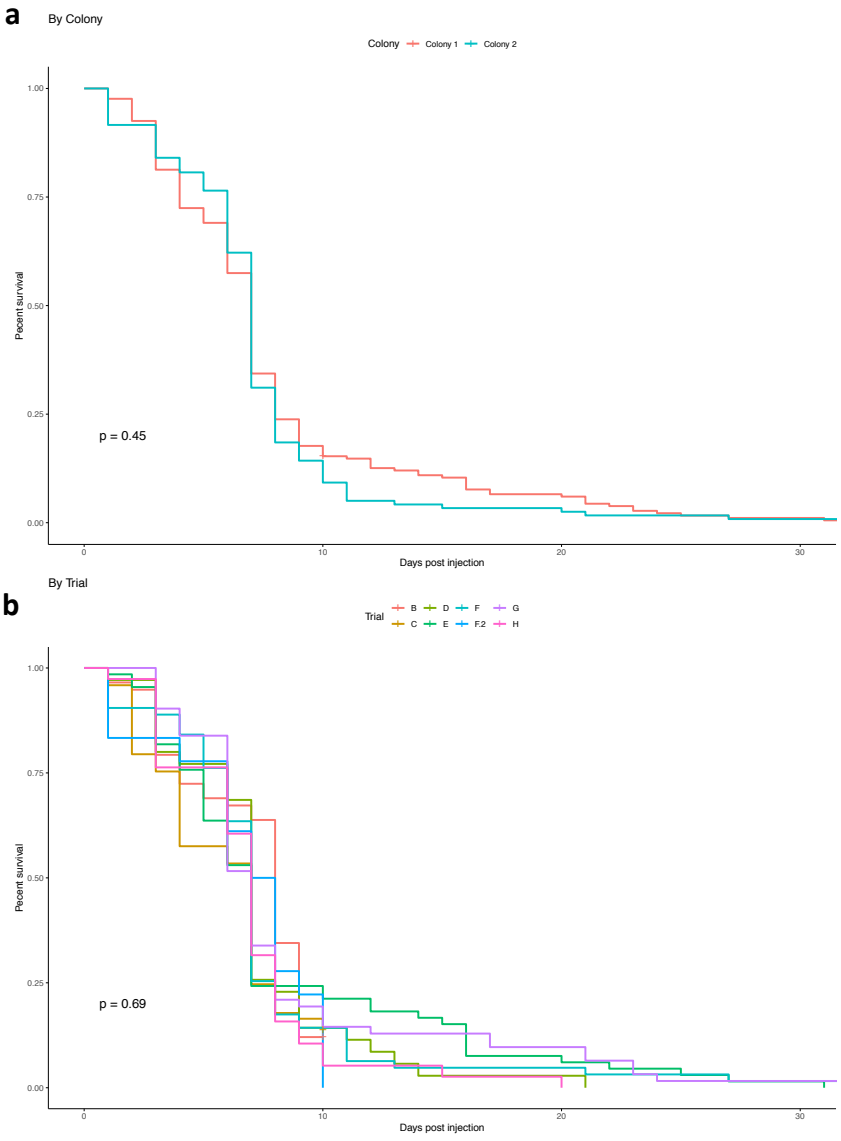
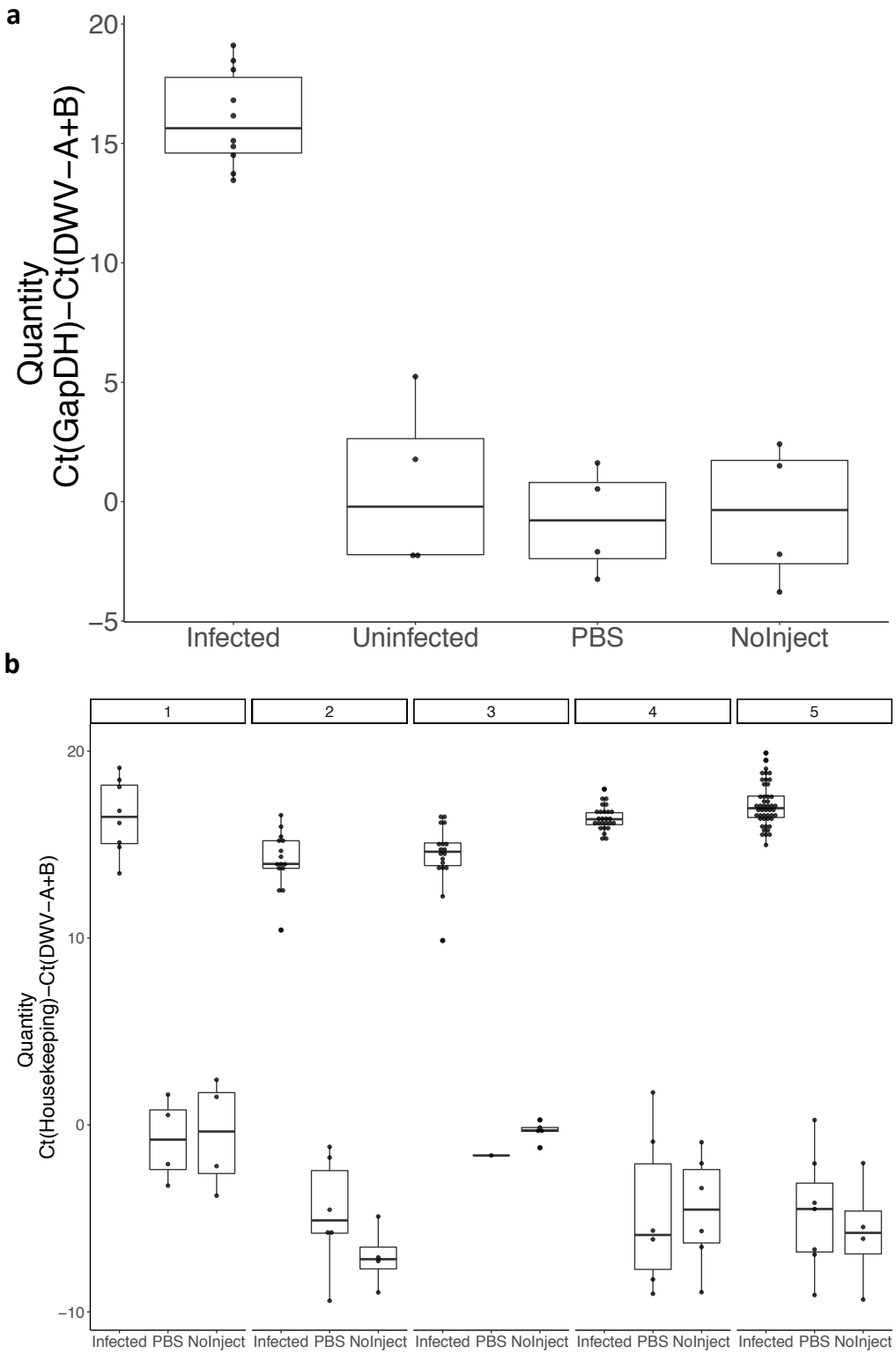
Simulated vector transmission differentially influences dynamics of two viral variants of deformed wing virus in honey bees (*Apis mellifera*) : Supplemental Figures

