Additional file 6. Assessing the influence of the sequencing depth on the performance of compared peak callers. (A) Two CTCF ChIP-seq datasets were merged to create a meta dataset of more than 36M reads; then subsets were derived by random sampling at indicated levels; each sub-sampling was done twice independently to obtain pseudo replicates. (B) Venn-diagrams illustrating the number of binding sites identified by different peak callers relative to MeDiChISeq for CTCF subset profiles with different total mapped reads (TMRs).