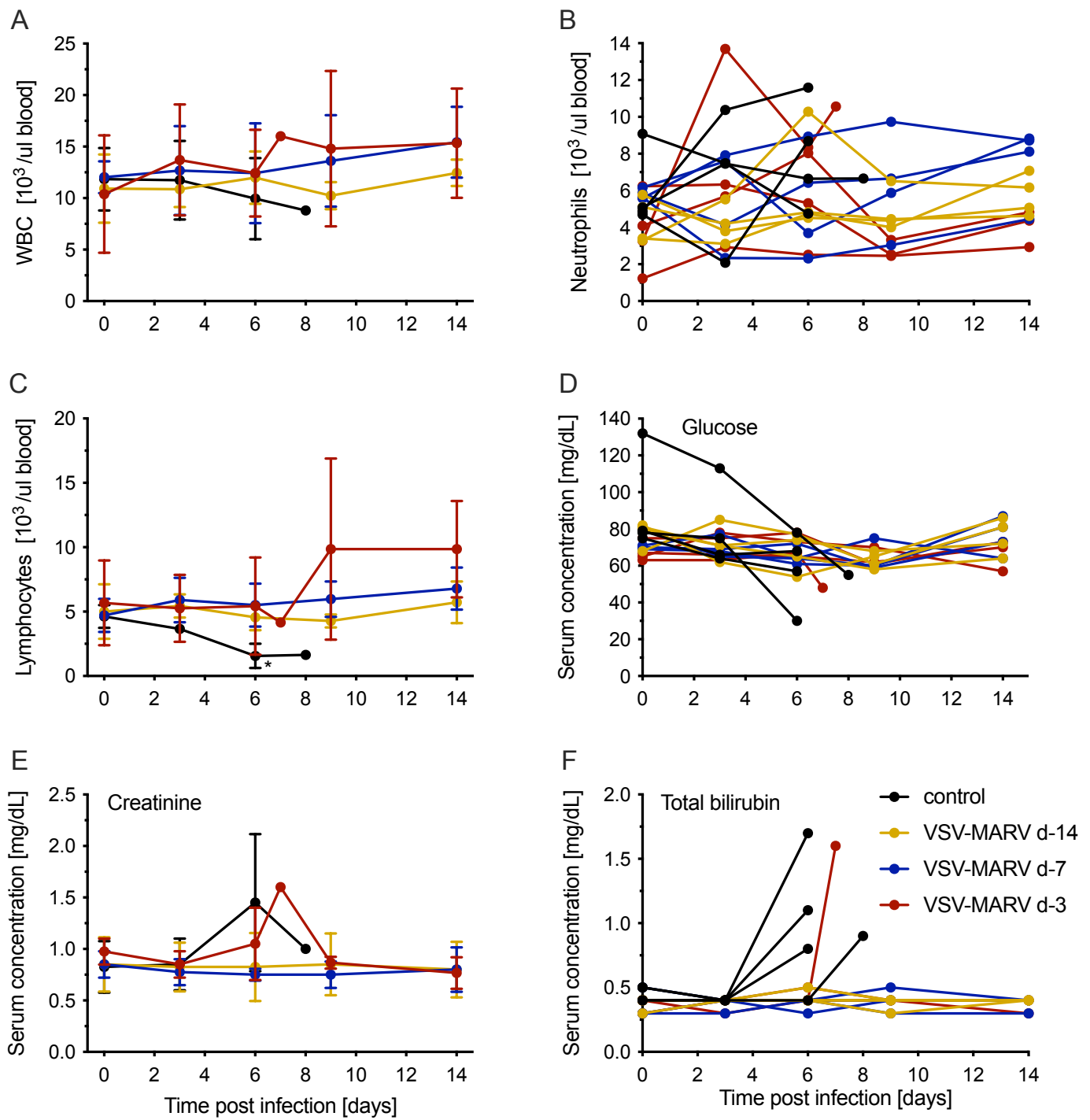
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### **Supplemental Materials**

