Save your files where they belong

MACS2 results go into peaks folder

BowTie2 BAM files go into the reads folder

BowTie2 BAM files of the controls go into the controls folder

Save your rna-seq comparison results in the rna folder

In the outputs folder, copy the “files.csv” and make the necessary edits

Work along the code and make changes to it as you go. Im hardly an expert so its not exactly “hit go” and it runs. There will be some edits you need to make to define like “where the files.csv that tells R where all your information is saved to”, “what colors do you want”, “what is the name of your RNA-seq files?” Read the comments in the code and if it does not work, you are probably missing something.

A common error that occurs is during the diffbind where it will say "Read block operation failed with error 1 after 0 of 4 bytes". Form online, that means that the file it encountered this at is corrupted. With your experimental files, you will need to redownload and keep doing so until it works. If its an input control file, just change the control file in the “files.csv” to a different input control, they should all be nearly identical in reality.