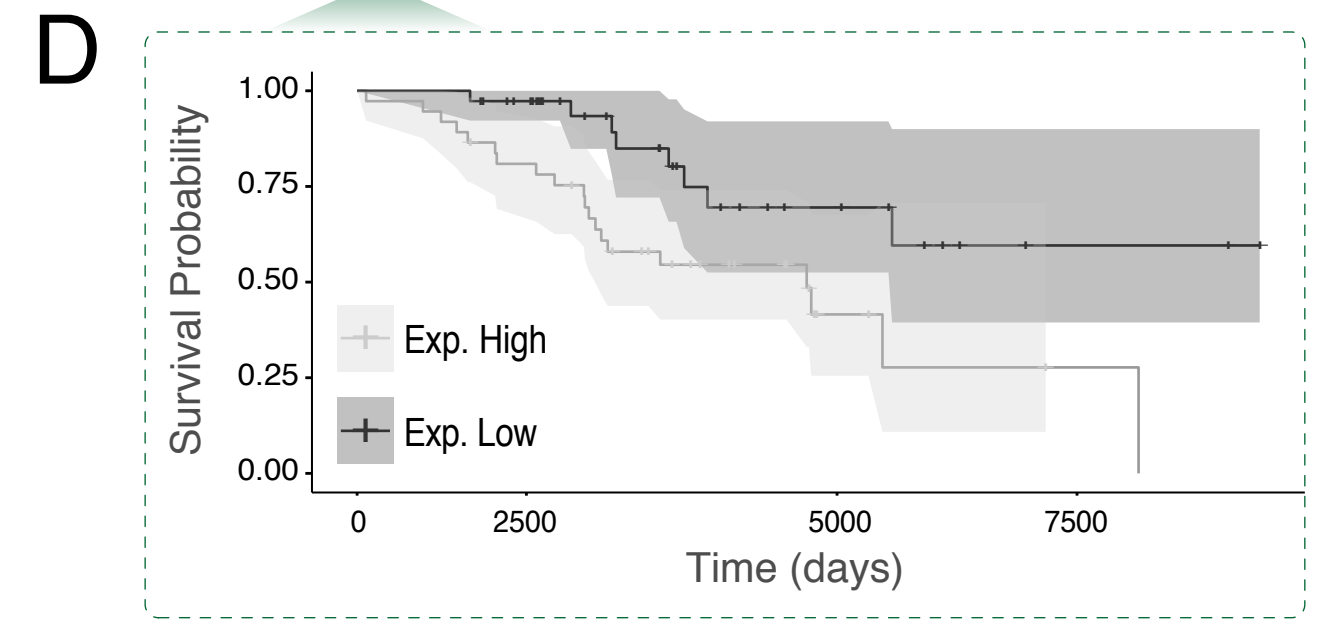
