|  | # bees | LSV1 | LSV2 | LSV3 | BQCV | DWV | *C.m./L.p.* | *Nosema* |
|---|---|---|---|---|---|---|---|---|
| **Rep 1** | 50 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
|  | 25 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
|  | 15 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
|  | 10 | 1 | 0 | 1 | 1 | 1 | 1 | 1 |
|  | 5 (set 1) | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
|  | 5 (set 2) | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
|  | 1 (set 1) | 1 | 0 | 1 | 1 | 1 | 1 | 1 |
|  | 1 (set 2) | 1 | 1 | 1 | 1 | 1 | 1 | 1 |

|  | # bees | LSV1 | LSV2 | LSV3 | DWV | *Nosema* |
|---|---|---|---|---|---|---|
| **Rep 2** | 50 | 1 | 1 | 1 | 0 | 0 |
|  | 25 | 1 | 1 | 1 | 0 | 1 |
|  | 15 | 1 | 1 | 1 | 0 | 1 |
|  | 10 | 1 | 1 | 1 | 0 | 1 |
|  | 5 (set 1) | 1 | 1 | 1 | 0 | 0 |
|  | 5 (set 2) | 1 | 1 | 1 | 0 | 0 |
|  | 1 (set 1) | 1 | 1 | 0 | 0 | 0 |
|  | 1 (set 2) | 1 | 1 | 1 | 0 | 0 |

|  | # bees | LSV1 | LSV2 | DWV | *Nosema* |
|---|---|---|---|---|---|
| **Rep 3** | 30 | NA | 1 | 1 | 0 |
|  | 5 (set 1) | 1 | 1 | 1 | 1 |
|  | 5 (set 2) | 1 | 1 | 1 | 1 |
|  | 5 (set 3) | 1 | 1 | 1 | 0 |

**Supplemental Table S6. Three replicates of pathogen detection in variable numbers of honey bees from a single colony.** The quantity of bees indicated in this table were processed as described in Supplemental Figure S10 / Methods. cDNA was prepared from these RNA samples, and was used in PCR for the pathogens listed above. 1 = pathogen detected; 0 = pathogen not detected; NA = pathogen not tested. Data from replicate 1 were presented in Supplemental Figure S10.