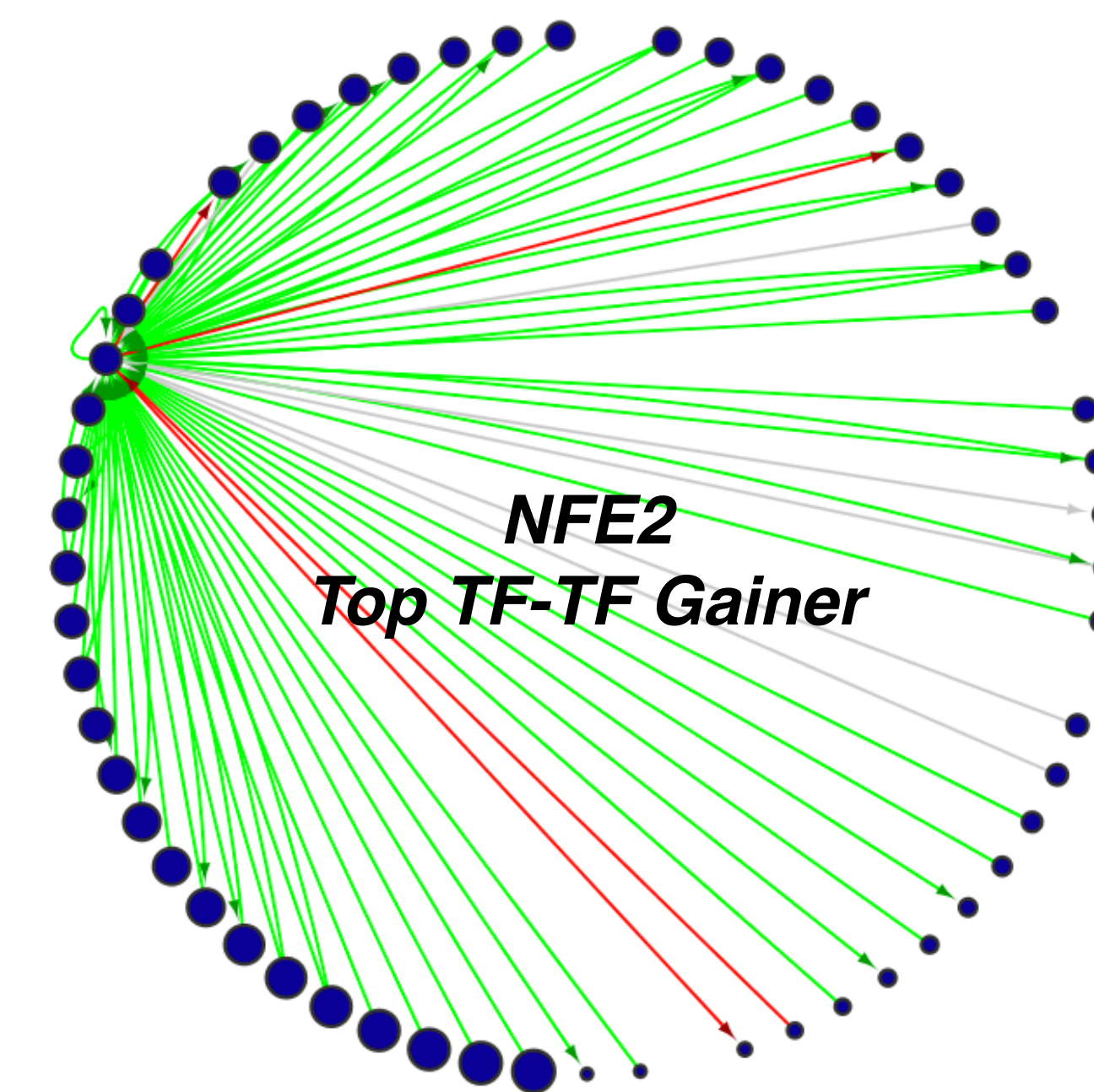
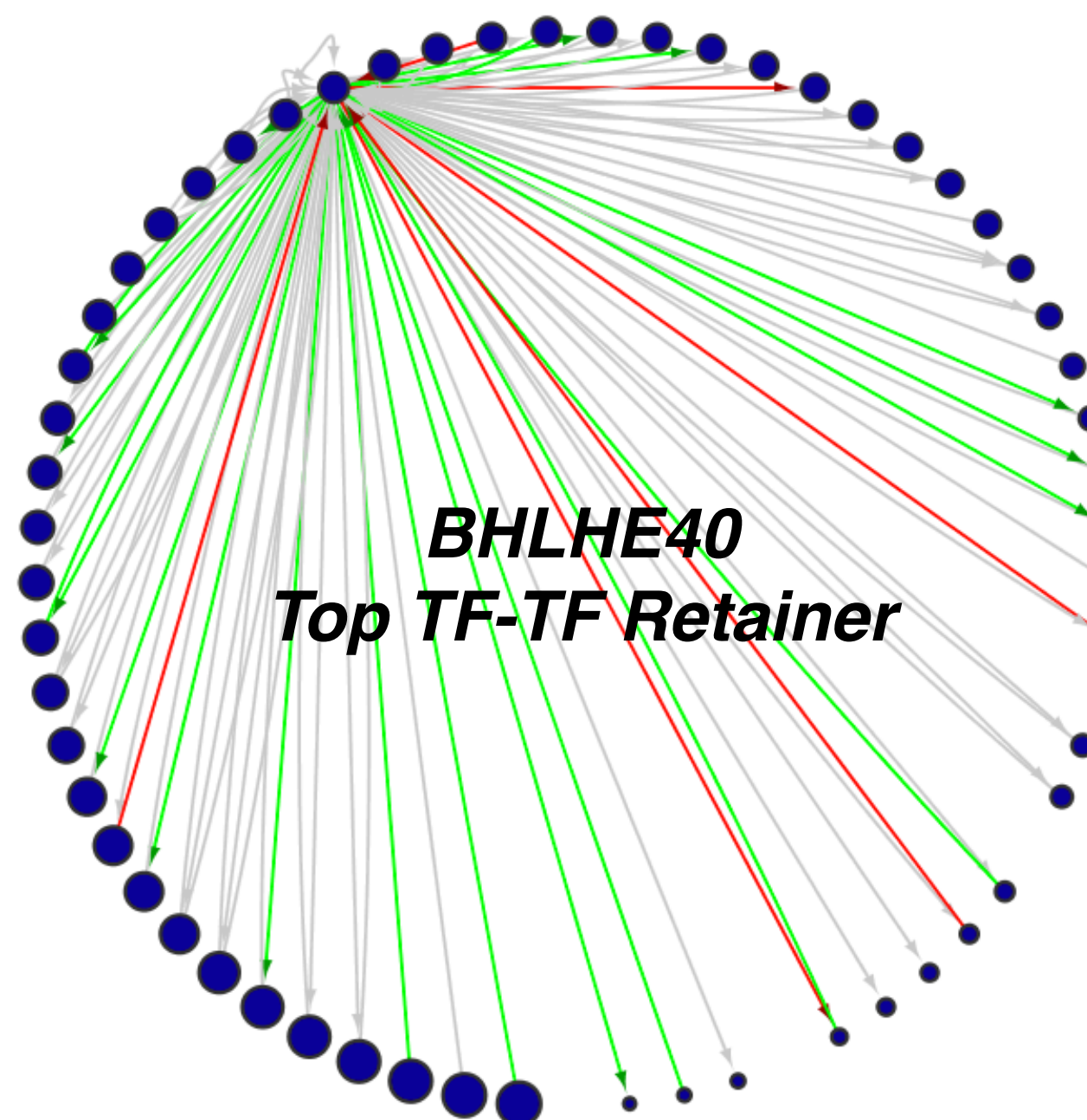
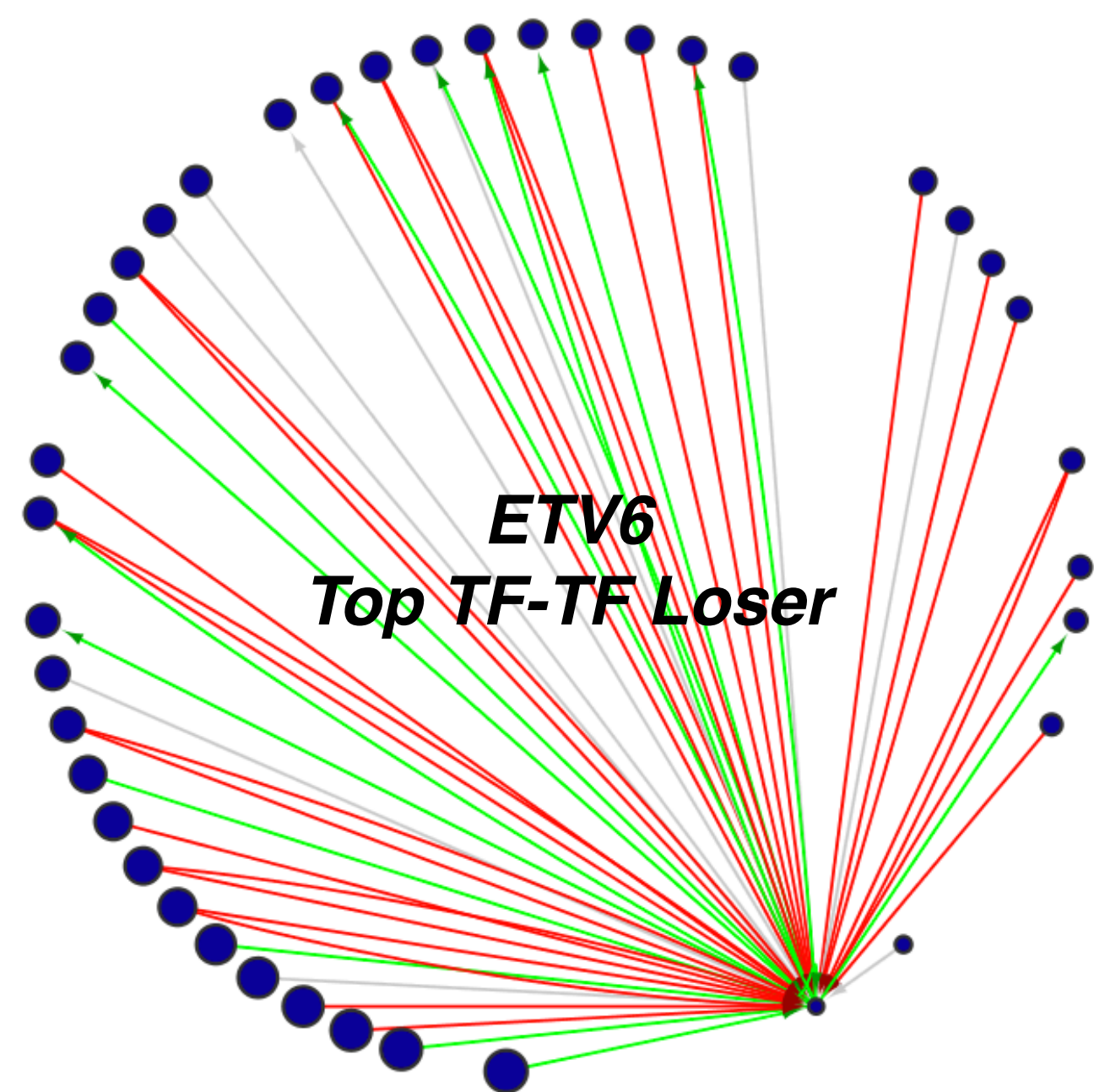
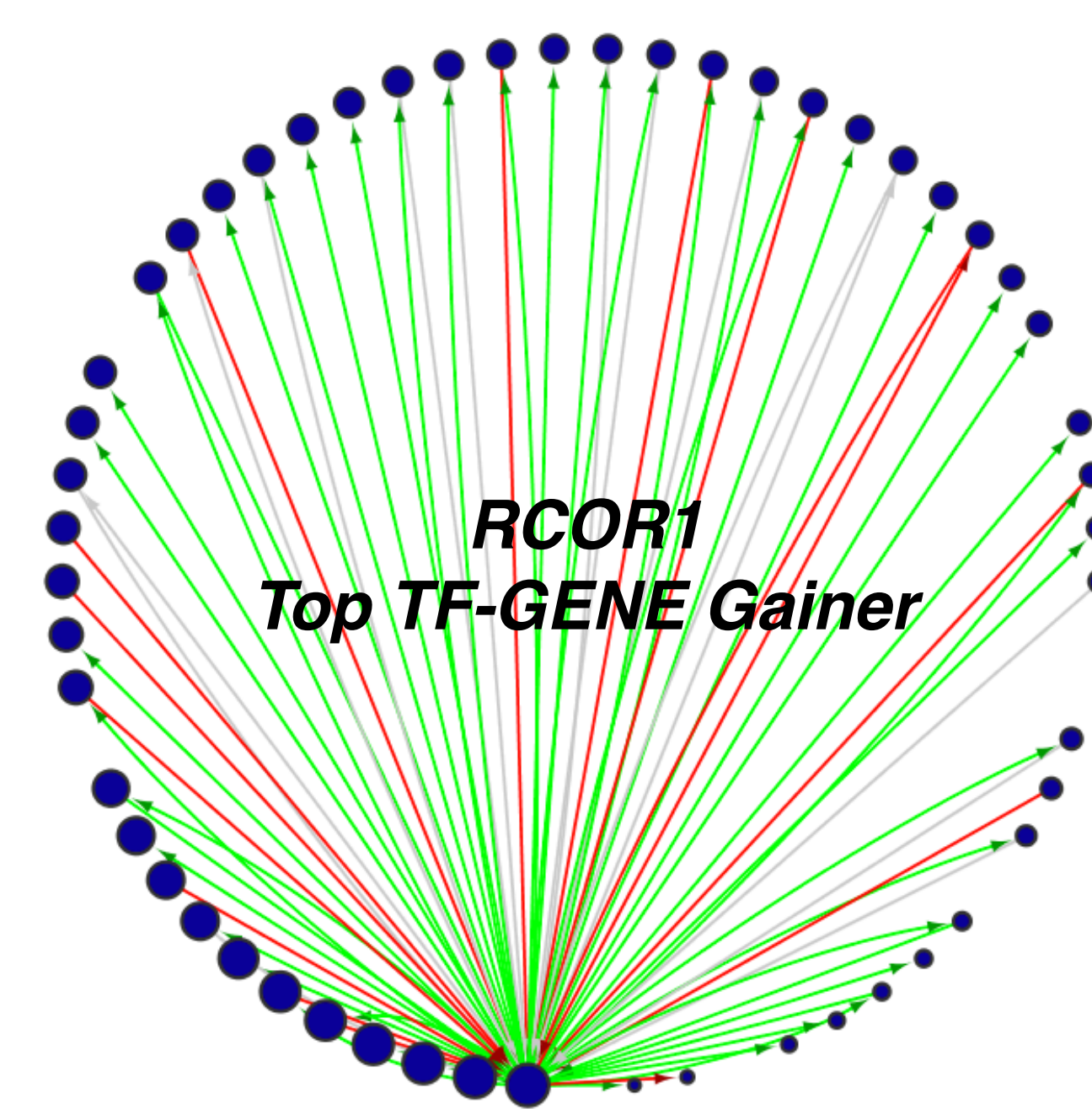
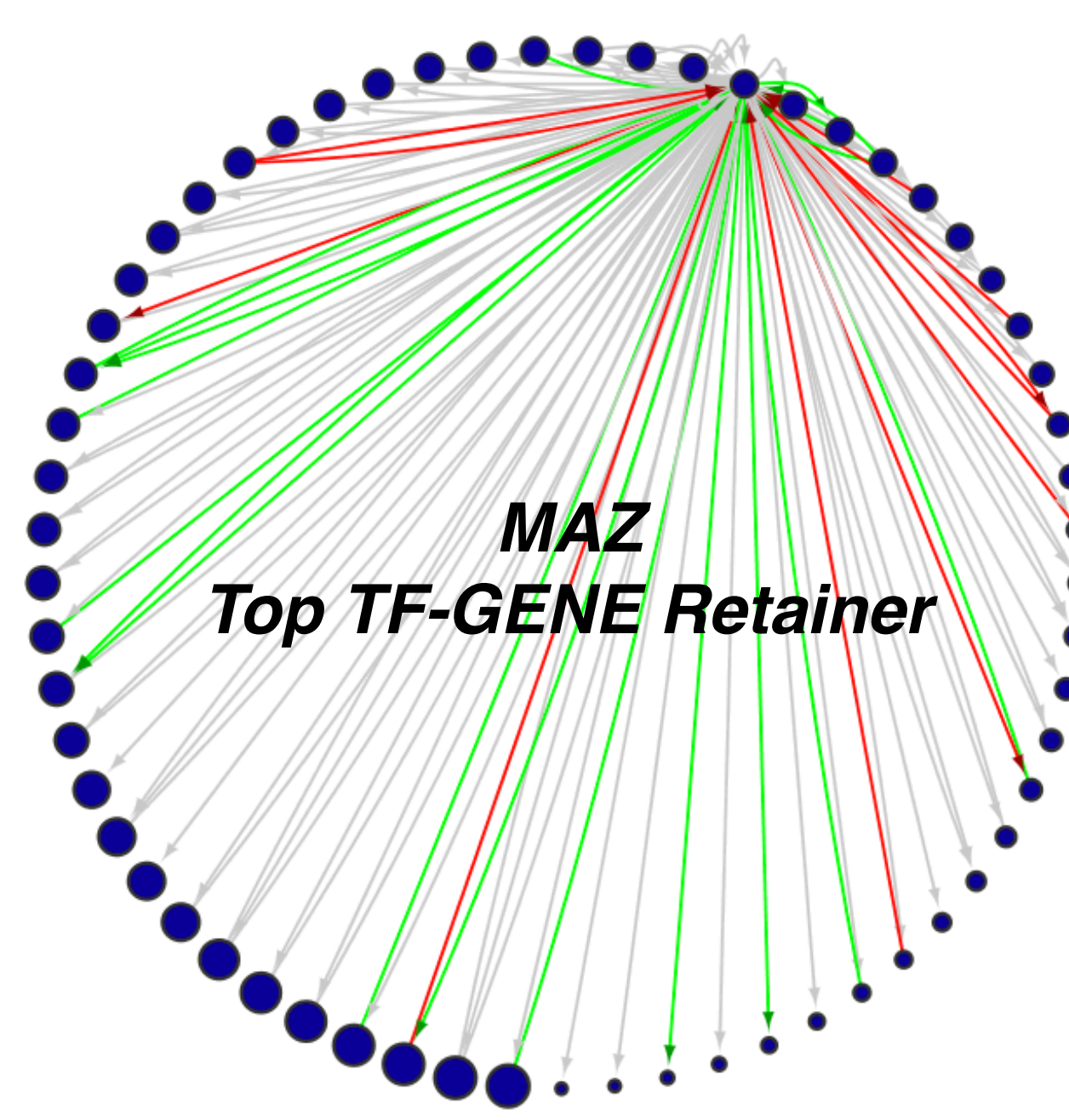
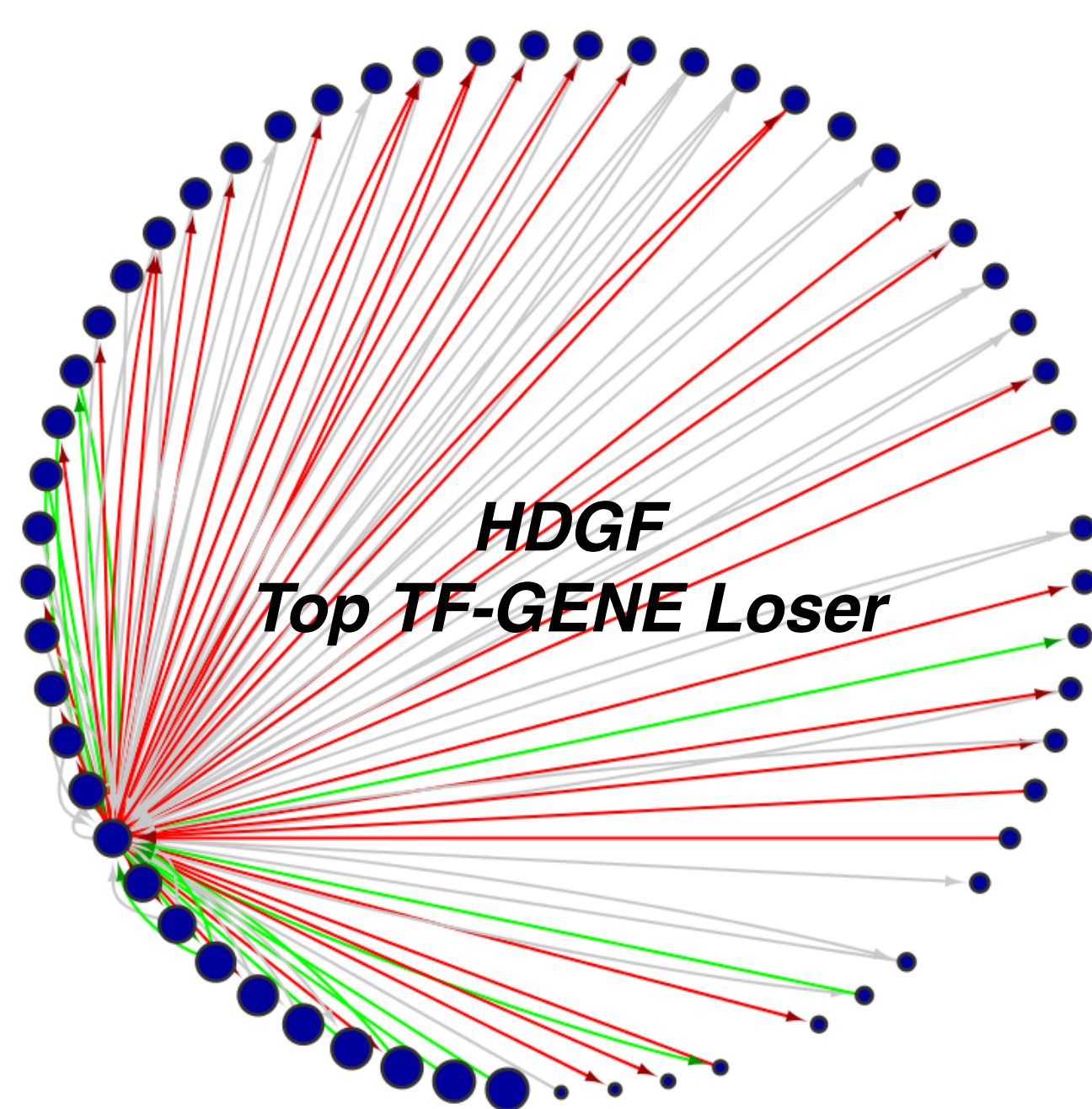


TF-GENE

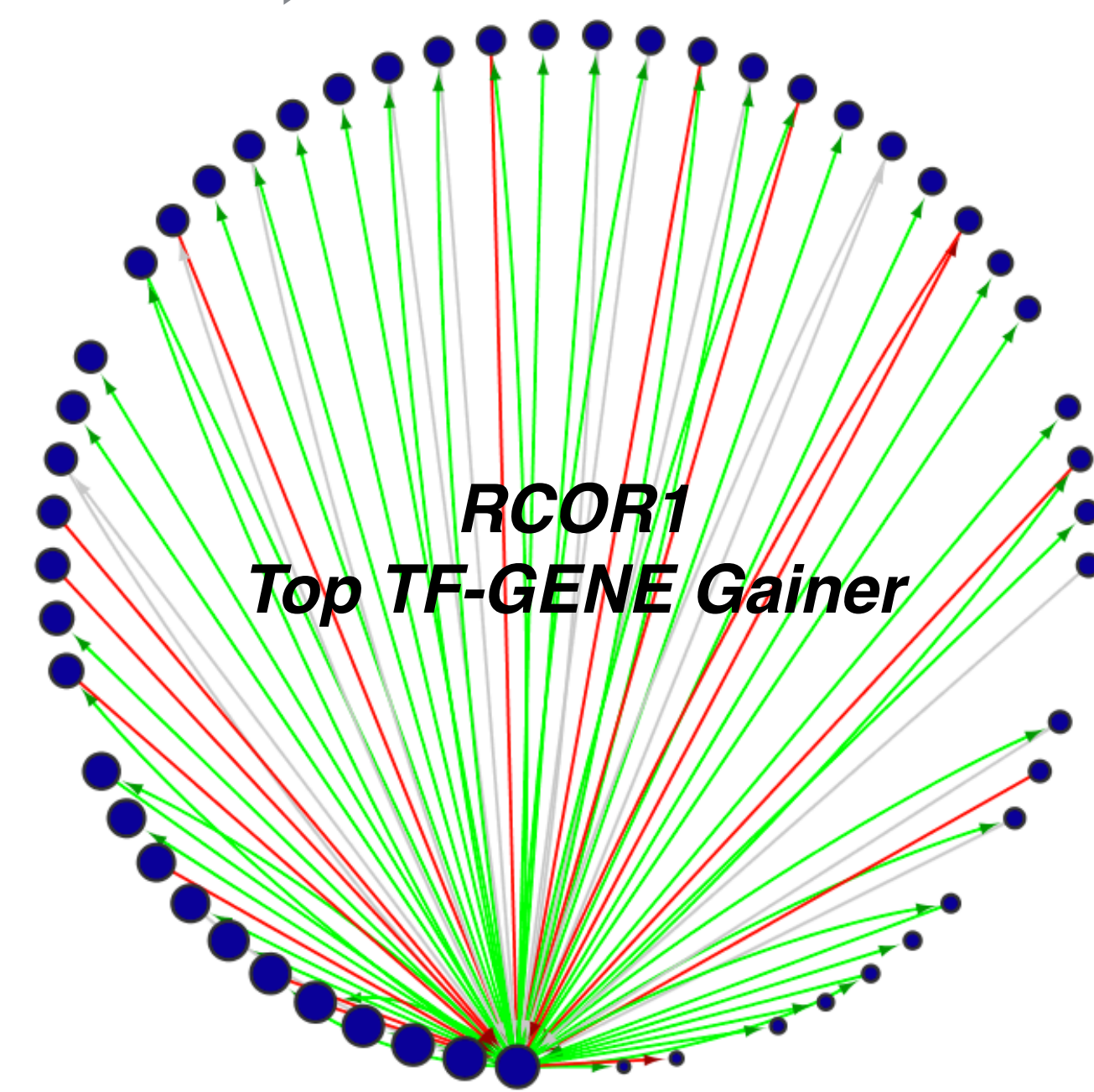
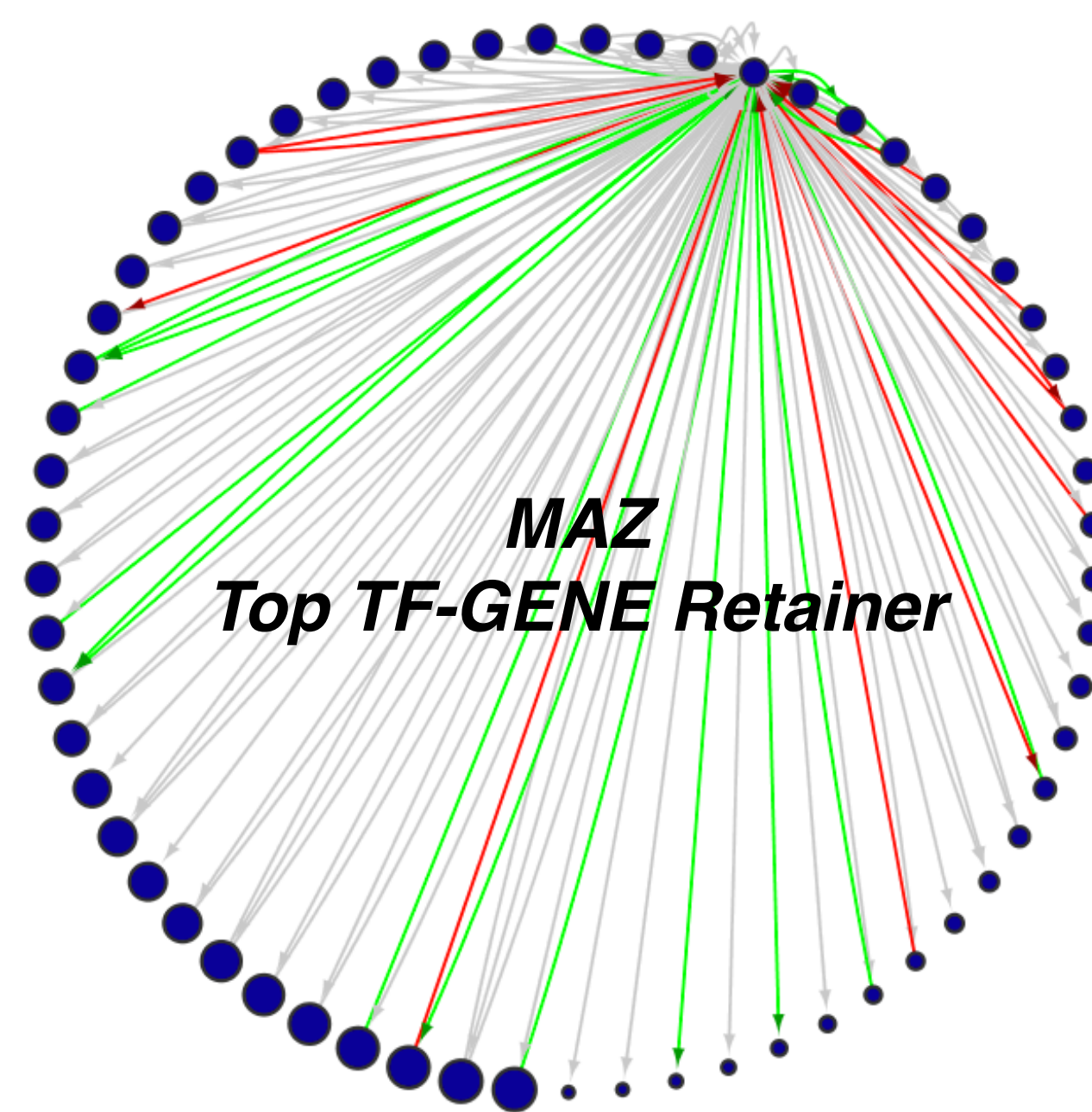
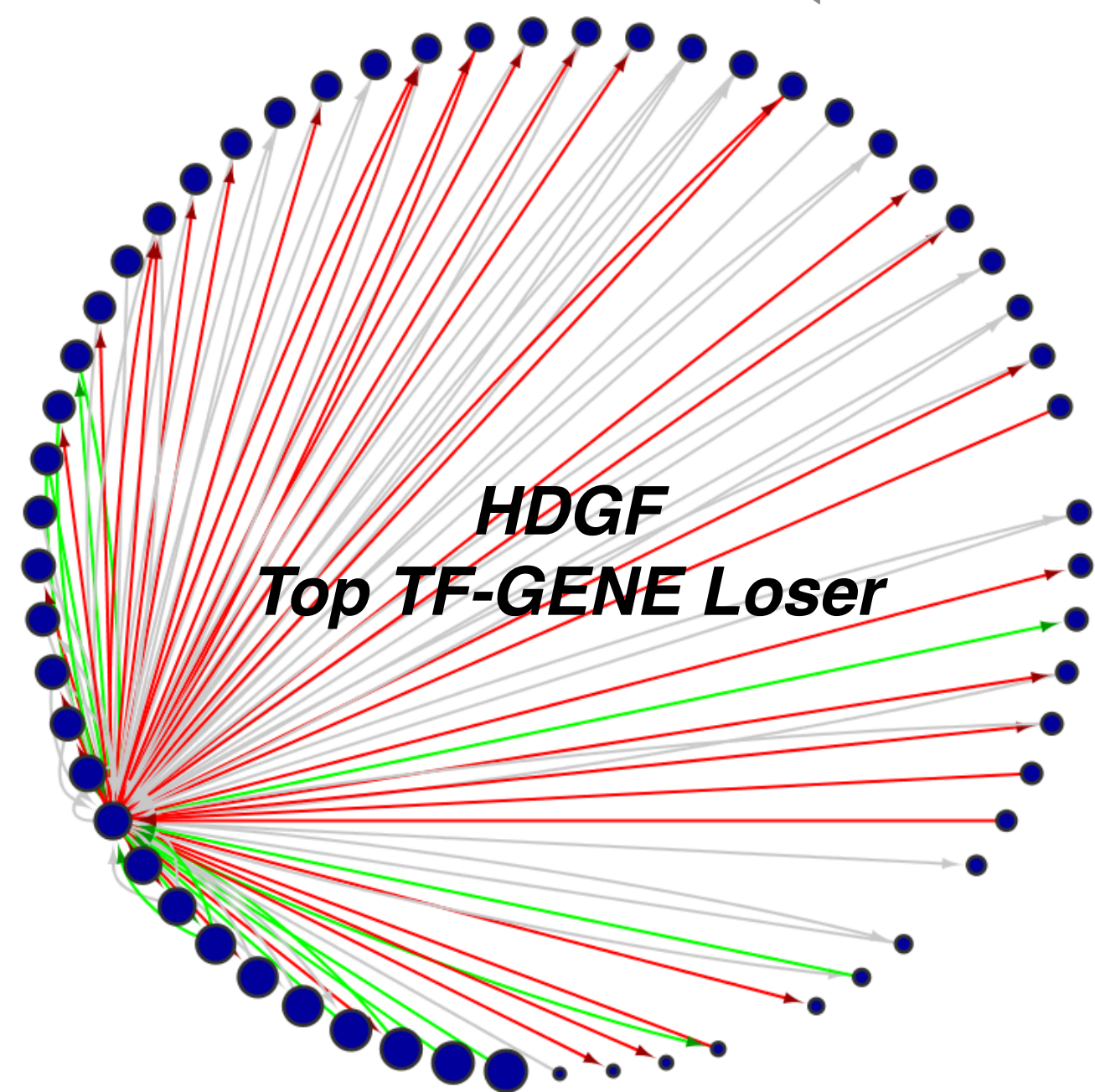
Gainer

