



Figure 6—figure supplement 4. CUT&RUN can map heterochromatin with a high dynamic range

CUT&RUN was performed for H3K27me3 in K562 cells either by extracting all the DNA after digestion followed by size selection or allowing cut fragments to diffuse out of the nuclei. For comparison ENCODE H3K27me3 X-ChIP-seq (GSM733658) dataset was analyzed. For each dataset 10 million reads were randomly selected and a typical genomic region is shown with the upper panels equally scaled and the lower panel rescaled for the ENCODE dataset.