

SUPPLEMENTARY FIGURE LEGENDS

Figure S1. Bacterial culturing of infected macaque lung. Tissue homogenates (0.1g/ml PBS) prepared from six samples taken throughout the left and right lungs of all macaques used in this experiment were cultured on blood agar plates, and concentrations (colonies/gram of lung tissue) of three different species were calculated for each sample. R1, Lung-right1 (upper); R2, Lung-right2 (middle); R3, Lung-right3 (lower); L1, Lung-left1 (upper); L2, Lung-left2 (middle); and L3, Lung-left3 (lower)

Figure S2. Viral RNA and total gene expression profiles of examined tissue. (A) Relative levels of viral HA or M1 RNA in lung lesions collected for microarray analysis were quantified using qPCR and compared to the global gene expression profiles in (B). Red arrows indicate the samples that were selected for downstream wave pattern cluster analysis. A color scale indicating expression levels for the heat map is shown at the bottom left.

Figure S3. Overview of temporal differential gene expression in rhesus macaques infected with Anhui/2. The total number of differentially expressed (DE) genes (± 2 fold-change relative to the mock-infected control) was plotted for each time point,

showing the number of both upregulated and downregulated genes. The exact number of DE genes per time point is indicated above each time point bar.

Figure S1

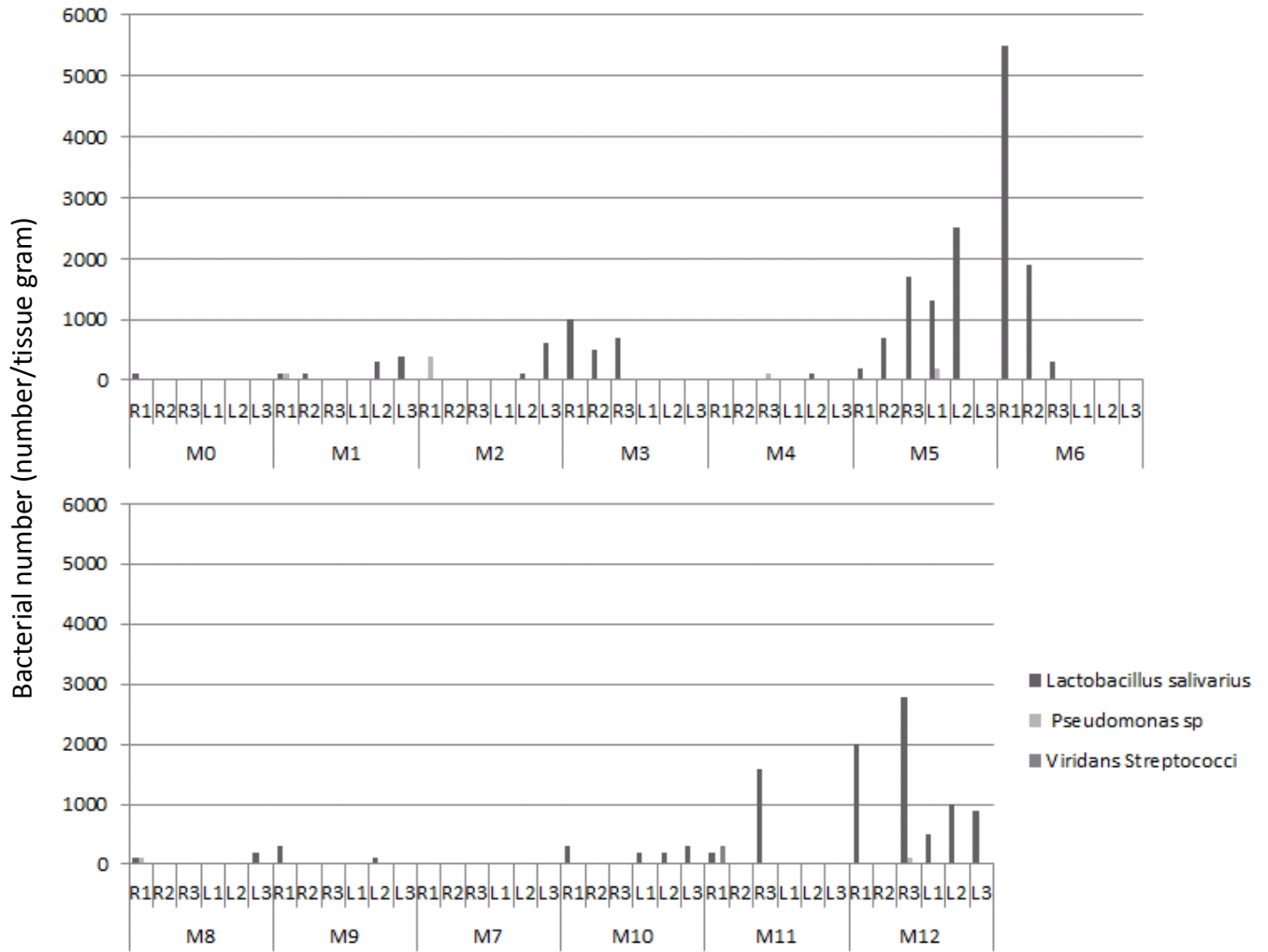
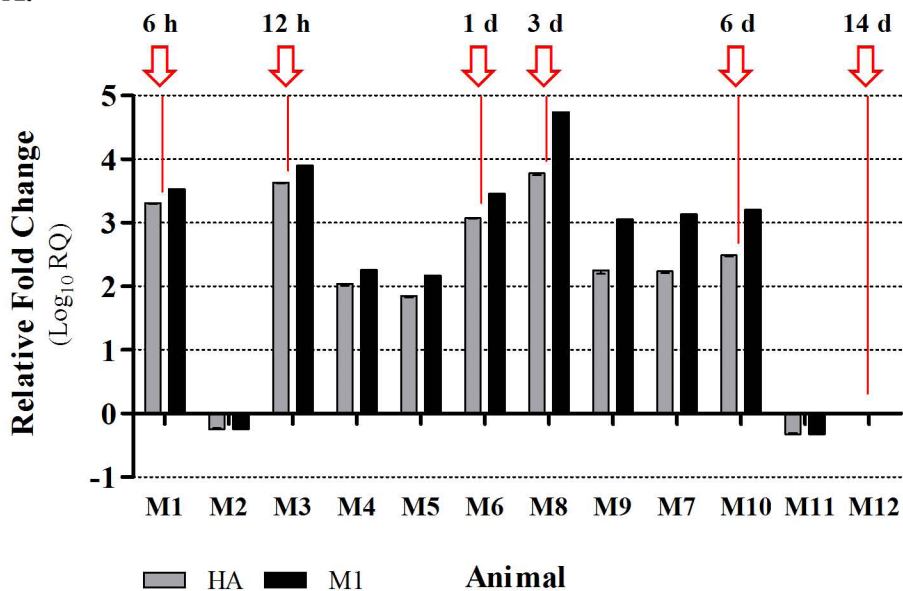


