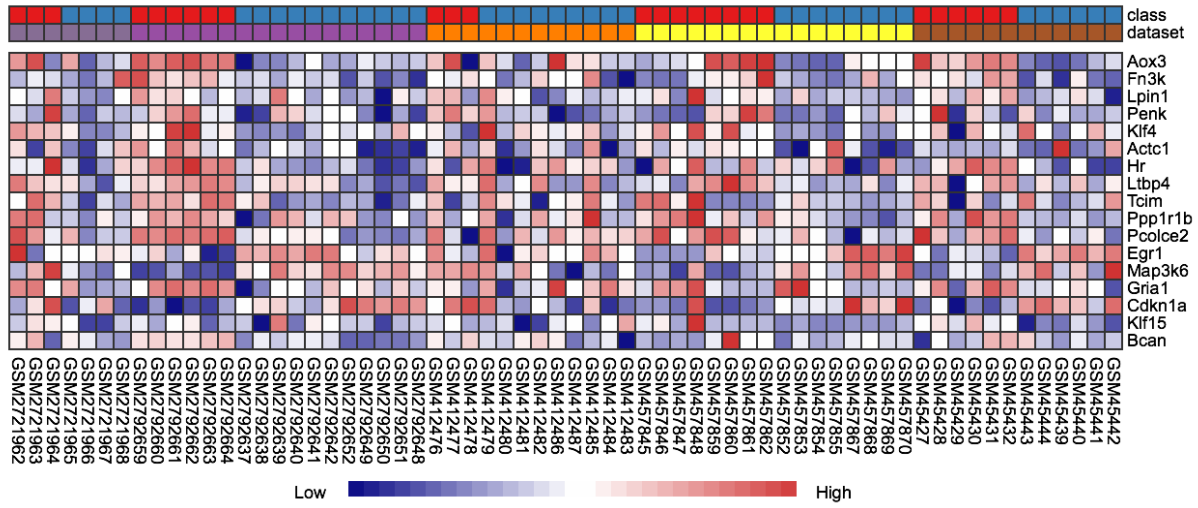
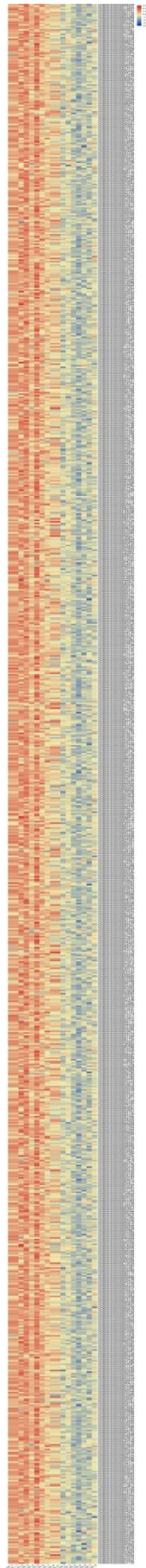


