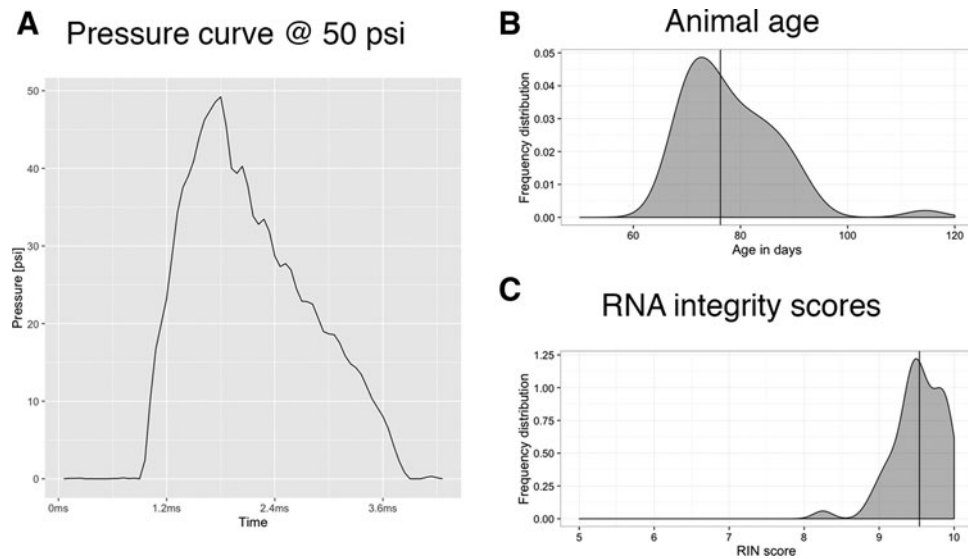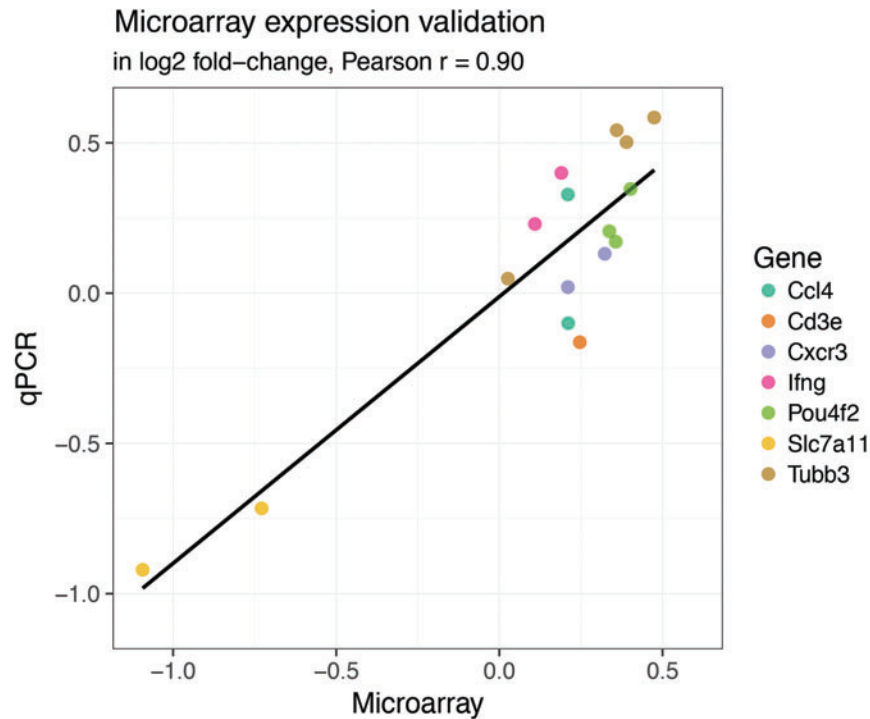# Supplementary Data

SUPPLEMENTARY FIG. 1. **(A)** A typical pressure curve produced by the blast gun. **(B)** Distribution of animal age for blast samples. **(C)** Distribution of ribonucleic acid (RNA) integrity number (RIN) scores for blast samples. The vertical line in (B) and (C) represents the median.

