

Predicting 8 chromatin states in held out chromosome in training cell type (GM12878 LCL)

Model + Input data types	8-class chromatin state accuracy (%)
Majority class (baseline)	42%
Gene proximity	59%
<u>Random Forest</u> : ATAC-seq (150M reads)	61%
Chromputer: DNase (60M reads)	68.1%
Chromputer: Mnase (1.5B reads)	69.3%
Chromputer: ATAC-seq (150M reads)	75.9%
Chromputer: DNase + MNase	81.6%
Chromputer: ATAC-seq + sequence	83.5%
Chromputer: DNase + MNase + sequence	86.2%
Label accuracy across replicates (upper bound)	88%