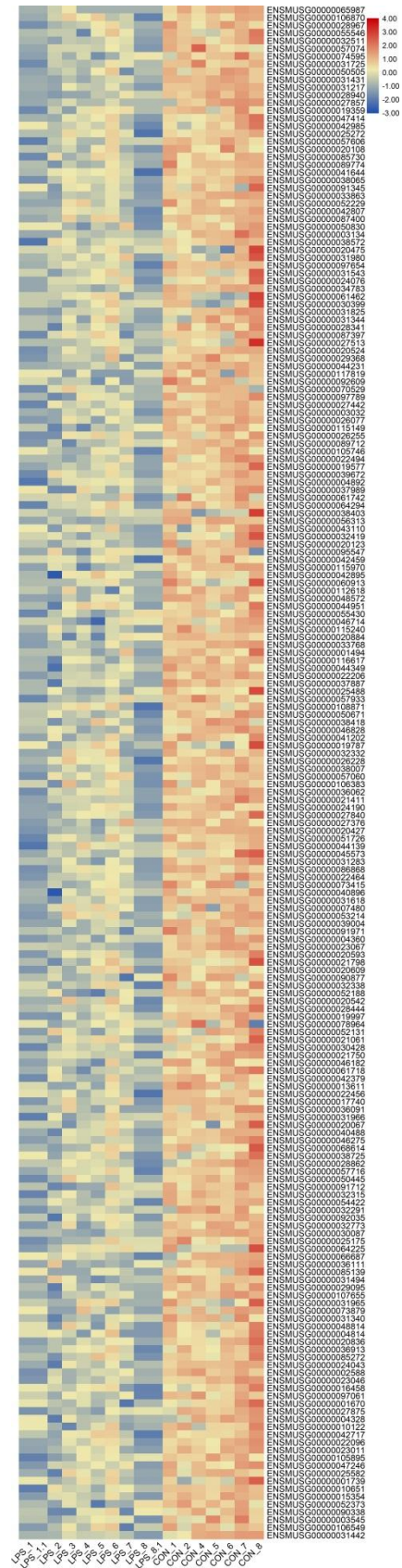
SUPPLEMENTARY FIGURES



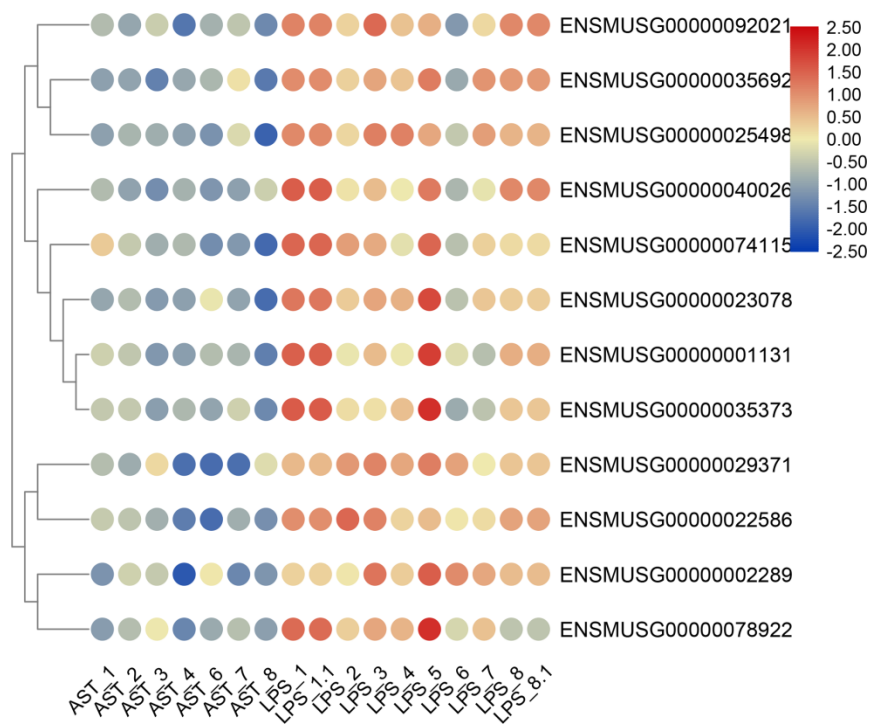
Supplementary Figure 1. Heat map of the 17 overlapping downregulated genes identified by both meta-analysis of published microarrays and our RNA sequencing experiments (control group vs. LPS group).



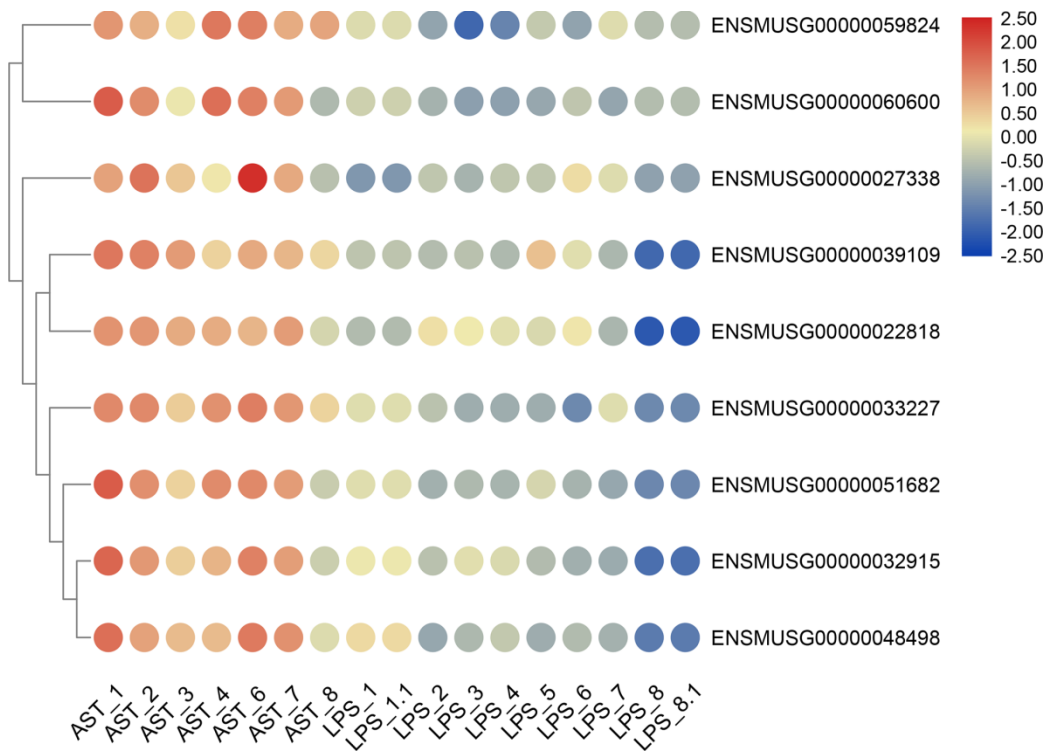
Supplementray Figure 2-1. Heat map of the 989 significantly upregulated genes in the LPS group compared to the control group identified by RNA sequencing.



