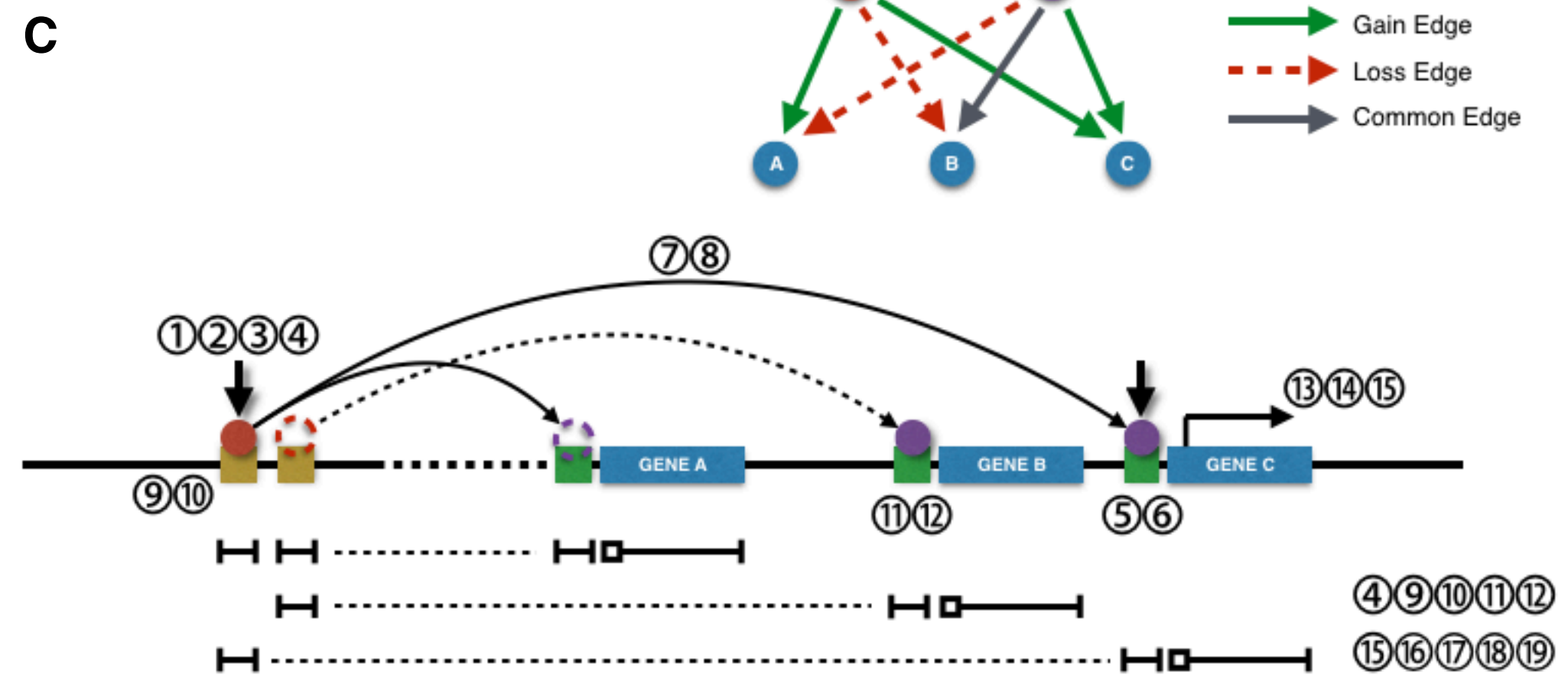
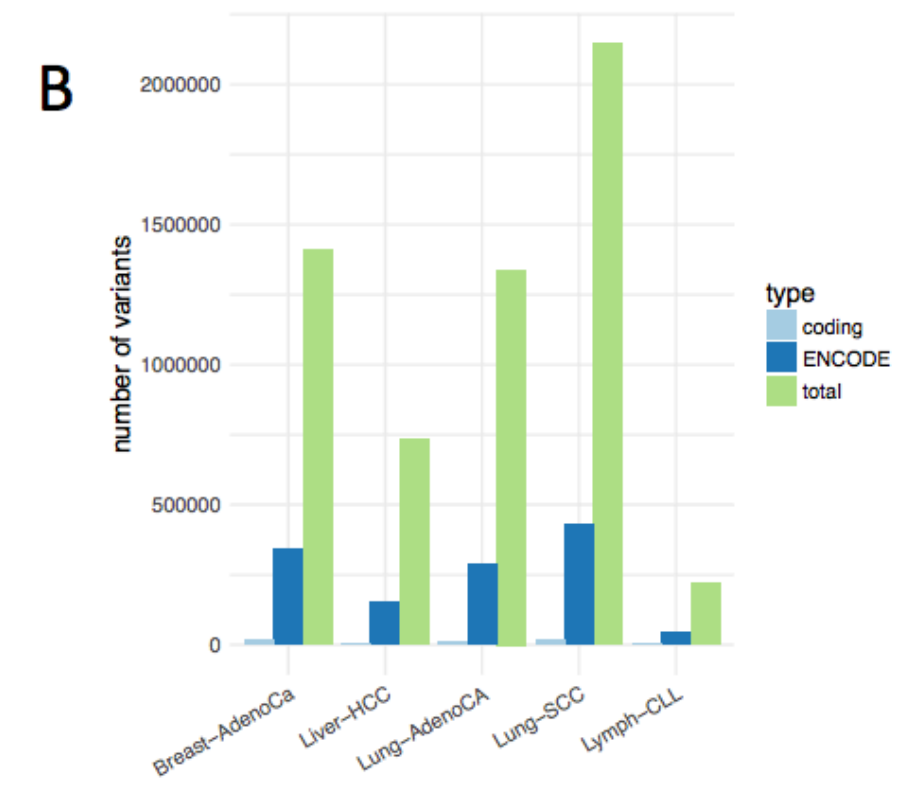


