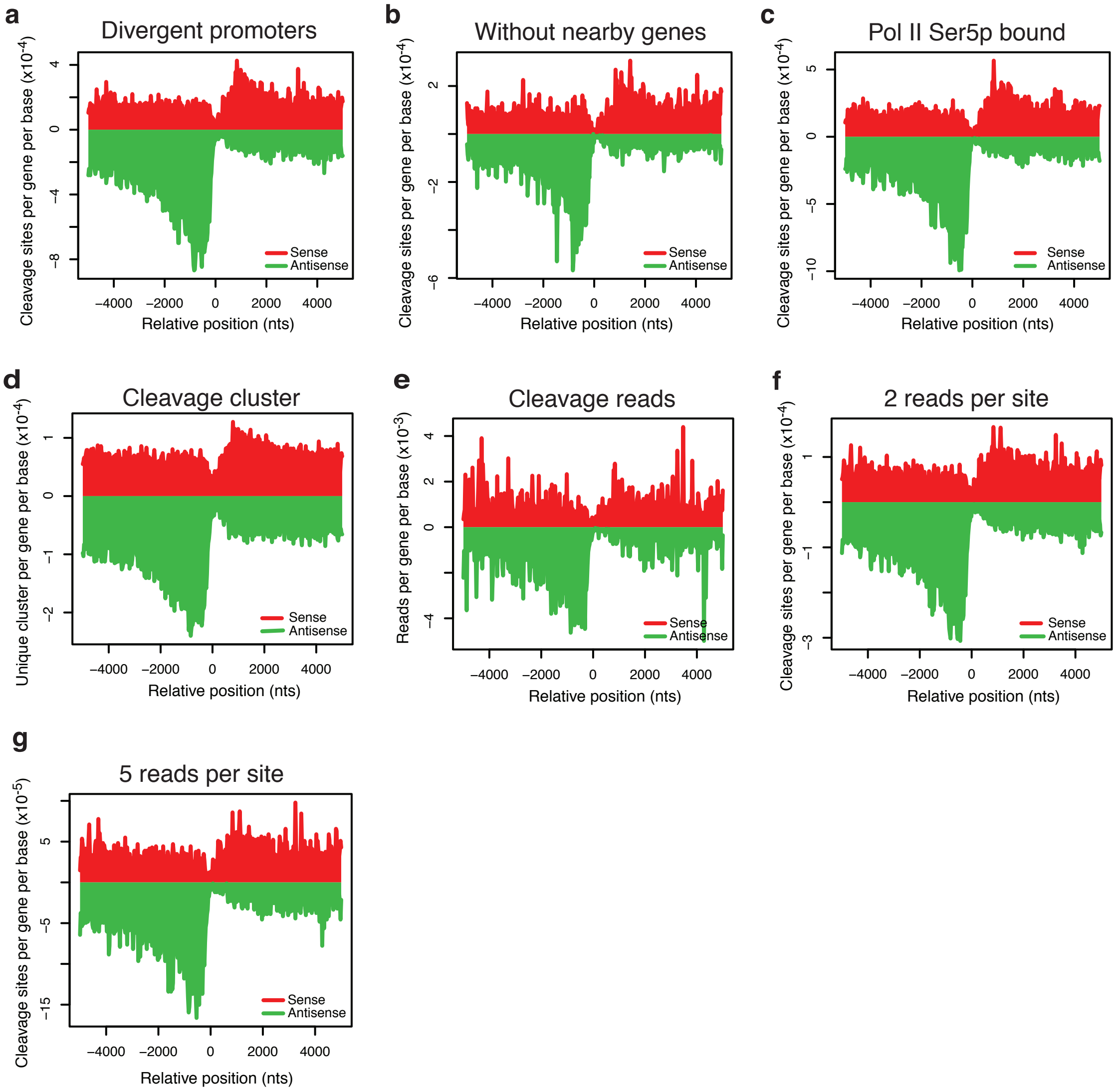

Supplementary Figure 3. Metagene analysis of cleavage sites near gene TSS. Displayed metagene plots (a-g) were generated in the same way as Figure 1a with the specified modifications. (a) Plot focusing on divergent promoters (details in methods), (b) or a subset of promoters where the gene is at least 6 kb in size and there are no other TSS or TES within the 10 kb window. Unlike Figure 1a, sites within 5 kb of TES were not removed. (c) A plot displaying a subset of promoters that showed significant Ser5 phosphorylated Pol II peaks in mESCs. For metagene plots a-c, only unique cleavage sites are being plotted. (d) Plotting the density of unique cleavage clusters (cleavage sites within 24 bps were clustered together and the most 5’ sites are used as a reference site of the cluster). (e) Plotting read density instead of unique cleavage sites. Sites with more than 500 supporting reads were removed from the plot since they could be unannotated gene ends. Metagene plots (f-g) were generated in the same way as Figure 1a except taking a subset of unique cleavage sites with at least two (f) or five (g) supporting reads.