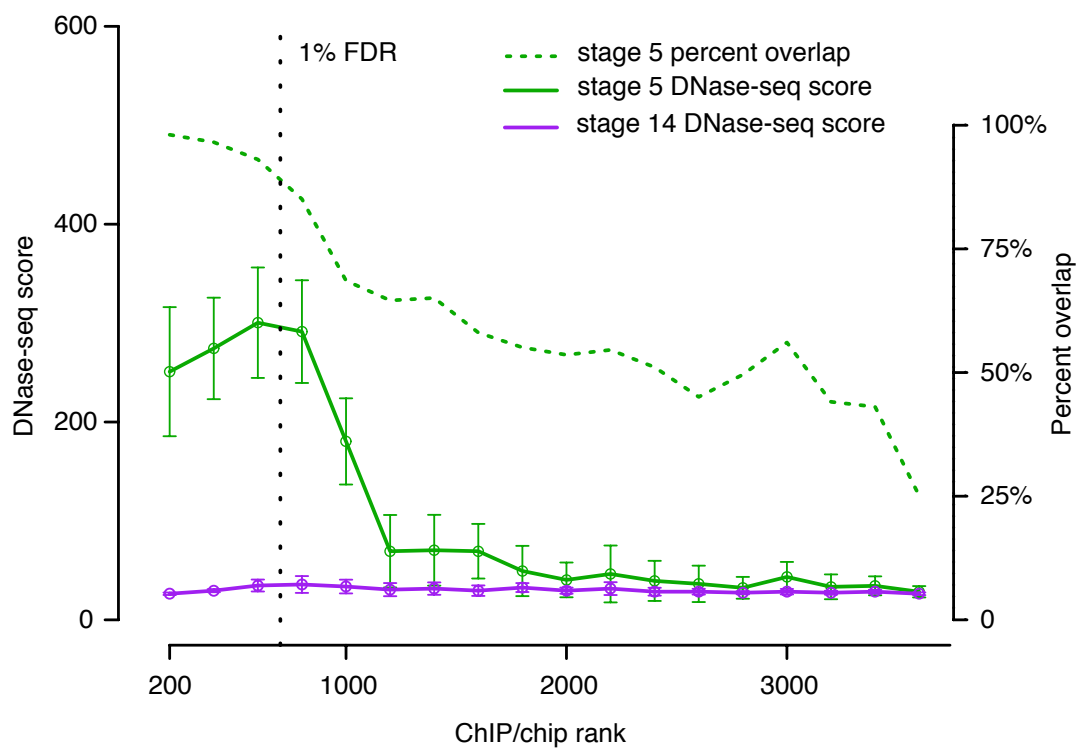
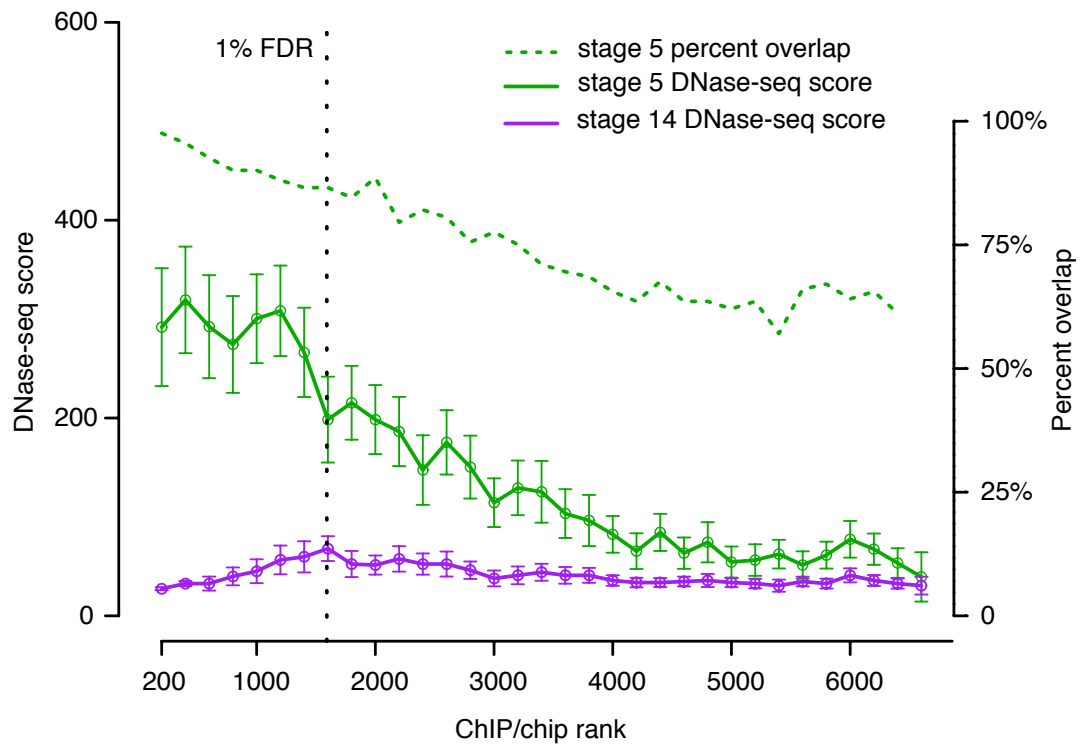


Additional data file 7. The level of transcription factor occupancy correlates with the degree of DNaseI accessibility. The median DNase-seq tag density in non-overlapping cohorts of 200 ChIP-chip 1 kb peaks is shown down to the ChIP-chip rank list (continuous lines). The ChIP-chip data are from stage 5 embryos and the DNaseI accessibility data is from stages 5 (green) and 14 (purple). 95% confidence limit for the median DNaseI accessibility of each cohort is indicated. Shown also is the percent of ChIP-chip peaks that are overlapped by 5% FDR DNaseI accessible regions in stage 5 embryos (dashed green line). The regions most highly bound by transcription factors are to the left along the x-axis and results are plotted as far as the ChIP-chip 25% FDR cutoff. The location of the ChIP-chip 1% FDR threshold is indicated by a black, vertical dotted line. Results for all 21 regulatory transcription factors are shown.

