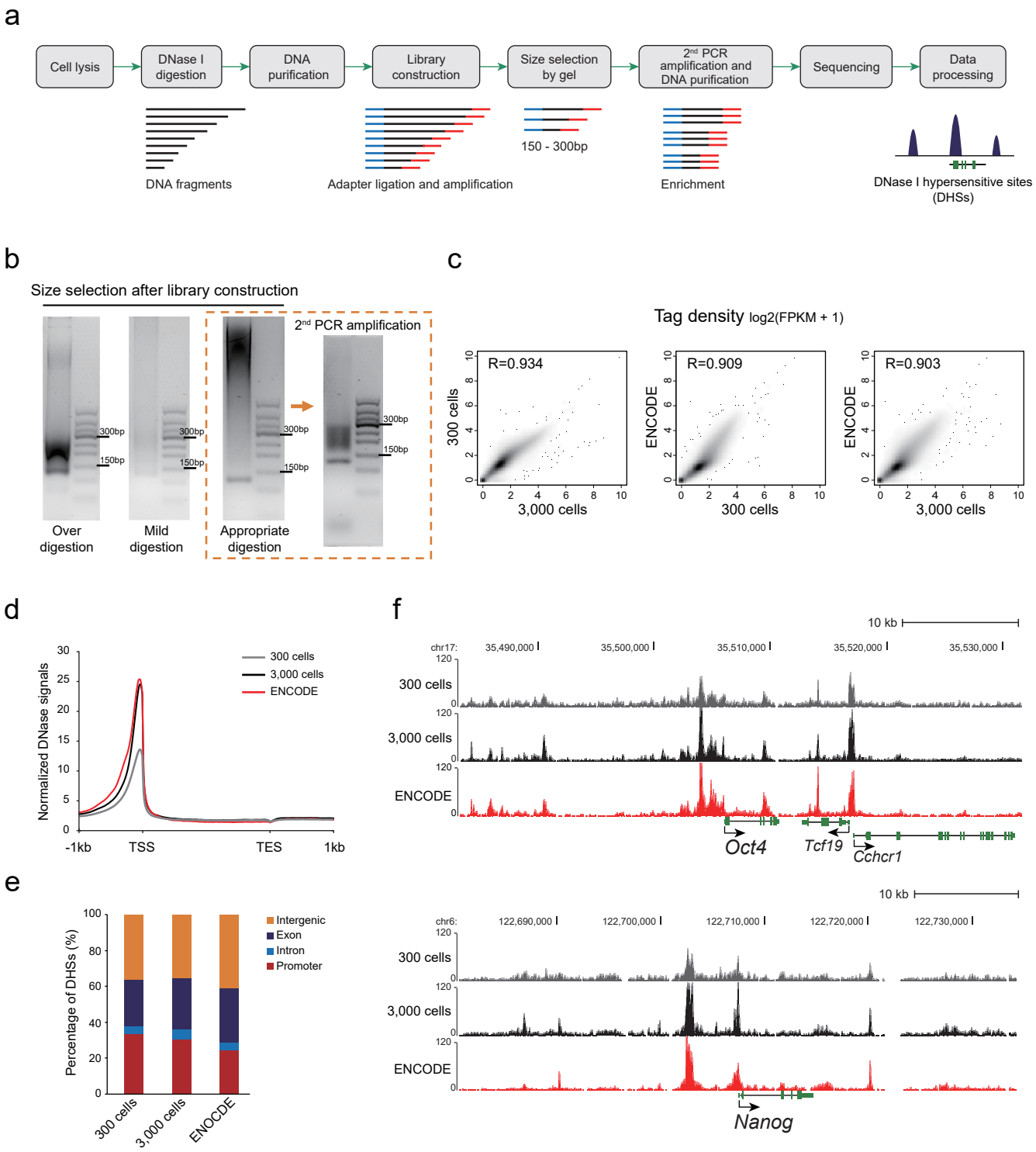

Fig. S1 Validation of low-input DNase-seq in mouse ESCs. **a** Workflow of low-input DNase-seq for probing accessible chromatin. **b** Electrophoresis showing over-digestion, mild-digestion and appropriate-digestion of ESC genomes after library construction. Only DNA fragments in the size range of 150 - 300bp were extracted for a 2nd PCR amplification and subsequent sequencing (see Materials and methods). **c** Scatterplots showing the correlation of ESC DNase signals generated by our low-input DNase-seq and ENCODE conventional DNase-seq. Pearson correlation coefficients are indicated. The genome was scanned with a 5-kb window. **d** Profiles of the average ESC DNase signal density for RefSeq genes. Transcription units are shown as metagenes, while upstream and downstream sequences are shown in absolute distances. **e** Distribution of ESC DHSs across genomic features. Regions of ± 1 kb surrounding the RefSeq TSS were annotated as promoters. **f** Genome browser view of mouse ESC DNase signal enrichment around the *Oct4* (top) and *Nanog* (bottom) loci.