Supplemental Material

Methods:

Determination of *S. aureus* load in tissues by quantitative PCR (qPCR):

For real-time PCR detection, log phase culture of *S. aureus* (10^9 CFU) was serially diluted and DNA was isolated by previously described protocol with minor modifications [1]. Briefly, bacterial cells were harvested lysed in 100 µl of NET buffer (50 mM NaCl, 125 mM EDTA, 50 mM Tris-HCl [pH 7.6]) containing 50 µl of 2.6 N NaOH solution and 100 µl of 24% sodium dodecyl sulphate (SDS; final concentration 3.4%). Lysates were incubated at 80°C for 10 min. and cooled to room temperature before adding proteinase K (200 µg/ ml) for digestion (50°C for 1.5 hour). DNA extracted from the lysates by standard phenol-chloroform, precipitated with isopropanol was quantified at A260 for analysis by real-time PCR to generate a standard curve (Bacterial CFU versus Ct value; Supplemental figure 1). To determine the *S. aureus* load in tissues, bacterial DNA isolated from the infected host tissue samples using the above protocol were subjected to real-time PCR. The Ct values thus obtained were used to determine the CFU in infected tissues from the standard curve generated as described above. For detection of *S. aureus* strain in brain, different parts of brain tissues like hippocampus, prefrontal and cerebral cortex, cerebellum, brain stem, parts of midbrain were mixed and homogenised.

Extracted *S. aureus* DNA was subjected to real-time PCR using primer that targets Staphylococcus 16S rRNA gene STPY [2]. The sequences of the primers used are provided below:

STPYF: 5'-ACGGTCTTGCTGTCACTTATA-3' and

STPYR2: 5'- TACACATATGTTCTTCCCTAATAA-3'

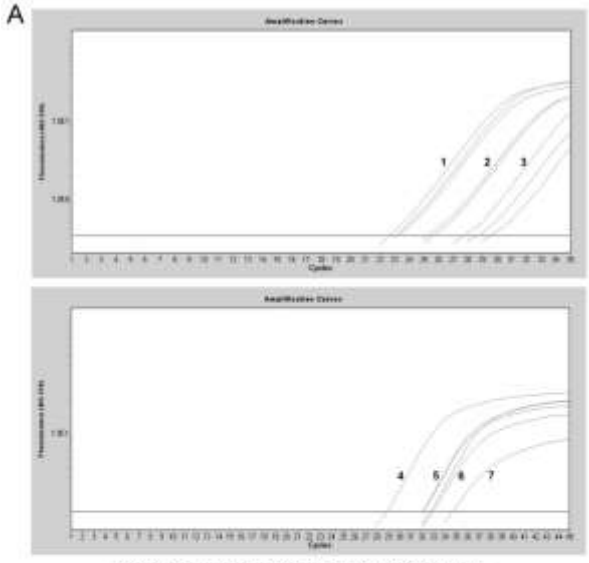
Real-time PCR was performed using 2X SYBR green master mix (KAPA SYBR FAST kit, KAPA BIOSYSTEMS, USA) in Light Cycler® 480 real-time PCR machine (Roche, Germany) with 1 µl of DNA samples in 10 µl reaction volume for 35 cycles of amplification [denaturation at 95°C for 10 sec; annealing at 57°C for 20 sec; extension at 72°C for 2 sec].

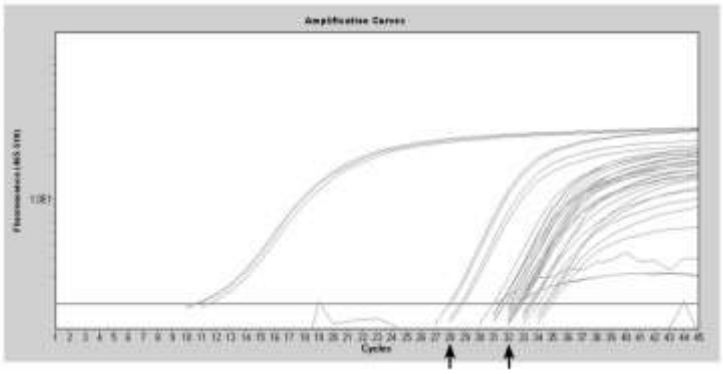
References:

[1] Romero C, Lopez-Goñi I. Improved method for purification of bacterial DNA from bovine milk for detection of Brucella spp. by PCR. Appl Environ Microbiol. 1999; 65:3735-7

[2] Johnson EJ, Zemanick ET, Accurso FJ, Wagner BD, Robertson CE, Harris JK. Molecular identification of Staphylococcus aureus in airway samples from children with cystic fibrosis. PLoS One 2016; 11:1–12. doi:10.1371/journal.pone.0147643.

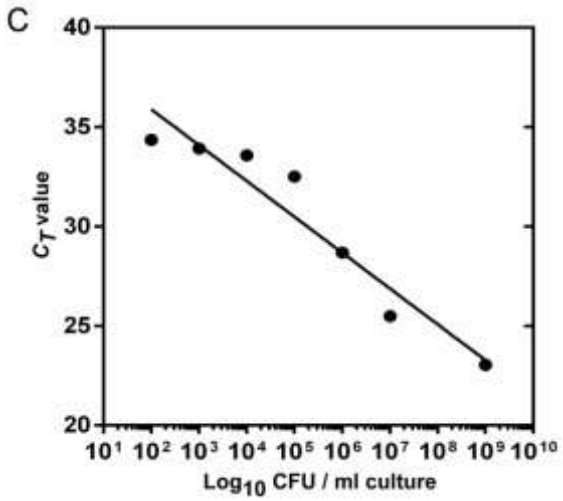
Supplementary Figure 1: Real time PCR amplification curve and standard curve for determination of bacterial load in tissues. (A) Amplification curves of real-time PCR generated for determination of C_T values for *S. aureus* STPY gene. Genomic DNA isolated from serially diluted log phase culture (10^9 CFU) of *S. aureus* were used for amplification using STPY gene specific primers. Intercept of the magnitude of the fluorescence signal with the horizontal threshold line represents the C_T value.





Information used for preparation of standard curve

Curve ID	Sample (CFU/ml of *S. aureus*)	C_T value
1	1×10^9	23.05
2	1×10^7	25.50
3	1×10^6	28.69
4	1×10^5	32.51
5	1×10^4	33.58
6	1×10^3	33.92
7	1×10^2	34.36



Number indicated in two graphs were curve ID of samples (10^9 CFU-10^2 CFU *S. aureus*), used for plotting the standard curve. All the corresponding C_T values were listed in the table. (B) Amplification

curve of real-time PCR showing corresponding C_T values for STPY gene products in spleen and blood samples indicated by arrows. (C) Standard curve for determination of bacterial load in tissues was generated by plotting C_T values from real-time PCR vs CFU per ml of culture. Each point represents the amount of DNA present in a given CFU of *S. aureus* corresponding to the C_T value. CFU = Colony Forming Unit.

Supplementary Figure 2

Histone acetylation and tyrosine hydroxylase expression profile in hippocampus of control animals with spectinomycin [Spec (+)] versus without spectinomycin [Spec (-)]. **(A)** Specific acetylated residues **(**K9, K27 and K14) of histone H3 were examined separately on immunoblots to quantify the residue-specific acetylation with respect to the total histone H3. Data presented as mean ± SEM. **(B)** Tyrosine hydroxylase (TH) protein expression in control animals with Spec vs without Spec. TH band intensities were normalized by GAPDH signal. (n = 4). Data was presented as mean ± SEM. Spec = Spectinomycin.