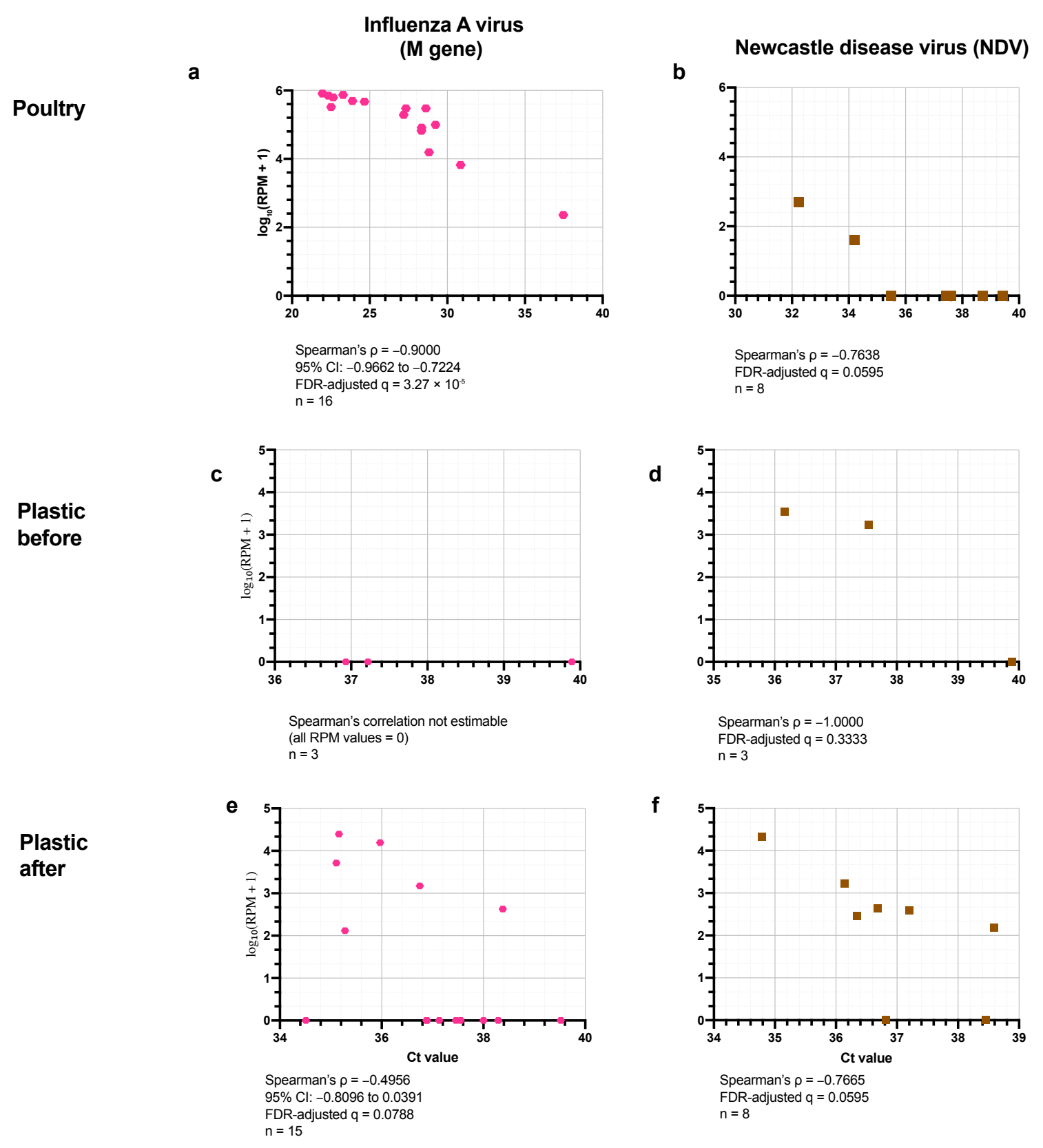


Supplementary Figure S5. Associations between targeted RT-qPCR Ct values and metagenomic relative abundance in pooled poultry and plastic-sheet samples. Scatter plots show Ct values versus $\log_{10}$(RPM + 1) for influenza A virus (M gene; left column) and Newcastle disease virus (right column) in pooled poultry samples (a, b) and plastic-sheet samples collected before (c, d) and after (e, f) the operational period. Each point represents one matched RNA pool. Only valid Ct values ≤40 were included in the correlation analyses, while zero RPM values were retained. Sample sizes were 16, 8, 3, 3, 15 and 8 for panels a–f, respectively. Associations were assessed using two-sided Spearman rank correlations across both intervention conditions. The AIV correlation in before-period plastic-sheet samples was not estimable because all three retained RPM values were zero. Benjamini–Hochberg correction was applied across the five estimable correlations, with 95% confidence intervals shown where available. Sampling was conducted over six dates, with three days per intervention condition. These exploratory sample-level analyses assessed correspondence between molecular methods rather than intervention effectiveness and did not account for within-day clustering.