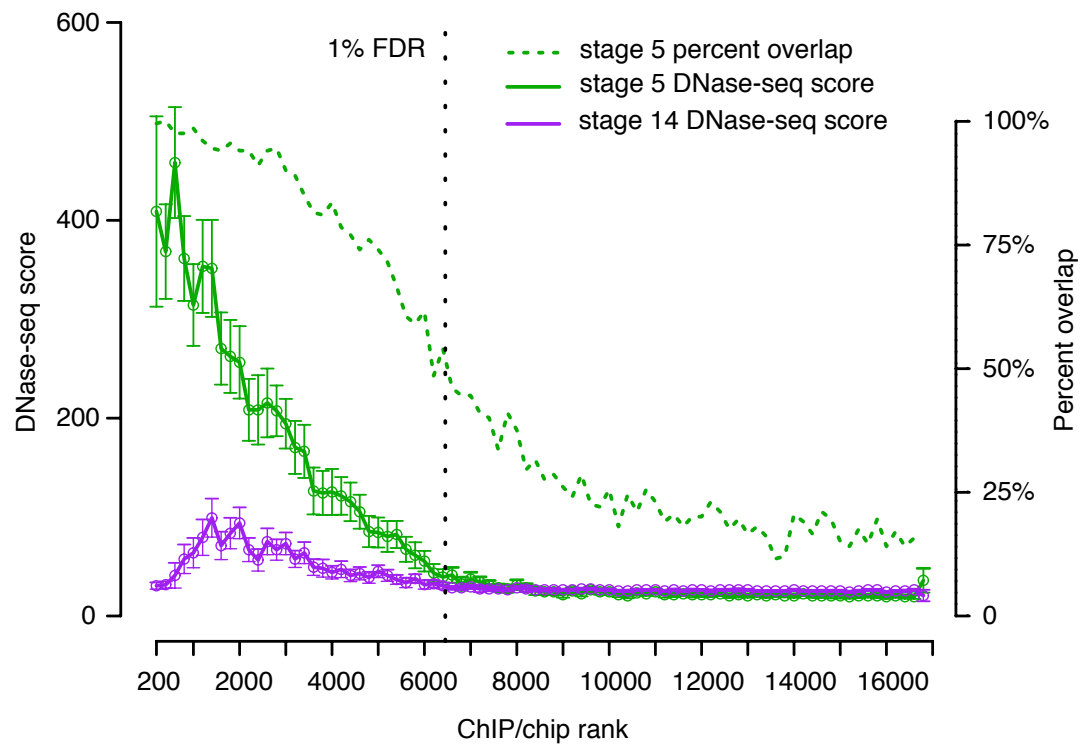
BCD

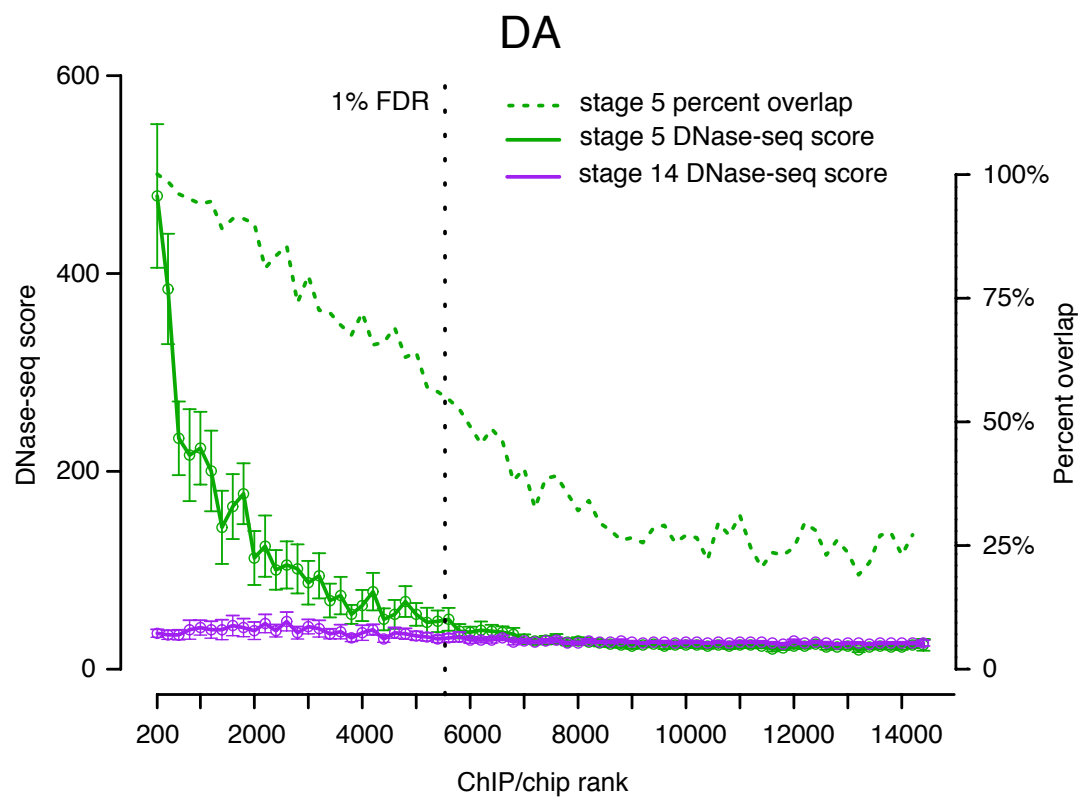


