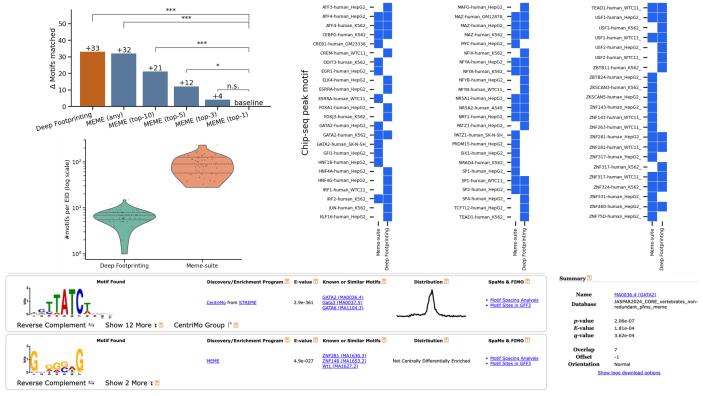
Week Report Sep W3

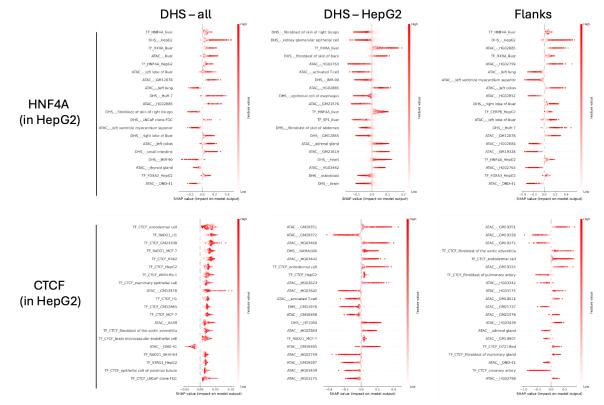
Comparative Analysis: Deep Footprinting vs. MEME-suite

- Conducted a comparative enrichment analysis between Deep Footprinting and MEME-suite (including tools such as FIMO, CentriMO, and STREME).
- Found that Deep Footprinting enrichment analysis yields more accurate results than MEME-suite. While MEME-suite can capture the transcription factor (TF) motif of interest, it underperforms in correctly identifying enriched motifs.
- · Observed a noticeable decrease in the number of correctly identified TF motifs in MEME-suite when narrowing the selection from top-10 to top-1 motifs.
- Included quantitative analysis on the number of output motifs per ChIP-seq peak for both methods, noting an order of magnitude difference (Deep Footprinting outputs significantly more accurate).
- Provided a heatmap and an example output for the GATA2 motif identified by MEME-suite for visual comparison.



Background Selection in Enrichment Analysis

- Initiated a comparative analysis on the impact of different background selections for enrichment analyses: DHS all-genome, DHS cell-line, and flanking regions.
- Early observations suggest differences depending on background choice. For cell-line specific TFs (e.g., HNF4A in HepG2) and for more ubiquitous TFs (e.g., CTCF in HepG2)
- \bullet Analysis on this aspect is ongoing and will continue next week.



Next Steps

- Finalize results for the background selection analysis.
- Start analysis on Enhancers.