CHANCE: ChIP-seq Analytics and Confidence Estimation

Main Output:

Export main output to text file

View IP strength

Compare with ENCODE

Multi IP normalization

Validate region list

View nucleotide frequency

View Phred score map

View read density bias

Welcome to CHANCE!
Reading wgEncodeBroadHistoneH1hescH3k4me1StdAlnRep1.bam... this may take a few minutes.
wgEncodeBroadHistoneH1hescH3k4me1StdAlnRep1.bam processed successfully, 8951369 tags proce
broad_data.mat loaded
6 samples loaded
Wrote matlab binary file broad_data_copy.mat

Samples:

Create sample

Delete sample

H1 HESC Broad H3K27me3 IP - # reads: 6434800 - genome: hg19 - broad_data.mat
H1 HESC Broad H3K36me3 - # reads: 6434800 - genome: hg19 - broad_data.mat
H1 HESC Broad H3K4me1 IP - # reads: 6434800 - genome: hg19 - broad_data.mat
H1 HESC Broad H3K4me2 - # reads: 6434800 - genome: hg19 - broad_data.mat
H1 HESC Broad H3K4me3 IP - # reads: 6434800 - genome: hg19 - broad_data.mat
H1 HESC Broad Input - # reads: 6434800 - genome: hg19 - broad_data.mat

Save samples to file

Restore saved samples