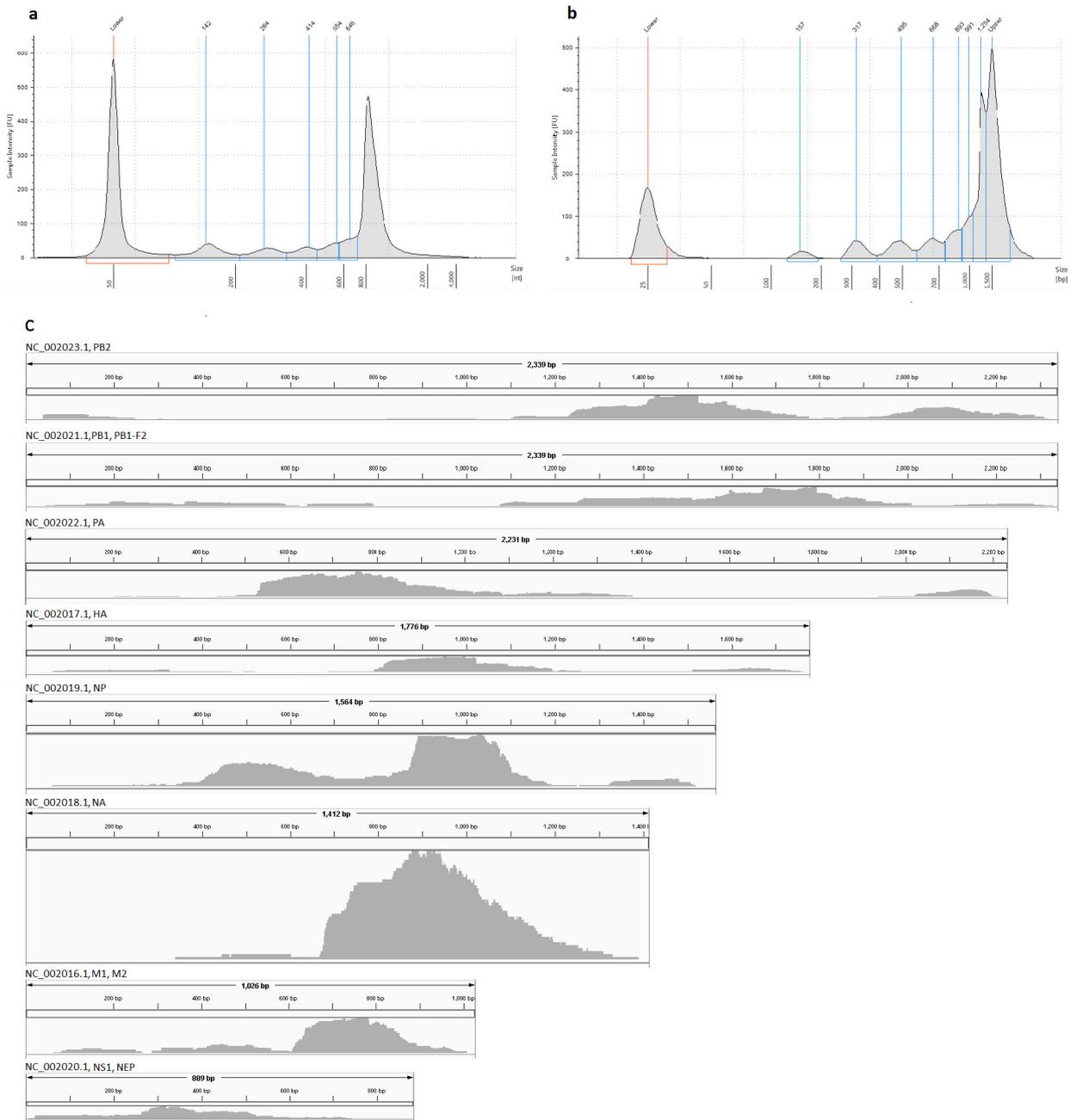


**Supplemental Figure S1:** Agilent tape station visualization of RNA, cDNA and Illumina reads of the influenza virus A sample. Panel **a**: input RNA (RNA tape) and **b**: cDNA (High sensitivity tape) shows distinct molecule sizes that are smaller than the influenza virus A RNA fragments. Panel **c** shows Illumina MiSeq read distribution aligned to the influenza virus A H1N1 reference with Bowtie. Maximum read depth for the fragments is: 4264 (NC\_002023.1), 1845 (NC\_002021.1), 6824 (NC\_002022.1), 2891 (NC\_002017.1), 12712 (NC\_002019.1), 41552 (NC\_002018.1), 9116 (NC\_002016.1), 908 (NC\_002020.1).



**Supplemental Figure S2:** HCMV regions of low coverage and read pileups, visualised in IGV. Panels a-d show OriLyt; Illumina coverage plot (a, maximum: 1008) and Bowtie-aligned read pileup (b), and Nanopore coverage plot (c, max. 16) and pileup (BLASR alignment, d). Panels e-h show the repetitive region at position 195000; Illumina coverage (e, max. 5438) and pileup (f), and Nanopore coverage (g, max. 83) and pileup (h) are shown. White reads in panel f indicate a mapping quality close to zero, here due to the redundancy of the sequence, that prevents the unambiguous mapping of short reads.

