



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) trypanosomatids (*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.