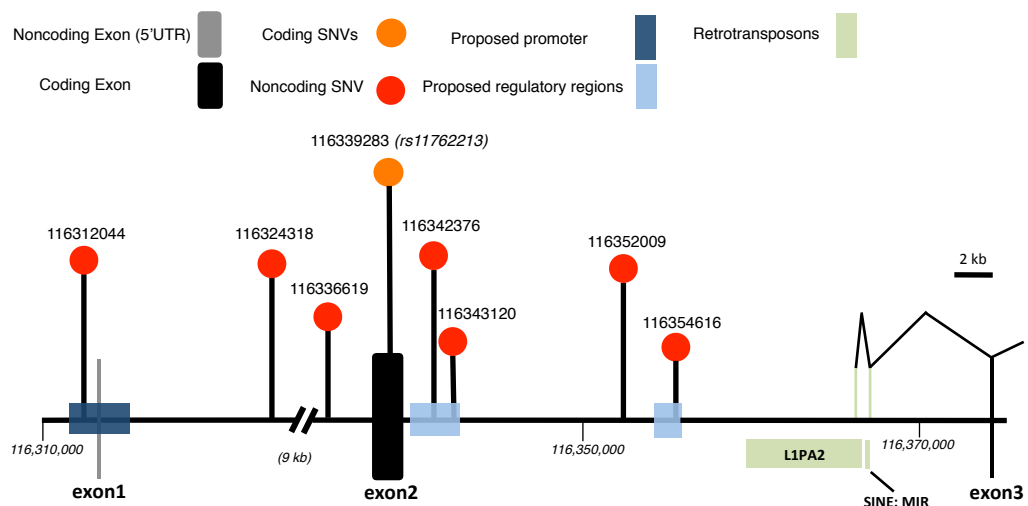


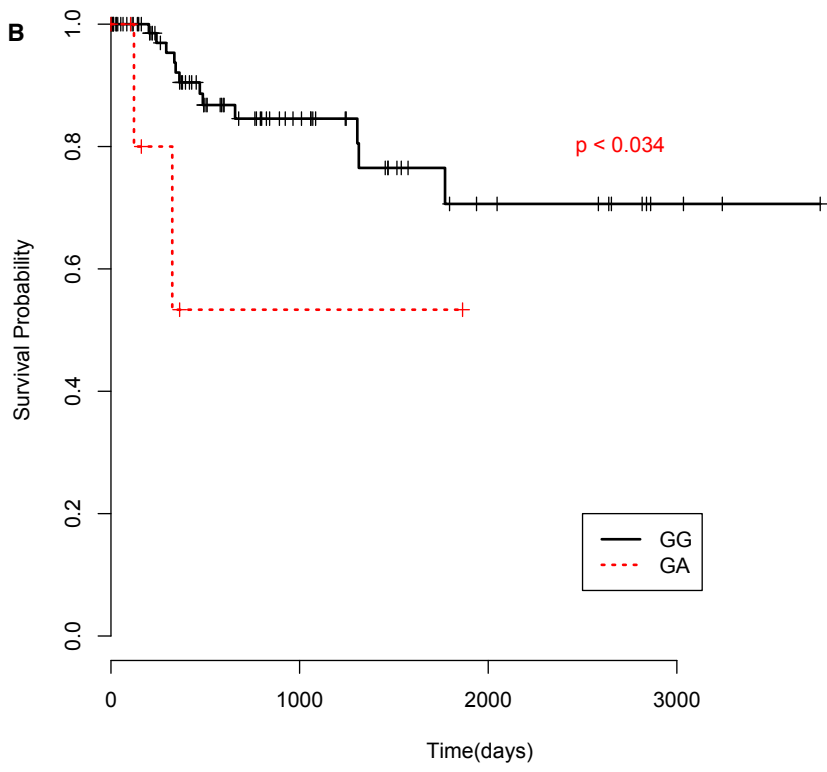
What's new

- Figure re-plot
- SV comparison
- New DHS/RepliSEQ
- Evolution tree

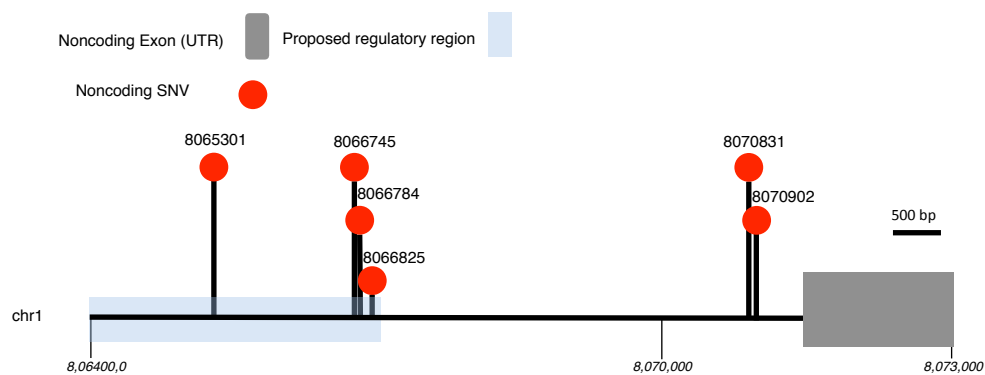
A MET



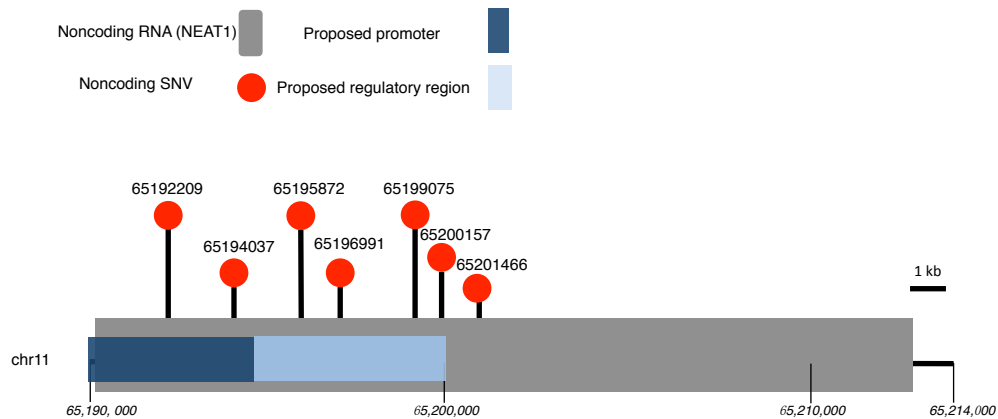
B



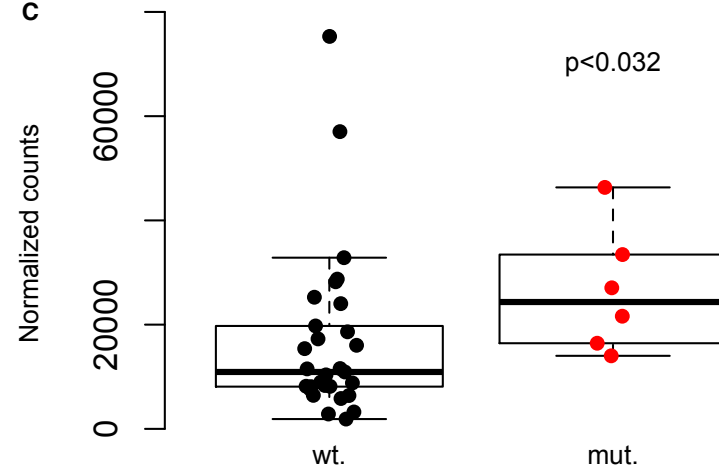
A ERRFI1



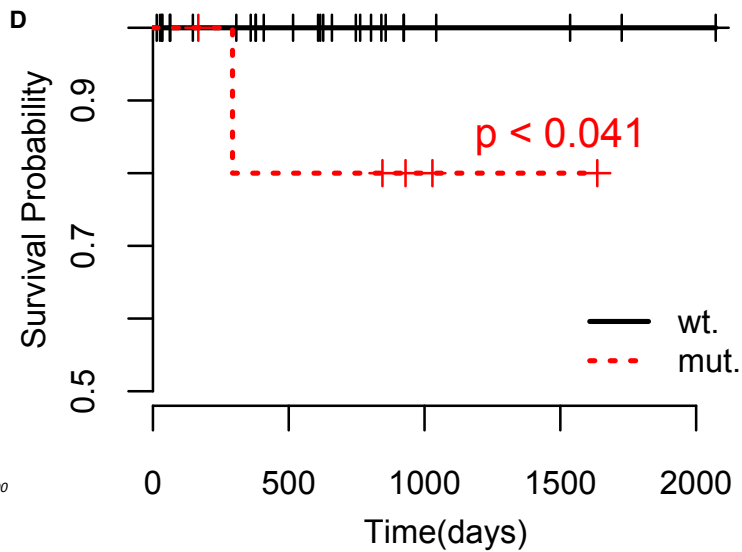
B NEAT1



C



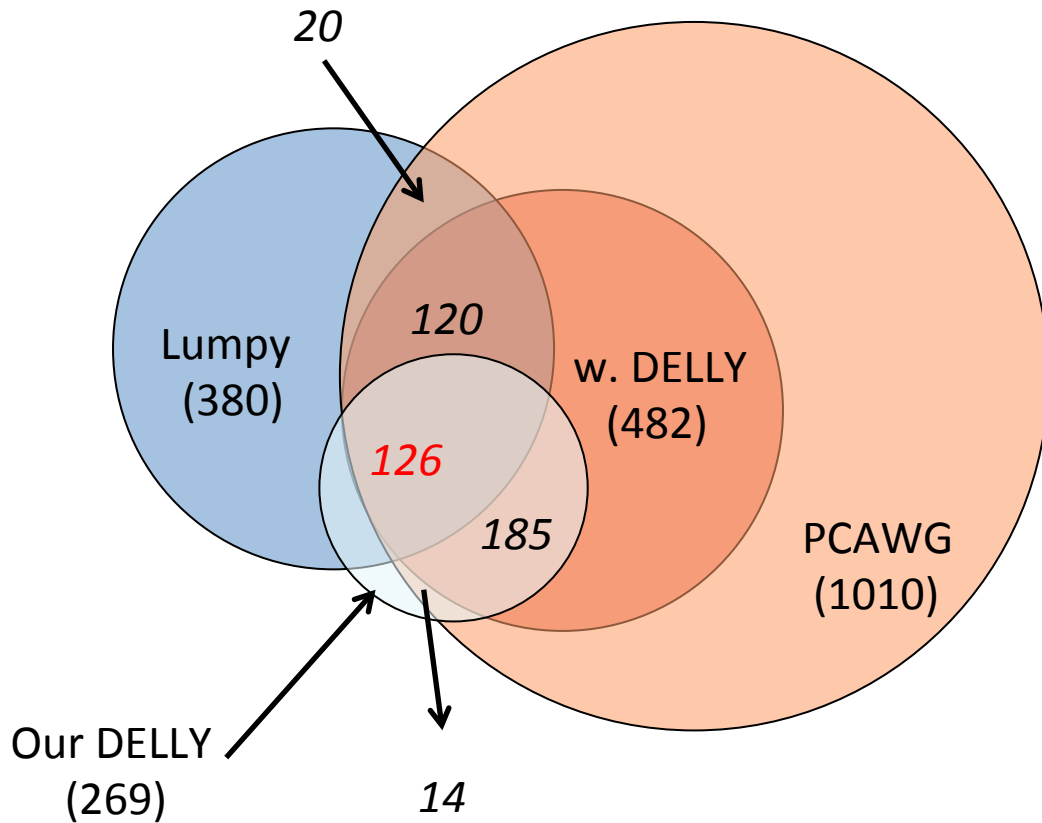
D



SV comparison

- First, why Lumpy/SVscore?
 - Our strength at bkpts (as to aCGH)
 - Overlapping bkpts with functional regions
 - What about bkpt labeled as IMPRECISE
 - Lumpy/SVscore gives the right normalization
 - Normalized CADD scores around bkpts
