

EN-CODEC
Main FigPack

v170530

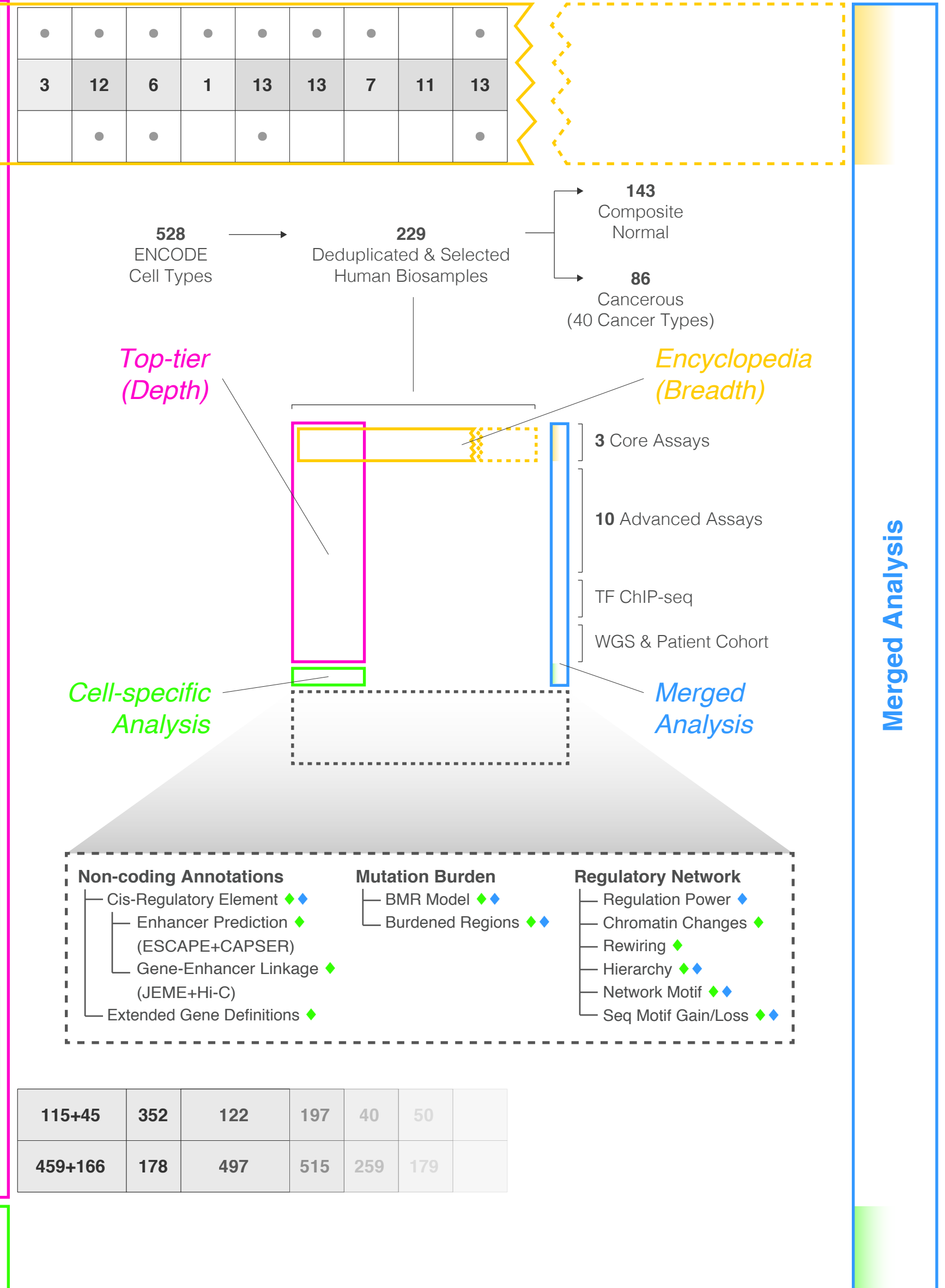
BIOSAMPLE →

← 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	▲		•	▲		▲									
	Enhancers SS	•	▲		•											
Methylation ME	WGBS	•	•		▲		•									
	RRBS	•	•	•	•	•	•									
Replication Timing RT	Repli-seq/chip	•	•		•	•	•									
	TF Total	207	95	31	52	59	49									
Transcription Factors TF	TFSS	125	69	23	34	34	32									
	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	▲			▲	▲									
Patient Data PD	SV	▲			▲	▲										
	Cohort	150	82	197	116			115+45	352	122	197	40	50			
	Expression	173	373	515	1100	546		459+166	178	497	515	259	179			