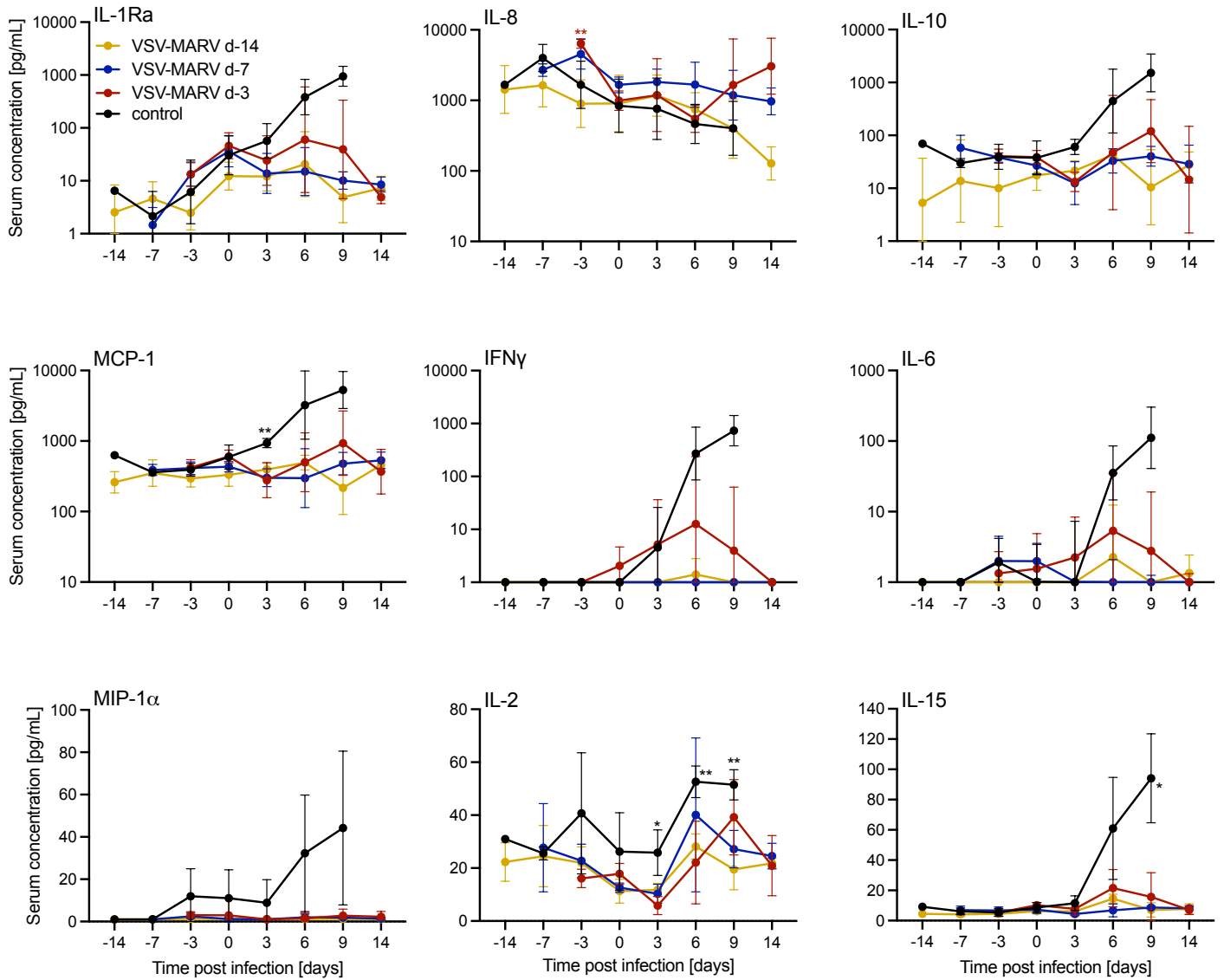
Figure S1. Blood cell counts and serum chemistry of NHPs.

Figure S2. Cytokine response in vaccinated and challenged NHPs.

