

Figure 1

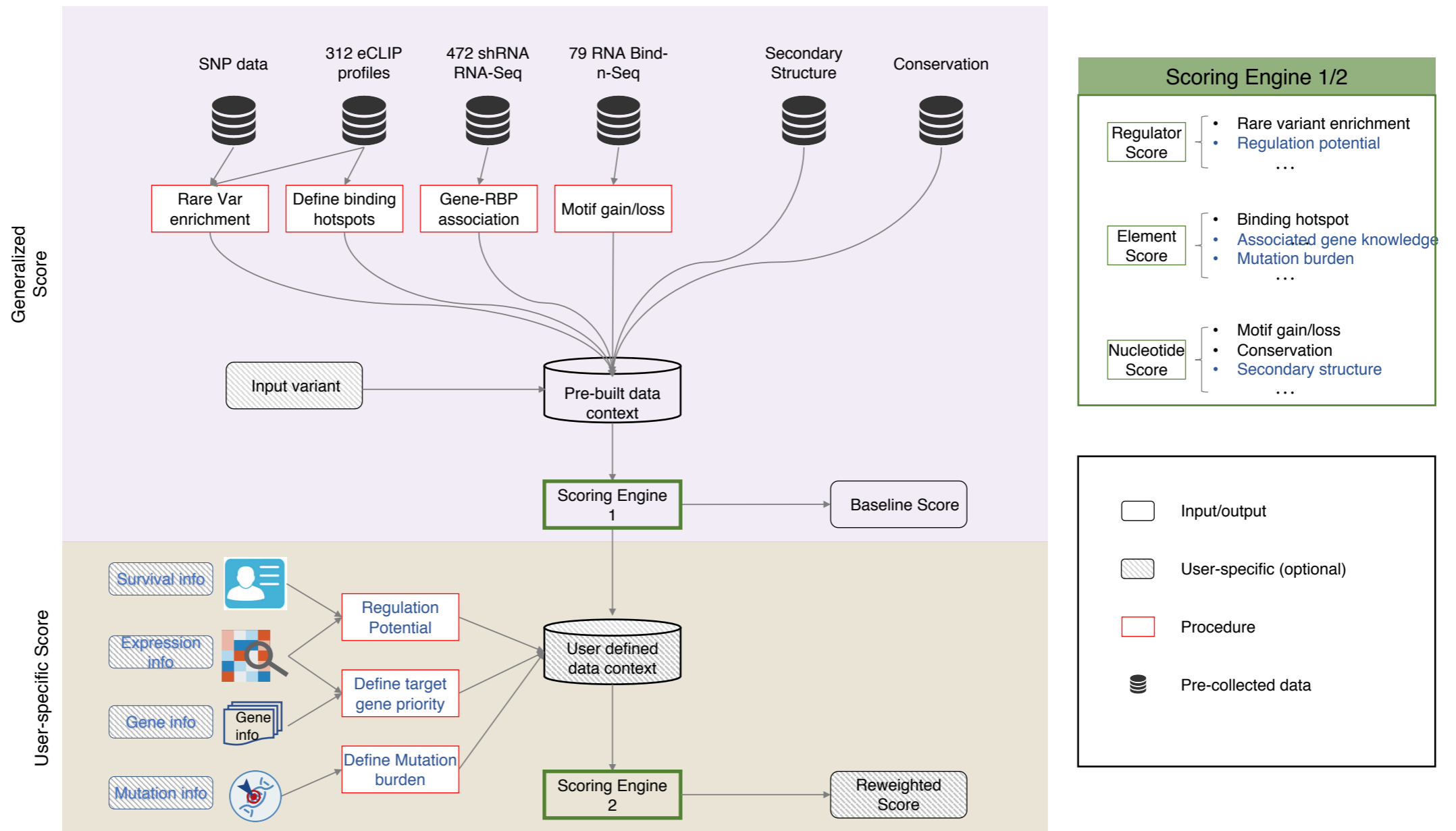


Figure 2

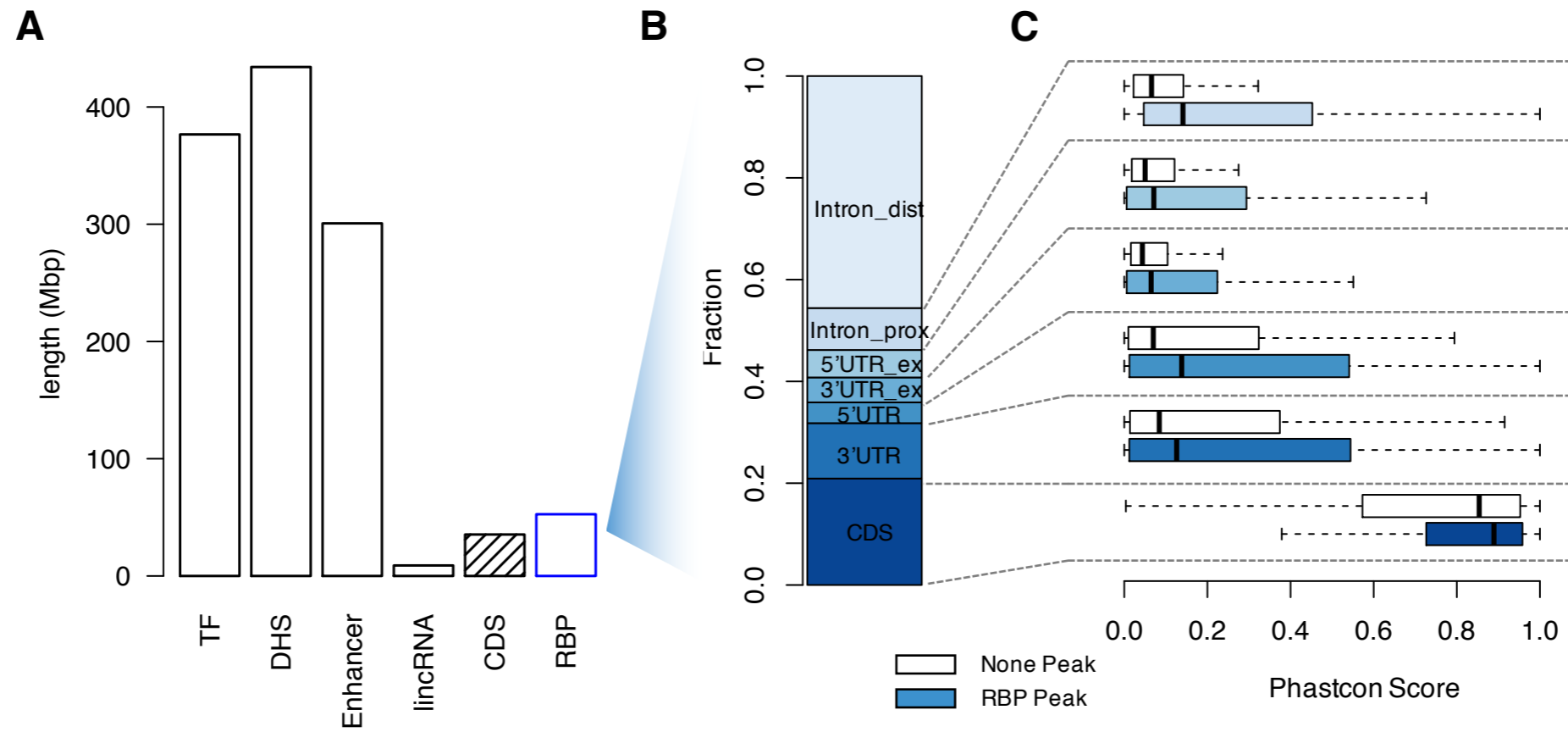


Figure 3

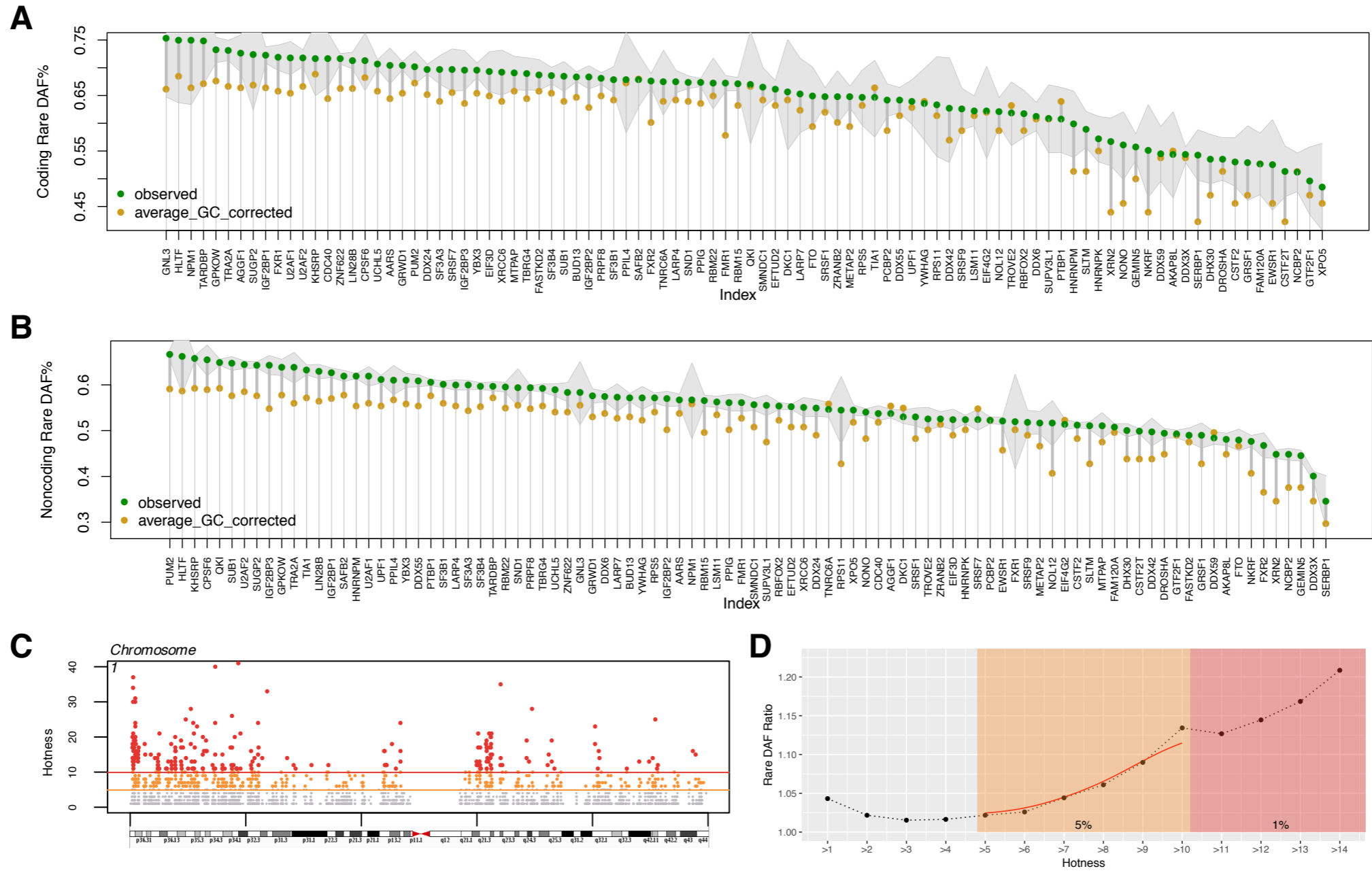


Figure 4

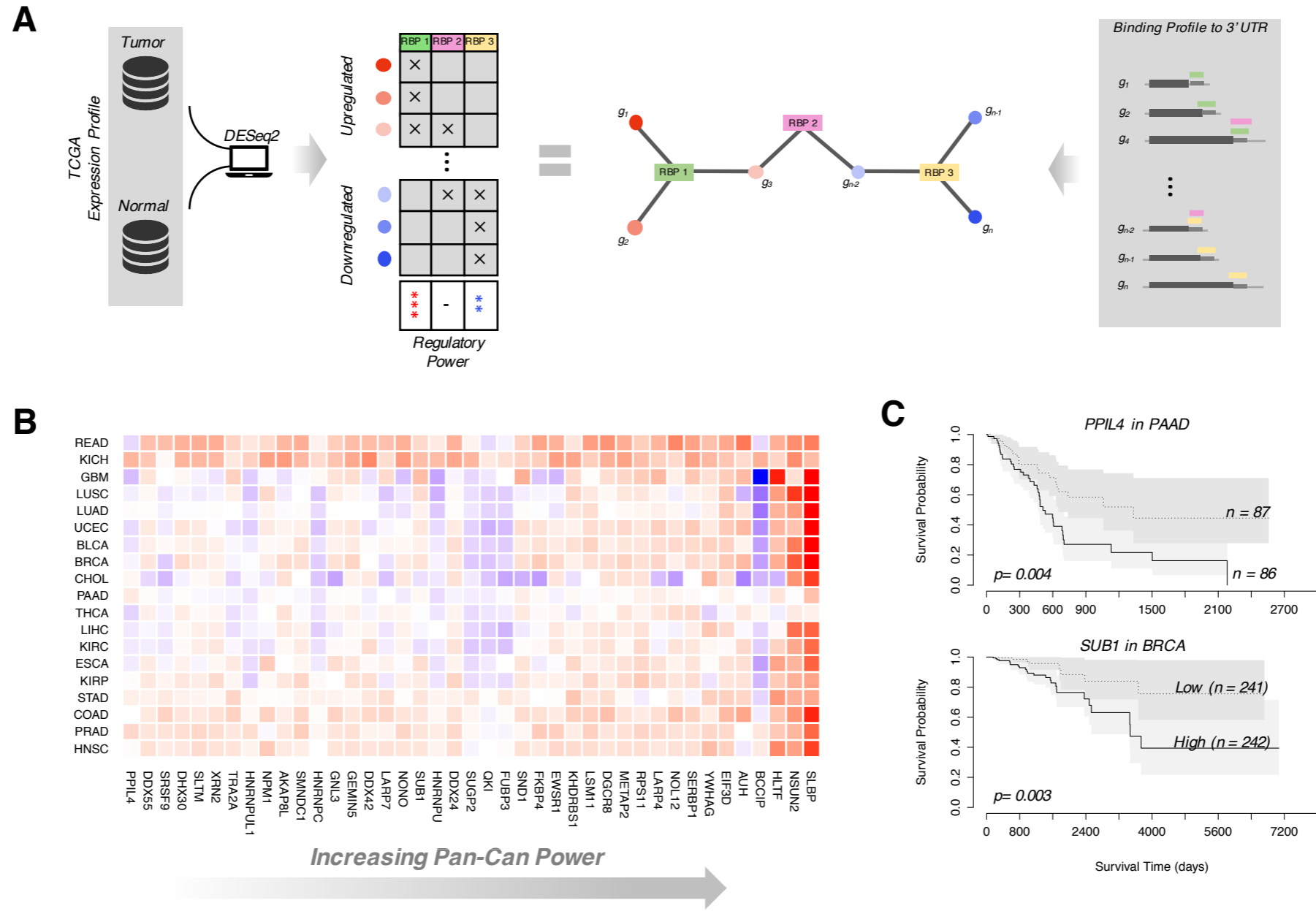


Table 1. Features used by RADAR

Category	Feature	Source	Scoring Scheme
Universal	RBP score	eCLIP	Weighted-entropy
	Binding hotspots	eCLIP	Weighted-entropy
	RBP-gene Association	shRNA RNA-seq	Entropy
	Motif	Bind-n-Seq/DREME	Entropy
	Structure sensitivity	RNAfold	Entropy
	Conservation	Gerp	Entropy
User-specific	RBP regulatory potential	Survival Expression	Entropy
	Key genes	Prior knowledge	Entropy
	recurrence	Mutation profiles	Entropy

