



## 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 wgEncodeBroadHistoneH1heschH3k4me1StdAlnRep1.bam... this may take a few minutes.  
wgEncodeBroadHistoneH1heschH3k4me1StdAlnRep1.bam processed successfully, 8951369 tags processed  
broad\_data.mat loaded  
6 samples loaded

## 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](#)