 - Report intervals as well
 - Issues: Quality & SVTyper
 - The genotyper works weirdly

SV comparison



This is on 32 samples
(we called SV from 35)

Criteria:

1. 0.5 reciprocal overlap
2. Matched sample
3. Matched SV CLASS

Only get **126** SVs if overlapping DELLY with Lumpy using 32 samples

SV comparison

- If we think PCAWG DELLY is the ground truth
 - Other methods rely on assembly...different searching space (complicated SV events produce way too many bkpts)
 - Not a fair comparison

	#SVs	FN	FP	Addl. catch
Lumpy	380	71%	63.2%	20 (5.26%)
Delly (ours)	269	61.6%	31.2%	14 (5.20%)

Bkpts&interval overlapping

- No overlapping with pRCC MutSig genes (~10)
- COSMIC genes
- Three overlapping with pRCC MutSig
 - Extensive SVs in TCGA-B9-4116
 - DEL of STAG2
 - A large INV involves NFE2L2

	bkpts
1	AFF3
1	AKAP9
1	ATRX
1	CDK6
1	CDKN2A
1	CLP1
1	CREBBP
1	ERCC2
1	LRP1B
1	MKL1
1	MLLT10
1	POLE
1	POT1
1	SND1
1	SOX2-OT
1	STAT5B
1	STK11
1	THRAP3
2	SPEN

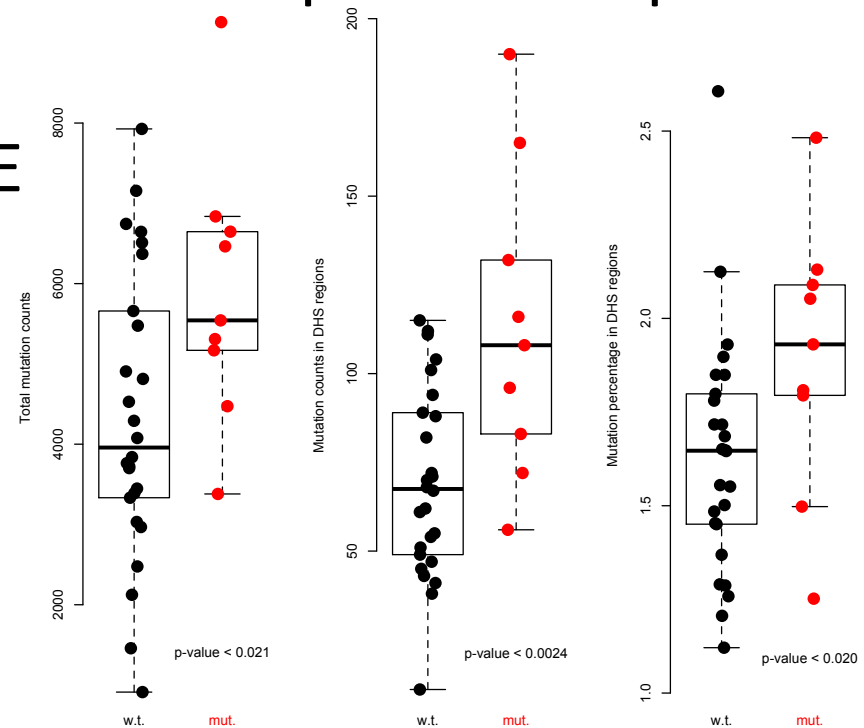
SV overlapping

- Some interesting COSMIC cases
 - 3 CDKN3A (confirmed NEJM 3/5 cases)
 - 2 SDHB deletion (interacts with FH and SDHA)
 - 1 EGFR duplication (pRCC responses to TKIs)
 - 1 HIF1A duplication (inhibited by VHL;)
 - 1 polyE bkpts (same case)
 - 1 DNMT3A deletion (affect methylation)
 - 1 MALAT1 *deletion*
 - 1 HGF *deletion (ligand for MET)*

