You will need to download SpearmanInputMaker.R and edit the file so that

* in the second line, HNSC\_CPM is changed to the name of your counts per million file for the cancer you are working on
* In the third line, adenosine correlated genes.txt is changed to the name of the list of genes/proteins you are interested in (this time we are using FINAL immune cell surface proteins.txt)

Put your edited SpearmanInputMaker.R file, Targets.txt file, your counts per million file, and the list of of genes/proteins you are interested in (download from the drive) in one folder. Save the list of genes/proteins of interest as a tab delimited text file. Change your working directory in R to this folder and run SpearmanInputMaker.R

This will output a file called SpearmanInput.txt

Open the file in excel, copy the cells in the first row, and move them to the right by 1 cell.

Save this file and use it to run SpearmanCorrelations.R.