1. Place you .atf file in the same folder as the script and run “complied\_sCRACM\_afcorrect.m” indicating
   1. filename
   2. cellspot = 8; % closest spot where cell soma is – this you need to match up with the image and the actual gridmap. (see grid\_adjust.xls)
   3. maptype = 5.; %laser intensity
   4. layer = 'L3\_'; %what layer is the pyramid in?
2. output should be two files “\_ca\_pA.csv” file and a “\_ca\_pA.png” file
3. Place all the .csv and .png file of the SAME genotype into a folder either name as “HO” or “HET”
4. Run mapping\_csv\_Het.m (for Het) or mapping\_csv\_HO.m (for HO)
5. Each of these will output you 1 csv file with the repective name: “HET15psCRACM\_avg.csv” or “HO15psCRACM\_avg.csv”
6. Place these csv file into a new folder call R-analysis.
7. Place in the csv file with cellid and depth info, see “cellid\_depth.csv”
8. The basic R-code file to be slightly modified is “ephys\_rcode\_sCRACM.R”
   1. Set the working directory where you have your csv files in step 5 and step 7
   2. The is the bulk where you can exclude and include cells, look at depth, etc…. it really depends what you want to plot once you have the data in R
   3. If you just run it, all the plots will be in the rstudio interface.