Supplemental Figure 1. No significant differences in survival across Trials and Colonies.



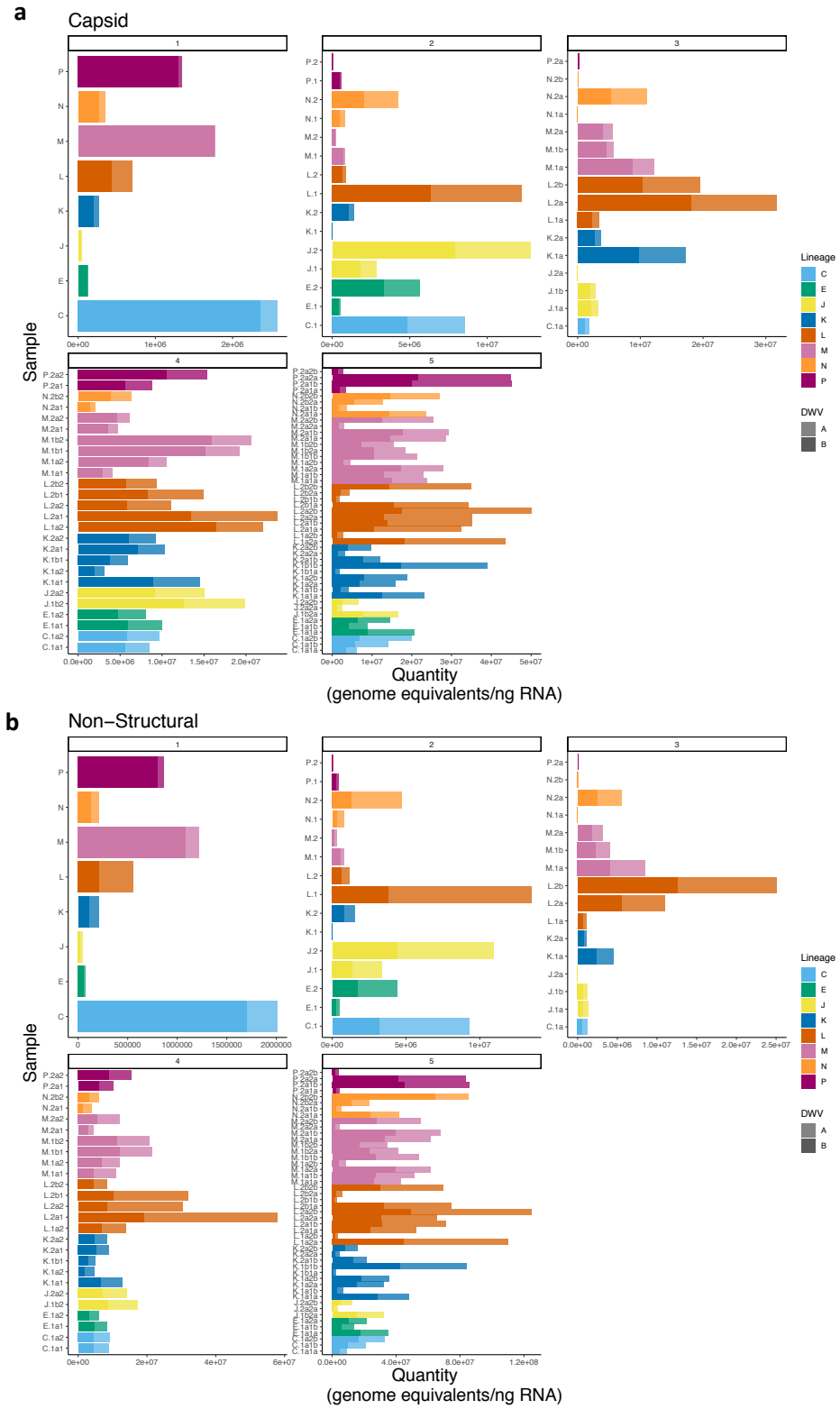

Percent survival across Trial (A) and Colony (B). There was no significant difference mortality across colony or trial.

Supplemental Figure 2. DWV levels of uninfected bees.



