

EN-CODEC
Main FigPack

v170517

BIOSAMPLE →

← ASSAY

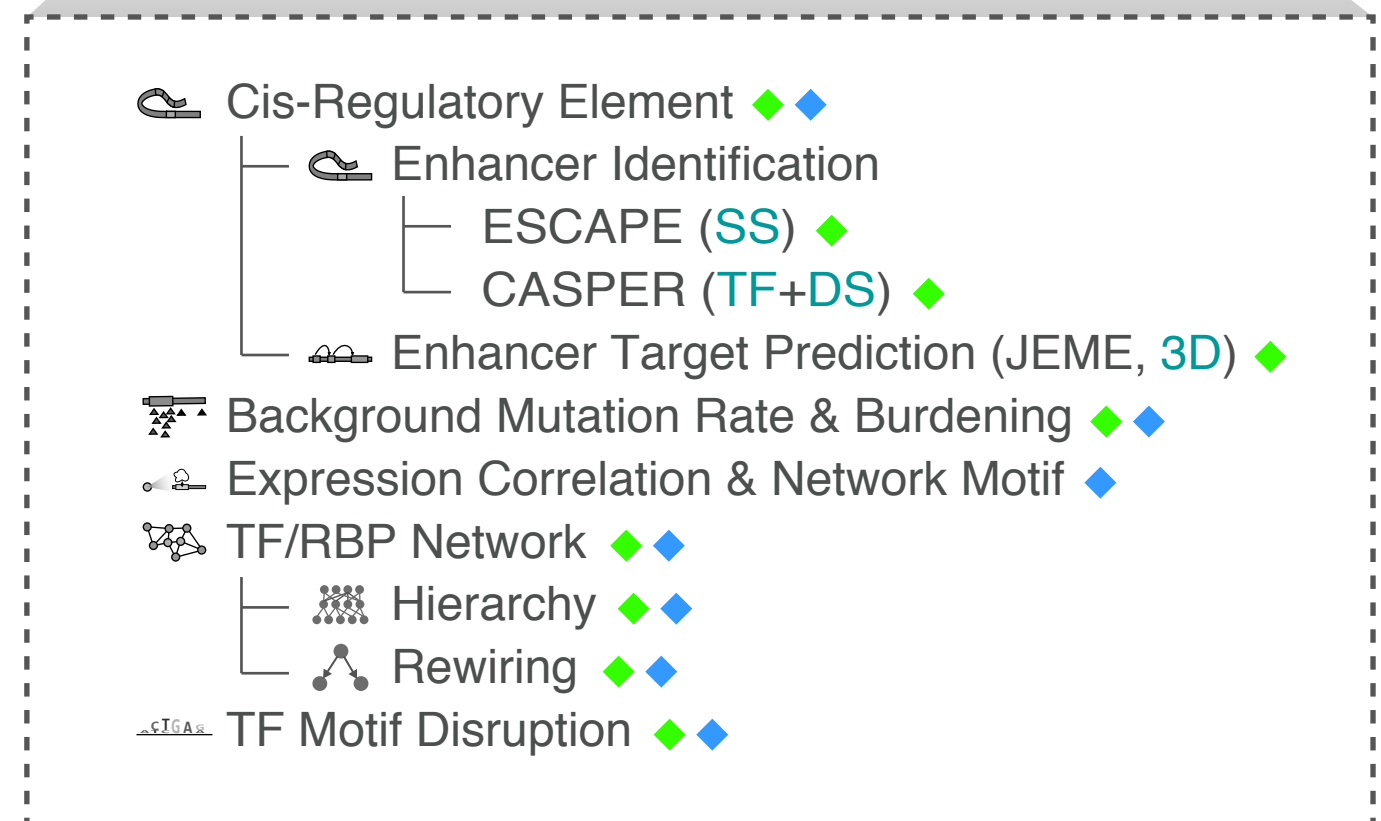
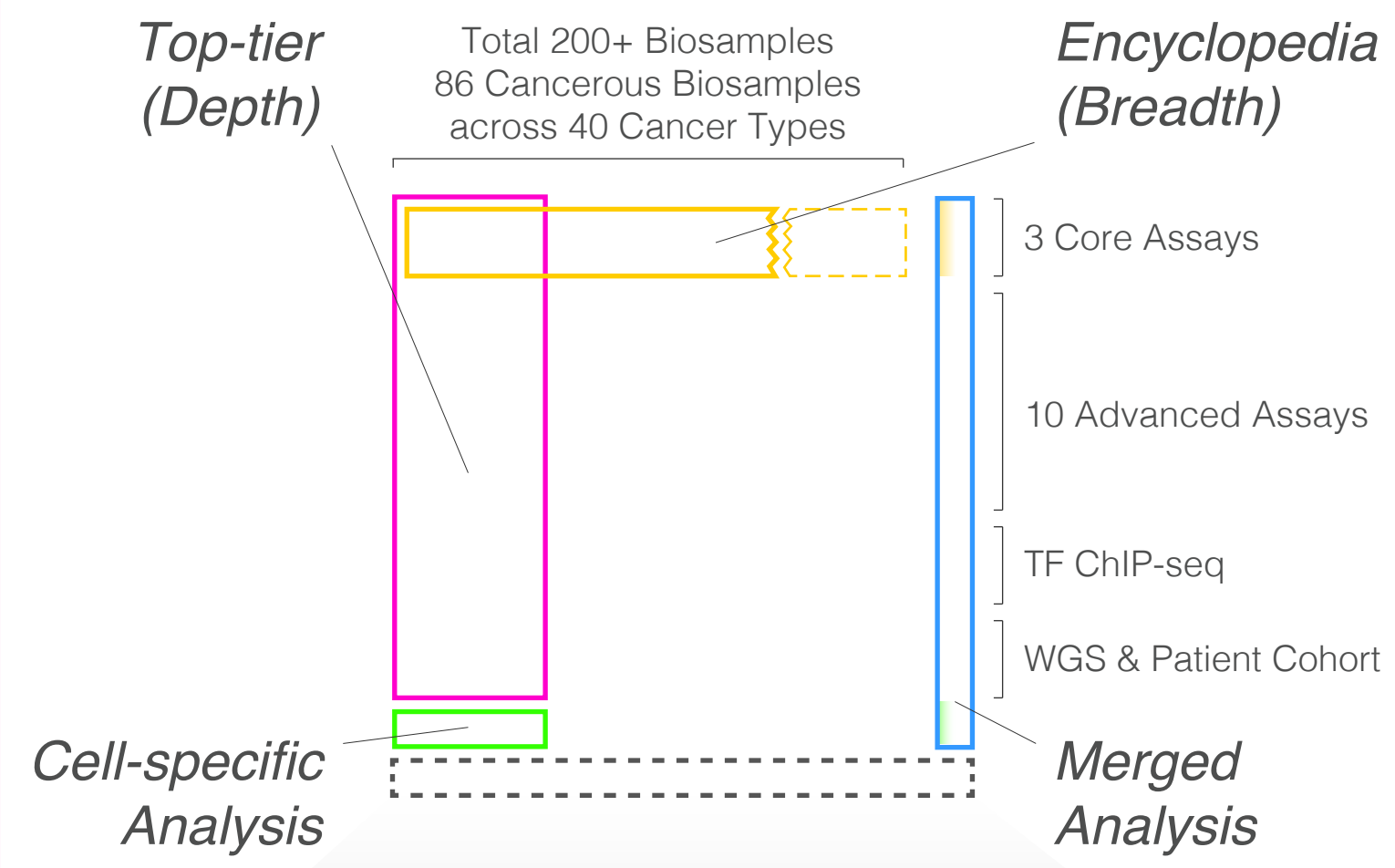
EN•CODEC

