

# 'Roxygen documentation for file create\_RNAmaps\_for\_regulated\_PAS.R '

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create\_RNAmaps\_for\_regulated\_PAS  
*iCLIP RNAmaps for regulated PAS*

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## Description

Create RNAmaps at pPASs and dPASs of transcripts with changes in 3'UTR length for two iCLIP libraries.

## Usage

```
create_RNAmaps_for_regulated_PAS(  
  PASs.gr,  
  iCLIP1.plus.bw,  
  iCLIP1.minus.bw,  
  iCLIP2.plus.bw,  
  iCLIP2.minus.bw,  
  upstream = 450,  
  downstream = 150,  
  DaPars = c("SRSF3", "SRSF7", "CPSF6", "Diff"),  
  UTR3.length = c("shorter", "longer")  
)
```

## Arguments

**PASs.gr** A GRanges object containing exact positions of PASs. Required metadata columns are 'PAS.type' as well as 'new.DaPars.SRSF3.regulation', 'new.DaPars.SRSF7.regulation', 'new.DaPars.CPSF6.regulation' and 'new.DaPars.Diff.regulation', which indicate the change in 3'UTR length of the hosting transcript in the different DaPars comparisons.

**iCLIP1.plus.bw** Path to the BigWig-File of the plus strand for iCLIP library 1.

<code>iCLIP1.minus.bw</code>	Path to the BigWig-File of the minus strand for iCLIP library 1.
<code>iCLIP2.plus.bw</code>	Path to the BigWig-File of the plus strand for iCLIP library 2.
<code>iCLIP2.minus.bw</code>	Path to the BigWig-File of the minus strand for iCLIP library 2.
<code>upstream</code>	Number of upstream nucleotides to include in the RNAmap.
<code>downstream</code>	Number of downstream nucleotides to include in the RNAmap.
<code>DaPars</code>	The DaPars comparison to look at. Choices are 'SRSF3' (Srsf3 KD/Ctrl), 'SRSF7' (Srsf7 KD/Ctrl), 'CPSF6' (Cpsf6 KD/Ctrl) and 'Diff' (Diff/Undiff).
<code>UTR3.length</code>	The set of transcripts to look at. Choices are 'shorter' (3'UTRs are getting shorter in the respective DaPars comparison) and 'longer' (3'UTRs are getting longer in the respective DaPars comparison).

**Details**

RNAmaps at pPASs and dPASs of transcripts with changes in 3'UTR length are generated for two iCLIP libraries in a user-defined window. In addition, for each PAS type and iCLIP library binding signals at not affected PASs are shown. Significant signal differences (adjusted P value  $\leq 0.01$ ) between regulated and not regulated PASs are indicated in black beneath the signals.

**Value**

RNAmap plot

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