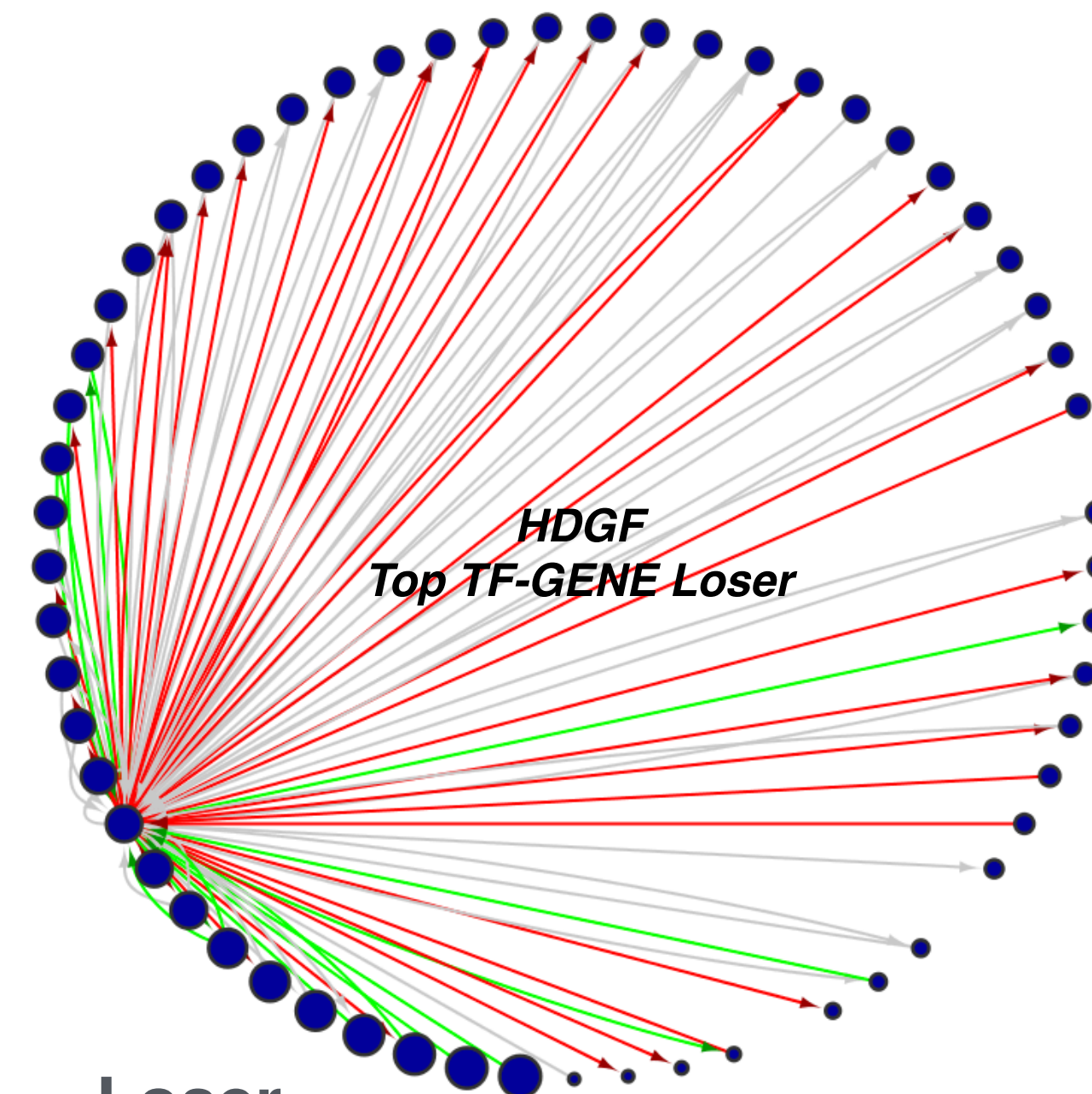
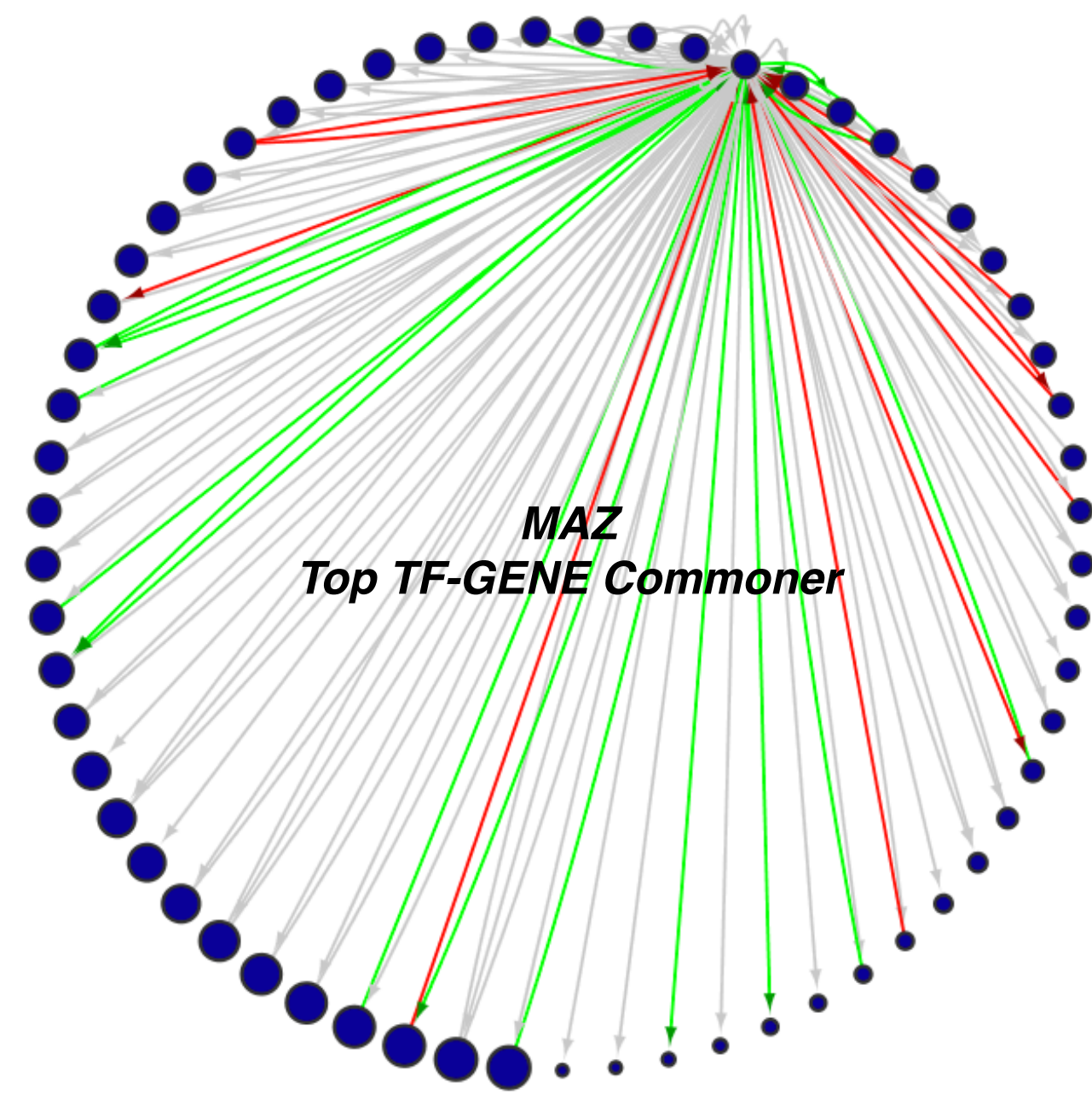
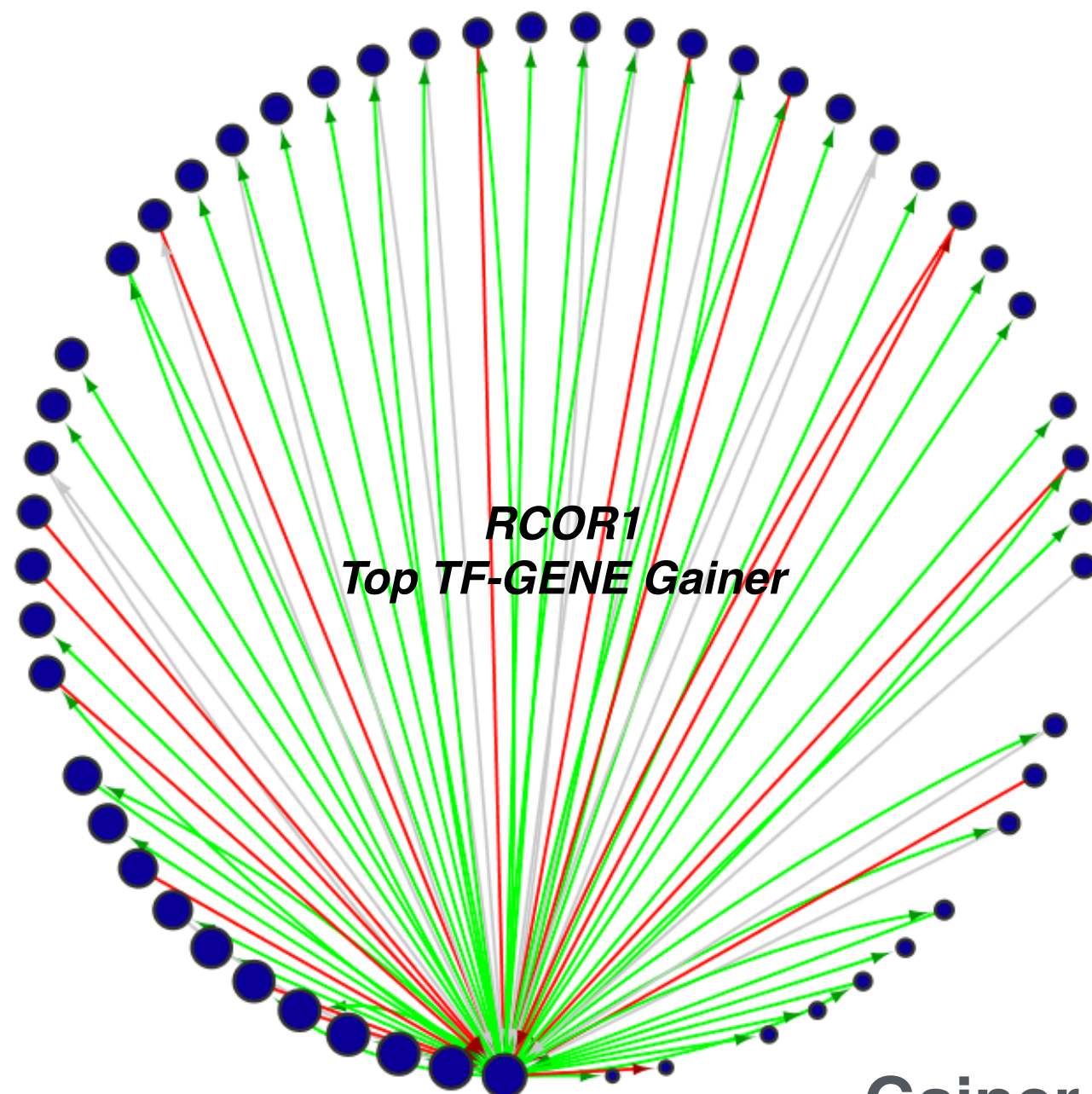
Loser

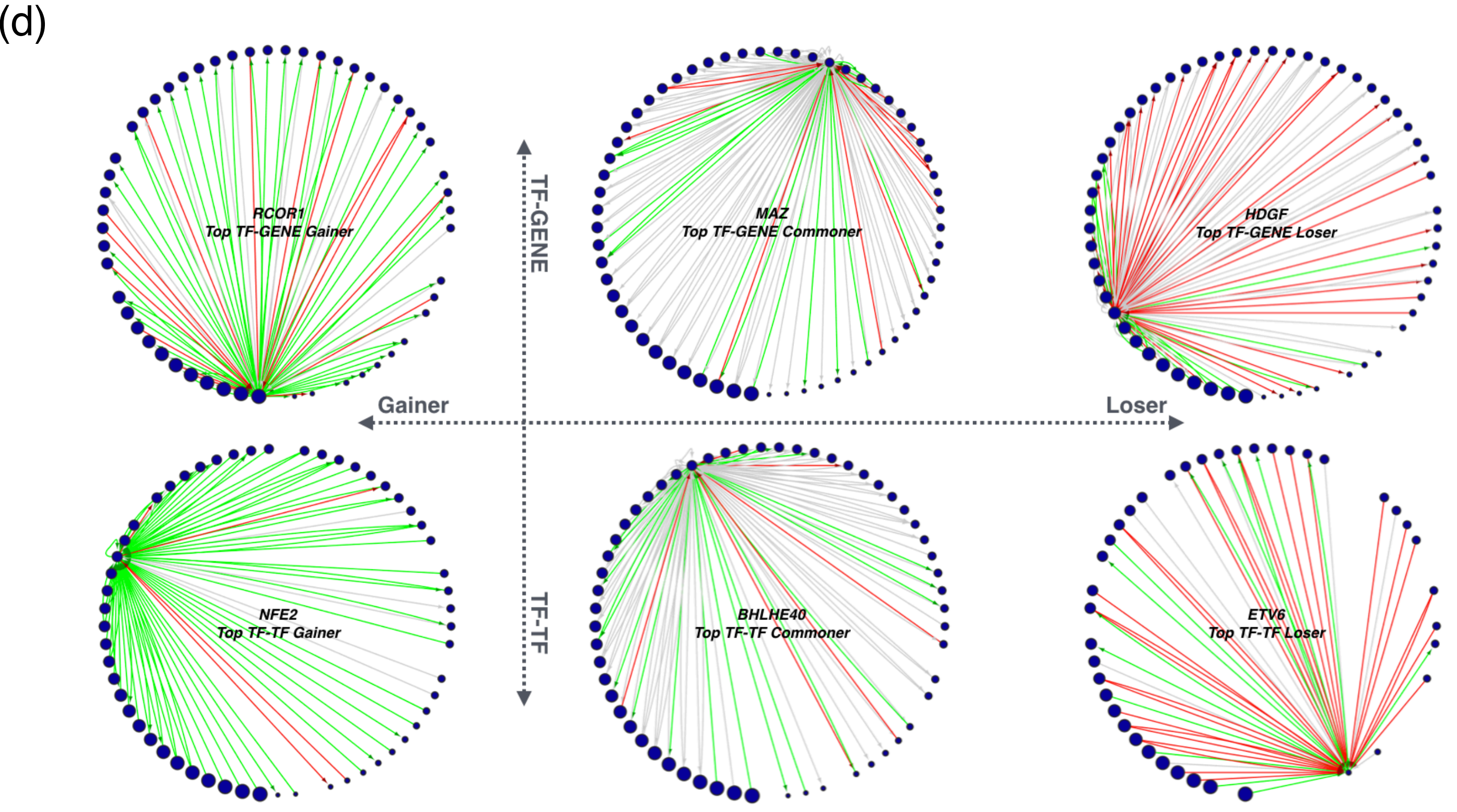
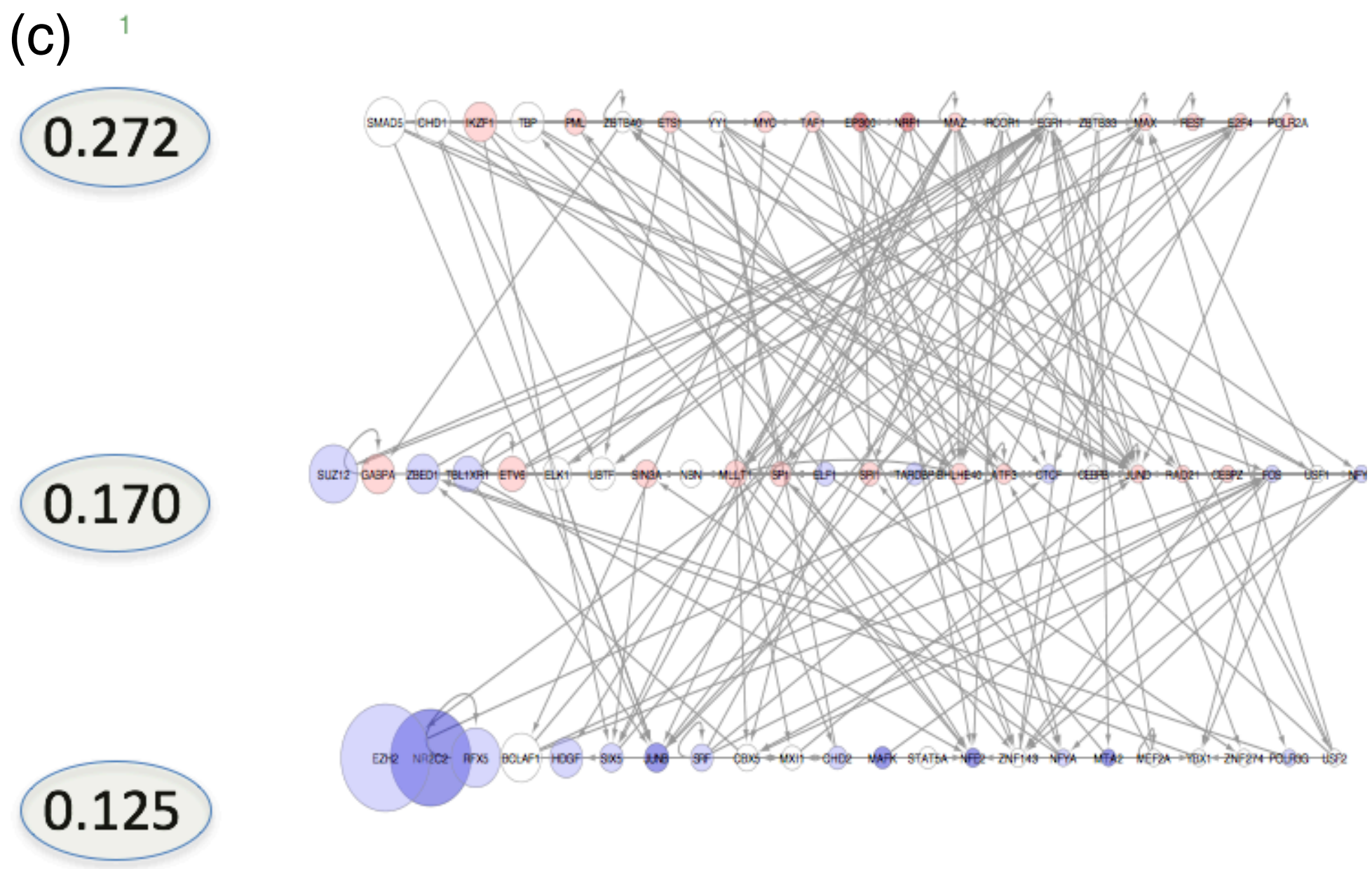
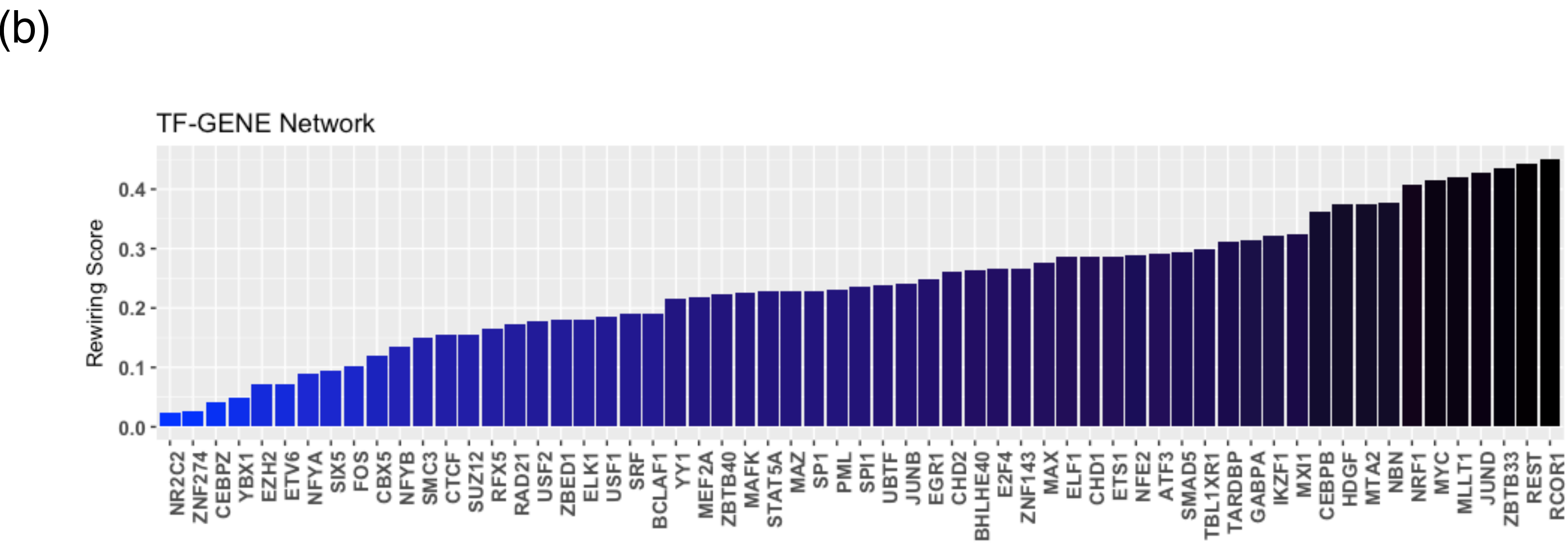
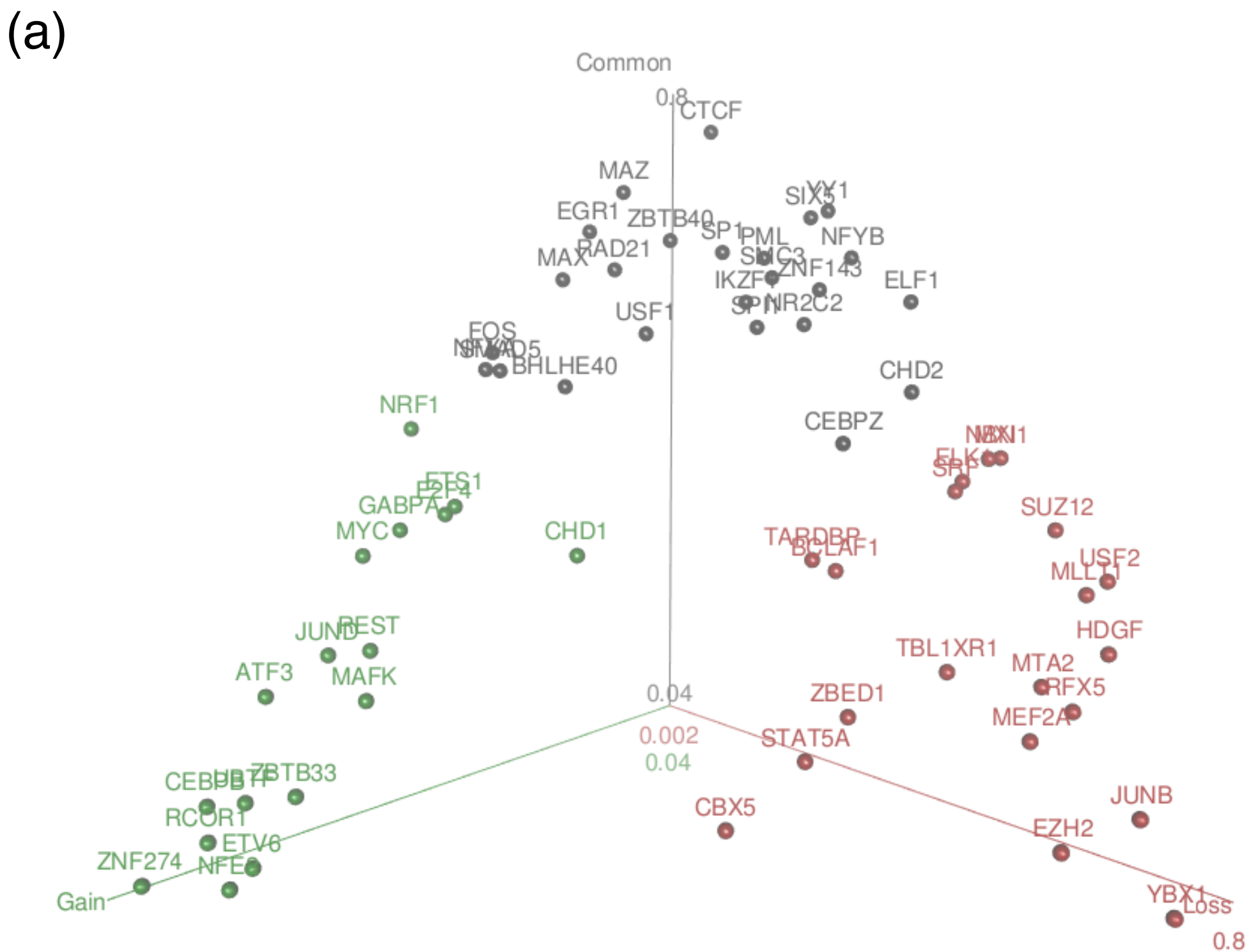
TF-TF