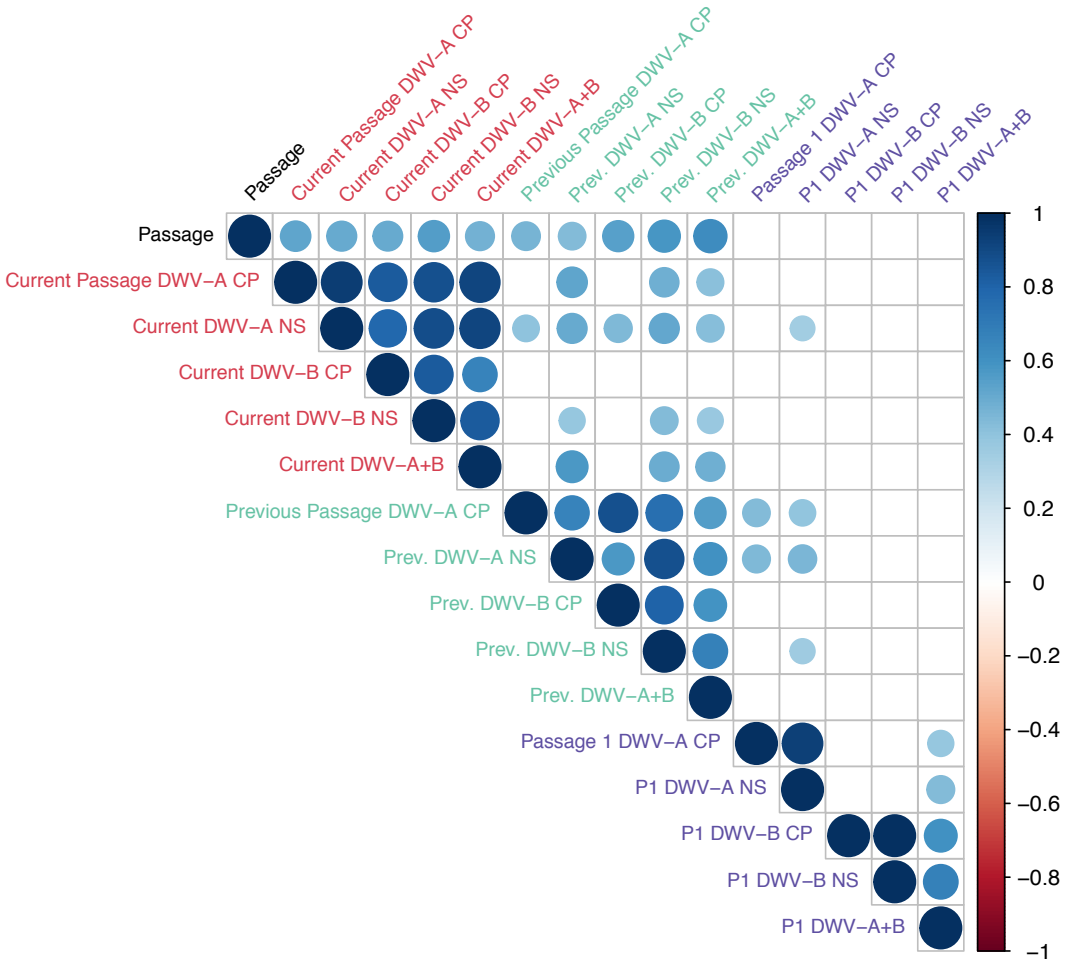
(A) DWV levels of Passage 1 bees, quantified by Ct value. ‘Infected’ bees were injected with DWV, resulting in high levels of infection, and utilized in the passaging paradigm. ‘Uninfected’ bees were also injected with DWV, but did not result in high levels of infection. PBS injection and No Injection were included as controls. (B) DWV levels of passaged DWV populations (‘Infected’) and controls (‘PBS’ and ‘No Inject’) across all Passaging rounds. (A-B) Ct values were normalized to an internal, honey bee housekeeping gene. Note that Passage 1 utilized the internal reference gene GapDH1 that