

Barplot Analysis of Cushing Results

This script produces bar plots. And it was last run on Fri Sep 25 09:38:00 2015.

```
## Creating a generic function for 'nchar' from package 'base' in package 'S4Vectors'
```

[illegible]

The data used is in the file `../data/processed/rpkm_table.csv`. This file was most recently processed on Fri Sep 25 09:40:20 2015.

Session Information

```
sessionInfo()
```

```
## R version 3.2.2 (2015-08-14)
## Platform: x86_64-apple-darwin13.4.0 (64-bit)
## Running under: OS X 10.10.5 (Yosemite)
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] ggplot2_1.0.1  plyr_1.8.3    reshape2_1.4.1 biomaRt_2.24.1
##
## loaded via a namespace (and not attached):
## [1] Rcpp_0.12.1      AnnotationDbi_1.30.1 knitr_1.11
## [4] magrittr_1.5     MASS_7.3-44      BiocGenerics_0.14.0
## [7] IRanges_2.2.7    munsell_0.4.2     colorspace_1.2-6
## [10] stringr_1.0.0    GenomeInfoDb_1.4.2 tools_3.2.2
## [13] grid_3.2.2       parallel_3.2.2    gtable_0.1.2
## [16] Biobase_2.28.0    DBI_0.3.1         htmltools_0.2.6
## [19] yaml_2.1.13      digest_0.6.8      formatR_1.2.1
## [22] S4Vectors_0.6.5  bitops_1.0-6      RCurl_1.95-4.7
## [25] evaluate_0.8     RSQLite_1.0.0     rmarkdown_0.8
## [28] labeling_0.3     stringi_0.5-5     scales_0.3.0
## [31] stats4_3.2.2     XML_3.98-1.3      proto_0.3-10
```