Figure 5

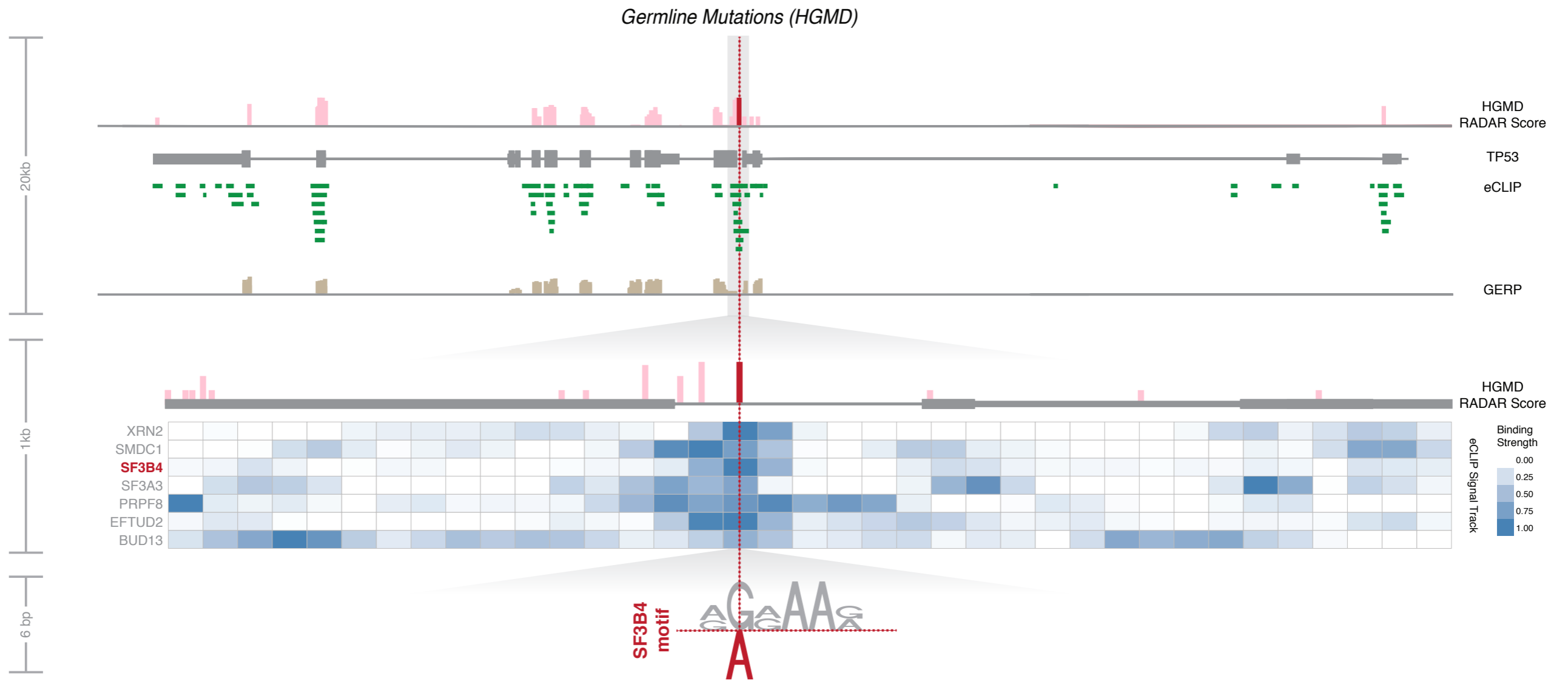
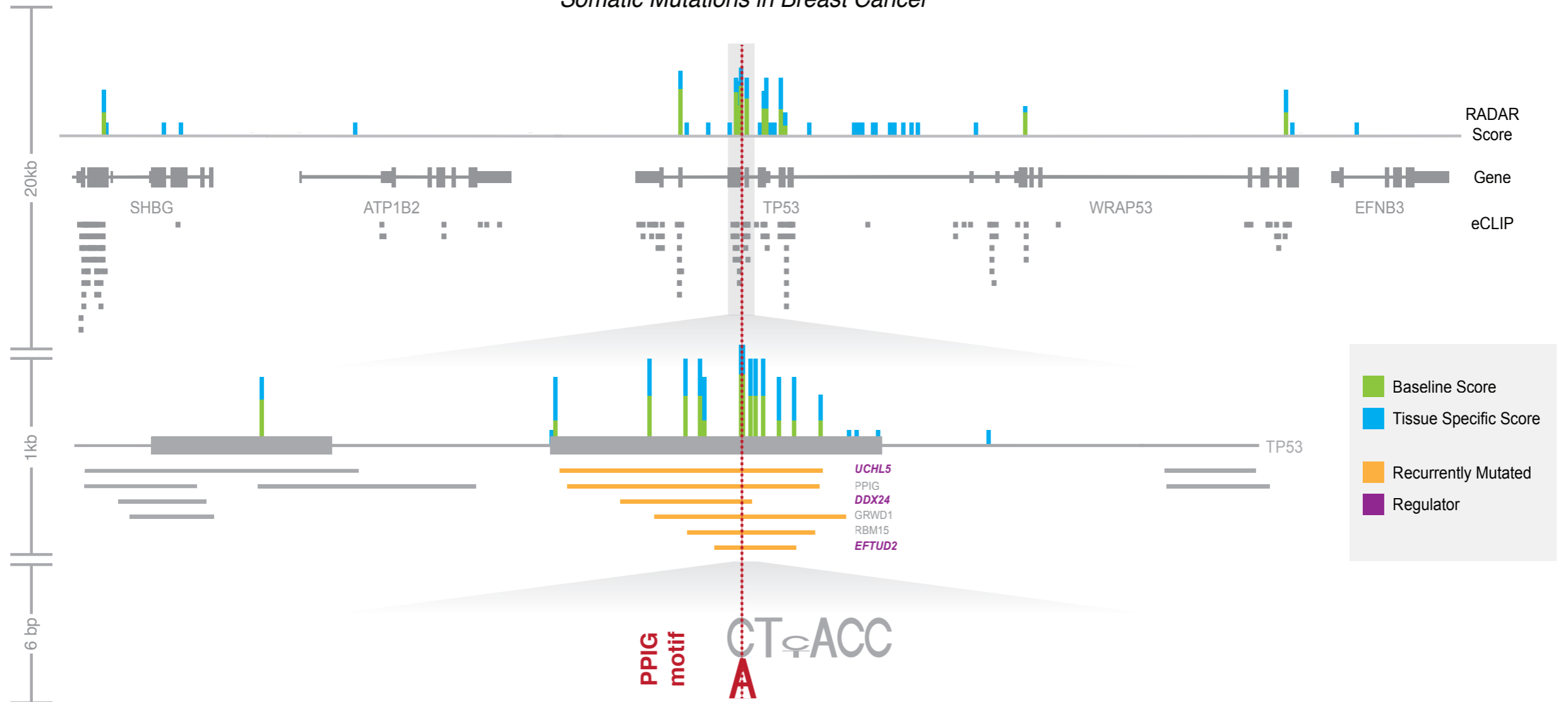


