This week, besides working on small details for some of our projects, I read and collected some more literature of SNPs on yeast and eQTLs that could be associated with genetic variation. Trying to define steps for studying this, I found a few sources (SCPD and MYBS) which can be useful for locating TF binding sites and analyze those sites and flank regions around it can be used for the previous step. The next step is to actually get the data and start playing with it to see if it will make sense.