\* Fig 1 - curr or modified

What about panel A? Illustrates more than just repl timing - Signal track

New photo instead of ROC

How well we do - Slide 20 + just genes - which shows that bcl6 as extended gene can be found - could be drawn like D

Survival analysis

==> \* Fig 2

Part A - undercutting by showing all the TF - too similar to rabit

Part B - eclip good & highlights SUB1

Part C

Part D - survival analsysis w sub1

DW loregic ? (does this go in figure)

\* Fig 3 - network? [shortened vers of 3 w/o hier just jund Jund rewiring]

==>\* Fig 4 - validation results

Outline:

1. Prioritizing Key elements through mutation burden analysis
   1. Integrating covariate matrix
   2. Accurate gene mutation rate estimation [[importance of many matched features from the encode data]]
   3. Extended gene annotation by linking various non coding elements
   4. Improved burden analysis by synthesizing signals from both nc and coding elements from each gene
2. Prioritizing Key elements through gene expression analysis
   1. TF analysis [[deemp]]
   2. RBP analysis
3. Prioritizing Key elements through network rewiring analysis
   1. How to build: Gene-gene mega network via proximal and distal regulatory elements
   2. Single node analysis
      1. Rank TFs according to rewiring measurements
      2. TFs Clustering according to rewiring status within K&G network
   3. Pairwise nodes analysis
      1. Disruption of co-associated TFs in tumor cells
      2. Change of co-association types (loregic)
   4. Topology analysis
      1. TF hierarchy changes in Tumor and normal cells
      2. TF motif gain and loss events in Tumor and normal [[FFL??]]
4. Prioritizing SNVs in Key elements discovered by 1-3
   1. Integrating element score and individual SNV score to have a finalized score [[flowchart or schematic]]
5. Experimental validation of key elements and SNV
   1. sh-RNAseq MCF-7
   2. Wild type and Mutant enhancers in MCF-7

Data Novelty:

1. Most comprehensive non-coding elements list that are linked to genes with high confidence in model tumor cell lines - good enhancers & linkages
   1. Experiments list includes:
      1. CHIP-seq (TF) -> TFBS
      2. CHIP-seq (Histone) + Enhancer-seq -> Enhancers
      3. Hi-C + CHIA-PET + CHIP-seq (Histone) -> Enhancer-gene linkage
      4. RAMPAGE -> accurate active promoter definitions
      5. iCLIP -> RNA-regulatory regions
2. Most comprehensive covariate list to better characterize the somatic mutational landscape
3. Most comprehensive list of CHIP-seq data for transcription factors activities in several cancer cells
4. Wild and mutation enhancer in luciferase assay for SNV effect analysis