

Supplementary Figures.

Fig. S1 STRING network model of ZFP57-interacting proteins. 41 of the 60 candidate ZFP57-interacting proteins were mapped on an interconnected network constructed by STRING analysis. The model revealed key sub-network clusters connected to ZFP57 and KAP1(TIF1B). Colours represent different subnetworks based on K-means clustering. Edge thickness is representative of the confidence in interaction based on database mining, experimental evidence and text mining.

Fig. S2 Heat-map showing that the great majority of the MSH2 Bio-ChIP-seq peaks overlapping with promoters are centered on Transcription Start Sites (TSS).

Fig. S3 Screenshots from the UCSC Genome Browser showing the ChIP-seq signals detected for biotin-tagged MSH2 in BirA-expressing E14 ESCs along eight cell growth-controlling genes with promoters overlapping CpGI. DNA methylation and binding profiles of MSH2 (2 replicates), ZFP57 and KAP1 are reported as in Figure 3a.

Fig. S4 (related to Figure 2f) Heatmaps showing the read enrichment of MSH2, MSH6, ZFP57 and KAP1 in the genomic regions overlapping (+/- 1.5 kbp) the KAP1 ChIP-seq peaks sorted on the basis of their overlap with various genomic elements.

Fig. S5 (related to Figure 2f) Heatmaps showing the read enrichment of MSH2, MSH6, ZFP57 and KAP1 in the genomic regions overlapping (+/- 1.5 kbp) the KAP1 ChIP-seq peaks sorted on the basis of their overlap with ZFP57 peaks.

Fig. S6 Screenshots from the UCSC Genome Browser showing the ChIP-seq signals detected for the Biotin-tagged MSH2 in BirA-expressing E14 ESCs along five non-ICR regions bound by ZFP57 [7]. DNA methylation and binding profiles of MSH2 (2 replicates), ZFP57 and KAP1 are reported as in Figure 3a.