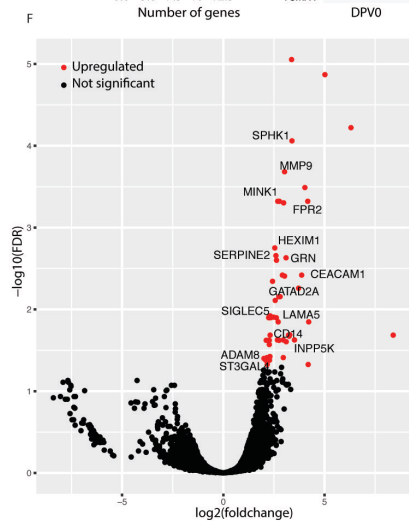
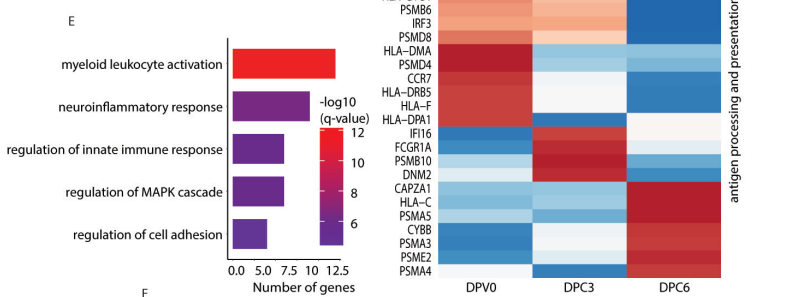
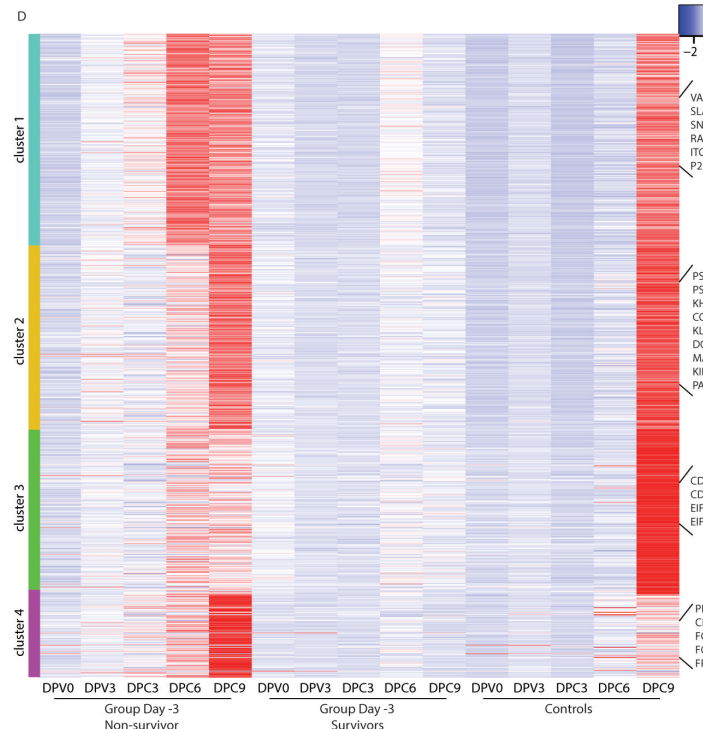
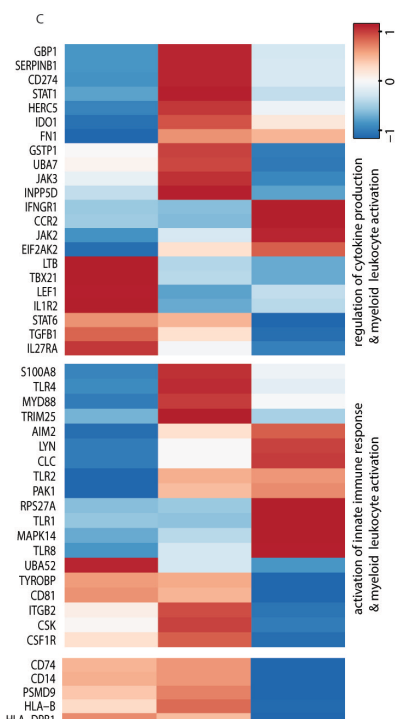
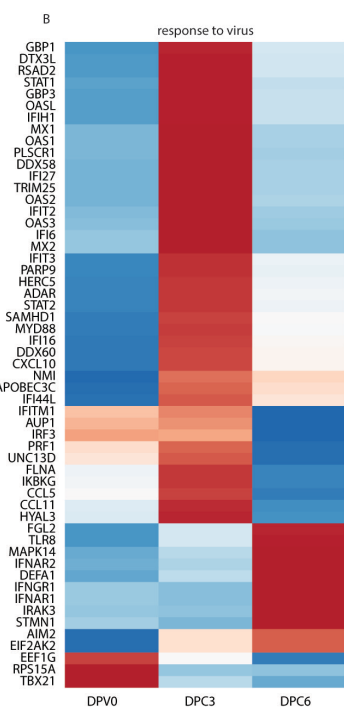
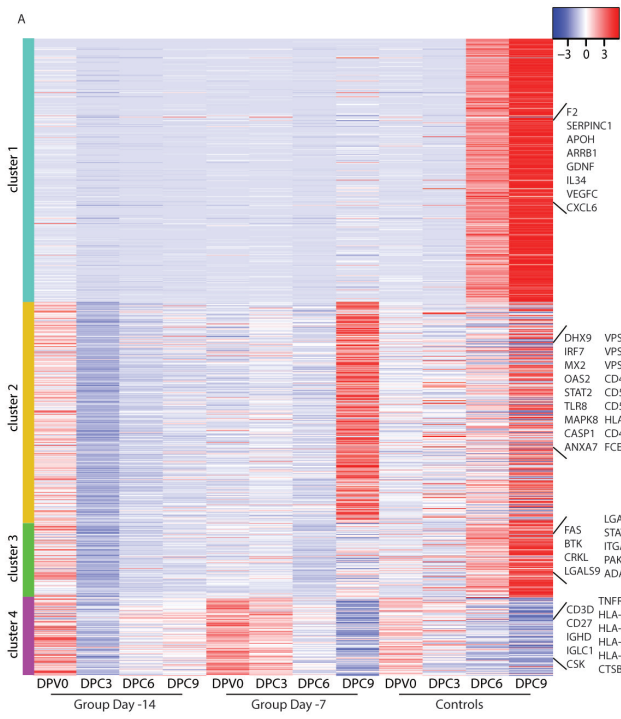
Figure S3. Transcriptional changes after challenge.



**Figure S1. Blood cell counts and serum chemistry of NHPs.** Levels of (A) white blood cells (WBC), (B) neutrophils, and (C) lymphocytes in whole blood samples over time are shown. Serum concentration of (D) glucose, (E) creatinine, and (F) total bilirubin over the course of the study are depicted. Mean and SD are depicted in (A, C, E). Statistical significance among groups was determined using two-way ANOVA with Tukey's multiple comparisons. Statistical significance is indicated as \* $p < 0.05$ .



**Figure S2. Cytokine response in vaccinated and challenged NHPs.** The concentration of selected cytokines in the serum of vaccinated and challenged NHPs was determined over time. Geometric mean and geometric SD are shown for IL-1Ra, IL-8, IL-10, MCP-1, IFN $\gamma$ , and IL-6. Mean and SD are depicted for MIP-1 $\alpha$ , IL-2 and IL-15. Statistical significance among groups was determined using two-way ANOVA with Tukey's multiple comparisons. Statistical significance is indicated as \*\*p < 0.01, and \*p < 0.05.



