



Figure 6—figure supplement 1. CUT&RUN recapitulates X-ChIP-seq but with higher dynamic range

For a direct comparison of genome wide dynamic range at previously identified CTCF binding sites, 10 million reads were randomly selected from ENCODE CTCF X-ChIP-seq (GSM749690) and CUT&RUN datasets and plotted at ENCODE peak called sites (GSM749690_narrowPeak) and ordered by genomic location. The upper plot shows the mean average of raw counts over these sites and heatmaps below are ordered by genomic location.