		K562	GM12878	HepG2	Liver	A549	IMR-90	MCF-7	MCF-10A	HeLa-S3	
DNA-binding Proteins (ChIP-seq)	TF	209	101	97	7	32	9	52	4	60	①
	TFSS	64	50	48	5	21	6	15	3	29	②
	Chromatin	17	6	7		3	1	3	1	4	③
	Histone	12	11	11	7	11	28	5		11	④
Knockdown	siRNA	29						2			⑤
	shRNA	219		221							⑥
3D Chromatin Structure	ChIA-PET	3	1	1				4		1	⑦
	Hi-C	•	•			•		•			⑧
Cis-regulatory Elements	DNase-seq	•	•	•		•	•	•		•	⑨
	EnhancerSeq	•	•					•			⑩
Methylation	WGBS	•	•	•	•		•				⑪
	RRBS	•	•	•	•	•	•	•	•	•	⑫
Transcription	RNA-seq	•	•	•	•	•	•	•		•	⑬
	RAMPAGE	•	•								⑭
Replication Timing	Repli-seq/chip	•	•	•		•	•			•	⑮
Cell Line WGS	SNV	•	•				•	•		•	⑯
	SV	•	•				•	•		•	⑰
TCGA	Cohort	95		327		38		198		2	⑱
	Expression	173		373		517		1100		546	⑲
		T	N	T	N	T	N	T	N	T	
		Blood		Liver		Lung		Breast			Cervix



*TCGA Cohort (PCAWG May):
 K562::CLLE, HepG2::LIHC, A549::LUAD, MCF-7::BRCA, HeLa-S3::CESC

**TCGA (1/28/2016):
 K562::LAML, HepG2::LIHC, A549::LUAD, MCF-7::BRCA, HeLa-S3::CESC

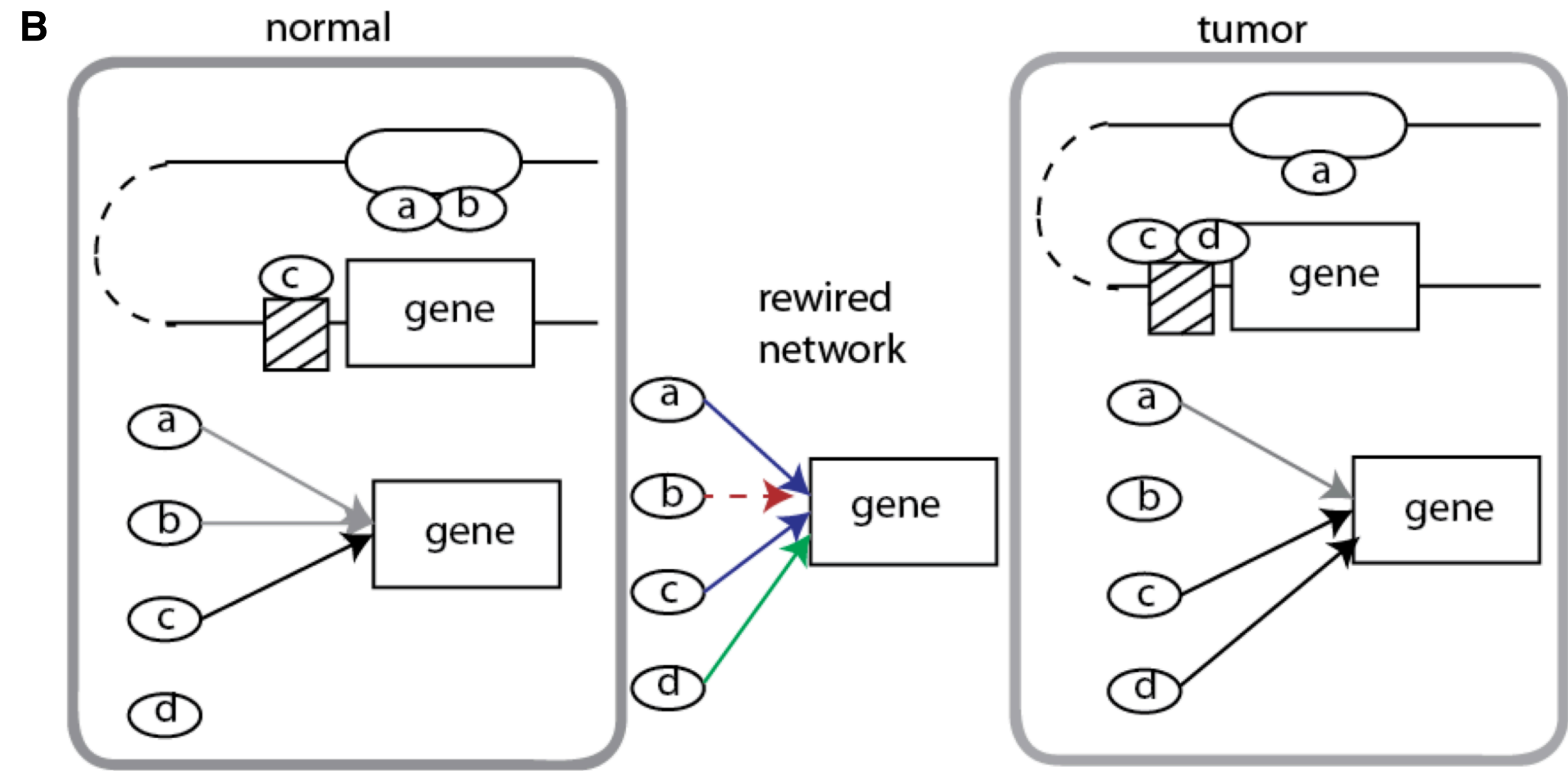
Figure 1

A

		K562	GM12878	HepG2	Liver	A549	IMR-90	MCF-7	MCF-10A	HeLa-S3	
DNA-binding Proteins (ChIP-seq)	TF	209	101	97	7	32	9	52	4	60	①
	TFSS	64	50	48	5	21	6	15	3	29	②
	Chromatin	17	6	7		3	1	3	1	4	③
	Histone	12	11	11	7	11	28	5		11	④
Knockdown	siRNA	29						2			⑤
	shRNA	219		221							⑥
3D Chromatin Structure	ChIA-PET	3	1	1				4		1	⑦
	Hi-C	•	•			•		•			⑧
Cis-regulatory Elements	DNase-seq	•	•	•		•	•	•		•	⑨
	EnhancerSeq	•	•					•			⑩
Methylation	WGBS	•	•	•	•		•				⑪
	RRBS	•	•	•	•	•	•	•	•	•	⑫
Transcription	RNA-seq	•	•	•	•	•	•	•		•	⑬
	RAMPAGE	•	•								⑭
Replication Timing	Repli-seq/chip	•	•	•			•	•		•	⑮
Cell Line WGS	SNV	•	•					•		•	⑯
	SV	•	•					•		•	⑰
TCGA	Cohort	95		327		38		198		2	⑱
	Expression	173		373		517		1100		546	⑲

T *N*
T *N*
T *N*
T *N*
T

Blood
Liver
Lung
Breast
Cervix



*TCGA Cohort (PCAWG May):
 K562::CLLE, HepG2::LIHC, A549::LUAD, MCF-7::BRCA, HeLa-S3::CESC

