

## METHODOLOGY ARTICLE

## Open Access

ATAC2GRN: optimized ATAC-seq and  
DNase1-seq pipelines ~~for rapid and~~  
~~accurate genome regulatory network~~  
~~inference~~



 very  
misleading  
title

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08.11.19, Journal Club, Evi Berchtold



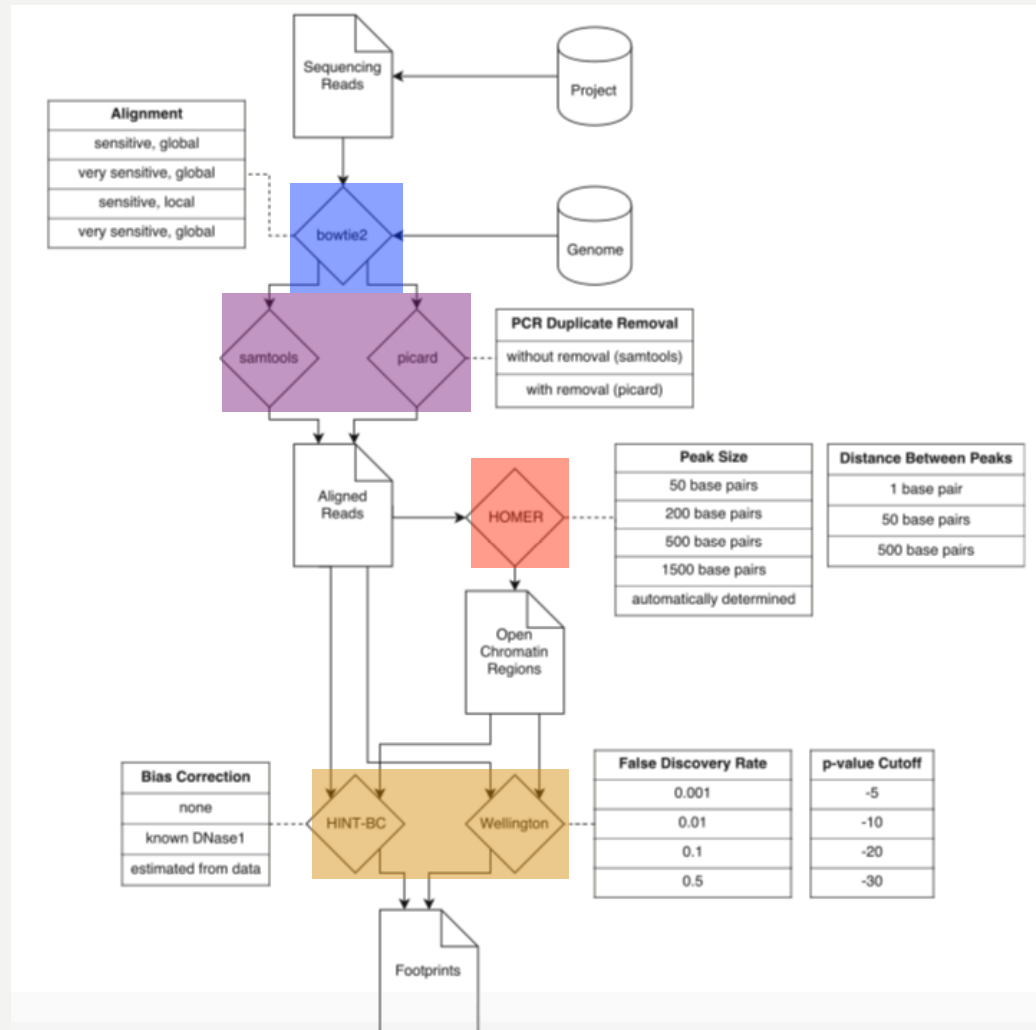


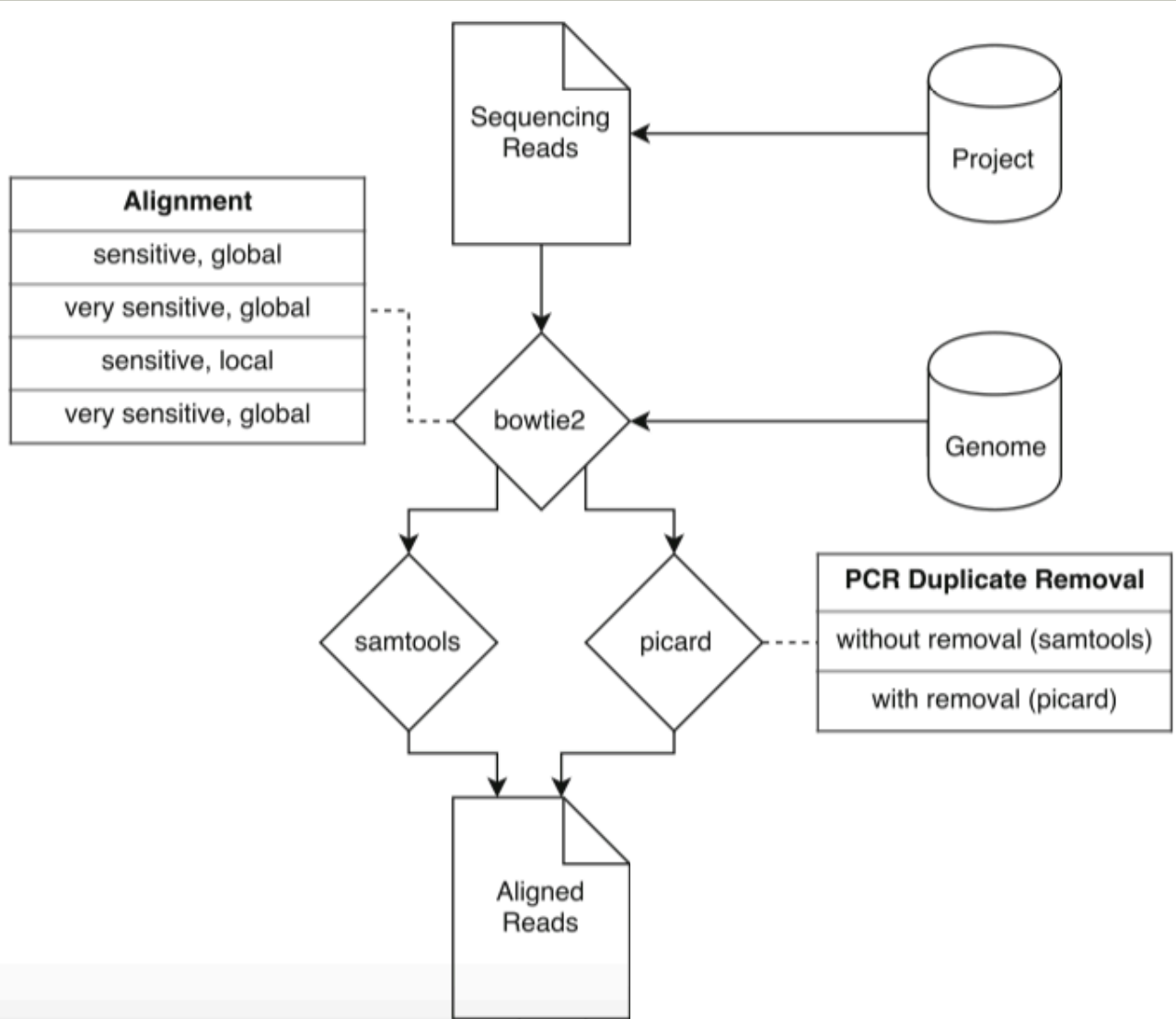
## Pipeline for ATAC/DNase-seq data

- mapping
- PCR duplicate removal
- peak calling
- footprint calling

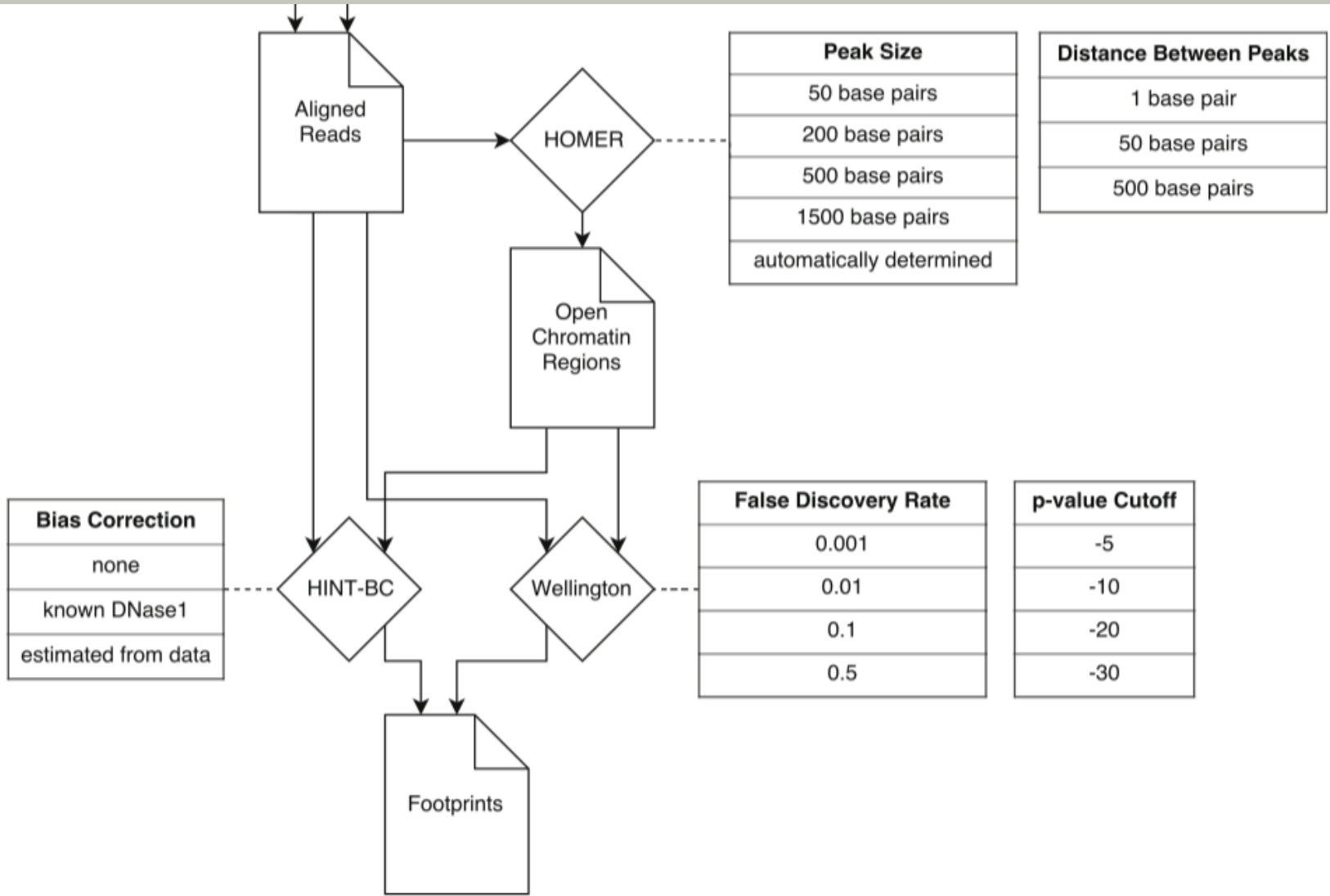
