Supplemental Figure 1A

Supplemental Figure 1B

Early infection-expressed genes

Defense response, inflammatory response, immune response

BTLA, CCL2, CCR5, CXCR6, CD62, CD180, EGF, IFNAR2, IL-1RL1, IL-6, IL-18R1, TLR7, TNFRSF17

Mid infection-expressed genes

Immune response, response to wounding, cytokine activity, defense response

CCL3, CCL3L1, CCL3L3, CCL7, CCL17, CD274, CEBPB, CLEC4A, CLEC4D, CLEC5A, CSF2RA, CSF2RB, CXCR1, DEFB1, IFNGR2, IL-1B, IL-1RAP, IL-1RA, IL-13RA1, IL-15RA, IL-18R1, IL-27, LILRB4, LTB4R, LY96, MR1, PDCD1LG2, PTX3, SOCS3, TLR2, TLR4

Late infection-expressed genes

Regulation of blood coagulation

ANXA8L2, CCL18, PLAU, PLG, SAA1, SAA2

Early   Mid   Late

log$_2$-fold

-3 -2 -1 0 1 2 3

down-regulated   up-regulated
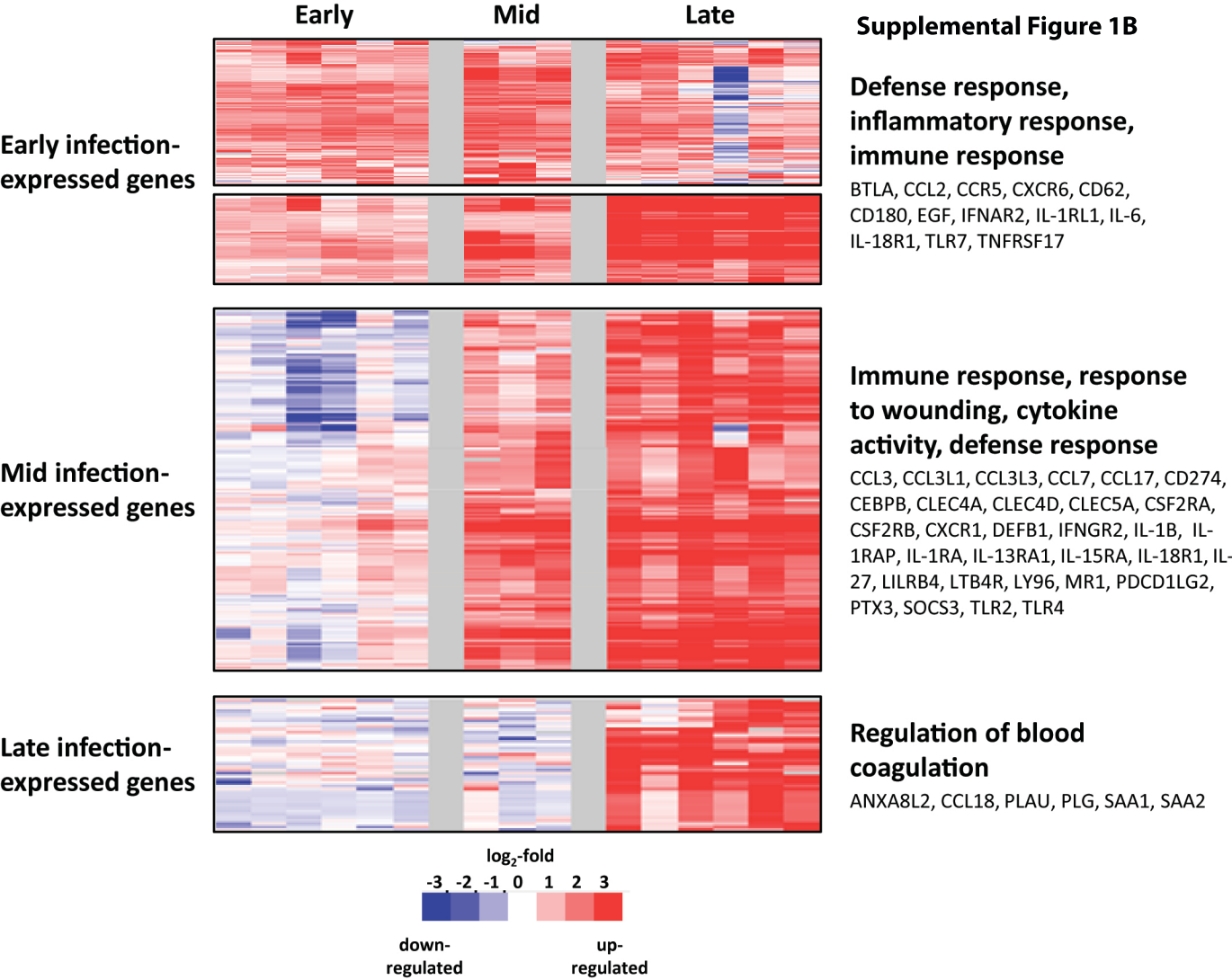
A

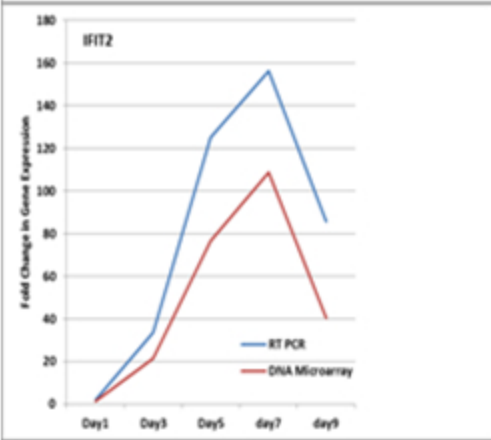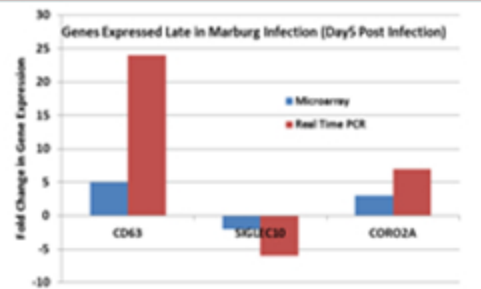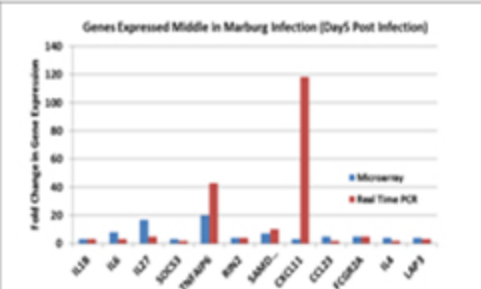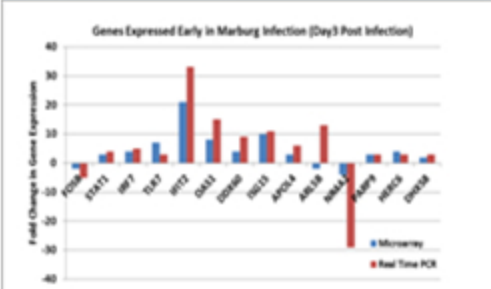| EARLY (DAY 3)	Microarray	Real Time PCR		MIDDLE (DAY 5)	Microarray	Real Time PCR		LATE (DAY 9)	Microarray	Real Time PCR
FOSB	-2	-5		IL1B	3	3		CD63	5	24
STAT1	3	4		IL6	8	3		SIGLEC10	-2	-6
IRF7	4	5		IL27	17	5		CORO2A	3	7
TLR7	7	3		SOCS3	3	2				
IFIT2	21	33		TNFAIP6	20	43				
OAS1	8	15		RIN2	4	4				
DDX60	4	9		SAMD4A	7	10				
ISG15	10	11		CXCL11	3	118				
APOL4	3	6		CCL23	5	2				
ARL5B	-2	13		FCGR2A	5	5				
NR4A2	-4	-29		IL4	4	2				
PARP9	3	3		LAP3	4	3				
HERC6	4	3								
DHX58	2	3								

B
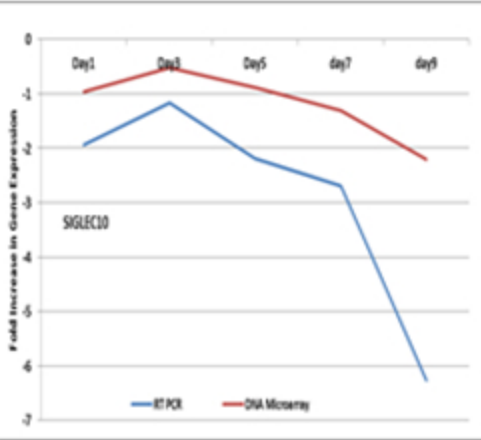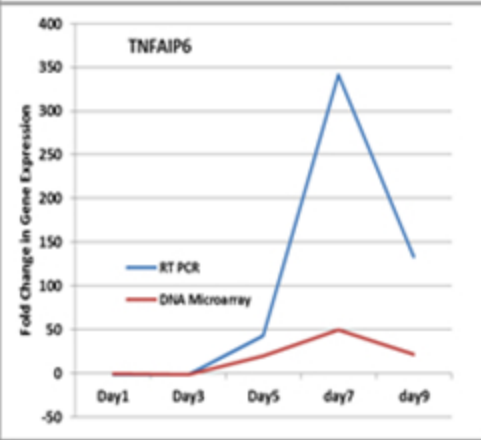
Figure S1. Temporal changes in gene expression following aerosol exposure to MARV.