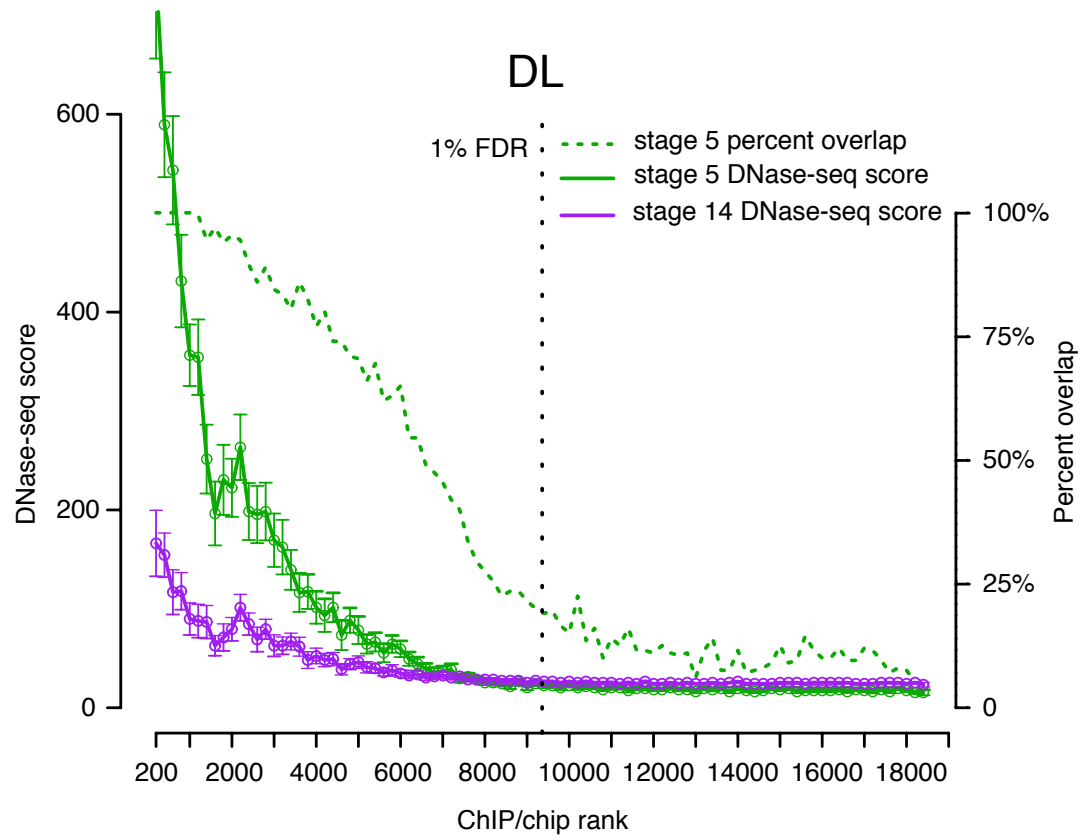
CAD



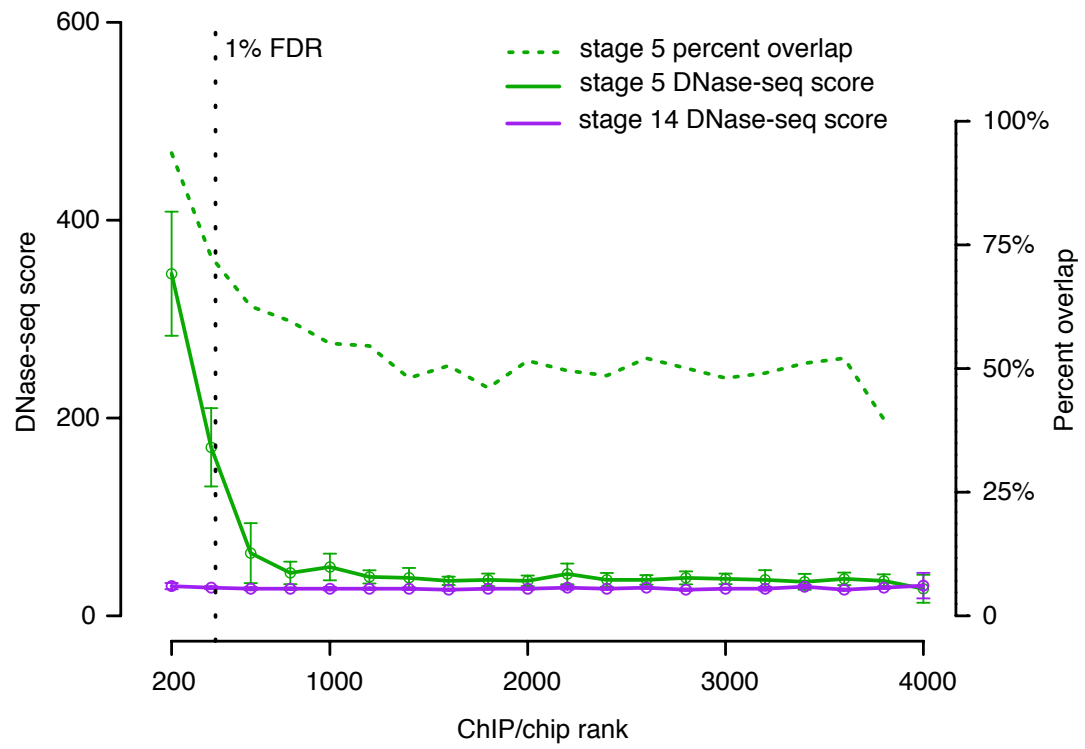
D

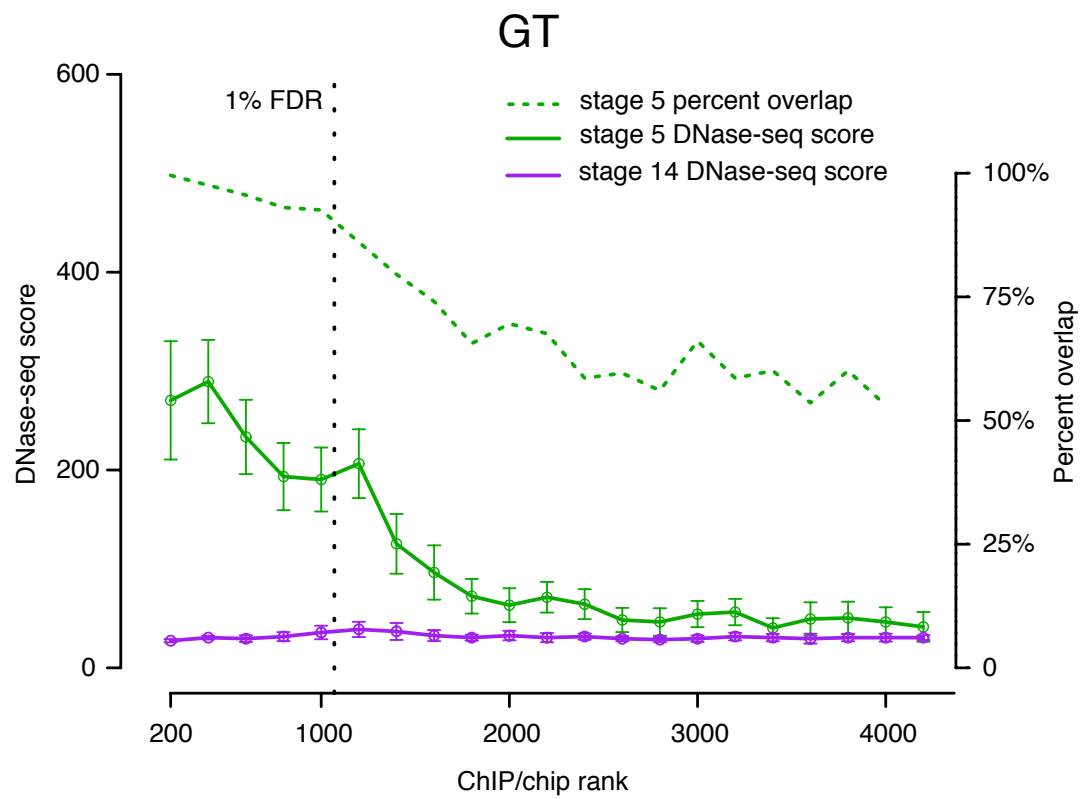


