'Roxygen documentation for file create_RNAmaps_for_all_PAS.R '

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R topics documented:

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create_RNAmaps_for_all_PAS

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

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. Metadata columns have to include the type of each PAS (i.e. 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.

1

upstream	Number of upstream nucleotides to include in the RNAmap.
downstream	Number of downstream nucleotides to include in the RNAmap.

Details

BigWig-Files are loaded as Rle, which allows a fast subsetting via the regions in the GRanges object. For the comparison of iCLIP signals of the two libraries a two proportions Z-test is performed. 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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