1	POLE2
1	DNMT3A
1	HIF1A
1	IDH1
1	MALAT1
2	EGFR
2	SDHB
3	CDKN2A
1	HGF

New DHS scheme

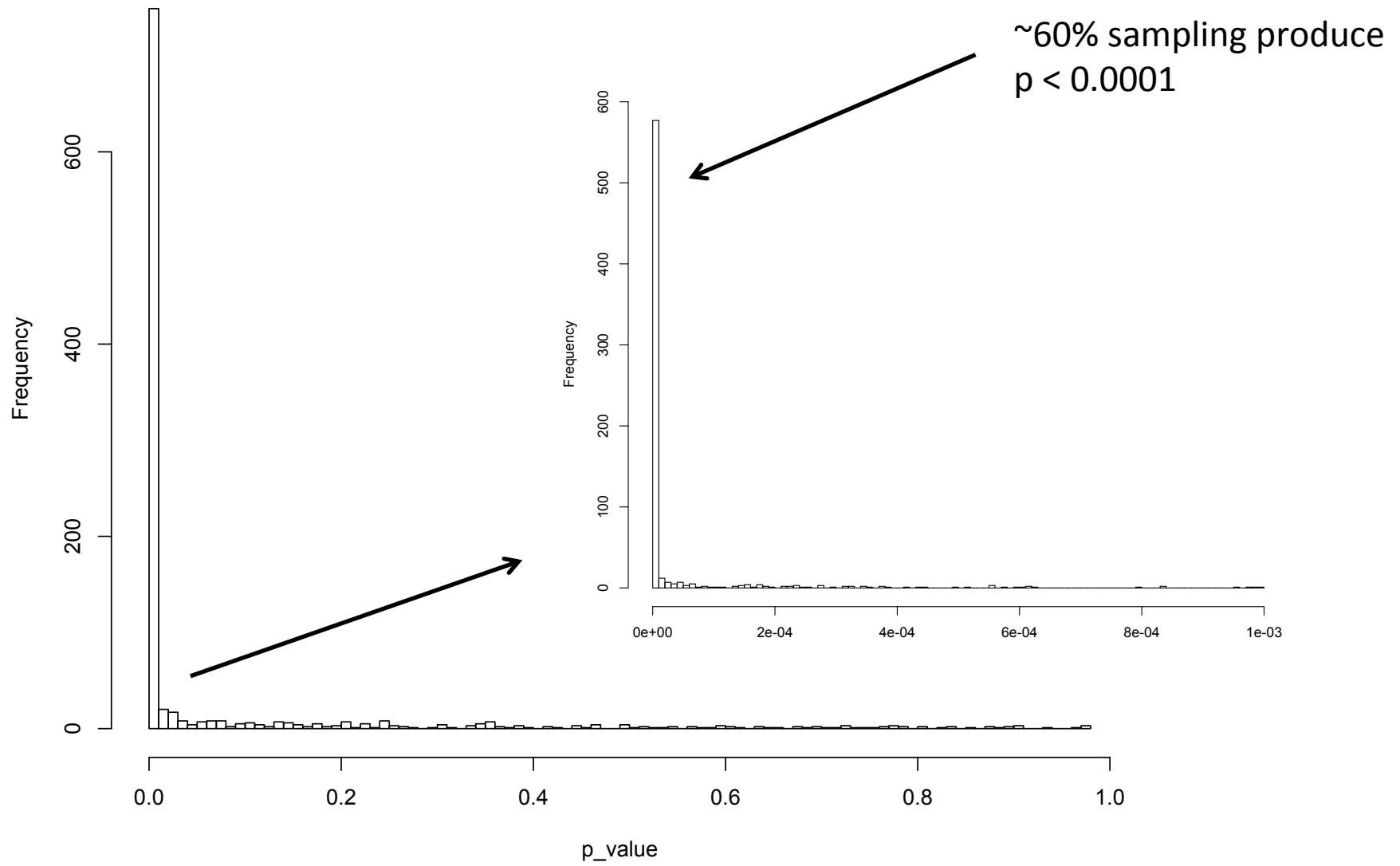
- Pulled fetal kidney cortex DHS from Roadmap
- 11 samples from different fetuses
 - Ultra-conservative: take the overlap of all samples
 - DHS percentage roughly matches ENCODE HEK293 narrowpeak (previously used)



RepliSEQ

- Newly defined CR-genes
 - Overlapping NEJM spreadsheet(pRCC-related) genes with CR&SWI/SNF pathway gene list
- Conservative RT signals (*Ref: NGen.*)
 - Taken median from 11 ENCODE cell lines
- Prudent adapted KS test (subsampling)
 - Q: does the RT dist. of SNVs from CR^{mut.} samples differ from CR^{wt.} samples
 - Randomly shuffle labels (9 v.s. 26) for 1,000 times to generate imperial TS distribution