Available from

- ENCODE
- ▲ External Resource
- ◆ EN-CODEC

Cell-specific Analysis

Merged Analysis

Fig 1

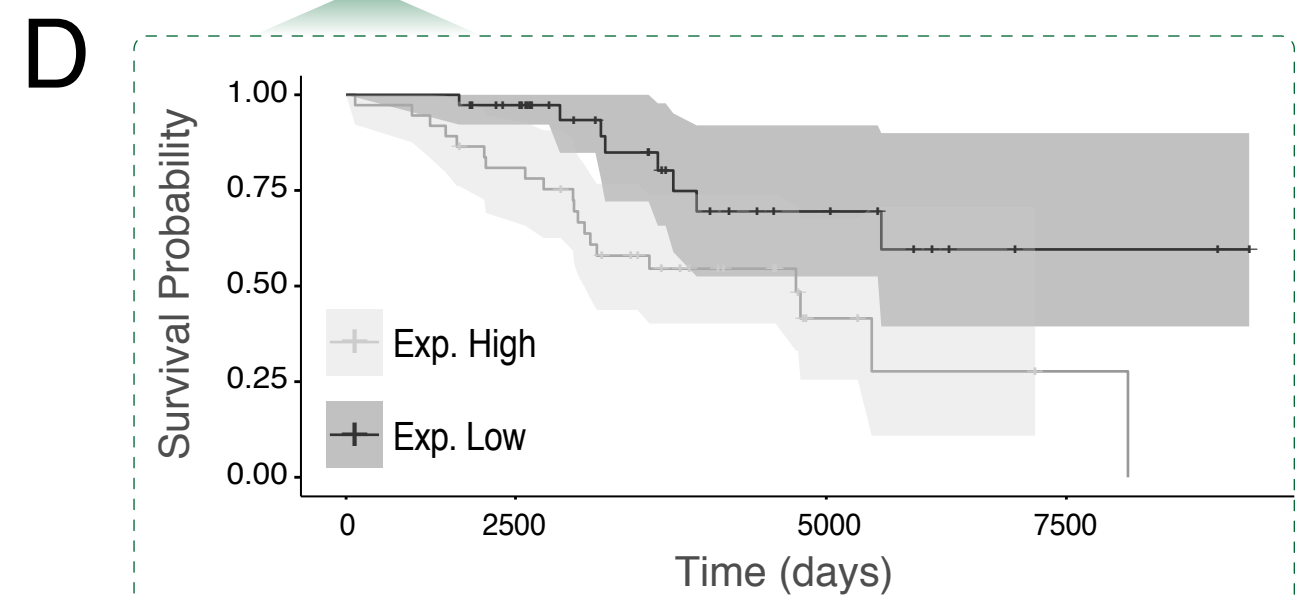