**TCGA (1/28/2016):
 K562::LAML, HepG2::LIHC, A549::LUAD, MCF-7::BRCA, HeLa-S3::CESC

Figure 1

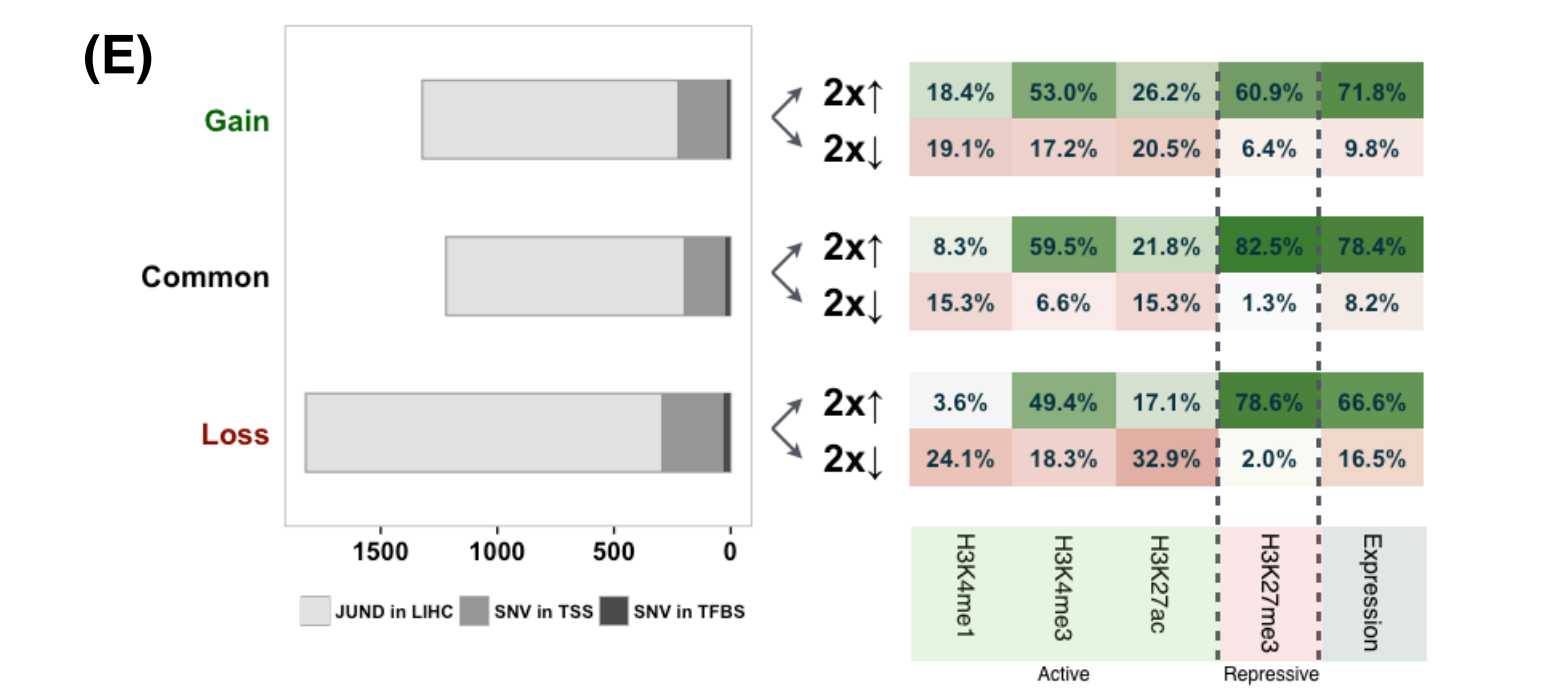
