



Figure 6–figure supplement 3. The high signal-to-noise ratio of CUT&RUN allows robust identification of DNA binding sites not possible with X-ChIP-seq

CUT&RUN was performed for Myc and Max in K562 cells and compared to ENCODE X-ChIP-seq datasets (GSM935410; GSM935539). For each dataset 10 million reads were randomly selected and (A) a typical genomic region is shown. Note for Myc different antibodies were used and therefore quantitative comparison is not possible. (B) Proportional Venn diagrams displaying the overlap between Myc and Max peak called sites identified by CUT&RUN or previously by ENCODE. (C) Heat maps showing CUT&RUN and ENCODE X-ChIP-seq signal plotted at peak called sites identified by Max CUT&RUN (n=20146). Sites were ranked by Max CUT&RUN score; note the change in the dynamic range of the heat maps.