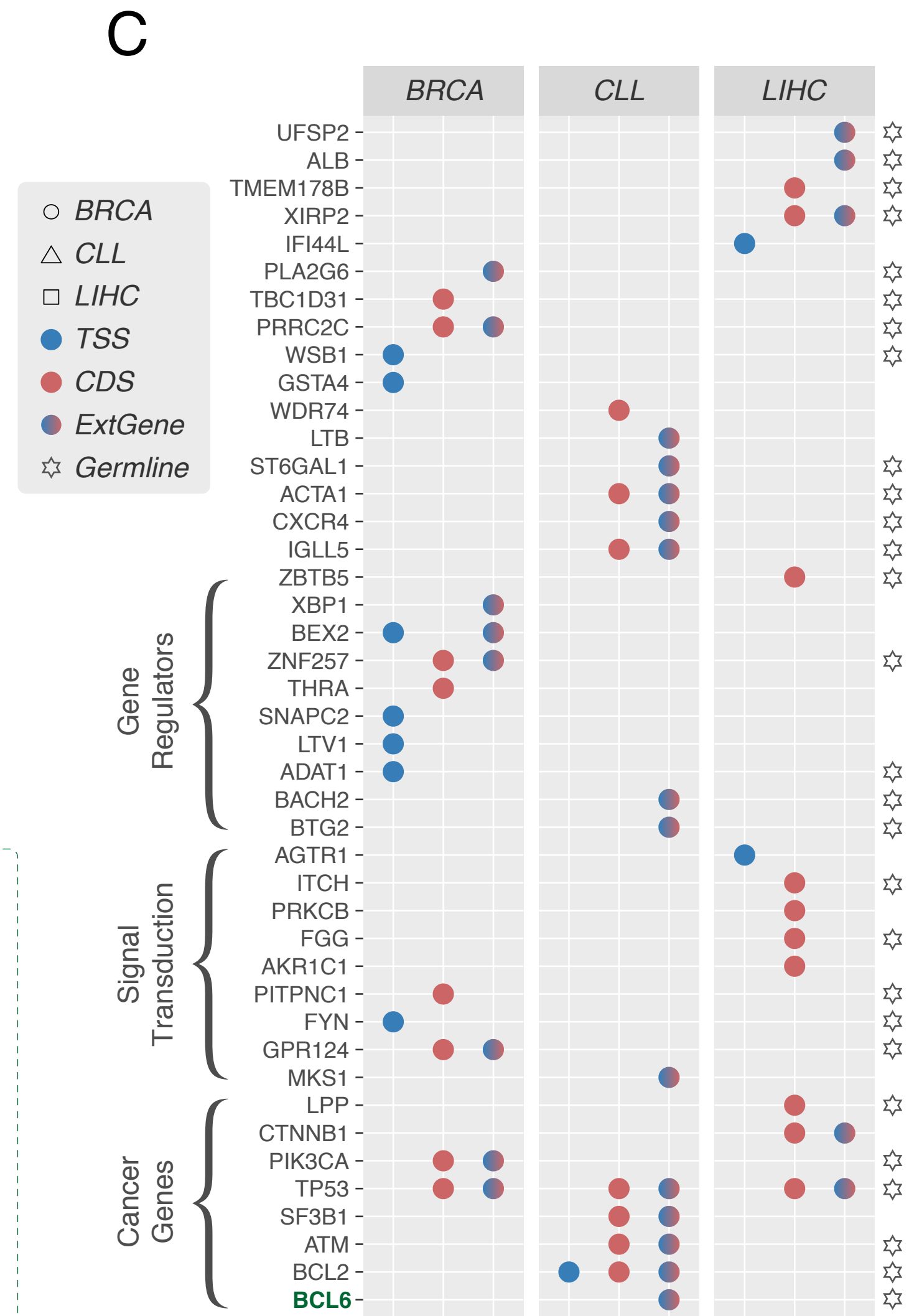
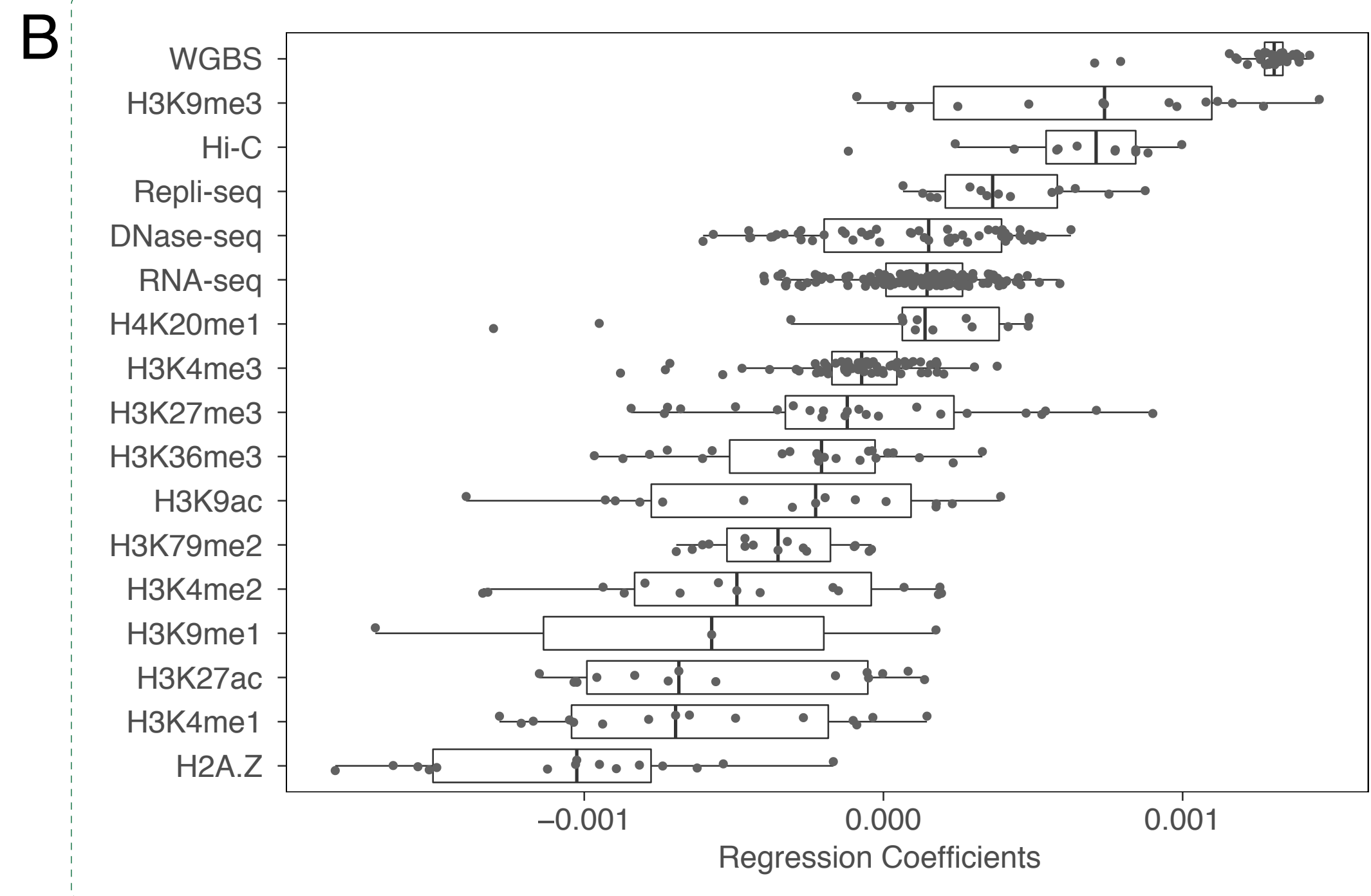
