

# Which genes are differentially regulated upon treatment?

↓  
**QuantSeq!**

**Organism**  
human

- well annotated
- many resources

**how many replicates?**

- large treatment & control groups
- how to accommodate sample number and read depth?

**how many reads/sample?**

- genes of interest are lowly expressed  
→ confirmed in pilot sequencing
- higher read depth per sample required  
↳ use 3' mRNA-Seq?  
↳ multiplex more samples ✓

**Sample type**  
blood

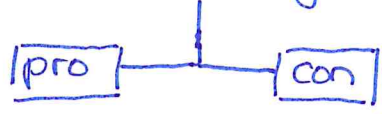
- mRNA analysis  
↓  
poly(A) selection to focus on poly-adenylated transcripts

**GENE EXPRESSION PROFILING**

- globin removal?

**extraction**

- pre-treatment "red blood cell lysis" can remove globin



- easy
- cheap
- quick
- can be used for WTS also
- samples need to be fresh  
→ non-frozen  
→ non-fixed

**WTS**

- transcript-level information
- isoform information obtained
- globin needs to be removed before library prep  
↳ using red blood cell lysis?  
↳ using globin depletion?
- higher read depth required → fragment on full transcript length

**3' mRNA-Seq**



- gene-level information ✓
- easy and fast to quantify  
→ easy data analysis ✓
- globin transcripts can be blocked ✓  
↓  
! Samples can be stored (stabilized) → easier to collect large numbers
- lower read depth requirement compared to WTS-Seq