

Transcription factor based Gene Set Analysis

Description

Perform Gene Set Analysis using camera of the limma package for signature lists derived from the transcription factor specific toptables.

Usage

TF_camera_gsa_FUN(TF_list, top_T = NULL, rma_obj, pltfrm = "Affy", d_m, cntrst = NULL, cnt_mat = NULL, TF_motifs = FALSE, wts = NULL, res_path)

Arguments

- TF_list
- character vector of transcription factors (either combined or motifs)
- top_T
- topTable generates after applying hg38_annot_FUN
- rma_obj
- object generated by oligo::rma or an MAList
- pltfrm
- either affy or agilent
- d_m
- design matrix
- cntrst
- the coeffecient to report for the camera output
- cnt_mat
- contrast matrix, not used
- TF_motifs
- logical, defaults to FALSE if no transcription factor motifs are used
- wts
- a vector of weights applied when running camera, defaults to NULL
- res_path
- path to save GSA files

Author(s)

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