

'Roxygen documentation for file create_RNAmaps_for_all_PAS.R '

November 3, 2020

R topics documented:

create_RNAmaps_for_all_PAS	1
Index	3

create_RNAmaps_for_all_PAS
<i>iCLIP RNAmaps for all PAS</i>

Description

Create RNAmaps at sPASs, pPASs and dPASs for two iCLIP libraries.

Usage

```
create_RNAmaps_for_all_PAS(  
  PASS.gr,  
  iCLIP1.plus.bw,  
  iCLIP1.minus.bw,  
  iCLIP2.plus.bw,  
  iCLIP2.minus.bw,  
  upstream = 450,  
  downstream = 150  
)
```

Arguments

PASS.gr	A GRanges object containing exact positions of PASs as single nucleotide region. A metadata column called "PAS.type" is required for each region and should be either sPAS, pPAS or dPAS.
iCLIP1.plus.bw	Path to the BigWig-File of the plus strand for iCLIP library 1.
iCLIP1.minus.bw	Path to the BigWig-File of the minus strand for iCLIP library 1.
iCLIP2.plus.bw	Path to the BigWig-File of the plus strand for iCLIP library 2.

iCLIP2.minus.bw

Path to the BigWig-File of the minus strand for iCLIP library 2.

upstream

Number of upstream nucleotides to include in the RNAmap.

downstream

Number of downstream nucleotides to include in the RNAmap.

Details

For each PAS type (i.e. sPAS, pPAS and dPAS) RNAmaps for two iCLIP libraries are generated in a user-defined window. For comparison of signal differences between the two iCLIP libraries, two proportions Z-tests are performed for each position. Positions with a significant signal difference (adjusted P value ≤ 0.01) are indicated in black beneath the signals.

Value

RNAmap plot

Index

`create_RNAmaps_for_all_PAS`, [1](#)