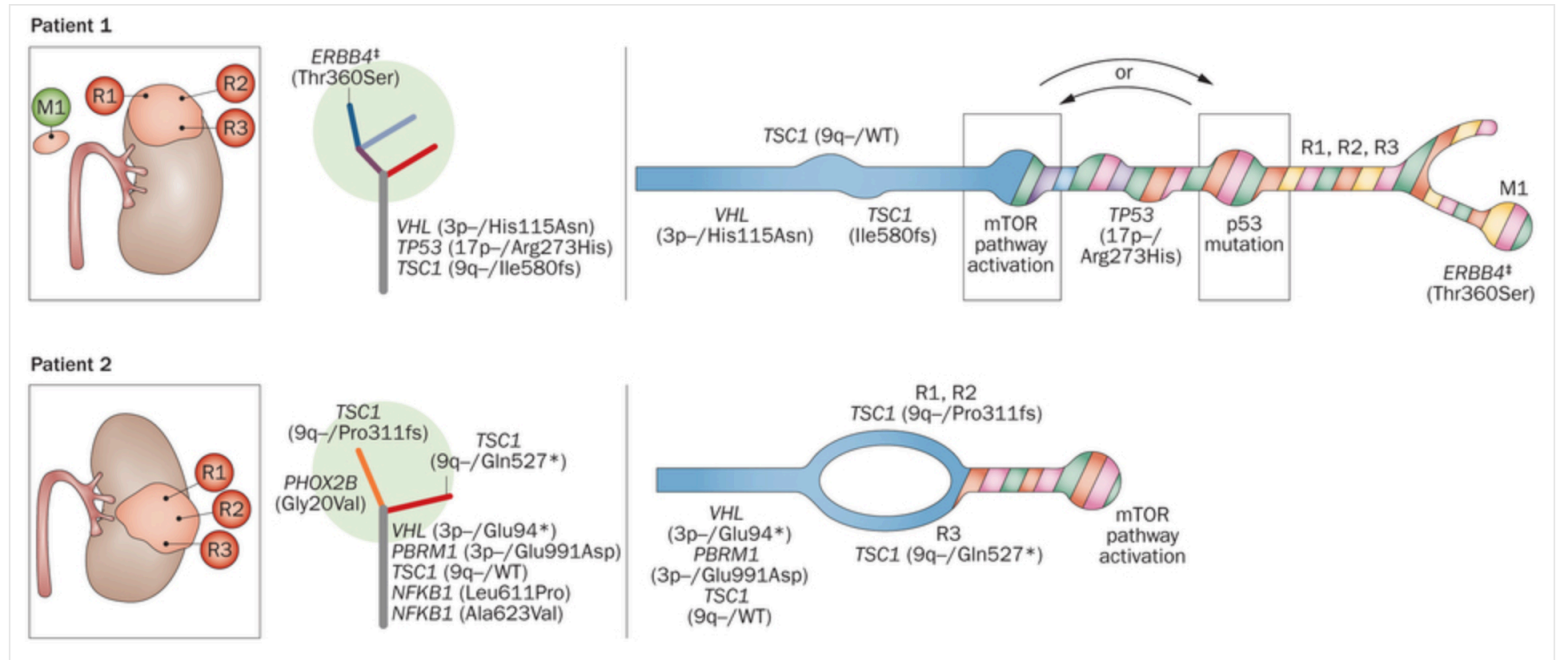
Why we need subsampling



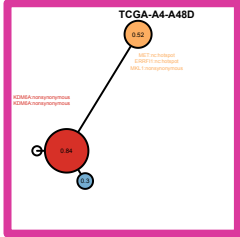
KS tests w/ subsampling: Issues

- A. p-value below limits
 - Our test produces $p < 2.2e-16$ (which becomes 0)
 - However, we observed 26% such cases
- B. test power not uniform
 - SNVs in each sample varies
 - Makes test statistic (D) not directly comparable
 - Worse: power is not uniform!

Evolution tree



- Less interesting because:
 - Single punch from each patient
 - Not ultra-deep sequence
 - Masked all CNV + MAF>0.6

