Supplementary information

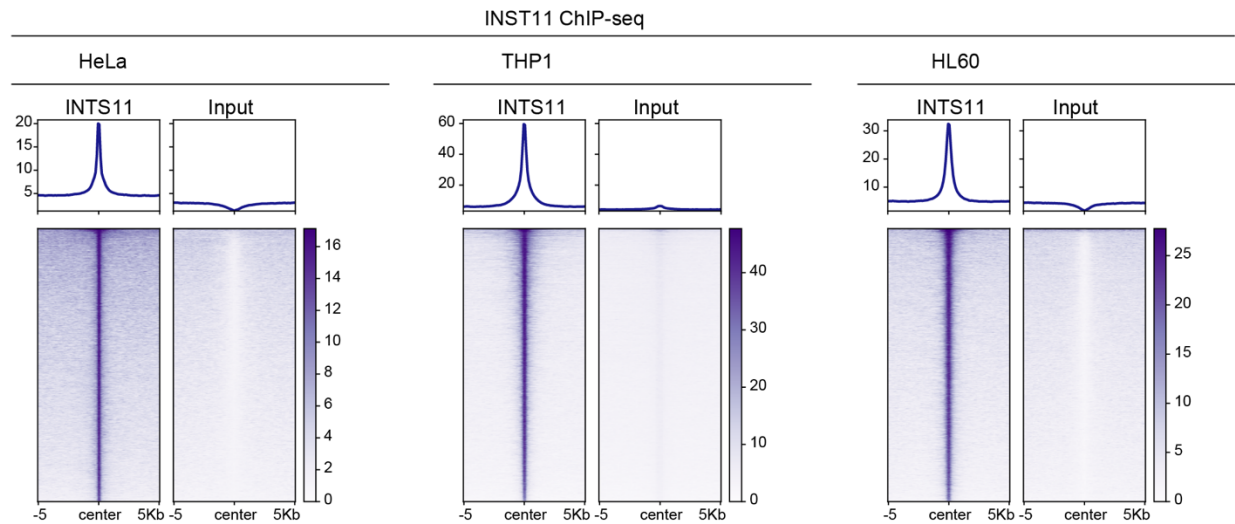# H3K4me3 regulates RNA polymerase II promoter-proximal pause-release

In the format provided by the
authors and unedited

Supplementary information

H3K4me3 regulates RNA polymerase II promoter-proximal pause-release

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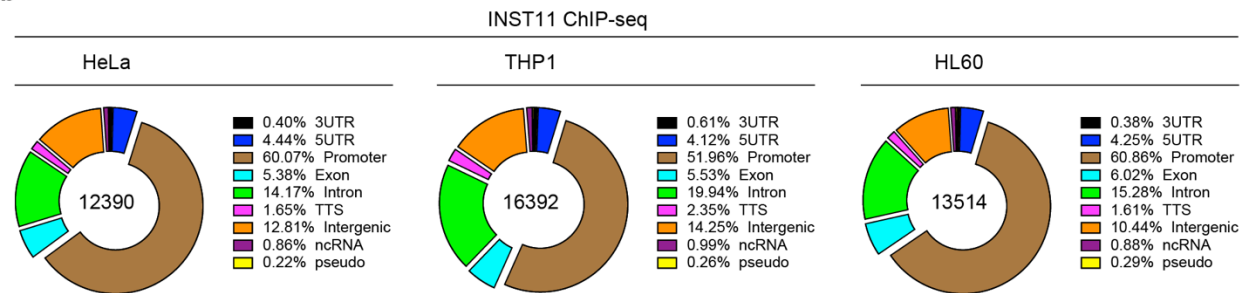
a

