

EN-CODEC
Main FigPack

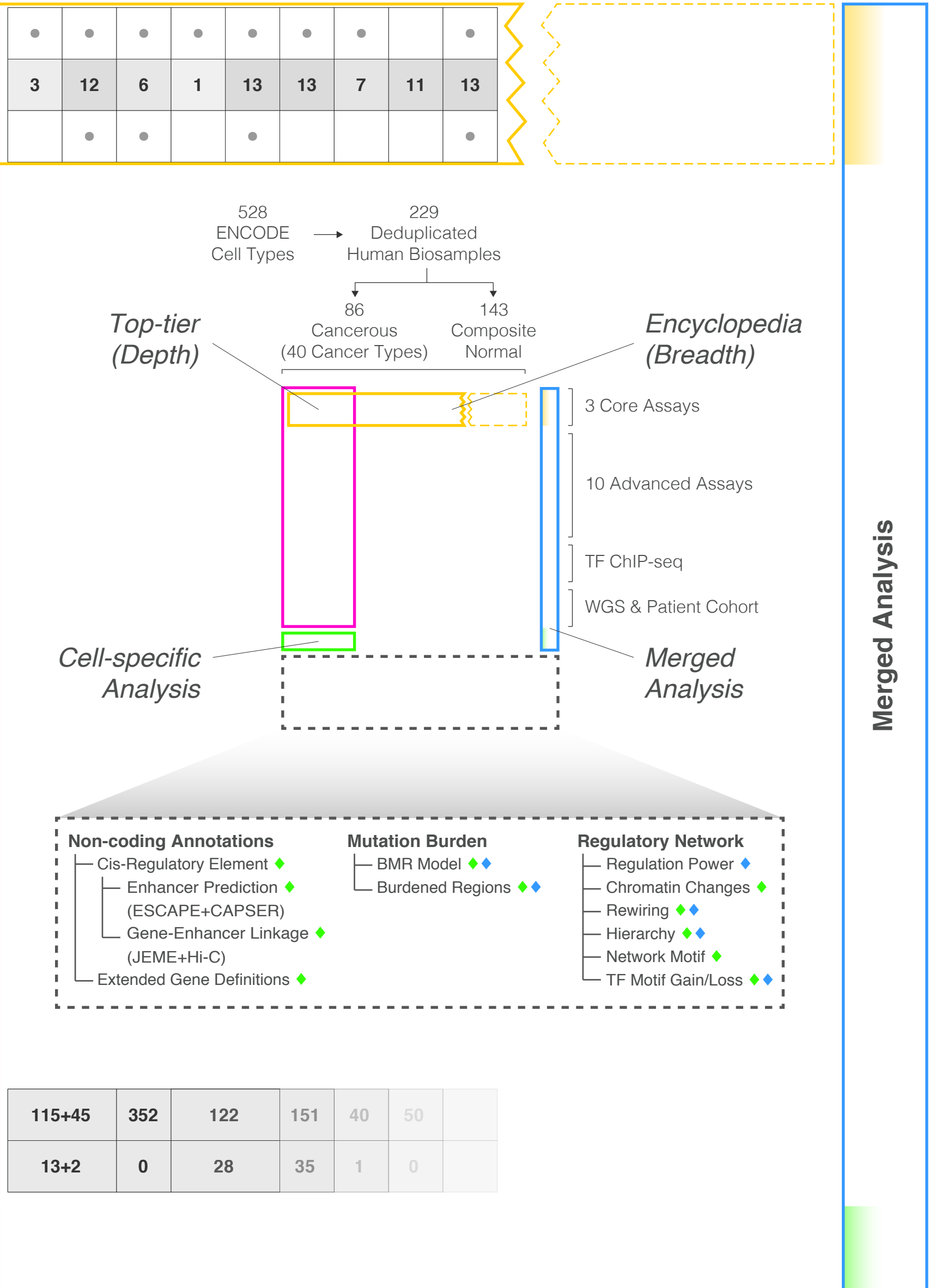
v170525

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													
shRNA/siRNA Knockdown KD	TF KD	85	61		2											
	RBP KD	234	225													
3D Chromatin Structure 3D	ChIA-PET	3	1		4	2										
	Hi-C	▲		•	▲		▲									
Enhancers SS	STARR-seq	•	▲		•											
Methylation ME	WGBS	•	•		▲		•									
	RRBS	•	•	•	•	•	•									
Replication Timing RT	Repli-seq/chip	•	•		•	•	•									
Transcription Factors TF	TF Total	207	95	31	52	59	49									
	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	▲			▲	▲										
	SV	▲			▲	▲										
Patient Data PD	Cohort	150	82	197	116											
	Expression	173	373	517	1100	546										