parameter search to optimize

- replicate consistency
- ChIPseq peak overlap



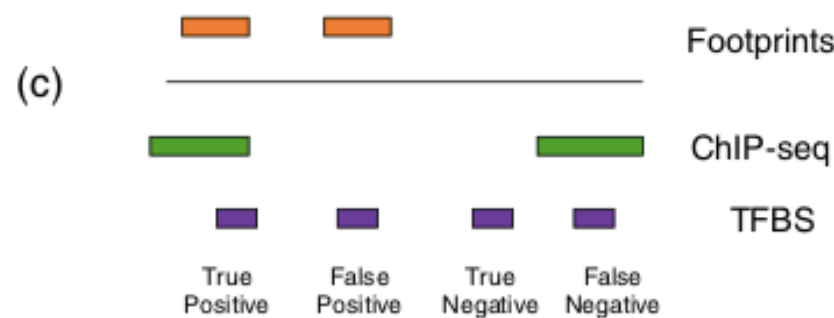
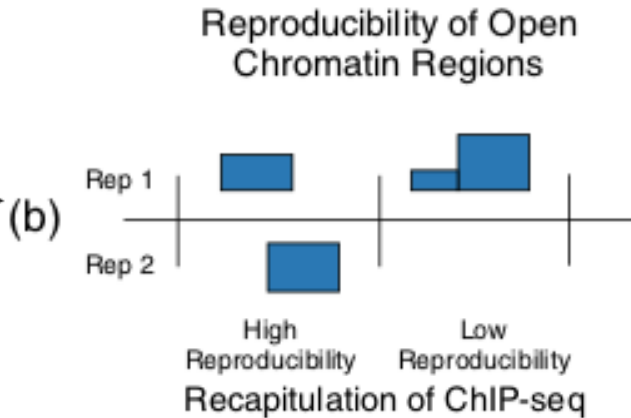
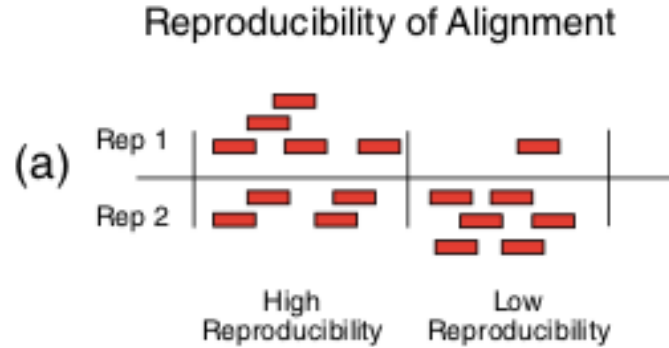
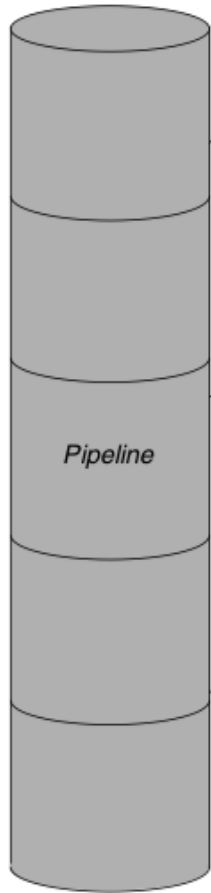