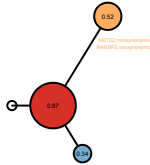


TCGA-AL-3473

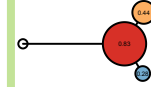
TCGA-A4-A4ZT



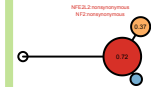
TCGA-AL-45DJ



TCGA-A4-A57E



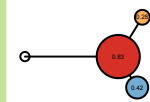
TCGA-B1-A47M



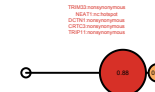
TCGA-AL-3466



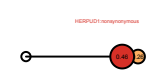
TCGA-B1-A47N



TCGA-AL-3468



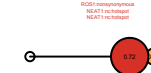
TCGA-B1-A47O



TCGA-AL-3472



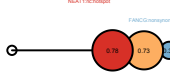
TCGA-B3-3925



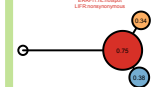
TCGA-B3-3926



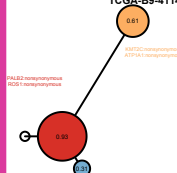
TCGA-B3-4103



TCGA-B9-4113



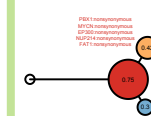
TCGA-B9-4114



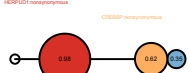
TCGA-B9-4115



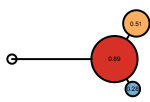
TCGA-B9-4116



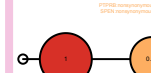
TCGA-B9-4117



TCGA-B9-4617



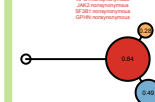
TCGA-B9-A44B



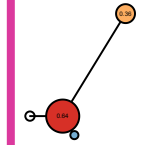
TCGA-GL-A4EM



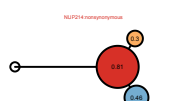
TCGA-GL-A59R



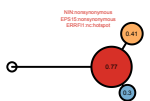
TCGA-HE-A5NF



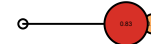
TCGA-HE-A5NH



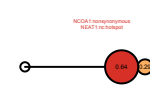
TCGA-HE-A5NI



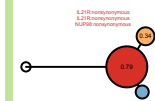
TCGA-HE-A5NJ



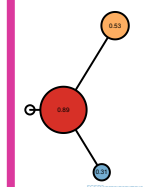
TCGA-HE-A5NL



TCGA-IA-A40X



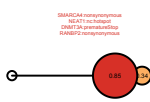
TCGA-IA-A40Y



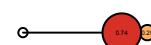
TCGA-MH-A55W



TCGA-MH-A55Z



TCGA-MH-A560



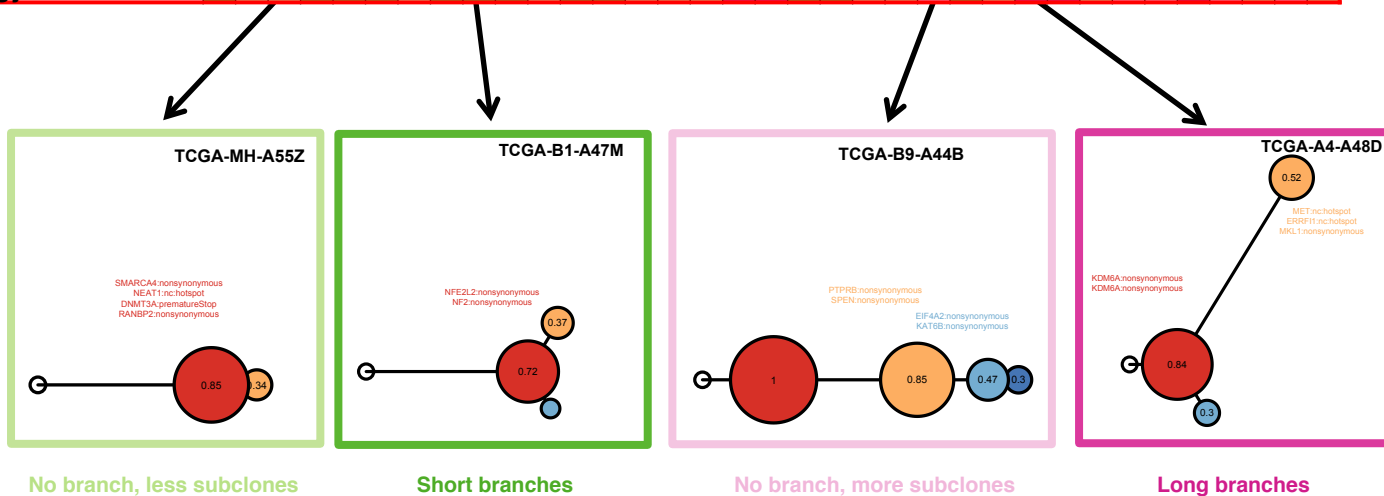
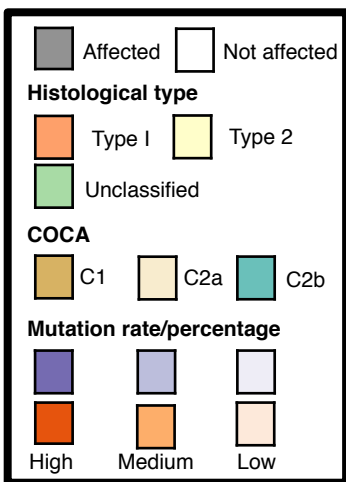
TCGA-MH-A561



TCGA-MH-A562



	Histological type	[Color-coded]										[Color-coded]										[Color-coded]									
	COCA	[Color-coded]										[Color-coded]										[Color-coded]									
Coding	MET copy number gain	[Color-coded]										[Color-coded]										[Color-coded]									
	MET somatic mut.	[Color-coded]										[Color-coded]										[Color-coded]									
	MET splicing event	[Color-coded]										[Color-coded]										[Color-coded]									
	MET germline mut.	[Color-coded]										[Color-coded]										[Color-coded]									
	BAP1/PBRM1/SETD2 somatic mut.	[Color-coded]										[Color-coded]										[Color-coded]									
	CDKN2A copy number loss	[Color-coded]										[Color-coded]										[Color-coded]									
	Noncoding	MET promoter mut.	[Color-coded]										[Color-coded]										[Color-coded]								
MET 1-2 intronic mut.		[Color-coded]										[Color-coded]										[Color-coded]									
NEAT1 somatic mut.		[Color-coded]										[Color-coded]										[Color-coded]									
ERRFI1 promoter mut.		[Color-coded]										[Color-coded]										[Color-coded]									
Mut. Processes	Whole genome mutation rate	[Color-coded]										[Color-coded]										[Color-coded]									
	DHS mutation percentage	[Color-coded]										[Color-coded]										[Color-coded]									
	1 - Max. population. frequency	[Color-coded]										[Color-coded]										[Color-coded]									
	Evolution tree topology	[Color-coded]										[Color-coded]										[Color-coded]									



