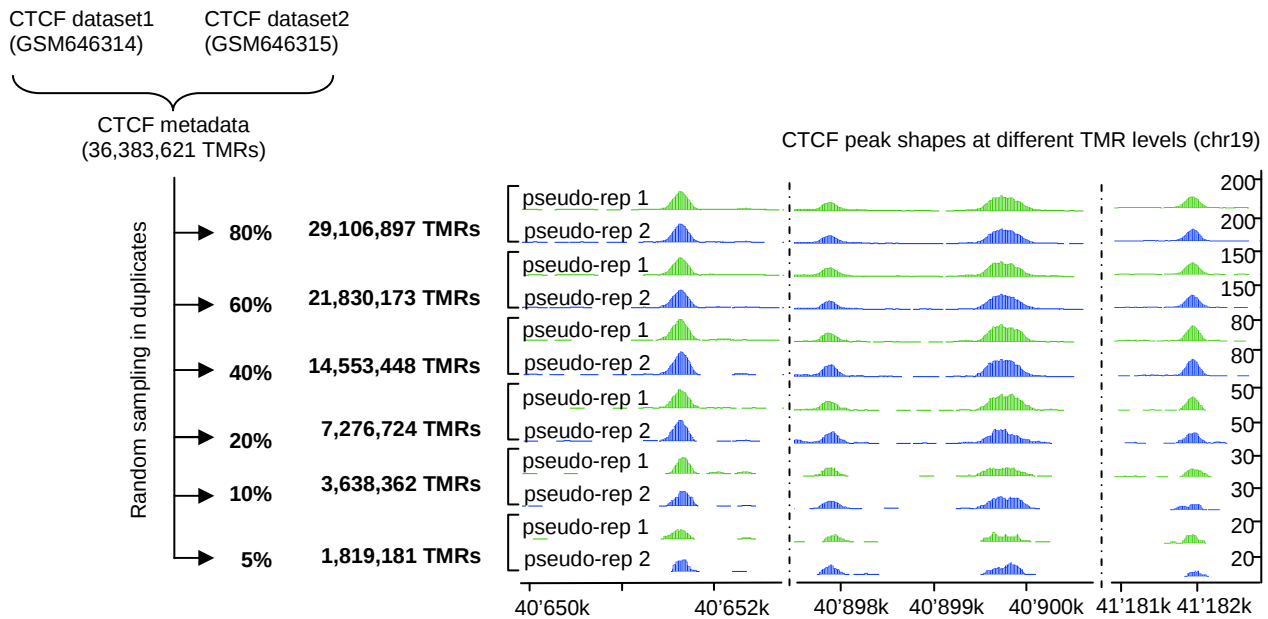
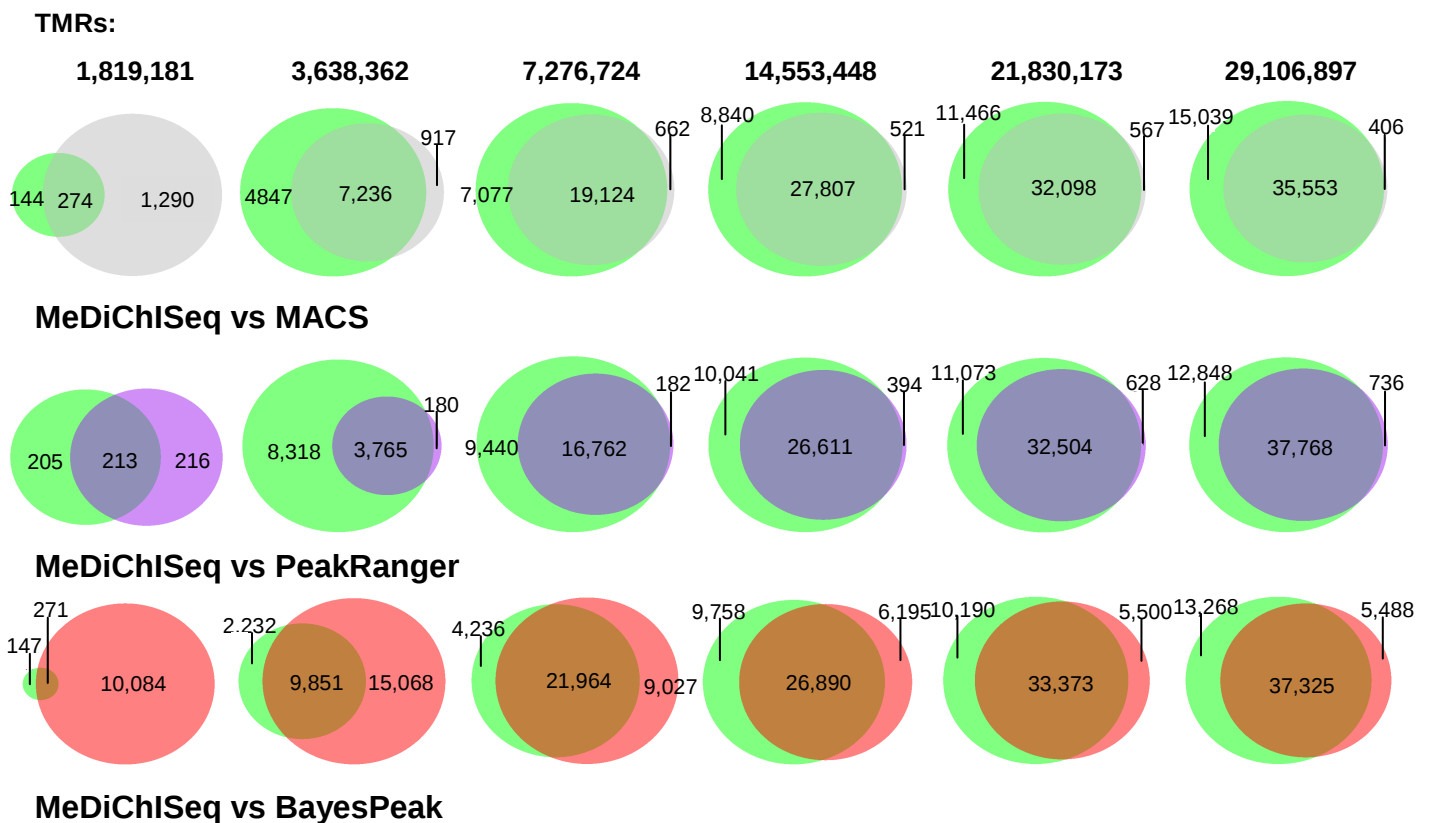


A



B



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).