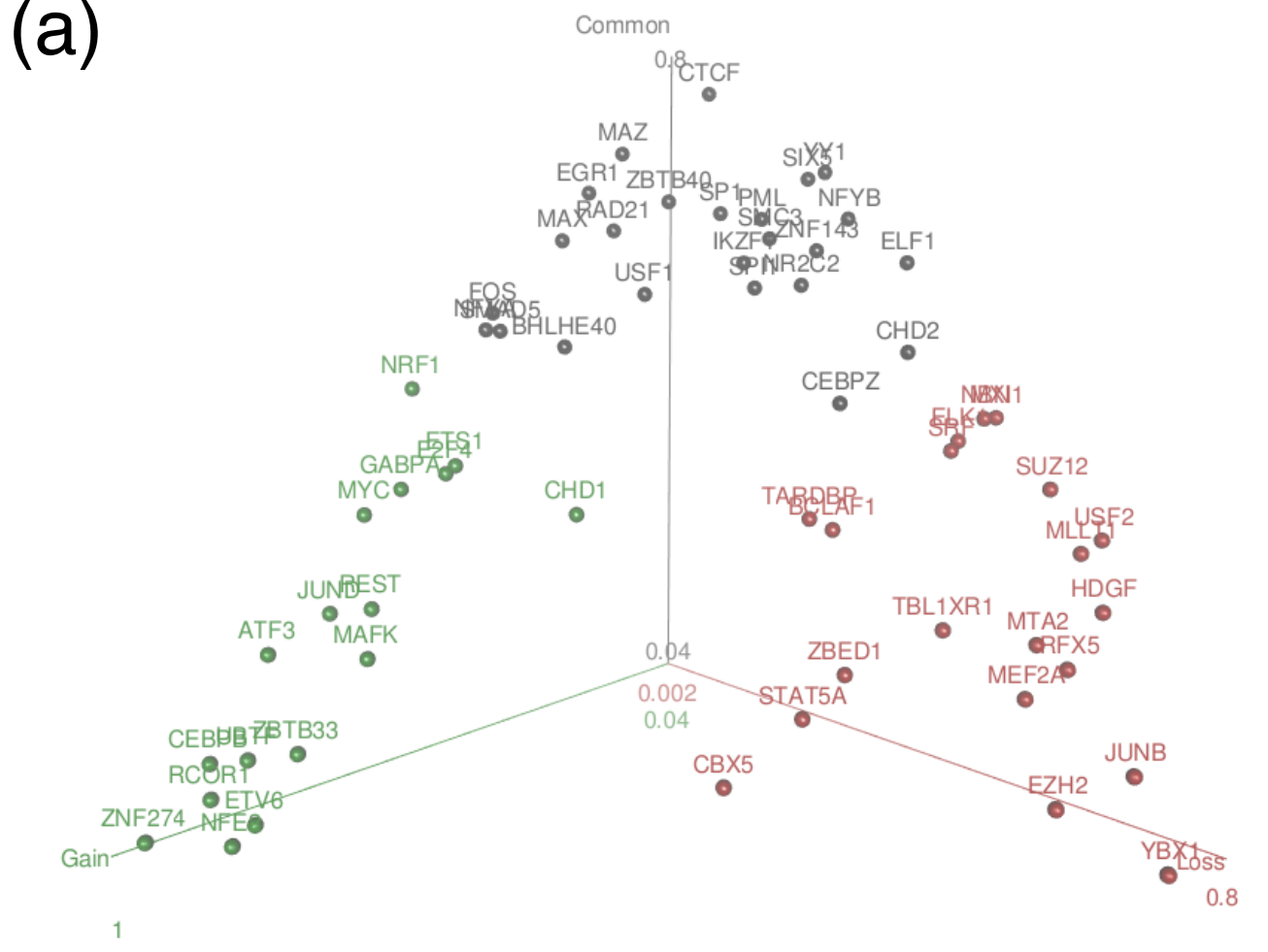
Loser ← *TF-GENE Network* → **Gainer**



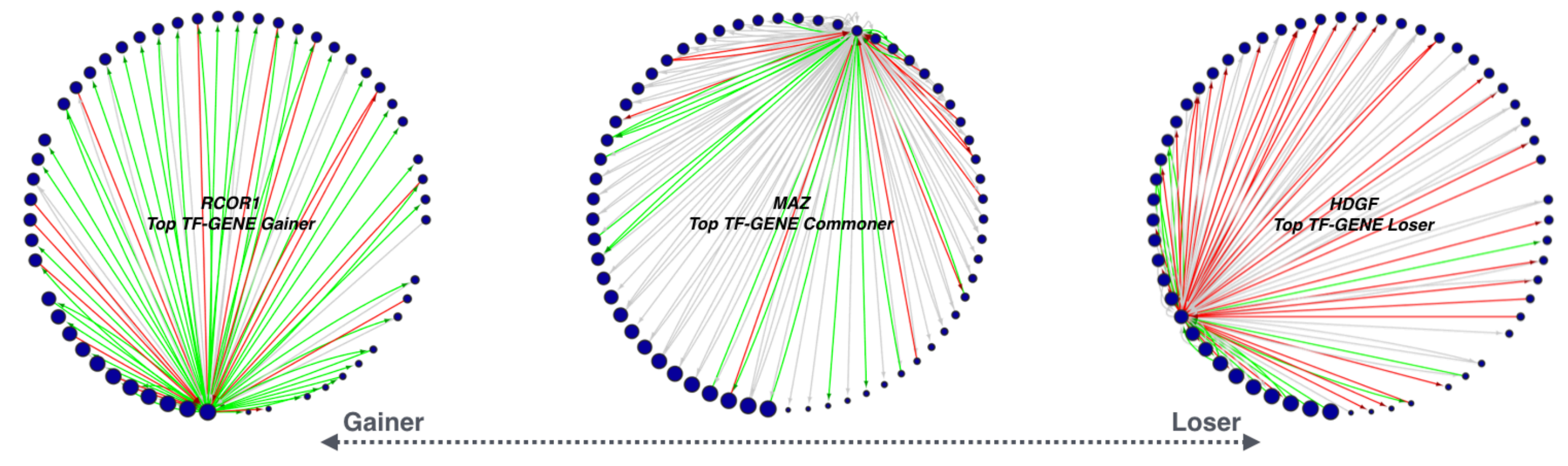




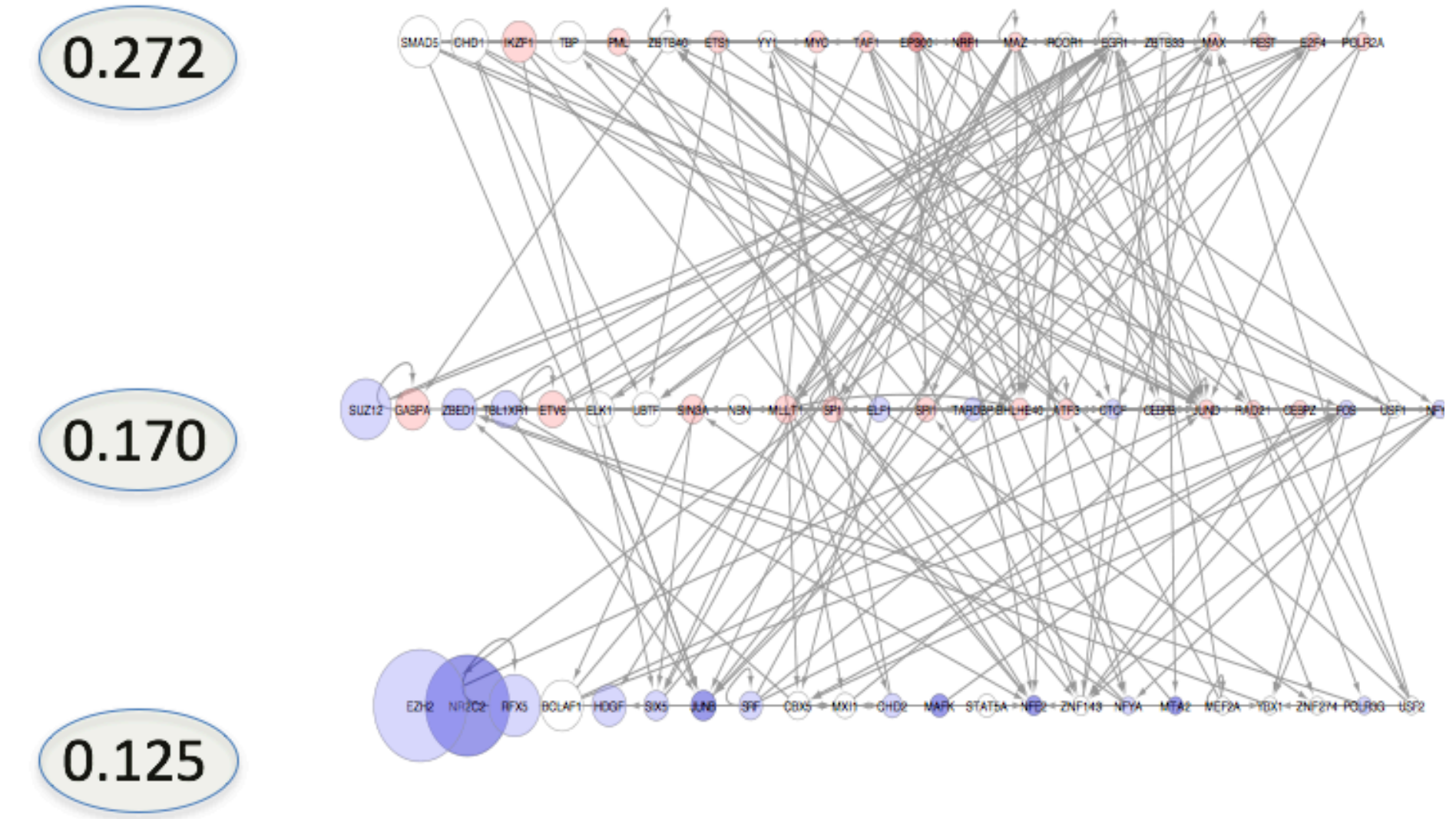
(a)



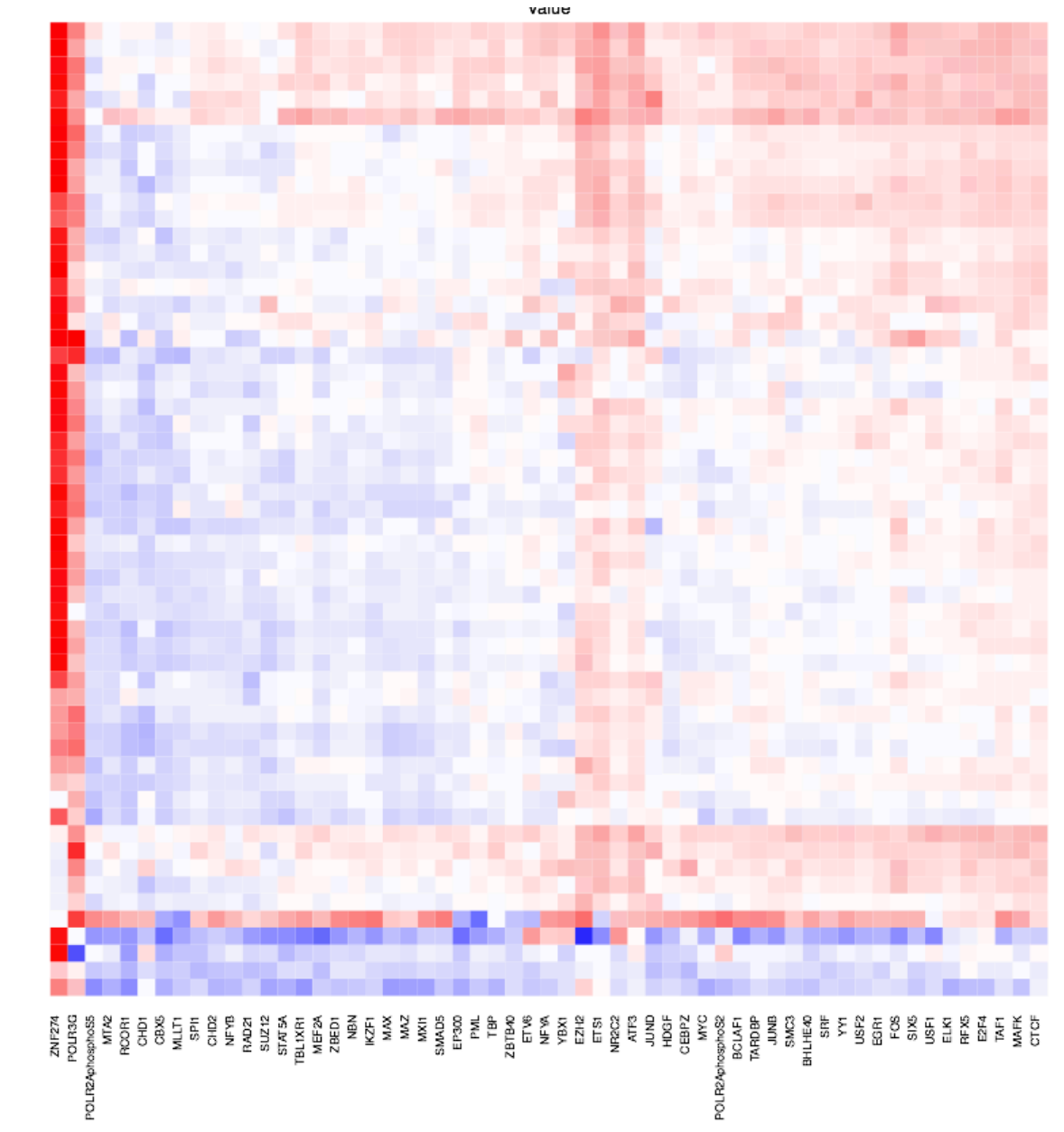
(b)



(c)

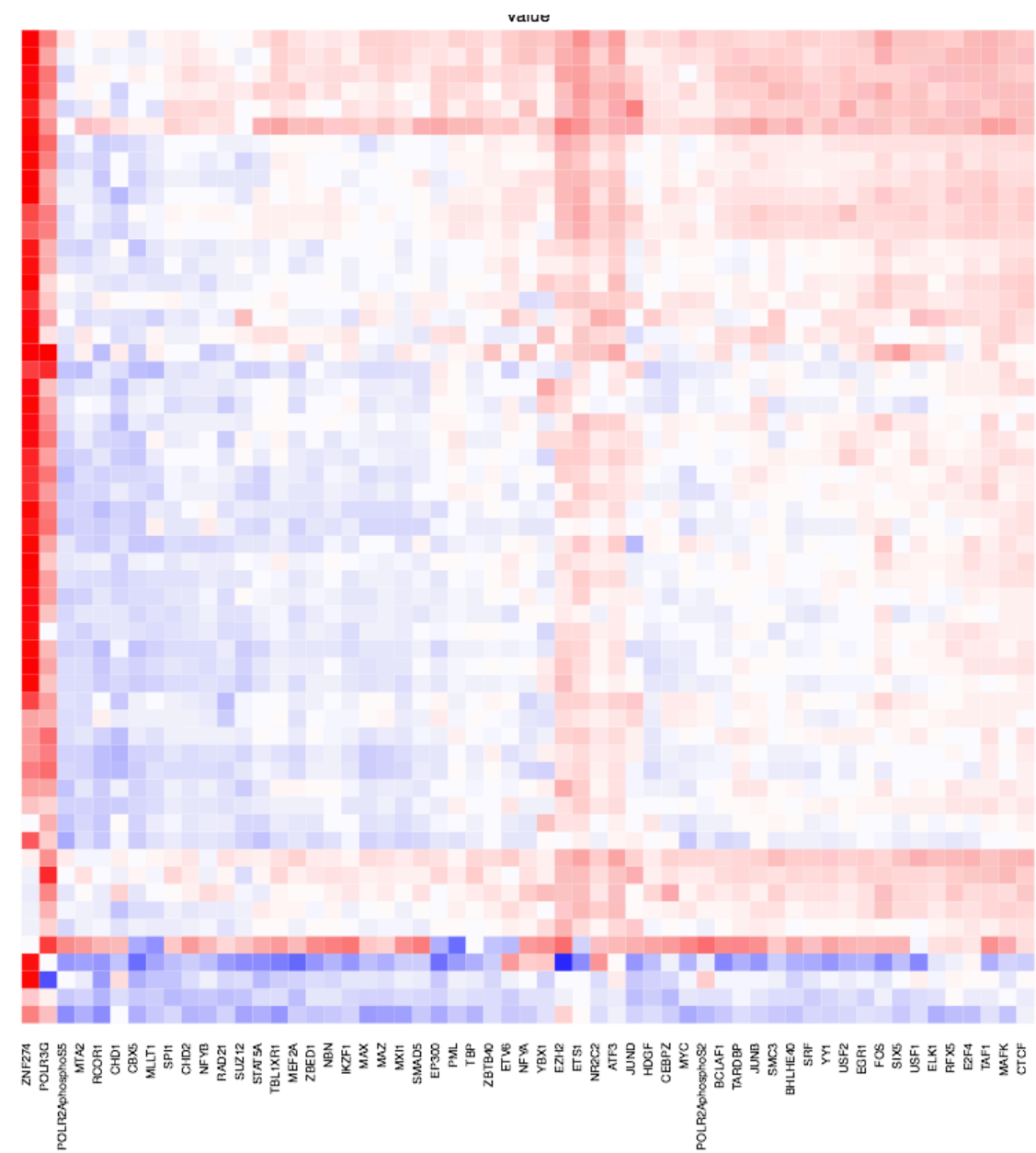


(d)

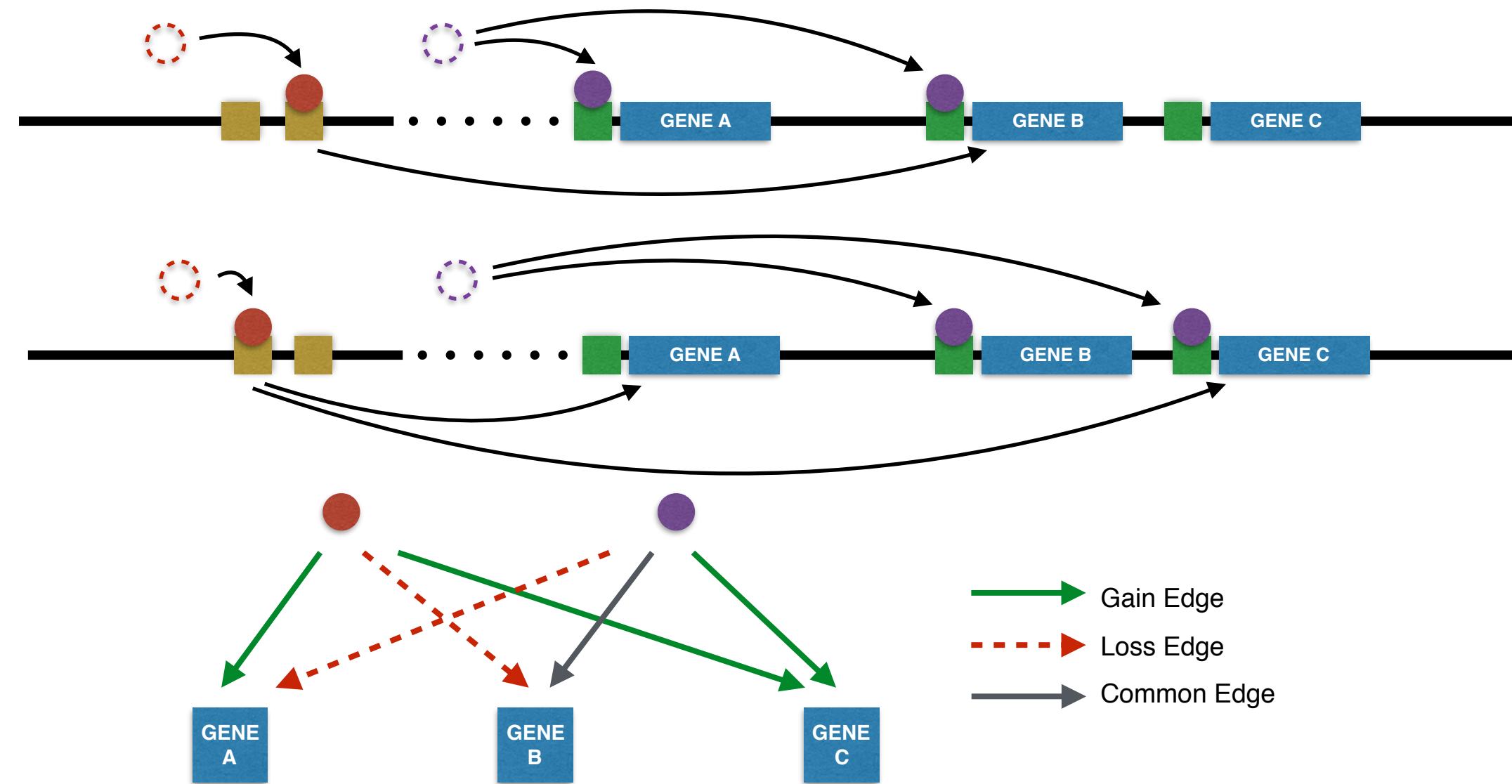


MTA2
STAT5A
MYC
RCOR1
SUZ12
POLR2AphosphoS5
SMI1
NBN
ZBED1
TBL1XR1
MAX
MAZ
IKZF1
SPI1
MEF2A
RAD21
JUNB
FOS
YBX1
NRX2
SRS
ATF3
MAFK
NFYA
NFYB
POLR2AphosphoS2
SMAD3
CHD2
CEBPZ
JUNB
SRF
BHLHE40
USP2
EGR1
YY1
TARDBP
BCLAF1
TAF1
SMC3
CTCF
E2F4
ELK1
RFX5
PML
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EP300
USP1
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POLR3G
EZH2
ETV1
CHD1

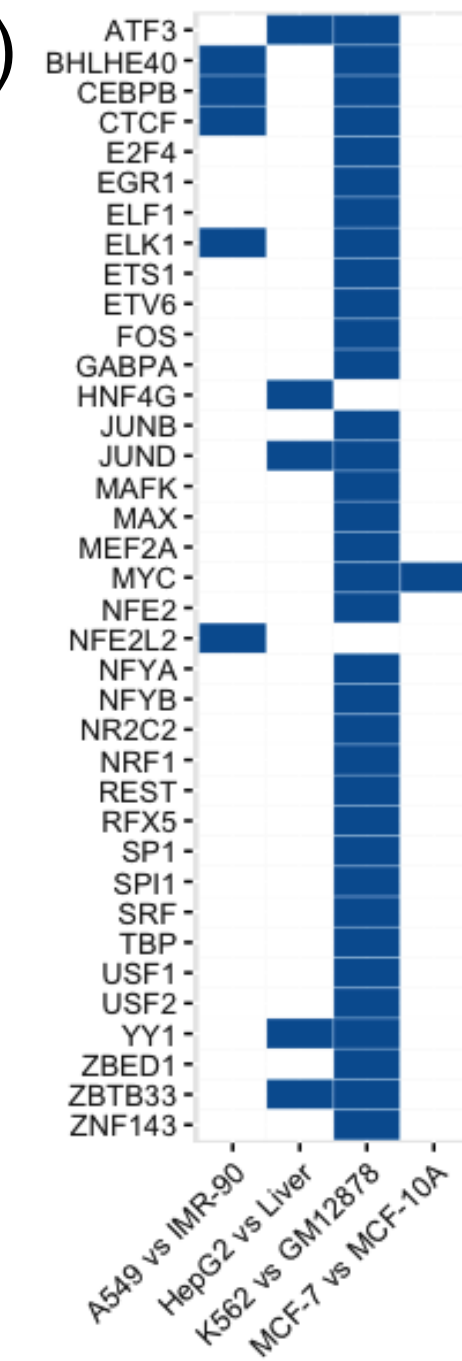
(a)



(b)

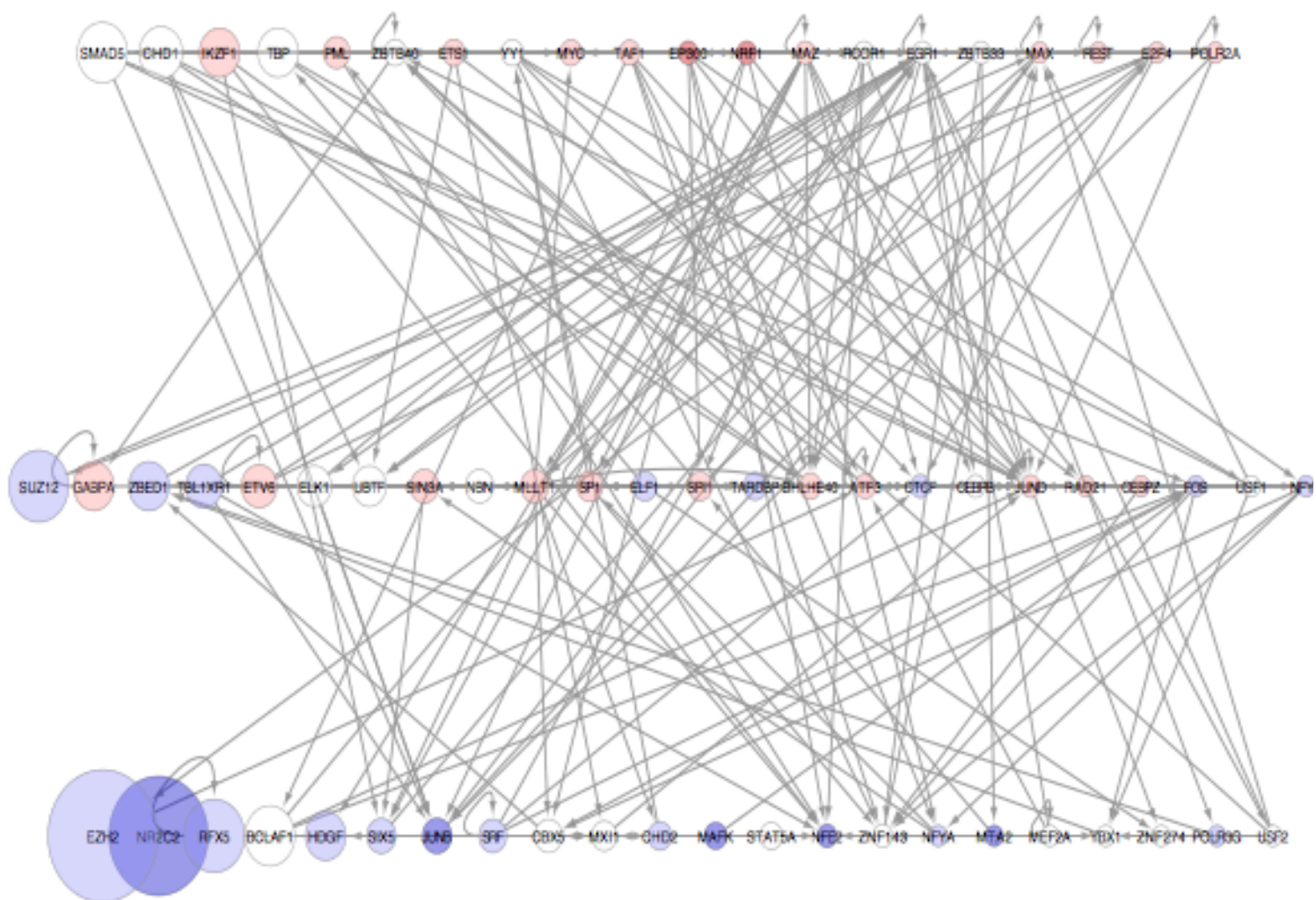


(c)



