S4 Fig. Increased chance of false negatives for low quality NTS samples, with high RPP30 Cq values. (A, B) Comparison of actual (Act) and RPP30-normalised (Norm) Cq values for SARS-CoV-2 targets shows that values cluster more strongly after normalisation, both when normalising to the worst (highest RPP30 Cq; A) and best (lowest RPP30 Cq; B). Increased clustering (i.e. reduced variability) demonstrates the impact of the correlation between quantity of human and viral nucleic acids in NTS samples (Fig 4C). This shows 1) that sample quality substantially impacts on assay sensitivity and 2) that variability in viral loads is smaller than non-normalised data suggest. Plots in (A) demonstrate that 4-6 positives (15-23%) would likely have been below the detection limit (above the red line, viral Cq > 40) in a worst quality sample scenario. Also, see Table 1, S4 Table, and S1 Data.