SUPPLEMENTARY INFORMATION FOR:

Intensity of *Nosema ceranae* infection is associated with specific honey bee gut bacteria and weakly associated with overall gut microbiome structure

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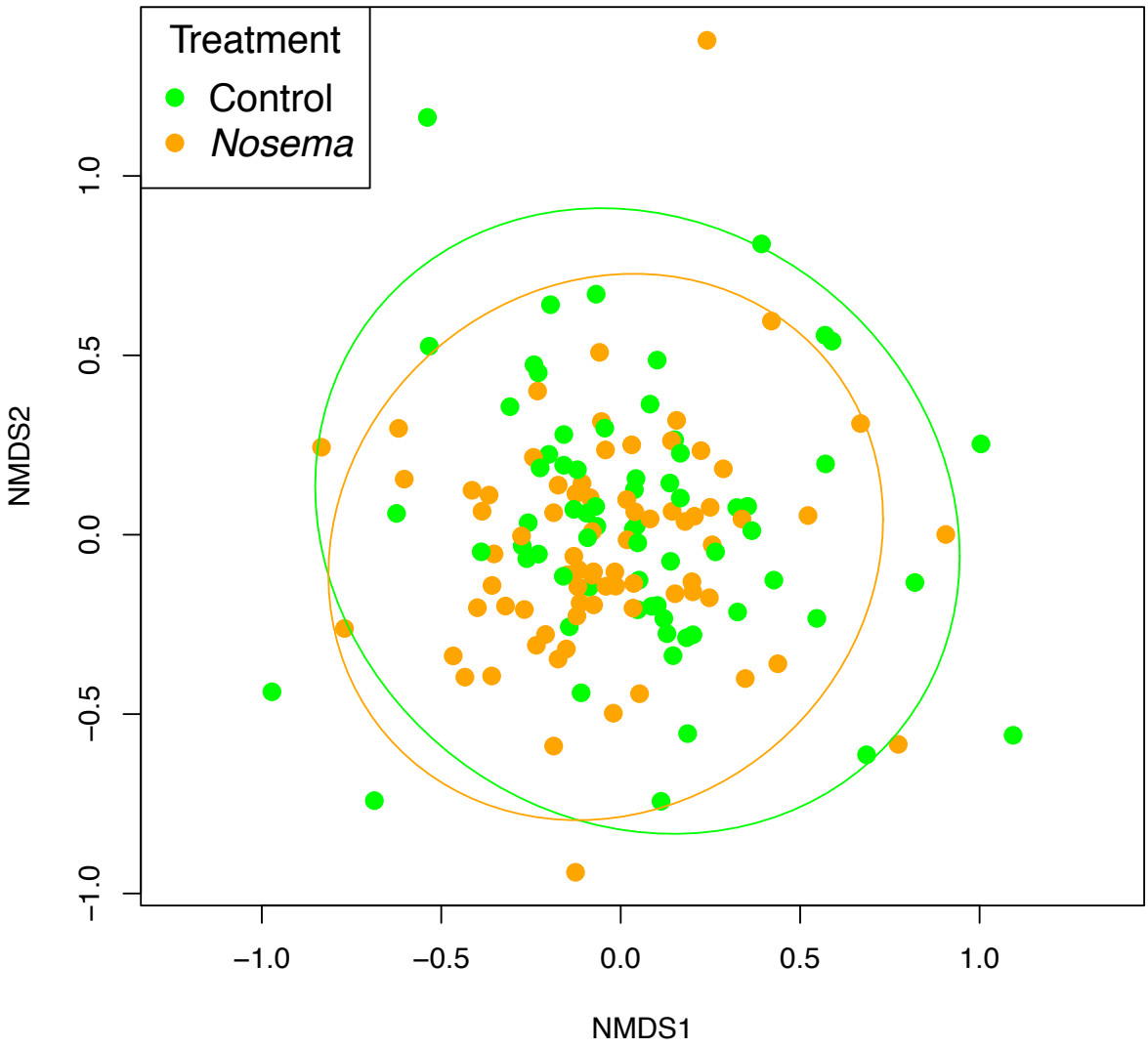

Fig. S1. NMDS ordination of Bray-Curtis distances of gut microbiota composition showed no significant difference in control versus infected bees (Adonis $F_{1,142} = 0.91$, $P = 0.56$).