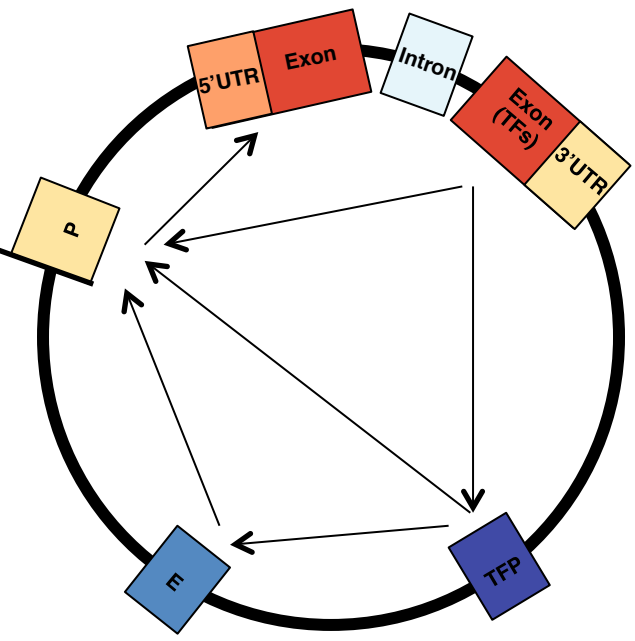
Paper E thoughts

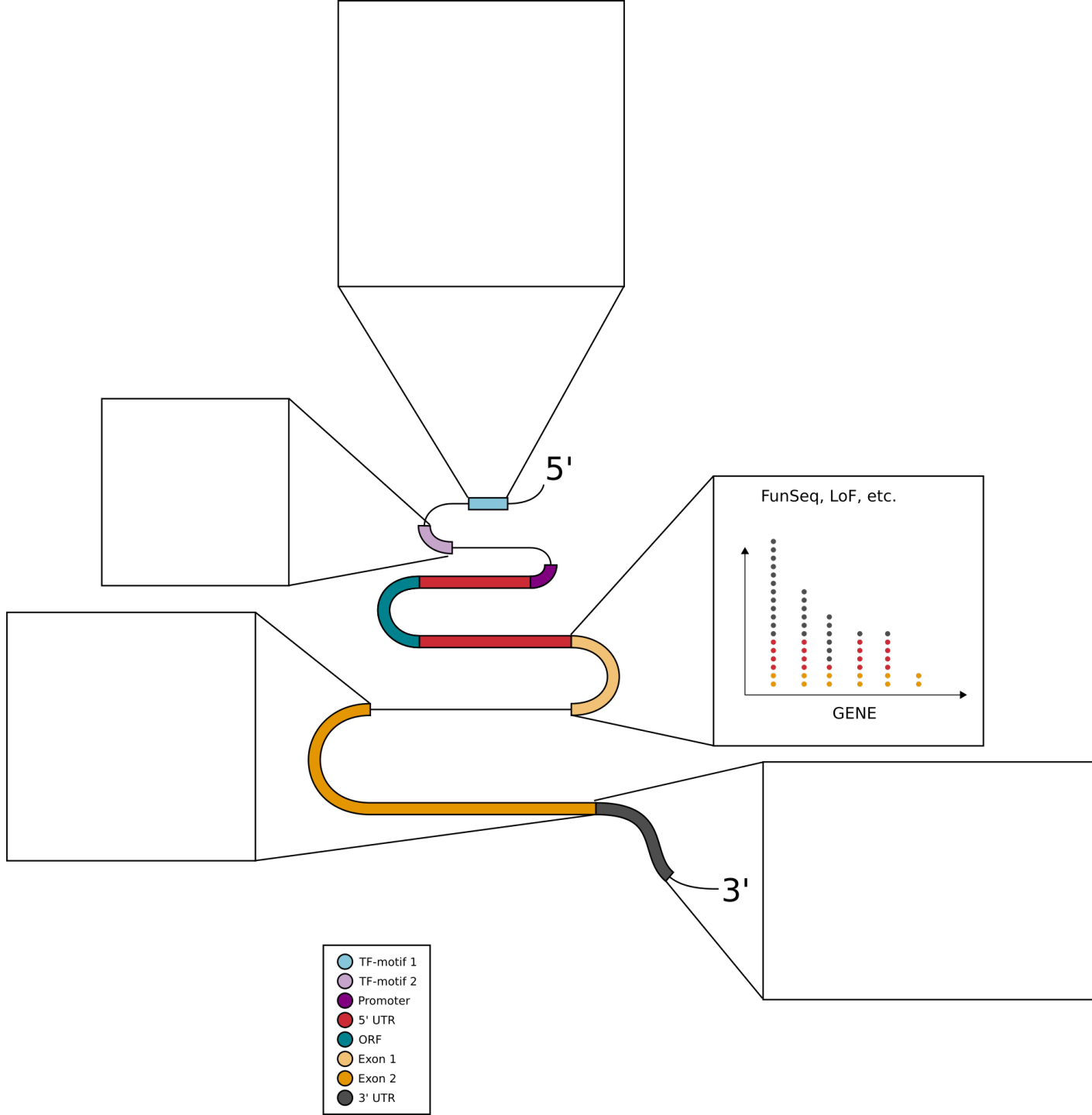
- What we want to sell
 - A complete “tumor portrait”
 - Completeness on several levels
 - Unprecedentedly large WGS cohort
 - Coding/**noncoding**/SVs...
- Fig1: a fancy figure to visualize the deluge of the data
 - Show a gene (“genecreek” or “-circle”)