Microarray expression validation
in log2 fold–change, Pearson r = 0.90

Gene	Strain	Microarray FC	qPCR FC
Cd3e	BXD27	0.246	−0.163
Tubb3	BXD27	0.026	0.048
Pou4f2	BXD42	0.337	0.206
Tubb3	BXD42	0.360	0.542
Slc7a11	BXD75	−1.093	−0.921
Pou4f2	BXD75	0.357	0.171
Tubb3	BXD75	0.390	0.502
Slc7a11	BXD85	−0.728	−0.716
Pou4f2	BXD85	0.402	0.347
Tubb3	BXD85	0.474	0.584
Cxcr3	B6	0.323	0.131
Ccl4	B6	0.210	0.328
Ifng	B6	0.190	0.400
Cxcr3	D2	0.210	0.020
Ccl4	D2	0.211	−0.100
Ifng	D2	0.109	0.230

Primers used (5' --> 3')

Slc7a11 fw	GGTGTGTAATGATAGGGCAGCA
Slc7a11 rev	CGGTCGTGACTTCCCCTTTG
Cd3e fw	TCTGGGCTTGCTGATGGTCAT
Cd3e rev	GTTCCTCGGGTCACAGGCTT
Ifng fw	TCAGCAACAGCAAGGCGAAA
Ifng rev	GCGACTCCTTTTCCGCTTCC
Pou4f2 fw	TGAACCCAGACCAAGCCAGG
Pou4f2 rev	GGTGCAGTTAAAGGGGACAGC
Tubb3 fw	CCTTTTCGTCTCTAGCCGCG
Tubb3 rev	CCTATCTGGTTGCCGCACTG
Ccl4 fw	CAAACCTAACCCCGAGCAACA
Ccl4 rev	GCAGGAAGTGGGAGGGTCAG
Cxcr3 fw	ACCAGCCAAGCCATGTACCTT
Cxcr3 rev	CGTAGGGAGAGGTGCTGTTTT

