

Supplementary Materials for

A conserved transcriptional response to intranasal Ebola virus exposure in nonhuman primates prior to onset of fever

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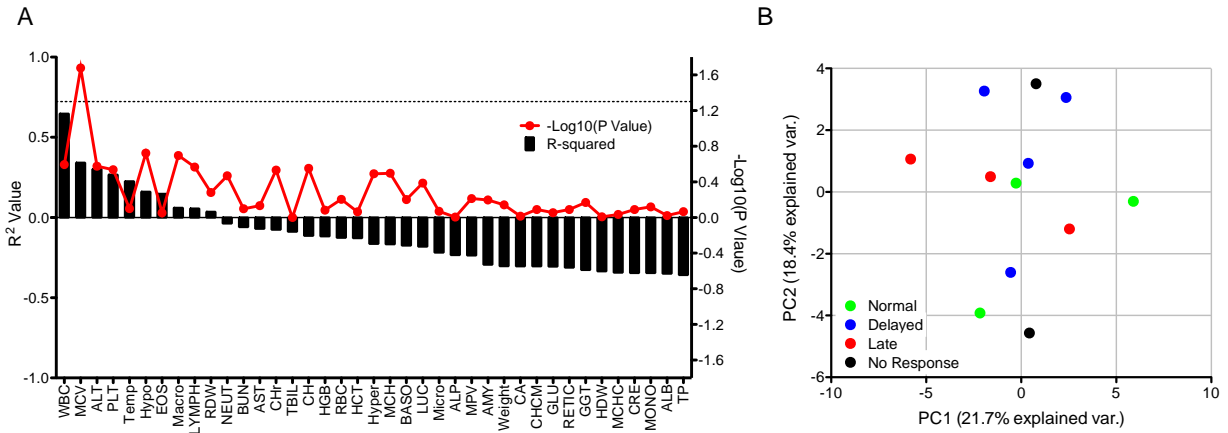
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The PDF file includes:

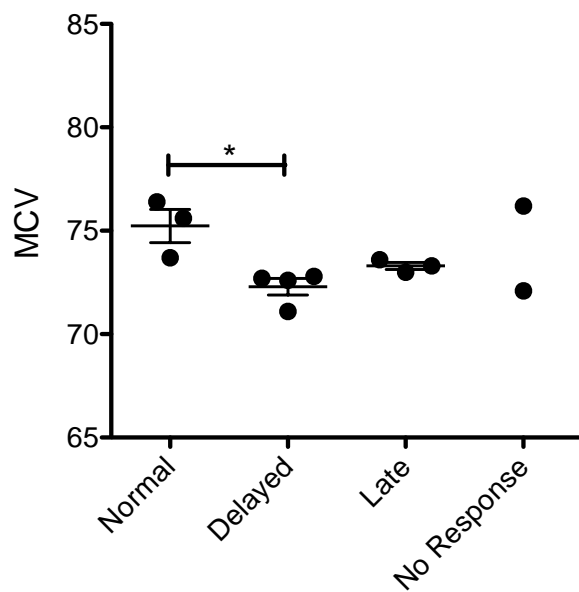
Fig. S1. Comparison of animals before exposure.
Fig. S2. Comparison of MCV between groups.
Fig. S3. Correlation of cytokine expression in symptomatic animals.
Fig. S4. Example genes from NanoString in Delayed animals.
Fig. S5. Interferon response in NanoString CodeSet.
Fig. S6. Histogram of deviances from curve fitting.
Legends for tables S1 to S3

Other Supplementary Material for this manuscript includes the following:
(available at
www.sciencetranslationalmedicine.org/cgi/content/full/10/434/eaq1016/DC1)