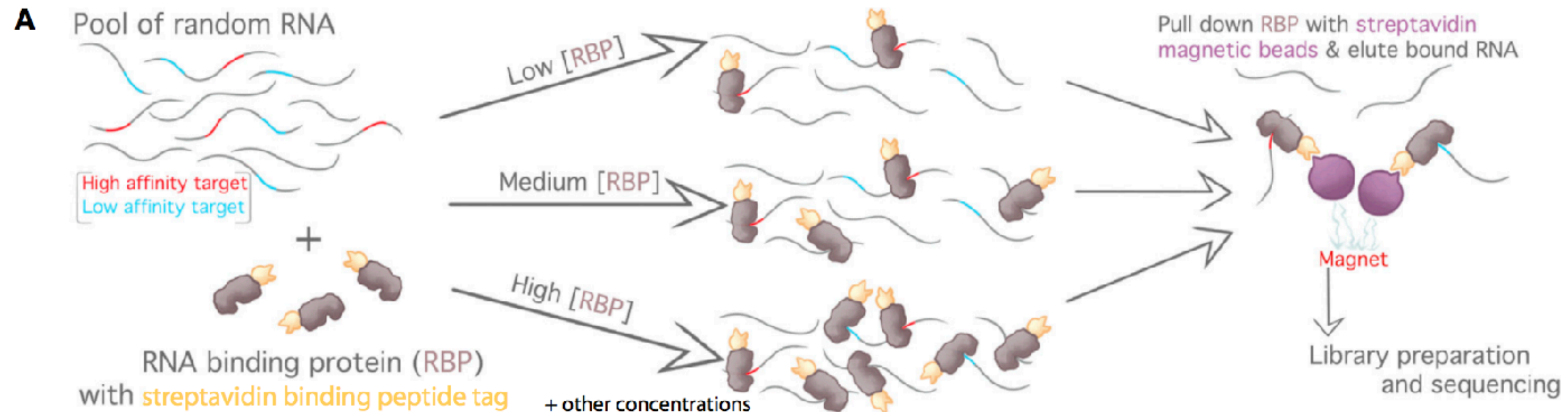
Figure 6

Somatic Mutations in Breast Cancer

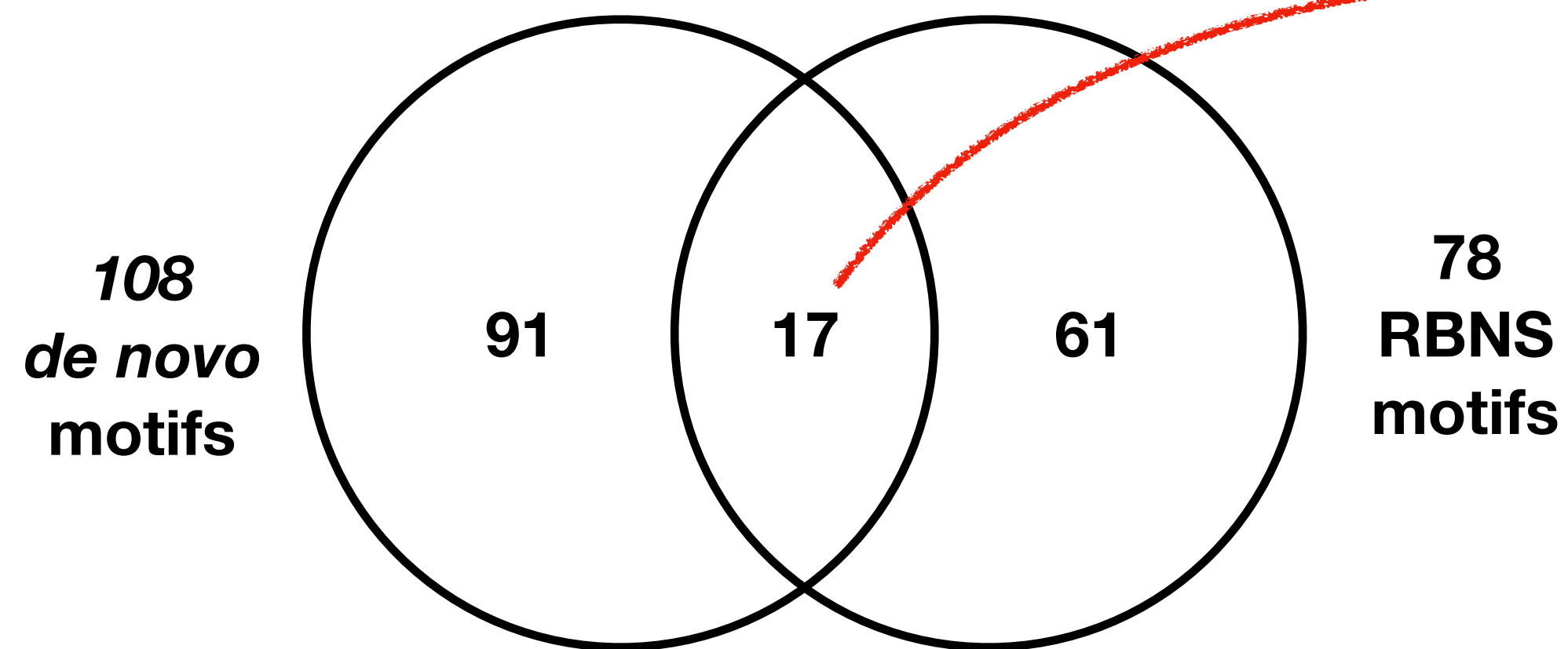
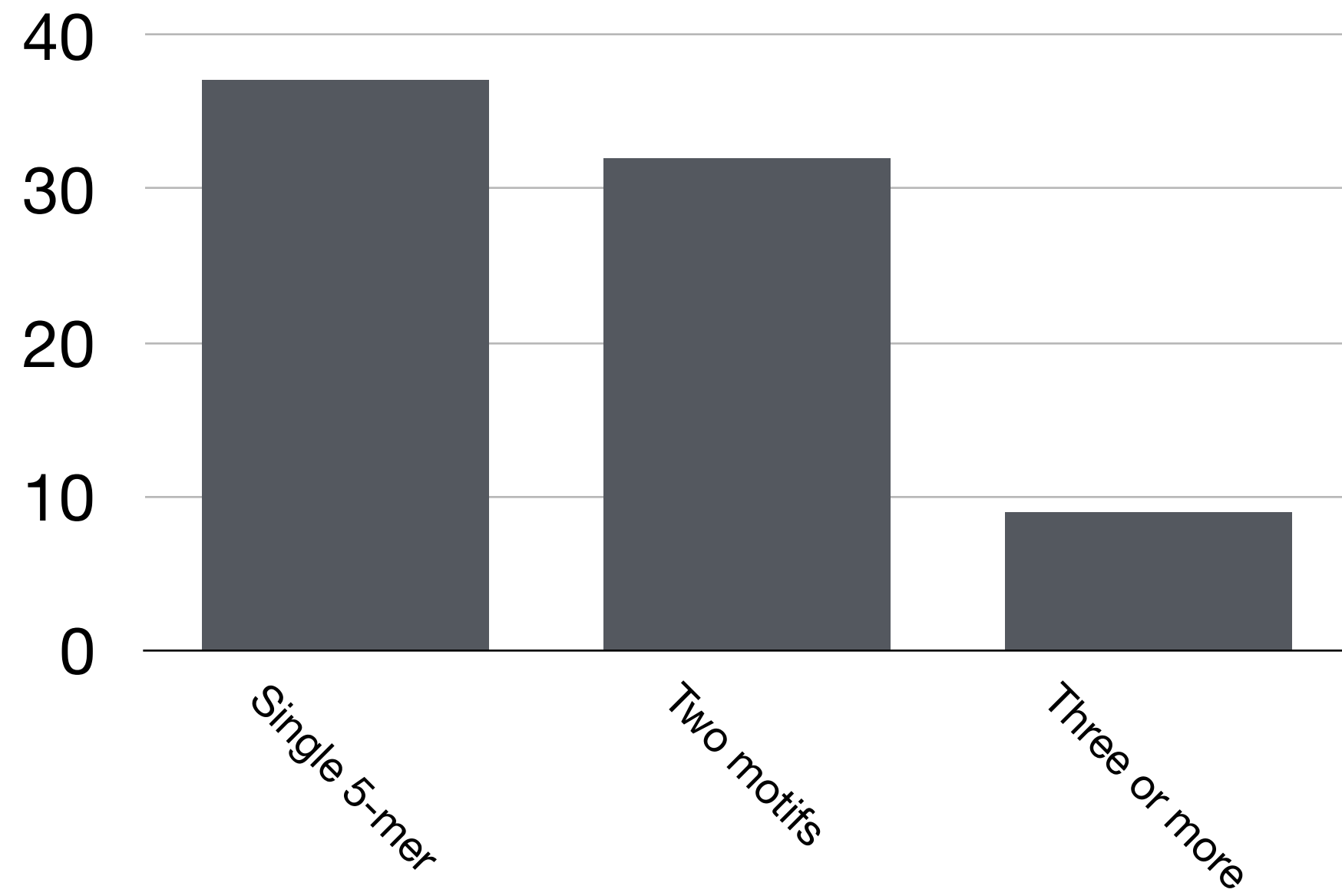


RNA Bind-N-Seq (RBNS)

- In vitro *high-throughput* assay to identify RBP binding motifs
- Lambert, N., Robertson, A., Jangi, M., McGeary, S., Sharp, P. A., & Burge, C. B. (2014). RNA Bind-n-Seq: quantitative assessment of the sequence and structural binding specificity of RNA binding proteins. *Molecular cell*, 54(5), 887-900.