Cell-specific Analysis



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

Fig 1

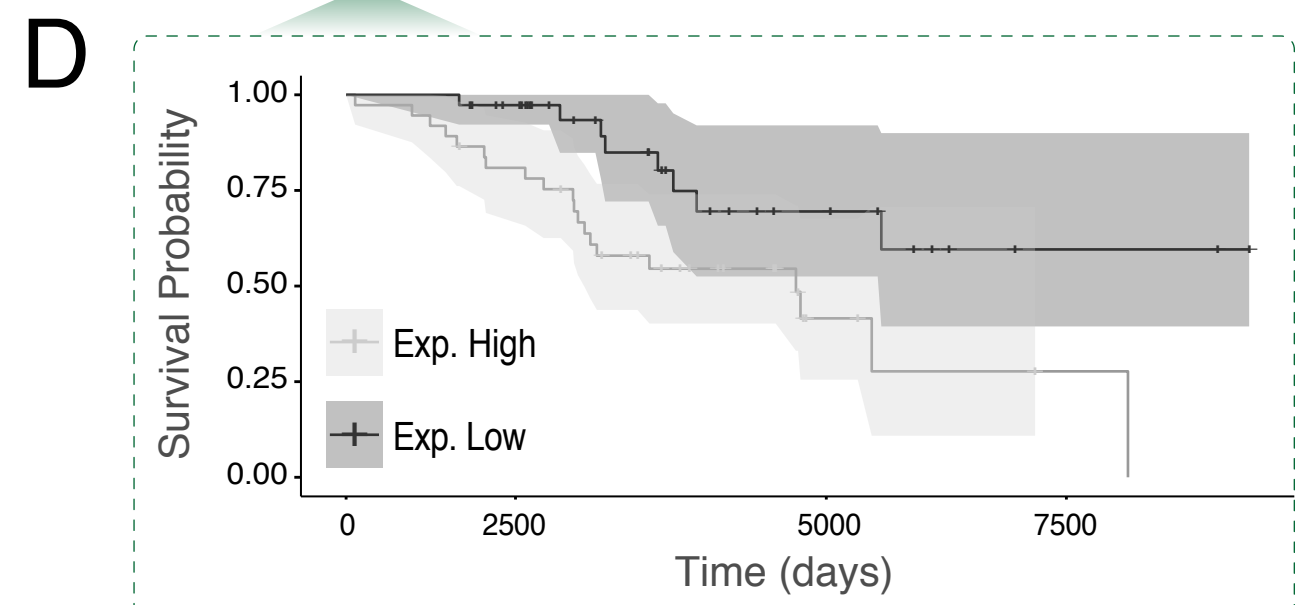