(d)

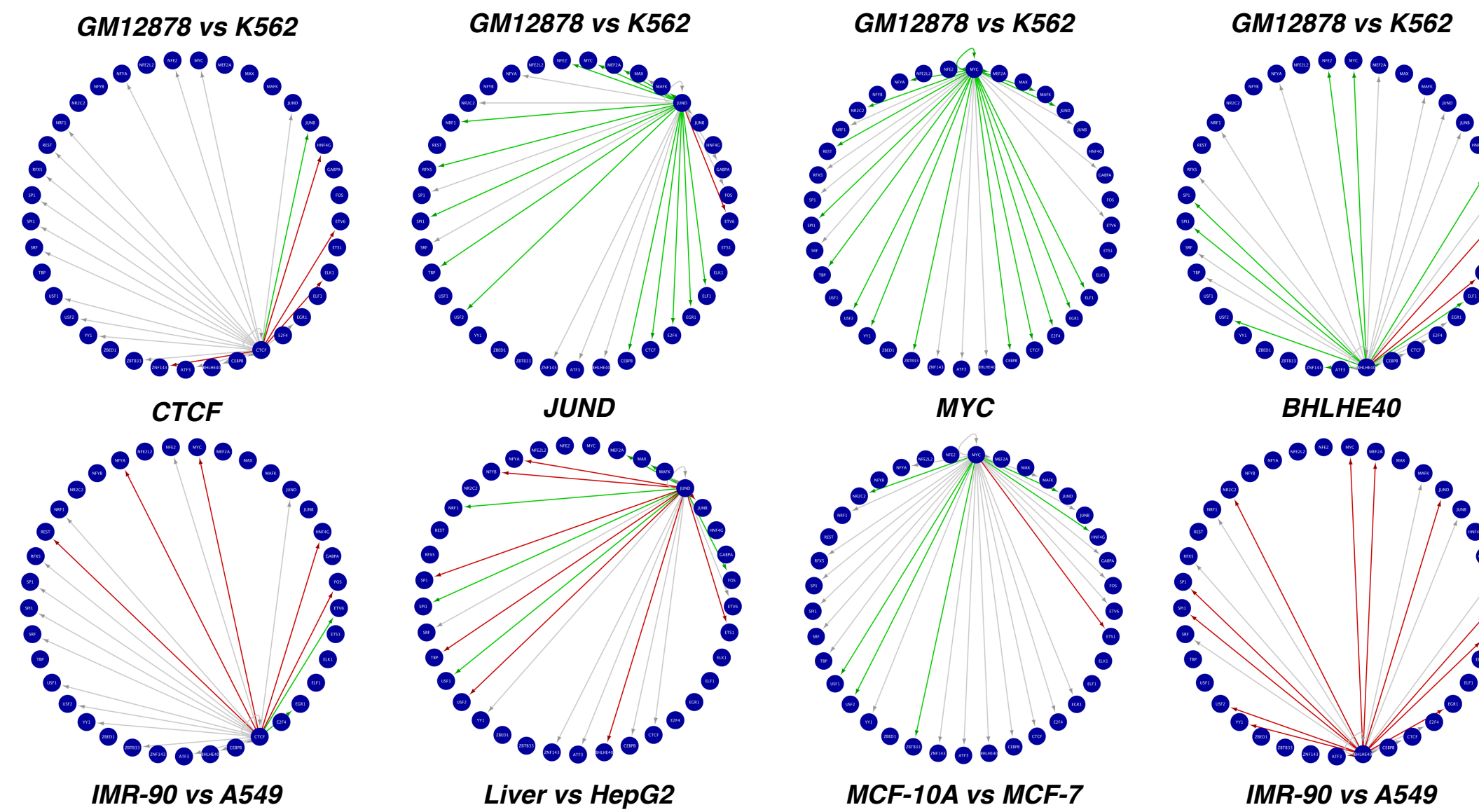
0.272



0.170

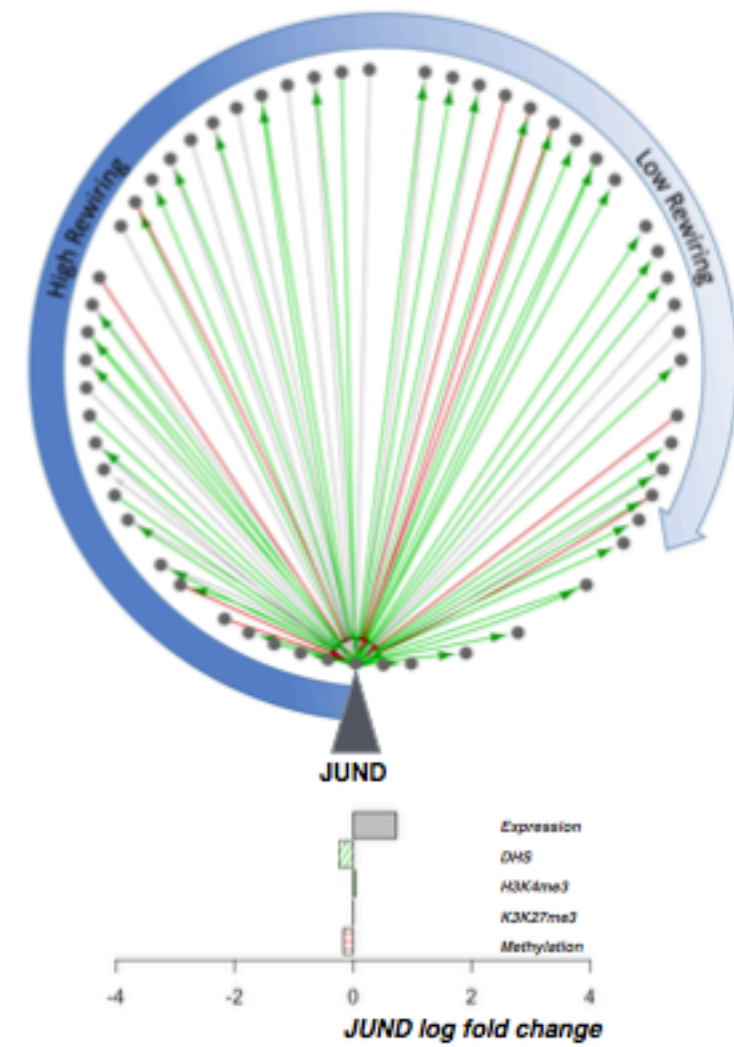
0.125

(e)

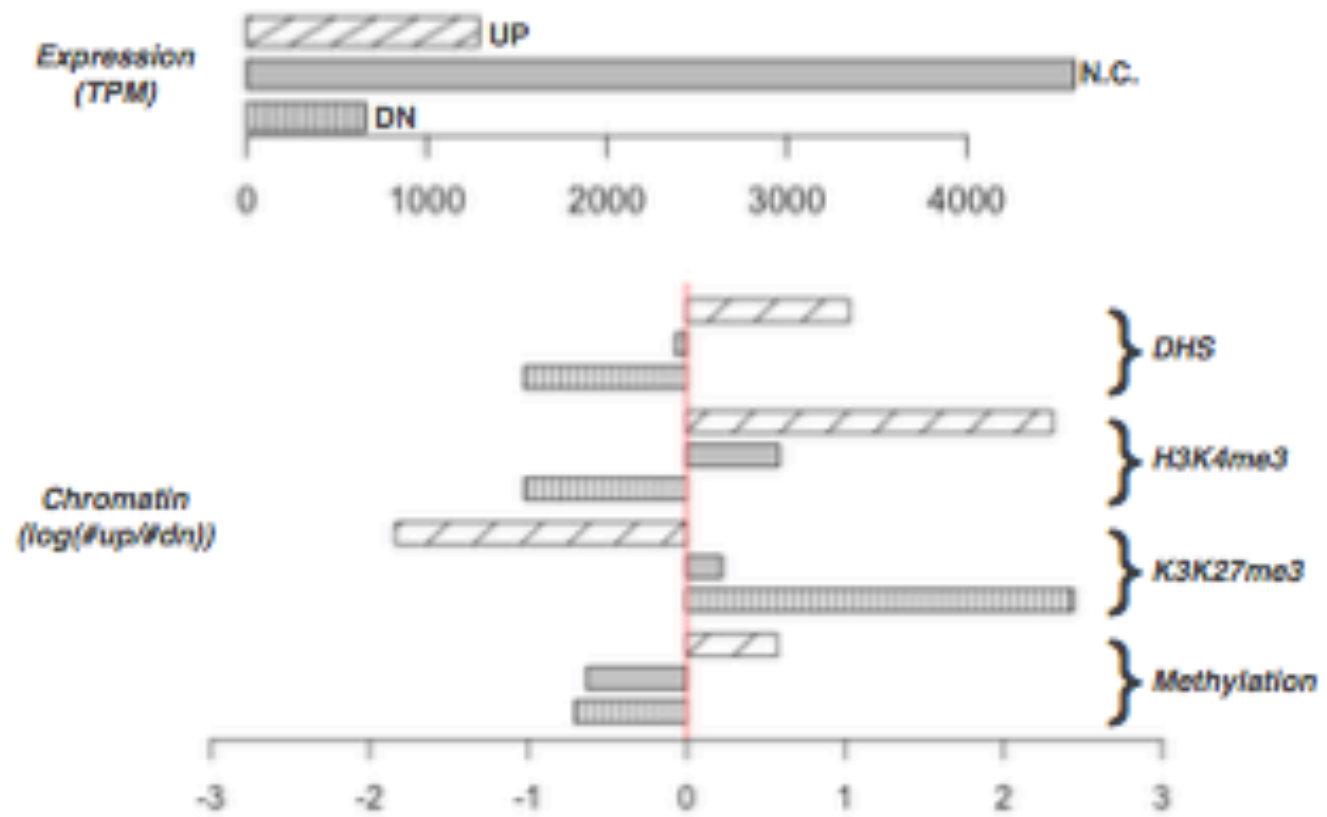


Overall Gene Target (n=15,189)

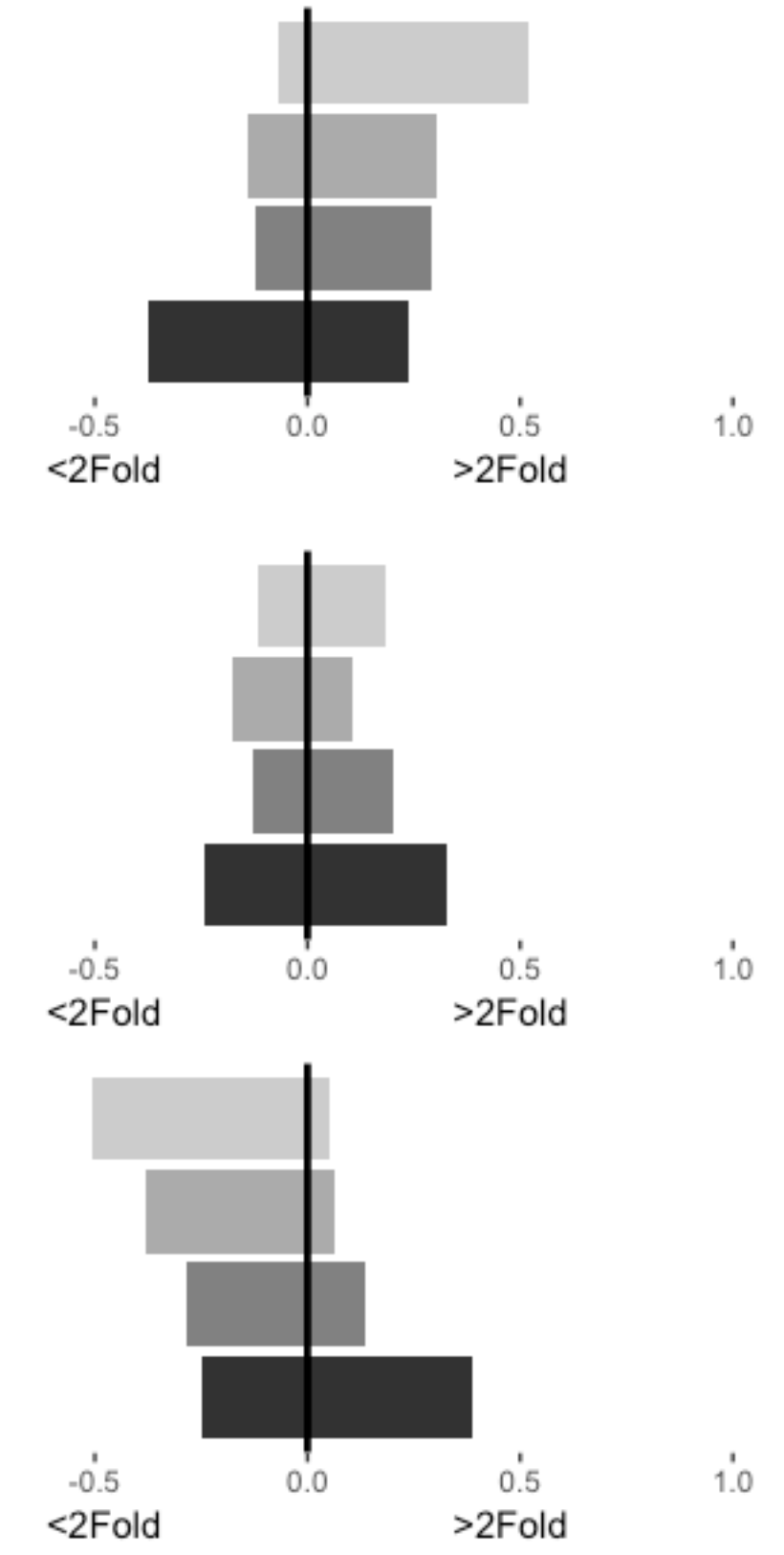
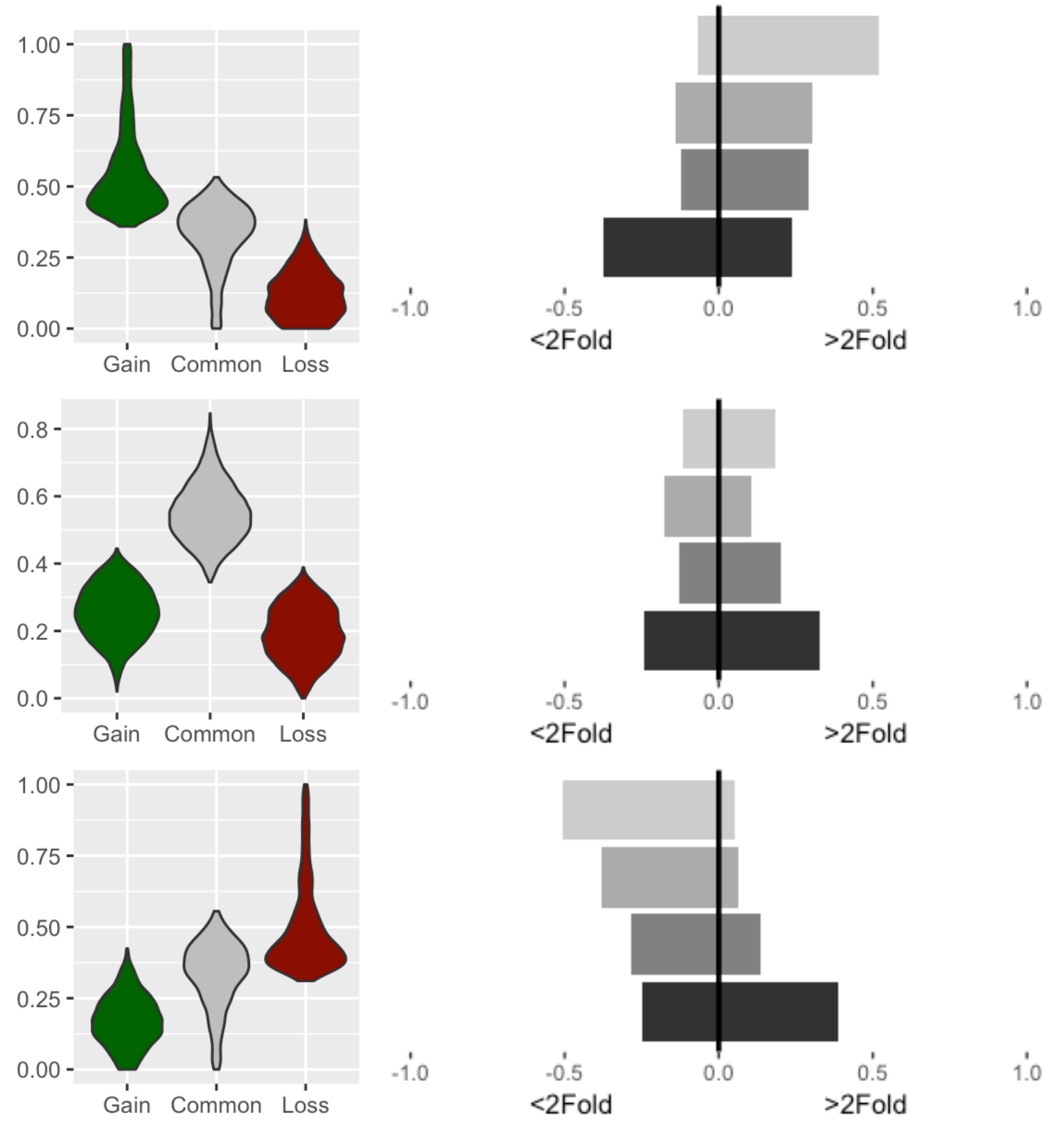
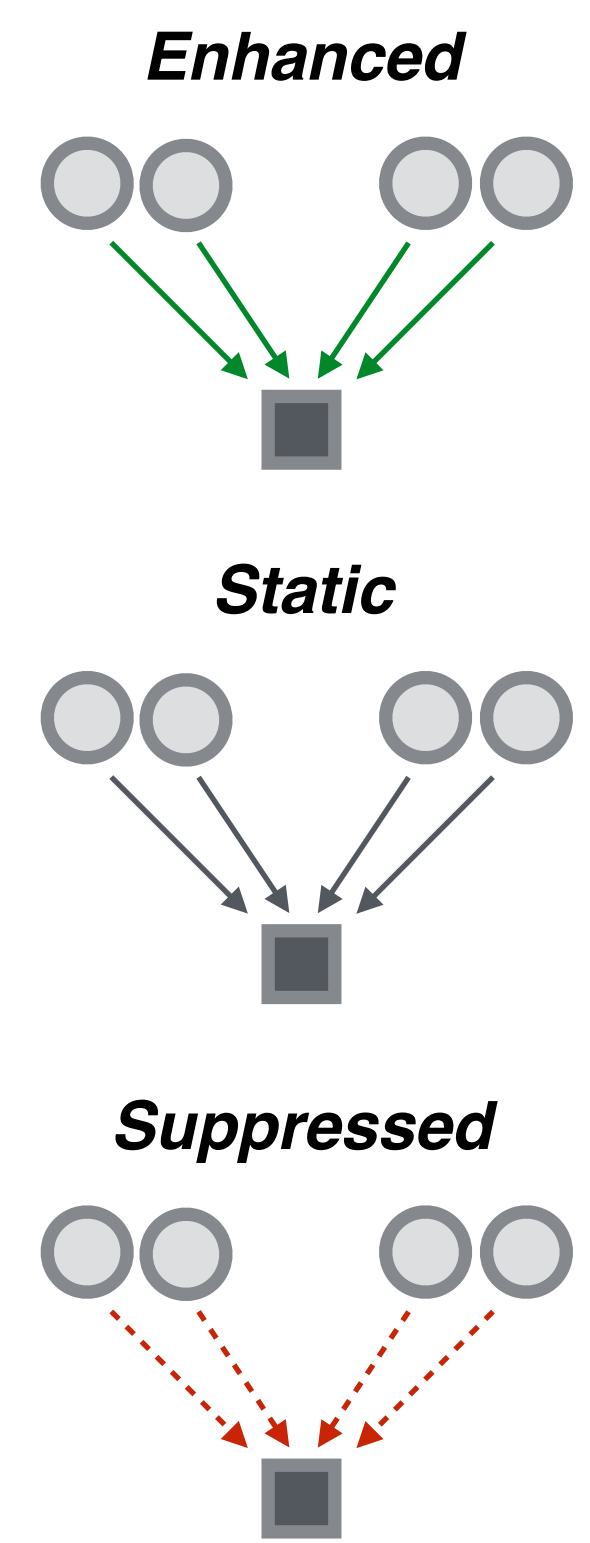
Expression (TPM)	UP			NC			DN		
n	2442			10294			2453		
%	16.1%			67.8%			16.1%		
DHS (TSS Cov) active	UP	NC	DN	UP	NC	DN	UP	NC	DN
n	622	1622	198	1280	7723	1291	108	1430	915
%	25.5%	66.4%	8.1%	12.4%	75.0%	12.5%	4.4%	58.3%	37.3%
H3K4me3 (TSS Cov) active promoter	UP	NC	DN	UP	NC	DN	UP	NC	DN
n	569	1817	56	801	8891	602	71	1753	629
%	23.3%	74.4%	2.3%	7.8%	86.4%	5.8%	2.9%	71.5%	25.6%
H3K27me3 (TSS Cov) inactive promoter	UP	NC	DN	UP	NC	DN	UP	NC	DN
n	25	2278	139	472	9446	376	237	2181	35
%	1.0%	93.3%	5.7%	4.6%	91.8%	3.7%	9.7%	88.9%	1.4%
Methylation (Sig Avg) repressive	UP	NC	DN	UP	NC	DN	UP	NC	DN
n	254	1994	194	741	8491	1062	117	2037	299
%	10.4%	81.7%	7.9%	7.2%	82.5%	10.3%	4.8%	83.0%	12.2%
Mutation ext.gene count	count > 1	has mut	no mut	count > 1	has mut	no mut	count > 1	has mut	no mut
	108	535	1907	402	2053	8241	117	548	1905
	4.4%	21.9%	78.1%	3.9%	19.9%	80.1%	4.8%	22.3%	77.7%
Mutation ext.gene pval < 0.05	29			138			57		
	1.2%			1.3%			2.3%		



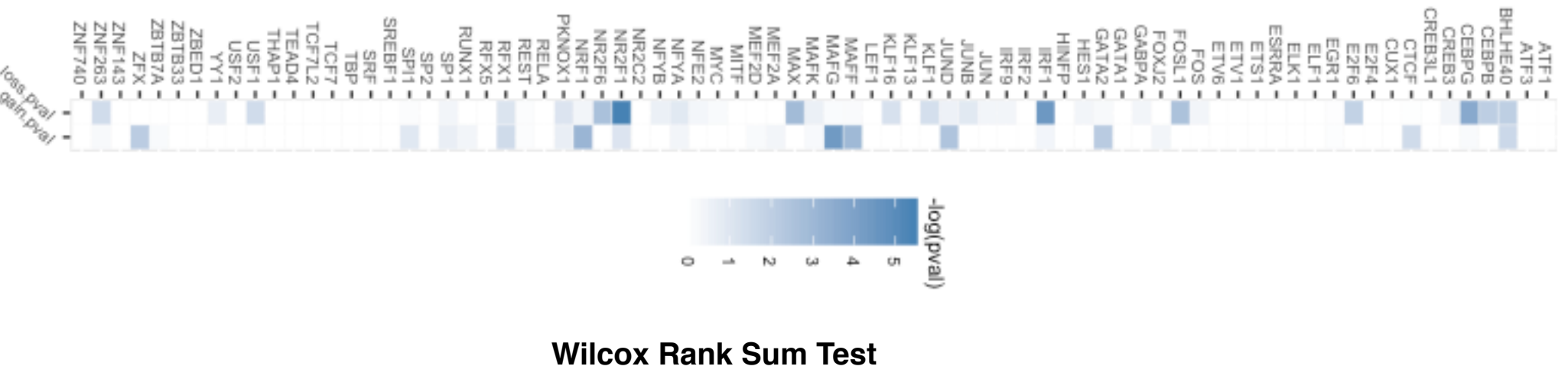
JUND Gained Targets



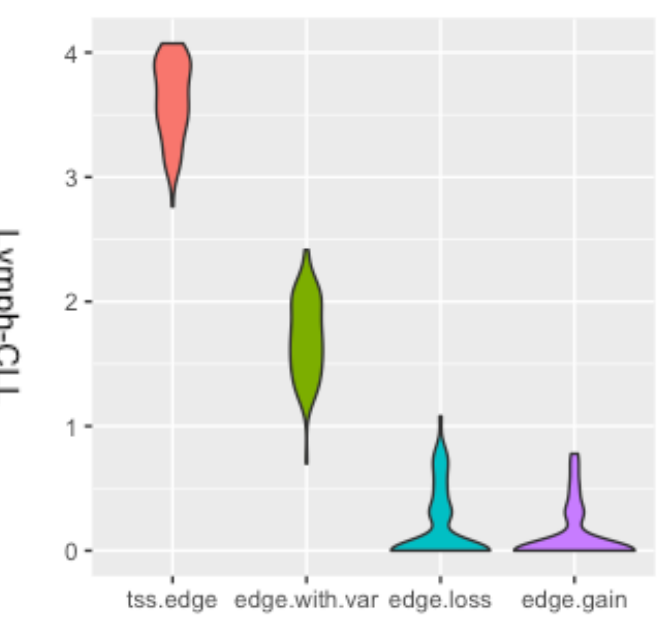
(a)



