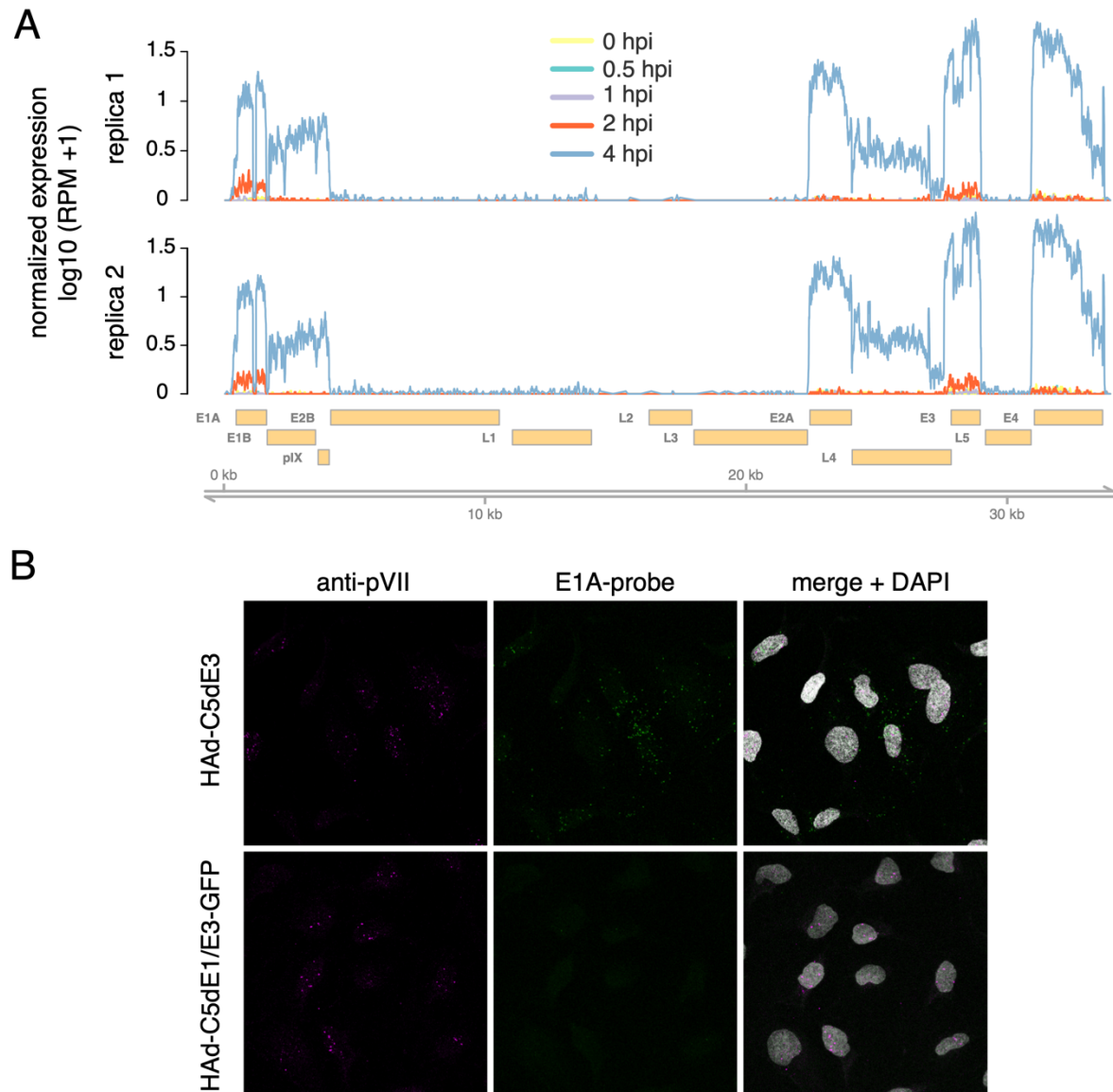


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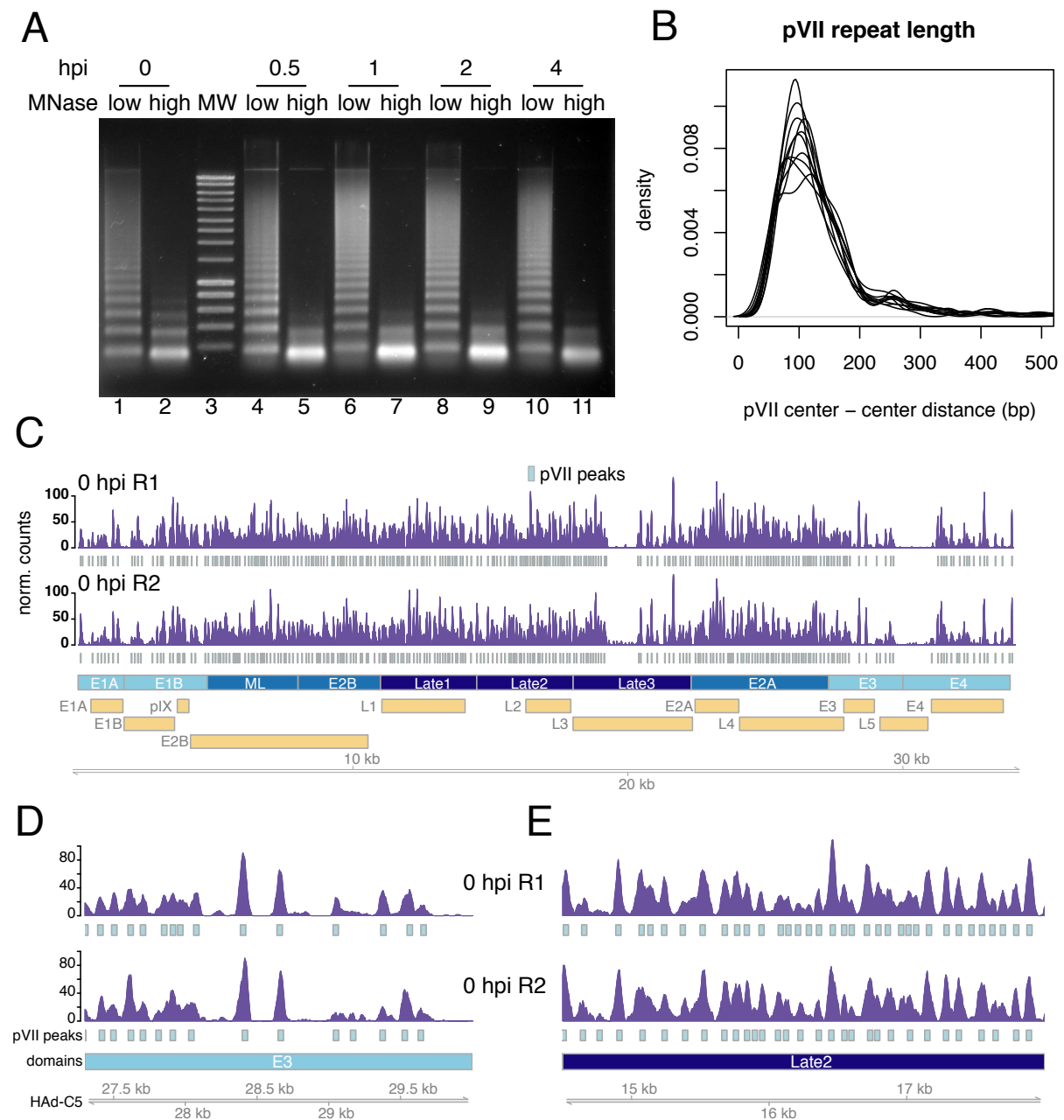
Appendix Figure S1



A Profiles illustrate HAd-C5dE3 genome coverage by RNA-seq reads. Measurements were replicated in two independent time series. Reads were normalized to RPM (reads per million mapped reads). Genomic location and underlying gene annotation of HAd-C5dE3 (NCBI accession: AY339865.1) are indicated at the bottom.

B Overview confocal images of cells infected with HAd-C5dE3 (top row) or an E1-deleted HAd-C5dE3 vector expressing GFP (bottom row). Detection of genomes using anti-pVII antibodies (left column, magenta signal) and E1A transcript with specific RNAscope probes (middle column, green signal), and merged with DAPI detecting the nucleus (right column, grey signal). An individual cell from each image is shown at higher magnification in Figure 2.