	K562	HepG2	A549	MCF-7	HeLa-S3	H1-hESC	Caco-2	HCT116	Panc1	LNCaP	PC-3	PC-9	SK-N-MC	DND-41	SK-N-SH	...
	CML	LIHC	LUAD	BRCA	Cervix	ESC	COAD+READ	PAAD	PRAD	LUAD	SARC	LAML	NB			

Chromatin Accessibility DS	DNase-seq	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•
	Histone Modifications HM	12	11	11	5	11	11	3	12	6	1	13	13	7	11	13
Transcription TX	RNA-seq	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•
	RAMPAGE	•														
RNA-binding Proteins RP	eCLIP	89	70													
	TF KD	85	61		2											
shRNA/siRNA Knockdown KD	RBP KD	234	225													
	ChIA-PET	3	1		4	2										
3D Chromatin Structure 3D	Hi-C	▲		•	▲		▲									
	STARR-seq	•	▲		•											
Enhancers SS	WGBS	•	•		▲		•									
Methylation ME	RRBS	•	•	•	•	•	•									
	Repli-seq/chip	•	•		•	•	•									
Replication Timing RT	TF Total	207	95	31	52	59	49									
	TFSS	125	69	23	34	34	32									
Transcription Factors TF	Chromatin Remodeller	31	13	3	7	9	9									
	Cofactor	20	7	3	4	6	3									
	General (GTF)	17	4	2	2	10	5									
	Other	14	2		5											
Cell Line WGS WG	SNV	▲			▲	▲										
	SV	▲			▲	▲										
Patient Data PD	Cohort	150	82	197	116											
	Expression	173	373	517	1100	546										

- Available in ENCODE
- ▲ Available as External Resource
- ◆ Available in EN-CODEC

