**Processing of scRNA-seq data.** FASTQs were aligned to the reference genome using the STARsolo feature of STAR v. 2.7.8a [doi: <https://doi.org/10.1101/2021.05.05.442755>] and the following filters: --soloCBmatchWLtype Exact, --outFilterScoreMinOverLread 0, --outFilterMatchNminOverLread 0, --outFilterMatchNmin 30. Cell-containing droplets were identified with the EmptyDrop-like filtering method [doi: [10.1186/s13059-019-1662-y](https://doi.org/10.1186/s13059-019-1662-y)] implemented in STARsolo via the following: --soloCellFilter EmptyDrops\_CR, modifying the default parameters to reflect the expected number of cells, the minimum UMI count to 50/75, and the number of simulations to 1000. To generate estimates of the levels of ambient RNA in each experimental condition, we used the calculateContaminationFraction function of the SoupX R package on barcodes for which >80% of the RNA-seq counts were assigned to one viral strain (i.e. H1N1 or H3N3), with genes of the other viral strain assumed to be non-expressed (i.e. contamination). This revealed that contamination rates for the IVT method were around 10% while the PCR method resulted in contamination rates around 20%. Log-transformed normalized expression values for the 16 possible gene segments were computed from the count matrices generated with STARsolo using the logNormCounts function of the scater R package. In addition, we attempted to estimate which cells genuinely expressed each segment when accounting for ambient RNA present in each library. To do this, we modified the estimateNonExpressingCells function of the SoupX R package as has been done previously [doi: https://doi.org/10.1101/2020.12.07.414151] to return the *p*-value associated with each barcode; this function estimates whether each cell contains significantly more counts of a specified gene or gene-set than would be expected under a Poisson model, given the estimated ambient RNA from its library of origin and the maximum contamination fraction. For each of the 8 segments of the IAV genome, we determined whether there exists statistical evidence for expression of the H1N1 strain, H3N2 strain, or both (or neither) using an an FDR threshold of 1%/5%. Any barcode with statistical evidence for expression of one or more segments from both viral strains was considered as a ‘potential doublet’ and excluded from further analysis. All remaining droplets were designated as ‘pure’ strains (with full or partial evidence, i.e. all 8 segments or less statistically expressed) or ‘reassortments’ (expression of distinct segments from each of the two strains).