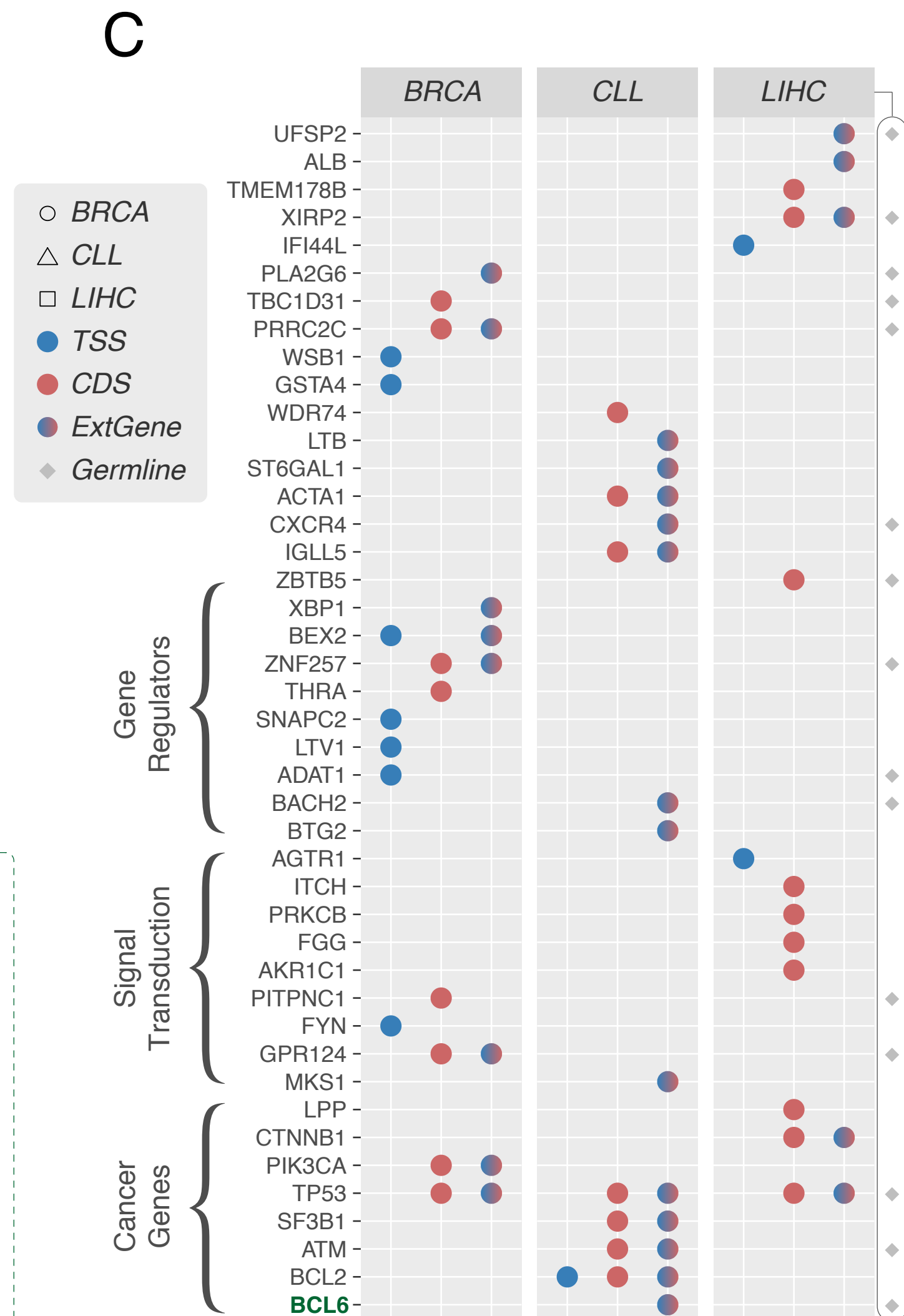
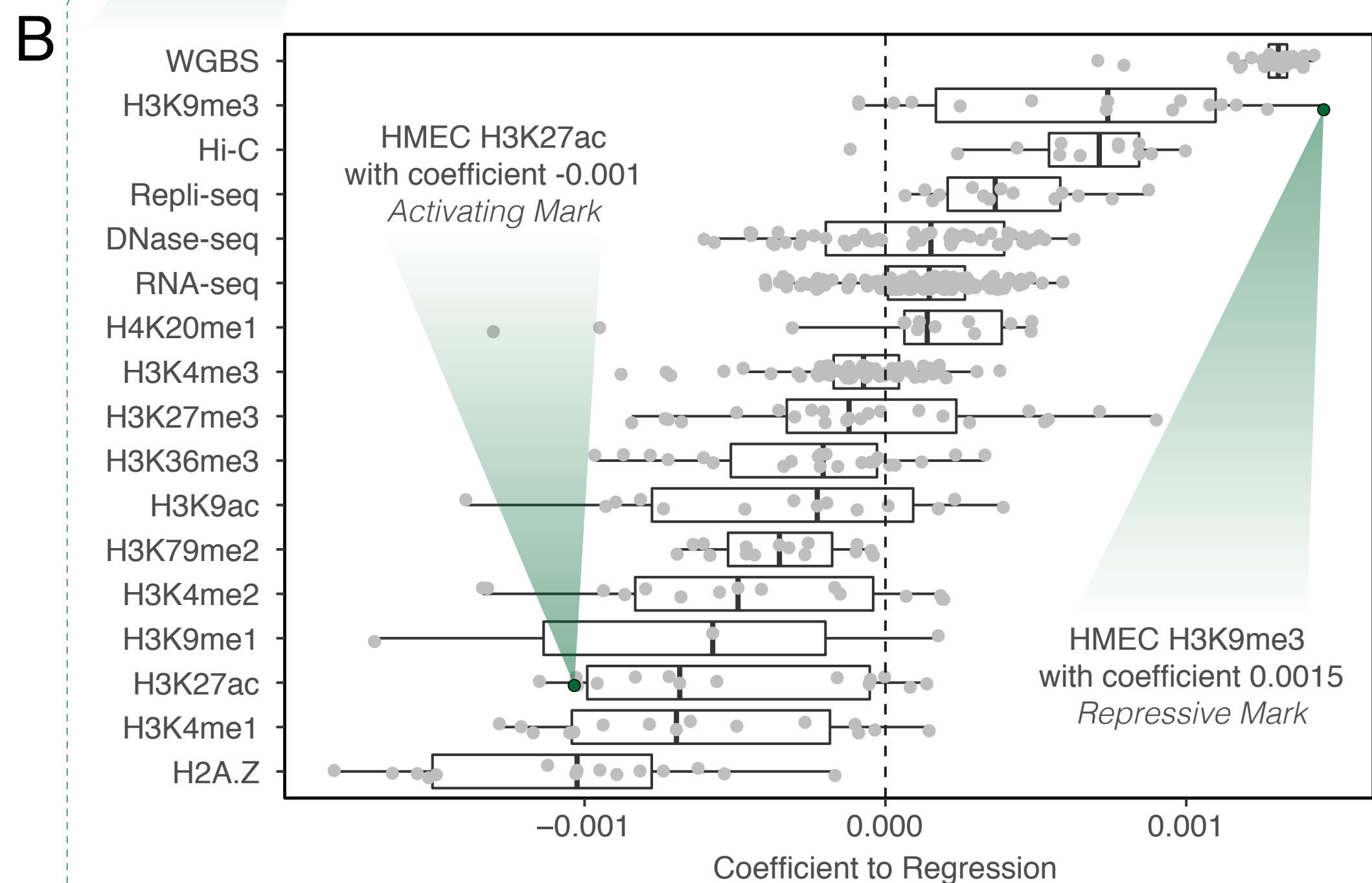
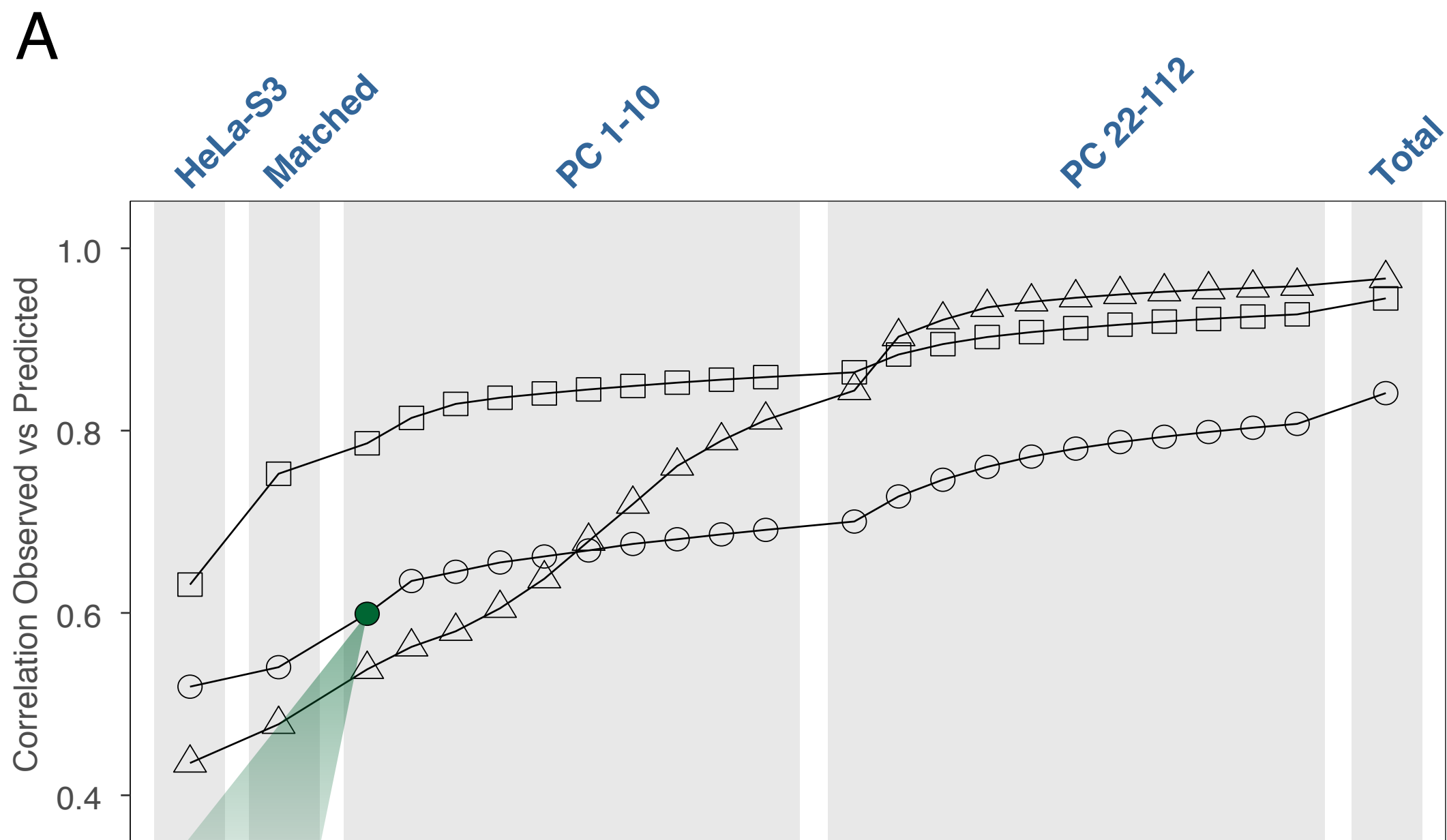