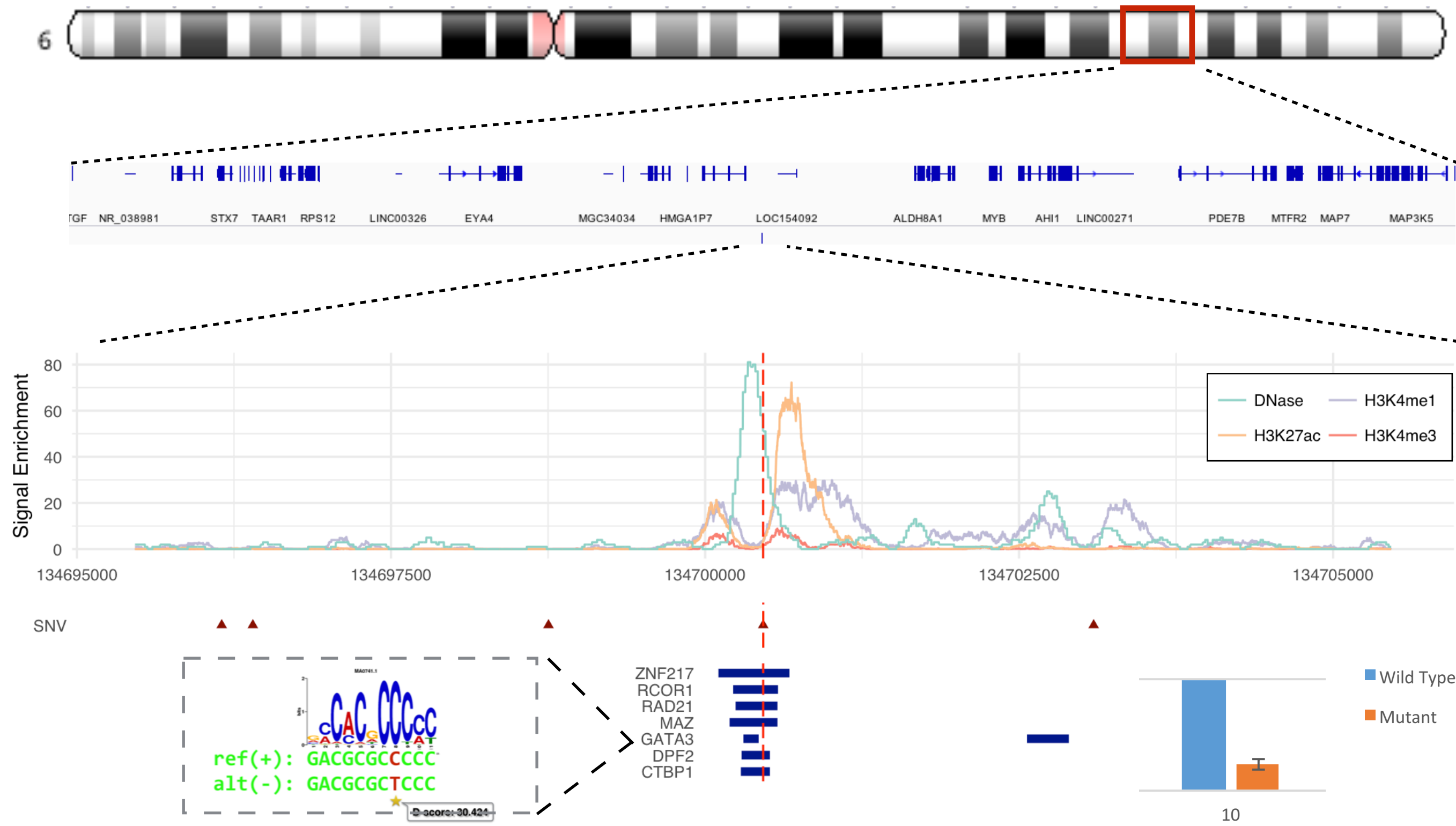
(b)



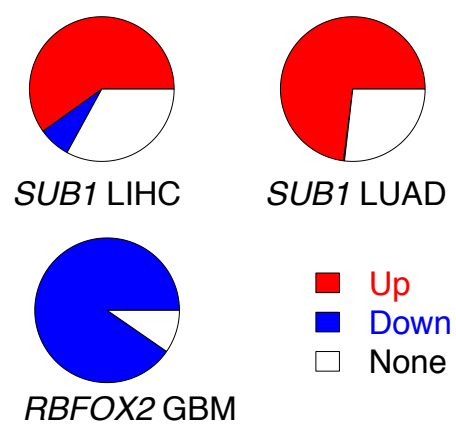
(c)



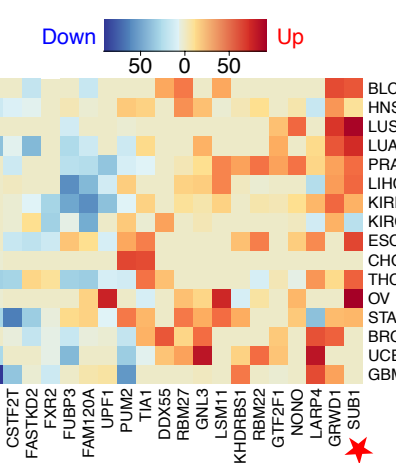
(a)



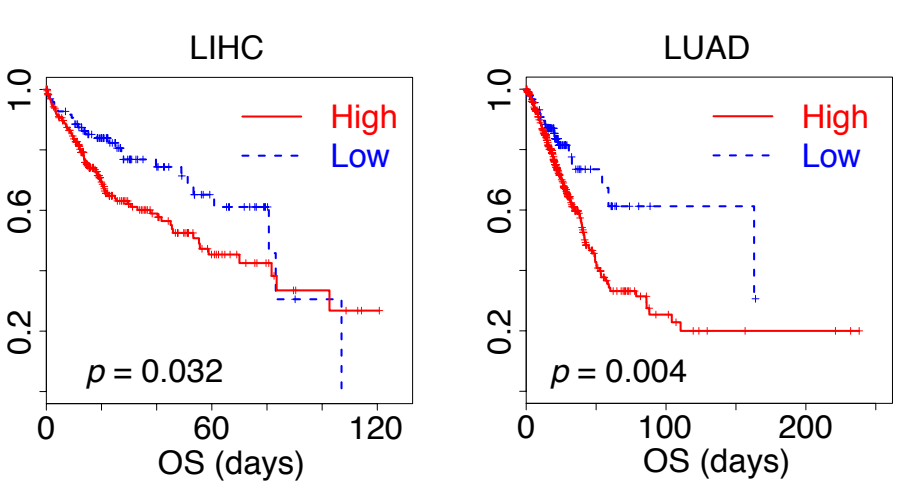
A



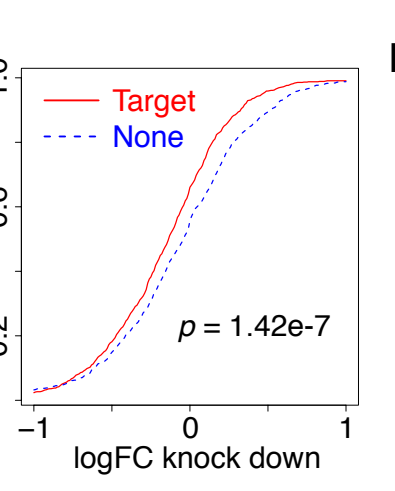
B



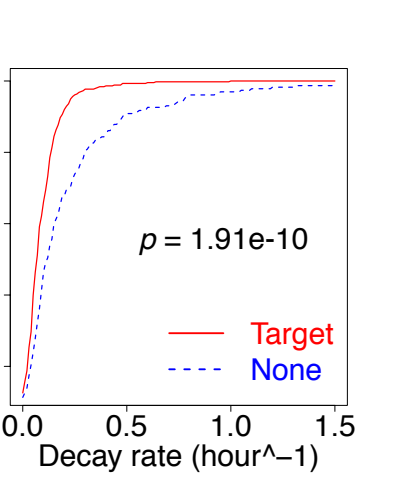
C

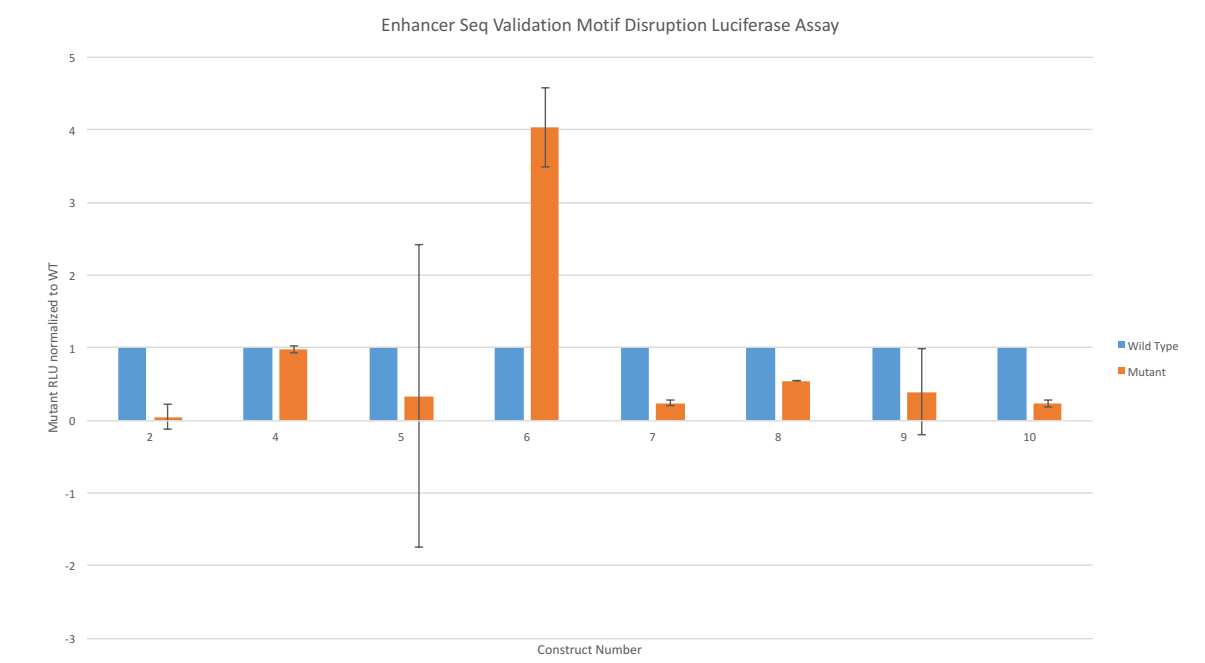


D

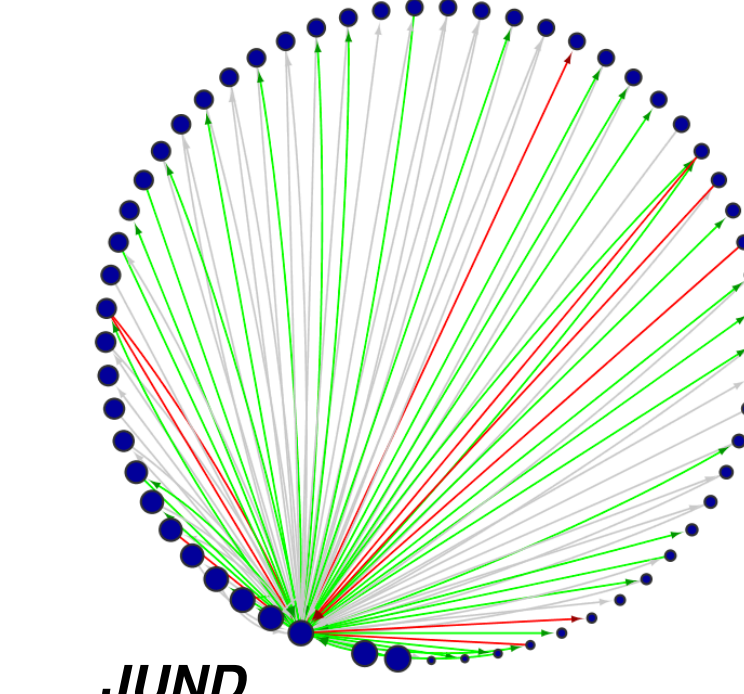
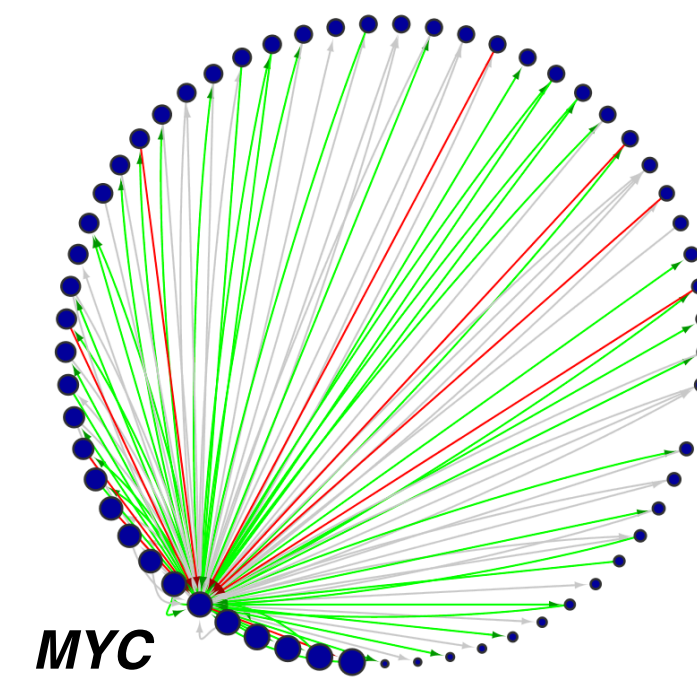
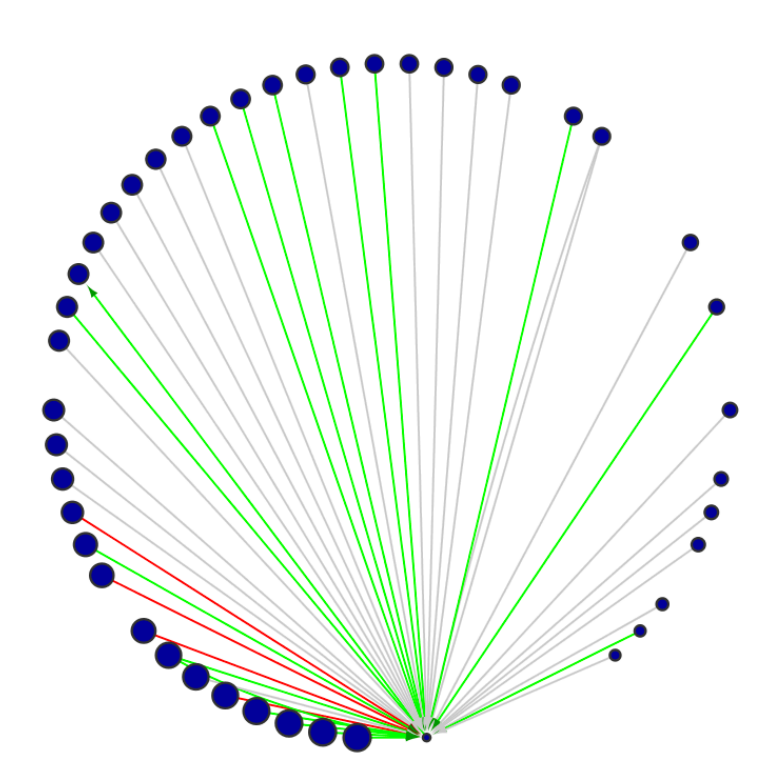
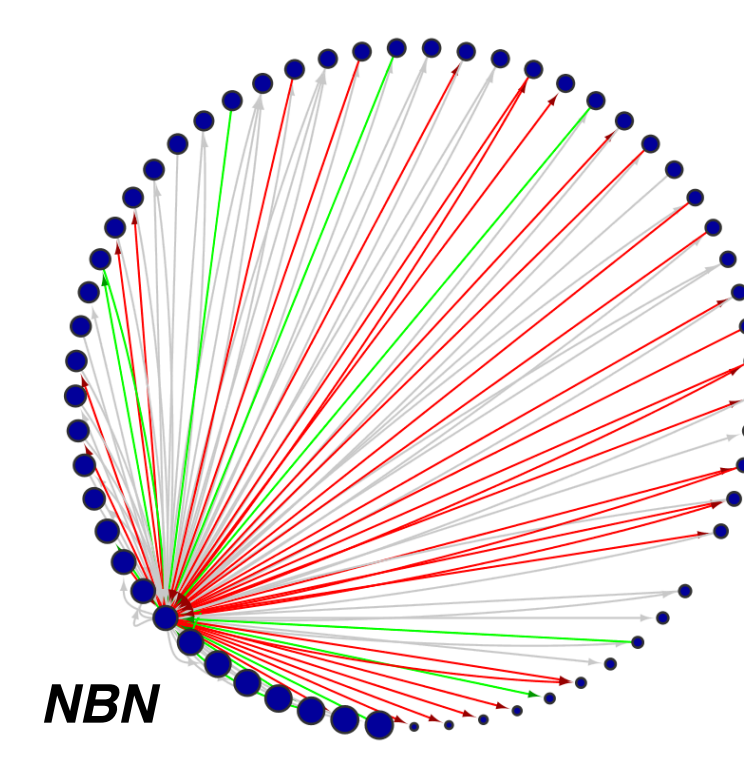
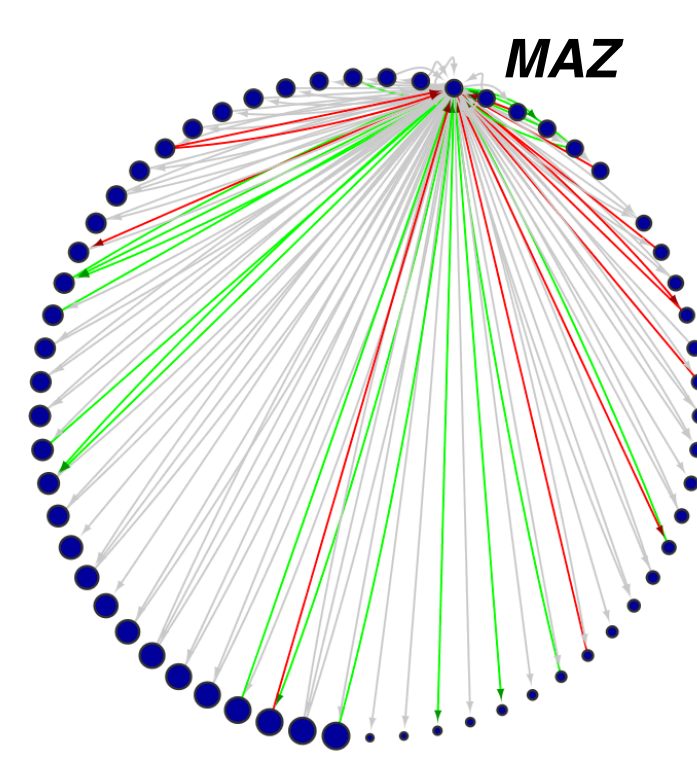


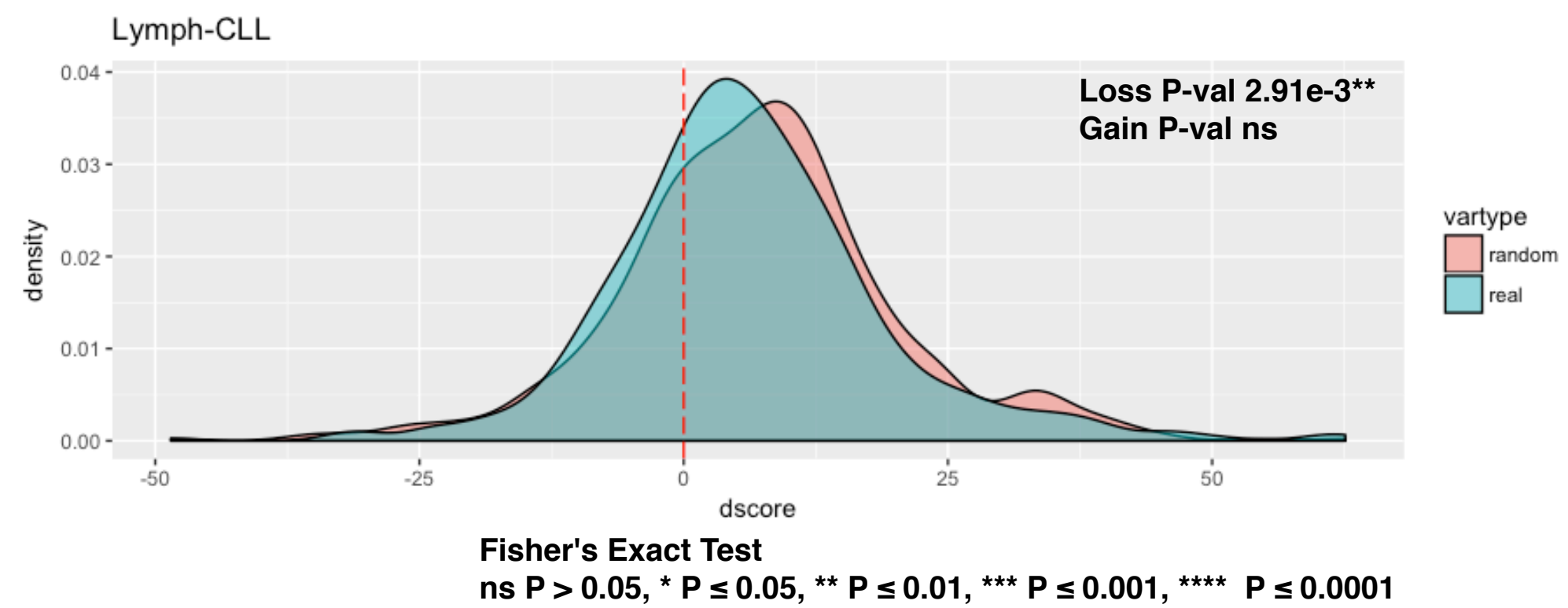
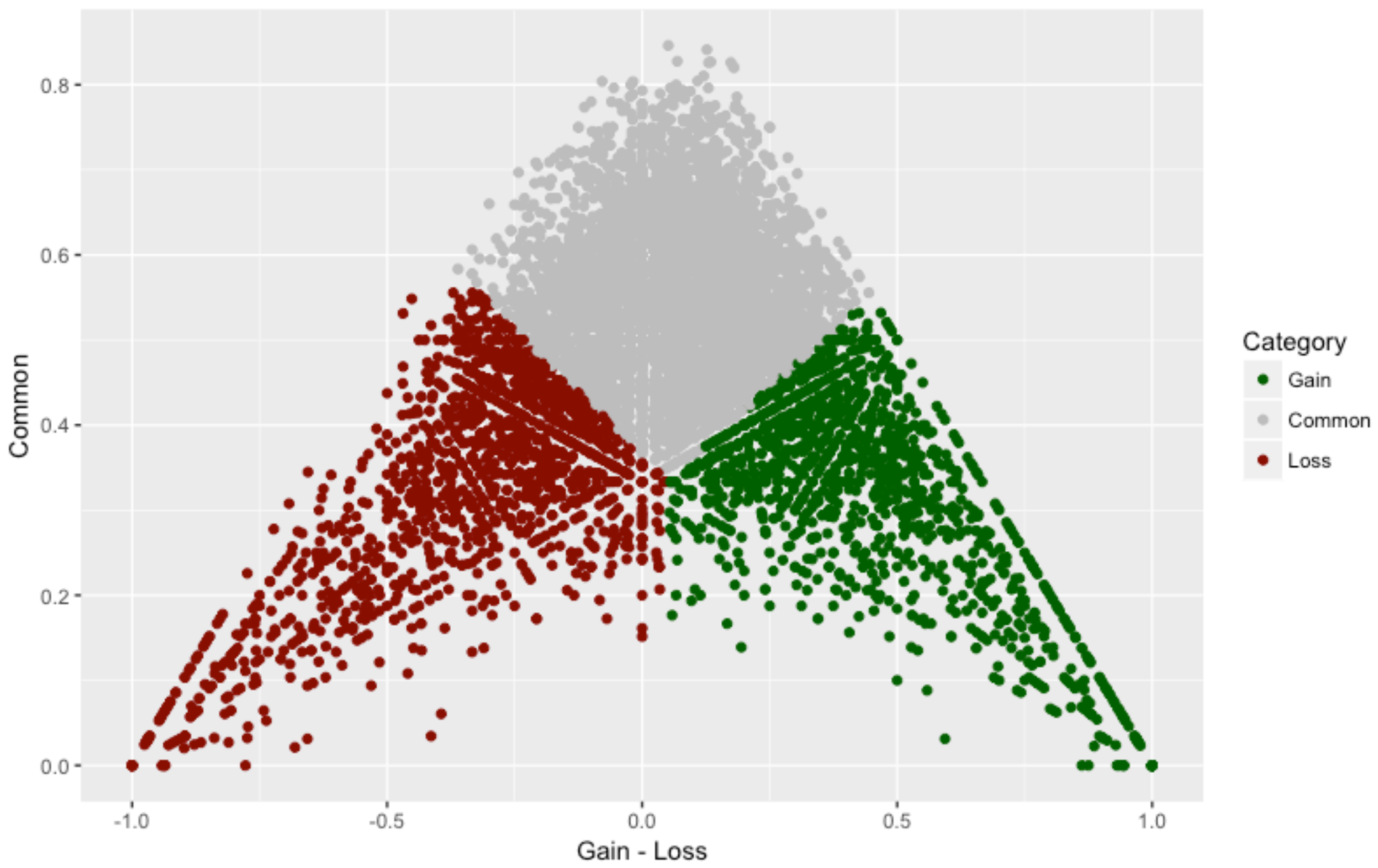
E



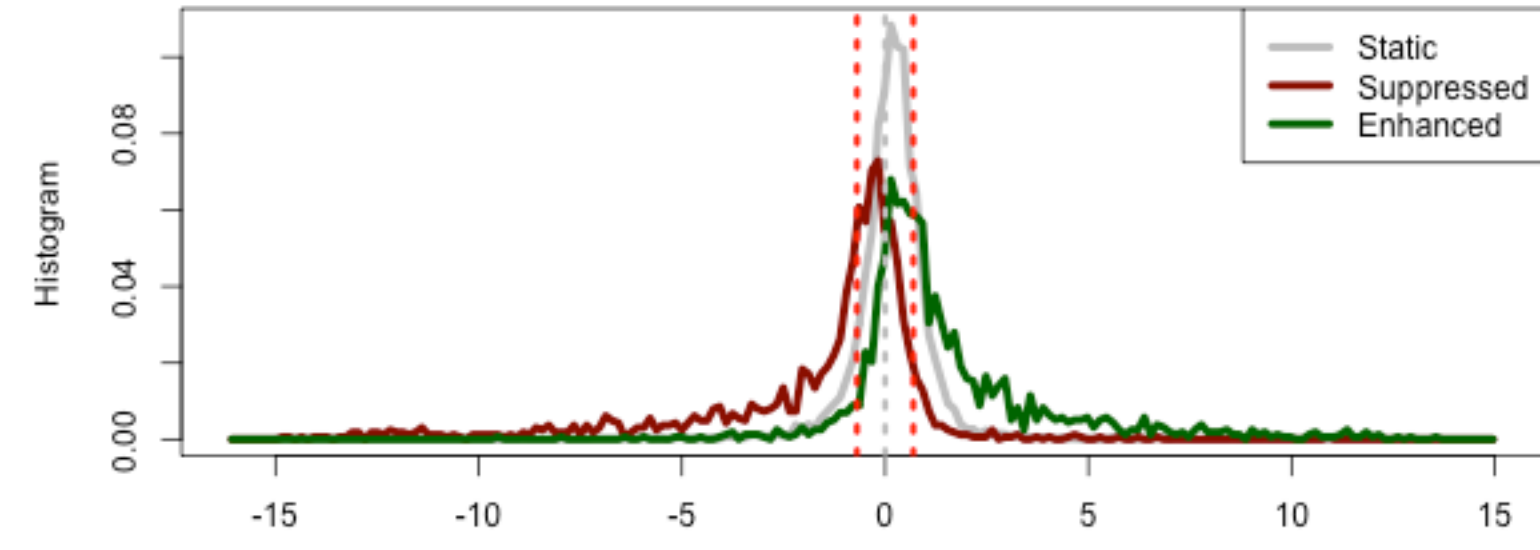


	Sample02	Sample04	Sample05	Sample06	Sample07	Sample08	Sample09	Sample10
chr	chr21	chr17	chr20	chr7	chr20	chr7	chr7	chr6
pos	27,541,982	38,474,408	43,971,343	1,598,567	58,563,412	150,759,483	5,596,005	134,700,462
ref	G	C	G	C	C	C	T	G
alt	A	G	C	T	T	G	G	T
D-score_min	20.361	16.910	3.665	15.746	7.217	13.959	13.372	13.989
D-score_mean	20.361	16.910	15.834	15.746	15.521	15.242	15.019	14.591
D-score_max	20.361	16.910	30.424	15.746	21.648	17.325	17.993	15.796

