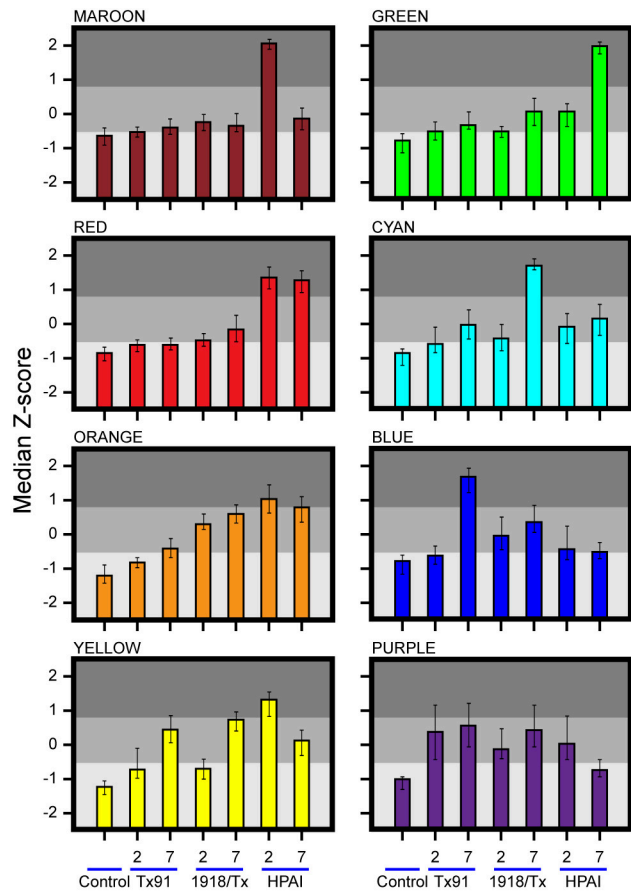
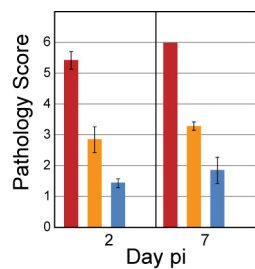


Macaque Response to Influenza

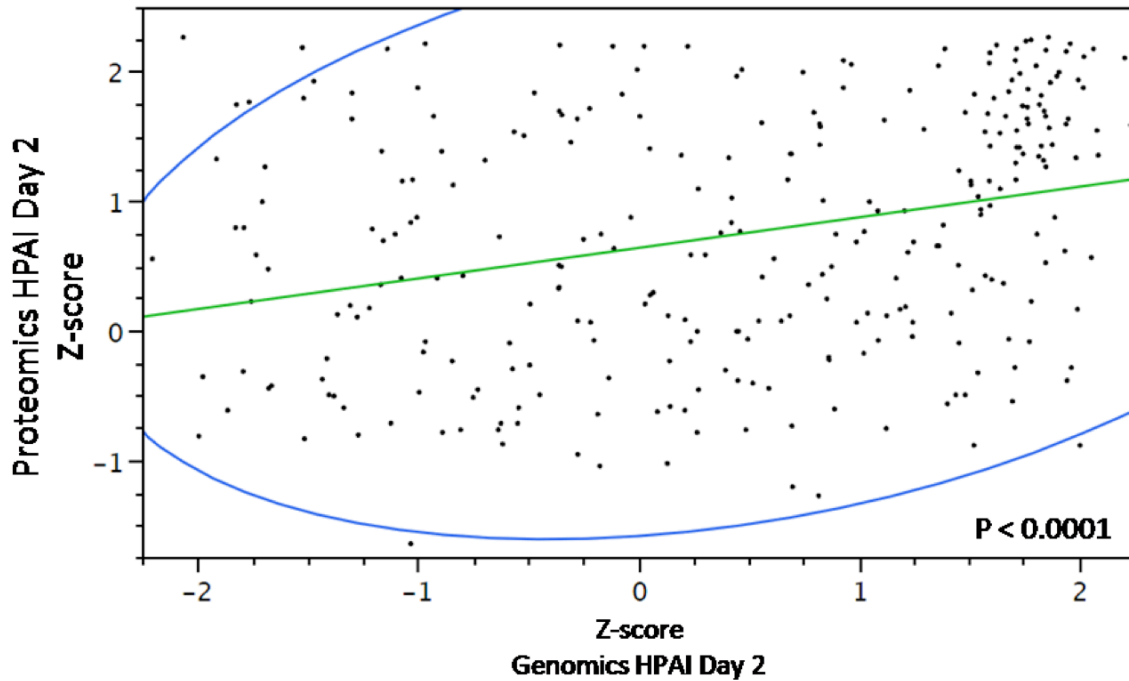


Supplemental Figure 1. Median z-scores of spectral counts for each of the 8 clusters are graphed relative to virus and time point. The graph is shaded according to response profiles from Fig. 2, with the darkest area REPRESENTING “high” ($\geq +0.8$), intermediate “core” ($< +0.8$ and ≥ -0.5), and lightest shading representing basal or normal levels of expression (< -0.5).

Macaque Response to Influenza



Supplemental Figure 2. Pathology scores from Baskin *et al.* study (3), which were used in correlation analysis for Fig. 4. Degree of pathology was scored from 0, no apparent signs of pathology, to 6, most several alterations from healthy. Bars represent the average pathology scores of the two macaques, and error bars indicate standard deviation. The average value was used to perform the correlation analysis. Red, orange, and blue represent HPAI, 1918/Tx, and Tx91. Control macaques presented no signs of pathology, and received scores of 0.



Supplemental Figure 3. Representative correlation analysis between proteomics and genomics z-score values for HPAI on day 2 post-infection. The green line represents the linear fit and the blue ellipse is the bivariate normal fit with $P = 0.950$. The correlation between proteomics and genomics data is weak (0.24 or 0.29 for the linear or bivariate estimates, respectively), although it did reach statistical significance. Results for other clusters in Figure 3 were comparable.