Functional Genomics 2.1.24

* Remember, for RNA-sq, different tissue types are going to tell you different things, because they are expressing different genes than one another.
* Different types of RNAs can have functions with other proteins, and they can be classified as coding RNA(mRNA), non-coding structural (rRNA), and non-coding functional (tRNA, siRNA, snRNA, gRNA, snoRNA, microRNA, lncRNA, Xist, Riboswitches).

RNA prep for library sequencing, what to target?

* Whole transcriptome sequencing – A sum of everything.
* Library prep
  + (Ribosomal depletion) Targeted hybridization removed abundant RNA (mRNA), to look at more valuable portions of the transcriptome. (Doing library prep in house and sending for sequencing is cheaper than having them do the library prep too.
  + (RNA enrichment) – If there is a subset of things you’re after and you already know the sequence, you can build probes to target just those and enrich them.
    - If you only wanted mRNA, you can do an enrichment using the poly-A tail.
    - You can also use size selection after enrichment.
  + (RNA amplicon) same as amplicon, but need to convert to cDNA.
    - PCR on cDNA

Going back to focal paper

* What were they thinking when they were going through this process.
* They had to make all these decisions, to come up with a plan, what were those decisions and how did they decide?