# Peak + FP calling





Replicate 1      Replicate 2



correlation bt #reads in 10kb bin

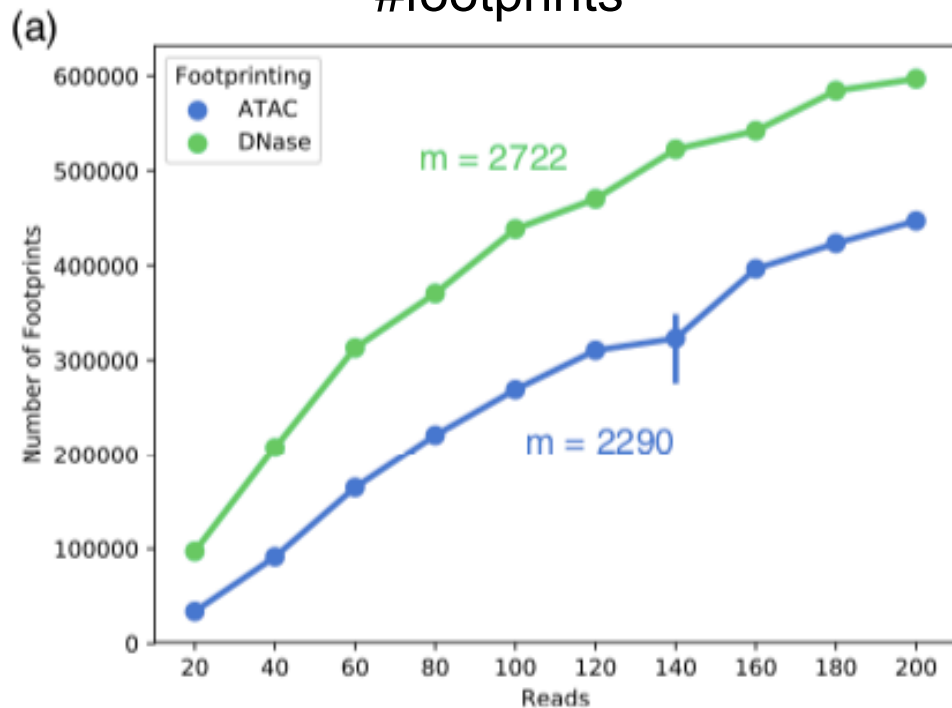
correlation bt avrg peak in 10kb bin

percentage of overlapping footprints