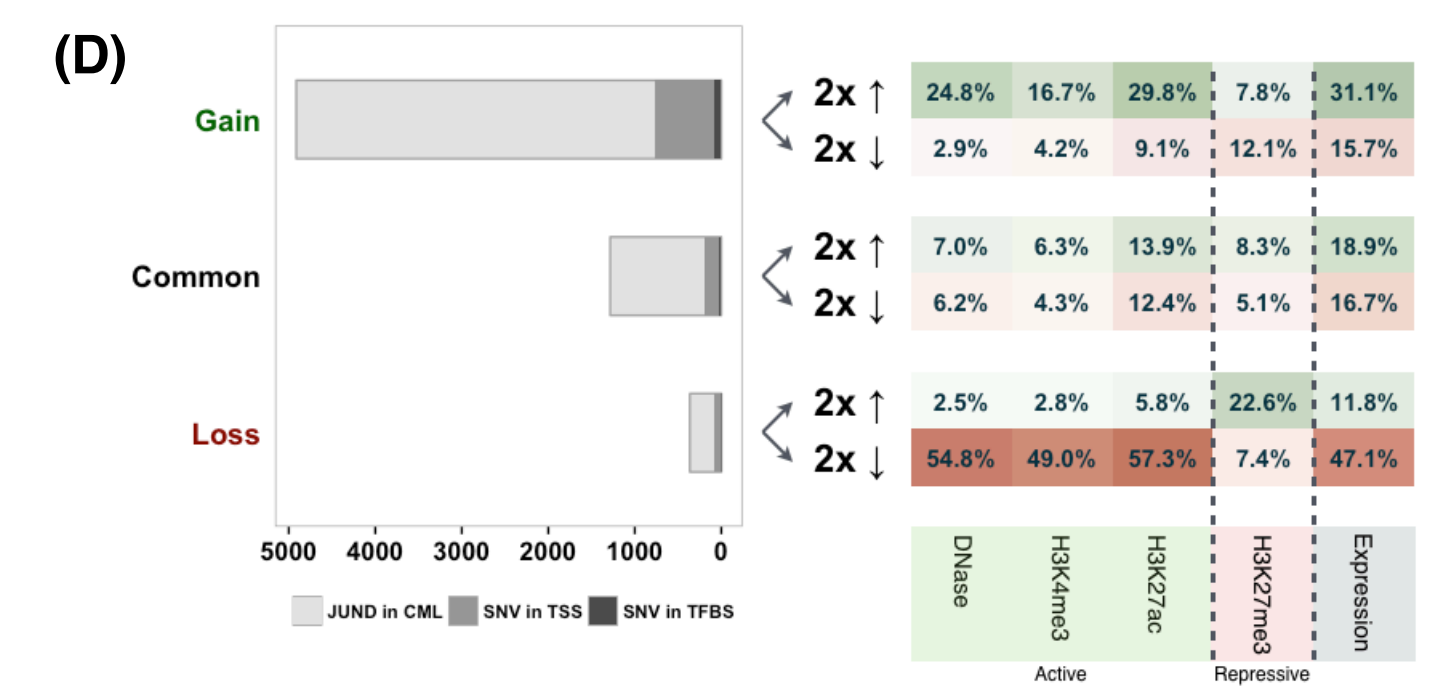
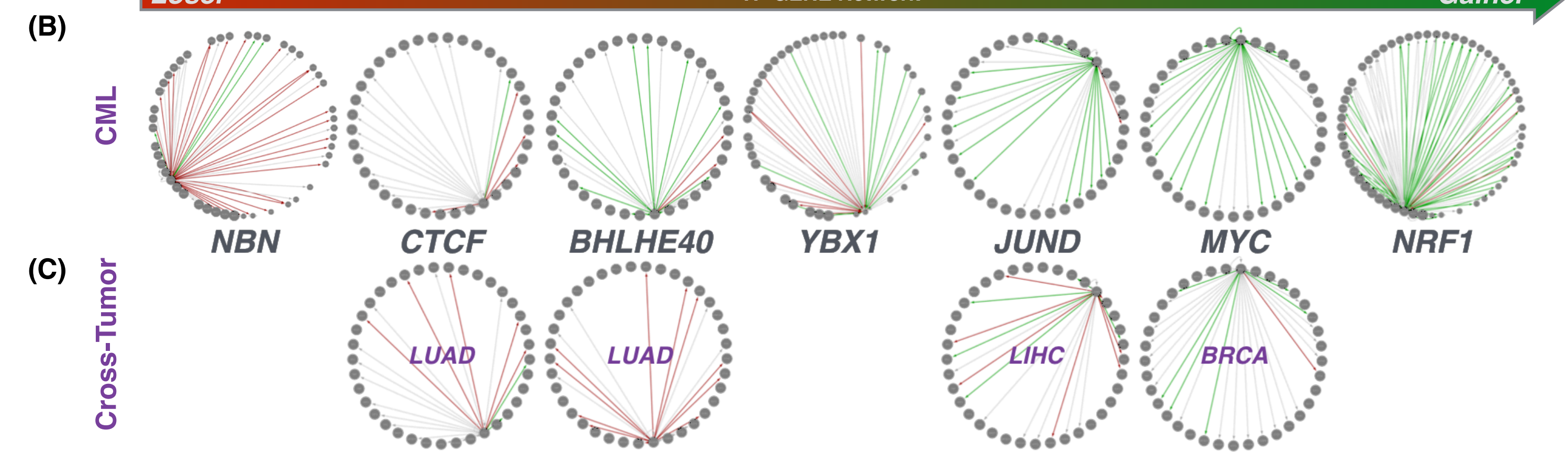
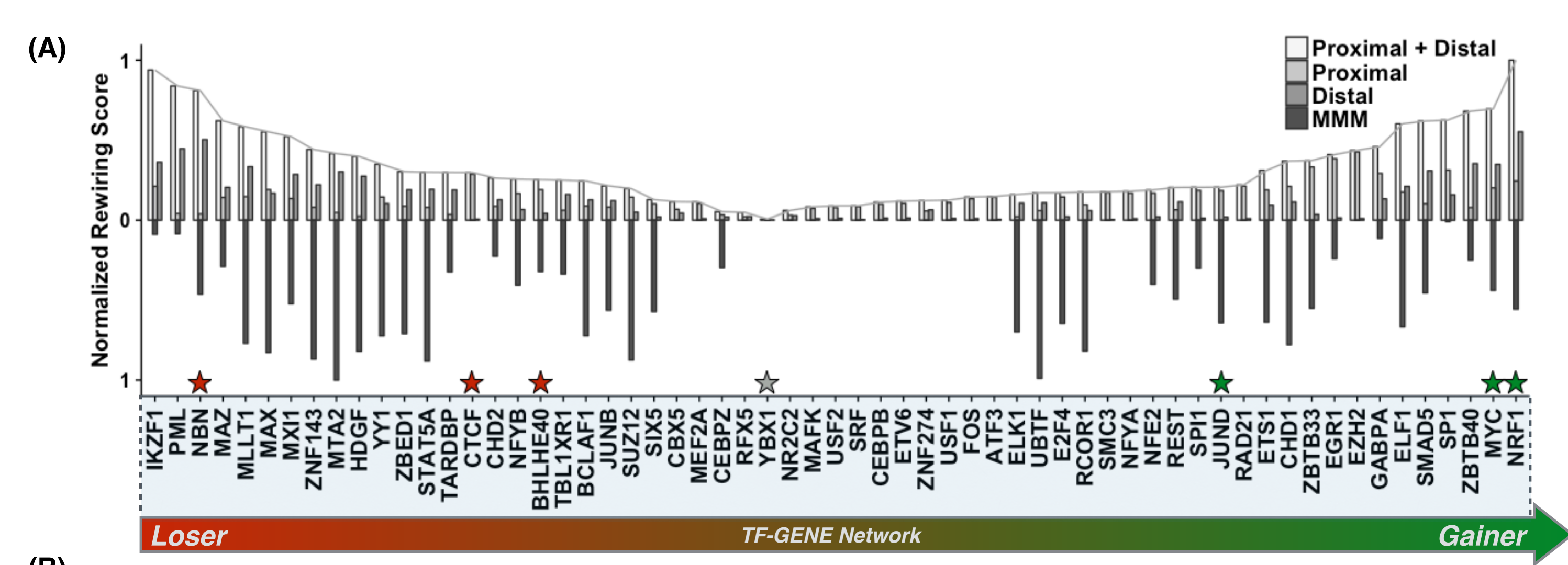


