

Sample				Total		Proper	
name	Raw reads	Clean Reads		Map		Map	
Mock-1	45332750	44743638	39590302	88.48%	36178764	80.86%	
Mock-2	81332450	80048738	69686755	87.06%	58175438	72.68%	
WSN	39496130	39074648	36448824	93.28%	33729024	86.32%	
WSN	45434642	44840648	41708707	93.02%	37800180	84.3%	
WSN	44262588	43624318	40572579	93.00%	37350580	85.62%	
WSN ad	39348744	38937330	36336954	93.32%	33220074	85.32%	
NS80	45552098	44983290	41681965	92.66%	38507578	85.6%	
NS80	40565552	40076928	36917427	92.12%	34146938	85.2%	
NS80	51294628	40739584	36615148	89.88%	33468954	82.15%	
NS80 ad	42170062	41539672	38674653	93.1%	35616364	85.74%	
NS80 ad	50142384	49519296	45826736	92.54%	42299136	85.42%	
NS80 ad	43139690	42753362	39745264	92.96%	36903794	86.32%	

**Table S1.** Summary of data obtained from the sequenced RNA-seq libraries.

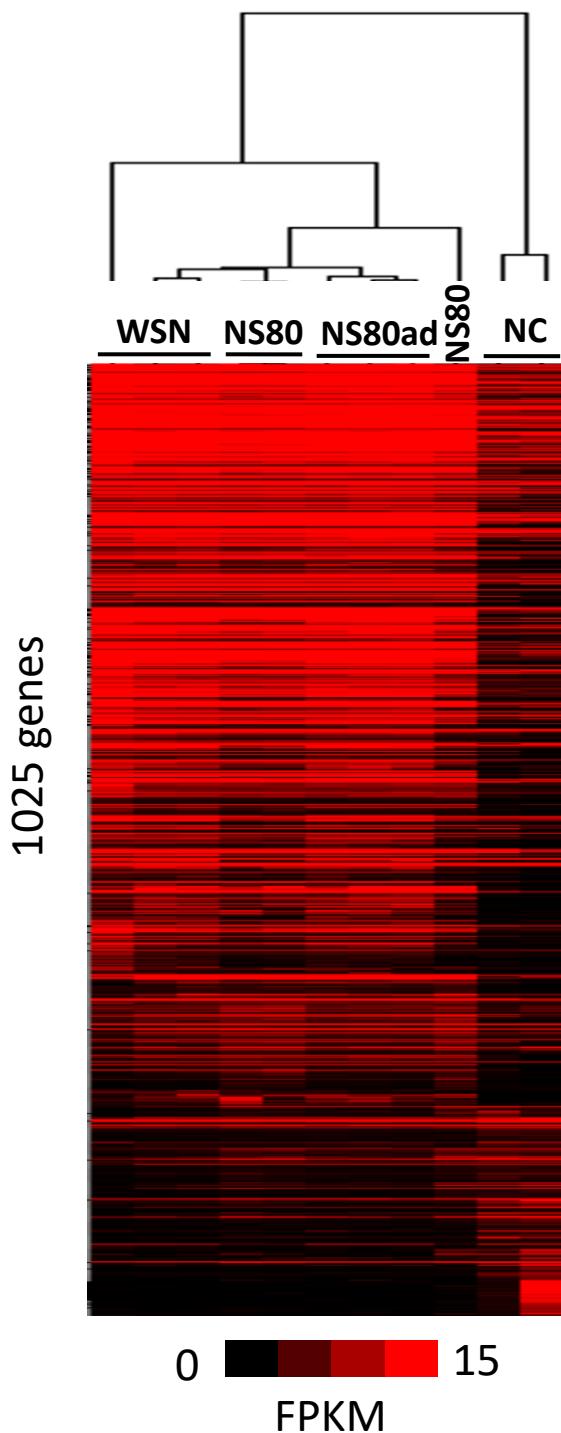
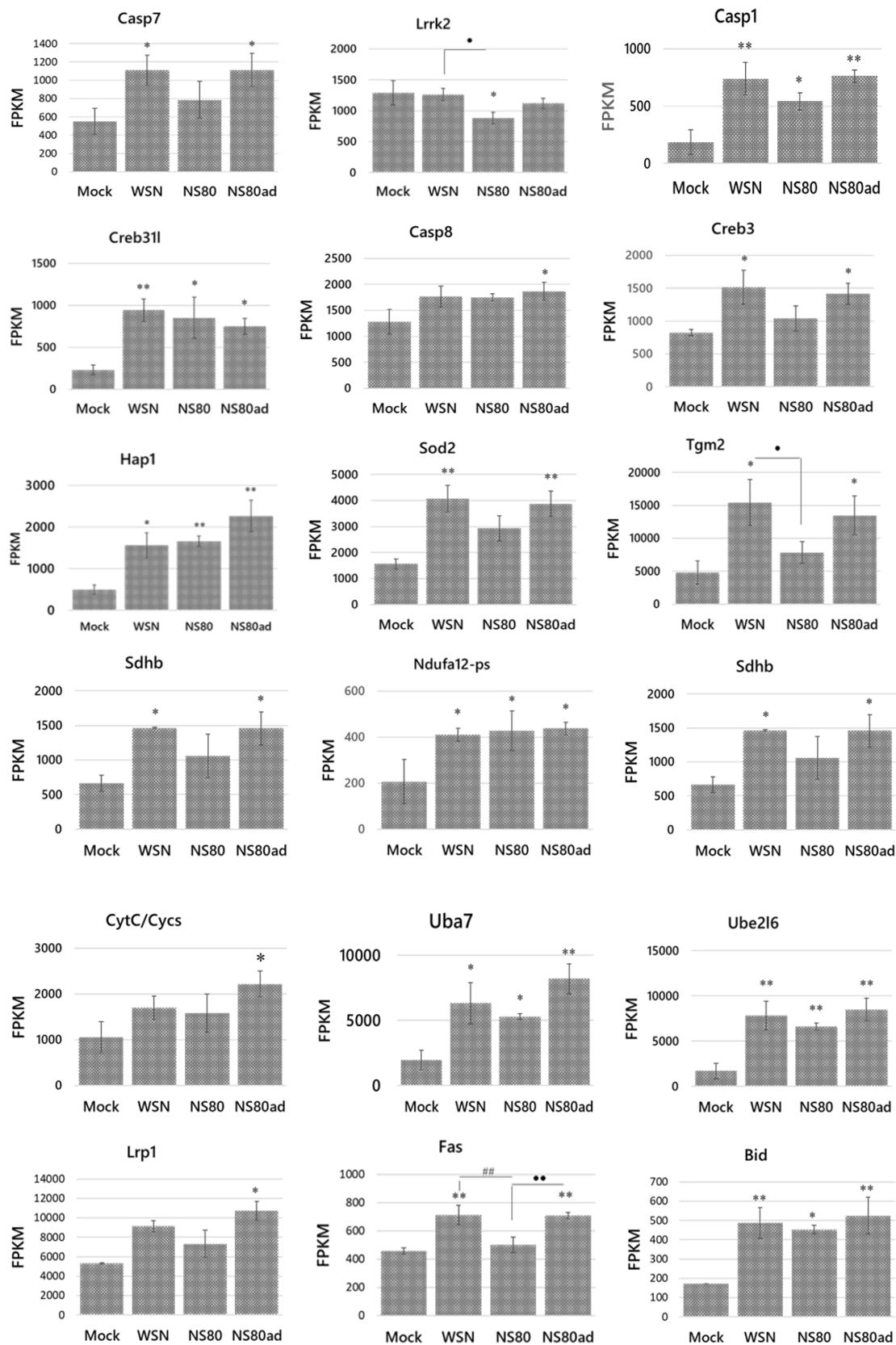
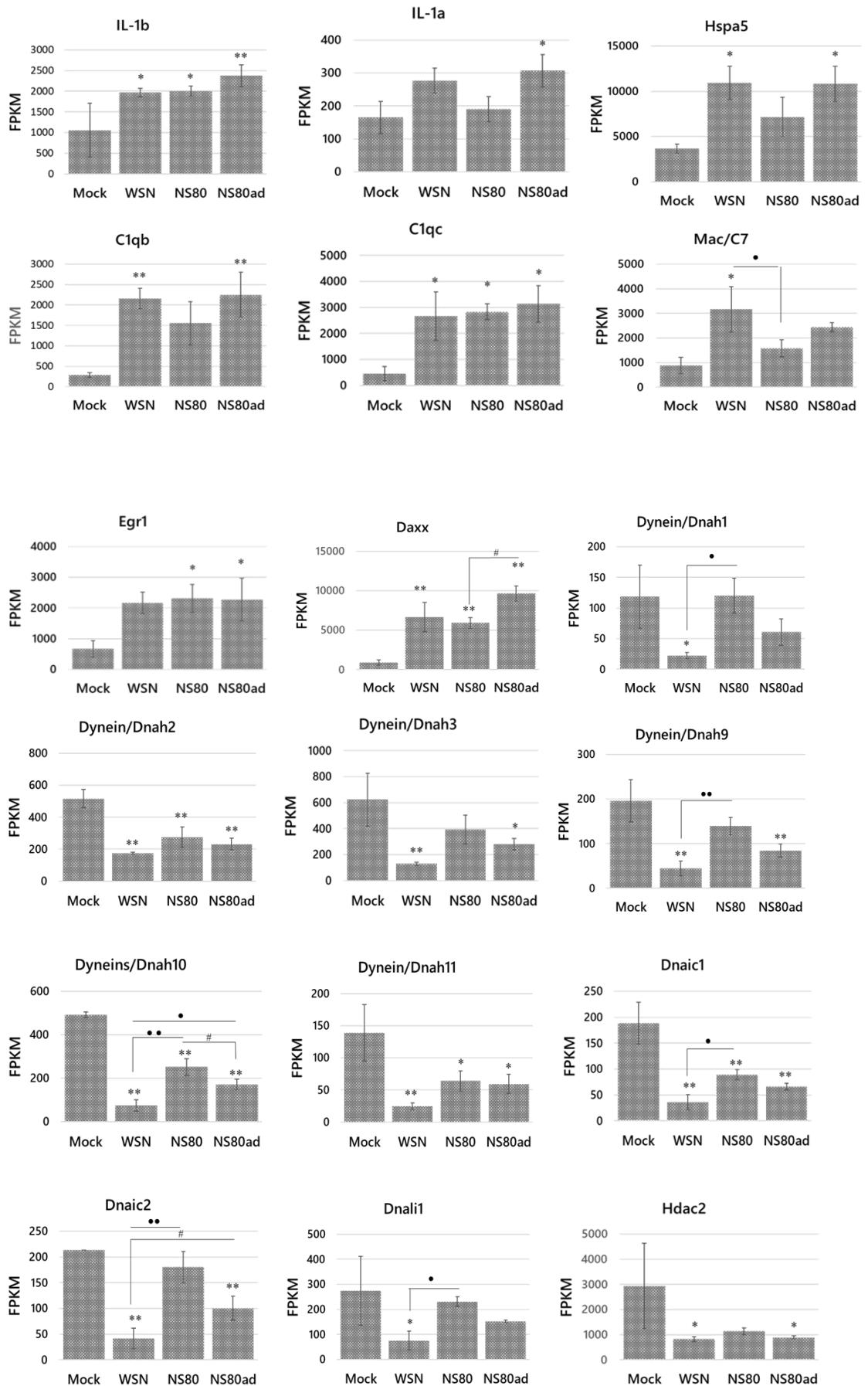