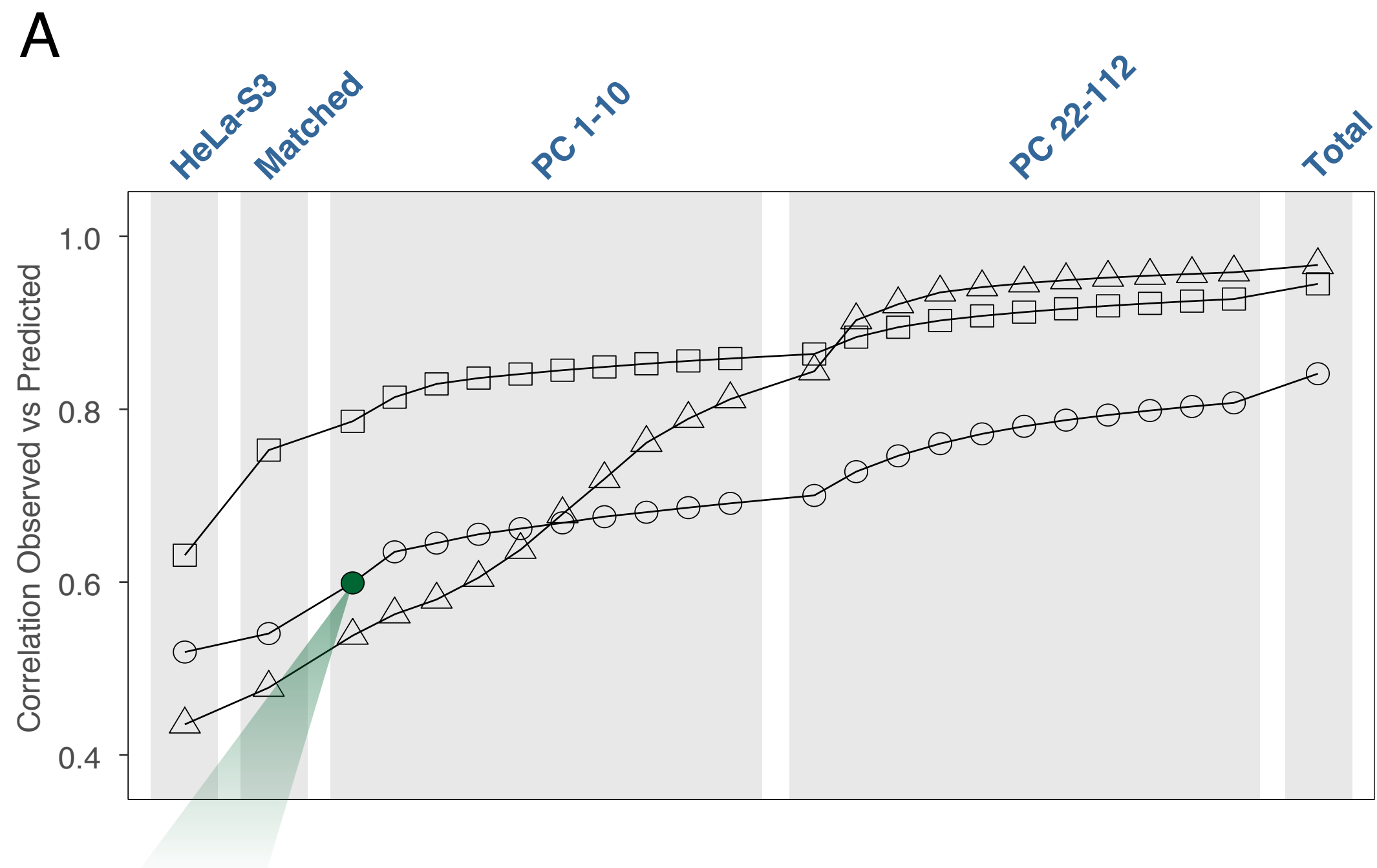


