'Roxygen documentation for file create_RNAmaps_for_all_PASs.R '

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R topics documented:

`create_RNAmaps_for_all_PAS` *iCLIP RNAmaps for all PAS*

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

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