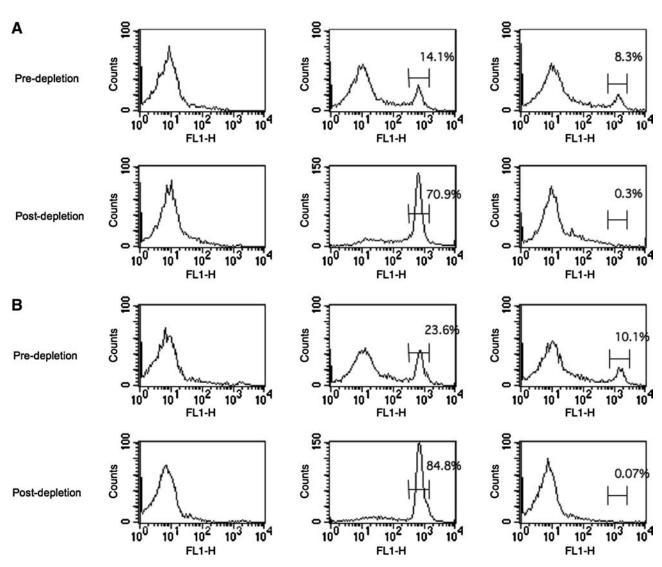
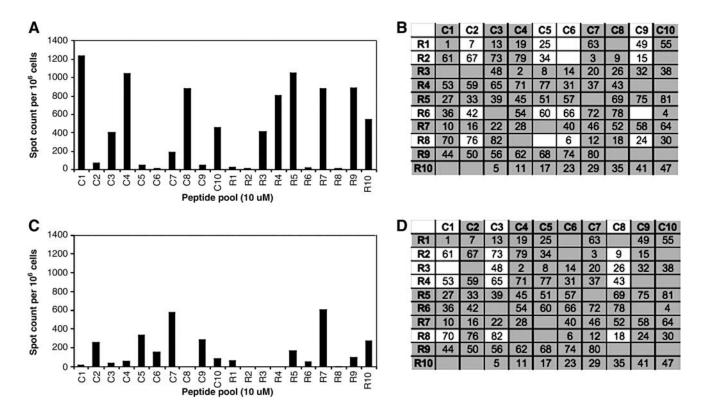
Protein	Size (aa)	Number of peptides <sup>a</sup>
Hemagglutinin	565	94
Nonstructural protein 1	230	37
Nucleocapsid protein	498	82
Neuraminidase	470	78
Matrix protein 1	252	41

<sup>&</sup>lt;sup>a</sup>Peptides screened were 17mers overlapping by 11 amino acids obtained through the NIH Biodefense and Emerging Infections Resources Repository, NIAID, NIH.



**SUPPLEMENTARY FIG. 1.** Example of flow cytometry demonstrating the enrichment of CD4 T cells following antibody and complement mediated lysis of CD8 T cells and APC. This figure is representative of the results from the CD4 enrichment of splenocytes. (**A**) Pre- and post-depletion results in C57BL/10 mice. (**B**) Pre- and post-depletion staining in SJL mice. There were <1% contaminating CD8<sup>+</sup> T cells present in any sample.



**SUPPLEMENTARY FIG. 2.** Screening of the NP protein utilizing a peptide pooling matrix approach. A matrix of pooled 17-mer peptides that contained no overlapping peptides in either rows or columns was constructed, as shown in panels **B** and **D**. Peptides were considered for further analysis if they were a member of both a positive row and column (shown in gray), with no row or column containing >40 spots per 10<sup>6</sup> CD4-enriched T cells excluded. All matrices were screened at least twice to ensure that no potential epitopes were falsely considered negative. The results from the NP matrix in both C57BL/10 (panels **A** and **B**), and SJL (panels **C** and **D**) mice are shown as examples. Panels **A** and **C** demonstrate the results from representative EliSpot assays, while panels **B** and **D** show the subsequent analysis of the matrix.