SUPPLEMENTARY FIG. 2. Validation of microarray expression data and samples/primers used. qPCR-derived fold changes values were $\log_2$ transformed and plotted against microarray expression data. There is good agreement of qPCR and microarray data (Pearson's $r = 0.90$). PCR, polymerase chain reaction.
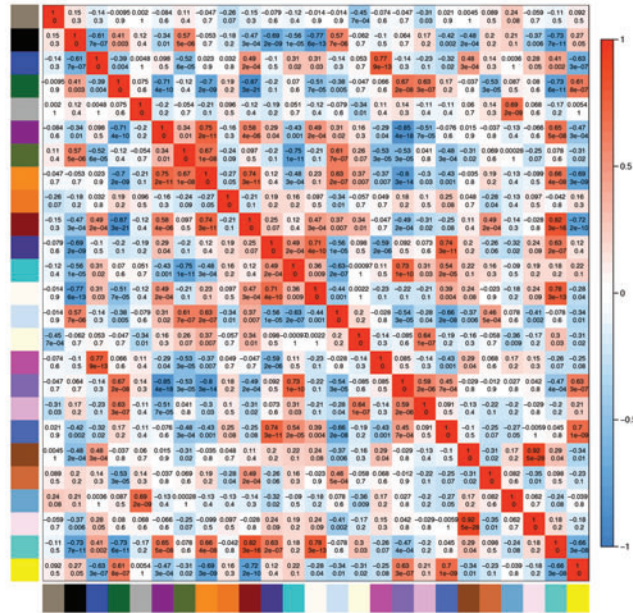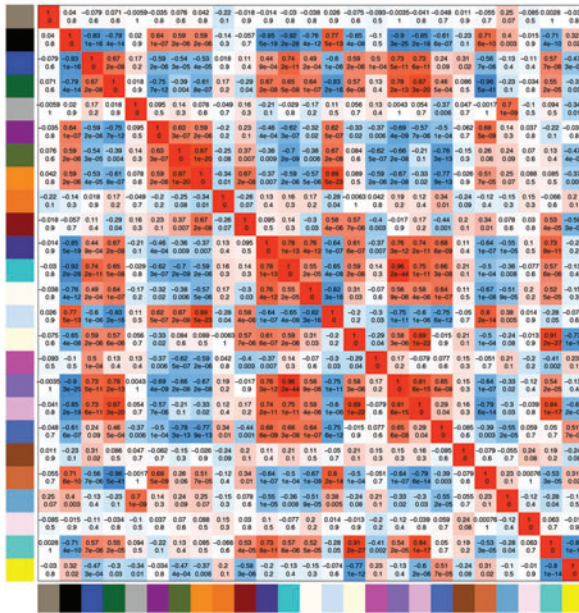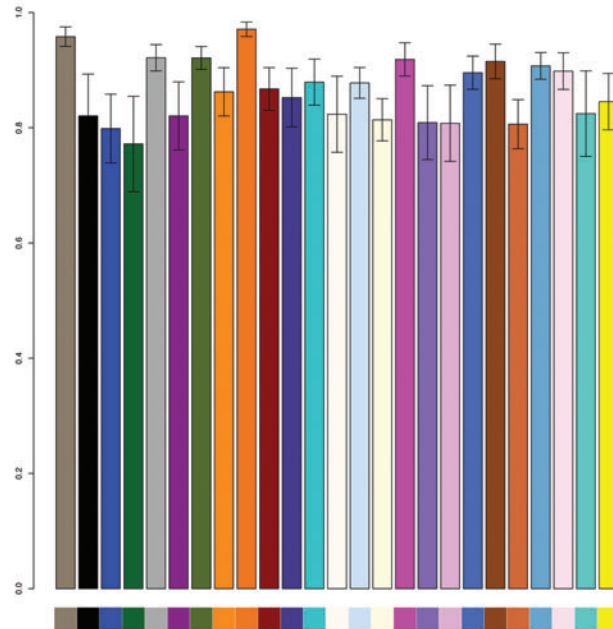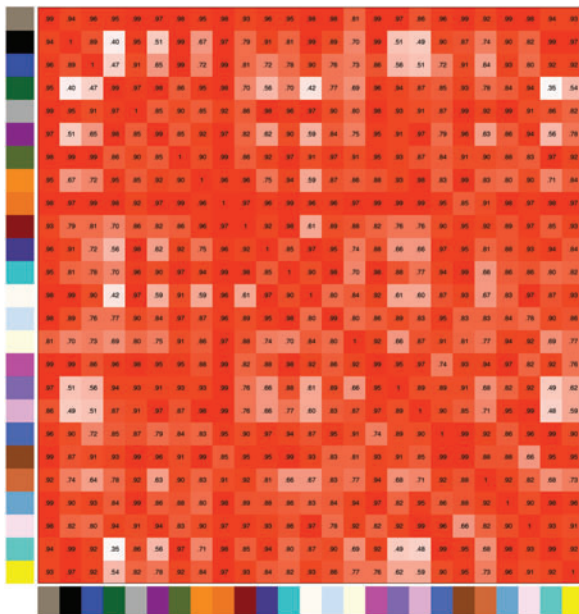
SUPPLEMENTARY FIG. 3. Top: Correlation matrices of weighted gene co-expression network analysis (WGCNA) modules identified for the blast and normal datasets. The colors on the *x*- and *y*-axis represent the module. Bottom left: Module eigengene preservation between both conditions. Lower values indicate higher intermodular changes. Bottom right: Module eigengene correlation between both condition. Lower values indicate stronger intramodular changes between conditions.