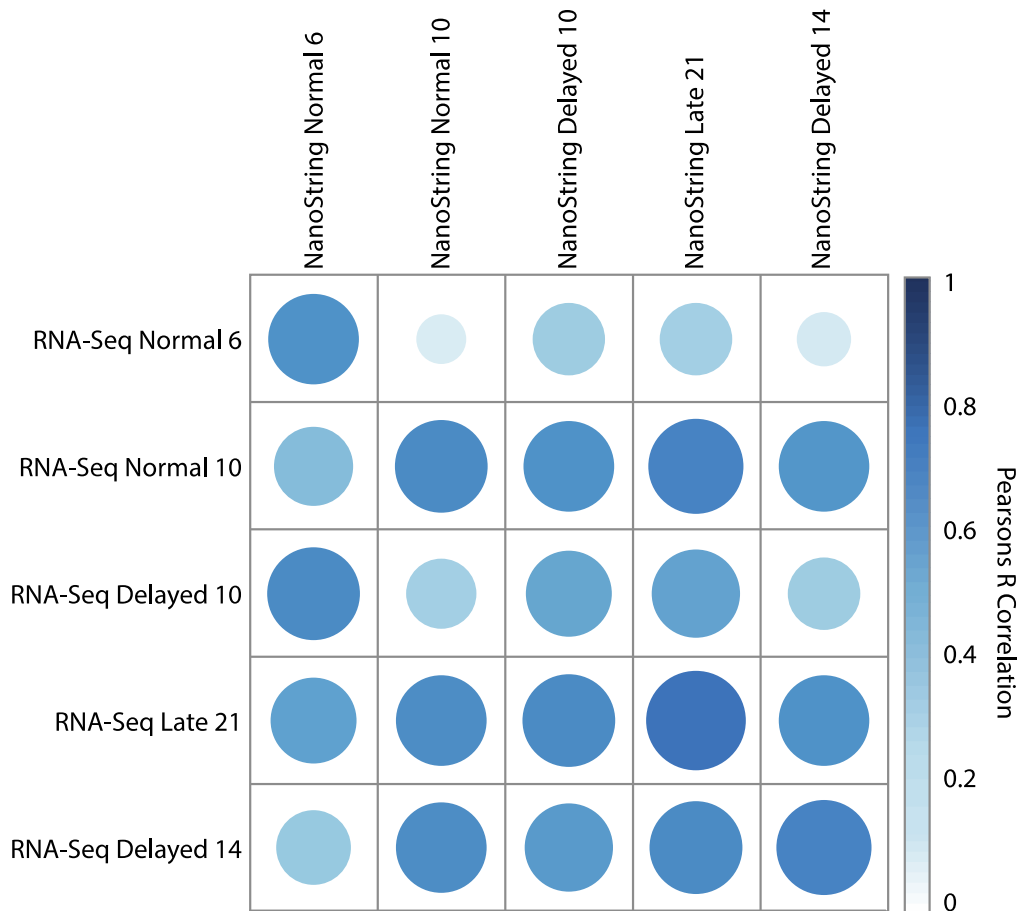
Table S1 (Microsoft Excel format). Cytokine expression in RNA-seq.
Table S2 (Microsoft Excel format). Early expressed genes in the Delayed group.
Table S3 (Microsoft Excel format). Normalized NanoString counts.



Supplemental Figure 1. Comparison of animals before exposure. Analysis of the pre-exposure samples to identify any significant differences in physiological or chemistry parameters. (A) Results of a one-way ANOVA with physiological/blood chemistry parameters shown on the x-axis. The left y-axis is the fitted R² value (black bars). The right y-axis is the -Log₁₀(p-value) (red points/line). The dashed line denotes where p = 0.05. Points above this line are within a significance threshold. (B) PCA plot of the same values in A for the different groups. Each point signifies an individual animal and the colors represent the different groups (green = Normal, blue = Delayed, red = Late, black = No Response).