on average had a higher Ct value than the later passages that utilized eIF3-S8 as the internal reference. DWV levels in (B) should therefore only be compared within a passage and not across passages.

Supplemental Figure 3. DWV variant level distributions



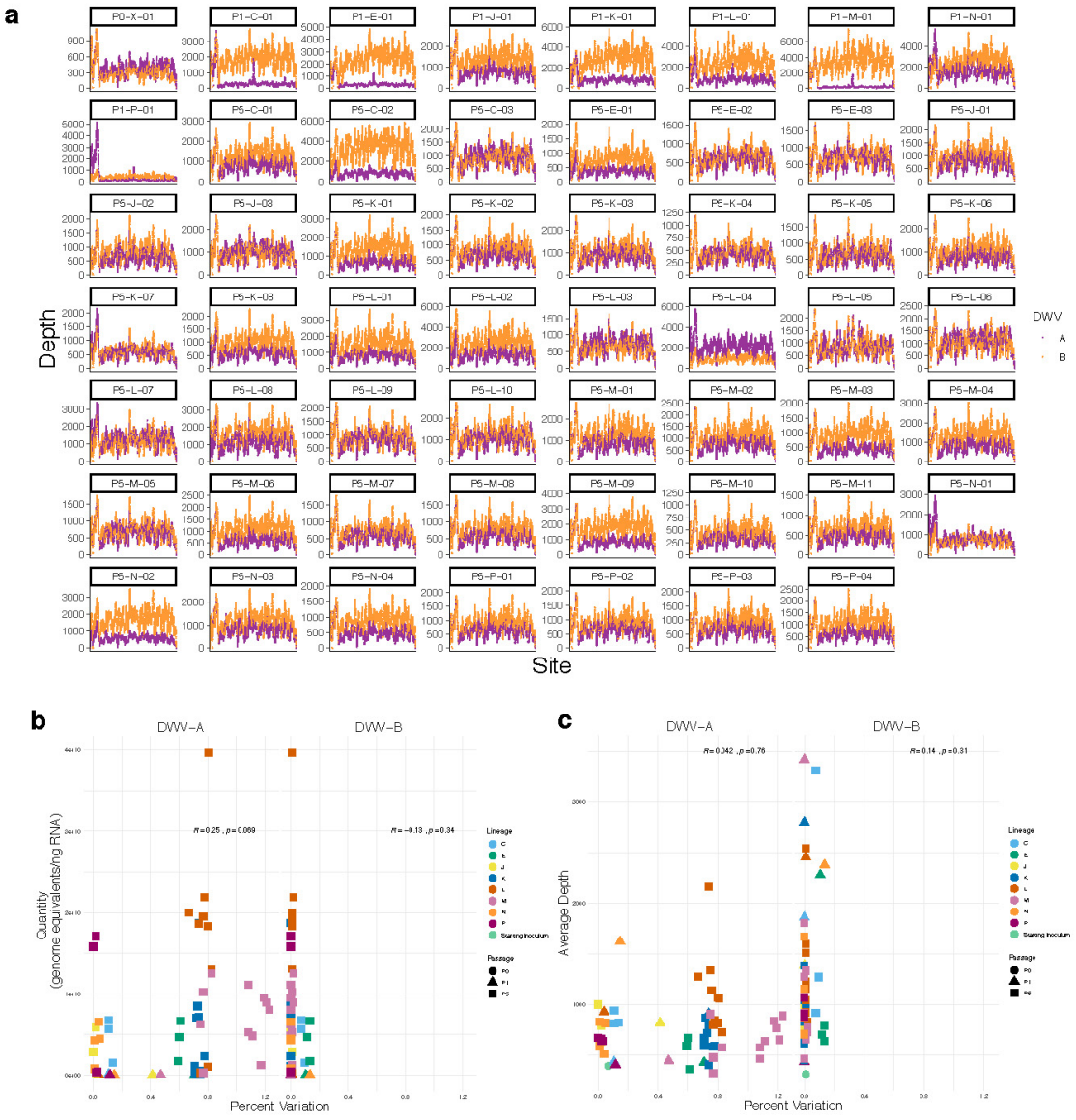
Distribution of individual DWV variant levels of all samples across passages, targeting the (A)  Non-structural region, and Capsid (B) region, determined by variant-specific qPCR. (A-B) DWV levels in controls (no-inject, PBS) were low to no detection, and therefore are not shown here, but can be found in Supplemental Figures and Tables.