Fig. S1

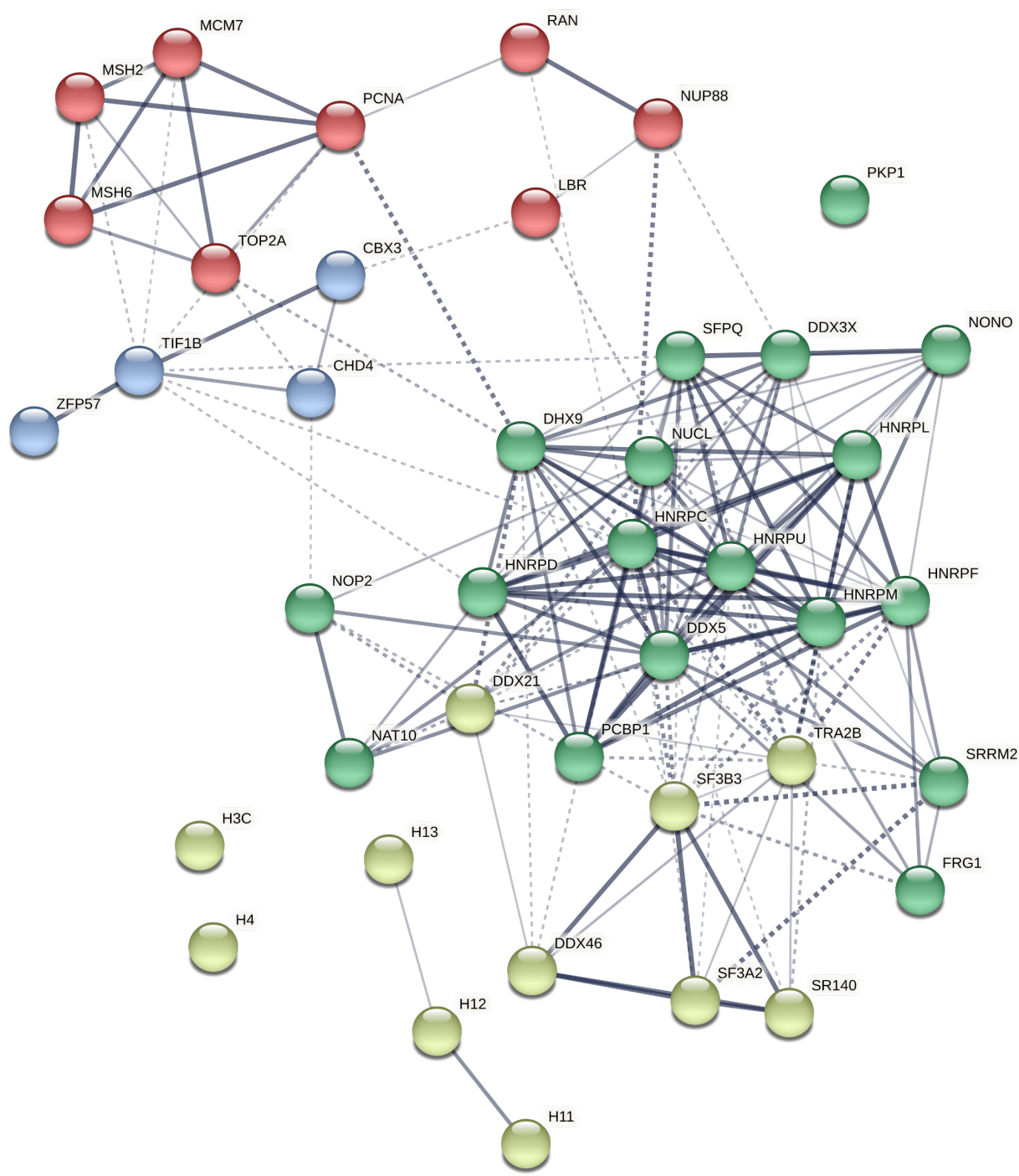


Fig. S2

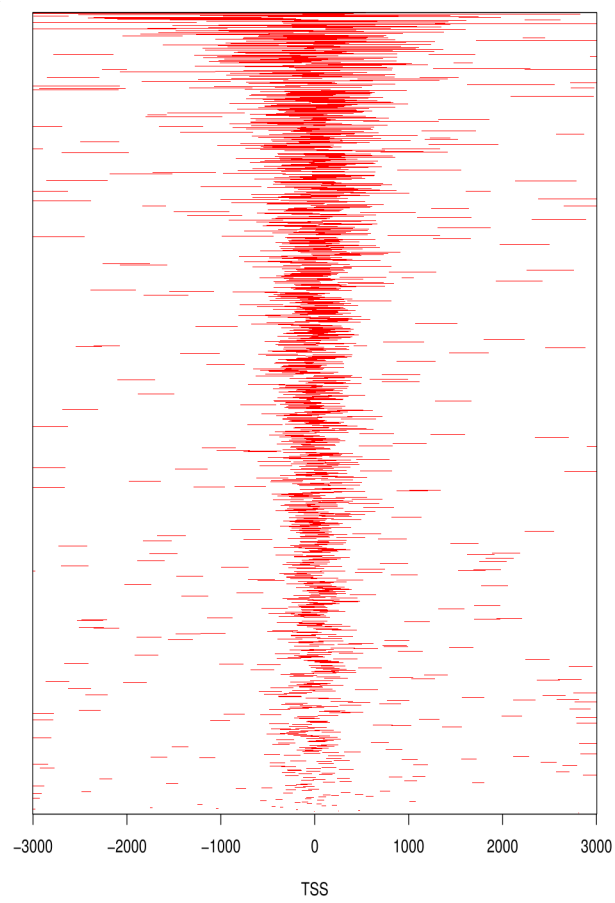


