## Setup steps for cloud platform access with google

These steps involve interaction with local browser and remote R session to authenticate to Google Cloud Platform so that you have access to TCGA data. Your local chrome session should be logged in with your google identity

```
# step 1) downgrade dplyr on the AMI to allow bigrquery
biocLite("Bioconductor/dplyr", ref="bioc-update") # say "n" to additional gueries
# alternate approach
#install.packages("https://cran.r-project.org/src/contrib/Archive/dplyr/dplyr_0.4.3.tar.gz",
#repos=NULL)
# step 2) install bigrquery with restrictions
library(devtools)
install_github("rstats-db/bigrquery", upgrade_dependencies=FALSE)
# step 3) install googlesheets package
options(httr_oob_default=TRUE)
biocLite("googlesheets") # say no to additional installs
# step 4) set a token
library(googlesheets)
gs_auth(new_user=TRUE)
# do as told -- after going to URL you get something to paste into a query in R
# step 5) now get to the TCGA platform
bq = src_bigquery("isb-cgc", "tcga_201510_alpha", "cgc-05-0011")
bq
```