Figure 2

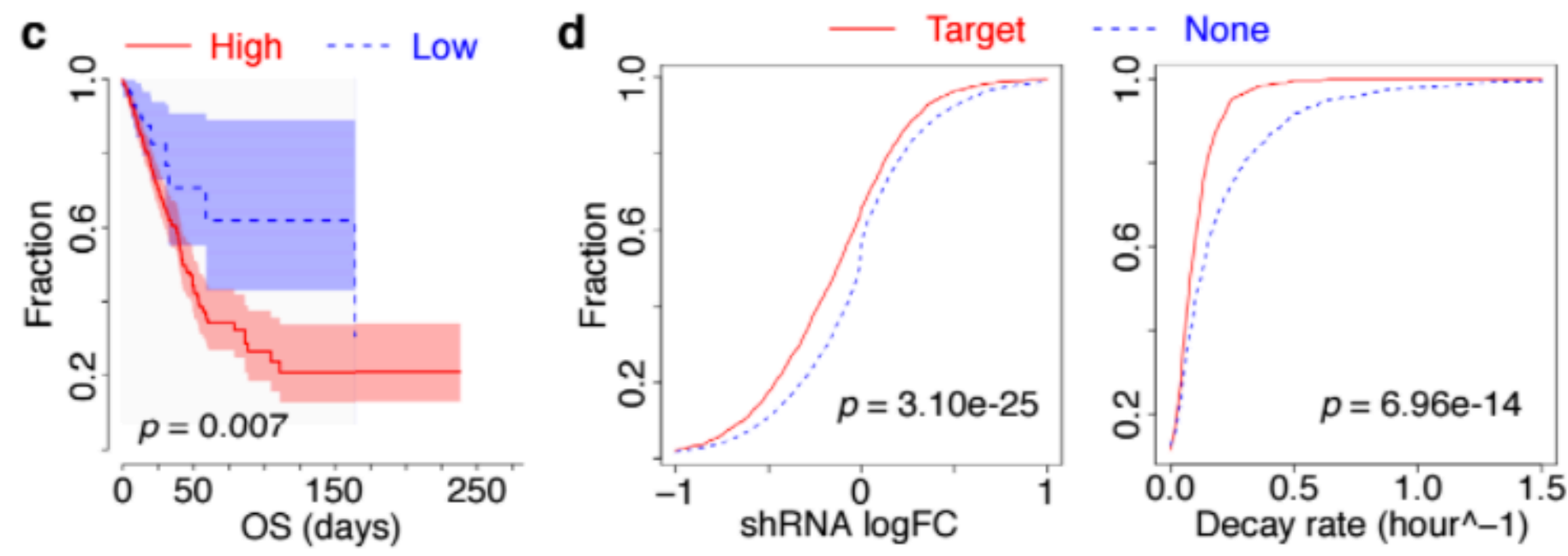
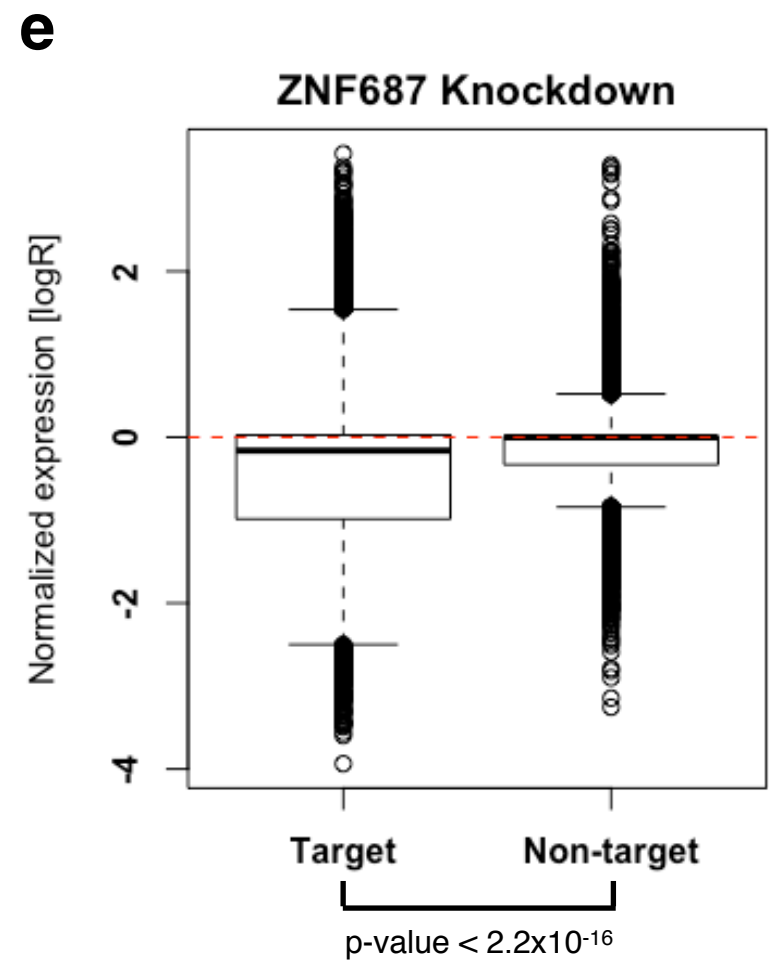
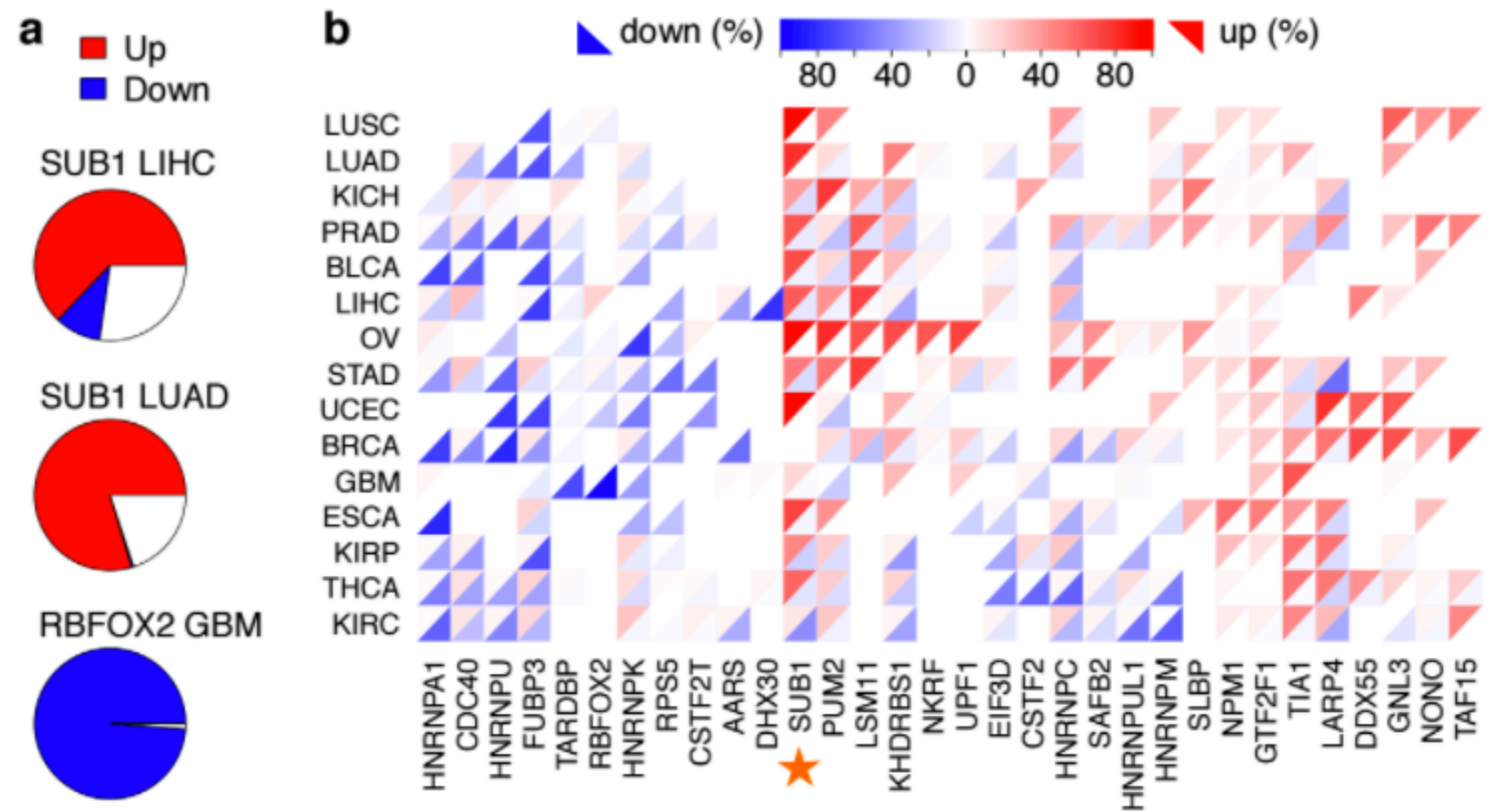