Fig. S3

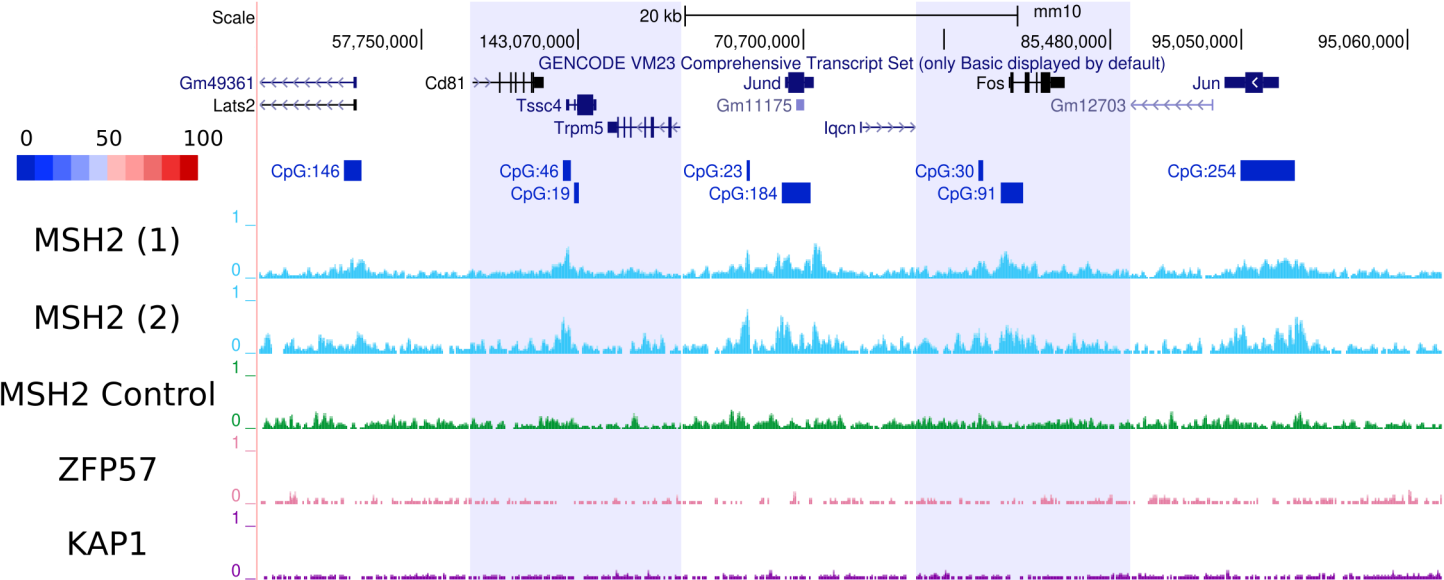


Fig. S4

