Complete list of ENCODE metrics EM

StrandShift: cross-correlation peak coordinate is fragment-length strand shift value on x-axis

PBC: number of genomic locations to which exactly one uniquely mapping read is located / the number of genomic locations to which at least one uniquely mapping read is located, i.e. the number of non-redundant uniquely mapping reads

readLength: length of the read

A: cross-correlation peak coordinate, y-axis

B: phantom-peak in cross-correlation profile, y-axis

C: baseline of cross-correlation coefficient values at extreme strand-shifts (height of line C on the y-axis)

NSC: NSC=A/C

RSC: RSC=(A-C)/(B-C)

QualityFlag: quality control tag

ALL_TAGS: number of mapped reads

UNIQUE_TAGS: number of uniquely mapped reads

UNIQUE_TAGS_LibSizeadjusted: adjusted by library size

UNIQUE_TAGS_nostrand: ignoring the strand direction

NRF: UNIQUE_TAGS/ALL_TAGS

NRF_nostrand: NRF ignoring the strand direction

NRF_LibSizeadjusted: NRF adjusted by library size

FDRpeaks: number of called peaks using FDR threshold

evalpeaks: number of called peaks using e-value threshold

FRiP_broadPeak: Fraction of reads under broad peaks

FRiP_sharpPeak: Fraction of reads under the sharp peaks

outcountsBroadPeak: number of broad peaks called

outcountsSharpPeak: number of sharp peaks called

Complete list of Global enrichment profile Metrics GM

X.axis: point of maximum distance between ChIP and Input, x-coordinate in the CHANCE plot

Y.Input: point of maximum distance between ChIP and Input, y-coordinate of Input in the CHANCE plot

Y.Chip: point of maximum distance between ChIP and Input, y-coordinate of ChiP in the CHANCE plot

DistanceInputChip: maximum distance between ChIP and Input

sign_chipVSinput: sign of the maximum distance

FractionReadsTopbins_chip: fraction of reads in the top 1% of bins with highest coverage for ChIP

FractionReadsTopbins_input: fraction of reads in the top 1% of bins with highest coverage for Input

Fractions_without_reads_chip: the fraction of bins without reads for ChIP

Fractions_without_reads_input: the fraction of bins without reads for Input