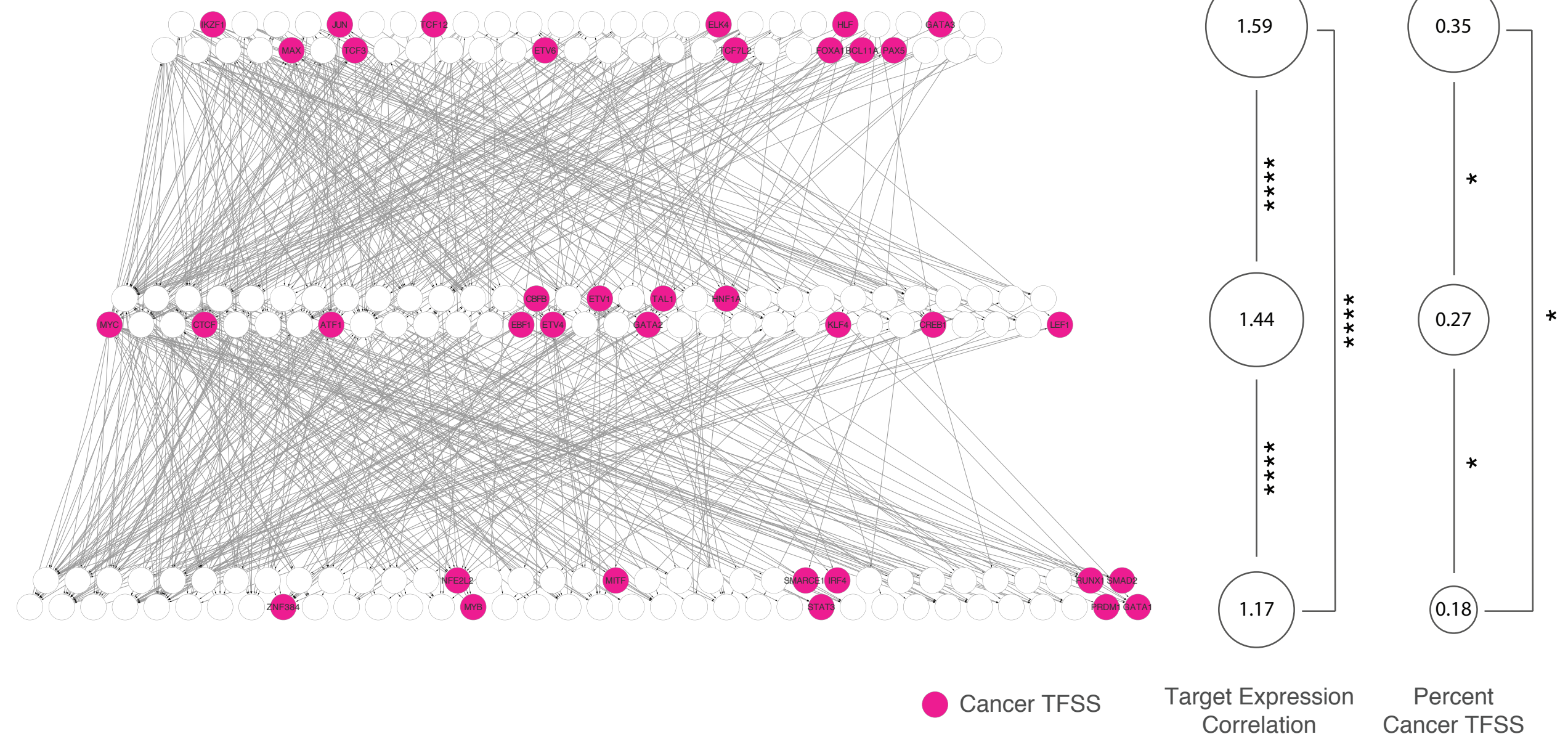
ENCODEC

v170418

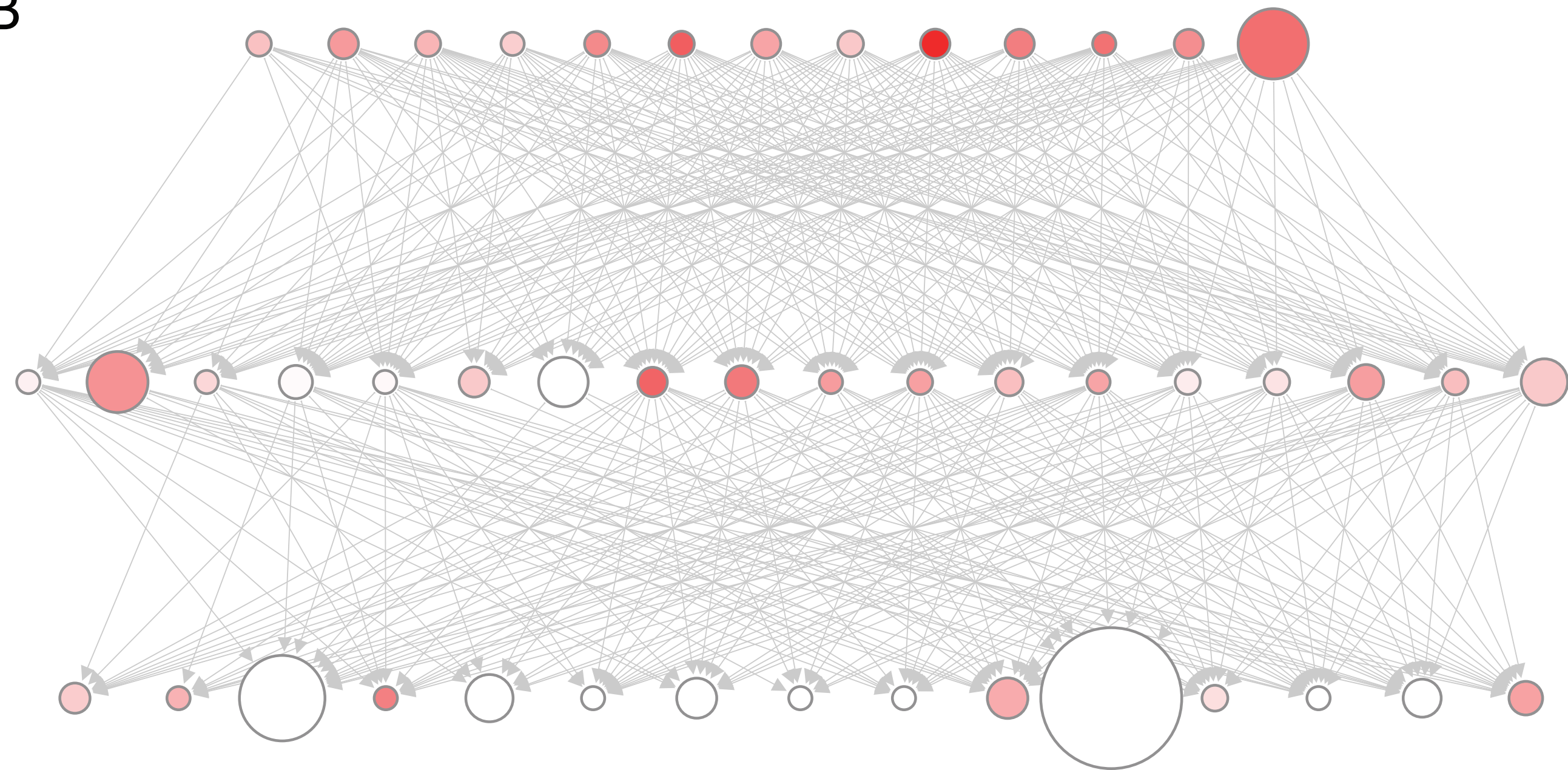
DL



A



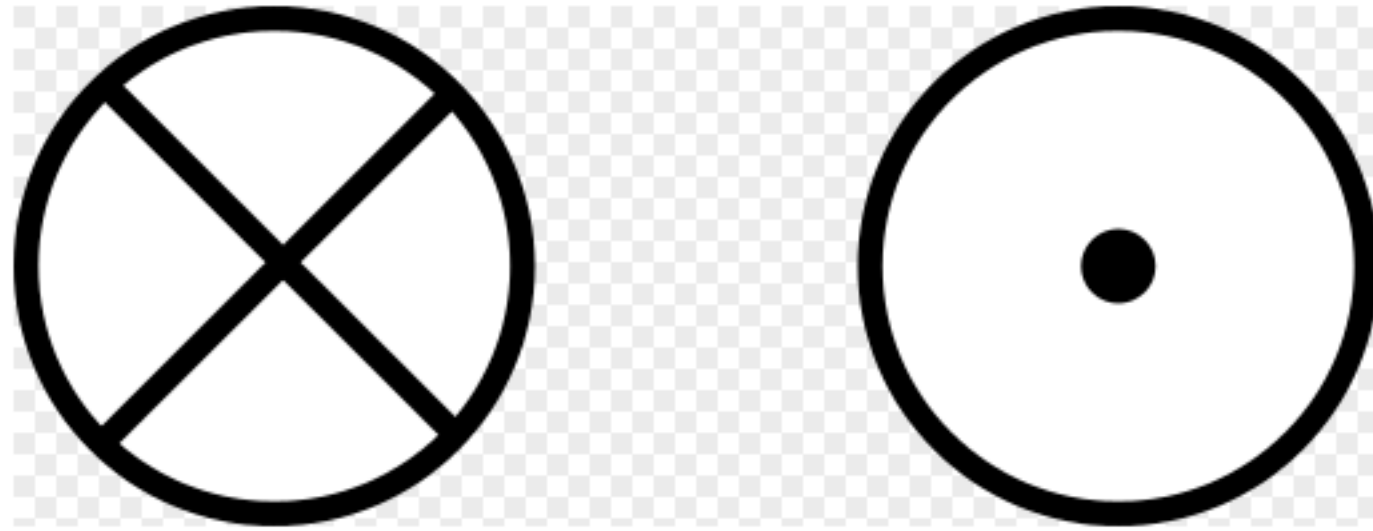
B



File:Notation for vectors in or out of a plane.svg

