

Annotation

ChIP-seq data

Expression data

Allelic imbalance data

hg19.gtf

H3K36me3.bigWig

H3K27me3.bigWig

input.bigWig

RNA-seq

MAE/BAE status

Process.R

calculate mean ChIP-seq and RNA-seq values per gene (with bwtools)

normalize ChIP-seq to input and calculate percentiles

percentile scores

Generate.R

train classifier

print classifier metrics

model

Analyze.R

predict

filter by expression and length