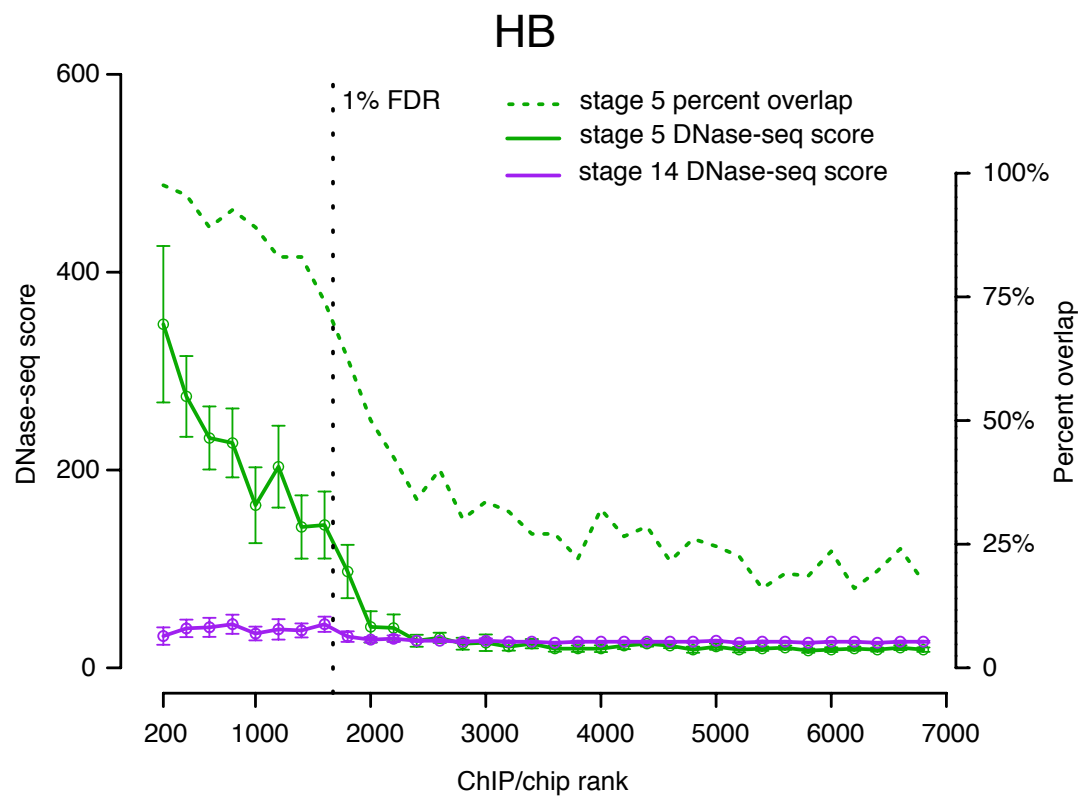




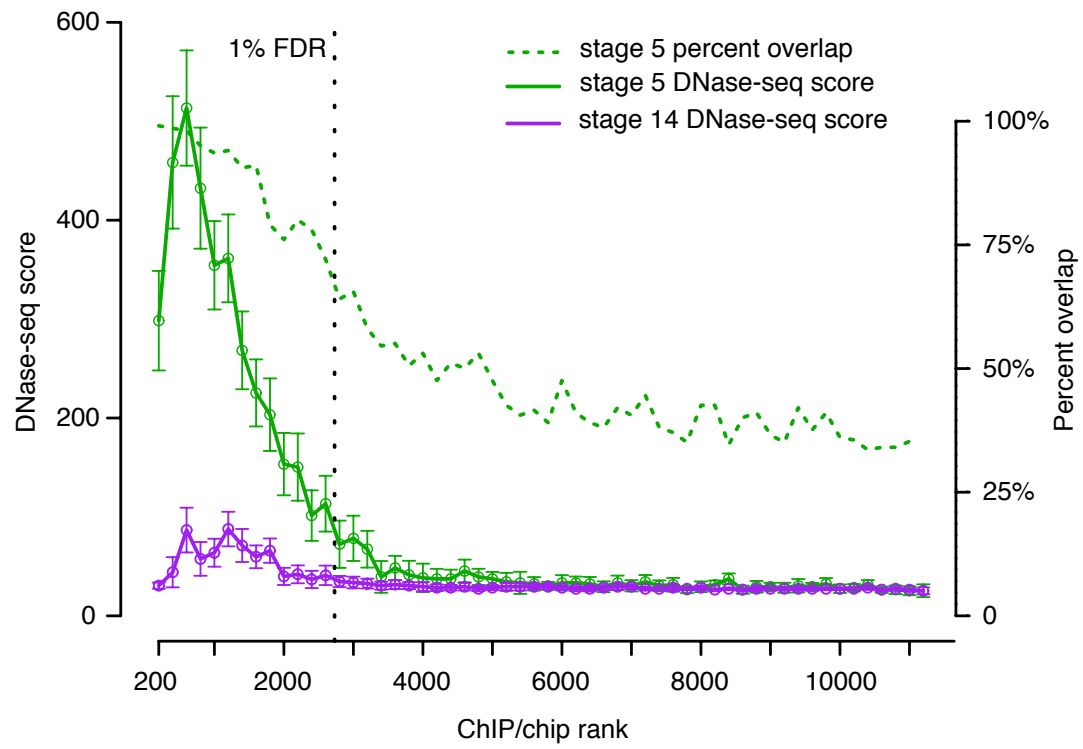