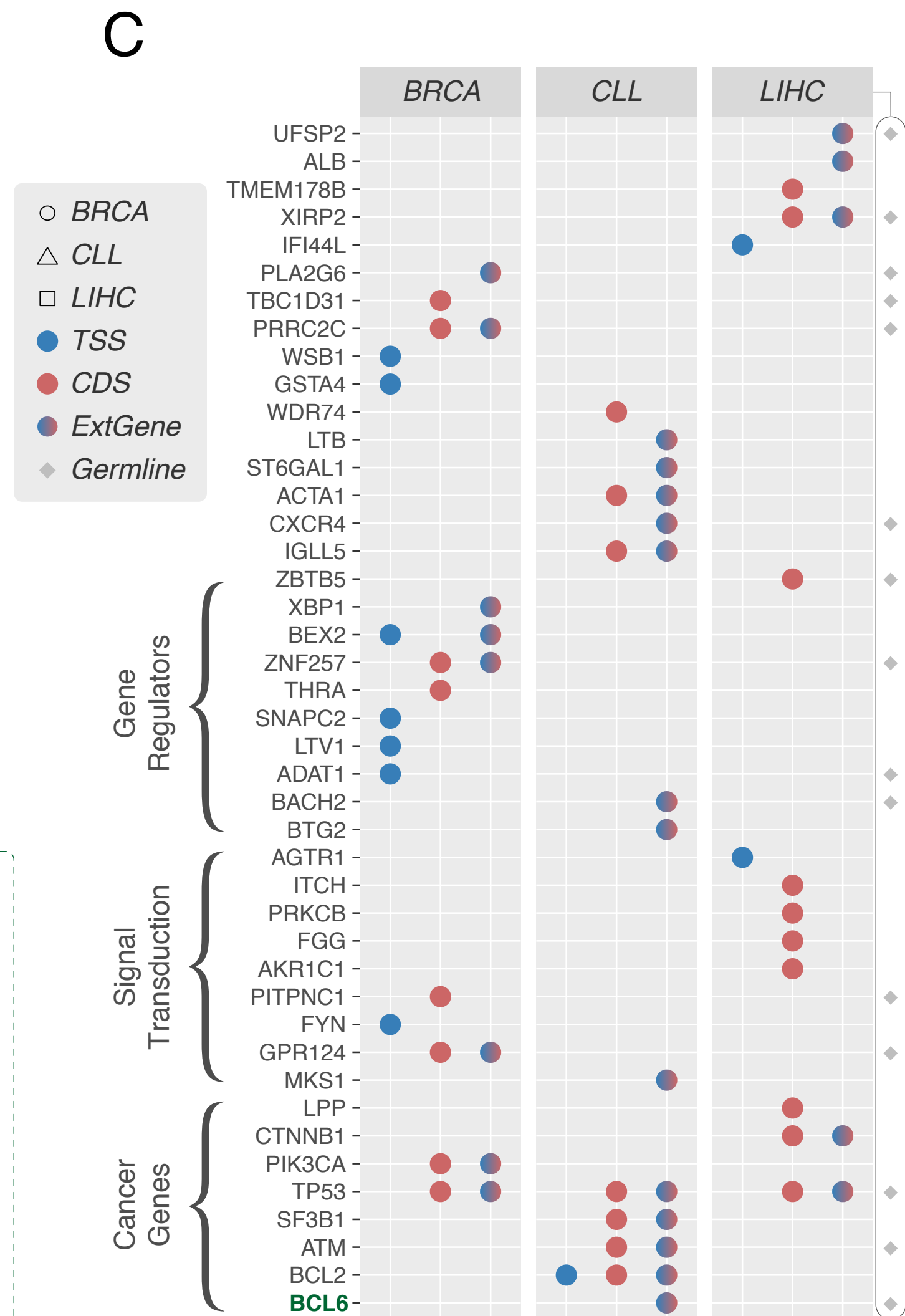
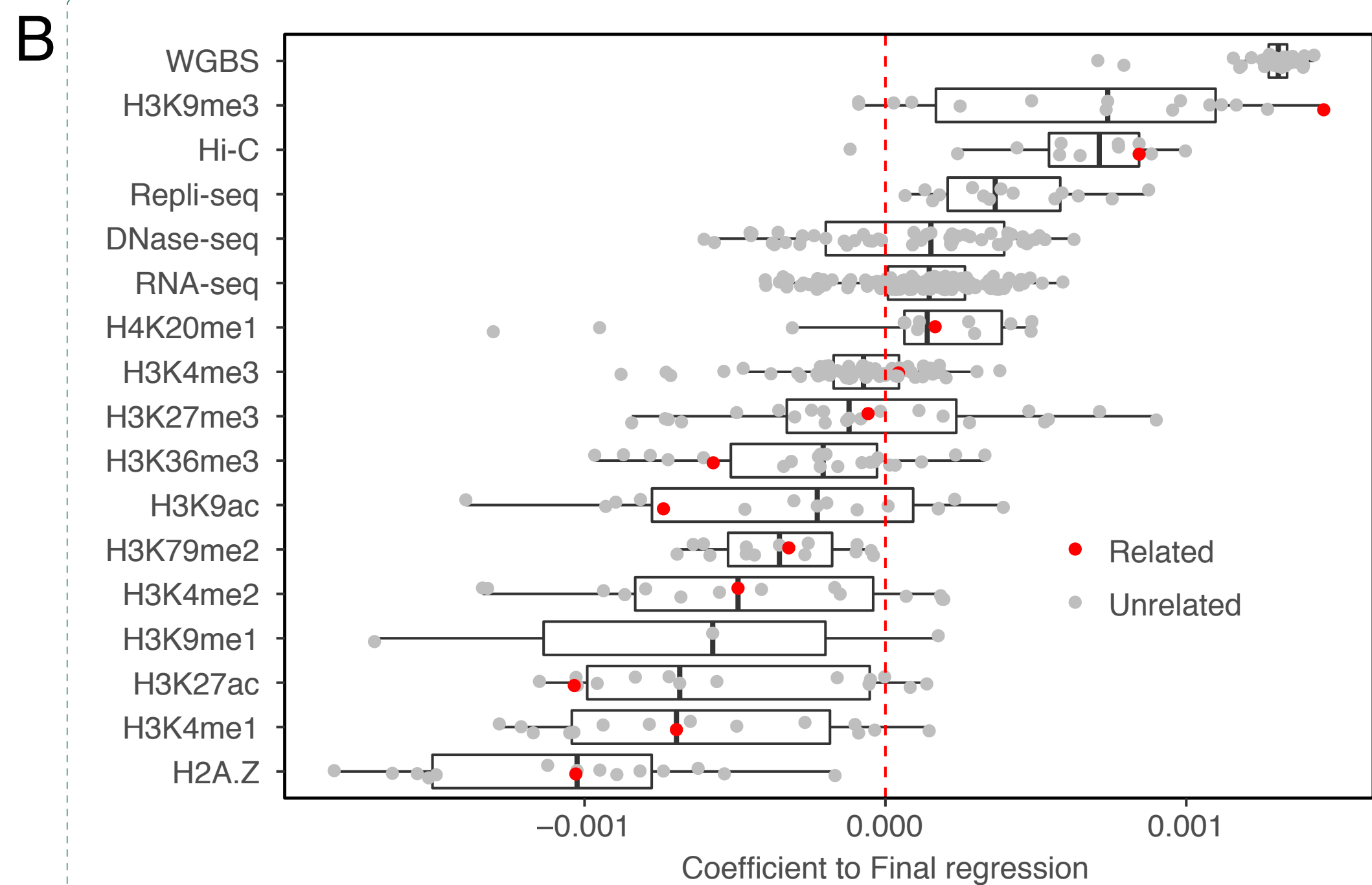
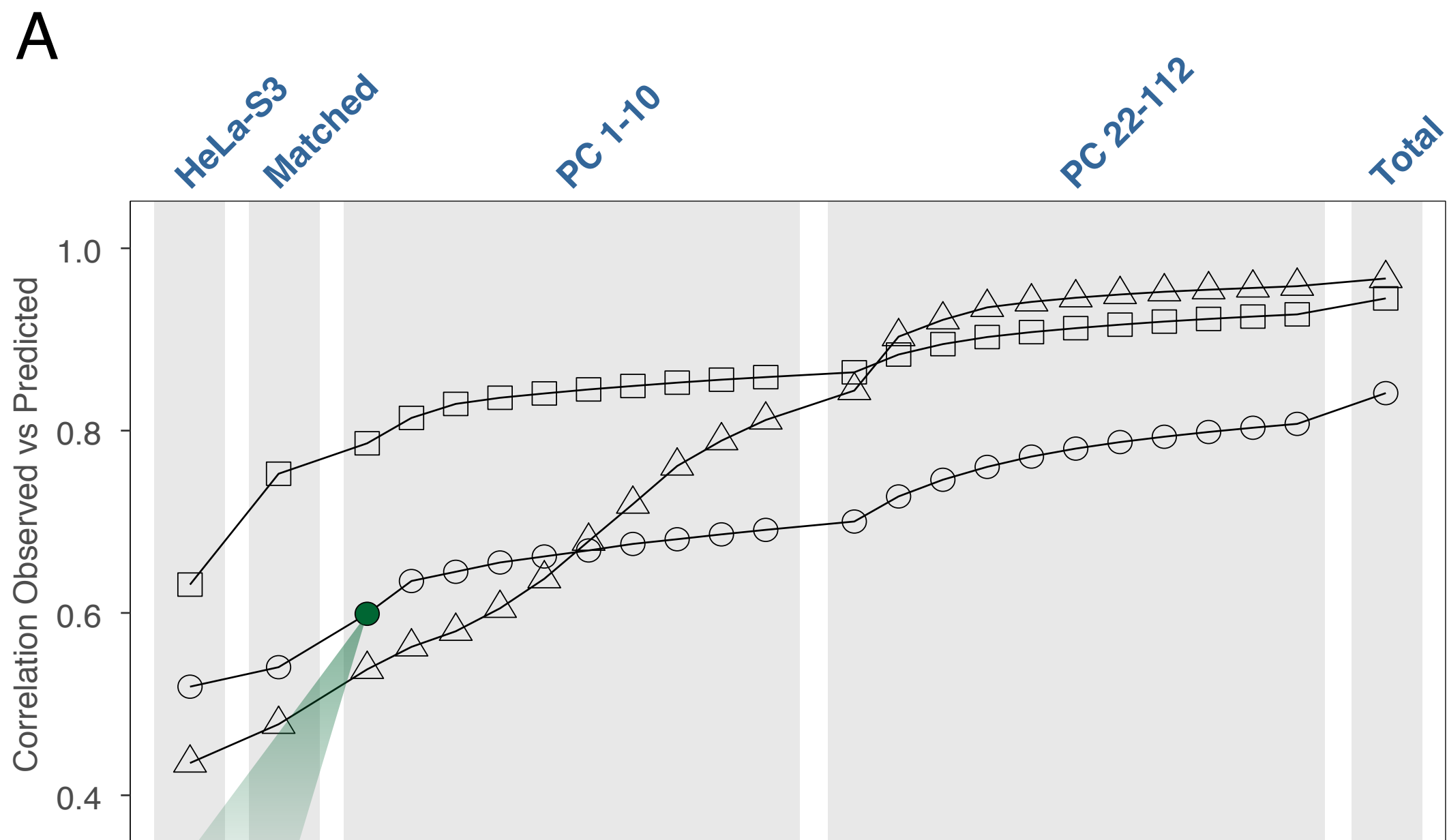


