

INPUTS

ASpli

OUTPUTS

TxDb
Annotation

experimental design

bam bai files
alignments

1 Extract features

binGenome()

ASpliFeatures

2 Count aligned reads to features

gbCounts()

ASpliCounts

targets

jCounts()

ASpliAS

3 Differential usage estimation

gbDUreport()

ASpliDU

jDUreport()

ASplijDU

4 Bin and junction signals integration

splicingReport()

ASpliSplicingReport

5 Region-based summarization

integrateSignals()

ASpliIntegratedSignals

6 Integrative reports

exportIntegratedSignals()

exportSplicingReports()

featuresg()
featuresb()
featuresj()
binMetadata()

countsg()
rdsg()
countj()
e1icounts()
ie2counts()
writeCounts()
writeRds()
irPIR()
altPSI()
esPSI()
allBins()
junctionsPJU()
junctionsPIR()
writeAS()

localec()
localej()
anchorj()
anchorc()
jir()
jes()
jalt()
writeJDU()

binbased()
localebased()
anchorbased()
writeSplicingReport()

signals()
filters()

genesDE(gb)
binsDU(gb)

DT interactive
HTML docs

CSV

HTML