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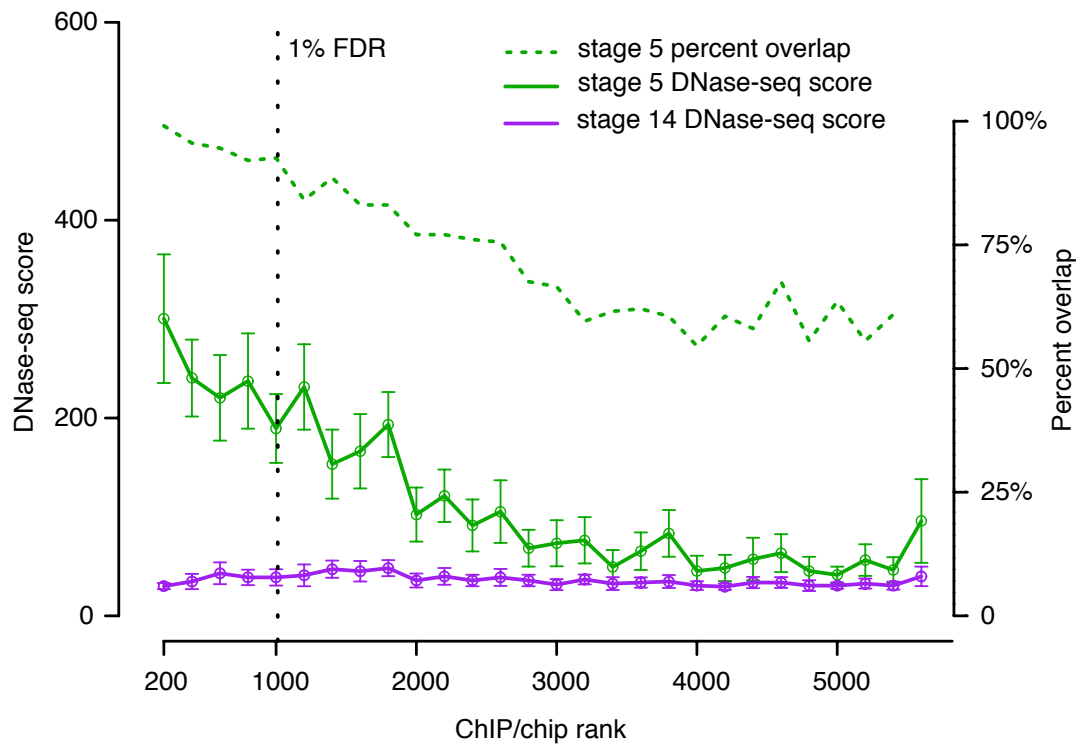