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Size of this PNG preview of this SVG file: 512 × 195 pixels. Other resolutions: 320 × 122 pixels | 640 × 244 pixels | 800 × 305 pixels | 1,024 × 390 pixels | 1,280 × 488 pixels.

[Original file](#) (SVG file, nominally 512 × 195 pixels, file size: 508 bytes)

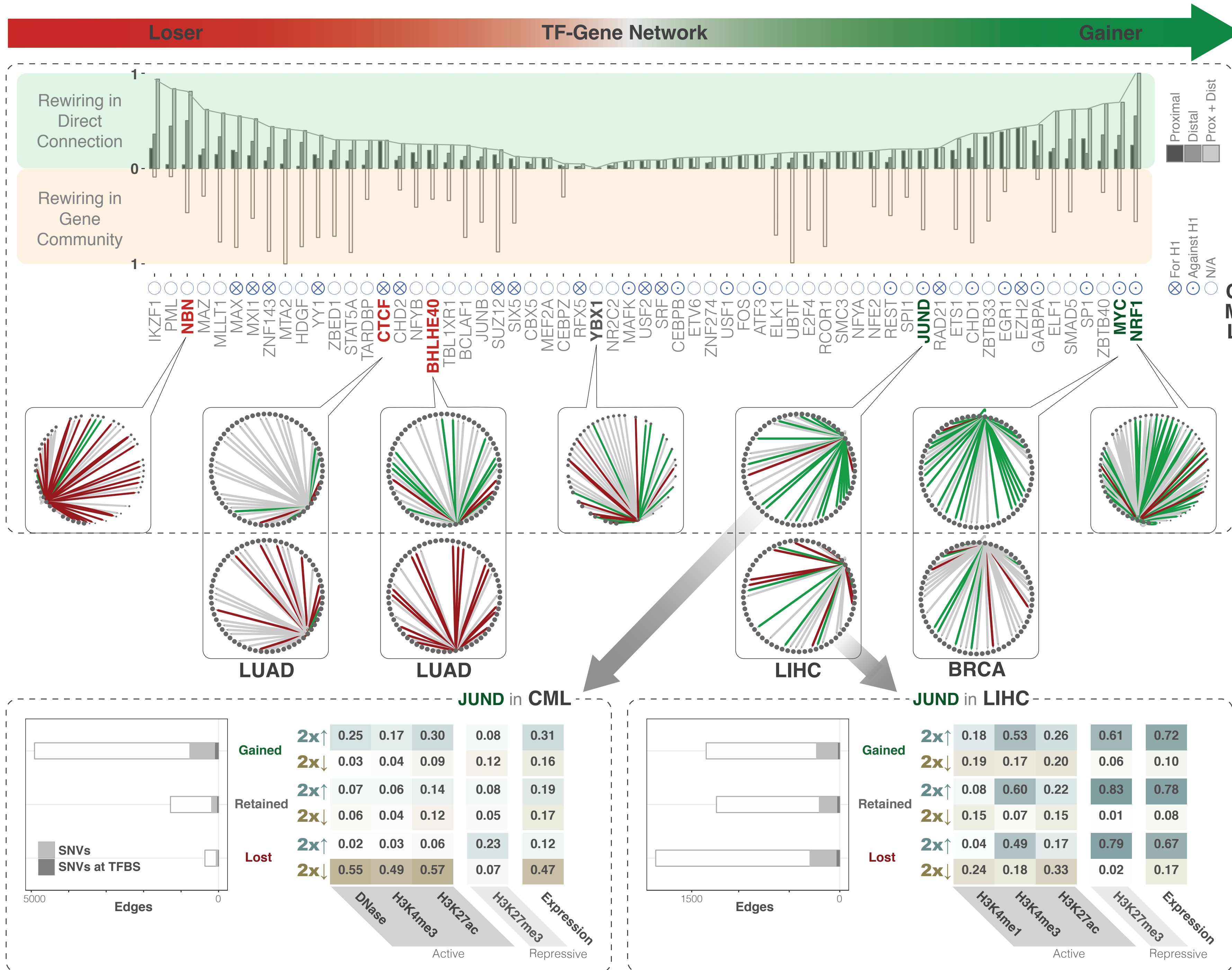
This image rendered as PNG in other widths: [200px](#), [500px](#), [1000px](#), [2000px](#).

