

A

ID	Assay	Sample
0	ATAC-seq	22-2a
1	ATAC-seq	22-4a
2	ATAC-seq	22-5a

Choose genome assembly:

Mouse mm10

Current selected: 22-2a ATAC-seq, 22-4a ATAC-seq, 22-5a ATAC-seq

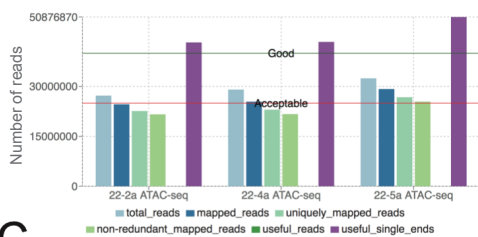
Update

Chart width: 800 px

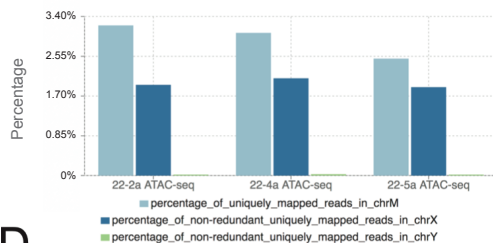
Chart height: 400 px

B Mapping

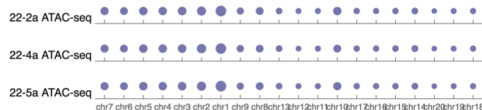
Standards based on useful single ends, Good: 40000000, Acceptable: 25000000



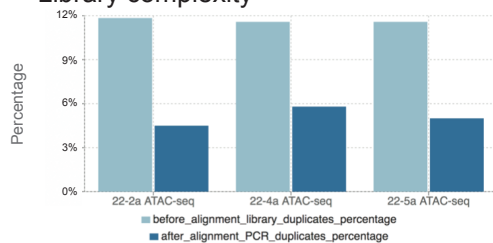
C chrM rate



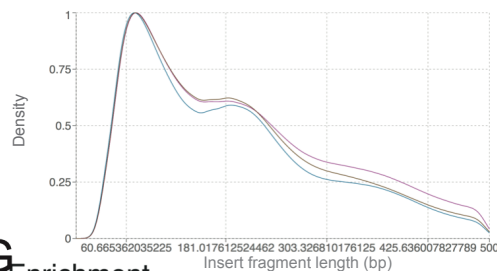
D Autosome mapping distribution



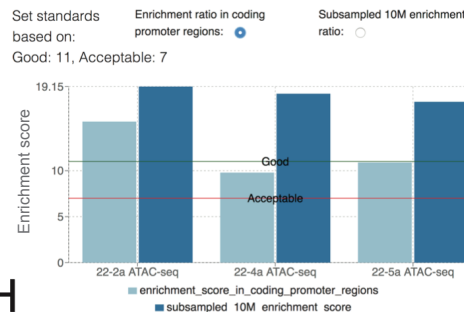
E Library complexity



F Insert size distribution



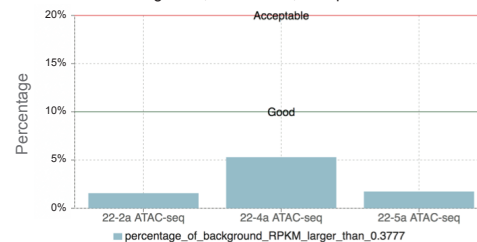
G Enrichment



H

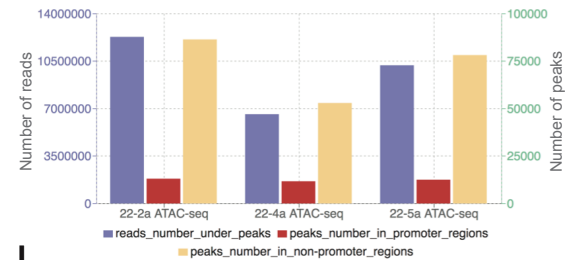
Background

Standards for background, Good: 10%, Acceptable: 20%



I

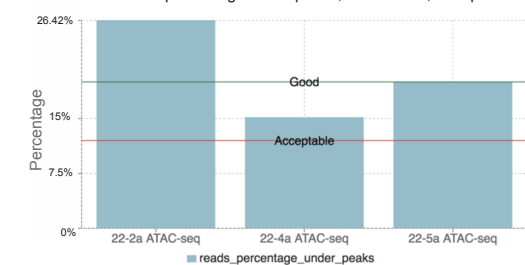
Peaks



J

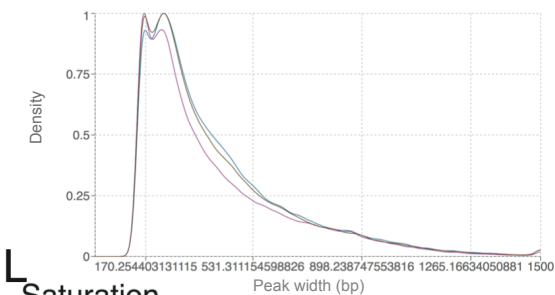
RUPr

Standards for reads percentage under peaks, Good: 20%, Acceptable: 12%



K

Peak size distribution



L

Saturation

