



Supplemental Figure S9. Statistical evaluation of LSV1, BQCV, Nosema, *C. mellificae* / *L. passim* abundance and colony health.

Honey bee colony health, pathogen prevalence (PCR) and pathogen abundance (qPCR) was monitored from January - March 2013. (Supplemental Table S3). Samples were obtained from six honey bee colonies at 3 or 4 different time points (n=6 colonies, 20 total sampling events). Overall weak colonies (< 5 frames, n=9 sampling events) had greater levels of pathogens relative to strong colonies (>9 frames, n=11 sampling events). The mean abundance of LSV2 was greater in weak colonies ($\log_{10}=7.55$) as compared to strong colonies ($\log_{10}=3.19$, $p=8.89 \times 10^{-5}$) (Figure 7). Likewise weak colonies had a higher mean abundances of (A) LSV1 (weak $\log_{10}=6.83$ vs. strong $\log_{10}=4.00$, $p=1.60 \times 10^{-3}$), (B) BQCV (weak $\log_{10}=6.25$ vs. strong $\log_{10}=4.06$, $p=7.57 \times 10^{-3}$), and (C) Nosema ceranae, (weak $\log_{10}=4.17$ vs. strong $\log_{10}=2.71$, $p=1.15 \times 10^{-3}$), whereas levels of (D) trypanosmatids (*C. mellificae* / *L. passim*) were not statistically different (weak $\log_{10}=2.40$ vs. strong $\log_{10}=2.60$, $p=0.35$) using a Welch Two Sample t-test to compare the mean pathogen abundance (\log_{10} qPCR copy number) in weak versus strong colonies.