Cell-specific Analysis



Merged Analysis

Fig 1

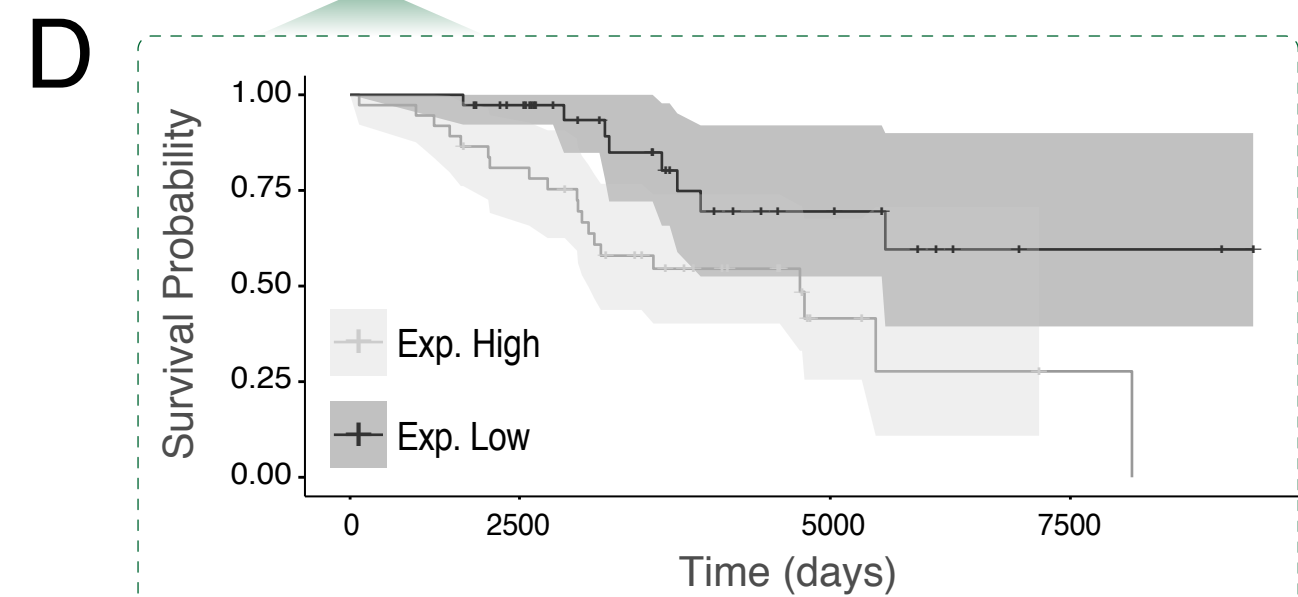