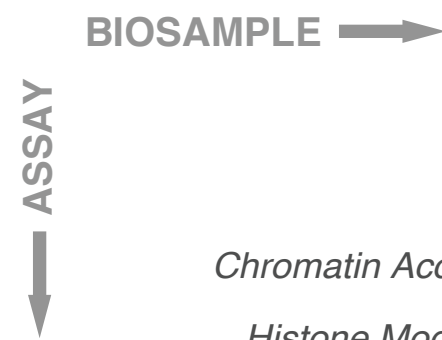
[Open in Media Viewer](#)

Summary [\[edit\]](#)

Description	English: The notations used to indicate that a vector is going into (left) or coming out of (right) the screen or a page Italiano: Rappresentazione grafica di un vettore entrante (sinistra) o uscente (destra) dal foglio (o da un piano geometrico)
Date	2 June 2007 (First version) 5 February 2014 (Latest version)
Source	Own work
Author	First version Created by bdesham with Inkscape. Second version hand-drawn by Krishnavedala
Permission (Reusing this file)	 <i>This image of simple geometry is ineligible for copyright and therefore in the public domain, because it consists entirely of information that is common property and contains no original authorship.</i> 
SVG development	 The source code of this SVG is valid .  This symbol was created with a text editor by Krishnavedala .

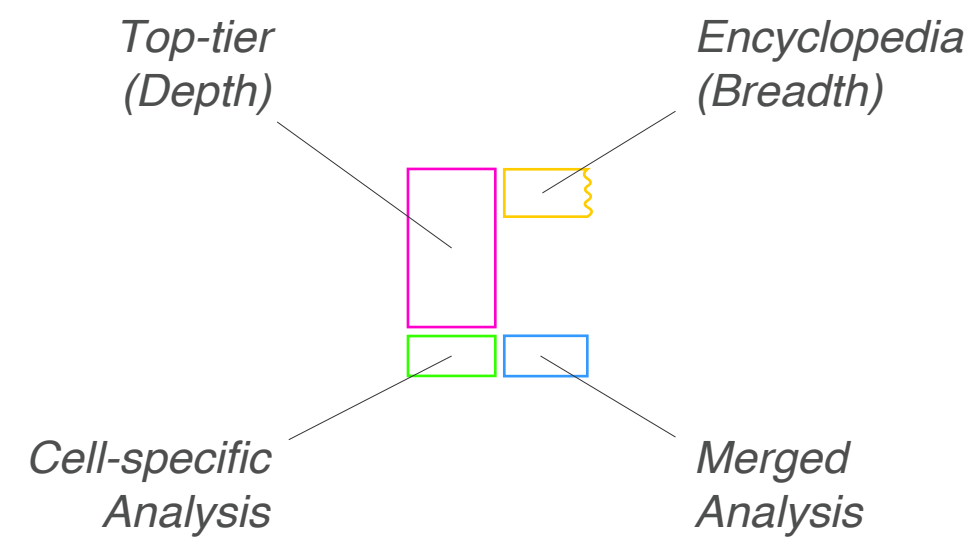
https://en.wikibooks.org/wiki/Physics_Study_Guide/Vectors_and_scalars