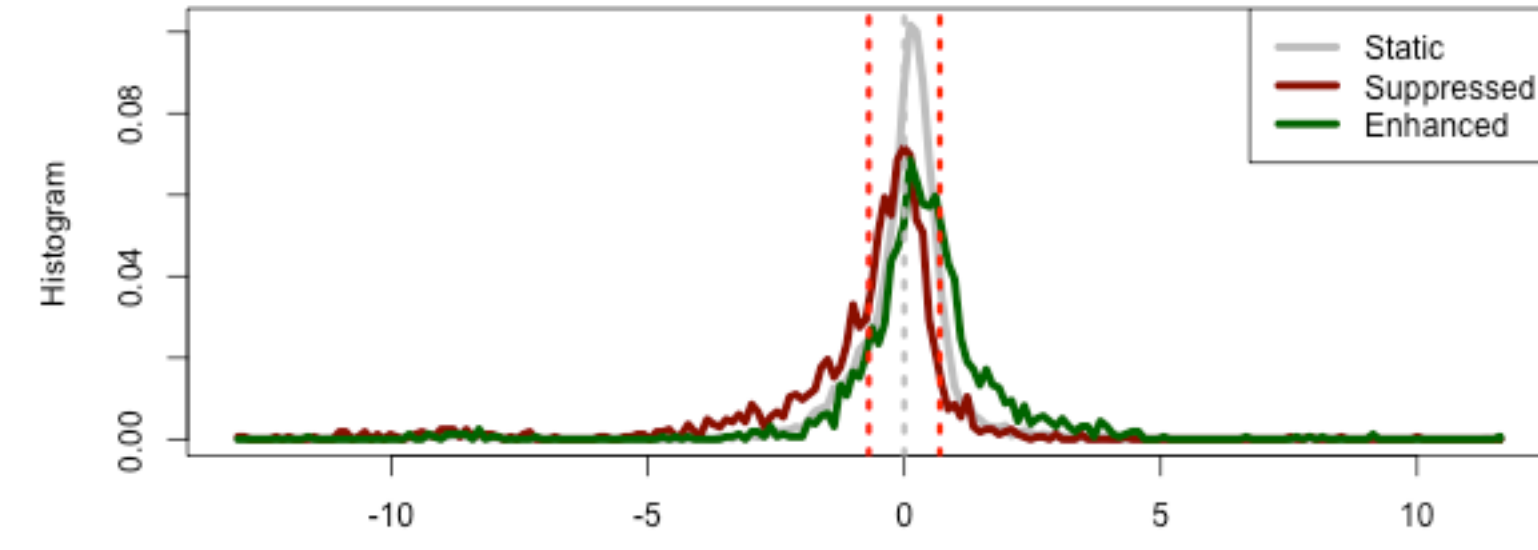




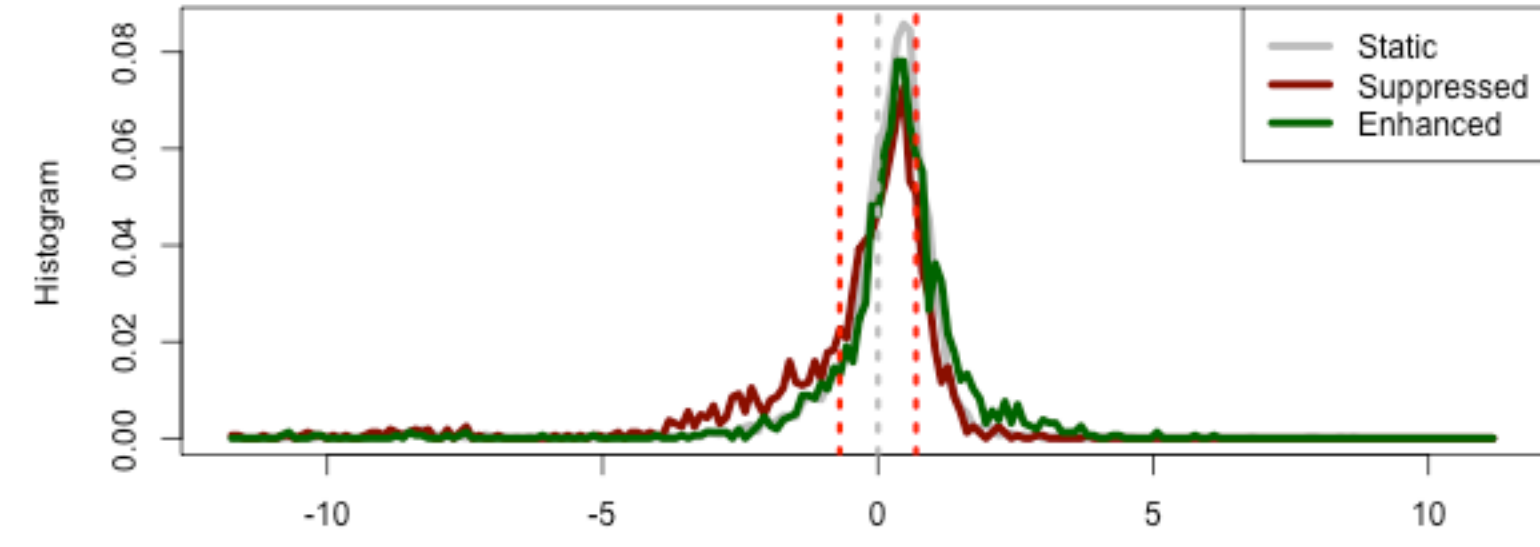
Expression(TPM) log(fc)



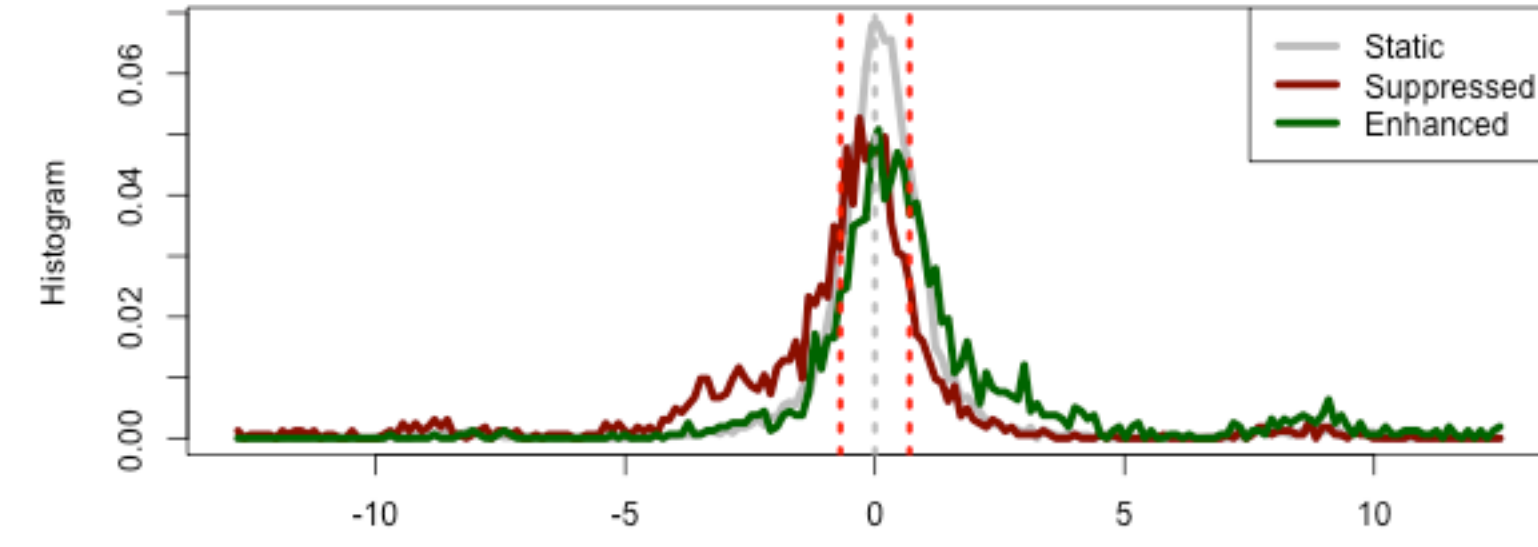
DNase I log(fc)



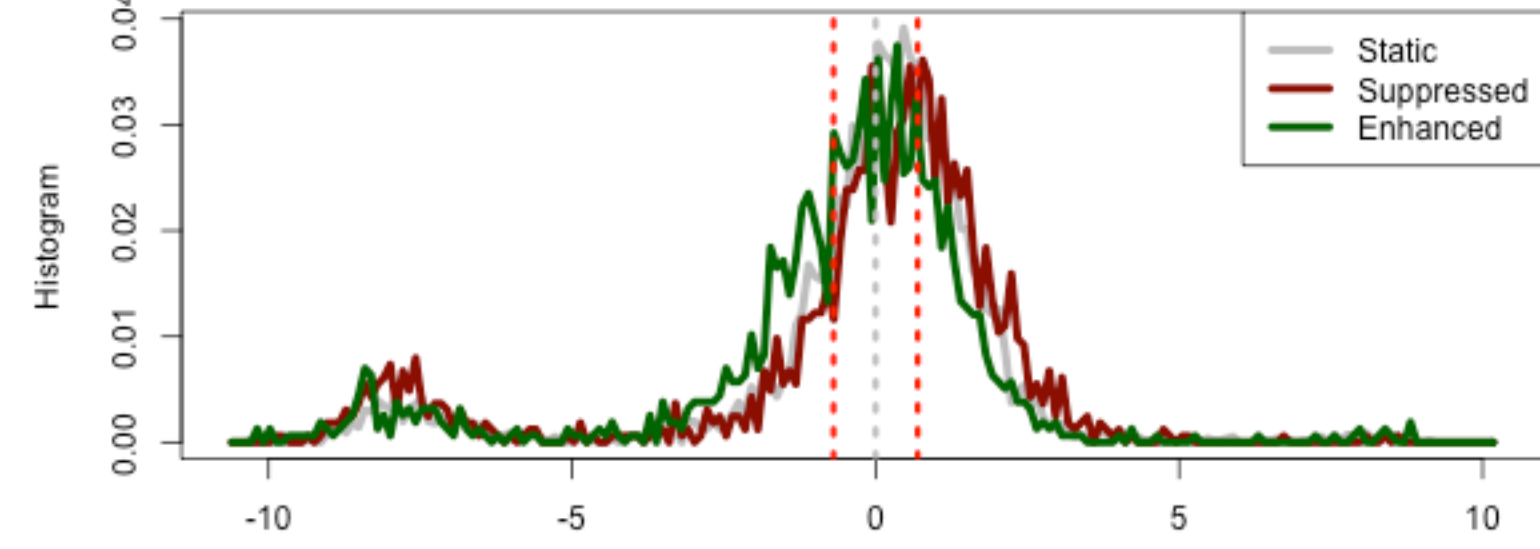
H3K4me3 log(fc)



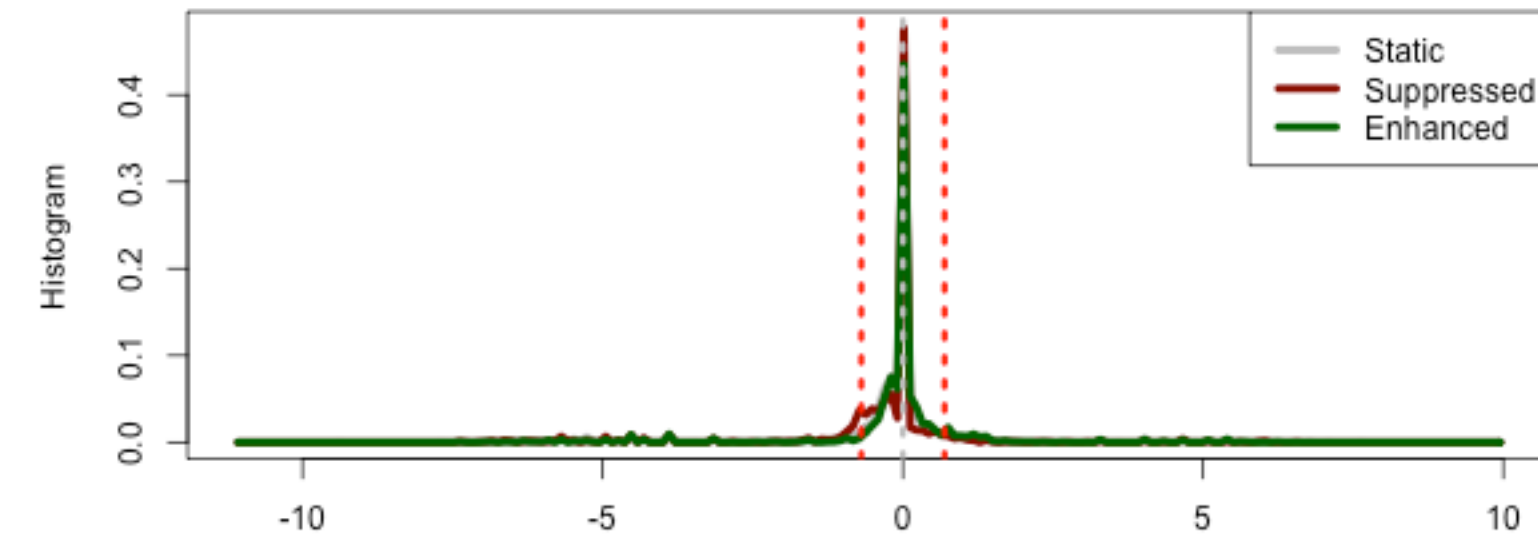
H3K27ac log(fc)



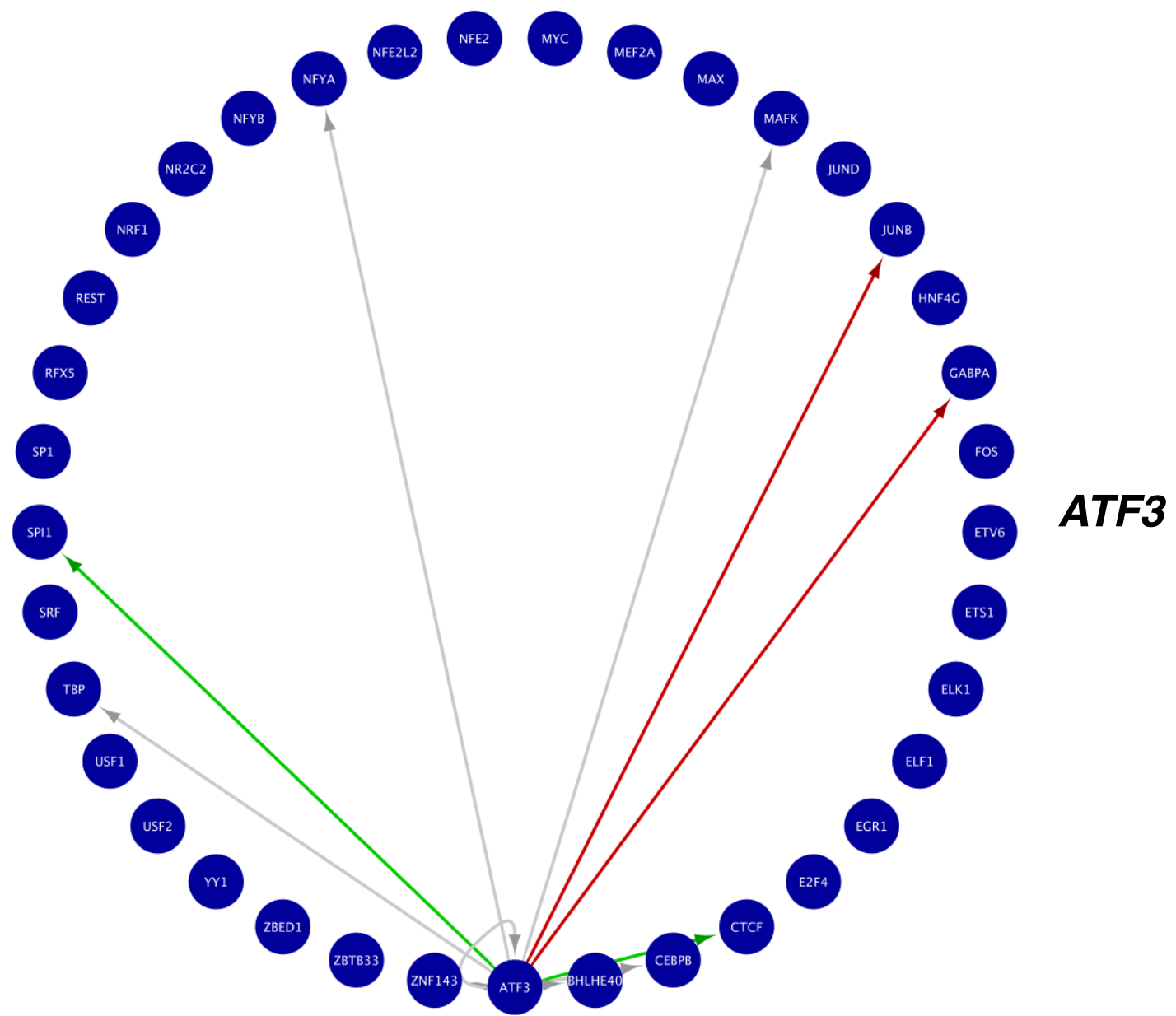
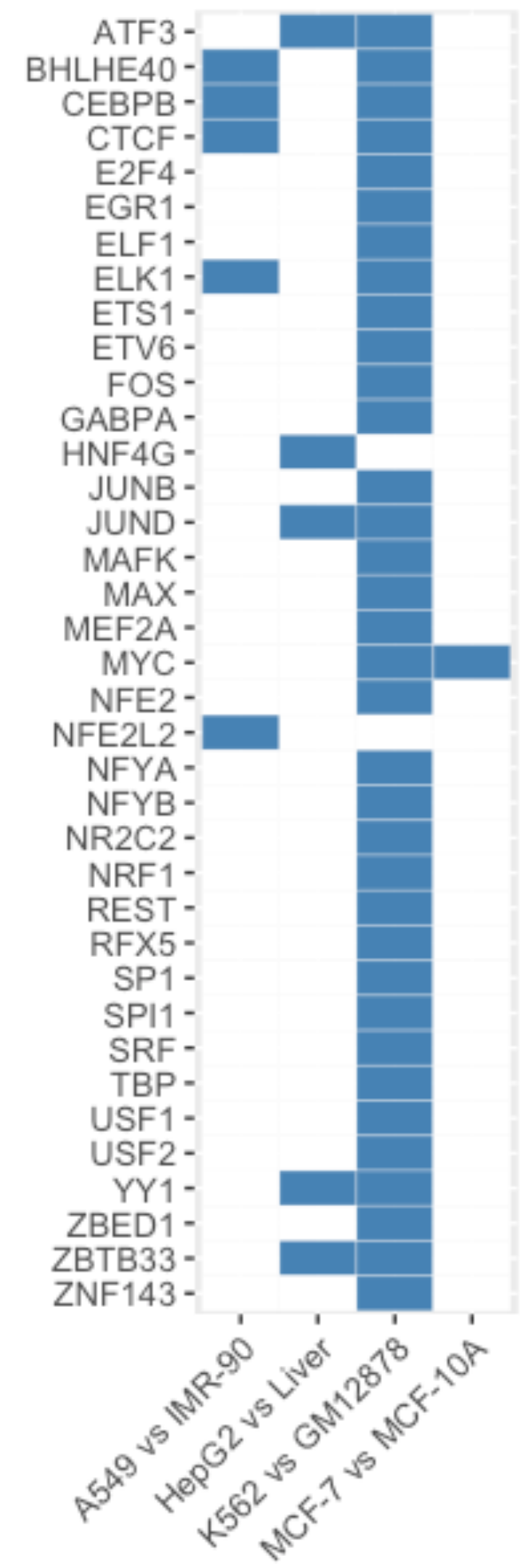
H3K27me3 log(fc)



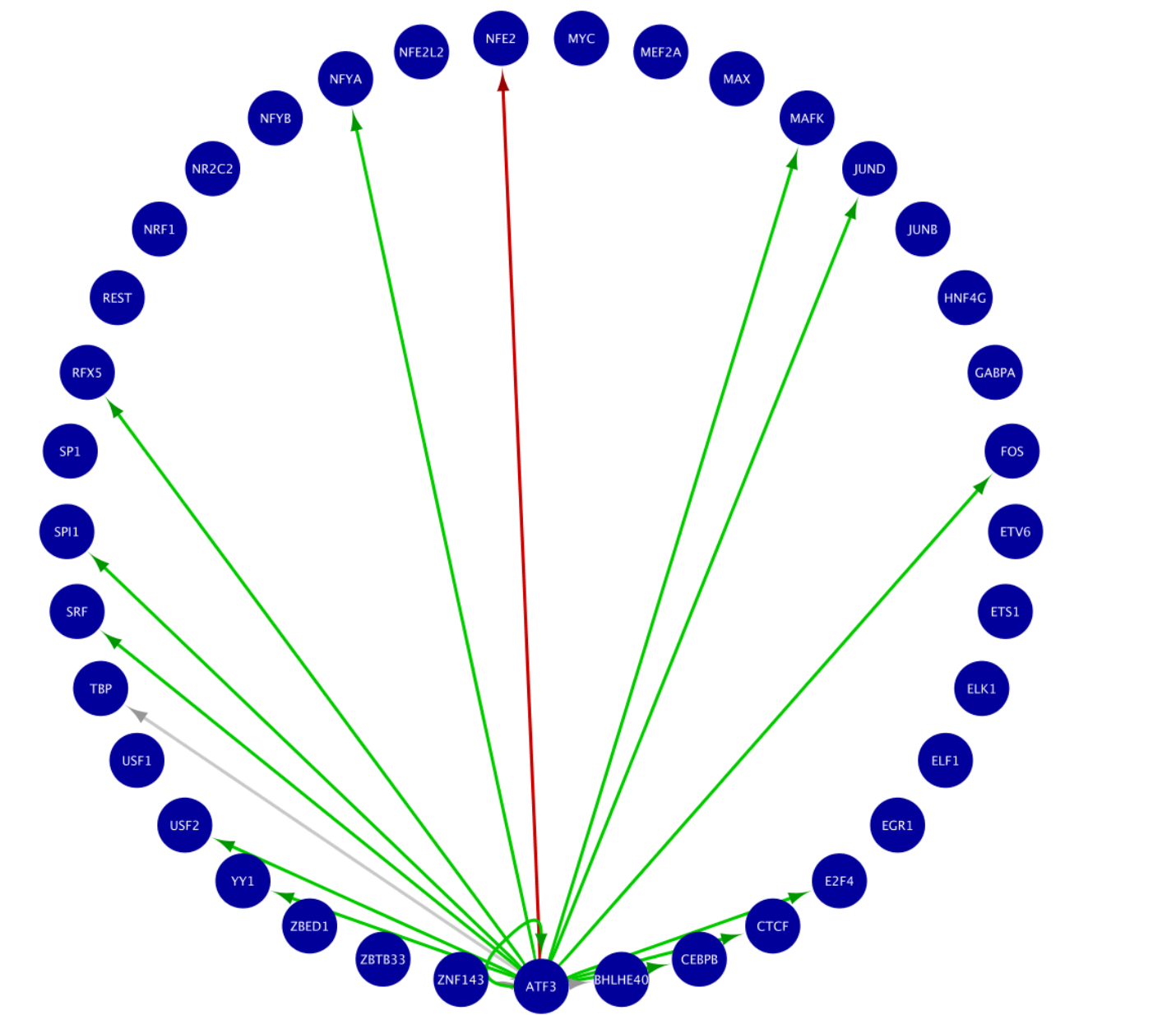
5mC log(fc)