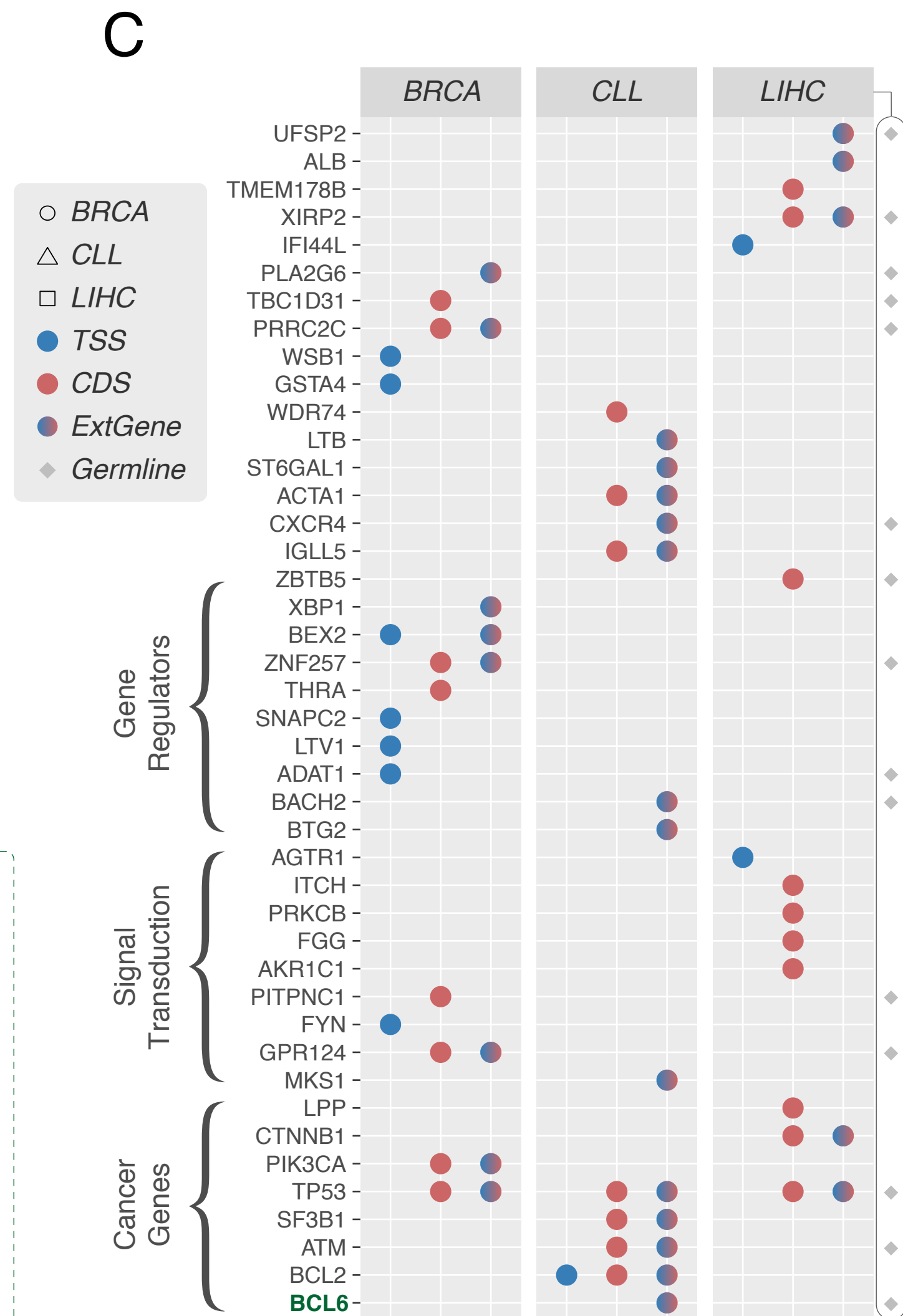
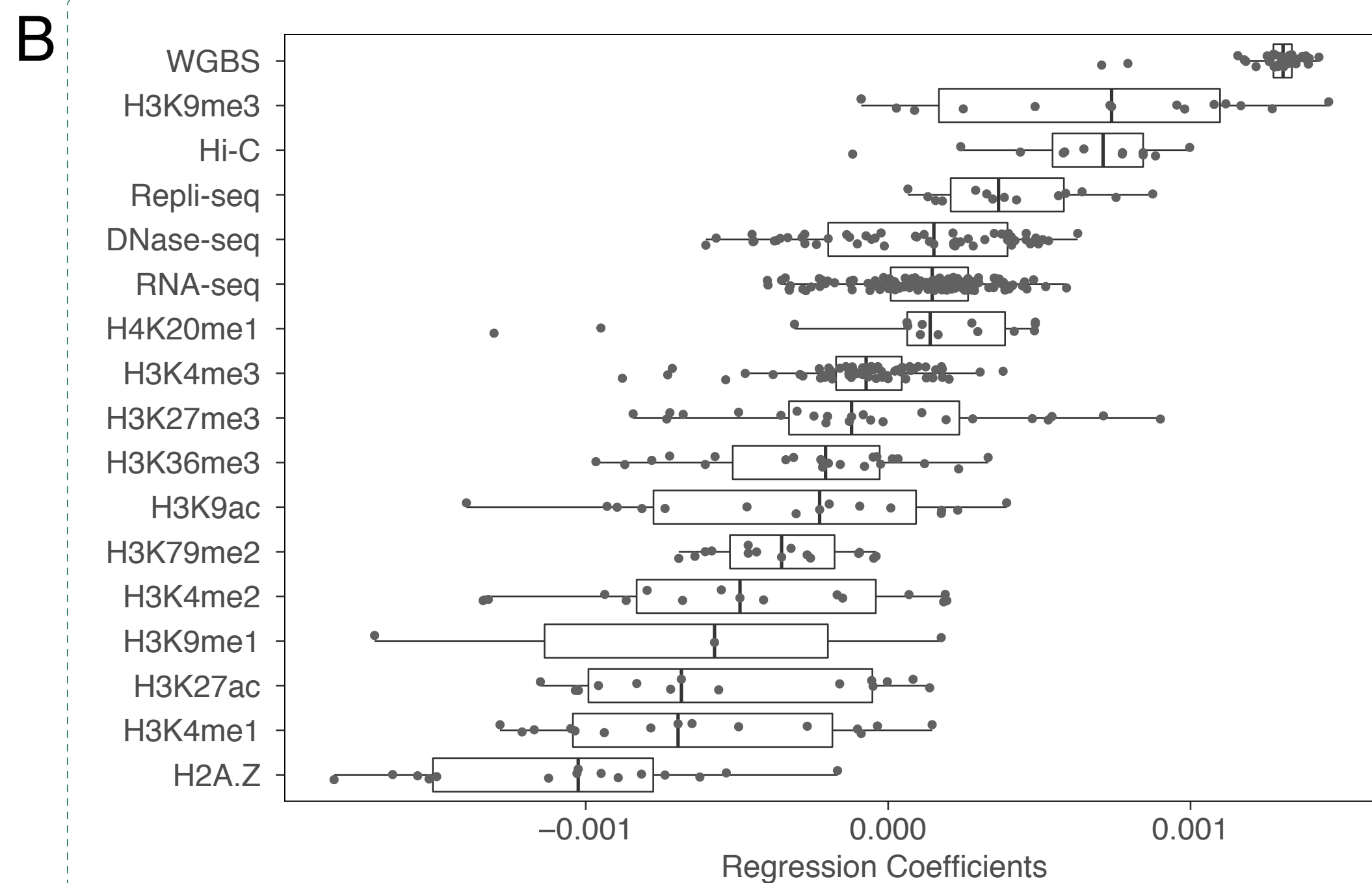
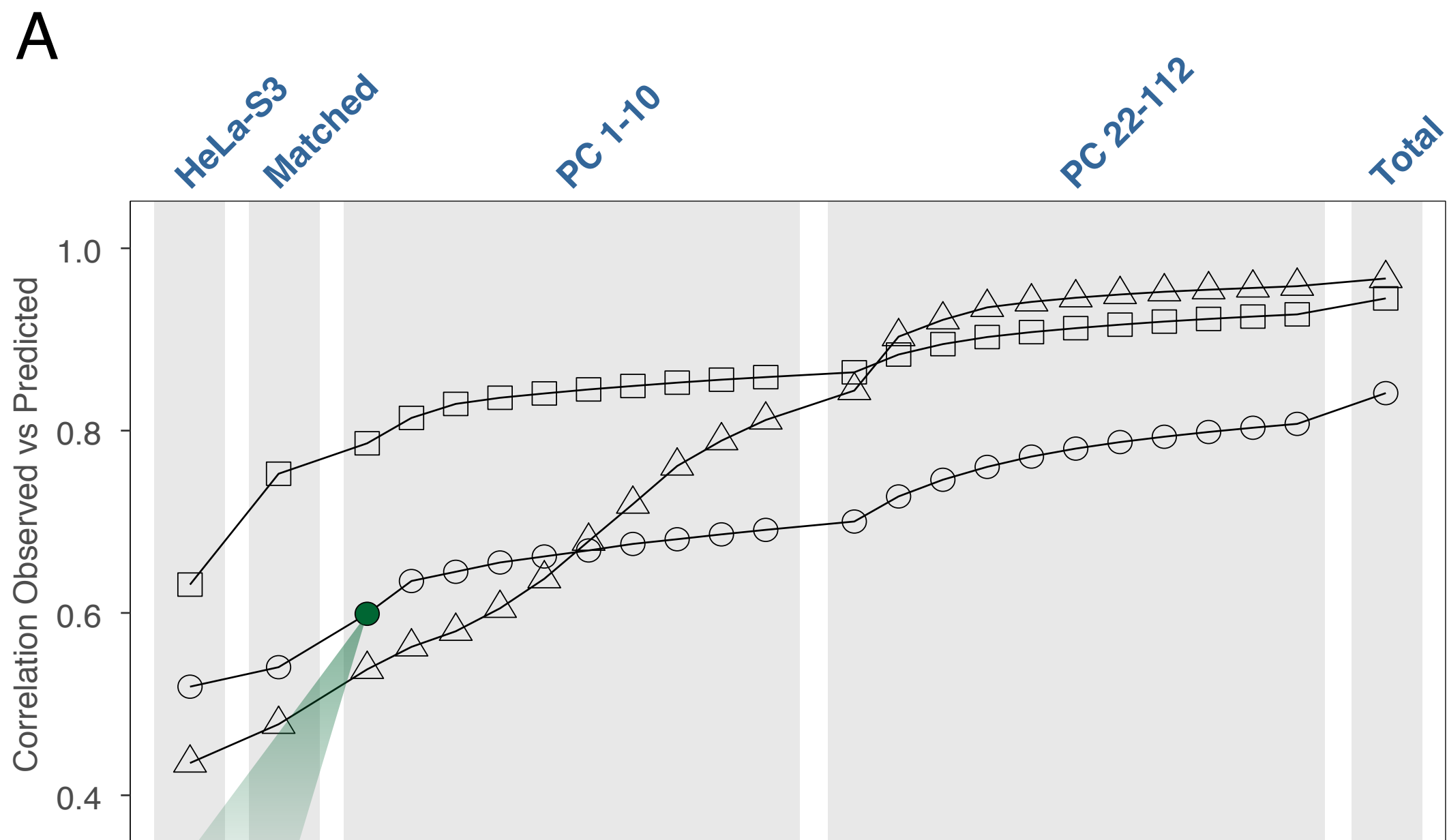