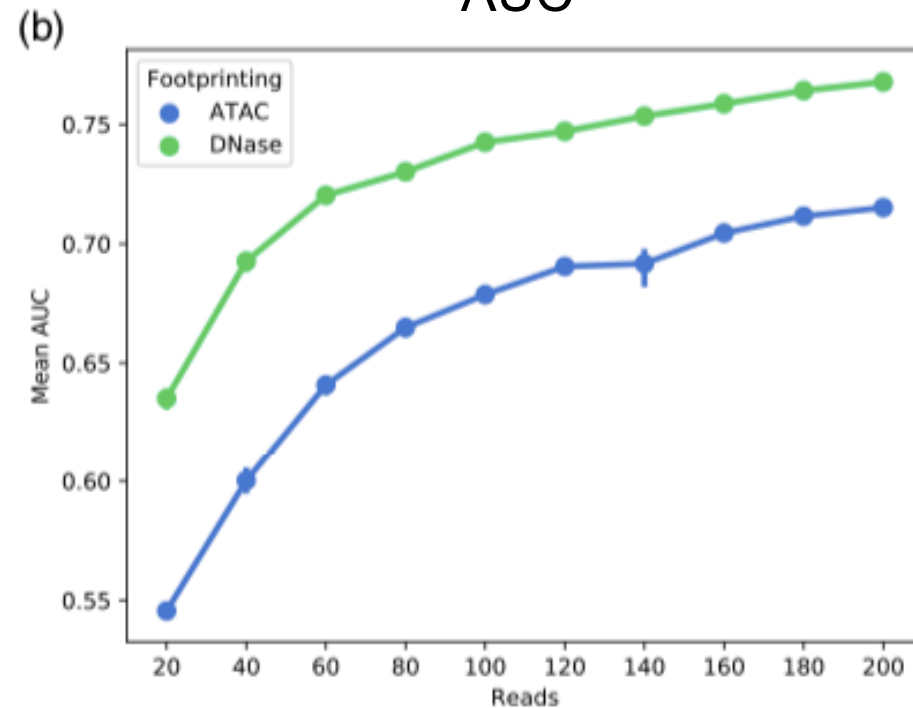
AUC

subsample #reads using seqtk

#footprints



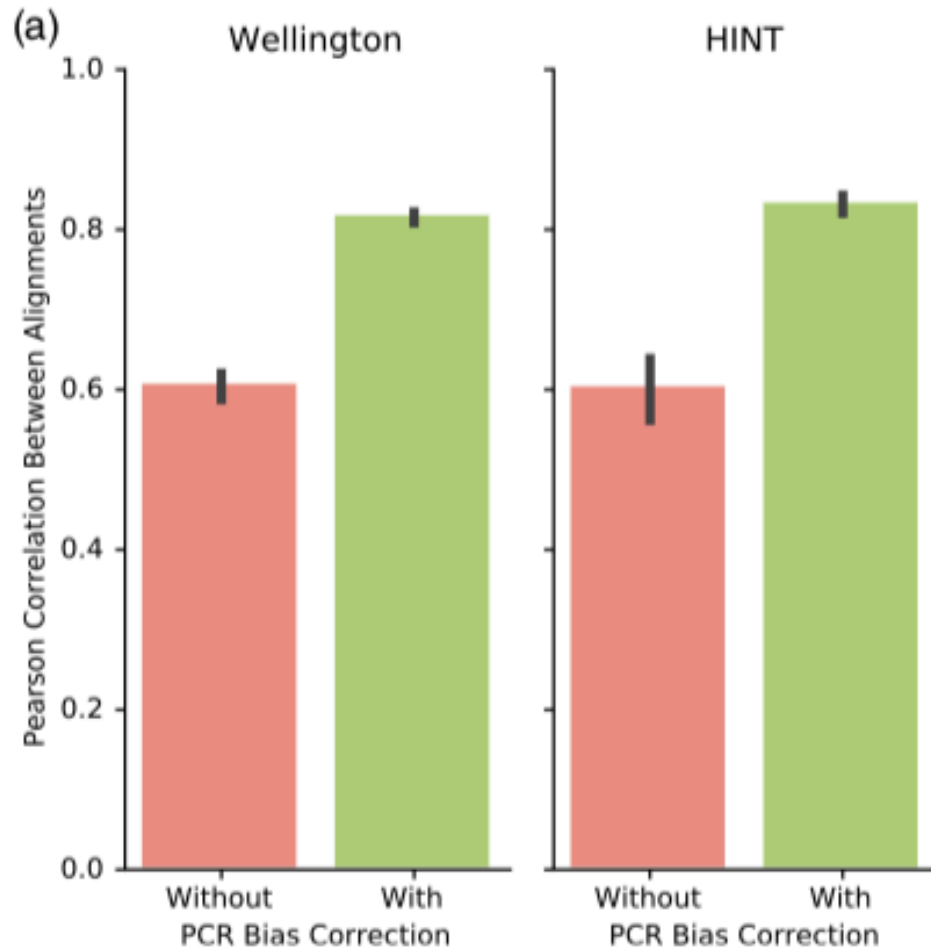
AUC



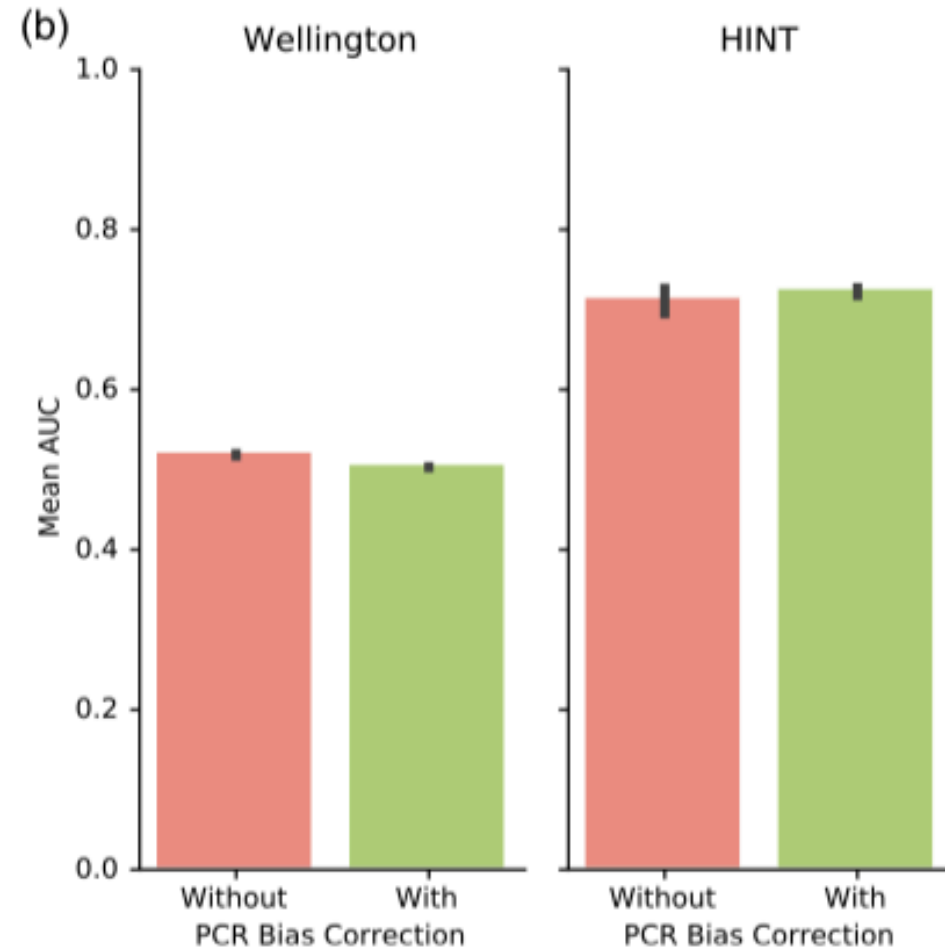
ATAC-seq: 2.85 billion reads for AUC=0.95