Appendix Figure S2

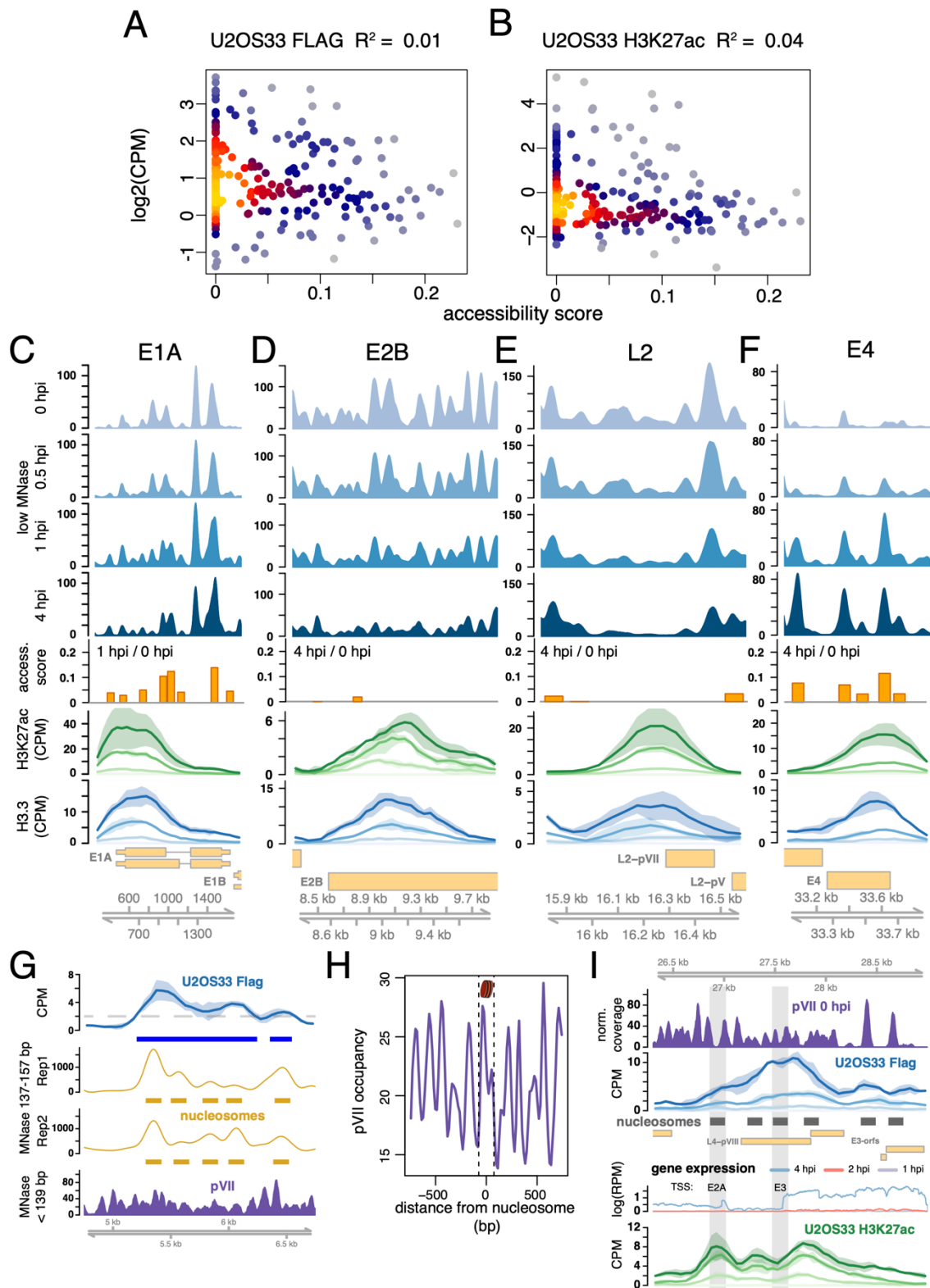


A Nucleosomal DNA ladder after chromatin digestion of HAd-C5dE3 infected H1299 cells using 100U (low) or 600U (high) of MNase.

B Distribution of pVII center-center distances of each sample along the HAd-C5dE3 genome.

C, D and E profiles illustrate HAd-C5dE3 genome coverage by MNase-seq reads of two biological replicates. pVII positions are represented by grey boxes. Partitioning of the genome into functional domains and the timing of their transcription is indicated by the color code (lightblue = early, darkblue=late). Snapshots of an open (D) and a tightly packaged genomic region (E).

Appendix Figure S3



A Scatter plots showing correlation of pVII accessibility score with H3.3 or **B)** H3K27ac abundance at 4 hpi in U2OS33. Each dot represents one pVII peak position derived from Fig. 4C. The coefficient of determination (R^2) is indicated.

C - F Genome browser tracks of H3K27ac enriched sites.

G Genome browser tracks showing nucleosome position calling. A H3.3 coverage > 2 CPM at 4 hpi was used to define nucleosome assembly regions (blue boxes). Middle tracks depict the smoothed profile of nucleosome-sized fragments, which was used to call exact nucleosome positions (golden boxes) of both replicates at 4 hpi. pVII occupancy at 0 hpi is depicted in the bottom panel.

H Average pVII occupancy at 0 hpi around predicted nucleosome positions. Dashed lines indicate nucleosome boundaries.

I Genome browser tracks showing pVII occupancy at 0 hpi (upper panel), the H3.3 (blue shades) / H3K27ac (green shades) accumulation over time, predicted sites of nucleosome assembly (blue boxes) using nucleosome sized fragments (137-157 bp) from 4 hpi MNase-seq samples and expression levels of early genes (middle panel).