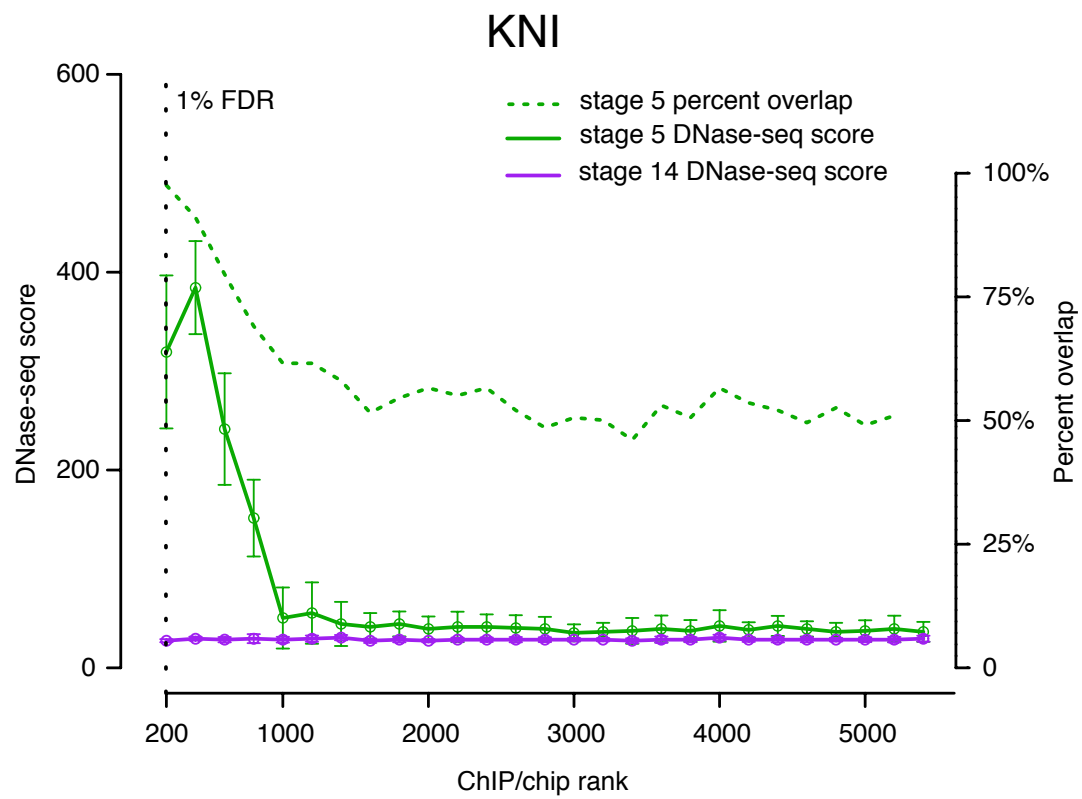


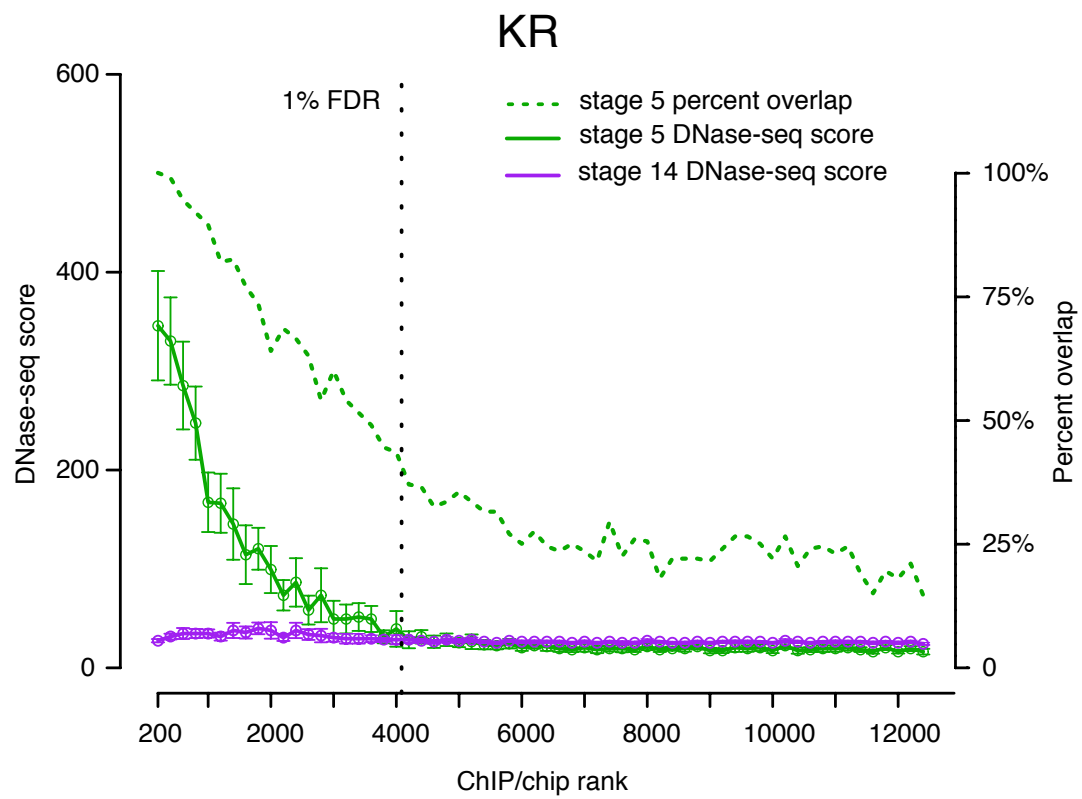
HRY



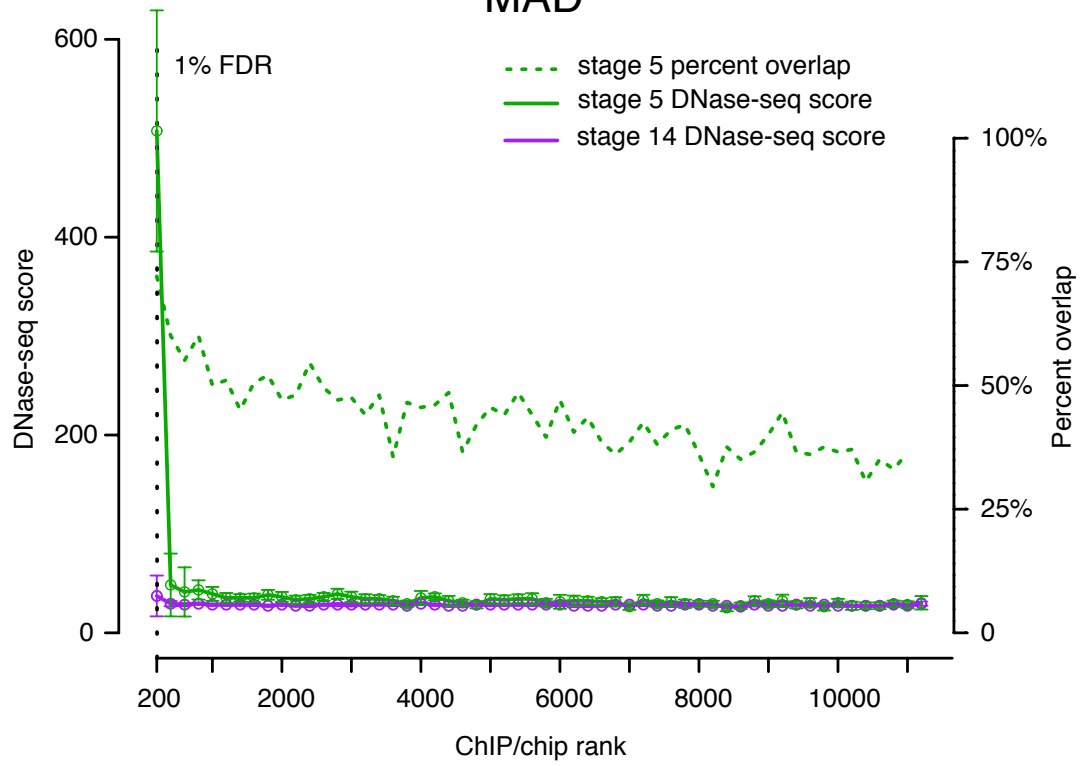