b

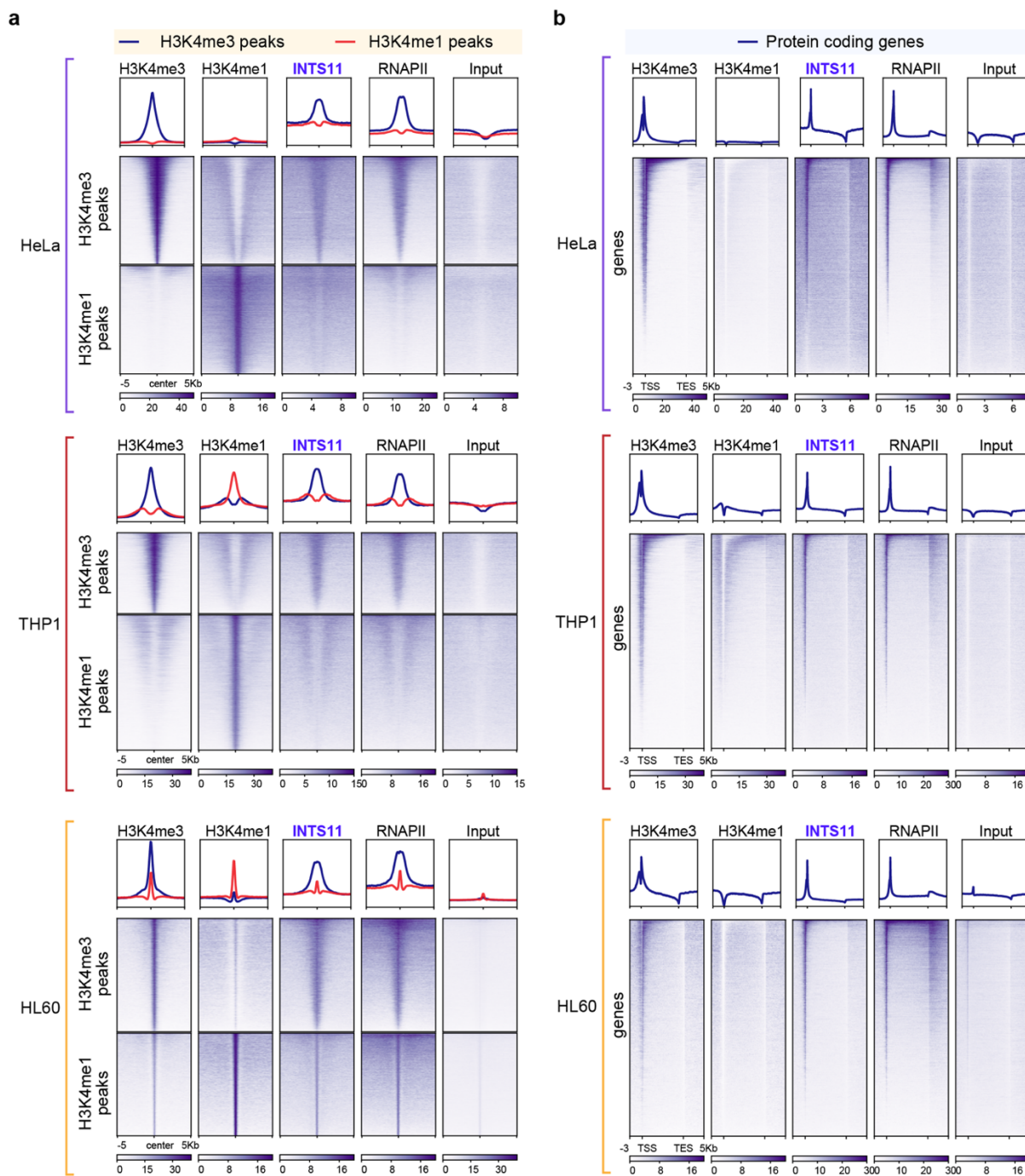**Supplementary Fig.1. INTS11 occupancy at genome wide.**

(**a**) INTS11 genomic binding sites as defined as enrichment over input by ChIP-seq.

(**b**) The genomic binding sites of INTS11 were predominantly localized to promoter region of genes.

The INTS11 ChIP-seq data for HeLa, THP1 and HL60 were obtained from published papers.

Supplementary Fig.2. INTS11 is enriched at H3K4me3-positive chromatin and binds promoter-proximal region of protein-coding genes.

(**a**) ChIP-seq heatmaps and profiles at H3K4me3 or H3K4me1 peak center in the depicted cell lines. Enrichments were plotted over the enrichment peak center (peak center ± 5 kb).