Fig 2

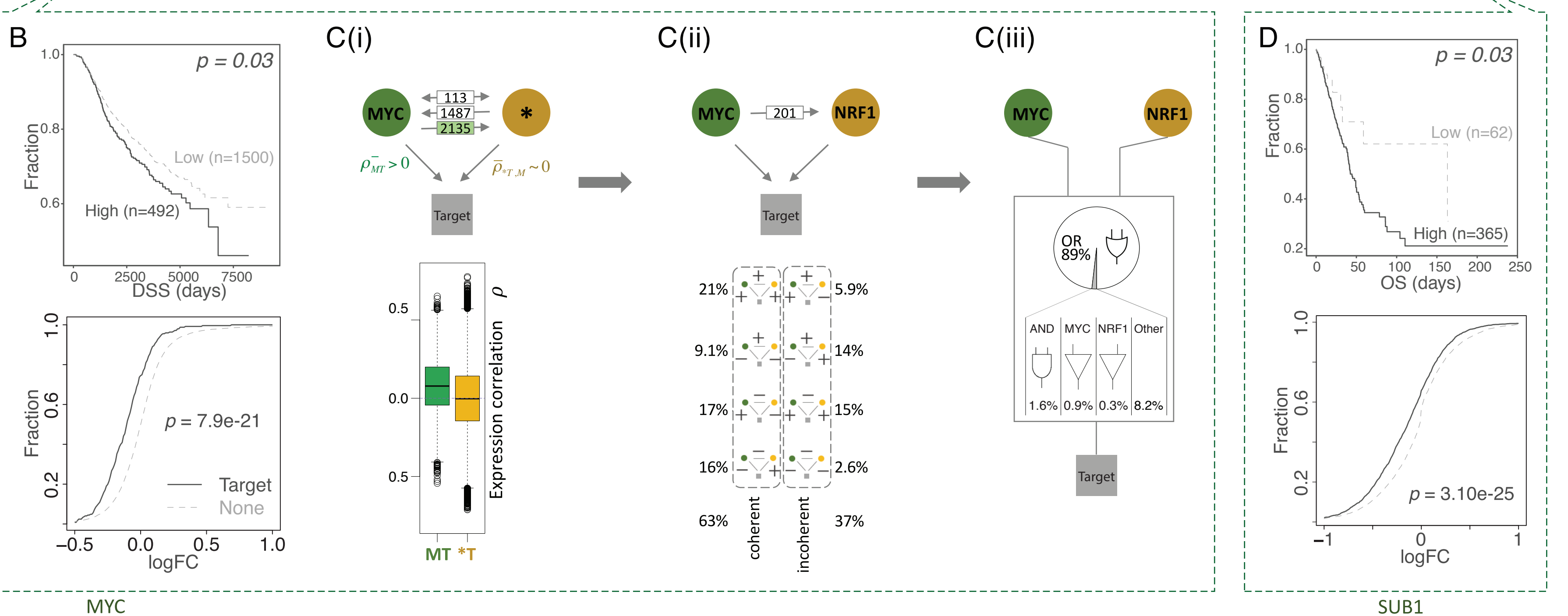
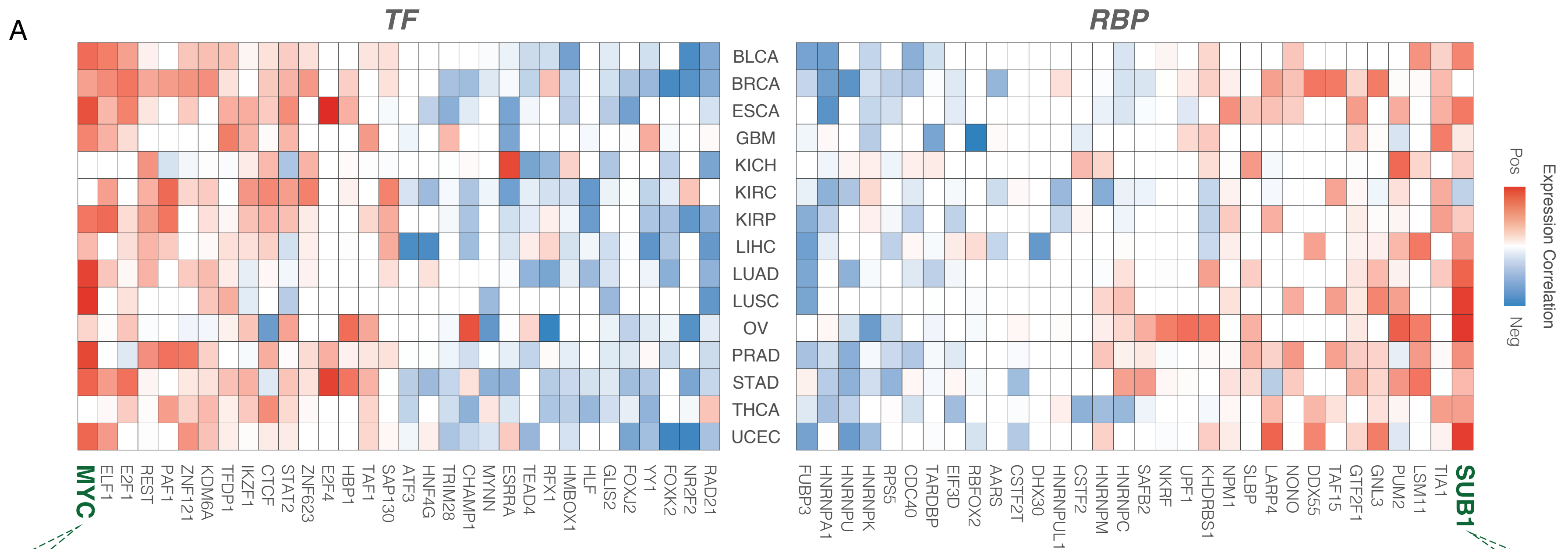
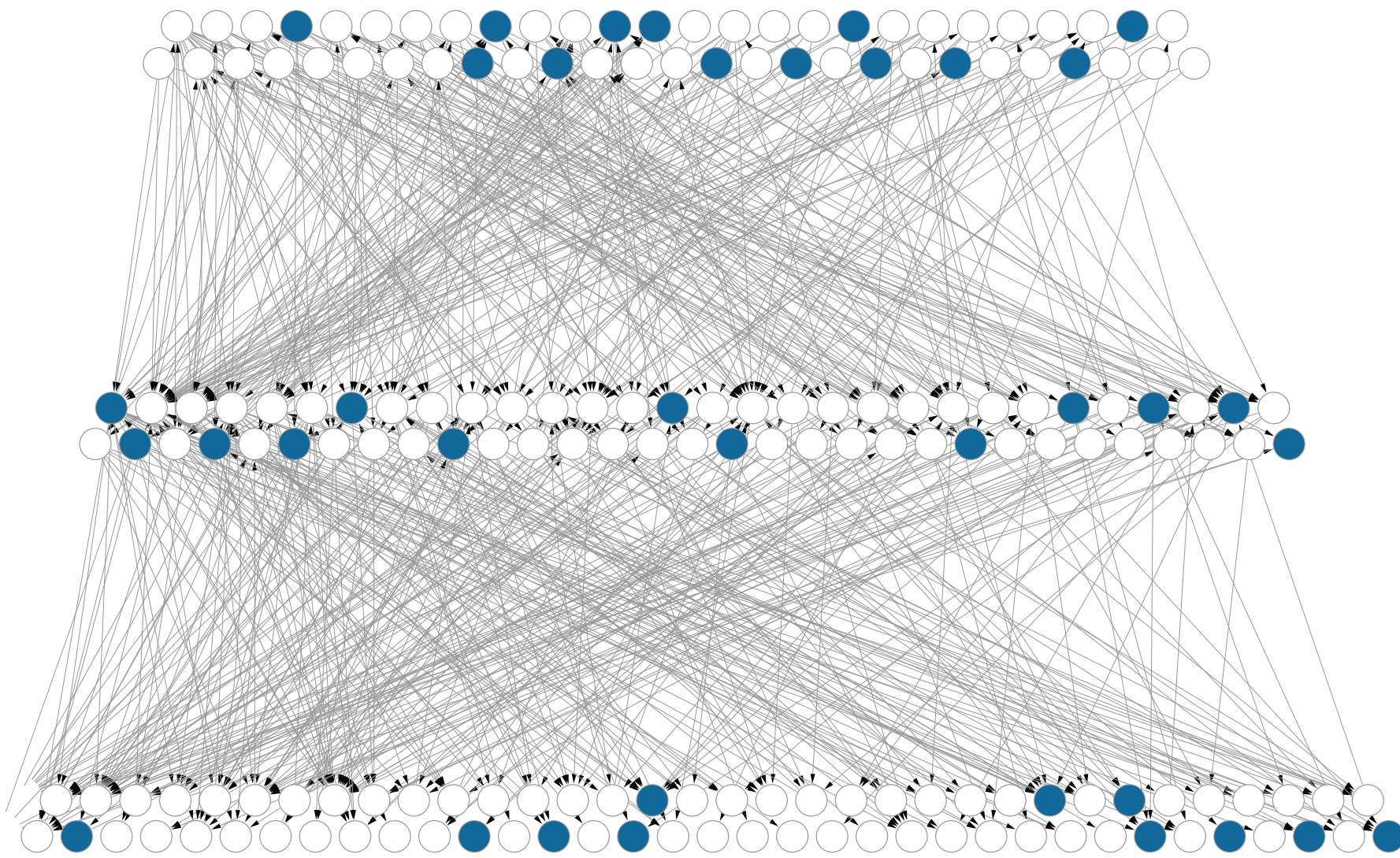
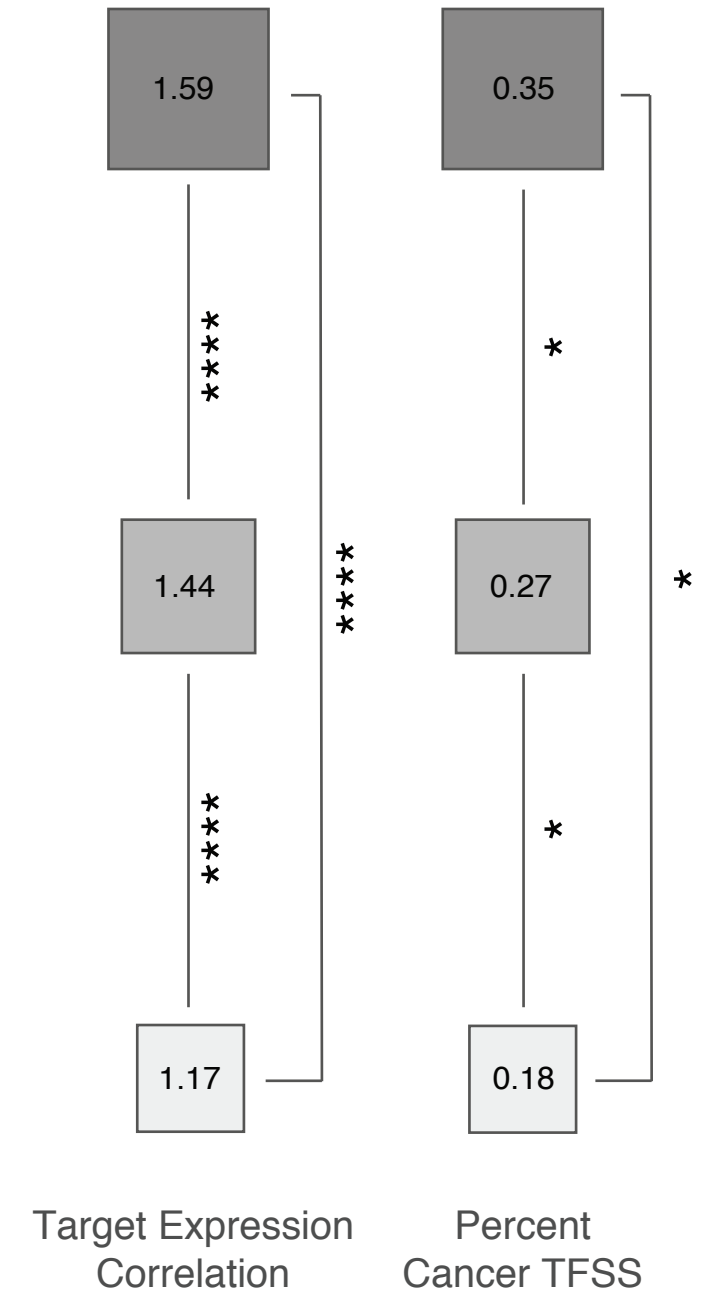