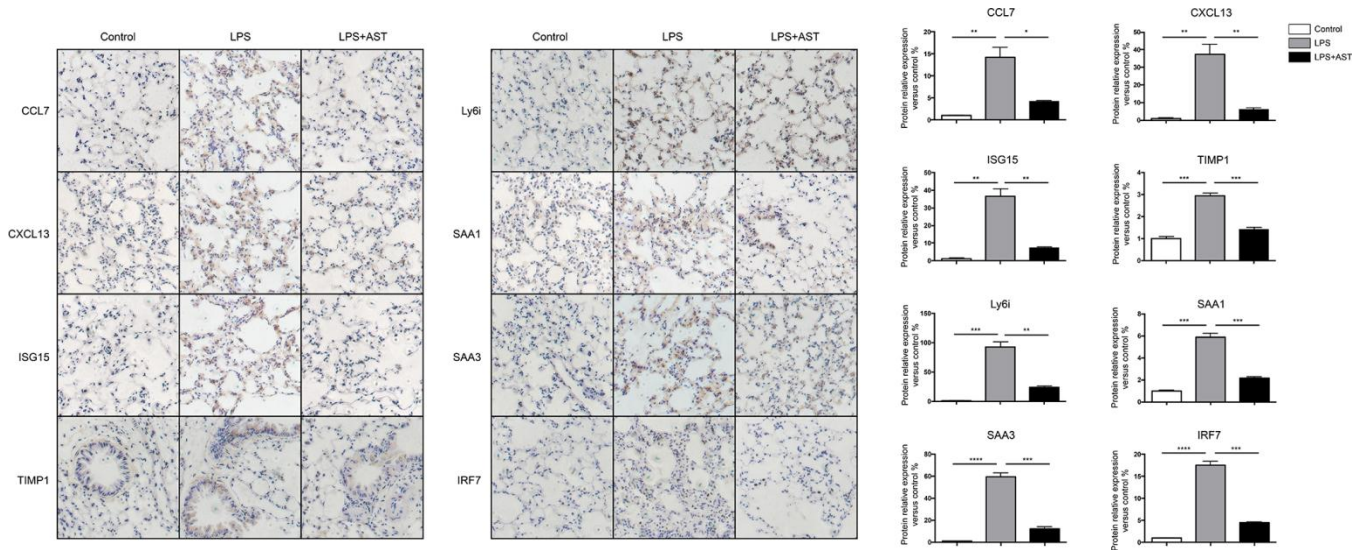
Supplementary Figure 2-2. Heat map of the 198 significantly downregulated genes in the LPS group compared to the control group identified by RNA sequencing.



Supplementary Figure 3-1. Heat map of the 9 significantly upregulated genes in the AST group compared to the LPS group identified by RNA sequencing.



Supplementary Figure 3-2. Heat map of the 12 significantly downregulated genes in the AST group compared to the LPS group identified RNA sequencing.



Supplementary Figure 4. Expression of the 8 core genes (*Ccl7*, *Saa3*, *Ly6i*, *Saa1*, *Irf7*, *Timp1*, *Isg15* and *Cxcl13*) determined by immunohistochemistry. Statistical analysis of the differences between groups was achieved with one-way ANOVA using Prism 7 software. ****p < 0.0001, ***p < 0.001, **p < 0.01, and *p < 0.05 were considered statistically significant.