(**b**) Genome-wide binding averages of ChIP-seq signal on protein-coding genes in different cell lines. The genomic binding sites of INTS11 were predominantly localized to the promoter region of genes. Data are displayed from 3 kb upstream of the transcriptional start site to 5 kb downstream of the end of each gene. TSS, transcription start site, TES, transcription end site. Rows of heatmap are sorted by decreasing H3K4me3 occupancy. The INTS11 ChIP-seq data for HeLa, THP1 and HL60 were obtained from published papers.
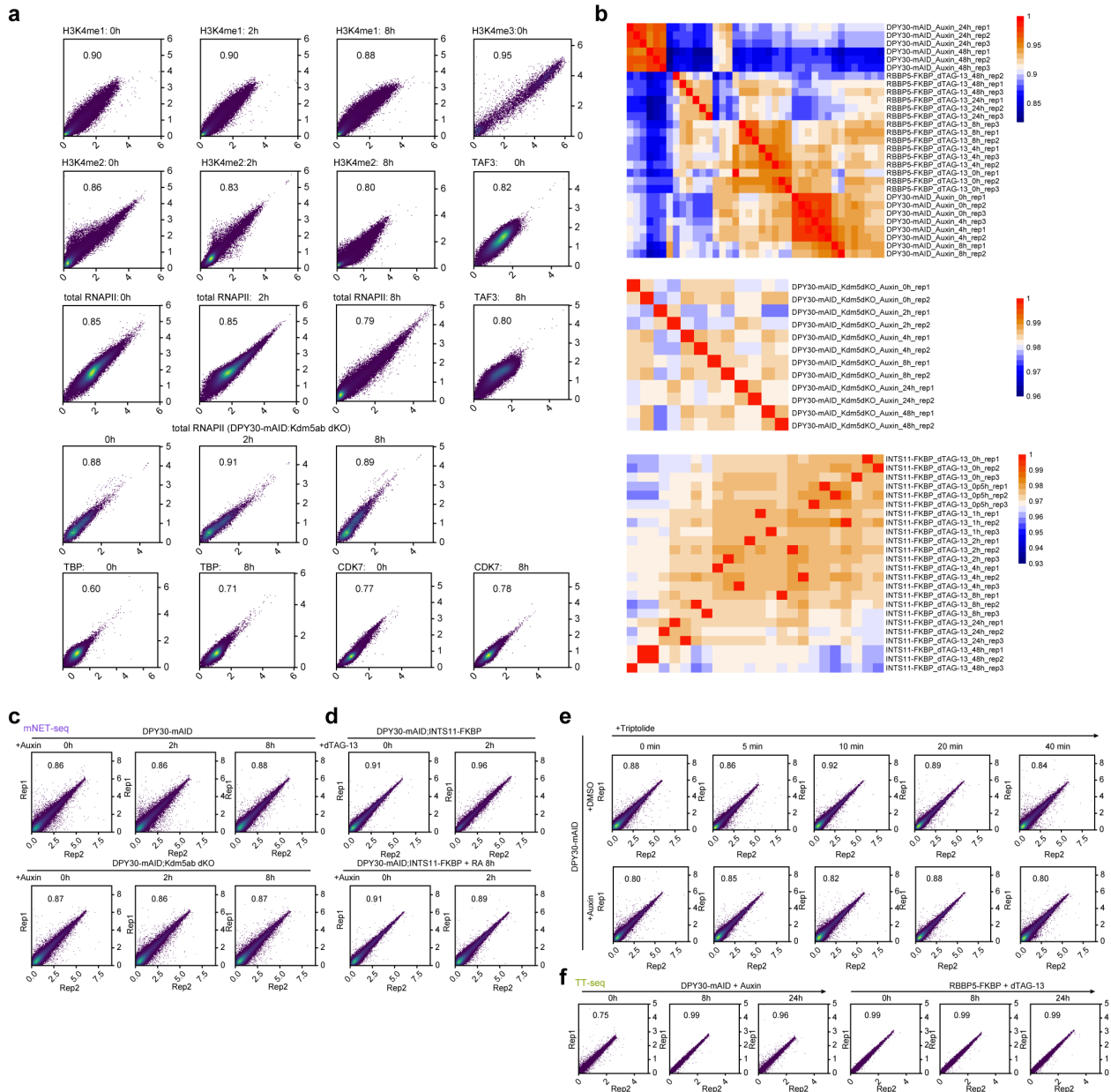
Supplementary Fig.3. Reproducibility of key sequencing data in this study.

