



Figure 7—figure supplement 2. Peaks identified by CUT&RUN have a more diverse range of motif scores than peaks from native ChIP.

Peak calling was performed on native CTCF ChIP (false positives were removed that did not contain a clear peak) and CUT&RUN. The underlying DNA sequence was extended in both directions by 100 bp and the best match and score to the JASPAR position frequency matrix (MA0139.1) calculated. Histograms plot the distribution of motif scores.