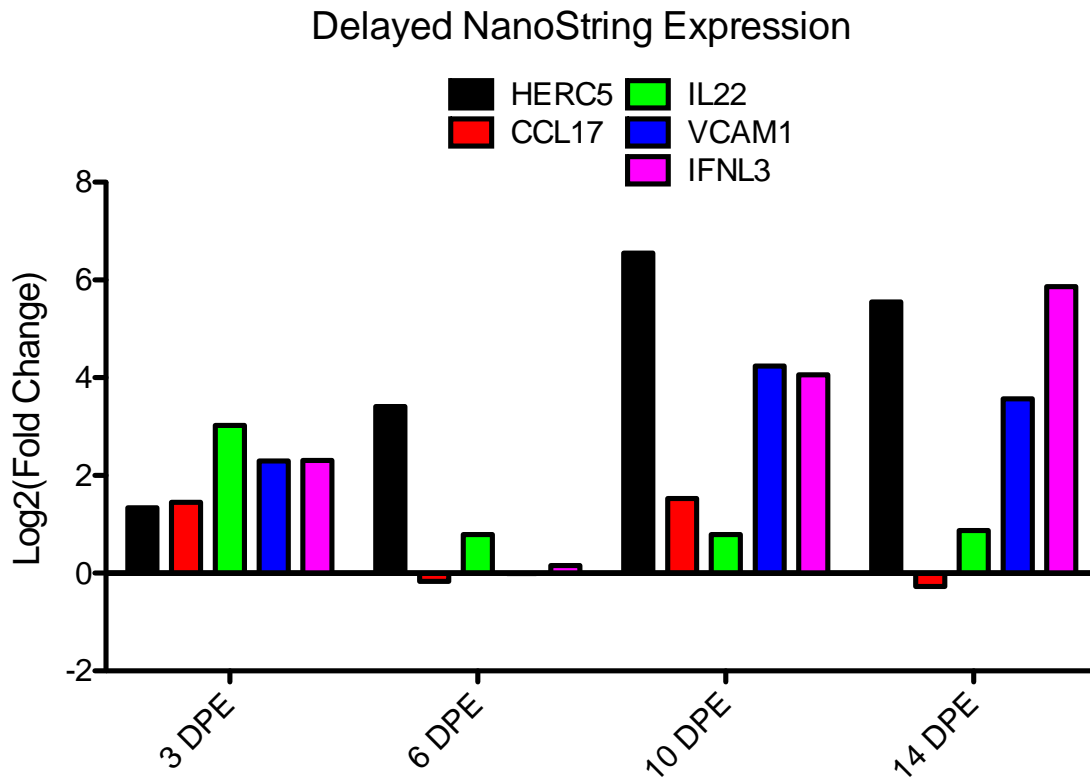


Supplemental Figure 2. Comparison of MCV between groups. Mean corpuscular volume (MCV) was measured in all animals on the day of infection. The only significant pair-wise difference (determined by pair-wise ANOVA) was between the Normal and Delayed animals ($p = 0.02$).