Fig 2

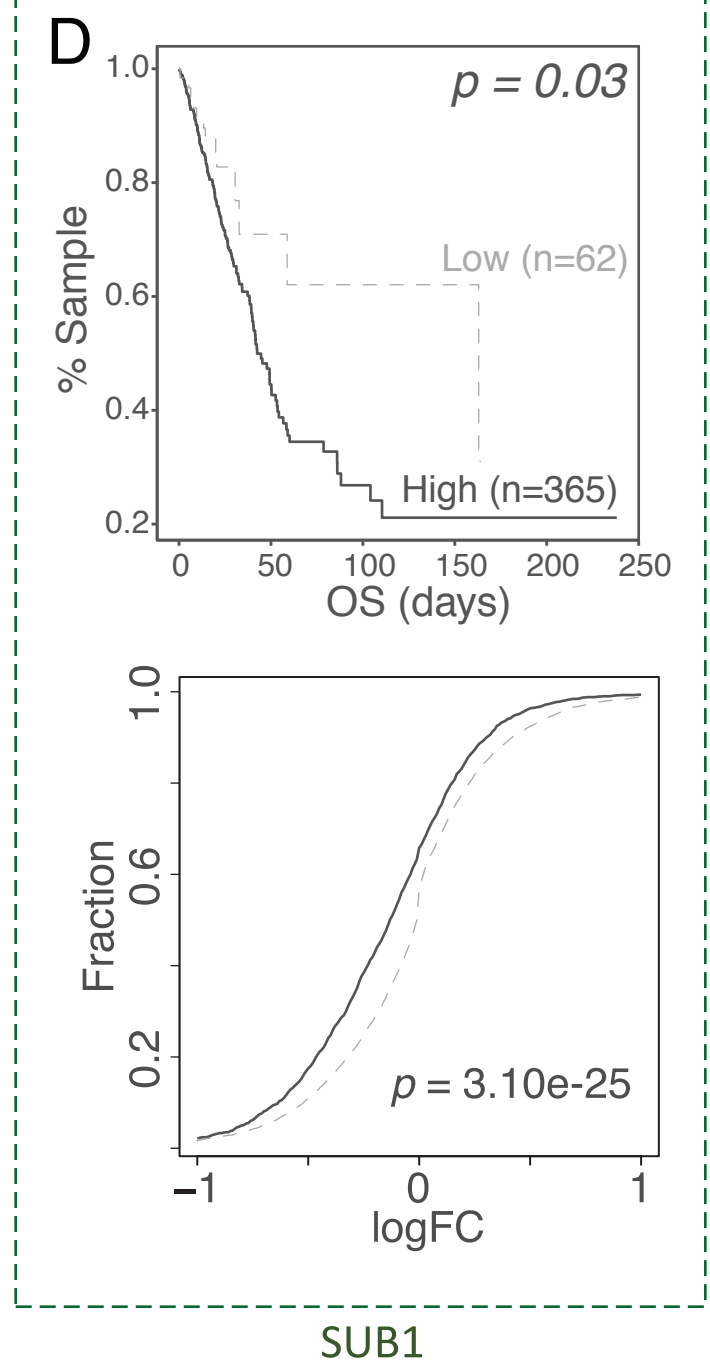
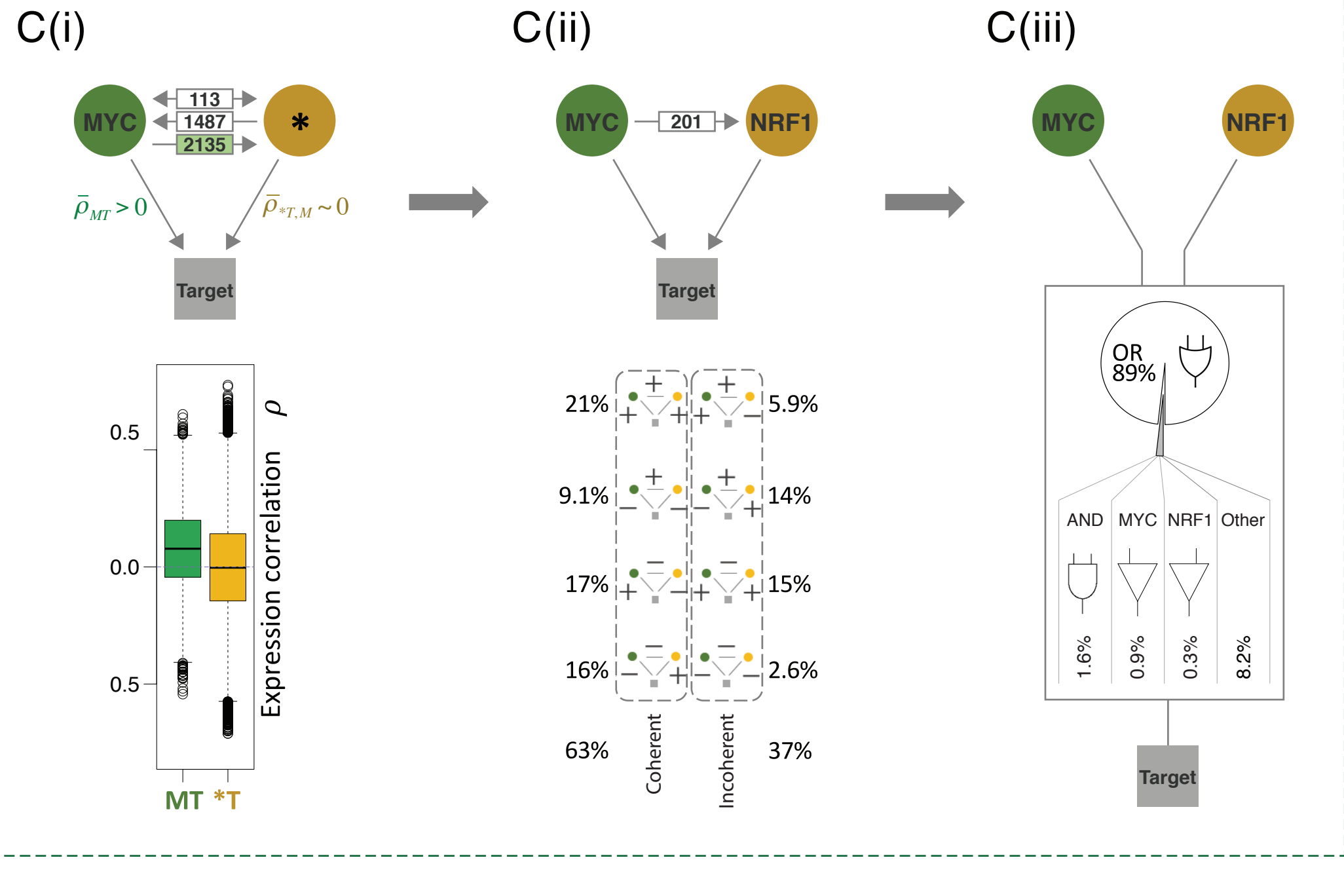
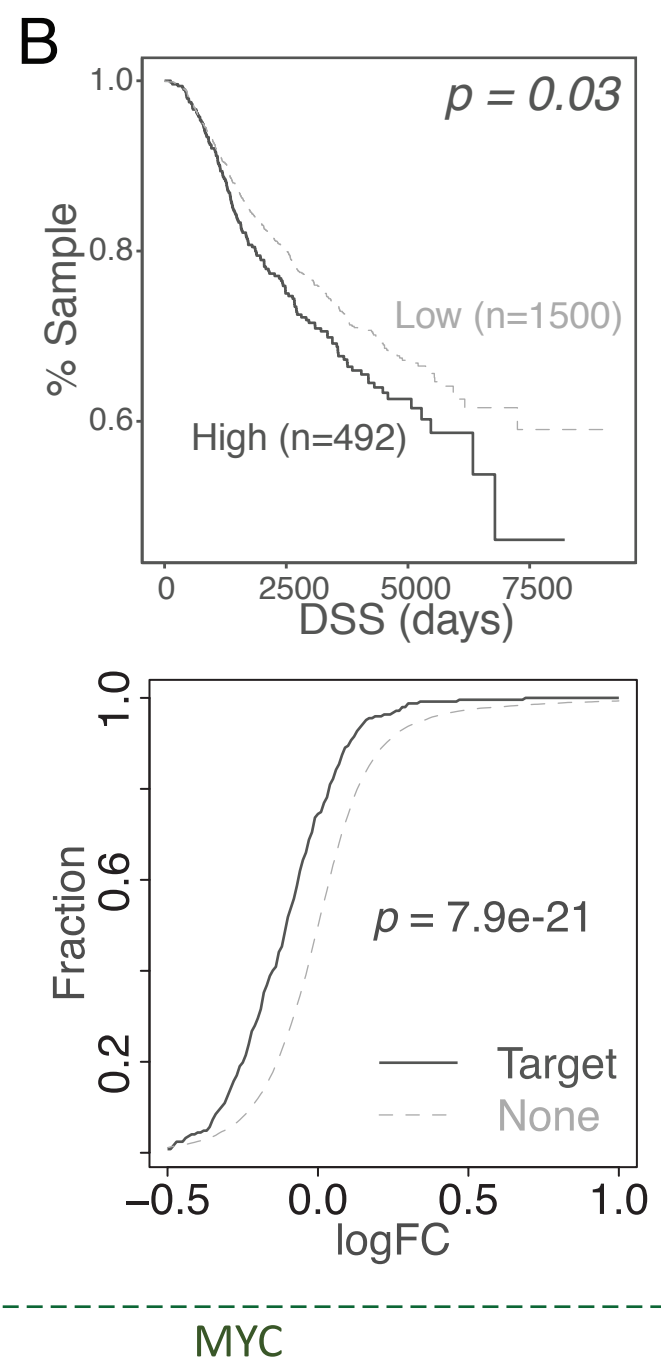
