



Figure S8. BAL RNA-sequencing. (A) Principal component analysis of bronchoalveolar lavage (BAL) samples from uninfected animals and vaccinated animals 3 days post challenge (control, intramuscular (IM) or intranasal (IN) vaccination). (B) Down- and up-regulated differentially expressed genes (DEGs). Heatmaps representing DEGs shared by all infected groups and enriching to Gene Ontology (GO) terms “myeloid cell activation” and “neutrophil degranulation” for (C) upregulated DEGs and (D) downregulated DEGs, and (E) “autophagy” and “positive regulation of cytokine production” for upregulated DEGs. Each column represents the median rpkms of the given group. Range of colors is based on scale and centered rpkms values of the represented DEGs. Red represents upregulated DEGs; blue represents downregulated DEGs. (F) Digital cell quantitation using ImmQuant IRIS database comparing challenged groups to uninfected controls. Red represents upregulation; blue represents downregulation. Each column represents the average relative predicted frequency of the given cell type. P-values are calculated relative to the uninfected animals. Statistical significance is indicated. For all heatmaps, range of colors is based on scale and centered rpkms values of the represented DEGs.