Fig 3

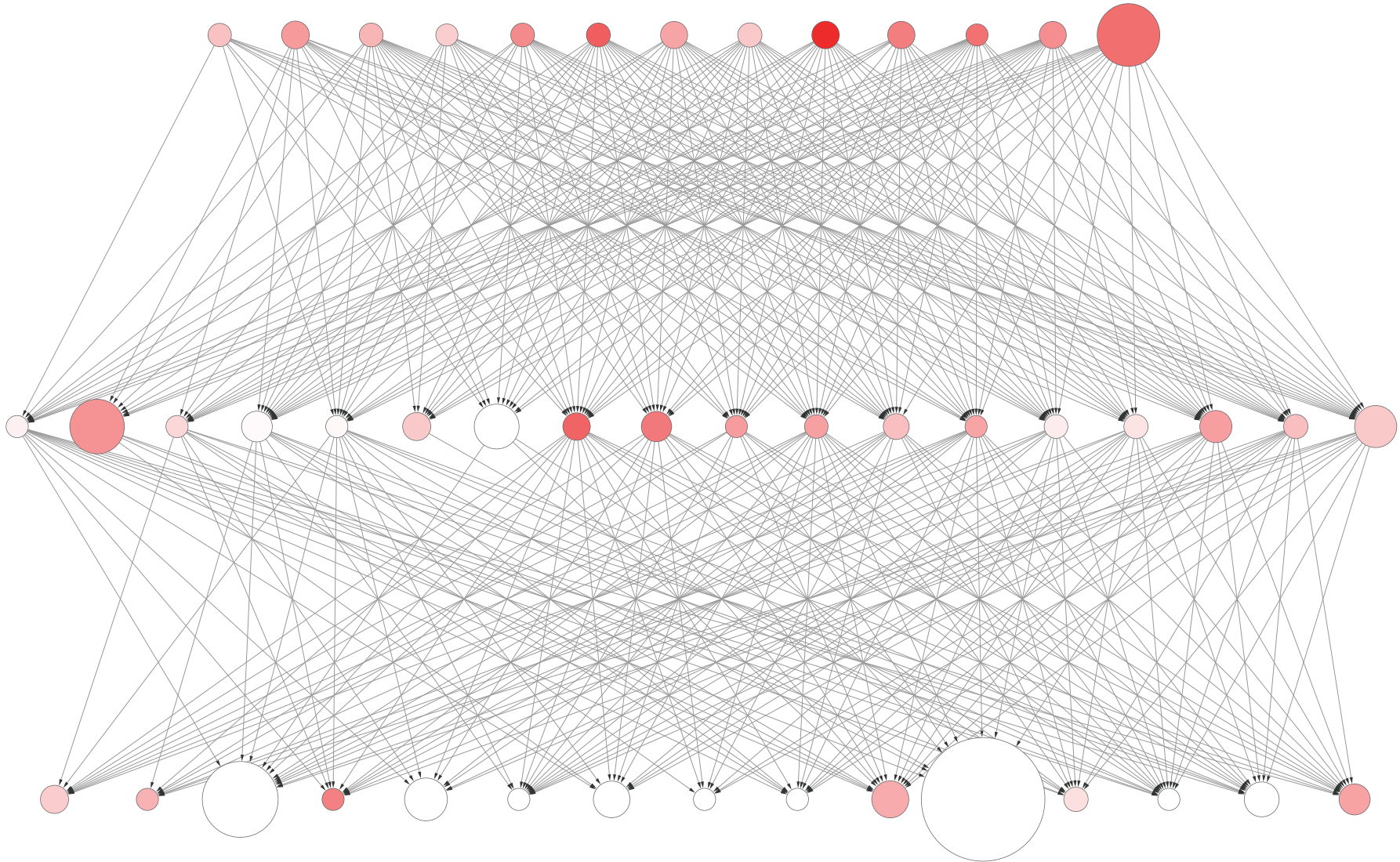
A



● Cancer TFSS



B



○ ● Exp. Correlation ○ ○ ○ TFBS Burden