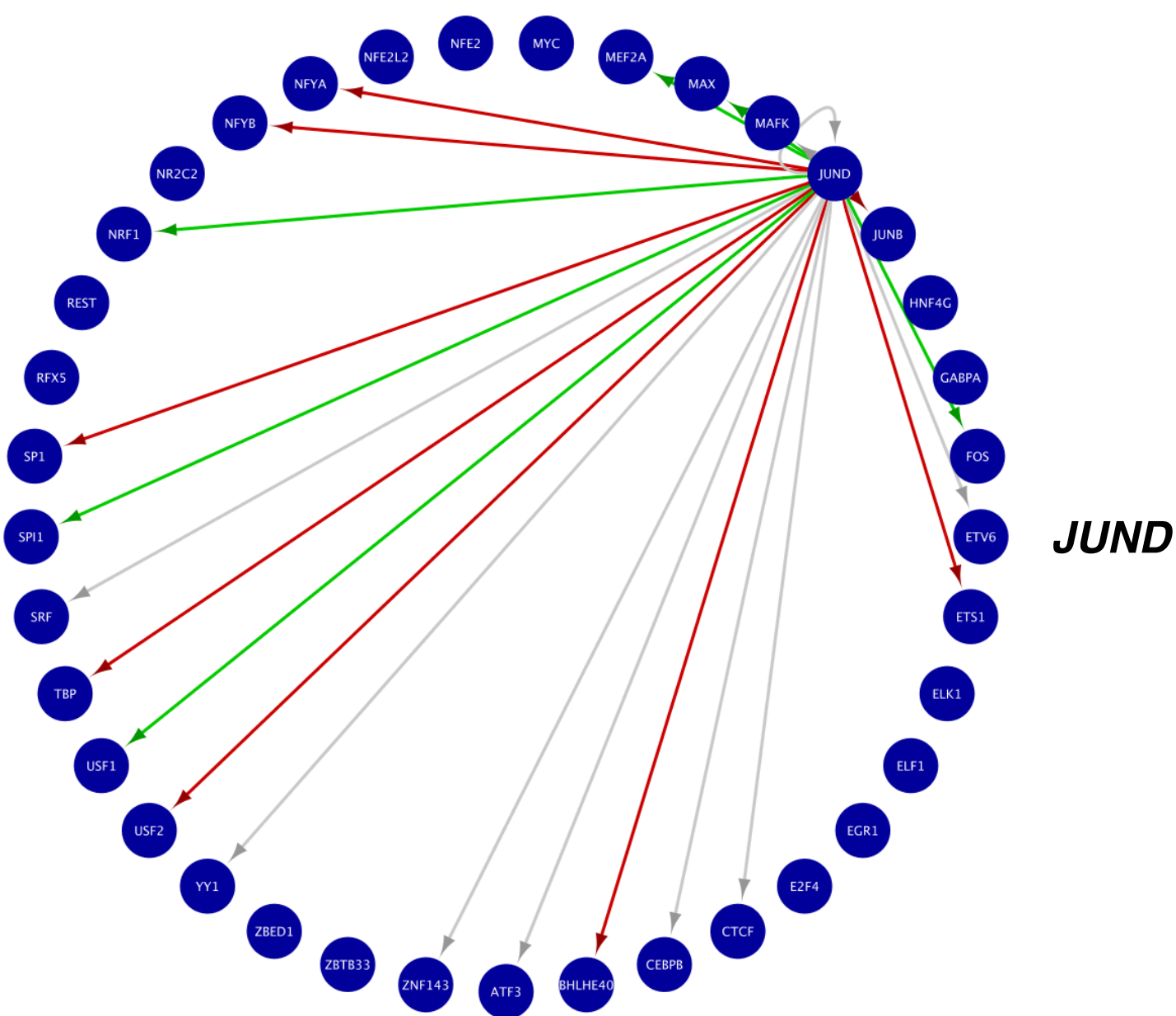
Cross-Cancer TFSS Matrix



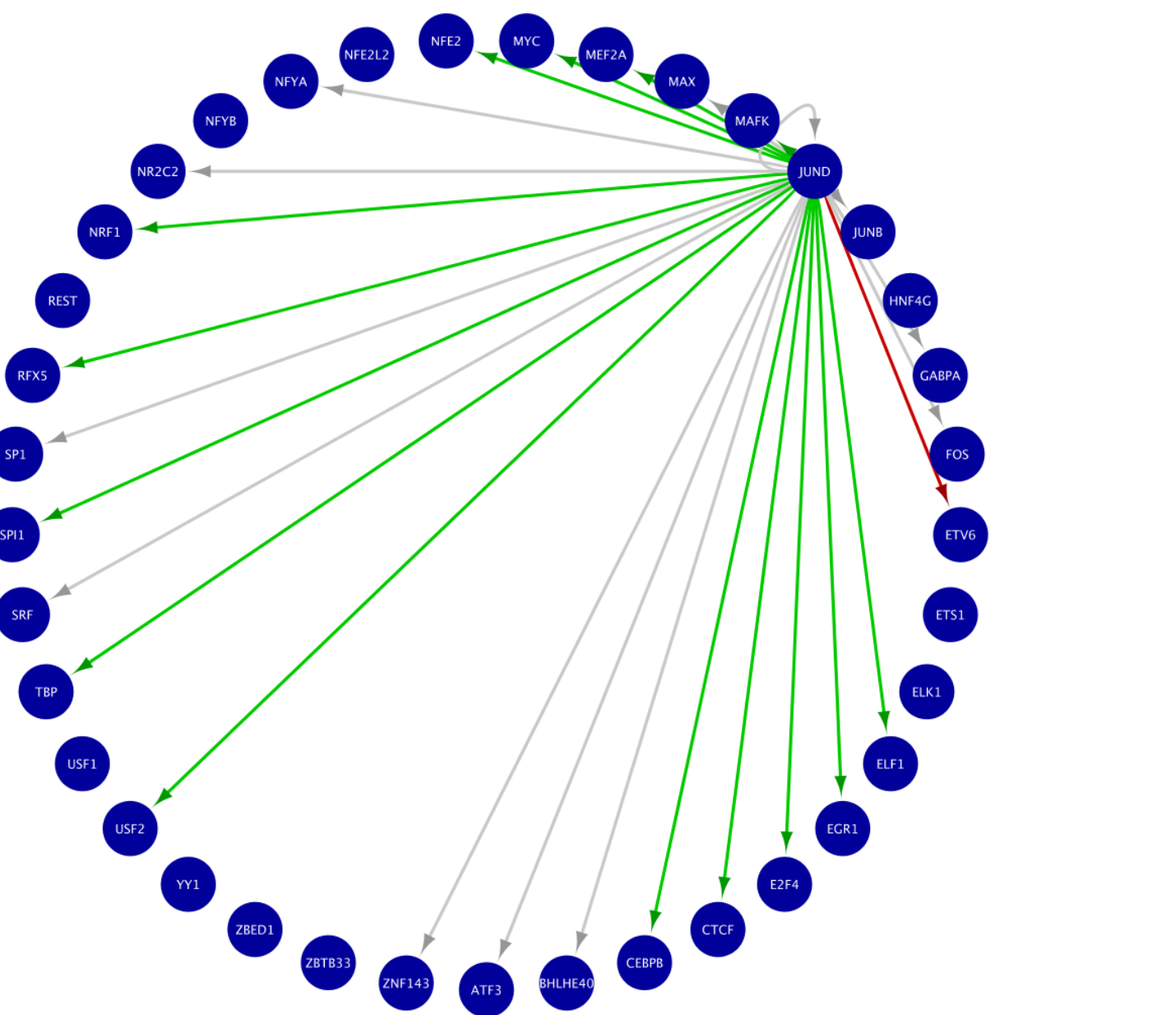
Liver vs HepG2

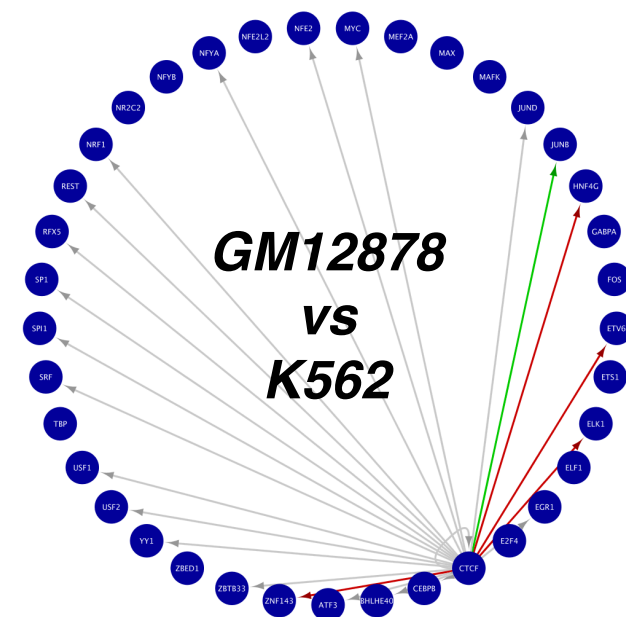


GM12878 vs K562

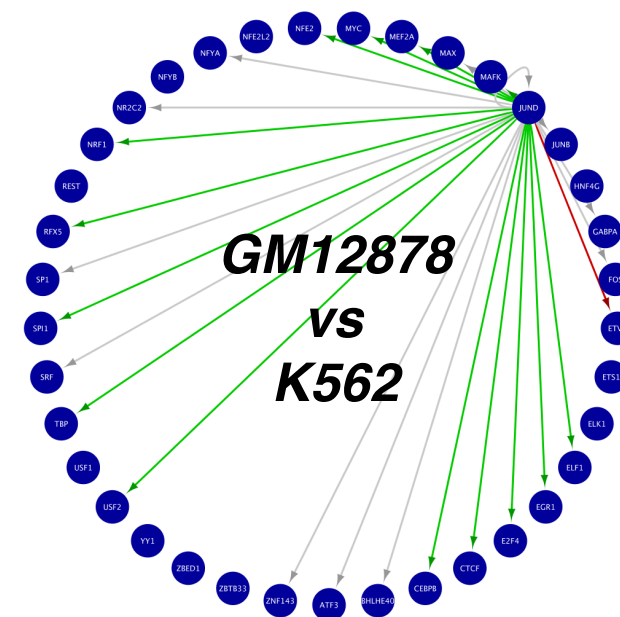


JUND

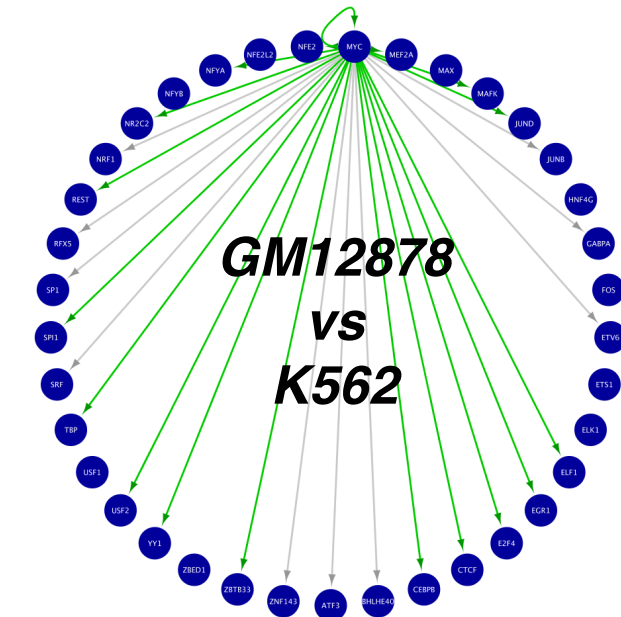




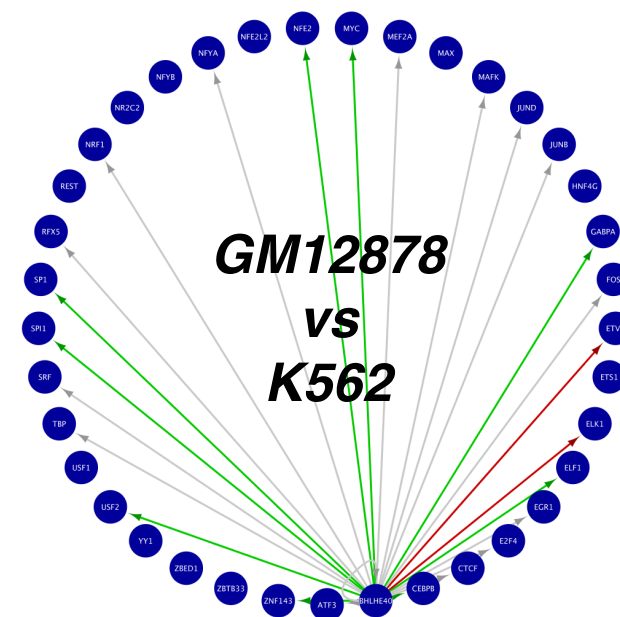
CTCF



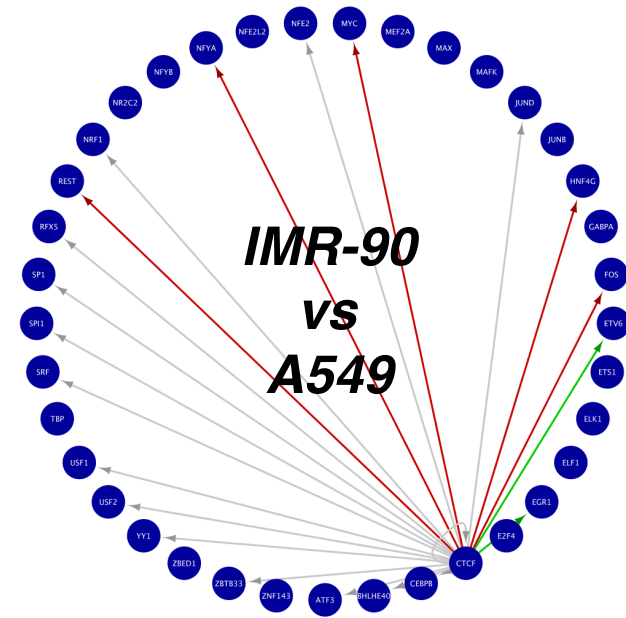
JUND



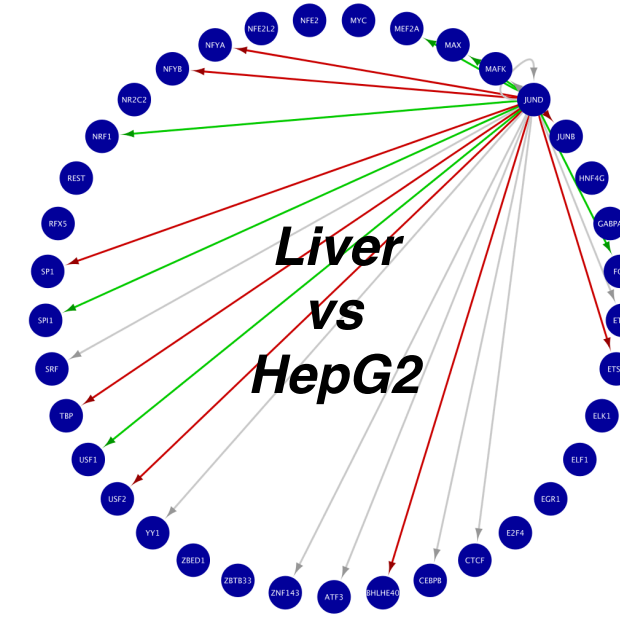
MYC



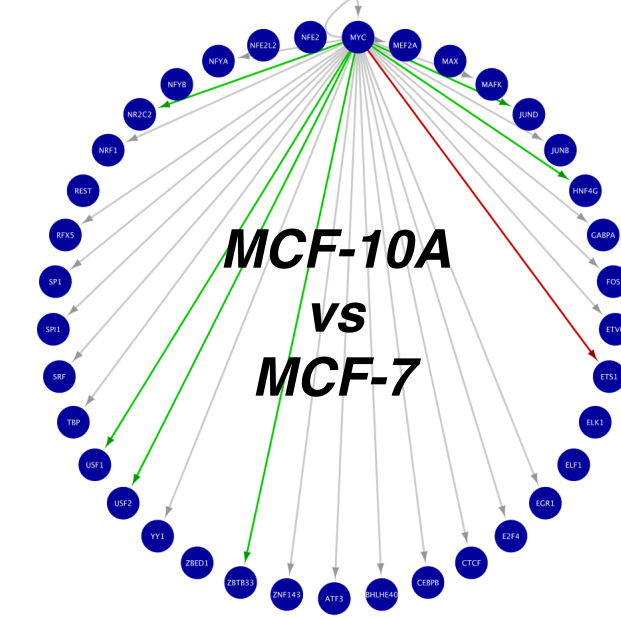
BHLHE40



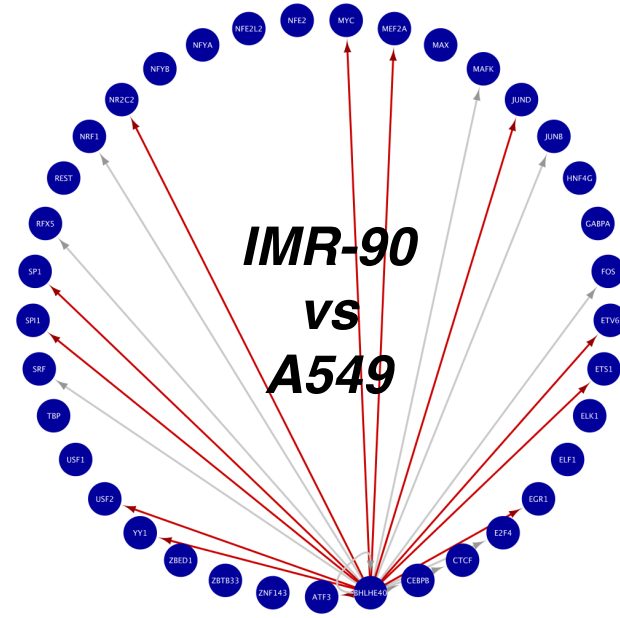
**IMR-90
vs
A549**



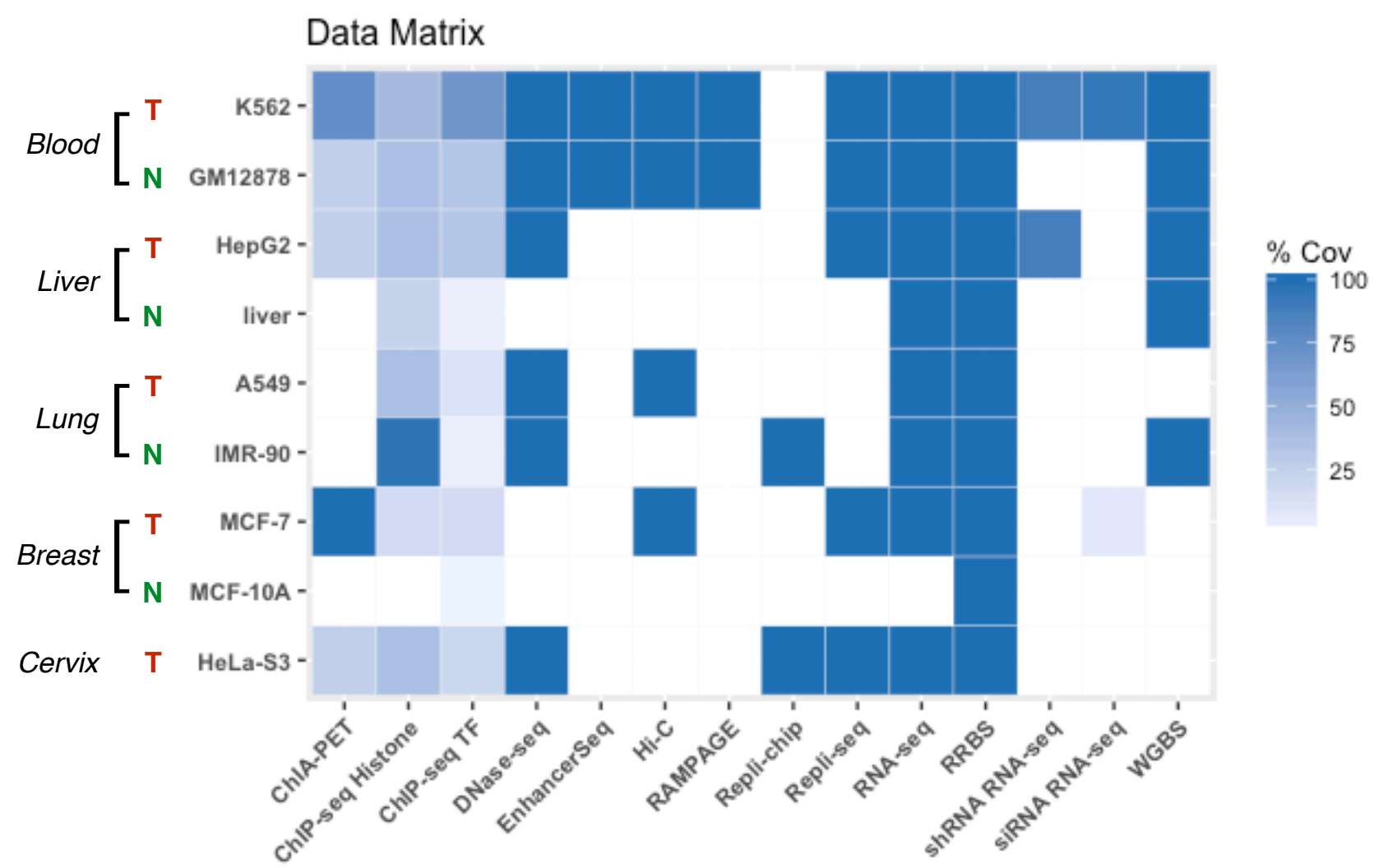
**Liver
vs
HepG2**



**MCF-10A
vs
MCF-7**



**IMR-90
vs
A549**



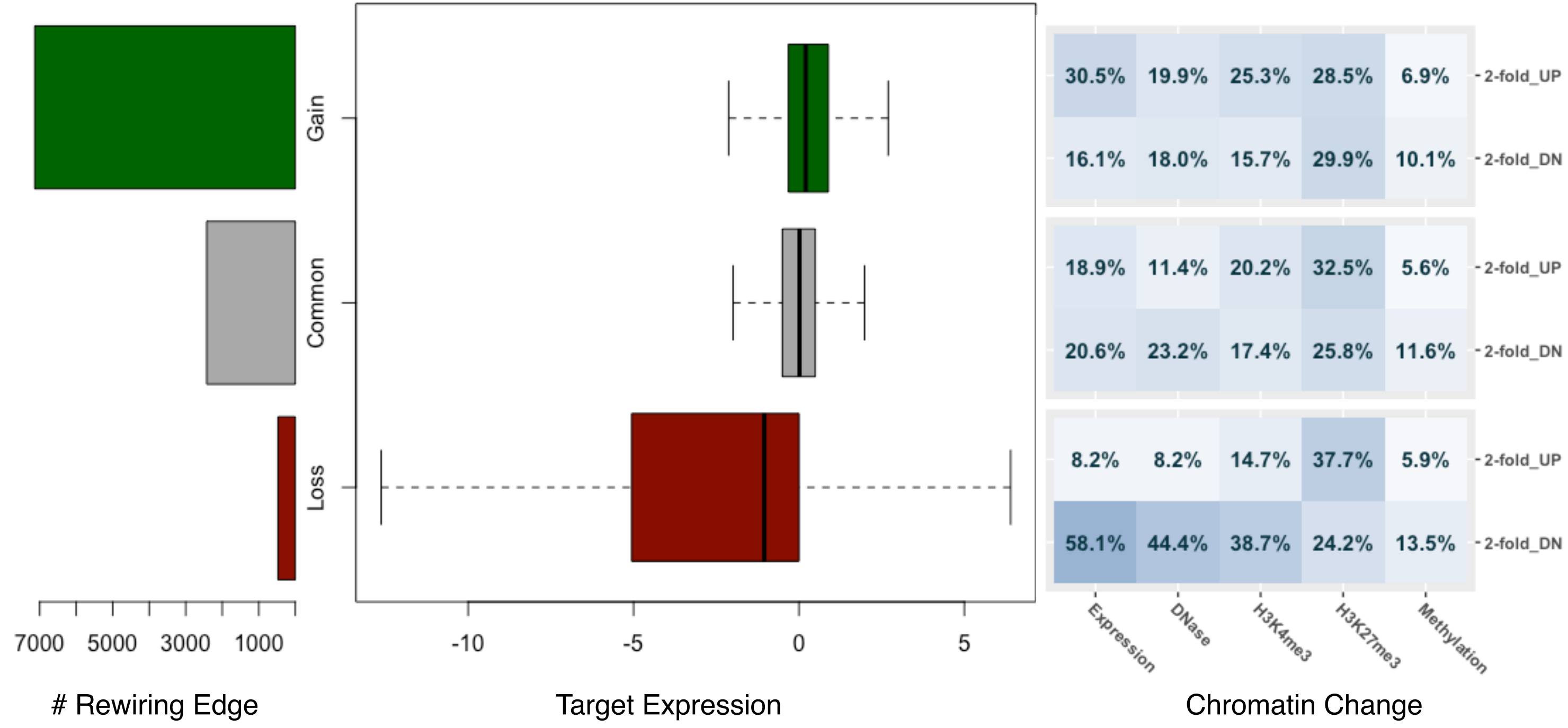
Data Matrix

Blood	T K562	209	64	17	1	12	1	1	1	1	3	1	0	1	219	29	1	1	1
	N GM12878	101	50	6	1	11	1	1	1	1	1	1	0	1	0	0	1	0	0
Liver	T HepG2	97	48	7	1	11	1	0	1	1	1	0	0	1	221	0	0	0	0
	N liver	7	5	0	0	7	1	0	1	1	0	0	0	0	0	0	0	0	0
Lung	T A549	32	21	3	1	11	1	0	1	0	0	1	0	0	0	0	0	0	0
	N IMR-90	9	6	1	1	28	1	0	1	1	0	0	1	0	0	0	0	0	0
Breast	T MCF-7	52	15	3	0	5	1	0	1	0	4	1	0	1	0	2	0	1	1
	N MCF-10A	4	3	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Cervix	T HeLa-S3	60	29	4	1	11	1	0	1	0	1	0	1	1	0	0	0	0	0

Data Matrix

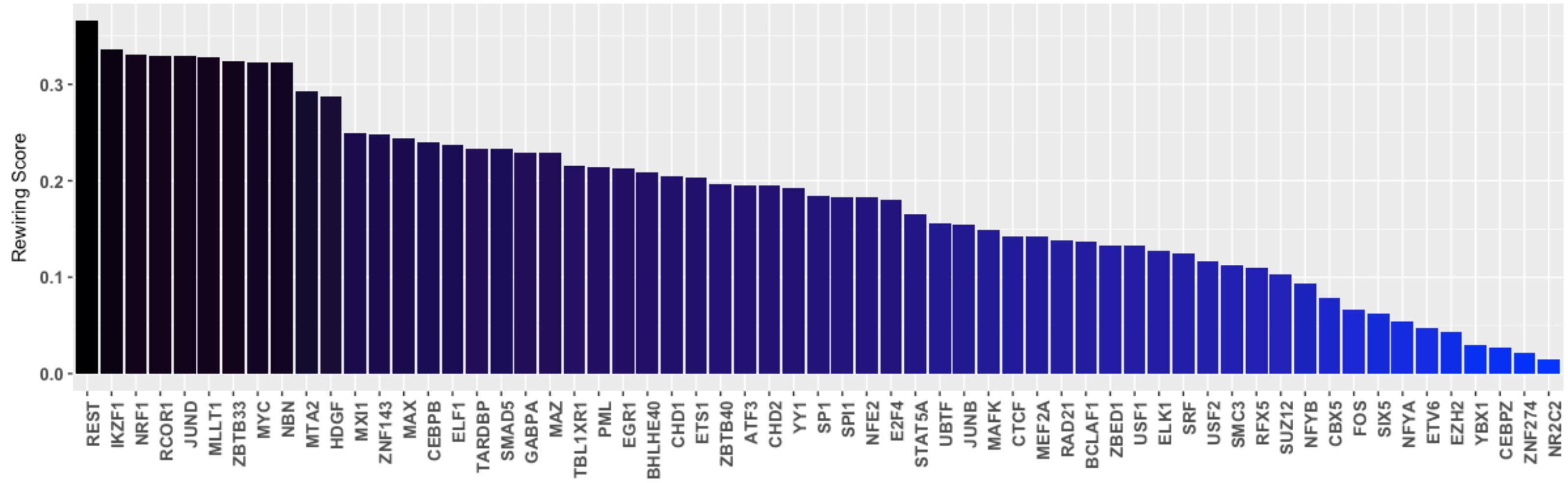
Blood	T K562	209	64	17	1	12	1	1	1	1	3	1	0	1	219	29	1	1	1	95
	N GM12878	101	50	6	1	11	1	1	1	1	1	1	0	1	0	0	1	1	1	0
Liver	T HepG2	97	48	7	1	11	1	0	1	1	1	0	0	1	221	0	0	0	0	327
	N liver	7	5	0	0	7	1	0	1	1	0	0	0	0	0	0	0	0	0	0
Lung	T A549	32	21	3	1	11	1	0	1	0	0	1	0	0	0	0	0	0	0	38
	N IMR-90	9	6	1	1	28	1	0	1	1	0	0	1	0	0	0	0	0	0	0
Breast	T MCF-7	52	15	3	0	5	1	0	1	0	4	1	0	1	0	2	0	1	1	198
	N MCF-10A	4	3	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Cervix	T HeLa-S3	60	29	4	1	11	1	0	1	0	1	0	1	1	0	0	0	0	0	2

JUND

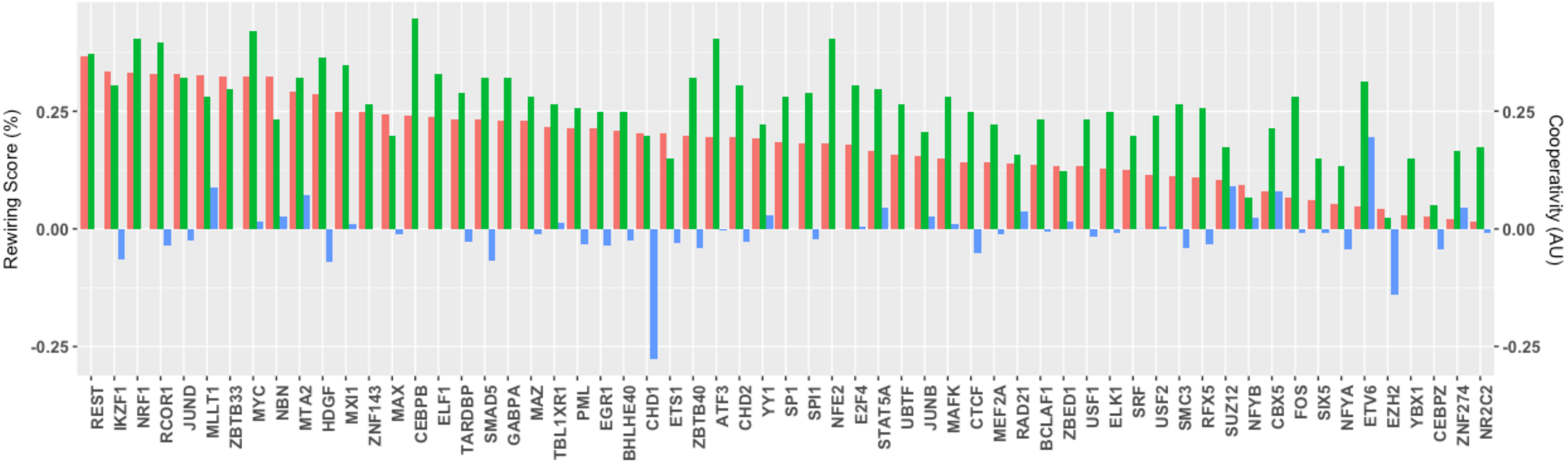


new TSS network, one TSS per gene

TF-GENE Network

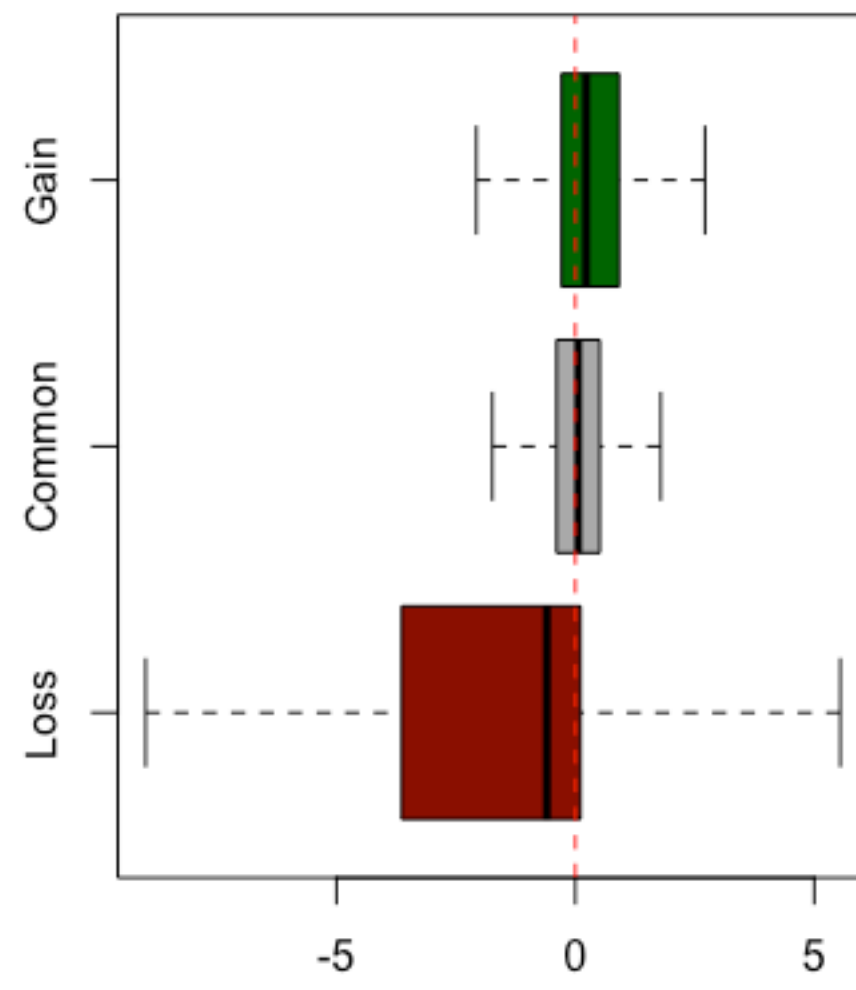
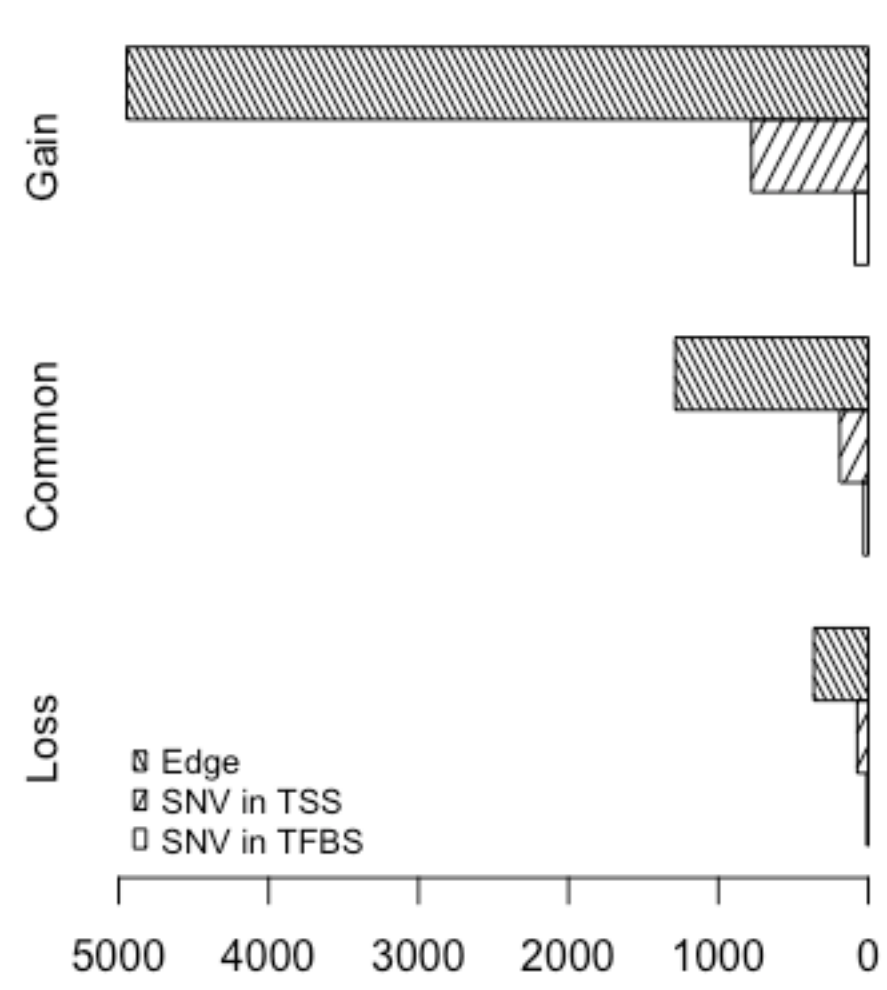