Figure S2

A.



B.

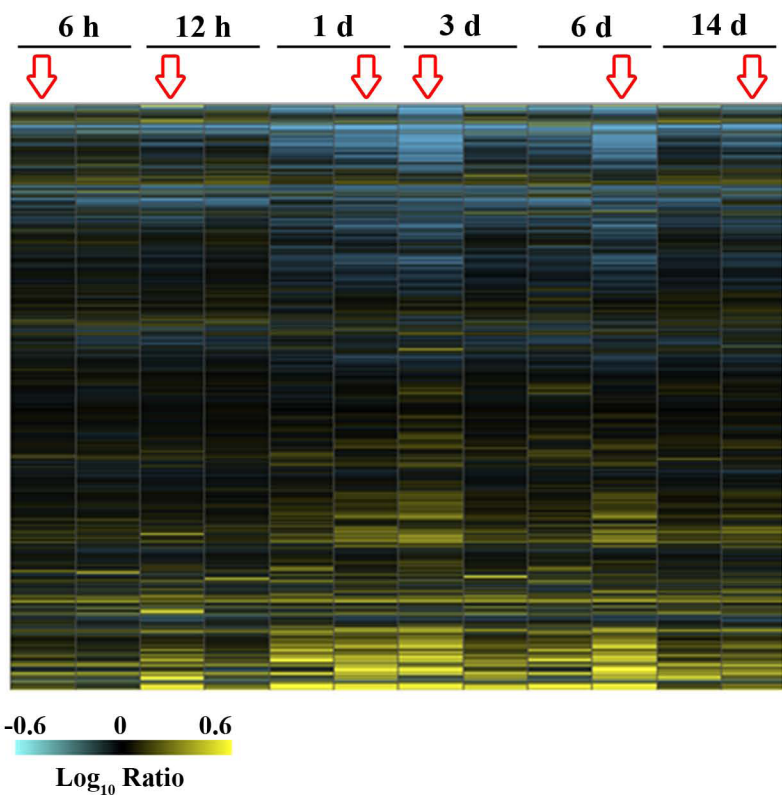


Figure S3