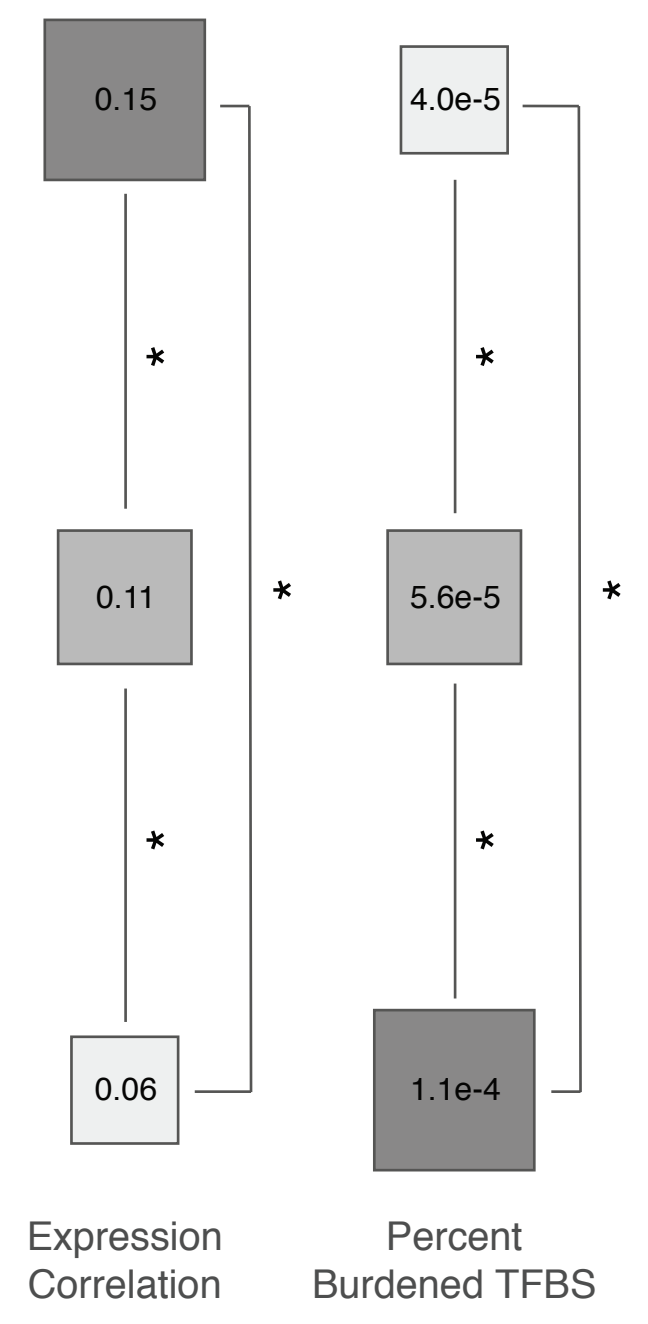


Fig 4

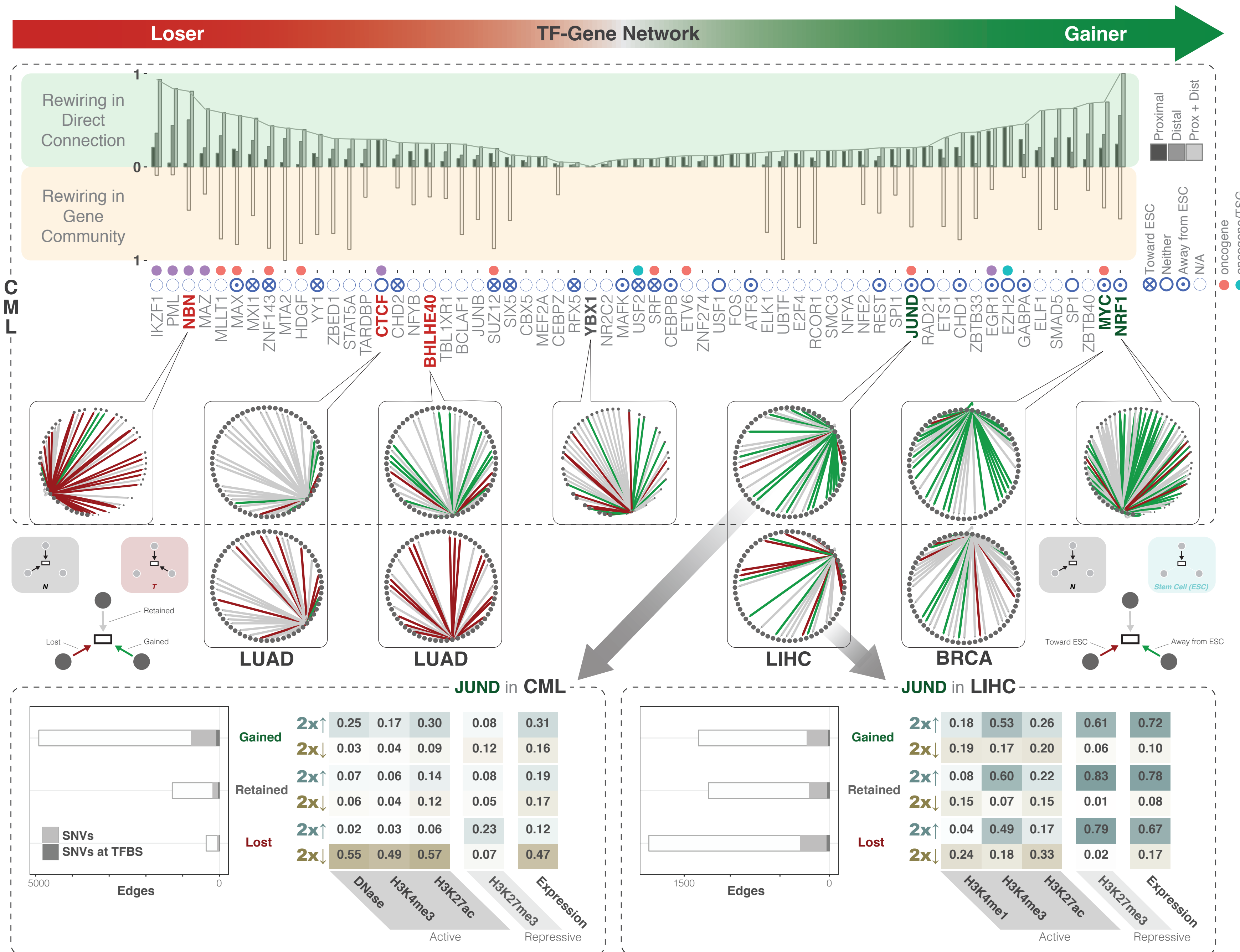
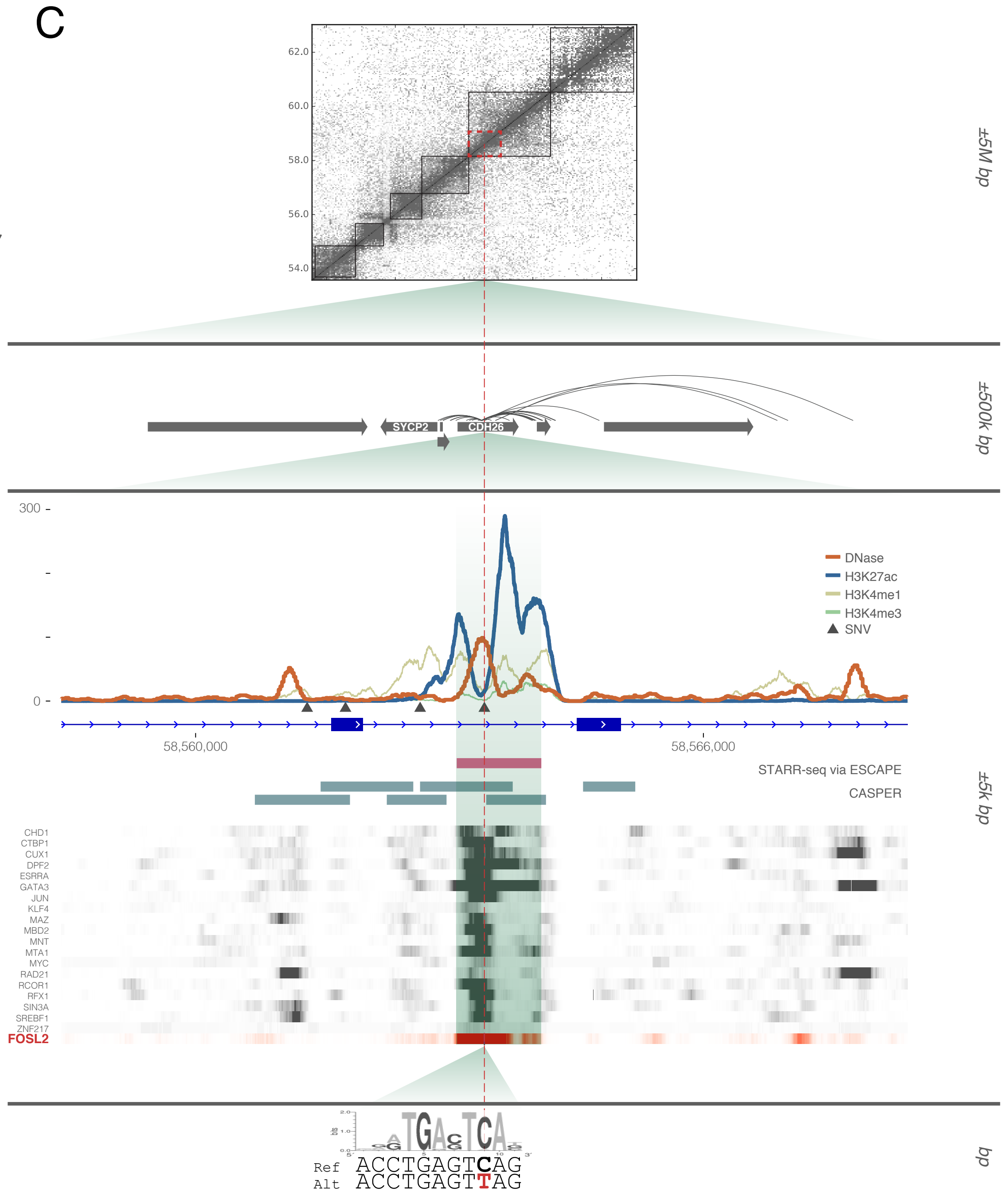