HKB

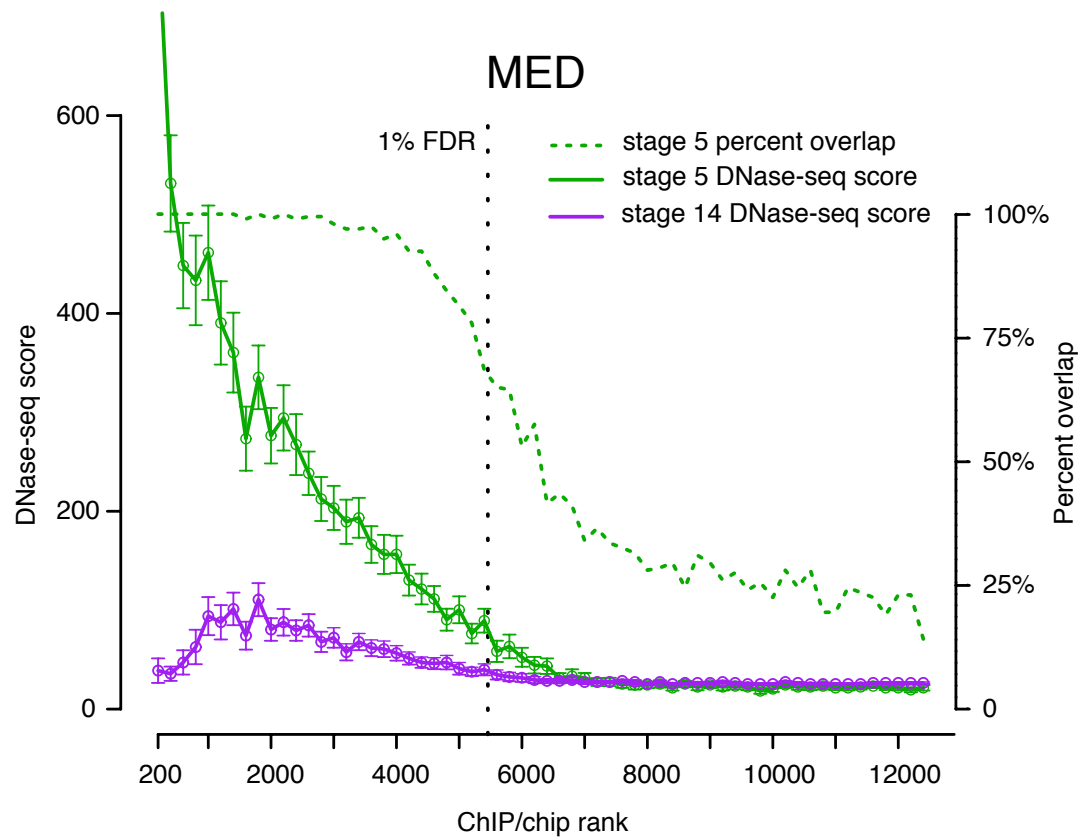




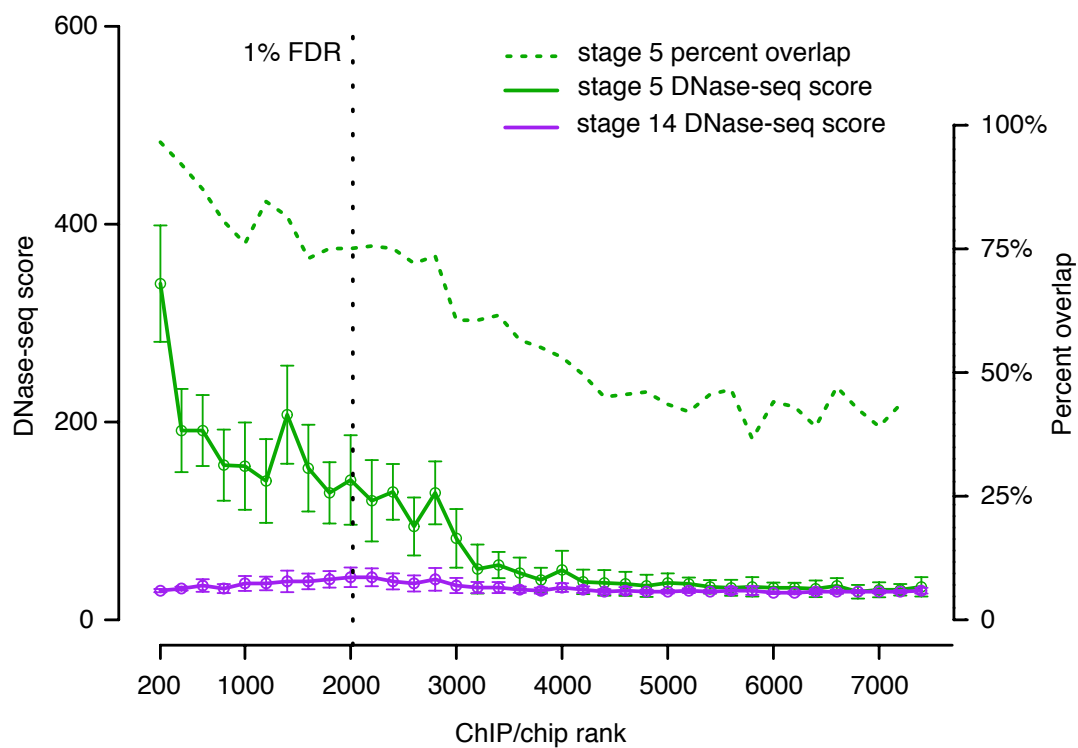


MAD

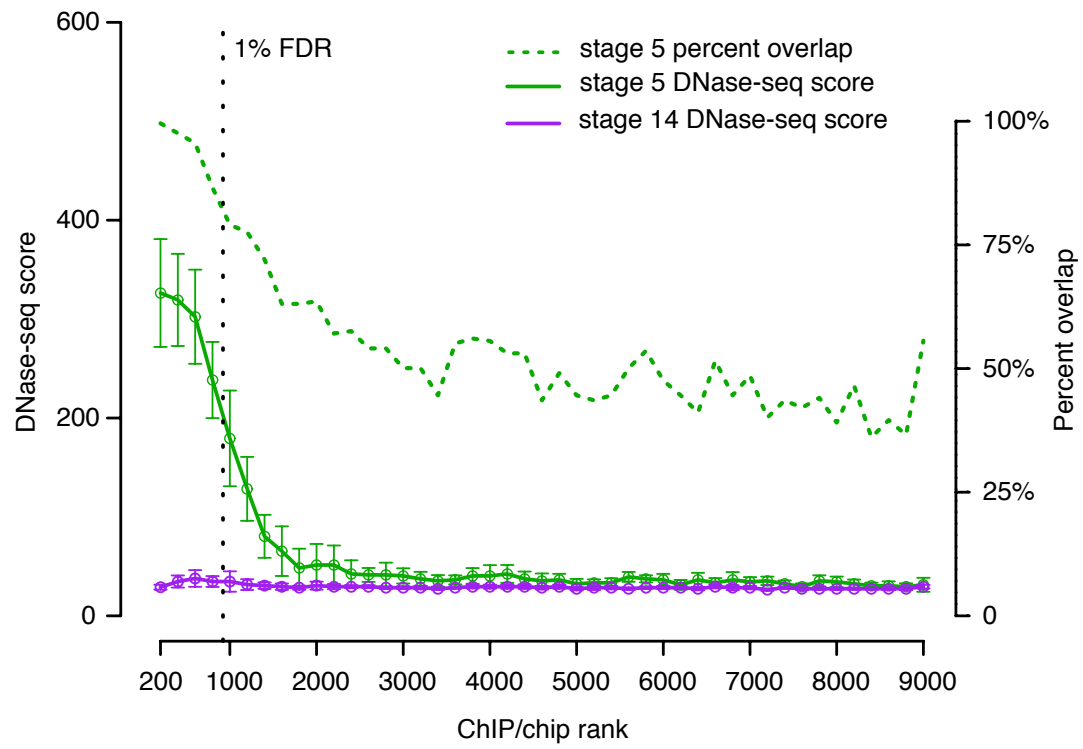