Fig 2

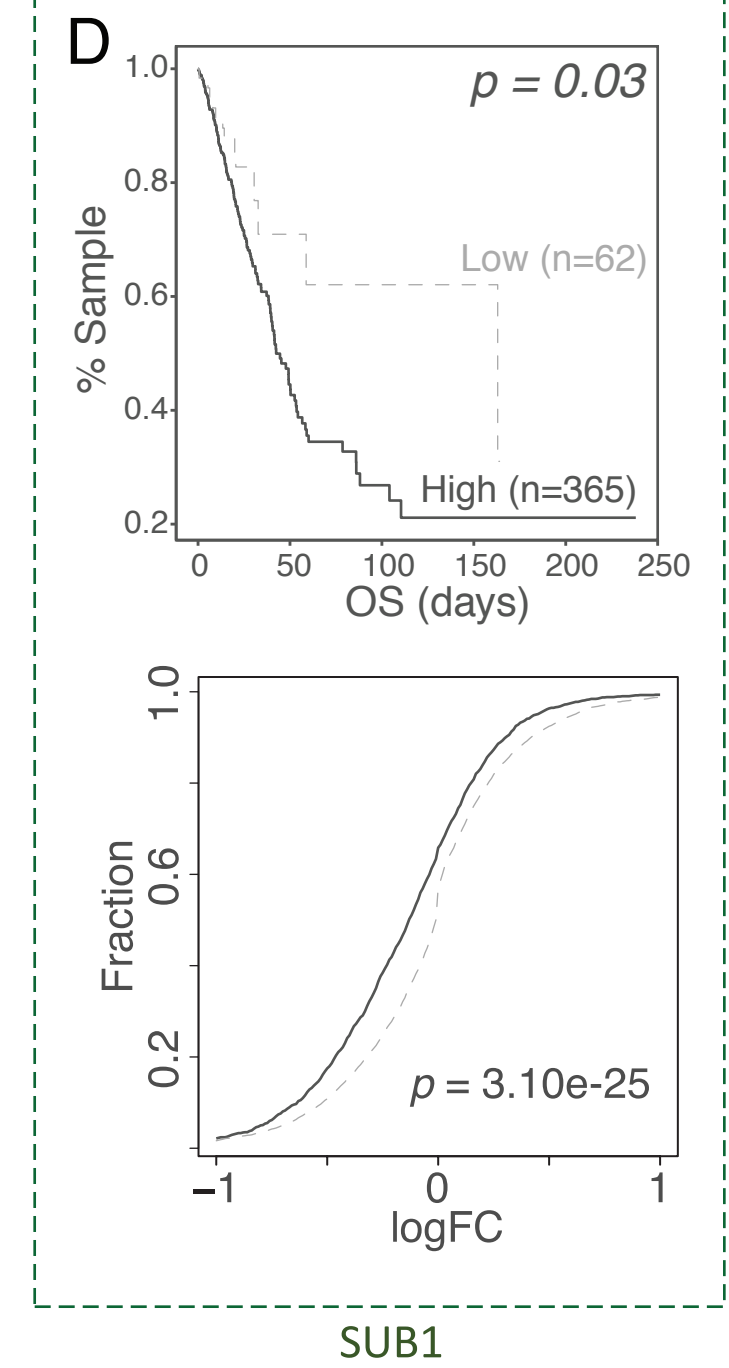
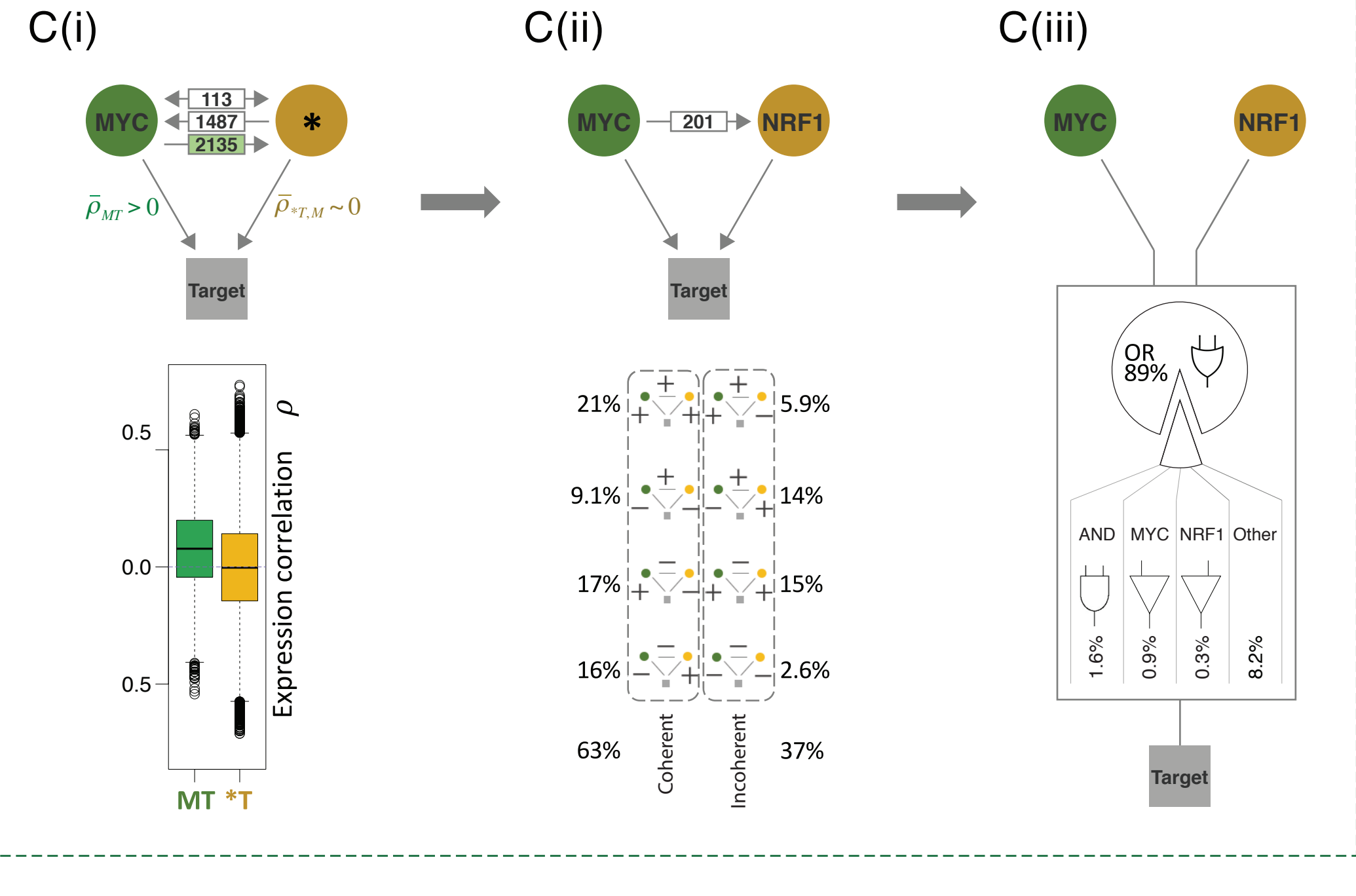
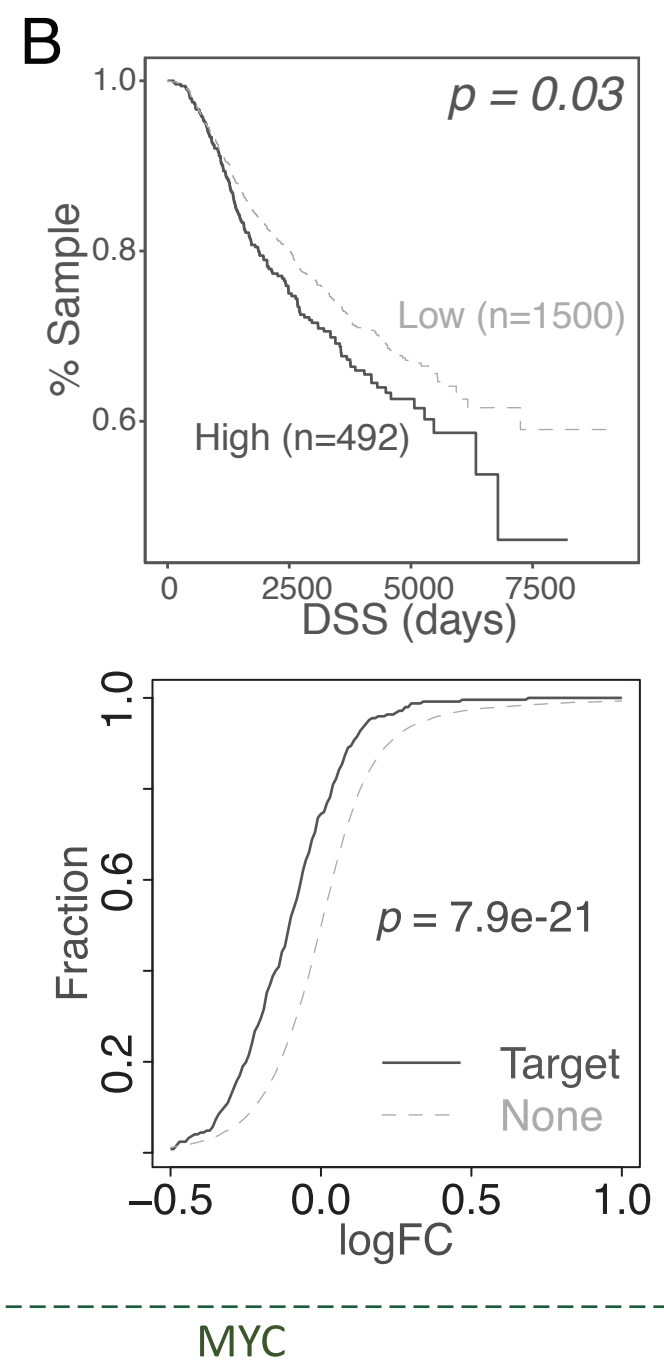
