

mRNA-Seq workflow

FASTQ

BAM

Counts

Reads QC

Adapter
trimming

Reads
mapping

BAM
processing

Expression
quantification

Differential
expression

FASTQC
(fastqc.sh)

BBDuk

STAR
(STAR.sh)

Samtool
(samtools.sh)

Feature count
featureCounts.sh

DESeq2
(differential_expression.R)

Peak calling and breakpoints identification workflow

BAM

BED

Call peaks

Overlapping

Breakpoint
analysis

MACS
MACS2.sh

Bedtools

create_two_windows_from_cosmic.R

closest-features.sh

Tests for different states and times

Tests for different states and times

Conditions

- es3Left_stats.r
- es3Right_stats.r
- es3LeftFlip_stats.r
- es3RightFlip_stats.r
- es4Left_stats.r
- es4Right_stats.r
- es4LeftFlip_stats.r
- es4RightFlip_stats.r
- es5Left_stats.r
- es5Right_stats.r
- es5LeftFlip_stats.
- es5RightFlip_stats.
- LSLeft_stats.r
- LSRight_stats.r
- LSLeftFlip_stats.r
- LSRightFlip_stats.r
- MSLeft_stats.r
- MSRight_stats.r
- MSLeftFlip_stats.r
- MSRightFlip_stats.r

Times

- NTvsNTleft_stats.r
- NTvsNTright_stats.r
- NTvsNTleftFlip_stats.r
- NTvsNTrightFlip_stats.r
- TCOdvsTCODleft_stats.r
- TCOdvsTCODright_stats.r
- TCOdvsTCODleftFlip_stats.r
- TCOdvsTCODrightFlip_stats.r
- TH2HvsTH2Hleft_stats.r
- TH2HvsTH2Hright_stats.r
- TH2HvsTH2HleftFlip_stats.r
- TH2HvsTH2HrightFlip_stats.r
- TTRANvsTTRANleft_stats.r
- TTRANvsTTRANright_stats.r
- TTRANvsTTRANleftFlip_stats.r
- TTRANvsTTRANrightFlip_stats.r