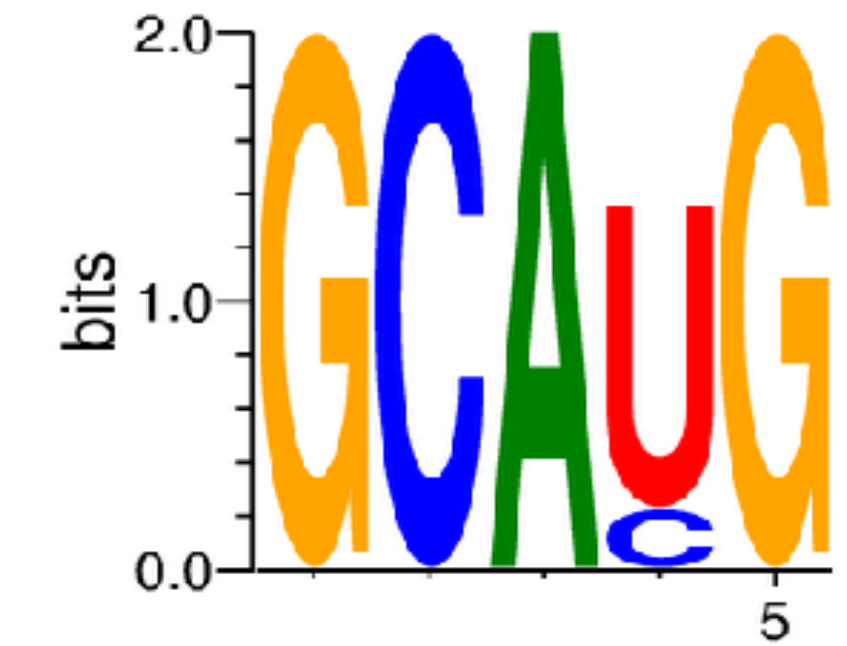
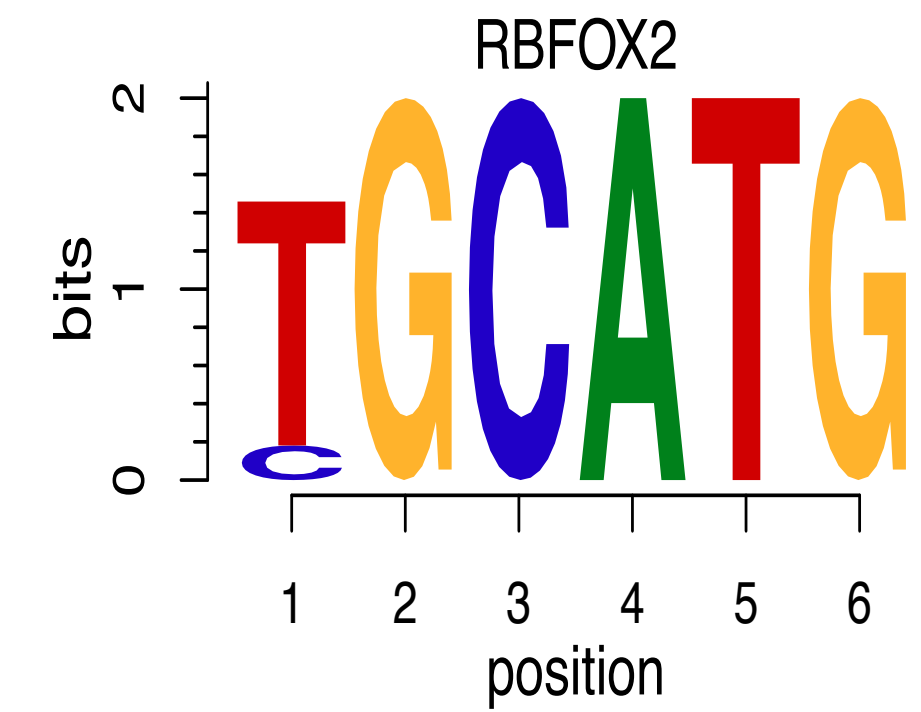
RBNS identified binding specificities of 78 RBPs (ranging from 5 to 9-mer)



- EIF4G2
- EWSR1
- FUBP3
- HNRNPC
- HNRNPK
- IGF2BP1
- IGF2BP2
- KHSRP
- PCBP2
- RBFOX2**
- RBM22
- SFPQ
- SRSF9
- TAF15
- TARDBP
- TIA1
- TRA2A

de novo

RBNS



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Identification and Classification of Conserved RNA Secondary Structures in the Human Genome

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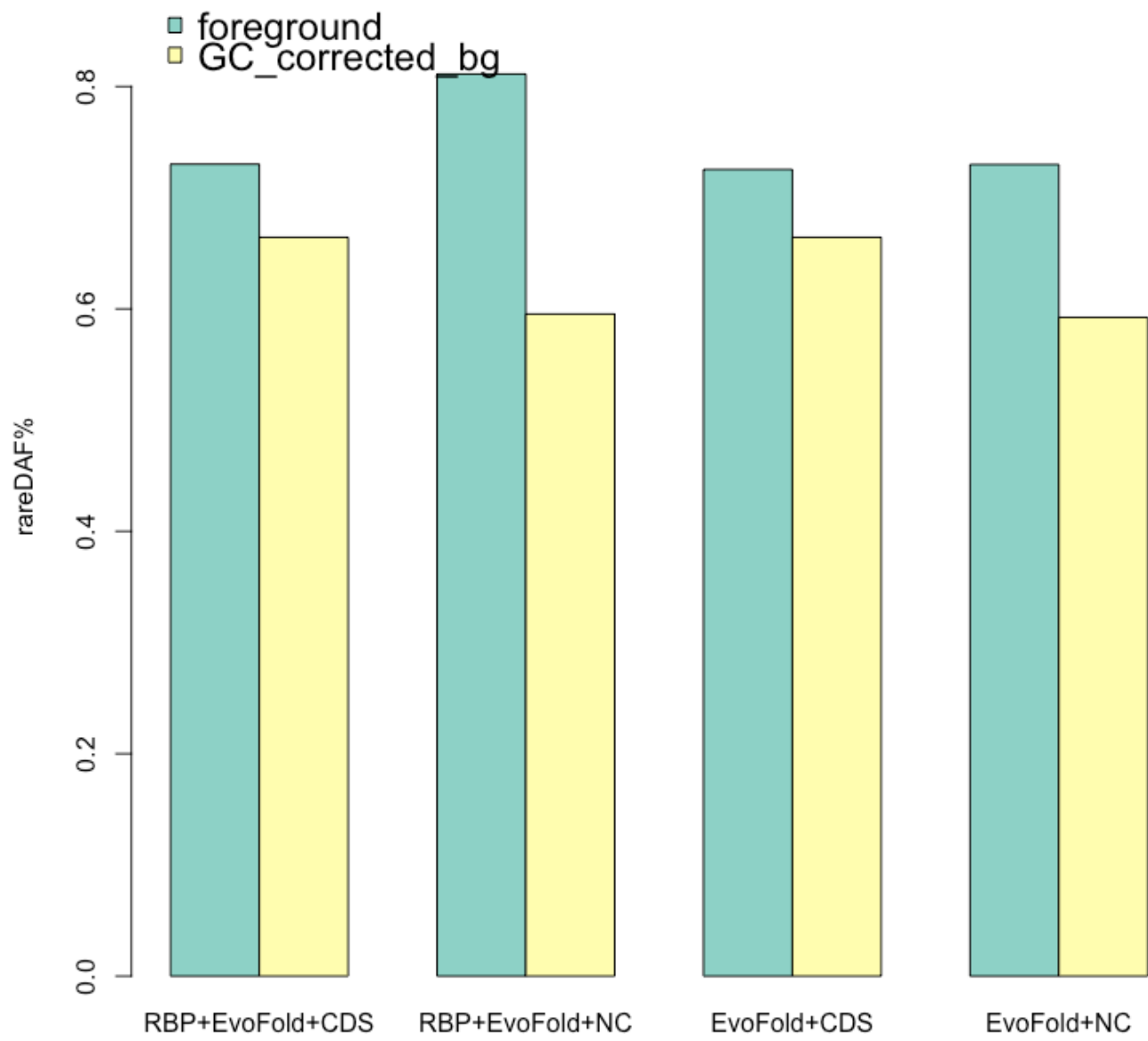
Richard Durbin, Editor

