



**Supplemental Figure S8. LSV1, BQCV, *Nosema*, *C. mellificae* / *L. passim* qPCR data plotted against colony health.**

Honey bee colony health and pathogen prevalence and abundance (n=6) was monitored from January – March 2013.

Honey bee colonies that were weak (< 5 frames, n=3) at the onset of the study are labeled W1, W2, and W3, and colonies

that were healthy (>9 frames, n=3) at the onset of the study are labeled S1, S2, and S3. Quantitative-PCR was used to

determine pathogen abundance of **A.** LSV1, **B.** BQCV, **C.** *Nosema ceranae*, and **D.** *C. mellificae* / *L. passim* throughout the course of the study.

Overall weak colonies had higher levels of LSV2, LSV1, and BQCV.