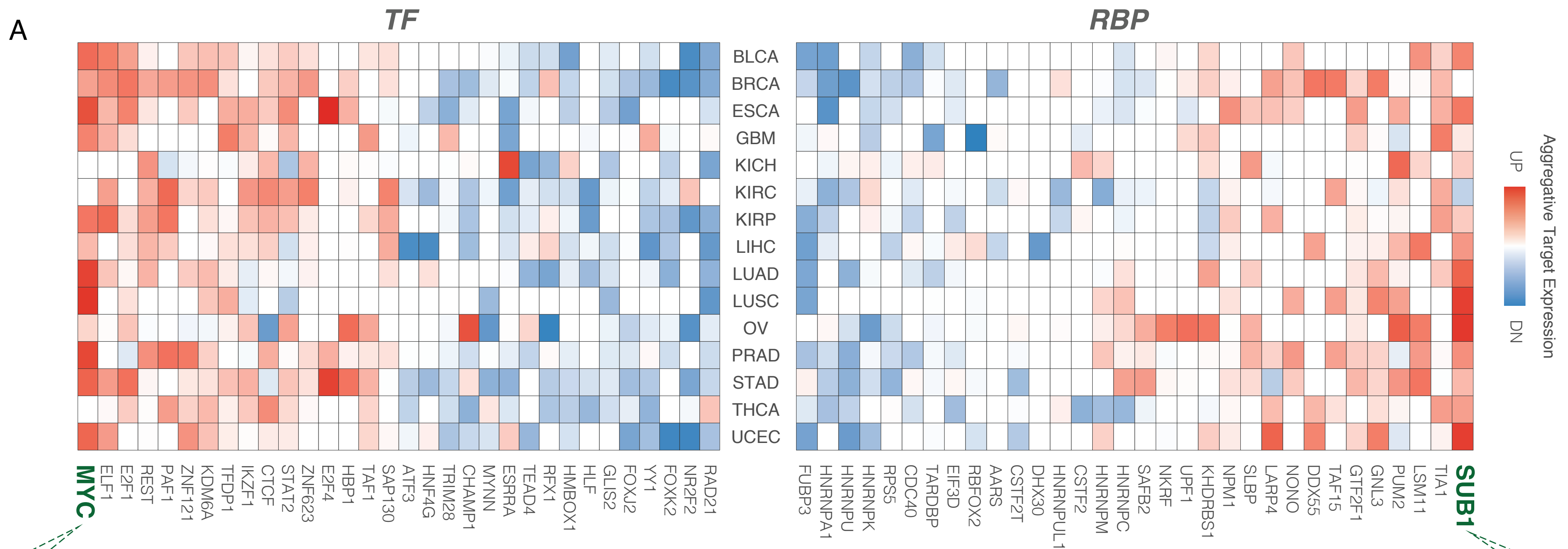
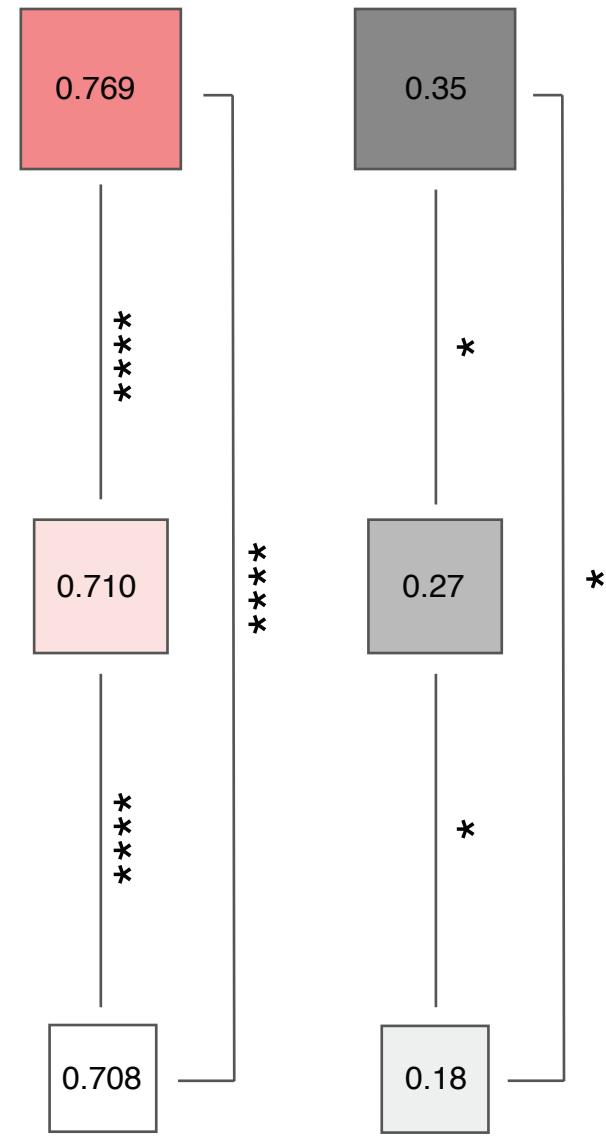
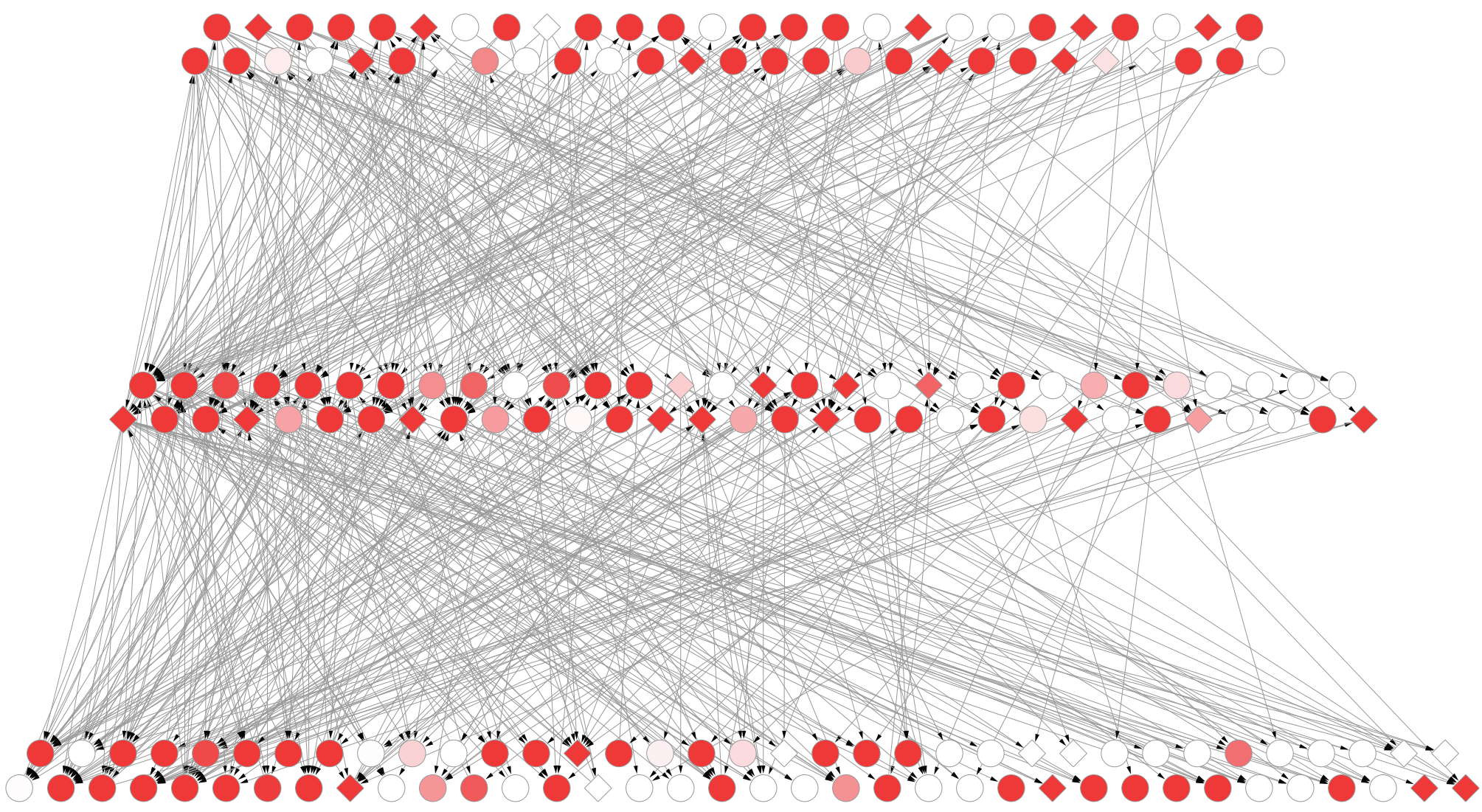