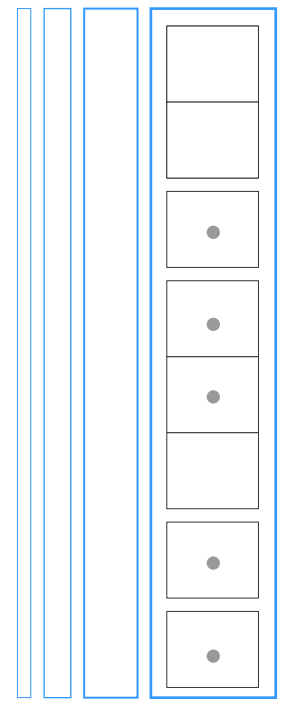
		K562		CD34+ PC GM12878		HepG2		Liver		A549		Lung IMR-90		MCF-7		HMEC MCF-10A		HeLa-S3		H1-HESC		Caco-2		HCT116		Panc1		LNCaP		PC-3		PC-9		SK-N-MC		DND-41		...	
		T	N	T	N	T	N	T	N	T	N	T	N	T	N	T	N	T	N	T	N	COAD+READ	PAAD	PRAD	LUAD	SARC	LAML												
Chromatin Accessibility DS	DNase-seq	●	▲	●		●	▲	●	▲	●	▲	●	▲	●	▲	●	▲	●	▲	●	▲	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●
	Histone	12	6	11	11	7	11	7	28	5	11	3	11	11	11	11	11	11	11	11	11	3	12	6	1	13	13	7	11	11									
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	3	1						4																													
3D Chromatin Structure 3D	Hi-C	▲	▲					●	▲	▲	▲									▲																			
	STARR-seq	●	▲	▲						●																													
Enhancers SS	WGBS	●	▲	●	▲			▲	▲	▲	▲									●																			
	RRBS	●	▲	●	●	●	●	▲	●	●	●	●								●																			
Methylation ME	Repli-seq/chip	●	▲	●						●	●									●																			
	TF Total	207	99	95	7	31	1	9	52	2	4	59	49																										
Transcription Factors TF	TFSS	125	68	69	6	23	1	6	34	1	3	34	32																										
	Chromatin Remodeller	31	11	13		3			7	1		9	9																										
	Cofactor	20	9	7	1	3		2	4			6	3																										
	General (GTF)	17	6	4		2		1	2		1	10	5																										
	Other	14	5	2					5																														
Cell Line WGS WG	SNV	▲	▲							▲				▲																									
	SV	▲	▲							▲				▲																									
Patient Data PD	Cohort	150			82	197			116																														
	Expression	173		373		517			1100																														

ENCODEC



- Available in ENCODE
- ▲ Available as External Resource

ESCAPE (SS) + CASPER (TF+DS)	●	●								●																														
Enhancer Target Prediction (JEME+3D)	●	●	●							●																														
Background Mutation Rate & Burdening																																								
TF/RBP Network	●		●		●		●		●																															
Network Hierarchy	●																																							
Network Rewiring	●		●		●		●		●																															
Expression Correlation & Network Motif																																								
TF Motif Disruption	●		●		●		●		●																															



- Σ ¶ 1.10 (HL) Reconcile with the main ENCODE encyclopedia
- Both promoter and enhancer annotations from ENCODEC were carefully consolidated with the main ENCODE Encyclopedia resources. The ENCODE Encyclopedia comprises of three levels, two levels of annotations and the raw data. The ground level includes peaks and quantifications produced by uniform processing pipelines for individual data types. The integrative level contains annotations produced by integrating multiple data types. The core of the integrative level is the Registry of candidate Regulatory Elements (cREs). The registry contains approximately ~1.31M human cREs and each cRE has a cell-type non-specific accession number, which then can be browsed from SCREEN (Search Candidate Regulatory Elements by ENCODE, <http://screen.umassmed.edu/>).
- Annotations from ENCODEC were merged against the Registry of candidate Regulatory Elements (cREs). We assigned cell type non-specific cRE accession numbers to ESCAPE and CASPER integrated enhancer annotations when the region had more than 1bp overlap. When there were more than one accession numbers associated with the annotation, we assigned multiple accession numbers to the element.
- For cases without an overlap, we assigned special accession numbers EH37EXXXXXXXX-C where XXXXXXXX are replaced with numbers starting from 0000001.
- For cases without an overlap, we assigned special accession numbers EH37CXXXXXXXX where XXXXXXXX are replaced with numbers starting from 0000001.
- To access the cRE using accession number, one can use the URL <http://screen.umassmed.edu/search/?q={accession}&assembly=hg19#> where {accession} is replaced with the cRE accession number. From SCREEN, one can look up H3K4me3, H3K27ac, CTCF, and DNase Z-scores and signal profiles across all available ENCODE cell types.