Figure 1: Inference of RNA binding proteins driving cancer expression patterns. Using ENCODE eCLIP data and TCGA tumor profiles, we applied RABIT framework to identify RNA binding proteins (RBP), whose target genes are differentially regulated in cancer. (a) The fractions of patients with target genes up or down regulated are shown for each combination of RBP and cancer type. (b) The fractions of patients with target genes differentially regulated are shown for all combinations of cancer types and RBPs whose targets are differentially regulated in at least 50% patients in one cancer type. (c) All lung adenocarcinoma patients are divided to two groups according to the *SUB1* activity predicted by RABIT. The overall survival was shown by KM plot. The association between RABIT regulatory activity and survival was tested through CoxPH regression. (d) In the left panel, the cumulative distributions of gene expression after *SUB1* knock down in HepG2 cell are shown for predicted *SUB1* targets and none-targets. In the right panel, the cumulative distributions of mRNA decay rates in HepG2 cell are shown. The comparison between two categories is done through Wilcoxon rank-sum test.

Figure 3

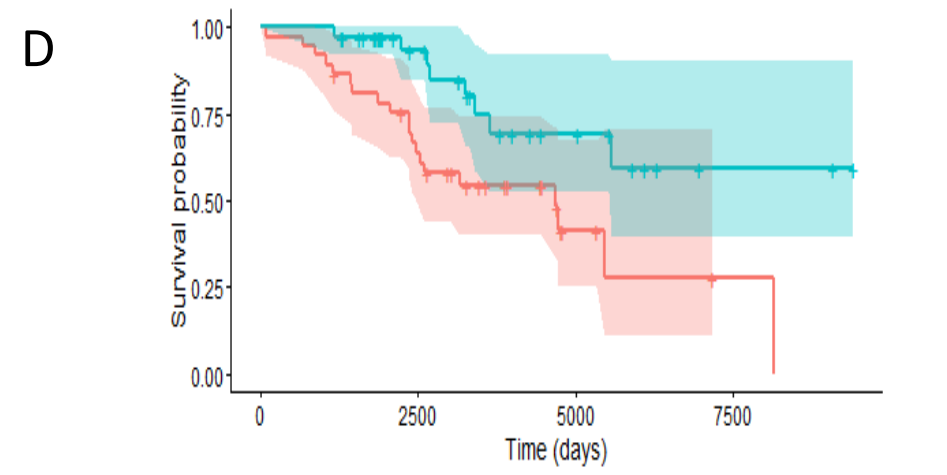
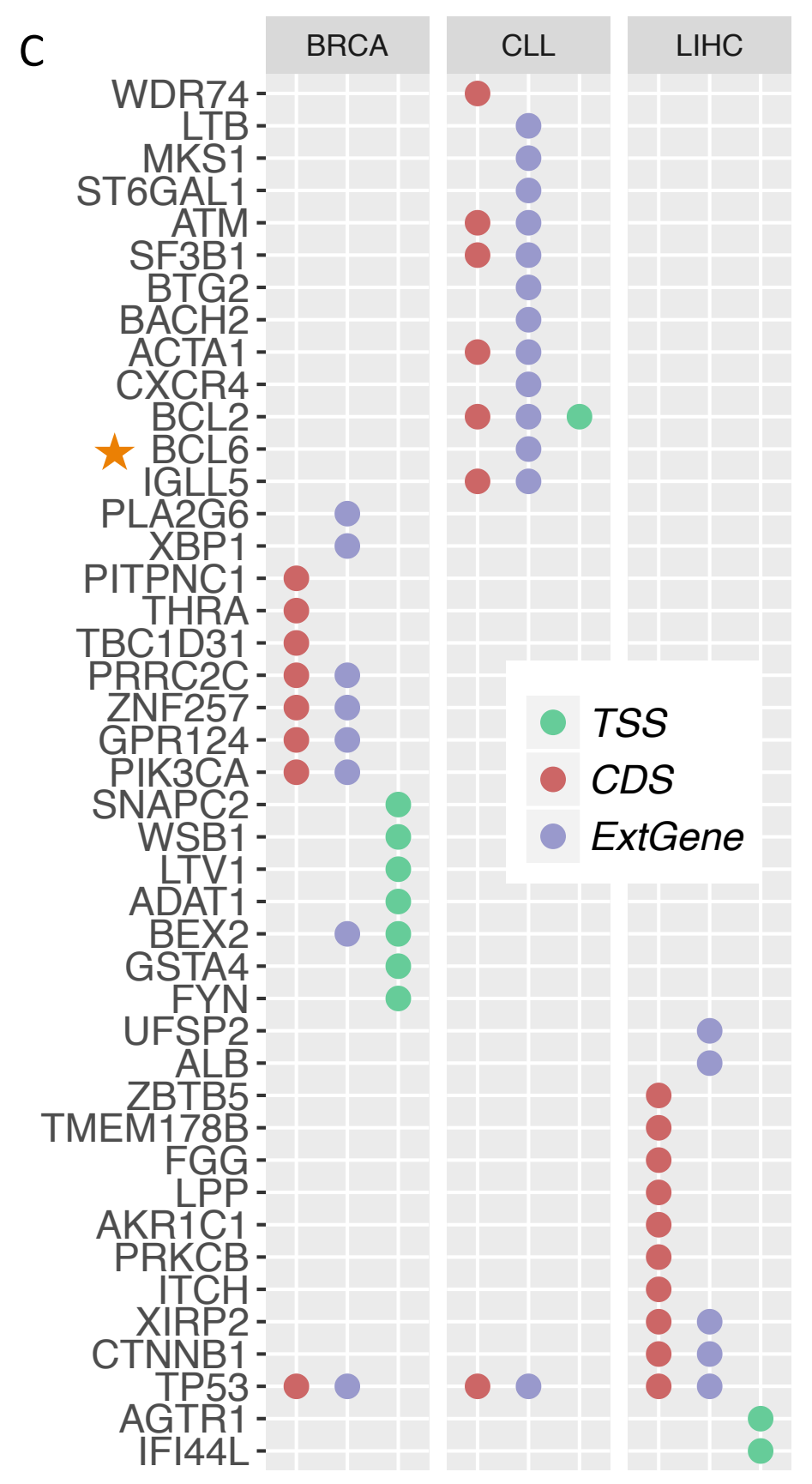
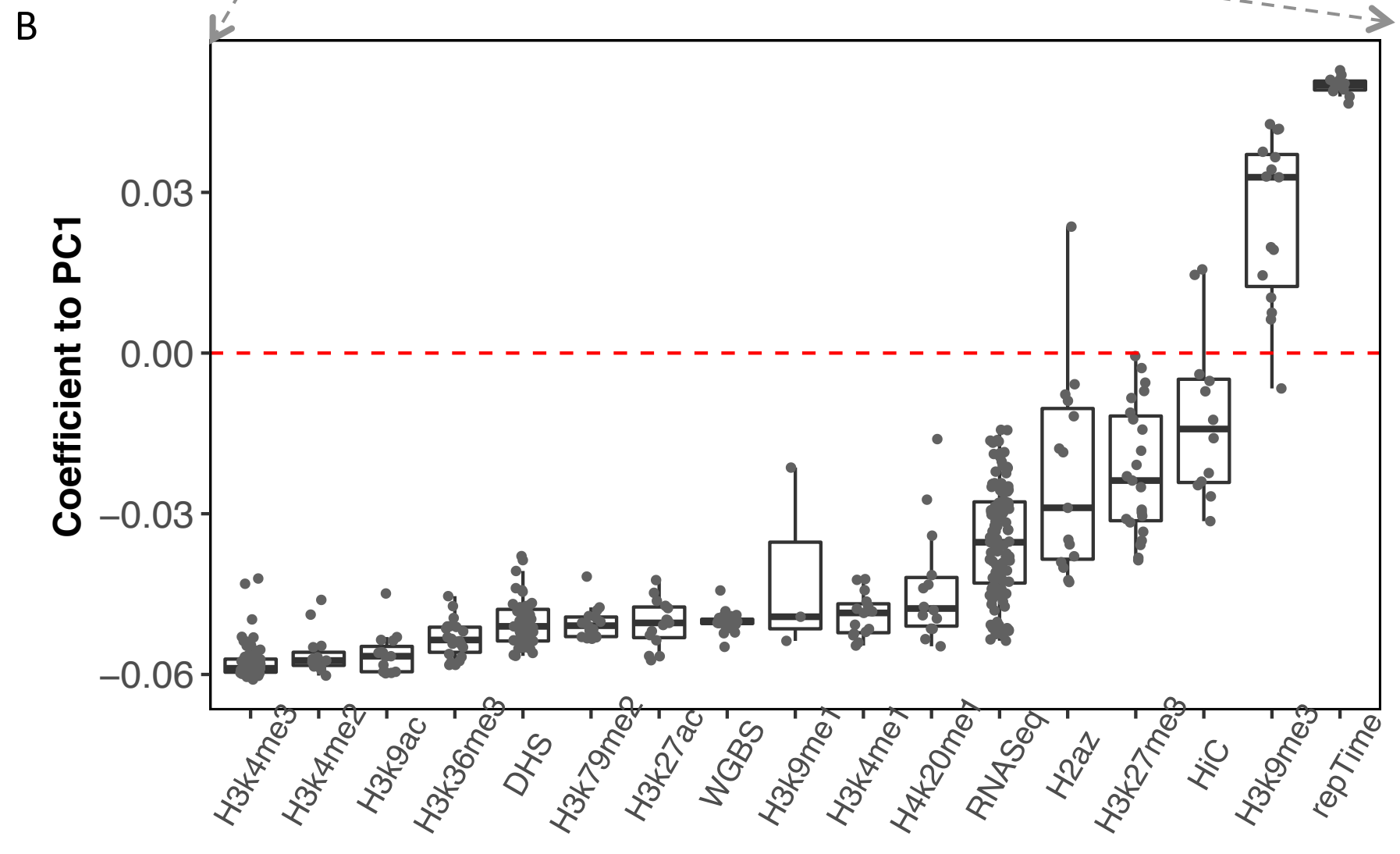
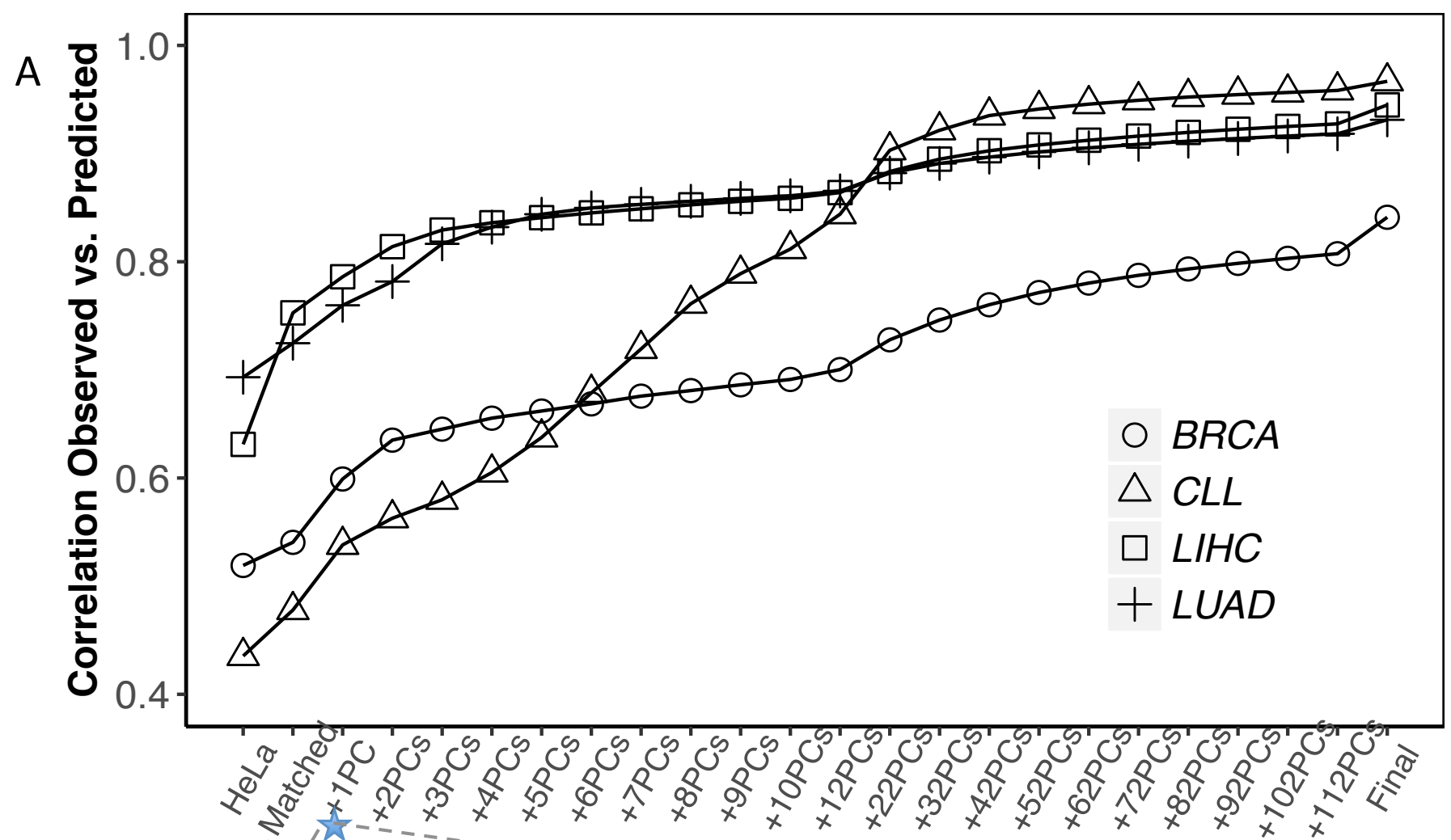