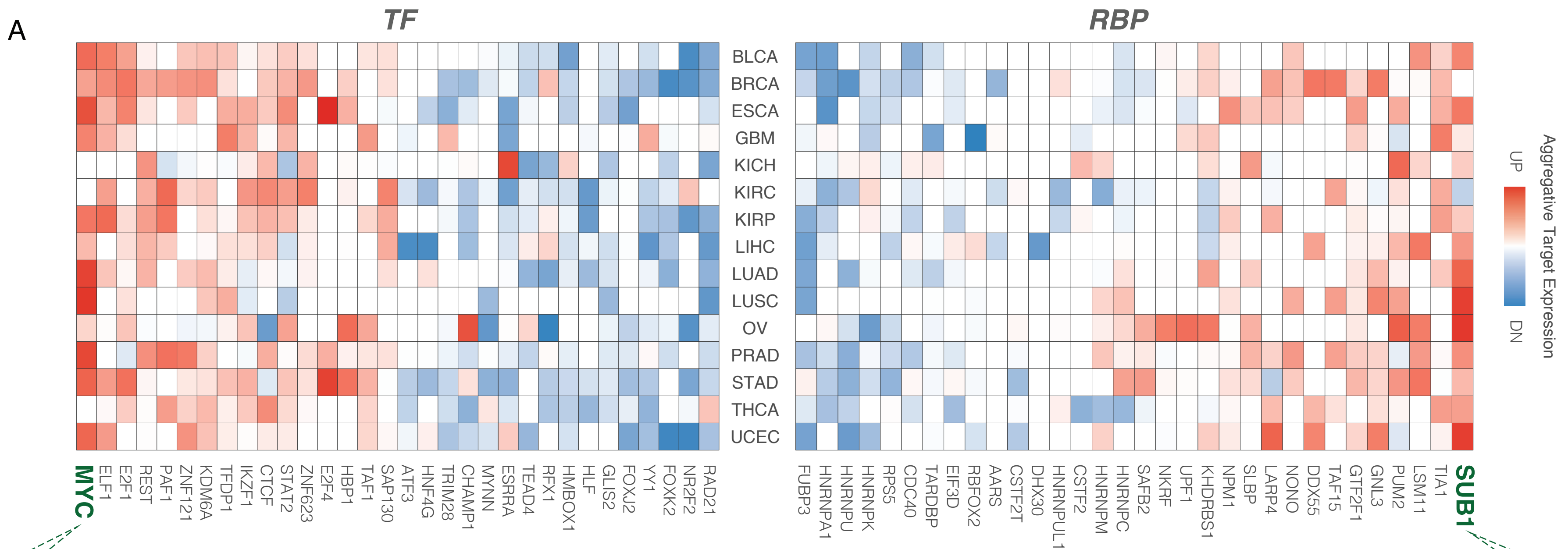
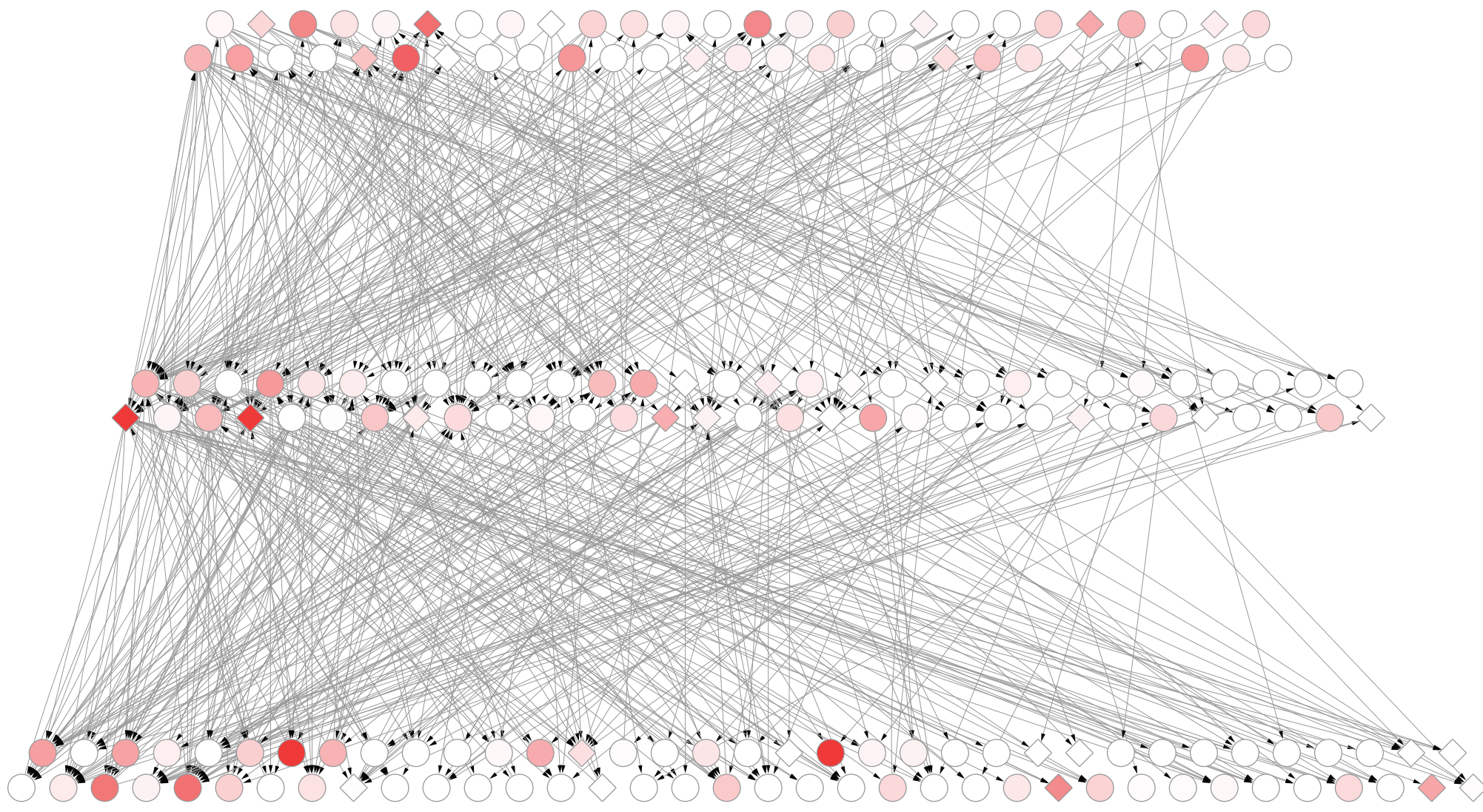
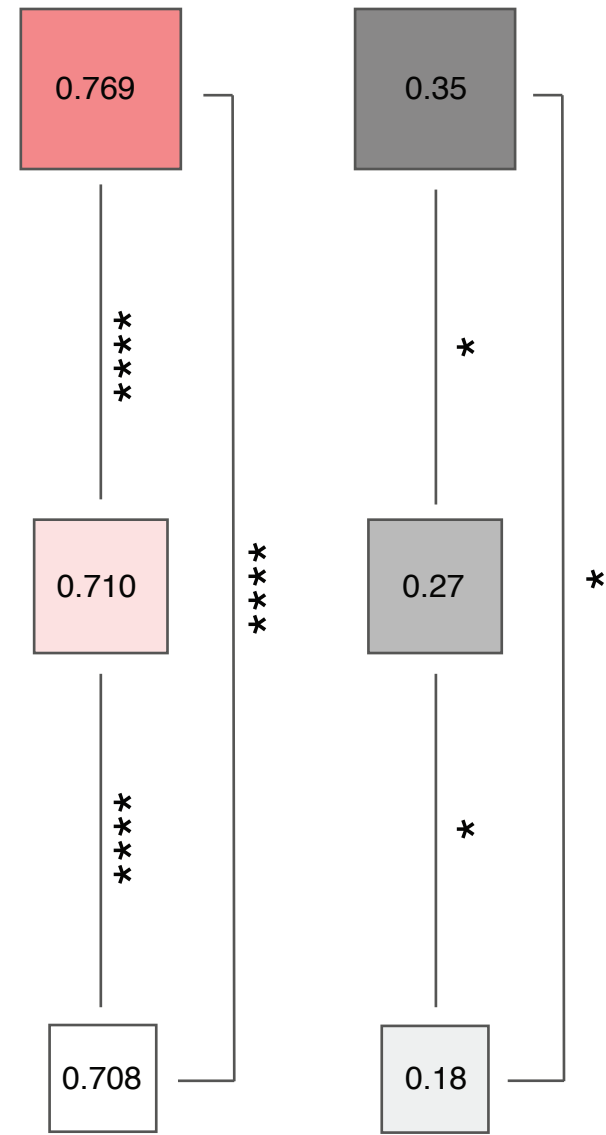


