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| Download Files in R  \*note: since I chose python for data analysis and reformating my files, perhaps it was easier to download the data initially in python. Possibly using package *pytcga*. But alas, I didn’t do it.  First install TCGAbiolinks package  Copy below to R console  source("https://bioconductor.org/biocLite.R") biocLite("TCGAbiolinks") |  |
| Download the file  The link below is a good how-to  http://bioconductor.org/packages/release/bioc/vignettes/TCGAbiolinks/inst/doc/download\_prepare.html |  |
| Export the Files in R to be loaded in Python for processing. |  |
| The data is not formatted correctly. See below. Barcode is unique identifier for each sample. Note length of unique barcode matches the number of files download from TCGA.  We need to make a table of unique barcodes and miRNA. |  |

