Barplot Analysis of Cushing Results

This script produces bar plots. And it was last run on Fri Sep 25 12:34:40 2015.

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

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The data used is in the file **../data/processed/rpkm_table.csv**. This file was most recently processed on `Fri Sep 25 12:37:04 2015`.

Session Information

```r
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
```