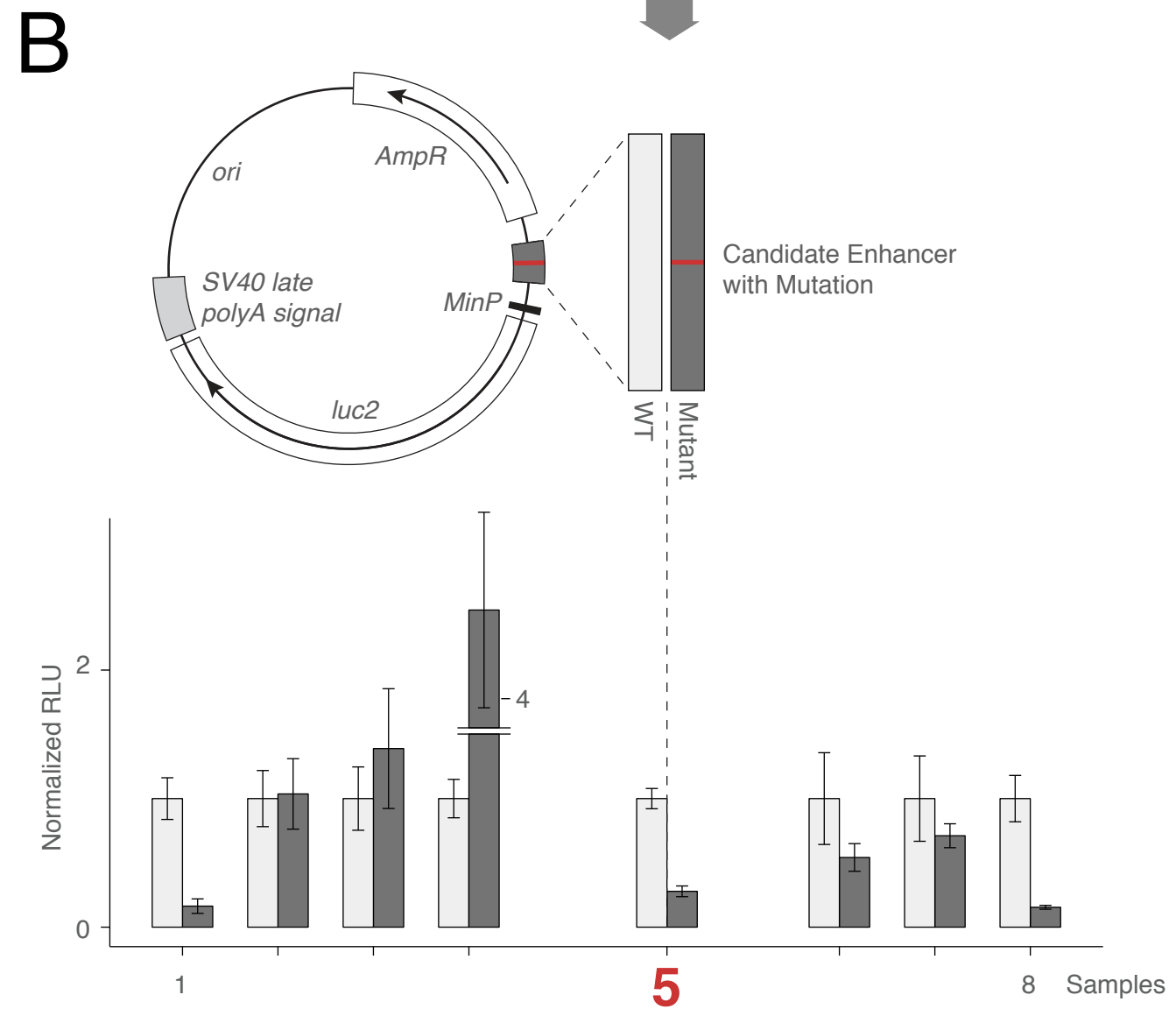
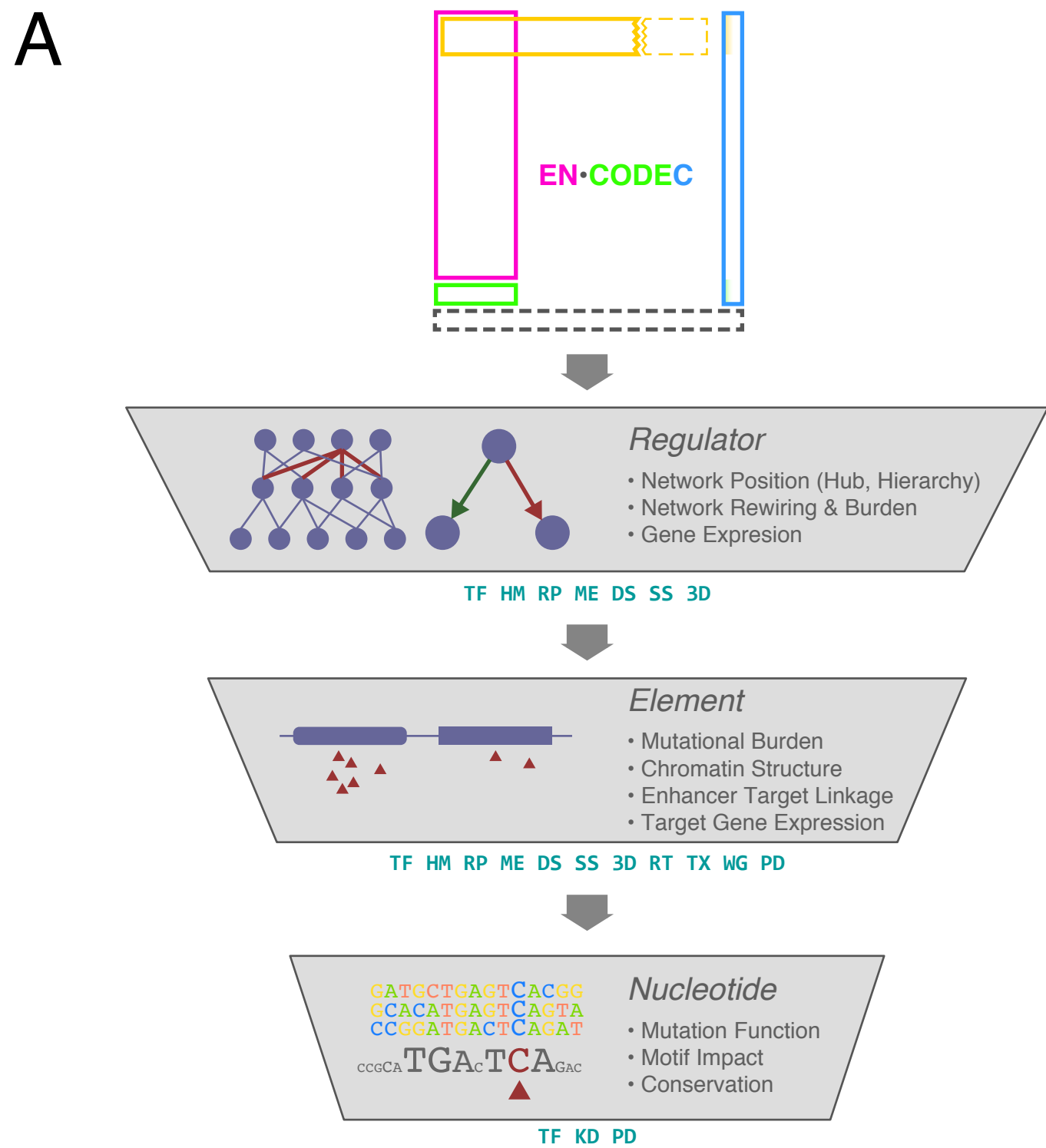


Fig 5



5M bp

500k bp

5k bp

bp

Fig 6