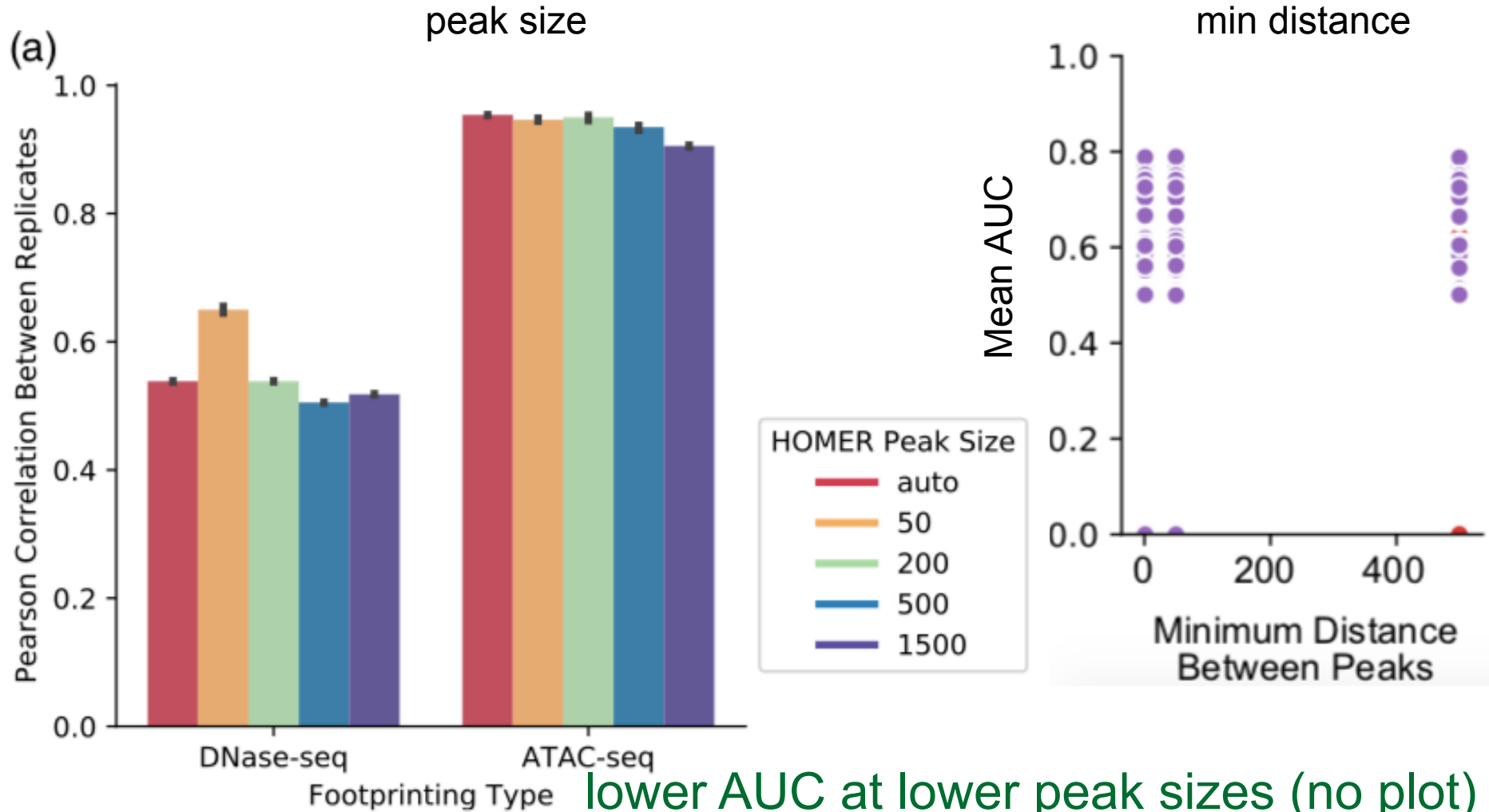
100 mio reads “defensable”, 160 mio “optimal” read depth