(A) Heatmap illustrating 1213 hierarchically clustered genes that showed at least a 2 $\log_2$-fold change in the differential gene expression following MARV exposure. Each row in the heatmap represents data from an individual gene, and each column represents the individual PBMC sample taken at a 1,3,5,7 or 9 postexposure (changes in gene expression are relative to the pre-infection control). Samples from the dataset were grouped into early (days 1–3), middle (day 5) and late (days 7-9) stages of infection . Major gene clusters are denoted by the colored vertical bars to the left of the heatmap and are labeled with DAVID-identified significant (p-value <0.001) functional groups to the right of that cluster. (B) The most significant functional groups (assigned by DAVID, p-value <0.001) found in major gene clusters are listed to the right of the heatmaps, along with the names of some representative genes. Red and blue colors denote expression levels greater or less than baseline (white), respectively.

Figure S2. Validation of mRNA changes observed in microarray through rt-PCR. A subset of mRNAs were selected for validation with rt-PCR from samples taken early (day 3 PE) during the middle of infection (day 5 PE) or late in infection (day 9 PE). (a) Fold Change in gene expression during early (left), mid (center) and late (right) MARV infection determined by microarray analysis (blue) and rtPCR assay (red). (B) The agreement of microarray and rtPCR gene expression trends throughout the time course of infection is illustrated using three different genes, IFIT2 (an up-regulated gene, left) TNFAIP (an up-regulated gene, center), and SIGLEC10, a down-regulated gene (right). Microarray values are shown in red, rtPCR values in blue.