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Abstract

Go to: 



Overview of LL's Part

- Investigate RNA folding characteristics of DREME motifs
- Probability of folding into different secondary structures
- Minimum free energy of original vs. mutant motifs

RNA secondary structure

- Calculated with CapR
 - <https://github.com/fukunagatsu/CapR>
- Motif sequence, plus 50 bp from upstream and downstream
- One probability matrix calculated, for each sequence, for these structures

- Bulge
- Exterior RNA
- Hairpin
- Internal RNA
- Multibranch
- Stem loop

```
>chr1,17421,17627,BUD13,0.00048828125,-  
Bulge 0 1.99455e-08 0.000464545 1.38286e-05 1.46406e-05 1.55022e-05  
2.05606e-05 1.17339e-05 0.000101196 1.01708e-05 1.64382e-05 5.04094e-05  
7.70172e-05 0.000106235 0.000439573 0.000711344 0.000736285 0.0015478  
0.00167642 0.000551169 0.000367372 0.000140471 4.96609e-05 1.16999e-05  
5.44293e-06 0.000633936 0.000813112 0.00062656 0.000674941 0.00101248  
0.00133008 1.65508e-05 0.000528675 2.33213e-05 0.000871995 0.0012408  
0.000984605 0.000910845 0.000142631 0.00158356 0.000121642 7.86675e-05  
9.54341e-05 0.000271989 0.00102157 0.0834383 0.0888513 0.0921426 0.115774  
8.94323e-05 1.00571e-05 0.088468 0.0835028 0.000350463 0.000544377  
0.000469329 0.000330232 9.56236e-05 0.463245 0.000113737 0.00331707  
0.00330224 0.0029775 0.0161246 0.00066284 0.0273265 ...
```

Minimum free energy

- RNAfold calculates minimum free energy (MFE) of RNA sequences
 - <https://www.tbi.univie.ac.at/RNA/RNAfold.1.html>
- Motif sequence, plus 20 bp from upstream and downstream
- Create mutant sequences from the original
 - Each bp has three mutant possibilities
 - Create each of these mutant possibilities with each bp
 - Run RNAfold on all mutants

Original:

```
>chr10,180989,181037,DDX3X,0.000152587890625,+  
GAGGGGCCGGUGGGGCCGAGCGGCCGCCCGCGCGCA  
UCGCCAUGUGA
```

Mutants:

```
>chr10,180989,181037,DDX3X,0.000152587890625,+1,G,A  
AAGGGGCCGGUGGGGCCGAGCGGCCGCCCGCGCGCAUCGCCAUGUGA  
>chr10,180989,181037,DDX3X,0.000152587890625,+1,G,C  
CAGGGGCCGGUGGGGCCGAGCGGCCGCCCGCGCGCAUCGCCAUGUGA  
>chr10,180989,181037,DDX3X,0.000152587890625,+1,G,T  
TAGGGGCCGGUGGGGCCGAGCGGCCGCCCGCGCGCAUCGCCAUGUGA
```

Minimum free energy

Original:

```
>chr10,180989,181037,DDX3X,0.000152587890625,+  
GAGGGGCCGGUGGGGCCGAGCGGCCGCCCGCGCGCAUCGCCAUGUGA  
((.(.(((((.((((((....))))).))))).)).)..... (-21.90)
```

Mutants:

```
>chr10,180989,181037,DDX3X,0.000152587890625,+,1,G,A  
AAGGGGCCGGUGGGGCCGAGCGGCCGCCCGCGCGCAUCGCCAUGUGA  
...(.((((((.((((((....))))).))))).)).((((...))) (-21.10)
```

```
>chr10,180989,181037,DDX3X,0.000152587890625,+,1,G,C  
CAGGGGCCGGUGGGGCCGAGCGGCCGCCCGCGCGCAUCGCCAUGUGA  
...(.((((((.((((((....))))).))))).)).((((...))) (-21.10)
```

```
>chr10,180989,181037,DDX3X,0.000152587890625,+,1,G,T  
UAGGGGCCGGUGGGGCCGAGCGGCCGCCCGCGCGCAUCGCCAUGUGA  
...(.((((((.((((((....))))).))))).)).((((...))) (-21.10)
```