GSA results barplots

Description

This function generates barplots of the top 20 (10 up- and 10 down) regulated enriched gene sets. If the number of up- or down regulated gene sets are less than 10, the remaining gene sets are added from the other group of gene sets. Only gene sets meeting the specific p.value cutoff are plotted, even if the number of gene sets are less than 20.

Usage

```
gsa_bar_plot_FUN(idx, gsa_ls, ts = 8, res_path, coi, wd, ht, pix = 600)
```

Arguments

idx	numeric vector of indeces of gene sets in a gsa result list
gsa_ls	gsa result list
ts	numeric, text size
res_path	path to save files
coi	cutoff of interest, used for the p.value reported
wd	width argument passed to ggsave
ht	height argument passed to ggsave
pix	the pixel per inch (ppi) value passed to ggsave

Author(s)

Ahmed Sadik

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