Fig 3

A



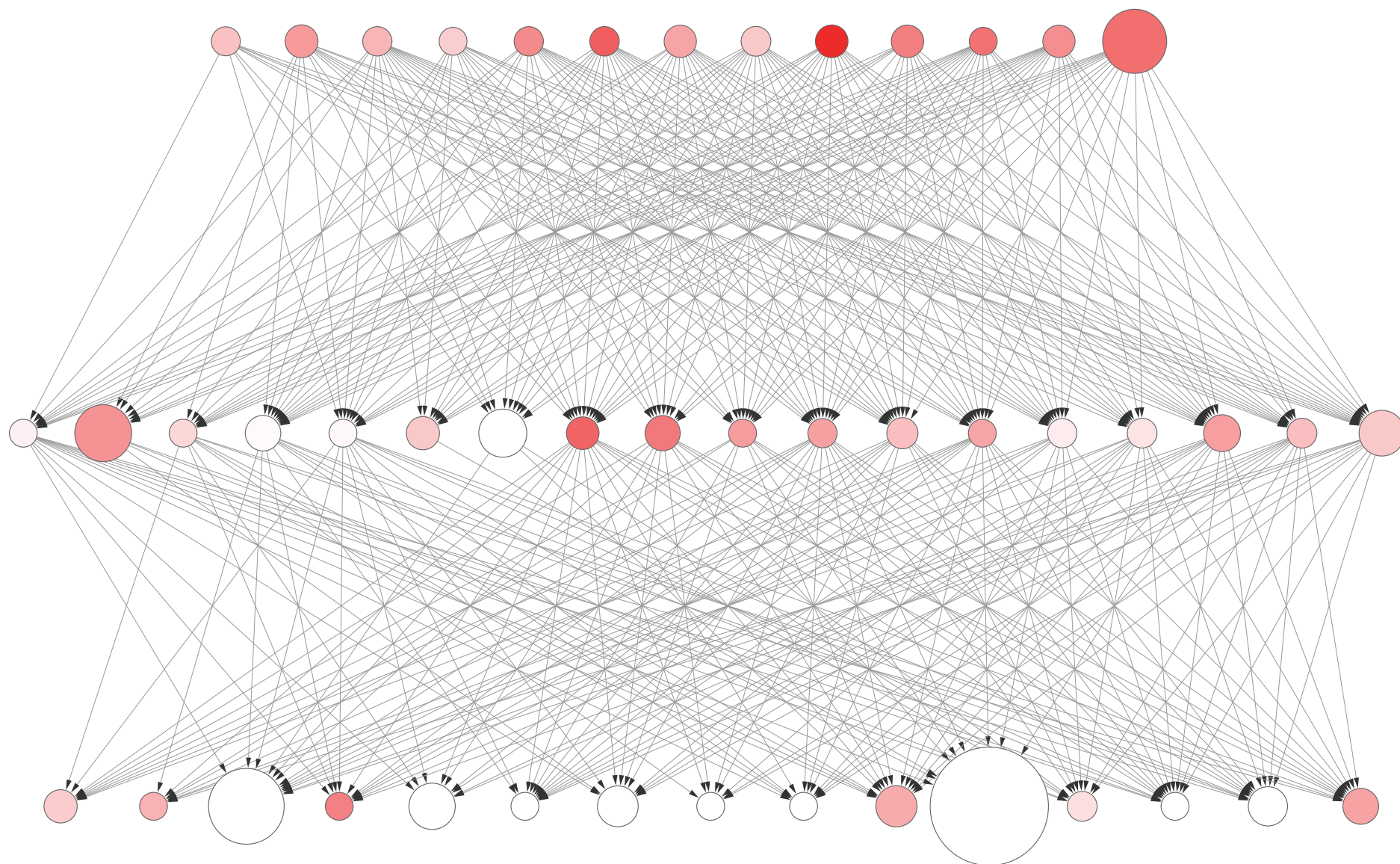
◇ Cancer TFSS



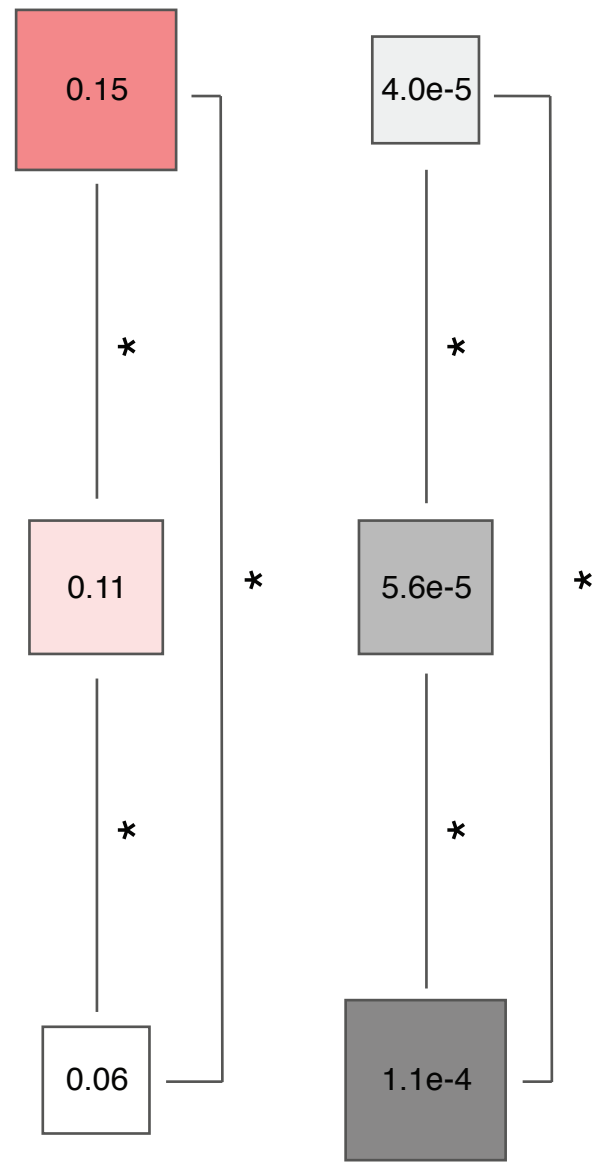
Target Expression Correlation

Percent Cancer TFSS

B