(**a**) Correlations between ChIP-seq experiments. Normalized reads per 100 kb bins for DPY30-mAID (y axis) and RBBP5-FKBP (x axis) degron cells in the indicated samples and time points were plotted. Spearman correlation coefficients are indicated in the panels.

(**b**) Correlations between SLAM-seq experiments. Spearman correlation coefficients are indicated in the panels.

(**c-e**) Correlations between replicates of mNET-seq experiments.

(**f**) Correlations between replicates of TTchem-seq and DRB/TTchem-seq experiments. Normalized reads per 100 kb bins for repeat 1 (y axis) and repeat 2 (x axis) in the indicated samples and time points were plotted. Spearman correlation coefficients are indicated in the panels.

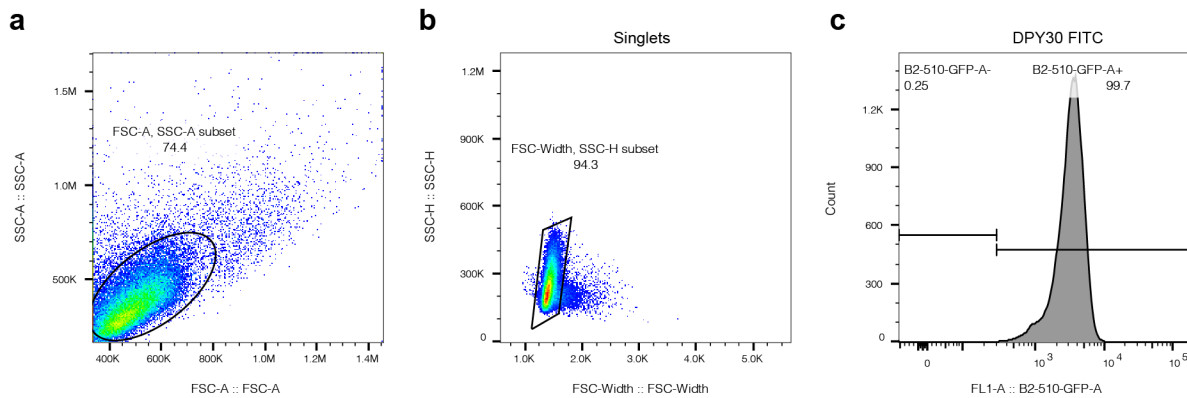**Supplementary Fig.4. Source Data of unprocessed western blots.**

