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This week, I focused on capturing motifs in enhancers across different cell lines, with most of the analysis centered on HepG2, K562, and WTC11 since more data were available for these. I generated figures that are still in progress, but they already highlight several observations. In HepG2, we derived an enhancer contribution score that clearly presents an HNF4a motif. By disrupting this motif, specifically by altering the nucleotide with the highest contribution, the sequence was no longer classified as an enhancer by the model (figure a).

Enhancer sequences in general contain several motifs, as shown in figures b and e, and their detection depends on the chosen q-value threshold (figure d). Some motifs appear more frequently than others, indicating stronger contributions to enhancer function, and their position within the enhancer is not always centralized (figure c).



The next steps are to continue working on this experiment, writing, and addressing the Genes review.