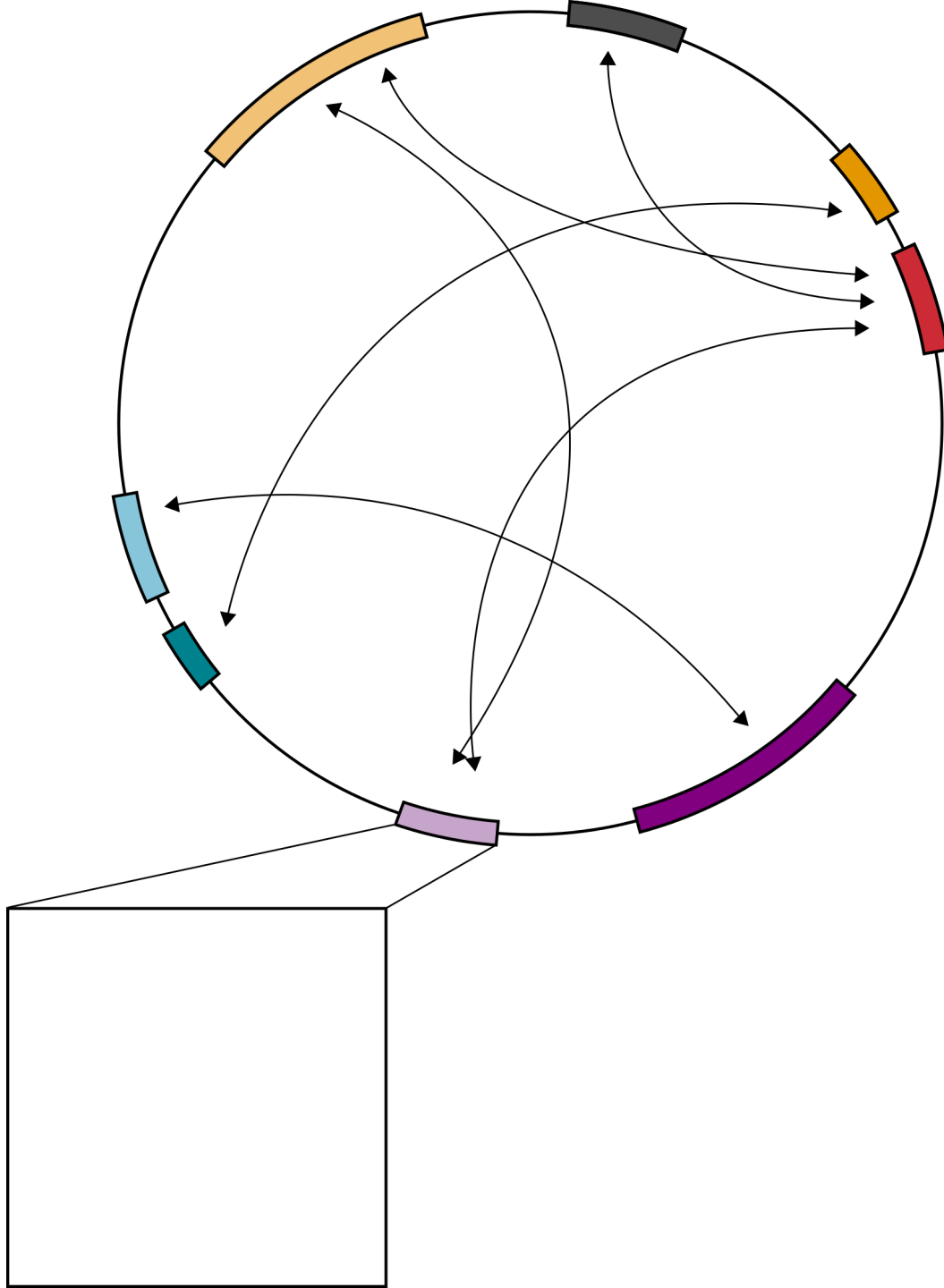
Issues

- One sample with 23 EPB41L2 promoter mutation?
 - And 9 has the identical FunSeq score!
 - Annotation issue? This promoter spans >170kb!
 - However, this is an excluded sample...
 - Still, another included sample has 8...

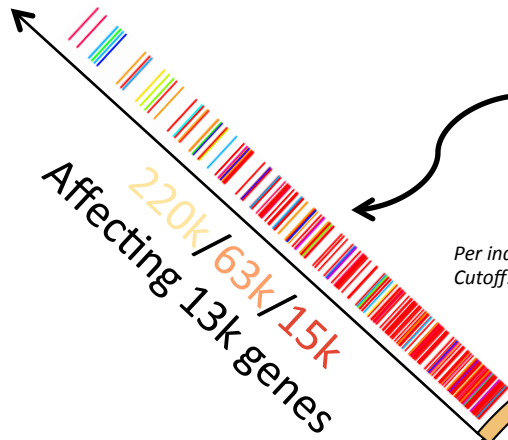
325k/92k/22k
Affecting 14.2k genes



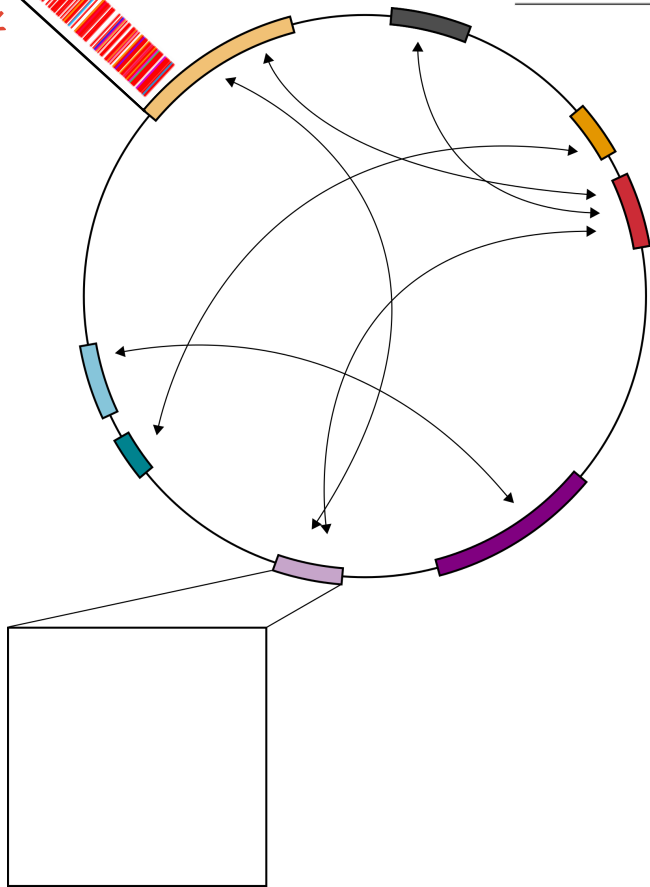




Gene functions? FunSeq breakdowns?



Per indiv. per gene (57k)
Cutoff: 1.5



108	TCF4
109	DUSP22
124	TERT
125	SEPT9
154	ZNF595

Annotation

```
51 volgesteinDriver.oncogene
58 volgesteinDriver.TSG
101 cellCycleGene.
114 apoptosisGene.
122 dnaRepairGene.
339 cancerPathwayGene.
385
1375 Metabolic_Genes_RCT
2646 essentialGene.
2905 immuneResponseGene.
9969 nonEssentialGene.
```

1. Normalize by the #gene
2. Normalize by the length of elements
3. Correct for RT/Trinucleotide context