**Figure S3. Transcriptional changes after challenge. (A, D)** Heatmaps representing four clusters of genes significantly associated with clinical outcome identified by maSigPro in **(A)** the day -14, day -7 vaccine groups and controls or **(D)** in the day -3 vaccine group and controls. Each column represents the median normalized transcript counts (RPKM) for each gene at each time point. The range of colors is based on scaled and centered RPKM values of the entire set of genes, with red indicating highly expressed genes and blue indicating lowly expressed genes. **(B, C)** Heatmaps of DEGs detected post VSV-MARV challenge in the day -3 vaccine group enriching to “response to virus”, and “regulation of cytokine production”, “activation of innate immune response”, “myeloid leukocyte activation”, and “antigen processing and presentation.” Each column represents the median normalized transcript counts (RPKM) for each gene at each time point. The range of colors is based on scaled and centered RPKM values of the entire set of genes, with red indicating highly expressed genes and blue indicating lowly expressed genes. **(E)** Volcano plot depicting DEGs detected 0 DPV between animals that survived versus the animal that succumbed to MARV challenge in the day-3 vaccine group. **(F)** Functional enrichment of the 55 DEGs detected in panel E. Horizontal bars represent the number of genes mapping to each GO term with color intensity representing the negative log of the FDR-adjusted p-value  $-\log(q\text{-value})$ .