Fig 3

A

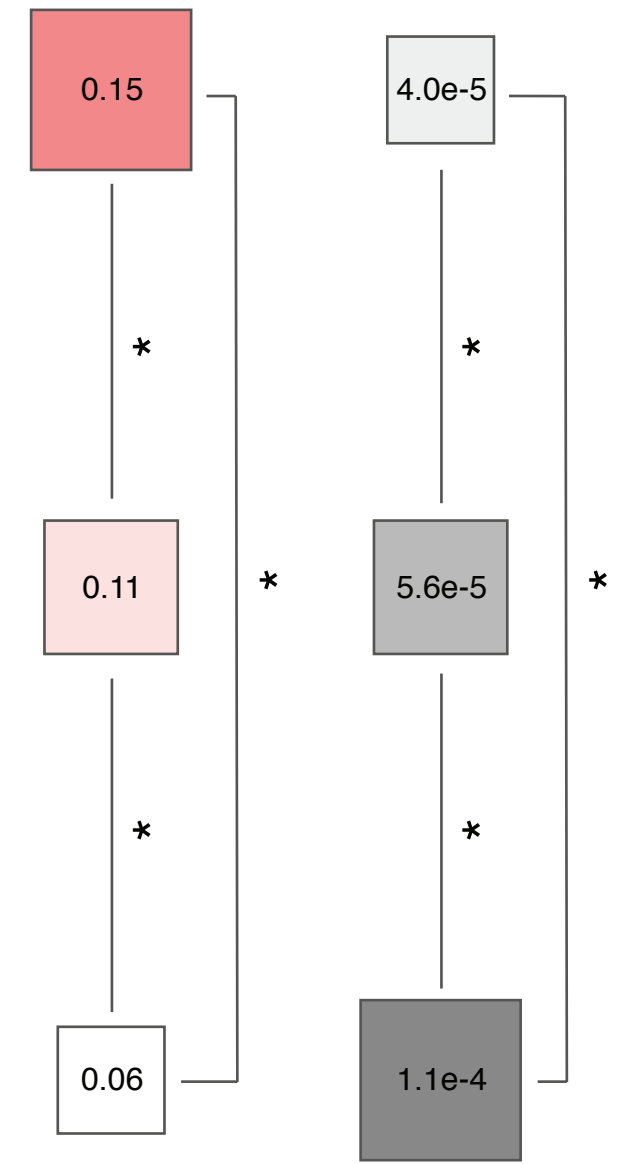
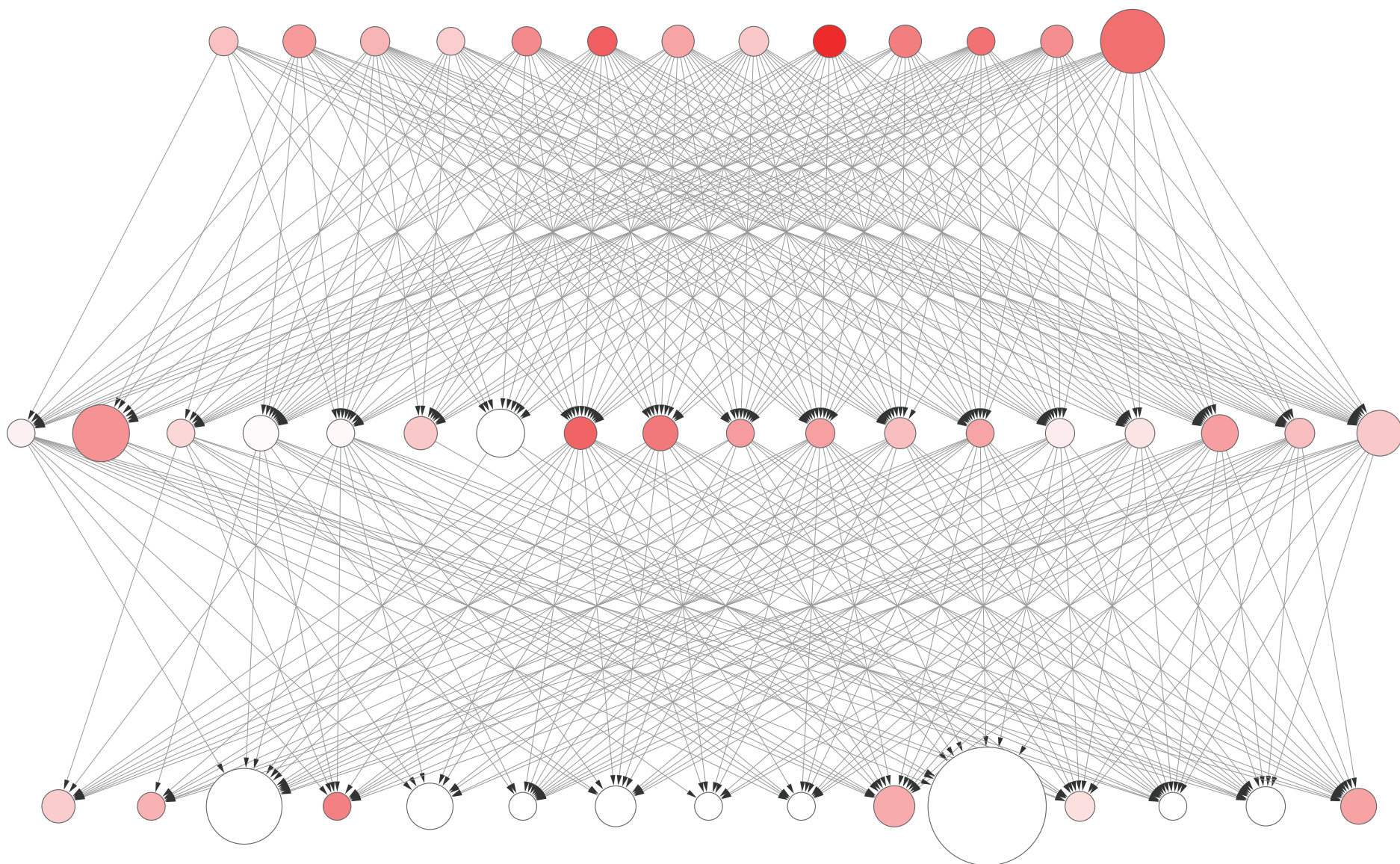