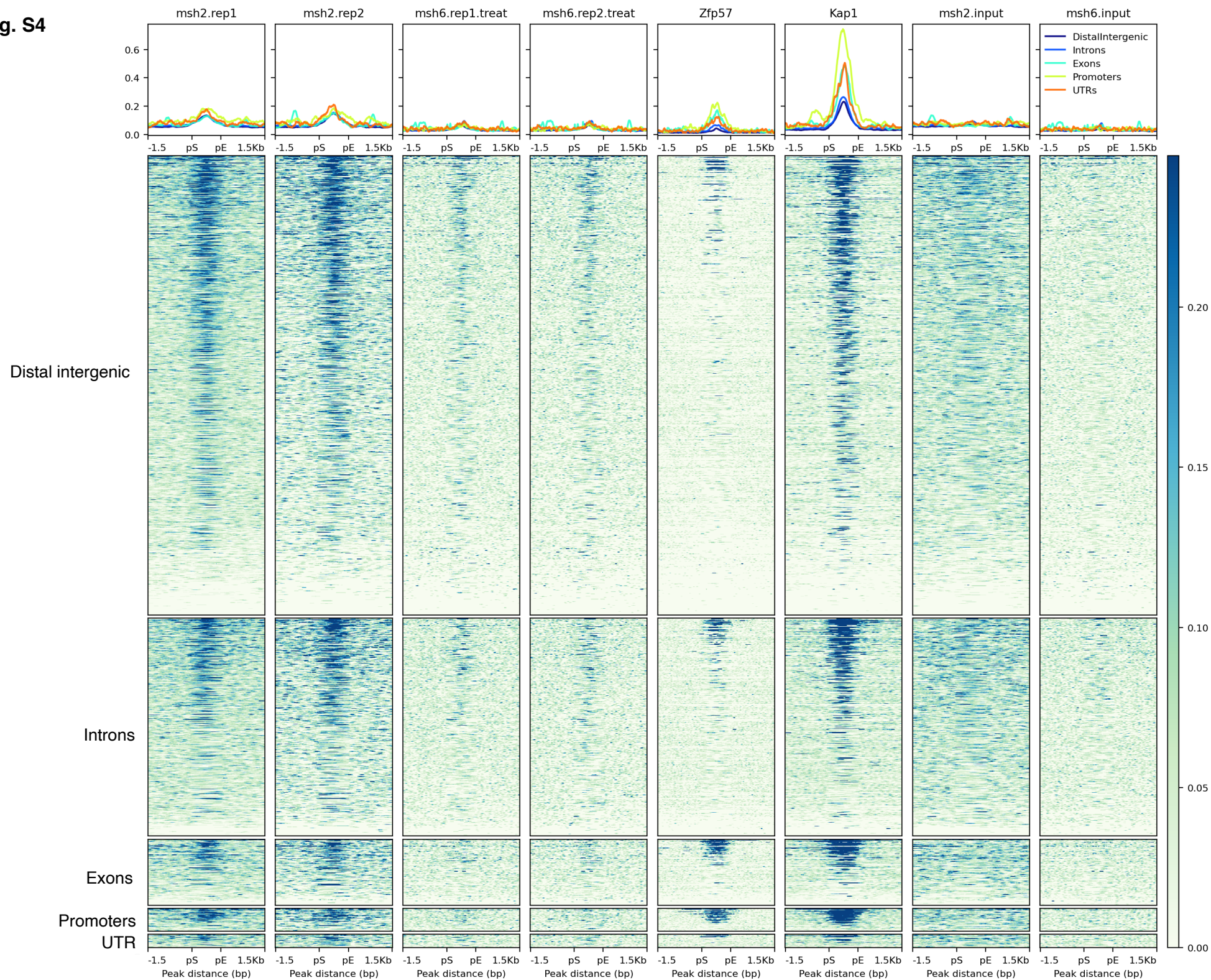


Fig. S5

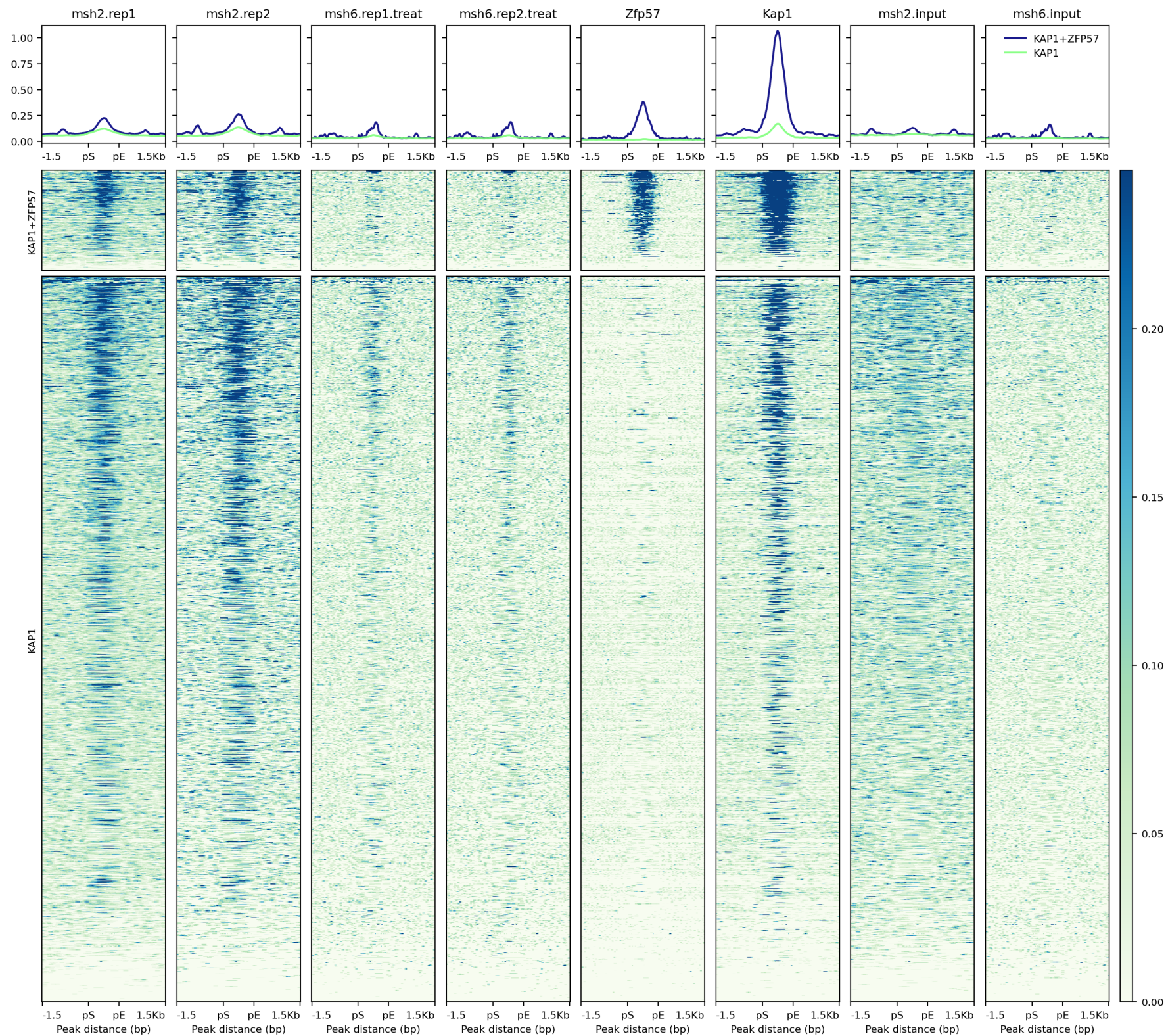


Fig. S6