○ TFBS Burden



Expression Correlation

Percent Burdened TFBS

Fig 4

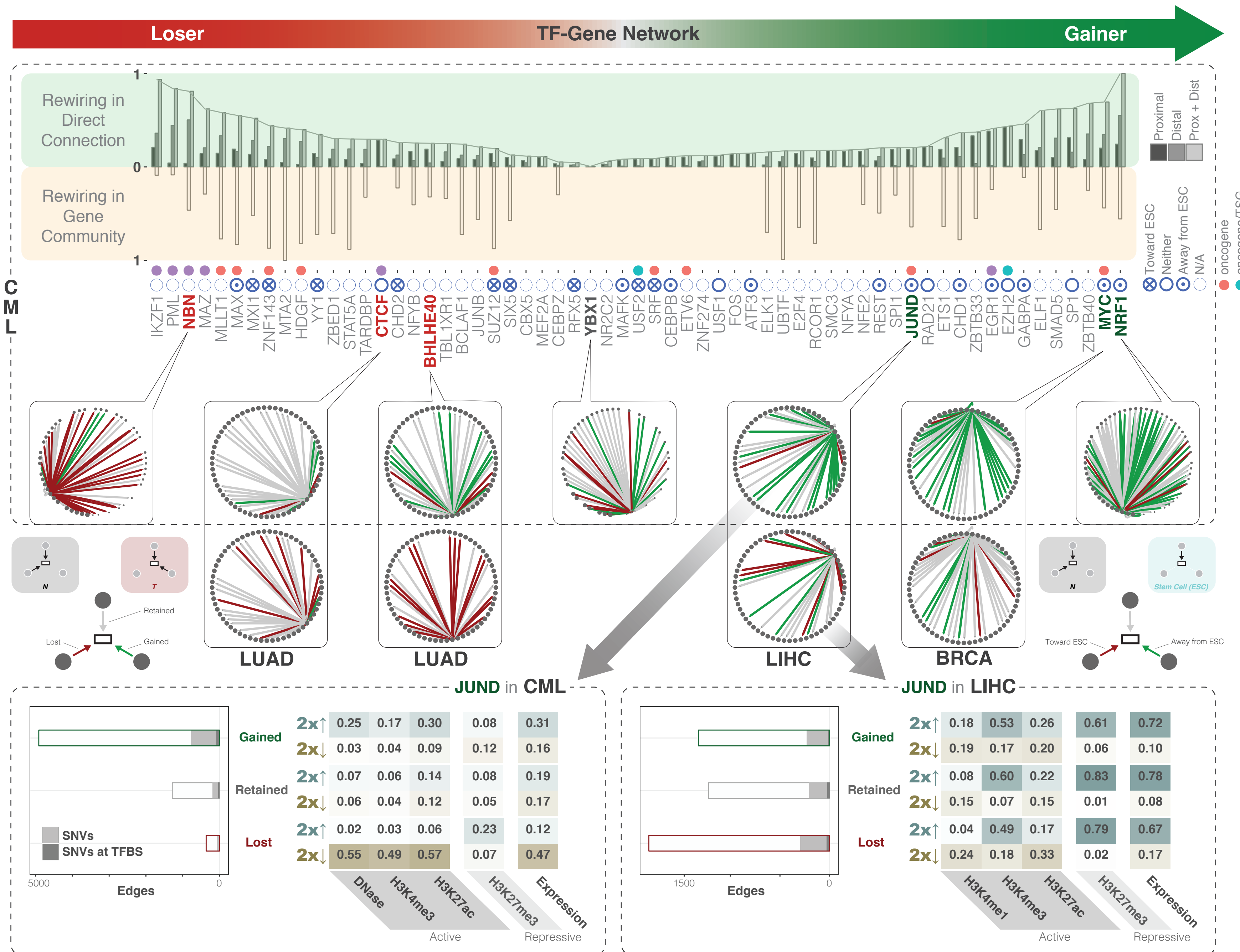


Fig 5

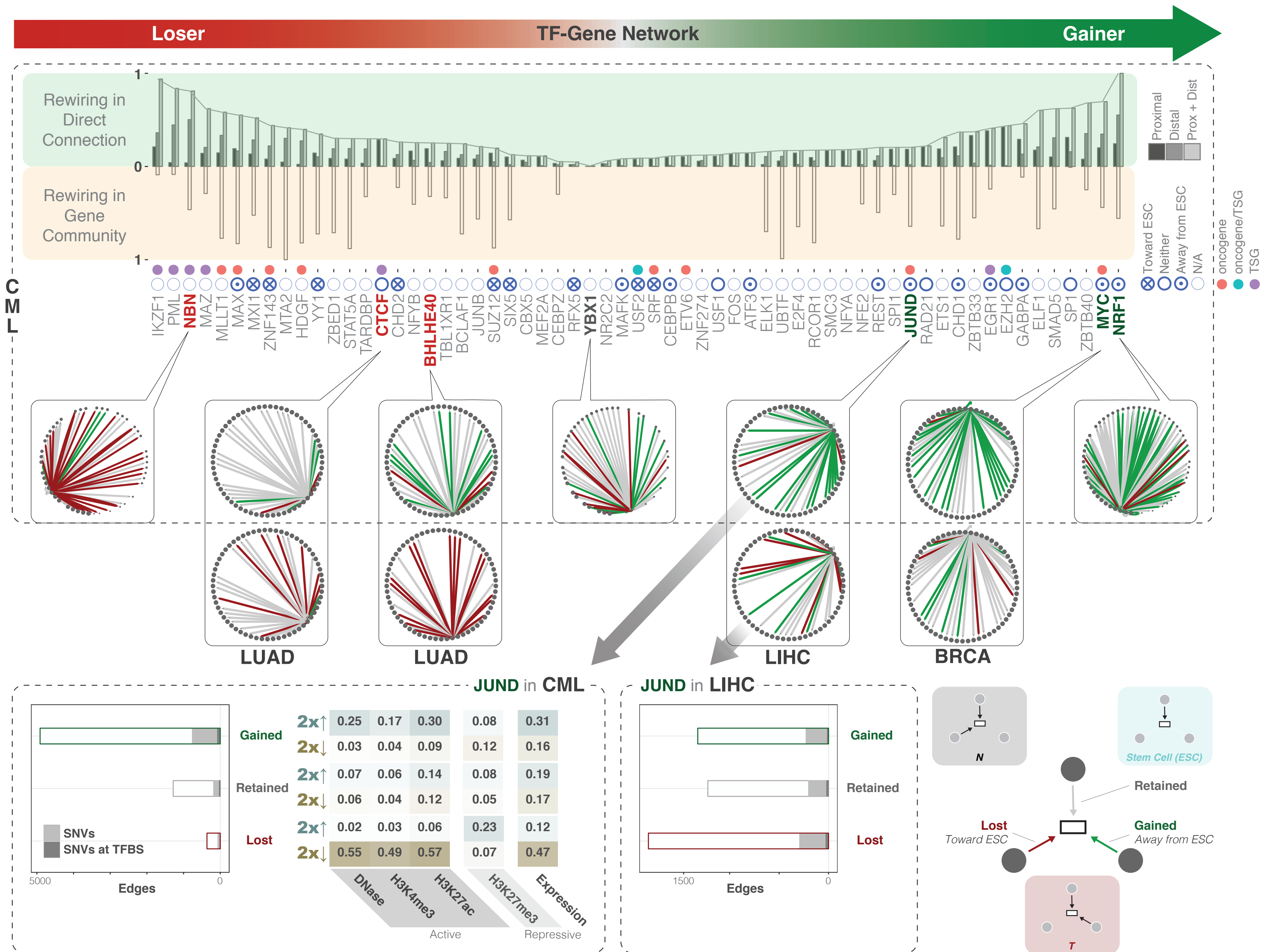


Fig 5