Correlation of #reads in bins



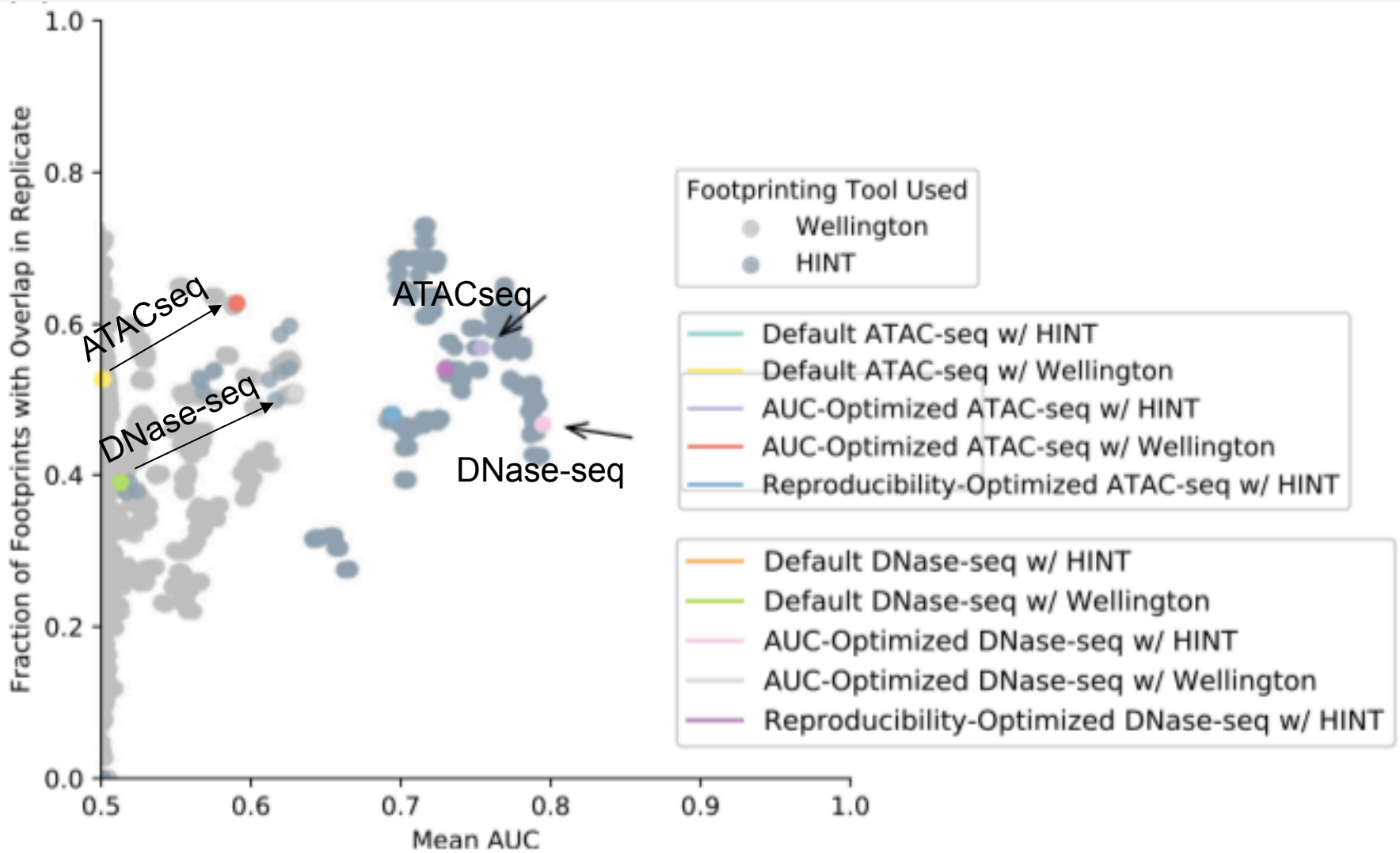
AUC

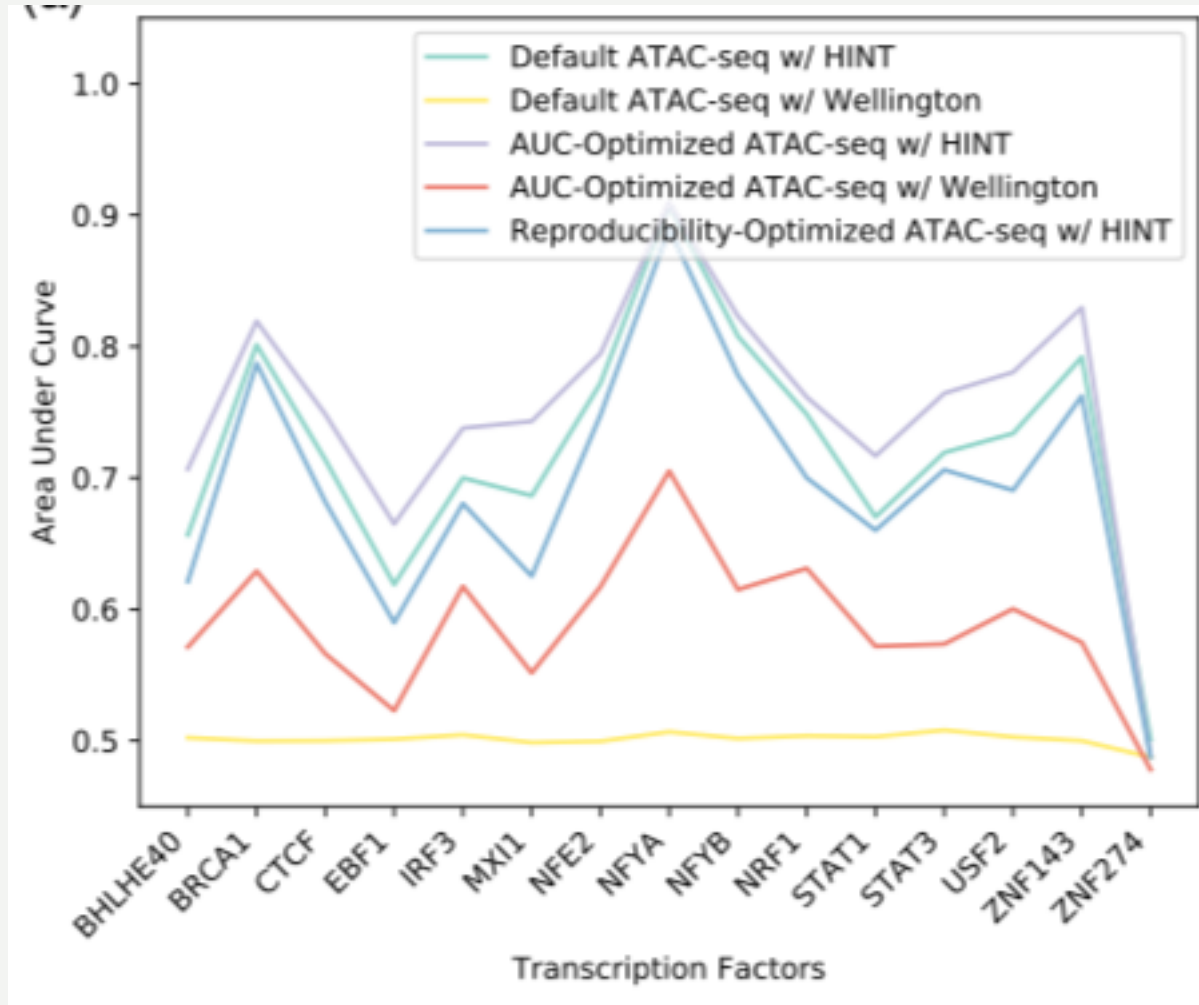




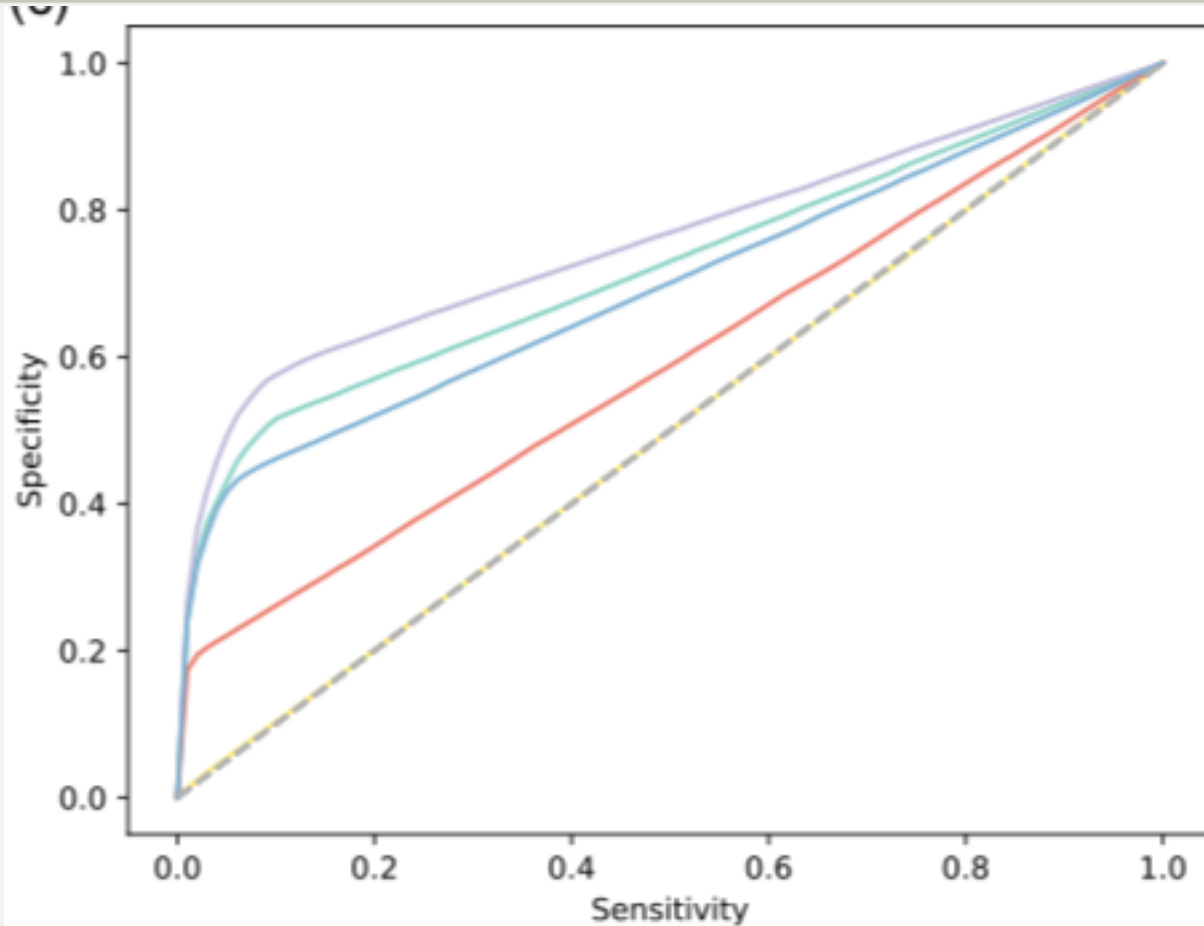
lower AUC at lower peak sizes (no plot)  
highest ChIPseq recovery at 200-500







imbalance of negative and positive TFBS of approx. 10:1



imbalance of negative and positive TFBS of approx. 10:1



- grid search over 4560 parameter combinations
  - but still limited to 1 mapper, 1 peak caller and 2 footprint caller
- claim that they produce a GRN is just wrong
- CHIP recovery plateaus at 160 mio reads
- PCR duplicate removal only affects reproducibility but not CHIP recovery
- smaller DHS peaks good for reproducibility but bad to AUC
- HINT's bias correction negatively affects AUC
- only little information in supplement, some conclusions only described in text without any figures/data available