Table S1. Primer and probe information for genes of interest.

Gene	Classification	Accession No.[1]	Assay ID[2]
BDNF	Neurotrophic factor	NM_214259	Ss03822335_s1
GAPDH	Reference	NM_001206359	Ss03374854_g1
TLR3	Pattern recognition receptor	NM_001097444	Ss03388861_m1
TLR4	Pattern recognition receptor	NM_001113039	Ss03389780_m1
PRRSV[3]	Virus	NA	NA

[1]NCBI GenBank accession number.

[2]Applied Biosystems TaqMan Gene Expression Assay identification number.

[3]*PRRSV* custom probe (Chen et al., 2009): forward primer, CGCACCAGATGGGACCTACTT; reverse primer, ACGGTGTTCAGTGAGGGCTTT; probe, CGCTGCGTTGACTGG

Figure S1. PRRSV infection significantly up-regulated expression of gene clusters encoding complement components (A), MHC-I and MHC-II isomers (B), and interferon induce proteins (C, FDR < 0.05).

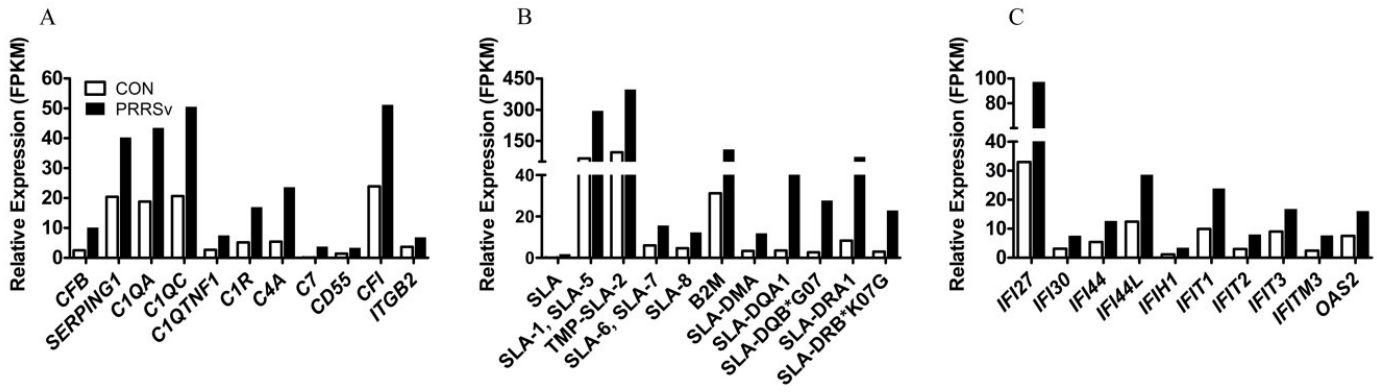

Figure S2. PRRSV infection altered the fractional composition and increased MHC-II expression of all subpopulations of CD11b+ that varied in expression levels of CD45 and/or forward scatter pattern (FSC-A). (A) Representative density plots characterized the fractions of CD11b+ cells based on expression level of CD45 and FSC-A. Two new fractions were observed for PRRSV cells with high FSC-A and intermediate or high expression of CD45. (B) Percentage of CD45low, intermediate, and high fractions in CD11b+ cells isolated from hippocampus of PRRSV (n=6) or control (n=6) piglets. Statistical analysis, one-way ANOVA, * $P < 0.05$. (C) Representative contour plot showing percentage of MHC-II+ populations from CD45low, intermediate, high and new fractions, respectively, in CON and PRRSV.