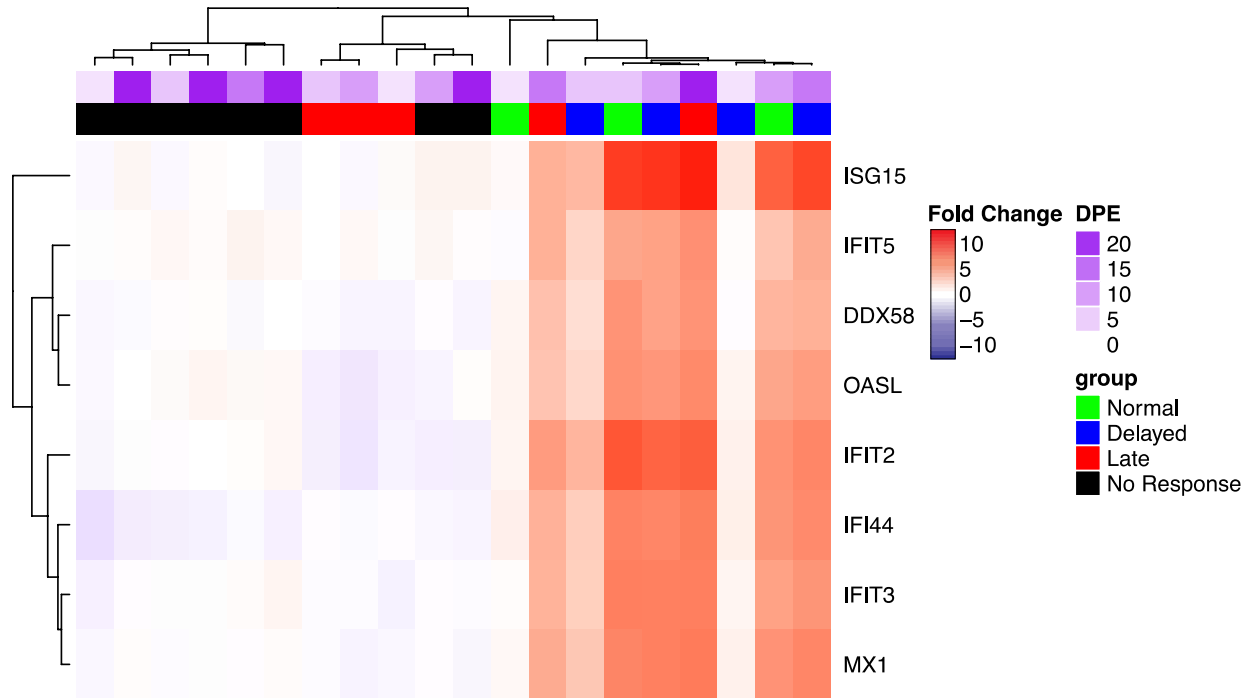


Supplemental Figure 3. Correlation of cytokine expression in symptomatic animals.

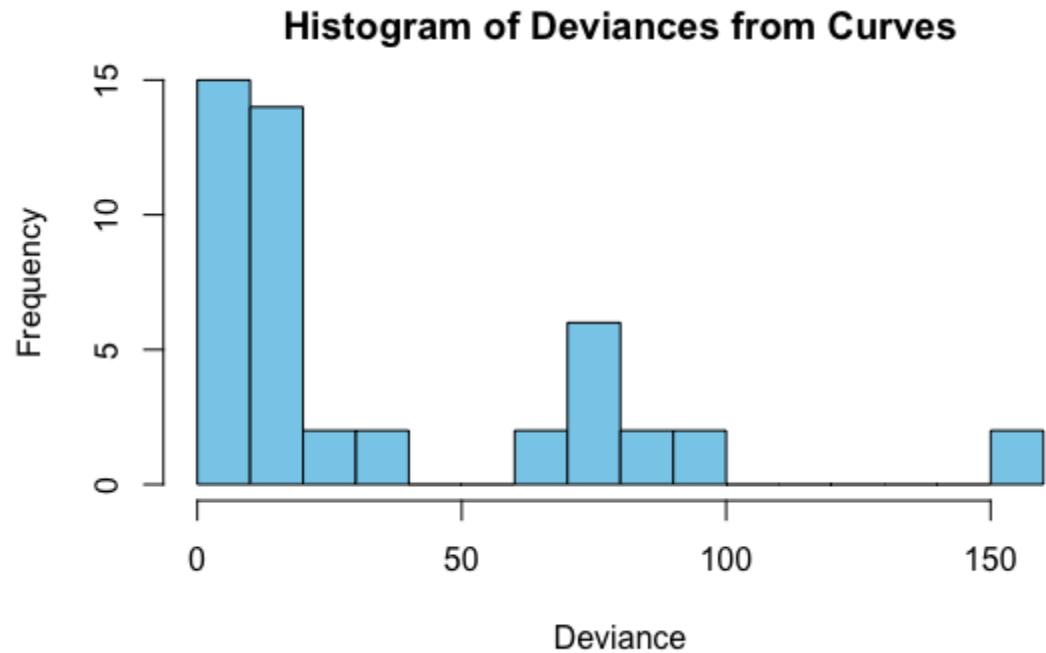
Correlation comparison of the symptomatic animals on NanoString and RNA-Seq for cytokine genes. The larger the circle and the darker the blue the stronger the correlation between the data sets.



Supplemental Figure 4. Example genes from NanoString in Delayed animals. Days post-exposure (DPE) are shown on the x-axis and the log₂ fold change relative to pre-exposure controls is on the y-axis. All data are from Delayed animals. Colored bars represent different genes (black = *HERC5*, red = *CCL17*, green = *IL22*, blue = *VCAM1*, purple = *IFNL3*).



Supplemental Figure 5. Interferon response in NanoString CodeSet. Overview of the principal ISGs detected in the NanoString CodeSet. The top color bar represents the day post-exposure with the darker purple colors representing later days. The second color bar represents the different groups (Normal = green, Delayed = blue, Late = red, No Response = black). The heatmap shows the fold change for a given day/group combination compared to day 0 with red for up-regulation, blue for down-regulation, and white for no change.



Supplemental Figure 6. Histogram of deviances from curve fitting. Deviances for logistic curve fitting. The x-axis is the deviance values for all genes tested and the frequency is displayed on the y-axis.

Supplemental Table 1. Cytokine expression in RNA-seq.

Supplemental Table 2. Early expressed genes in the Delayed group.

Supplemental Table 3. Normalized NanoString counts.