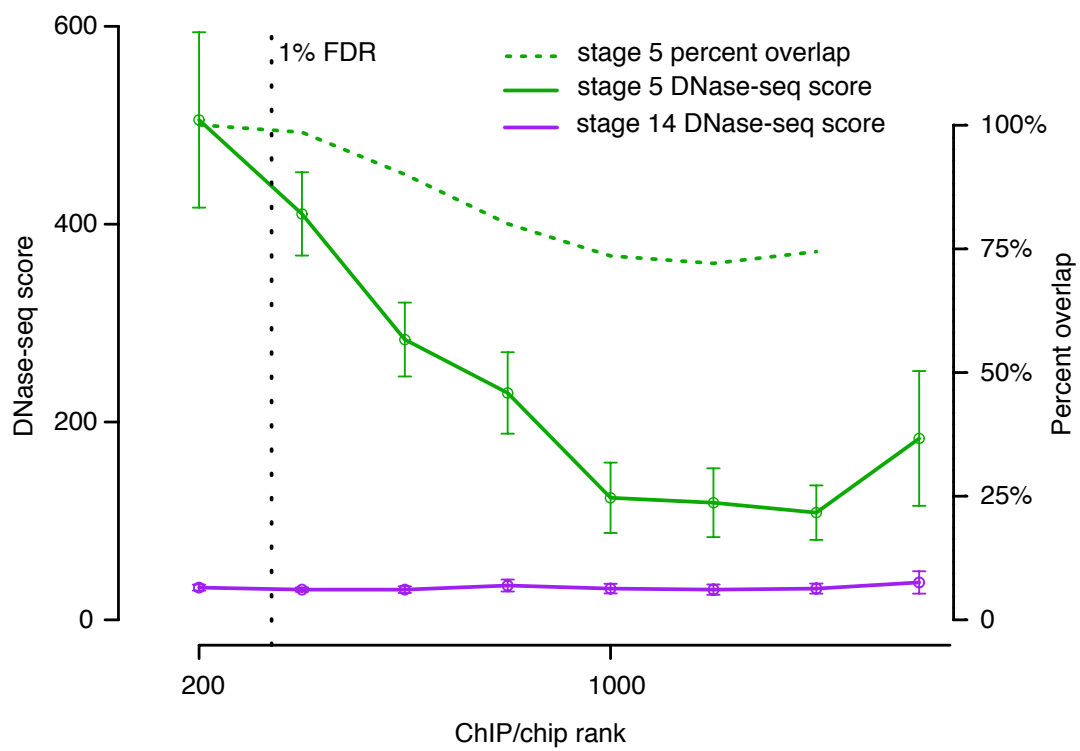
PRD



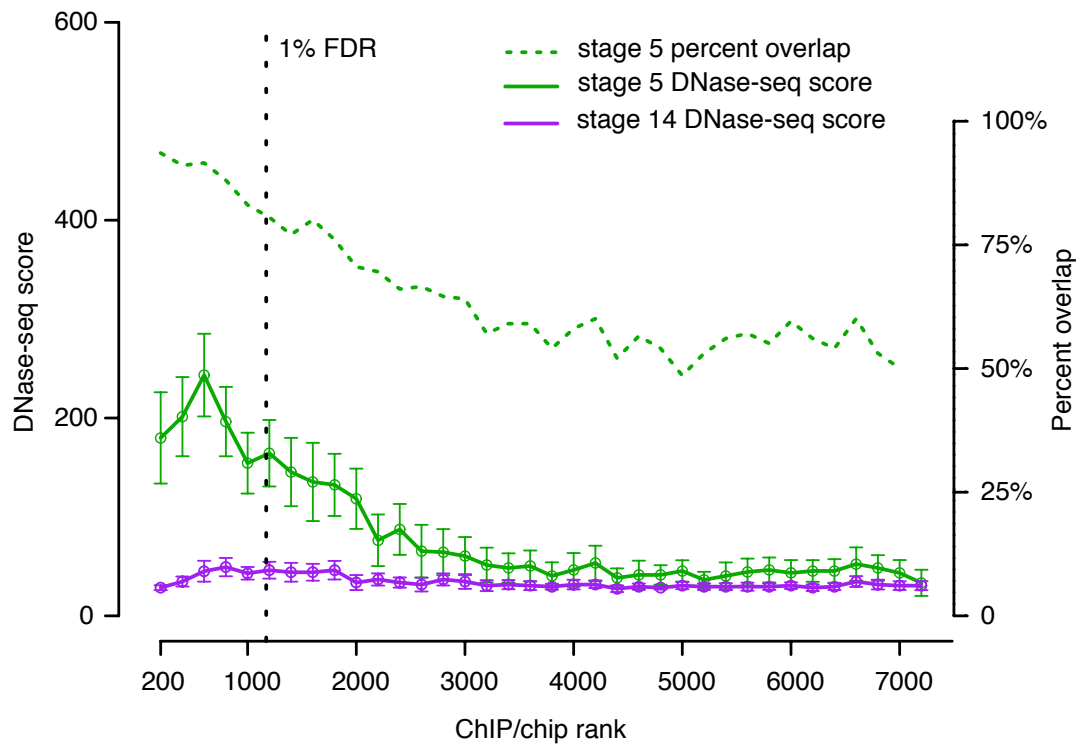
RUN



SHN



SLP1



SNA