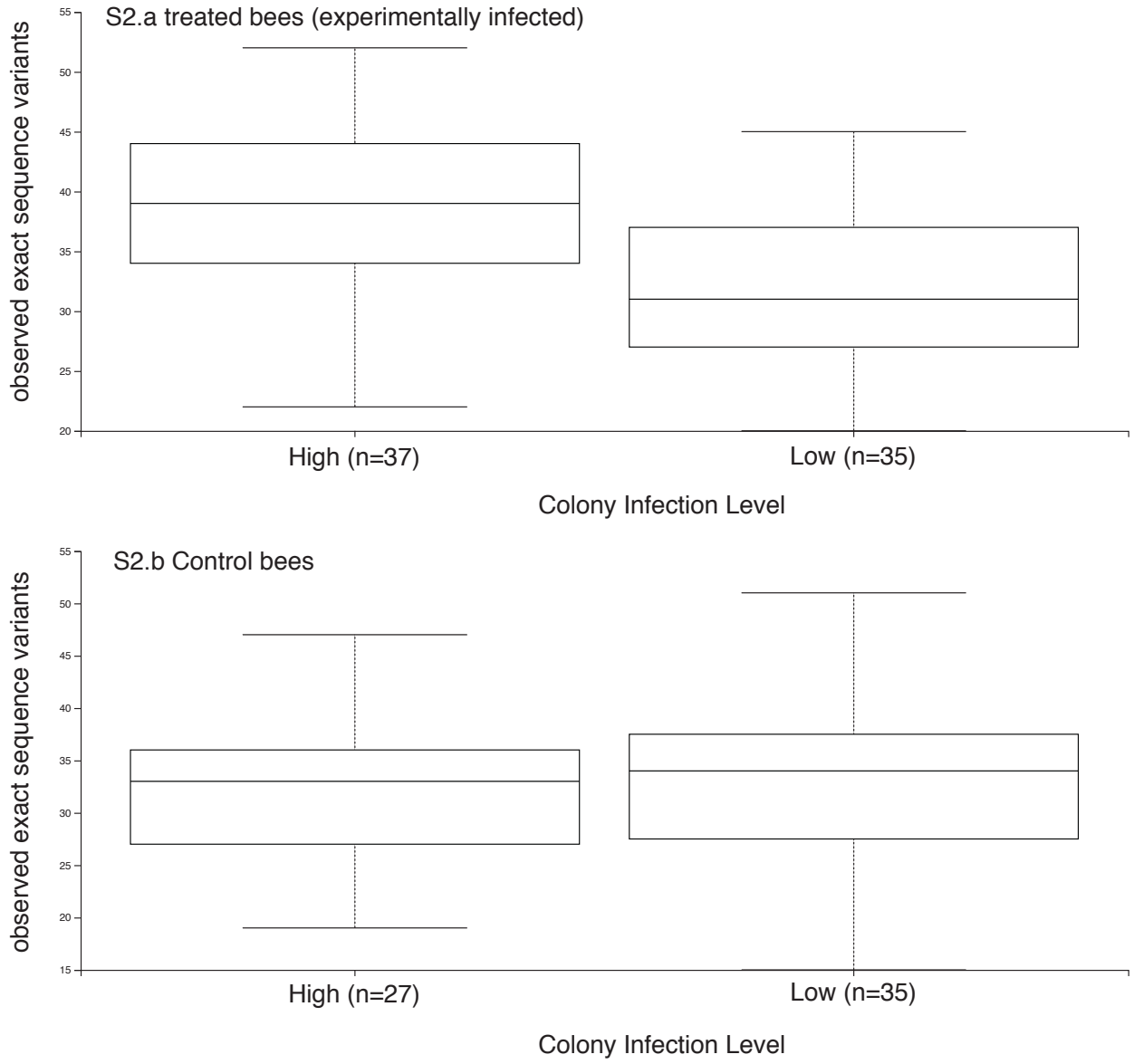

Fig. S2. For *Nosema* treated samples, high infection level colonies exhibited more ESVs per sample compared to low infection colonies (Fig. S2.a, Kruskal-Wallis $H_{71} = 12.07$, $P < 0.0006$). For control bees alpha diversity did not differ between high and low infection level colonies (Fig. S2.b, Kruskal-Wallis $H_{64} = 0.12$, $P = 0.75$).

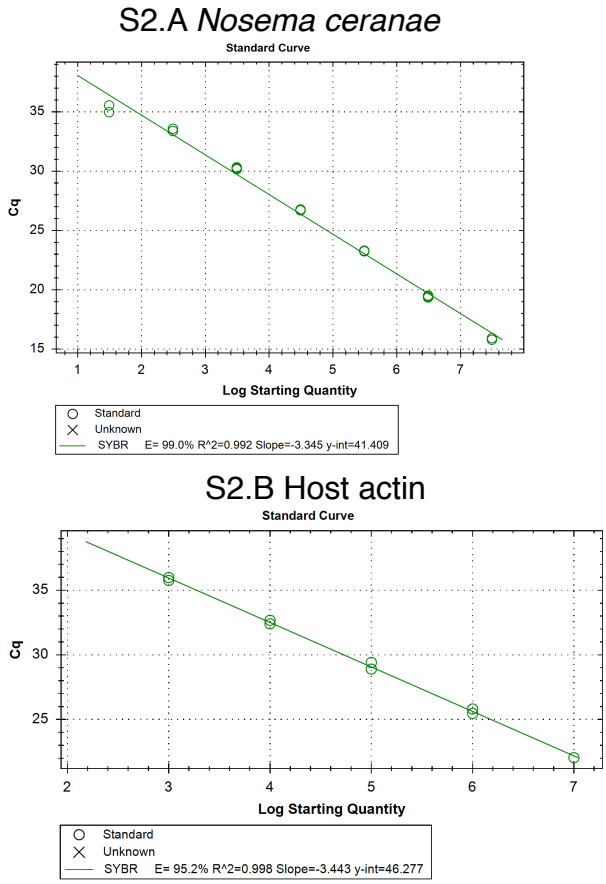

Fig. S3. Example standard curves showing qPCR amplification efficiency (calculated by the BioRad CFX manager software). All efficiencies ranged between 90-110% with most in the mid 90% range.