**FIG S1** Maximum likelihood (ML) tree of the 55 RNA/pvDNA paired samples. This was inferred with the Generalised Time Reversible (GTR) nucleotide substitution model with gamma-distribution of rates among site heterogeneity, a proportion of invariable sites (GTR+I+Γ_5) and 1,000 bootstrap replicates. Paired samples were identified by a bootstrap support >70%. The ML phylogenetic tree was inferred with the MEGA6 software.
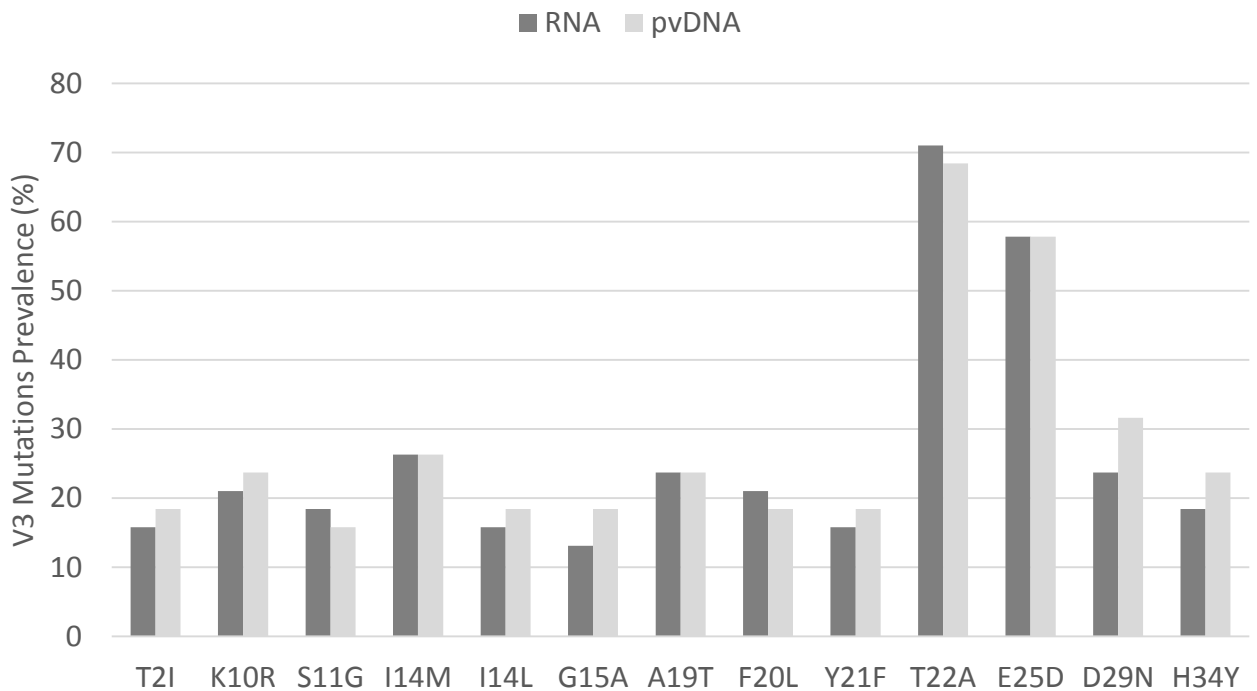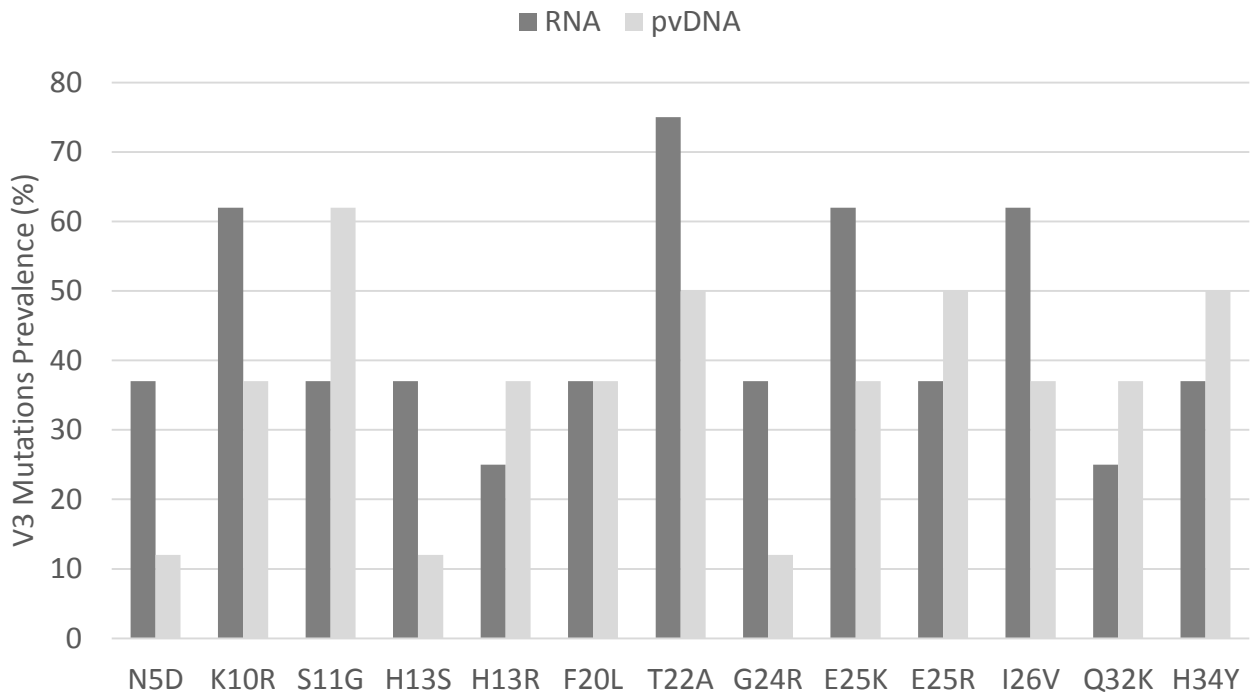
FIG S2 Prevalence of V3 mutations in concordant DNA/RNA samples. (A) Concordant RNA/DNA samples (N=8) with X4/DM tropism. (B) Concordant RNA/DNA samples (N=38) with R5 tropism. All mutations found at the 35 V3 positions with an overall prevalence ≥ 10% were evaluated.