Supplemental Figure 4. Correlation between viral population factors in the passaging paradigm.



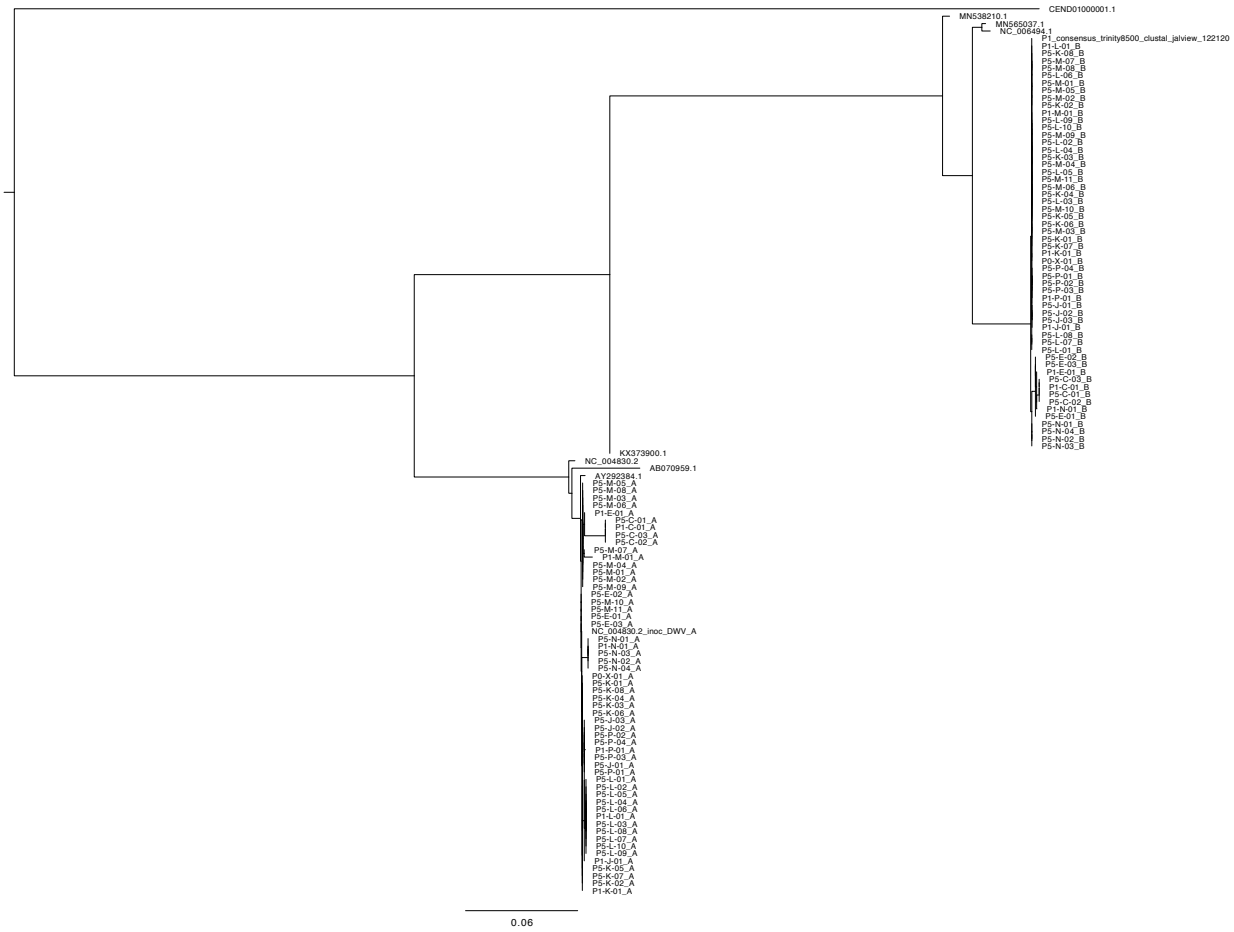

Correlation matrix was calculated in R using cor() with the use="pairwise.complete.obs" option. The matrix was then plotted using the corrplot() function, excluding all correlations with a p-value of > 0.0004. Size of the circle indicates correlation (larger = stronger) and color indicates direction (positive or negative); all correlations were positive.

Supplemental Figure 5. Average Depth, variation and titer, variation and depth.



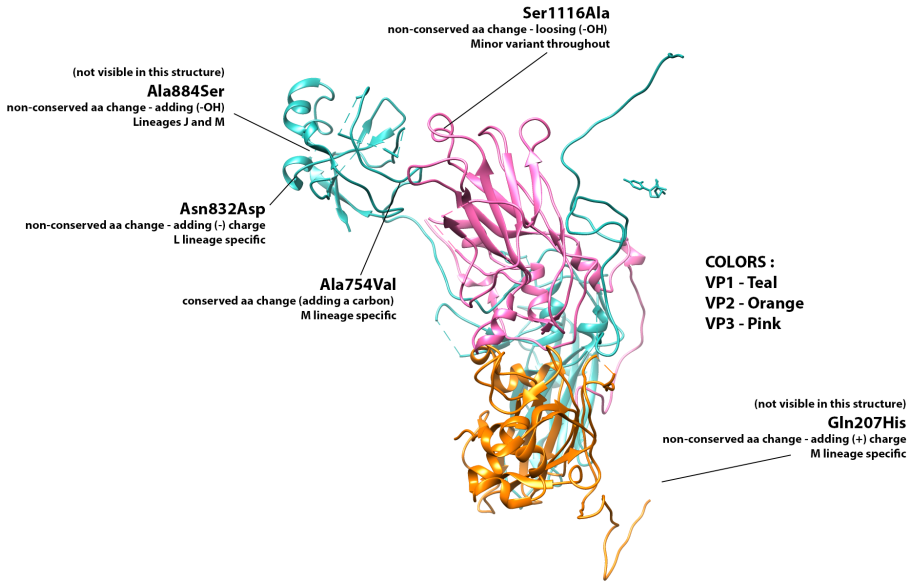

(A) Overall read depth across DWV-A (maroon) and DWV-B (orange) consensus genomes across all individual samples. (B-C) Average variation within each sample was plotted against over viral levels (B) and average read depth (C) across DWV-A and DWV-B. No significant association was found between average variant and overall levels nor average depth.

Supplemental figure 6. Full Maximum likelihood trees without collapsing.




Tree construction was supported by 1000 bootstrap replicates and generated from full nucleic acid genome sequences for all consensus DWV-A and DWV-B populations.

Supplemental figure 7. Variable sites on DWV-A capsid proteins.




Variable sites with missense mutations annotated by SNPeff were located and labeled within the DWV-A crystal structure PDB 5MV6 (VP1=teal, VP2=orange, VP3=pink), along with hypothesized effects on protein structure and function.