◇ Cancer TFSS

Target Expression Correlation

Percent Cancer TFSS

B



○ ○ ○ TFBS Burden

Expression Correlation

Percent Burdened TFBS

Fig 4

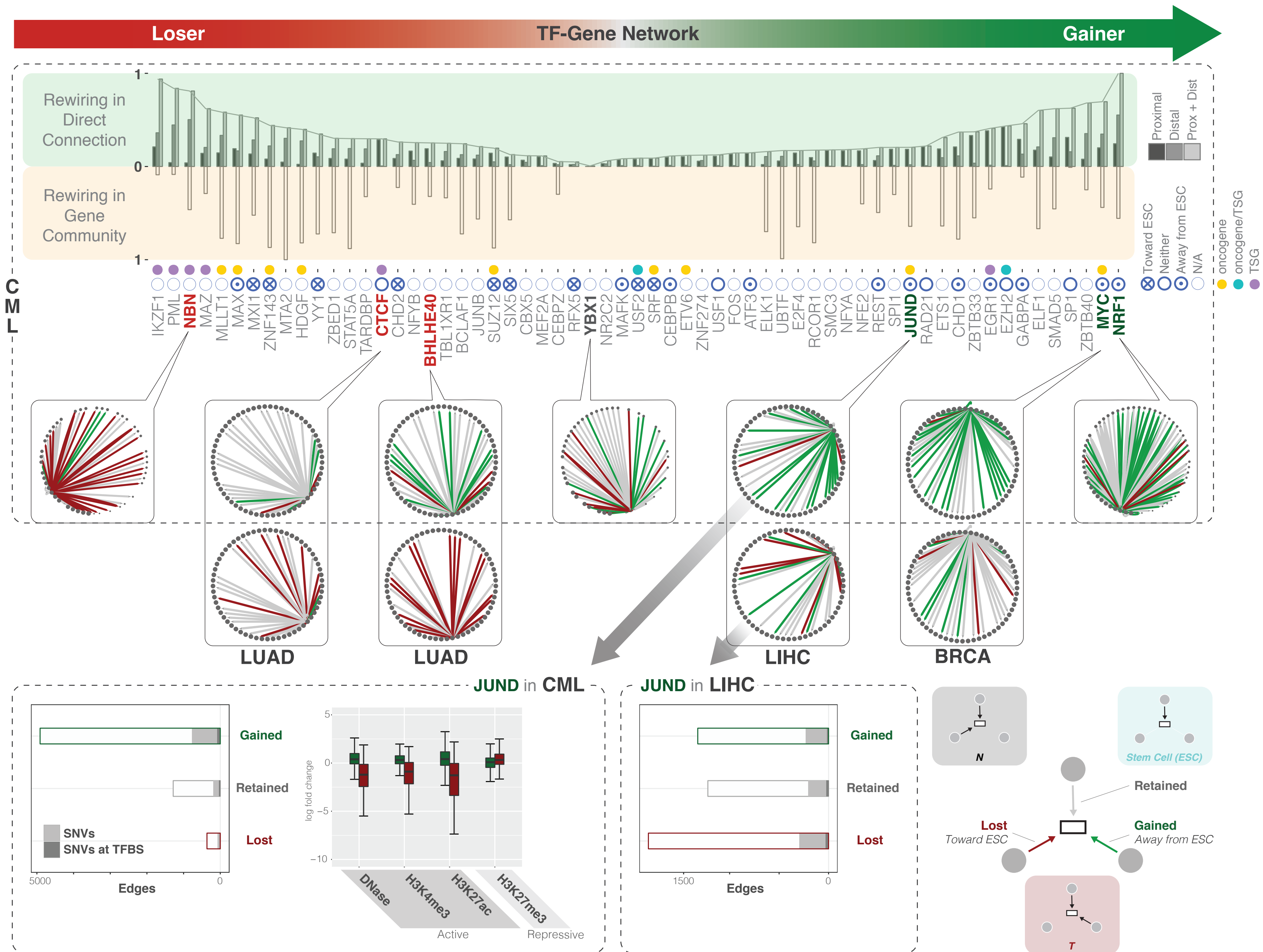


Fig 5

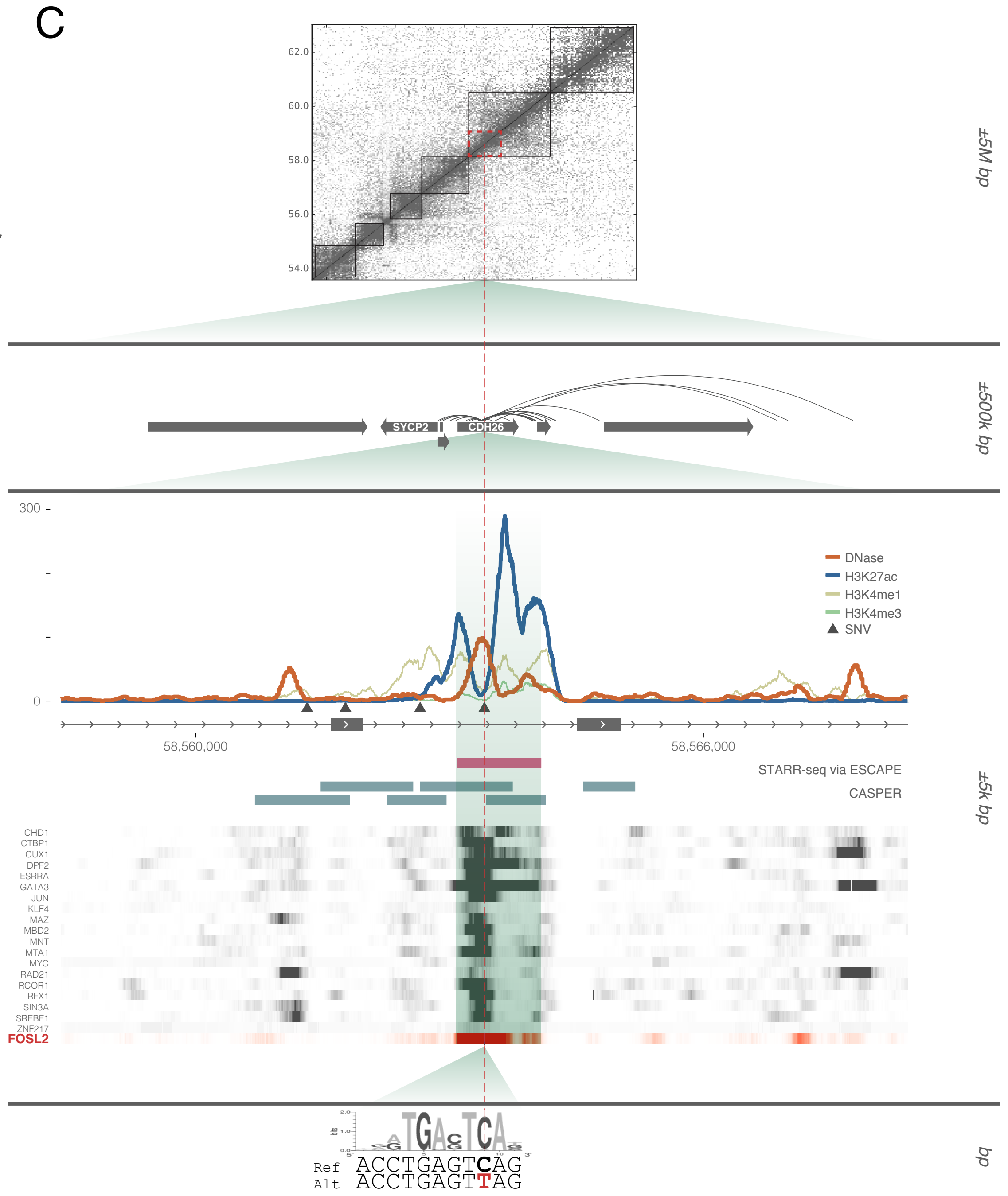
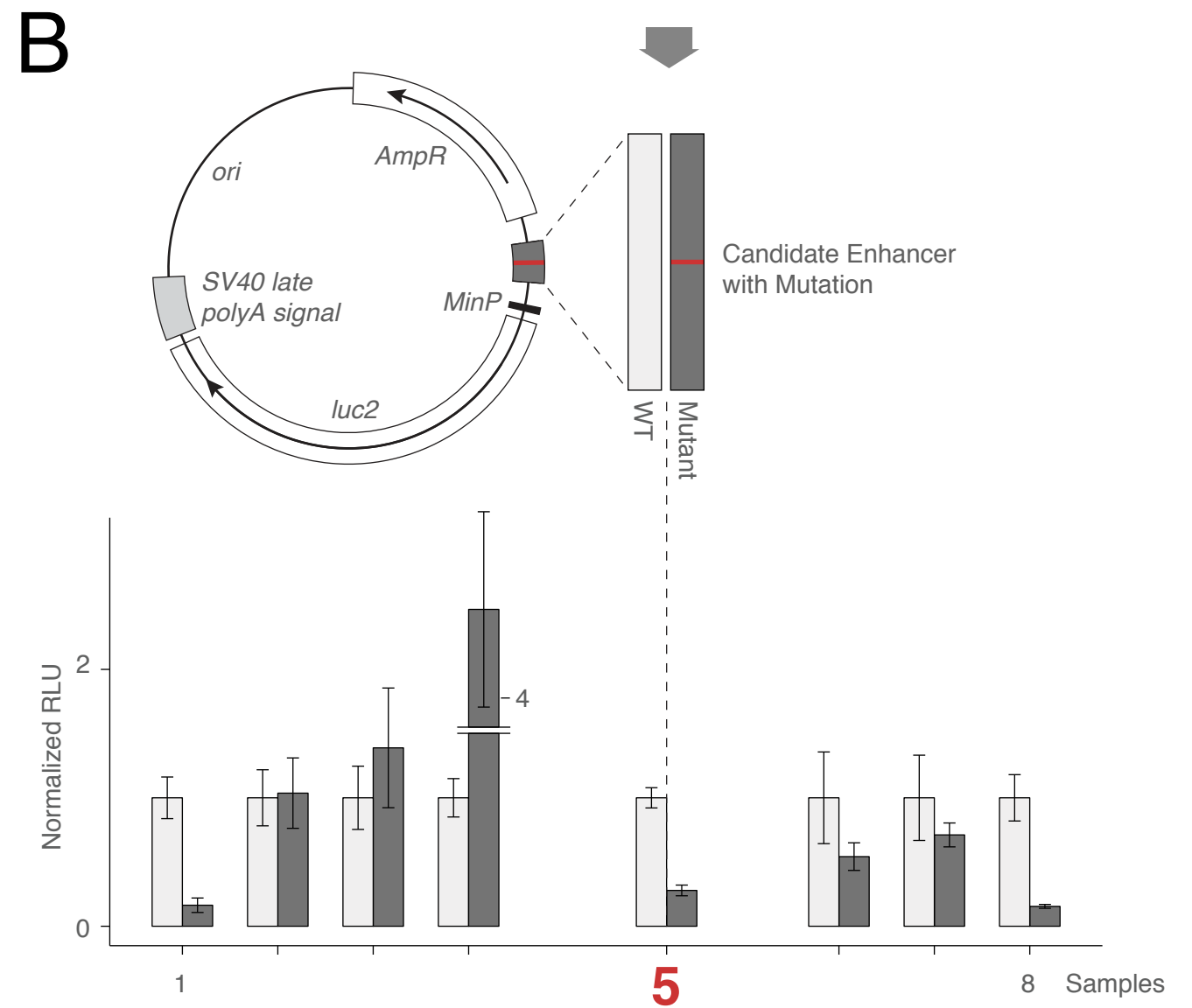
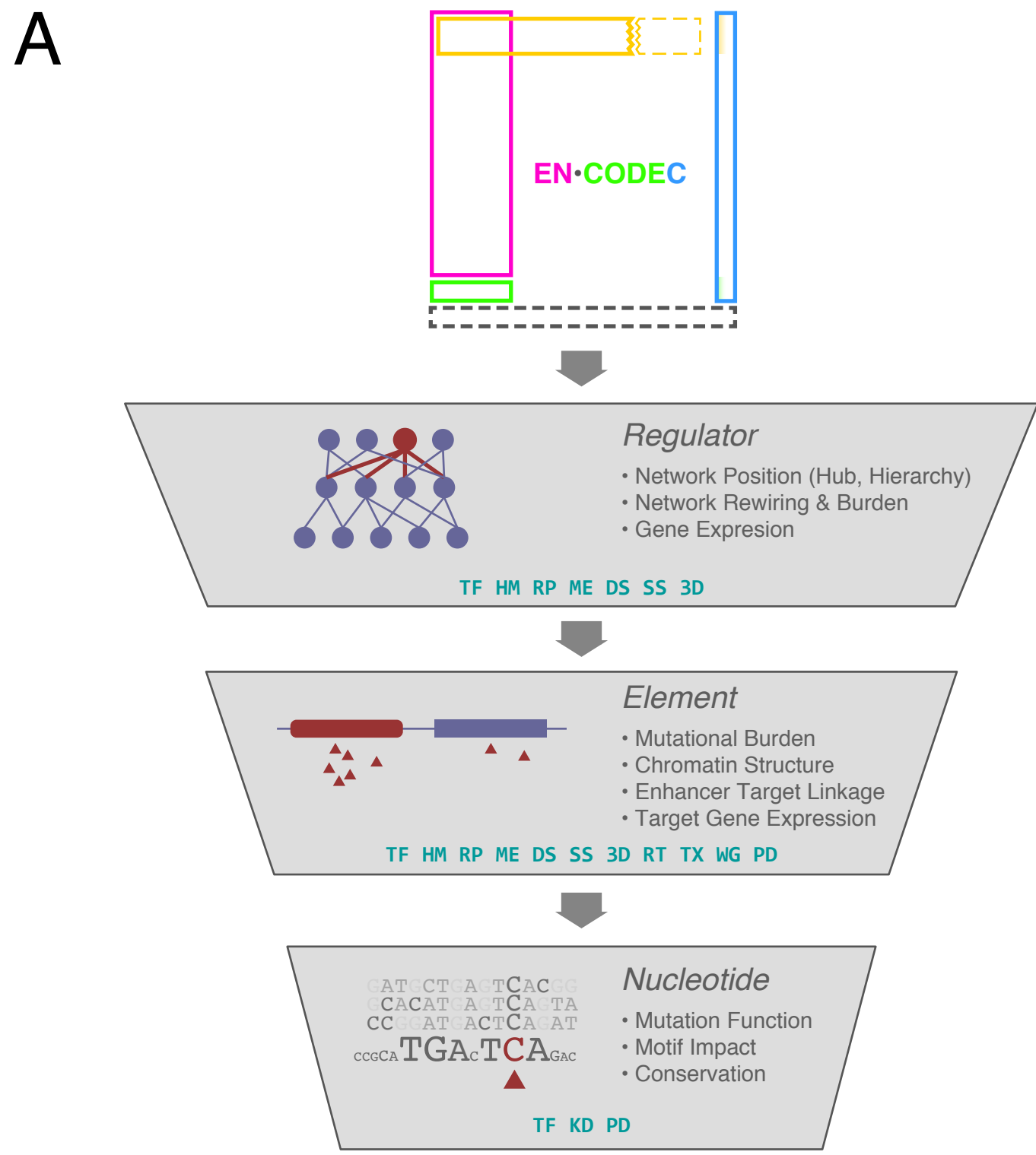


Fig 6