Figure S1. Hieratical clustering of FPKM values from lungs infected with WSN, NS80, NS80ad and uninfected control (NC). Selection of 1025 genes was done by comparing expression value between WSN and NS80 infected cells relative to uninfected controls (Figure 2A).





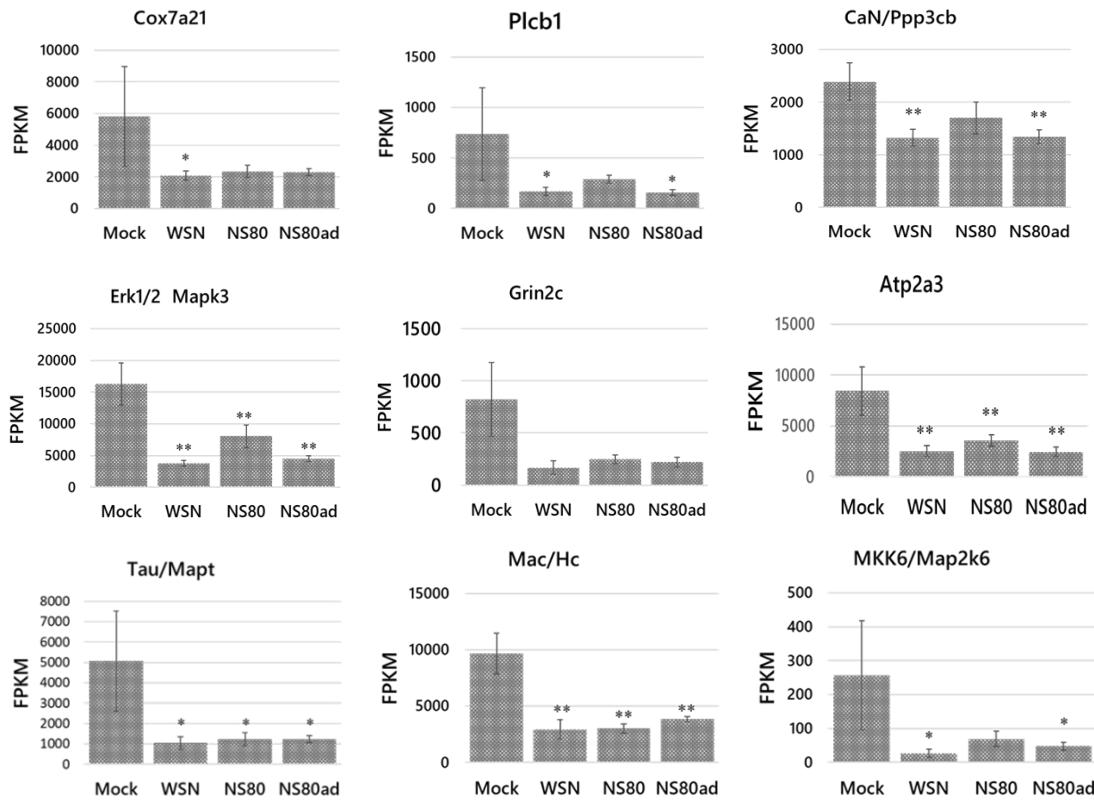


Figure S2. The FPKM values obtained from RNA seq data analyses from brains (n=3) infected with WSN (n=3), NS80 (n=3), and NS80ad(n=3). Data are presented as the mean  $\pm$  SD. Data were statistically evaluated using one-way ANOVA and post hoc Tukey's HSD test; #, •, \* p < 0.05; ••, \*\* p < 0.01; \*\*\* p < 0.001.