M2D8:Cell viability; quantitative PCR; identification of regulatory motifs 04/10/2018

- 1. Treat cells with DNA damaging agents and inhibitors for cell viability
- 2. Analyze qPCR results
- 3. R: Identify regulatory motifs in RNA-seq data

Extra Office Hours

- Leslie: Tuesday April 17th 56-322 (lab), 10:30am-1:30pm
- Josephine: Wednesday April 18th 56-322, 10:00am-1:00pm
- Noreen: Tuesday and Wednesday 56-322, 2:00-4:00pm

Mod2 Research Report (20% of final grade)

Due Saturday 4/21 at 10pm

- Title, Abstract
- Introduction
- Methods
- Results (Figures and captions)
- Discussion
- References

Last week of Mod2!



Etoposide is a drug/chemotherapy that causes DNA double strand breaks

- mechanism of action: forms a ternary complex with DNA and topoisomerase II enzyme and prevents re-ligation of the DNA strands = dsDNA strand break
- cancer cells (quickly dividing cells) rely on topoisomerase II more than normal cells



Measuring synthetic lethality in our parental and BRCA2-/- cell line

What is synthetic lethality? Combination of deficiencies (knockouf, LOF, drug treatment) in 2 or more genes leads to cell death

What parallel pathways are we perturbing in this experiment? double strand breaks > HR (BRCAZ-1-) > NHEJ (drug - Lop. or Mib.)

What is the output of this assay?

Six compounds identified that target NHEJ and / or HR 1= DMSO, we effect D= total loss of activity

	Repair activity	
Drug name	NHEJ	HR
Pimozide	0.28	0.55
→ Loperamide	0.20	0.57
> Mibefradil	0.28	0.57
Etoposide	0.65	0.08
SR 59230A	0.27	0.58
AMN082	0.19	0.92

- Loperamide = slows contractions of intestines, treatment for gastrointestinal ailments
- Mibefradil = blocks calcium channels, treatment for heart conditions

(Slide from Noreen's Lecture 4/5)

Goglia et al. (2014) Molecular Cancer Therapeutics 14:326-342

Synthetic lethality part 1: experiment overview

- 1. Choose miberfradil or loperamide, sign up at front bench
- 2. Induce double strand breaks (etoposide 37°C for 60min)
- 3. Remove etoposide media and incubate with appropriate concentration of miberfradil or loperamide till M2D9



qPCR (quantitative PCR) is used to detect and quantitate gene expression

- Fluorescence is a function of ds MA concentration via SYBR green dye
- dsDNA concentration is proportional to <u>RNA</u> purified from cells and used to make complementary DNA (cDNA)
- We can compare <u>of the compare</u> of a particular gene in different conditions by measuring the abundance of the gene-specific transcript
- Expression of the gene of interest is normalized to a housekeeping gene, <u>GAPDH</u>
- Plot the exponential transformation (log2) of the change in the threshold values (ΔC_T) for each condition



Threshold cycle (C_T) is calculated from qPCR after all cycles complete



- What would be a C_T value for a gene expressed lower than the transcript in blue? pink, Ct=25
- Higher?

No Template

https://bitesizebio.com/24581/what-is-a-ct-value/

qPCR melt curve indicates the number of dsDNA products in rxn

negative derivative of fluorescence

vs. temperature



What would cause multiple peaks? Multiple de DNA products Typrimers created off target product, Seq. Similarly Typplice variants

Computational exercise—transcription factor binding site motifs

- Calculate position weight matrices
- Search public database of transcription factor binding
- Scan sequences to look for matching motifs
- Practice expectation-maximization algorithm for de novo motif discovery



Today in lab

- 1. Drug treat cells in tissue culture:
 - 1st: Red, Orange, Yellow, Green
 - 2nd: Blue, Pink, Purple, White, Grey
- 2. Analyze qPCR data
- 3. Complete "Transcription Factor Motifs" R exercise
- HW due M2D9:
 - Create figure with qPCR analysis/RNA seq analysis (including figure title and caption)
 - associated results section
 - associated discussion section