Return number of TF targets present in tt

Description

This function saves to disk tables that show the number of target genes of each transcription factor (combined and single motifs) represented in the toptable. Different cutoffs are applied using log2FC, p.value, adj.p.value to show how much change occurs in the number of gene representations after applying these cutoffs. The table includes the log2FC value of the transcription factors. Additionally, a list is returned with both representation tables and transcription factor specific tobtables.

Usage

```
TF_genes_tt_FUN(ptrns, t_table, fc_filt = NA, rtrn_value = "dim", pv = NA, apv = NA)
```

Arguments

ptrns	vector of gene symbols
t_table	topTable genrated after running the hg38_annot_FUN
fc_filt	numeric, log2 fold change cutoff
rtrn_value	can be "dim" if only the number of genes are required, or "tt_fc" if toptable subsets for TF are required
pv	numeric, p value cutoff
apv	numeric, adjusted p value cutoff

Author(s)

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