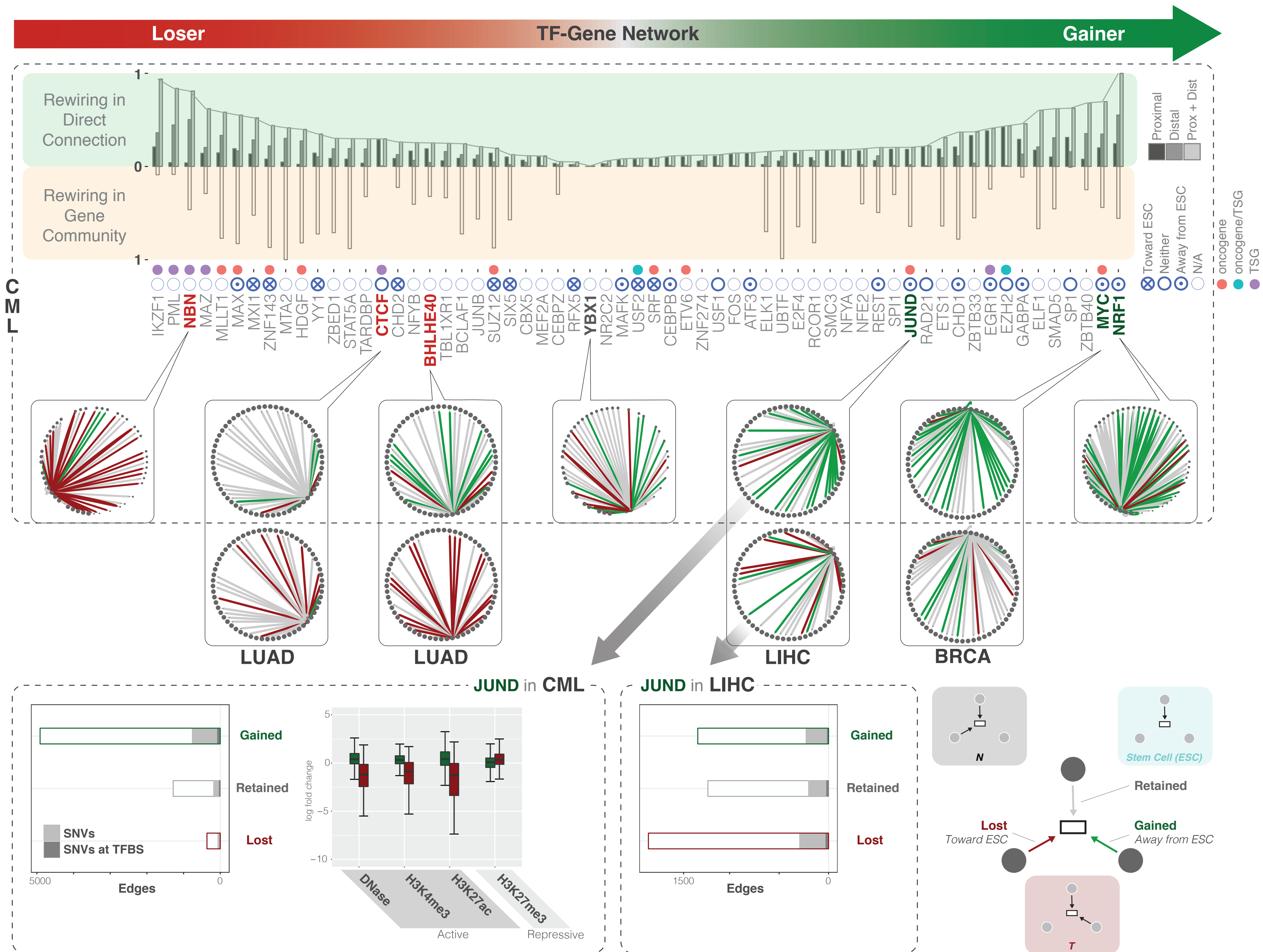


Fig 5

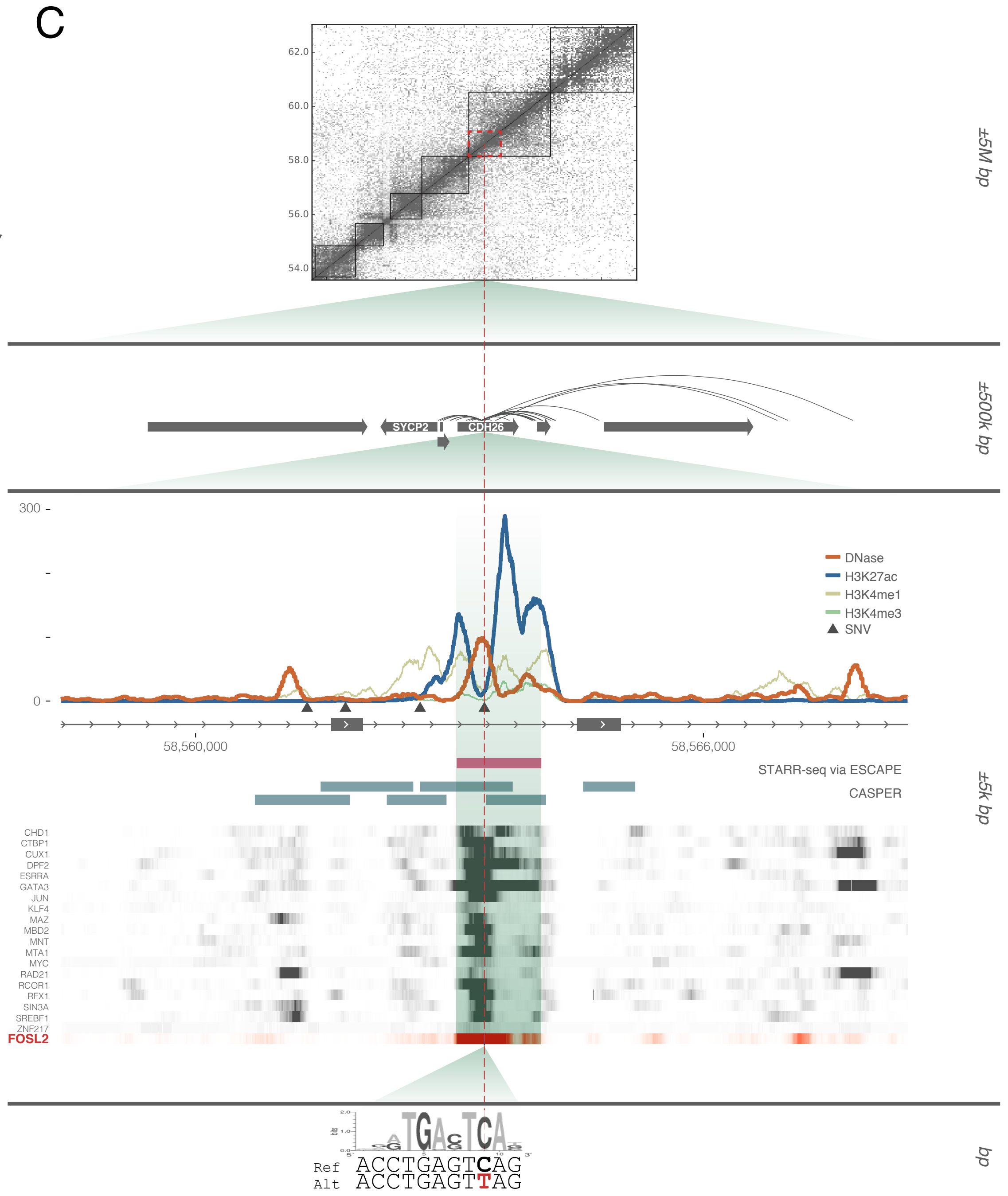
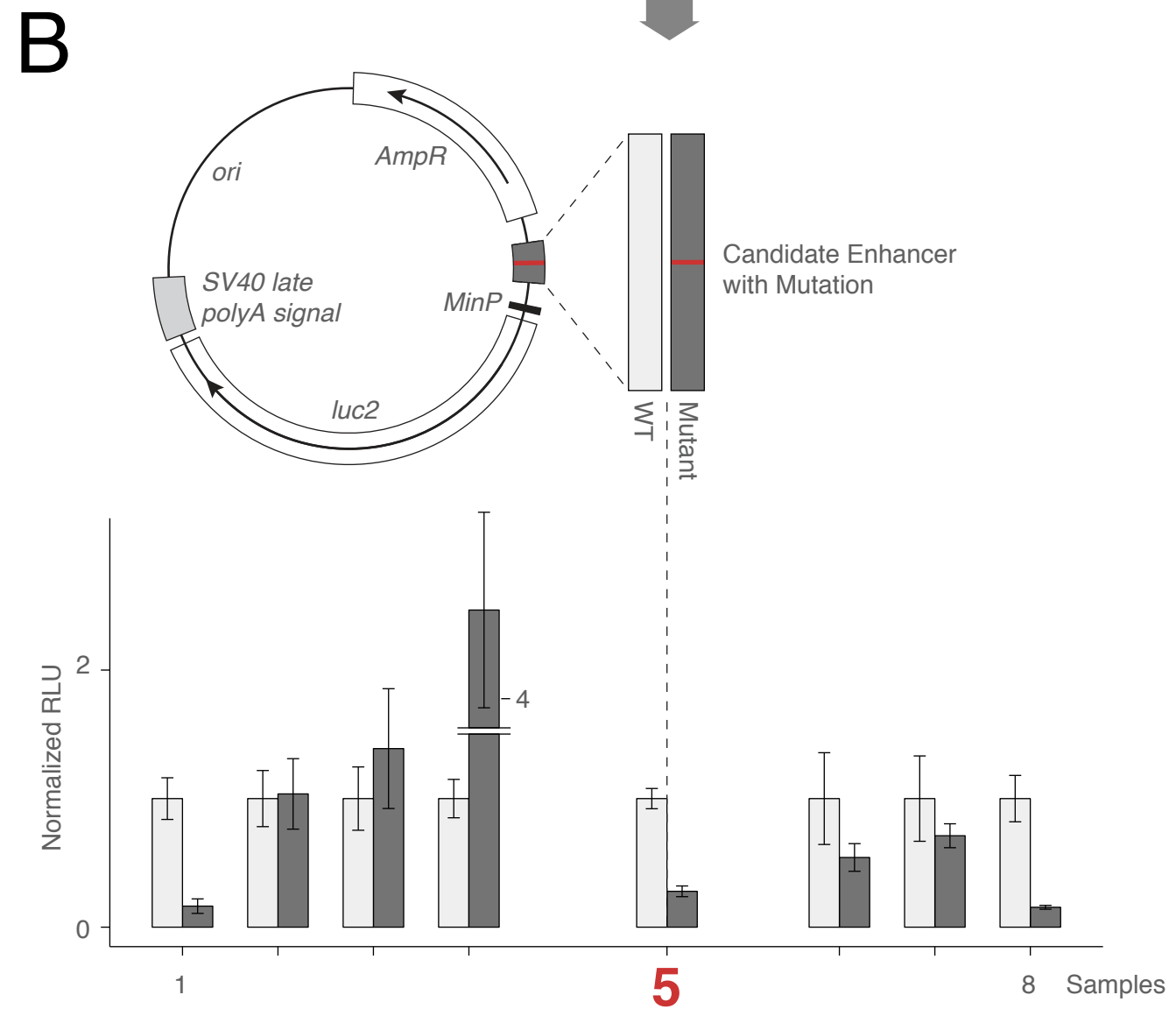
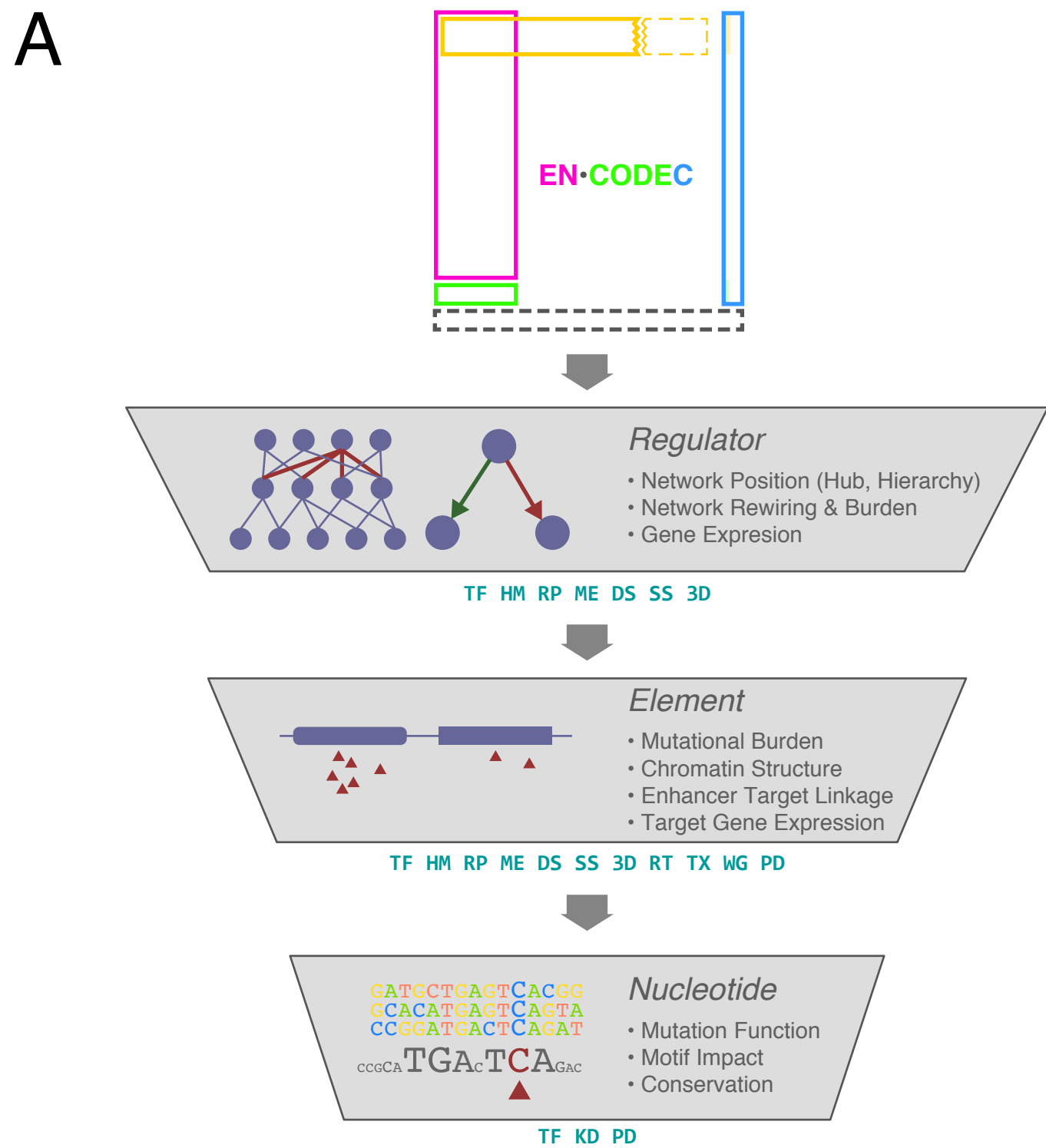


Fig 6