

Barplot Analysis of Cushing Results

This script produces bar plots. And it was last run on Sun Aug 23 19:37:46 2015.

```
## Warning: package 'ggplot2' was built under R version 3.1.3
```

[illegible]

The data used is in the file `../data/processed/rpkm_table.csv`. This file was most recently processed on Sun Aug 23 19:40:38 2015.

Session Information

```
sessionInfo()
```

```
## R version 3.1.2 (2014-10-31)
## Platform: x86_64-apple-darwin13.4.0 (64-bit)
##
## 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_2.22.0
##
## loaded via a namespace (and not attached):
## [1] AnnotationDbi_1.28.2 Biobase_2.26.0      BiocGenerics_0.12.1
## [4] bitops_1.0-6         colorspace_1.2-6    DBI_0.3.1
## [7] digest_0.6.8         evaluate_0.7.2      formatR_1.2
## [10] GenomeInfoDb_1.2.5   grid_3.1.2          gtable_0.1.2
## [13] htmltools_0.2.6      IRanges_2.0.1       knitr_1.10.5
## [16] labeling_0.3         magrittr_1.5        MASS_7.3-43
## [19] munsell_0.4.2        parallel_3.1.2      proto_0.3-10
## [22] Rcpp_0.12.0          RCurl_1.95-4.7      rmarkdown_0.7
## [25] RSQLite_1.0.0        S4Vectors_0.4.0     scales_0.2.5
## [28] stats4_3.1.2         stringi_0.5-5       stringr_1.0.0
## [31] tools_3.1.2          XML_3.98-1.3        yaml_2.1.13
```