Figure 4

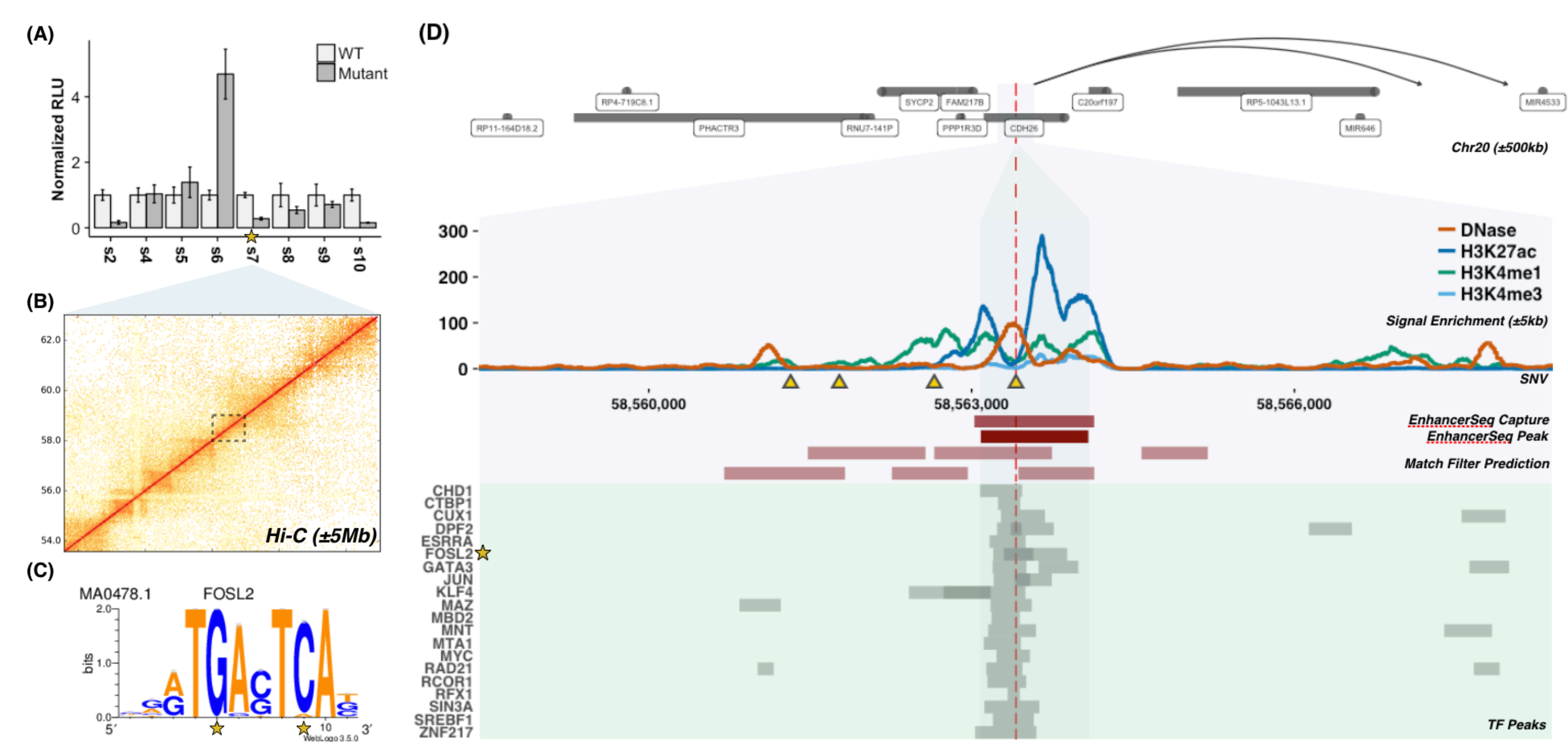


Figure 5