Fig. 3a
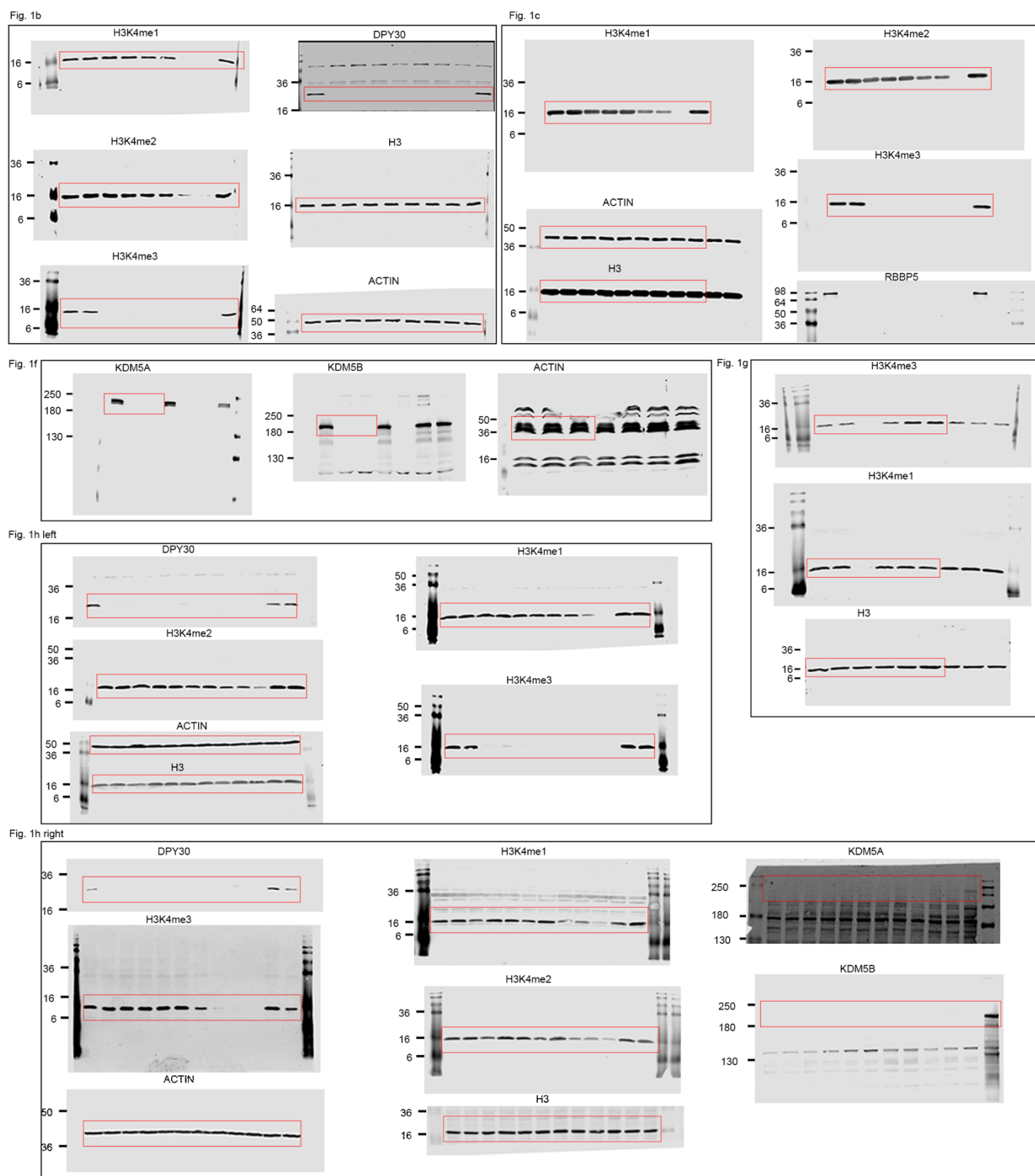
Supplementary Fig.4. Source Data of unprocessed western blots.
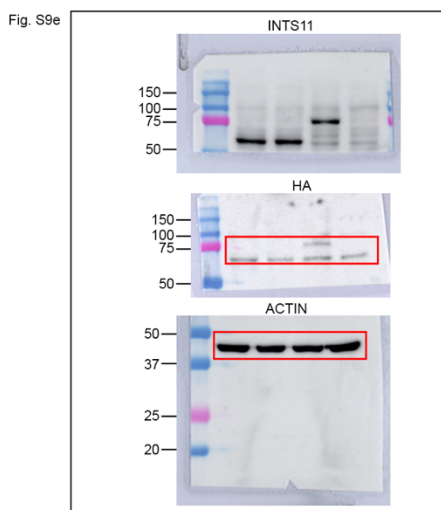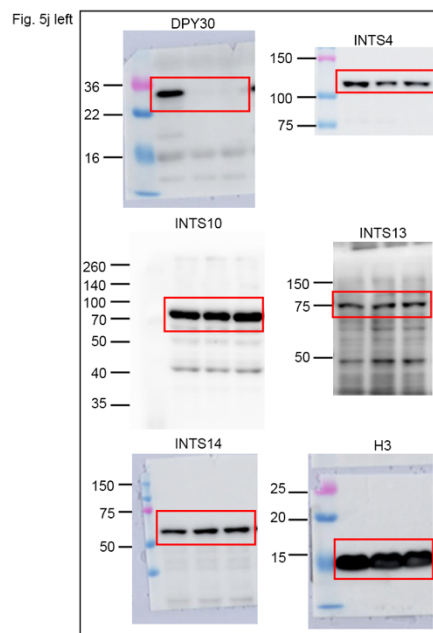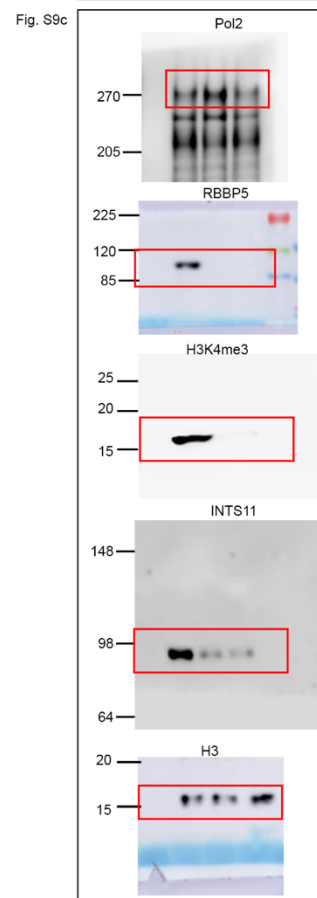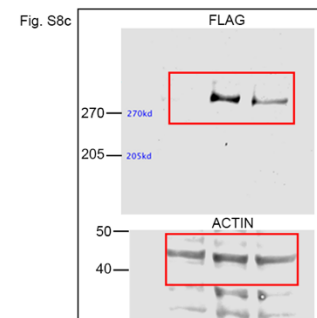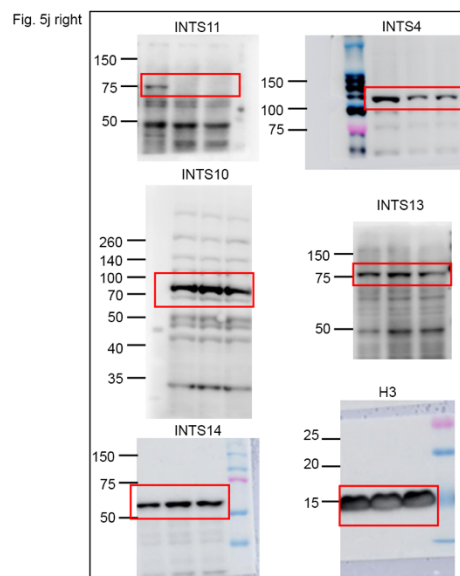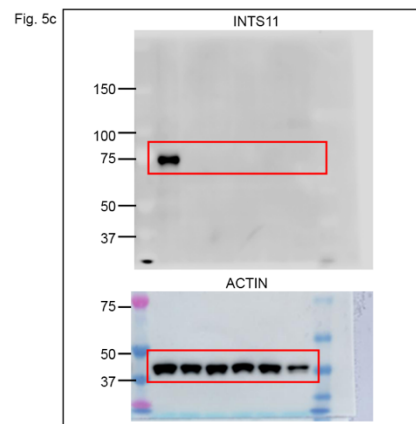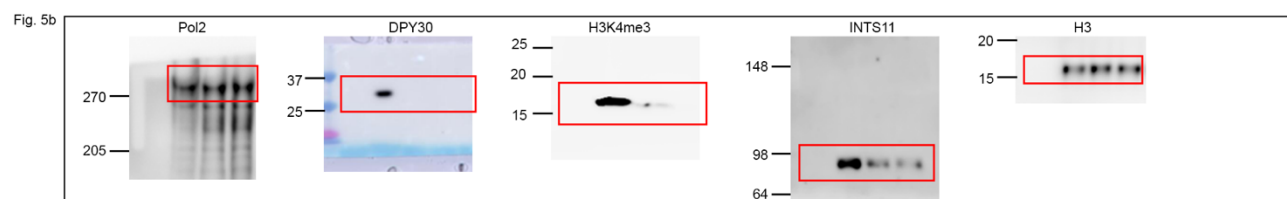
Supplementary Fig.4. Source Data of unprocessed western blots.

Supplementary Fig.5. Gating strategy for flow cytometry analysis

(**a**) Representative gating for cells in E14 mESCs.

(**b**) Representative gating for singlets in E14 mESCs.

(**c**) Representation of DPY30-positive cells in E14 mESCs.