K562-GM12878 Network



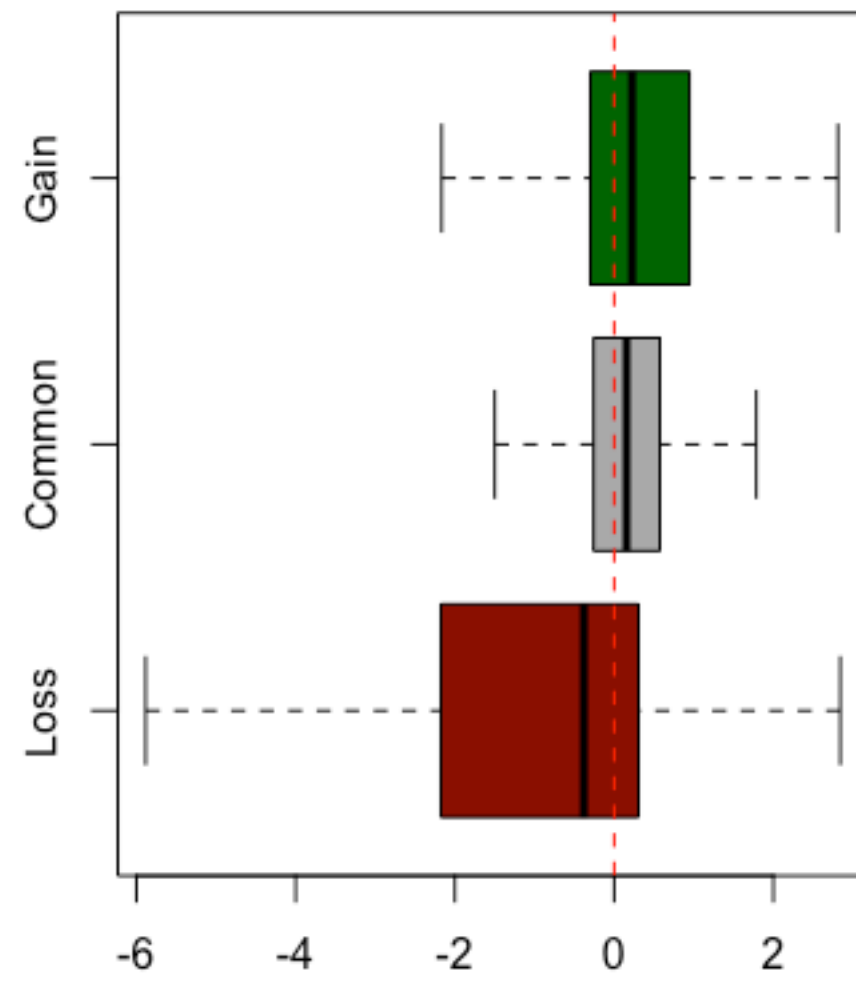
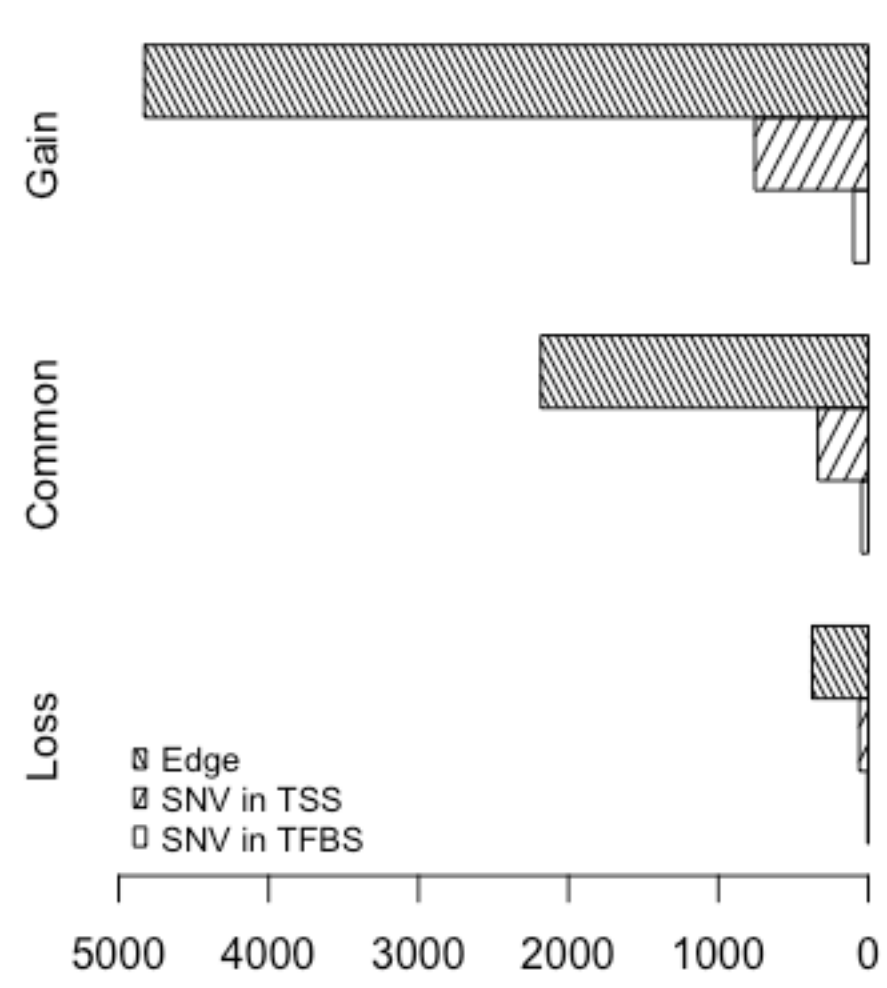
■ rScore_TF2GENE
■ rScore_TF2TF
■ Cooperativity

JUND



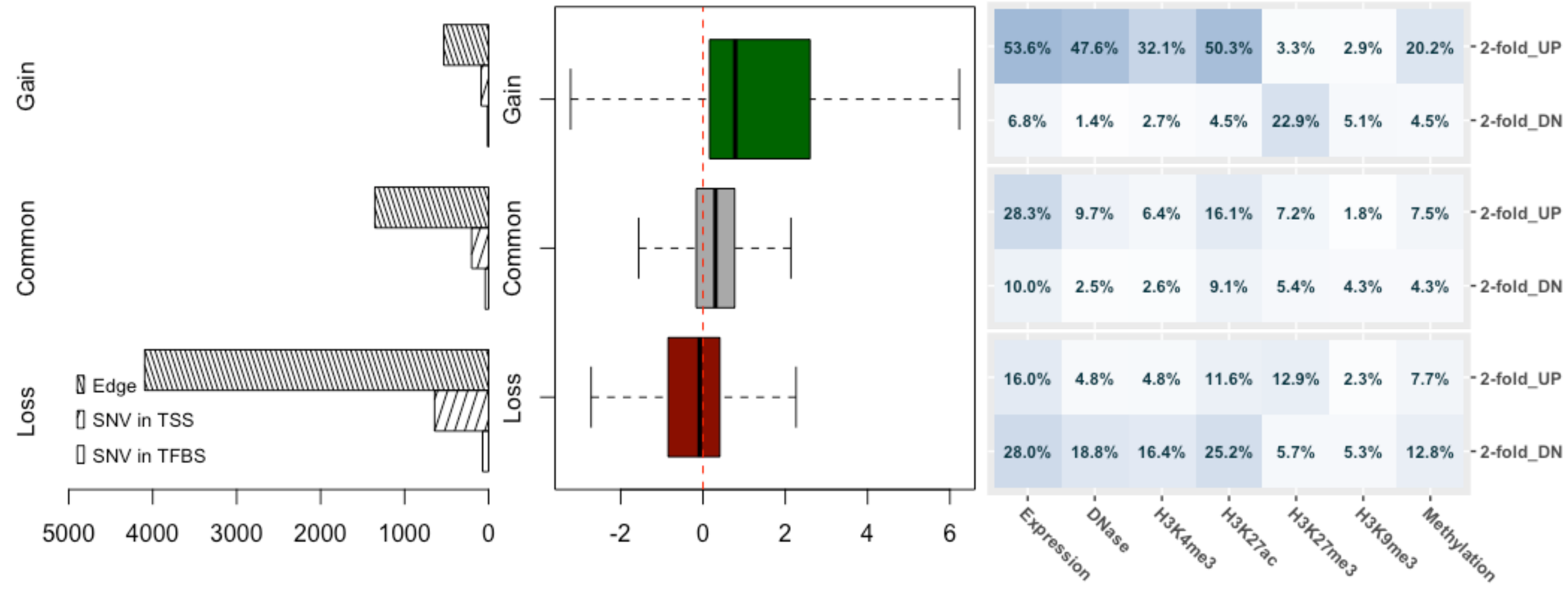
31.1%	24.8%	16.7%	29.7%	7.8%	3.2%	9.9%	-2-fold_UP
15.7%	2.9%	4.2%	9.1%	12.1%	5.3%	7.9%	-2-fold_DN
18.9%	7.0%	6.3%	13.9%	8.3%	0.8%	3.6%	-2-fold_UP
16.7%	6.2%	4.3%	12.4%	5.1%	4.3%	9.8%	-2-fold_DN
11.8%	2.5%	2.8%	5.8%	22.6%	2.2%	8.0%	-2-fold_UP
47.1%	54.8%	49.0%	57.3%	7.4%	10.5%	11.6%	-2-fold_DN
Expression	DNase	H3K4me3	H3K27ac	H3K27me3	H3K9me3	Methylation	

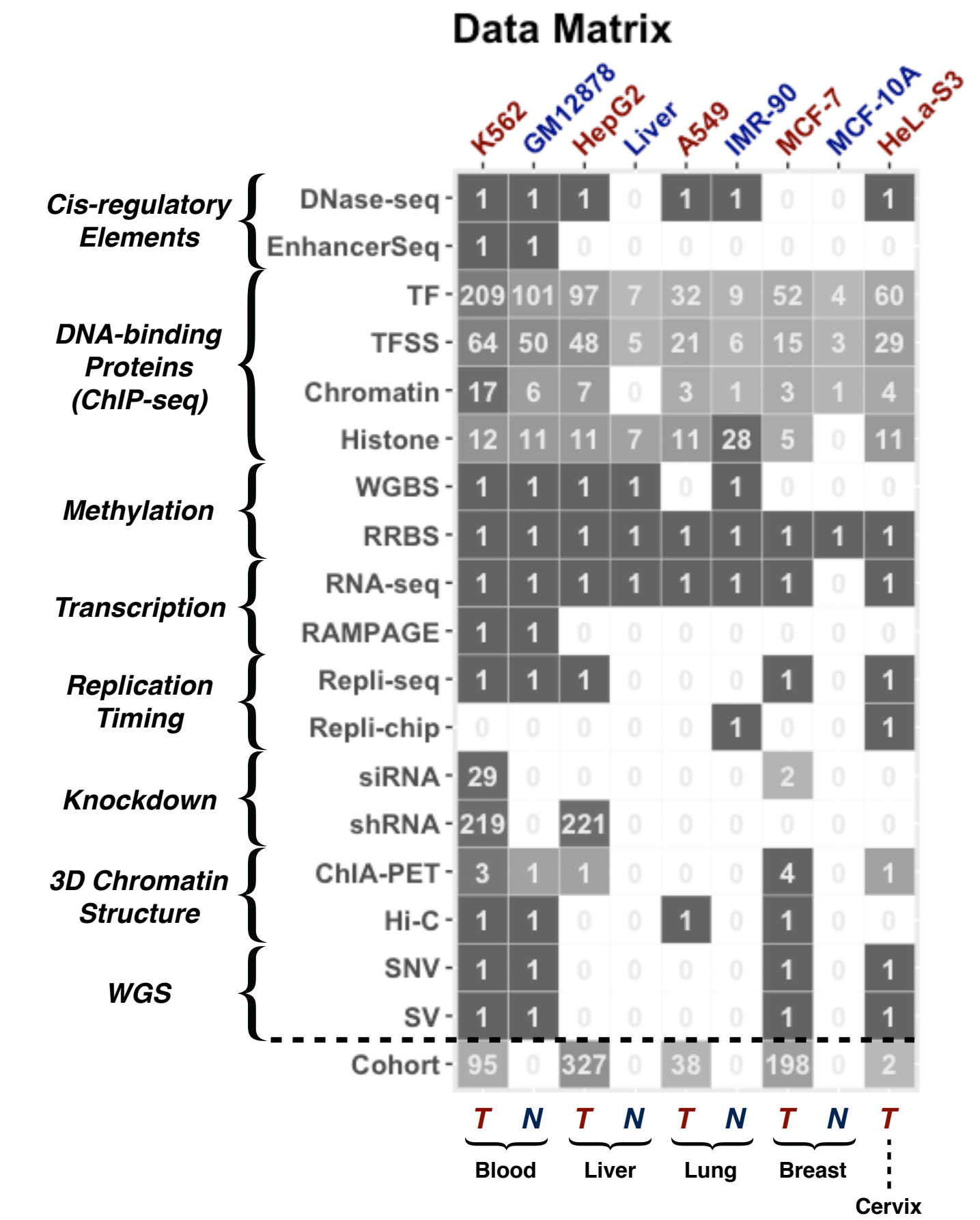
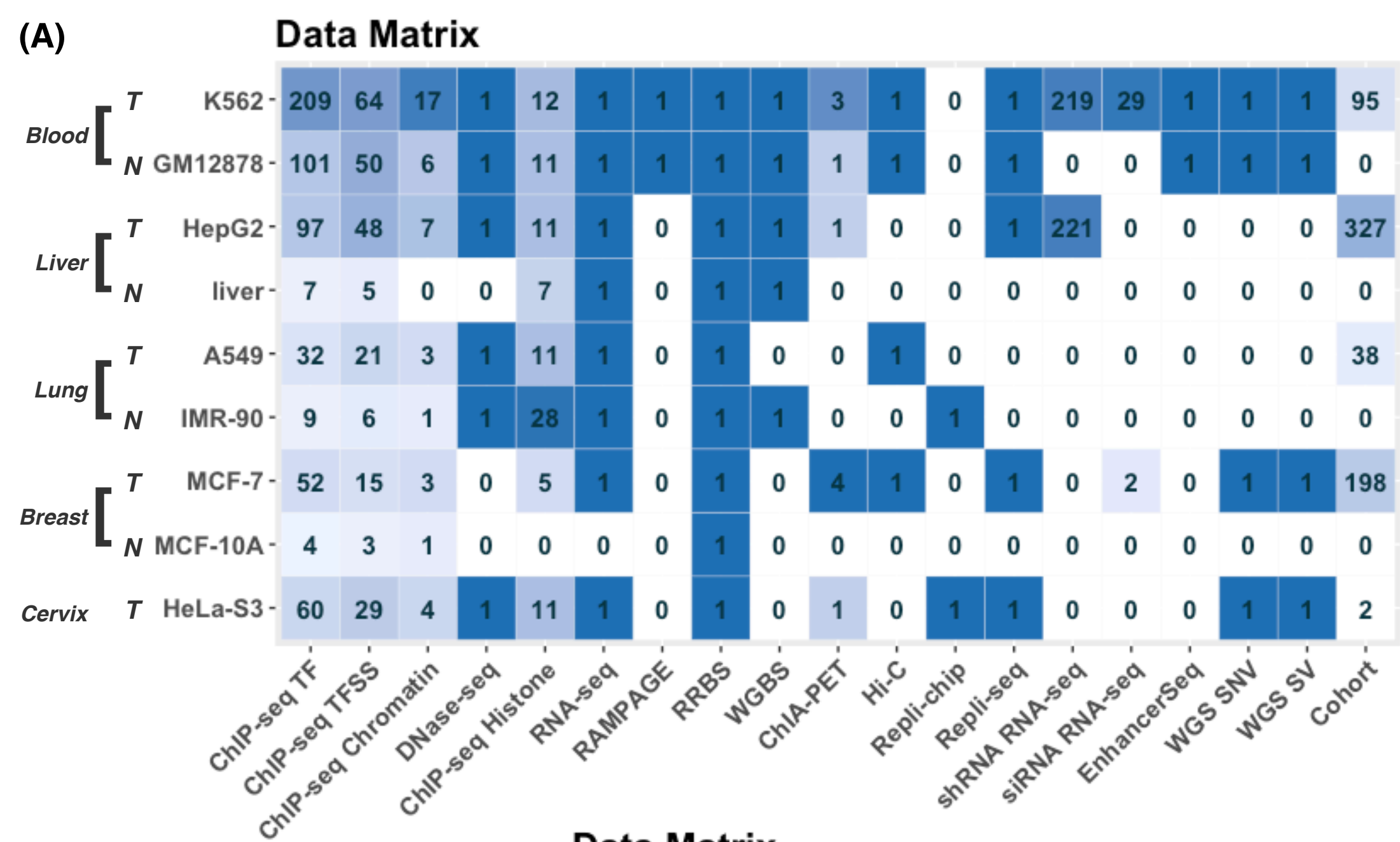
MYC



31.8%	21.6%	16.2%	28.5%	6.4%	2.2%	8.7%	-2-fold_UP
15.7%	4.2%	3.7%	10.7%	13.9%	5.9%	8.4%	-2-fold_DN
19.8%	4.9%	4.4%	12.1%	8.8%	1.5%	4.0%	-2-fold_UP
11.7%	4.1%	2.2%	8.2%	3.8%	4.1%	10.1%	-2-fold_DN
13.2%	6.2%	3.5%	9.7%	20.0%	5.1%	14.3%	-2-fold_UP
40.8%	34.6%	34.3%	43.5%	4.1%	7.0%	10.8%	-2-fold_DN
Expression	DNase	H3K4me3	H3K27ac	H3K27me3	H3K9me3	Methylation	

HDGF





*Cohort: K562::CLLE, HepG2::LIHC, A549::LUAD, MCF-7::BRCA, HeLa-S3::CESC

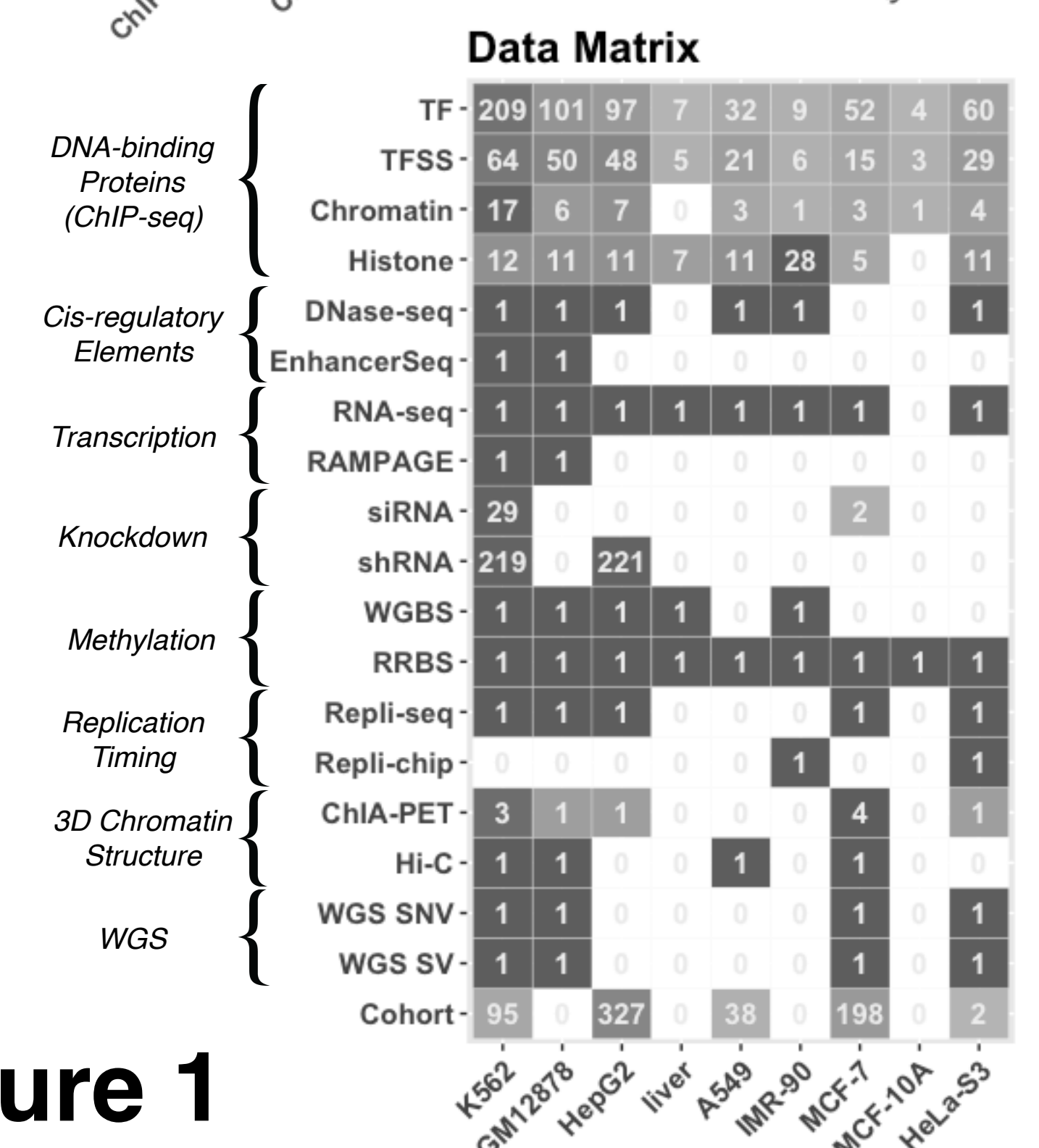


Figure 1

Data Matrix

		K562	GM12878	HepG2	Liver	A549	IMR-90	MCF-7	MCF-10A	HeLa-S3
Cis-regulatory Elements	DNase-seq	1	1	1	0	1	1	0	0	1
	EnhancerSeq	1	1	0	0	0	0	0	0	0
DNA-binding Proteins (ChIP-seq)	TF	209	101	97	7	32	9	52	4	60
	TFSS	64	50	48	5	21	6	15	3	29
	Chromatin	17	6	7	0	3	1	3	1	4
	Histone	12	11	11	7	11	28	5	0	11
Methylation	WGBS	1	1	1	1	0	1	0	0	0
	RRBS	1	1	1	1	1	1	1	1	1
Transcription	RNA-seq	1	1	1	1	1	1	1	0	1
	RAMPAGE	1	1	0	0	0	0	0	0	0
Replication Timing	Repli-seq	1	1	1	0	0	0	1	0	1
	Repli-chip	0	0	0	0	0	1	0	0	1
Knockdown	siRNA	29	0	0	0	0	0	2	0	0
	shRNA	219	0	221	0	0	0	0	0	0
3D Chromatin Structure	ChIA-PET	3	1	1	0	0	0	4	0	1
	Hi-C	1	1	0	0	1	0	1	0	0
WGS	SNV	1	1	0	0	0	0	1	0	1
	SV	1	1	0	0	0	0	1	0	1
Cohort		95	0	327	0	38	0	198	0	2
TCGA		173	0	373	0	517	0	1100	0	546
		<i>T</i>	<i>N</i>	<i>T</i>	<i>N</i>	<i>T</i>	<i>N</i>	<i>T</i>	<i>N</i>	<i>T</i>
		Blood		Liver		Lung		Breast		Cervix

***Cohort:**

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

A

Data Matrix

		ChIP-seq TF	ChIP-seq TFSS	ChIP-seq Chromatin	DNase-seq	Histone	RNA-seq	RAMPAGE	RRBS	WGBS	ChIA-PET	Hi-C	Repli-chip	Repli-seq	shRNA	RNA-seq	siRNA	RNA-seq	EnhancerSeq	WGS SNV	WGS SV	Cohort
Blood	T K562	209	64	17	1	12	1	1	1	1	3	1	0	1	219	29	1	1	1	1	1	95
	N GM12878	101	50	6	1	11	1	1	1	1	1	1	0	1	0	0	1	1	1	1	1	0
Liver	T HepG2	97	48	7	1	11	1	0	1	1	1	0	0	1	221	0	0	0	0	0	0	327
	N liver	7	5	0	0	7	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0
Lung	T A549	32	21	3	1	11	1	0	1	0	0	1	0	0	0	0	0	0	0	0	0	38
	N IMR-90	9	6	1	1	28	1	0	1	1	0	0	1	0	0	0	0	0	0	0	0	0
Breast	T MCF-7	52	15	3	0	5	1	0	1	0	4	1	0	1	0	2	0	1	1	1	1	198
	N MCF-10A	4	3	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Cervix	T HeLa-S3	60	29	4	1	11	1	0	1	0	1	0	1	1	0	0	0	0	1	1	1	2

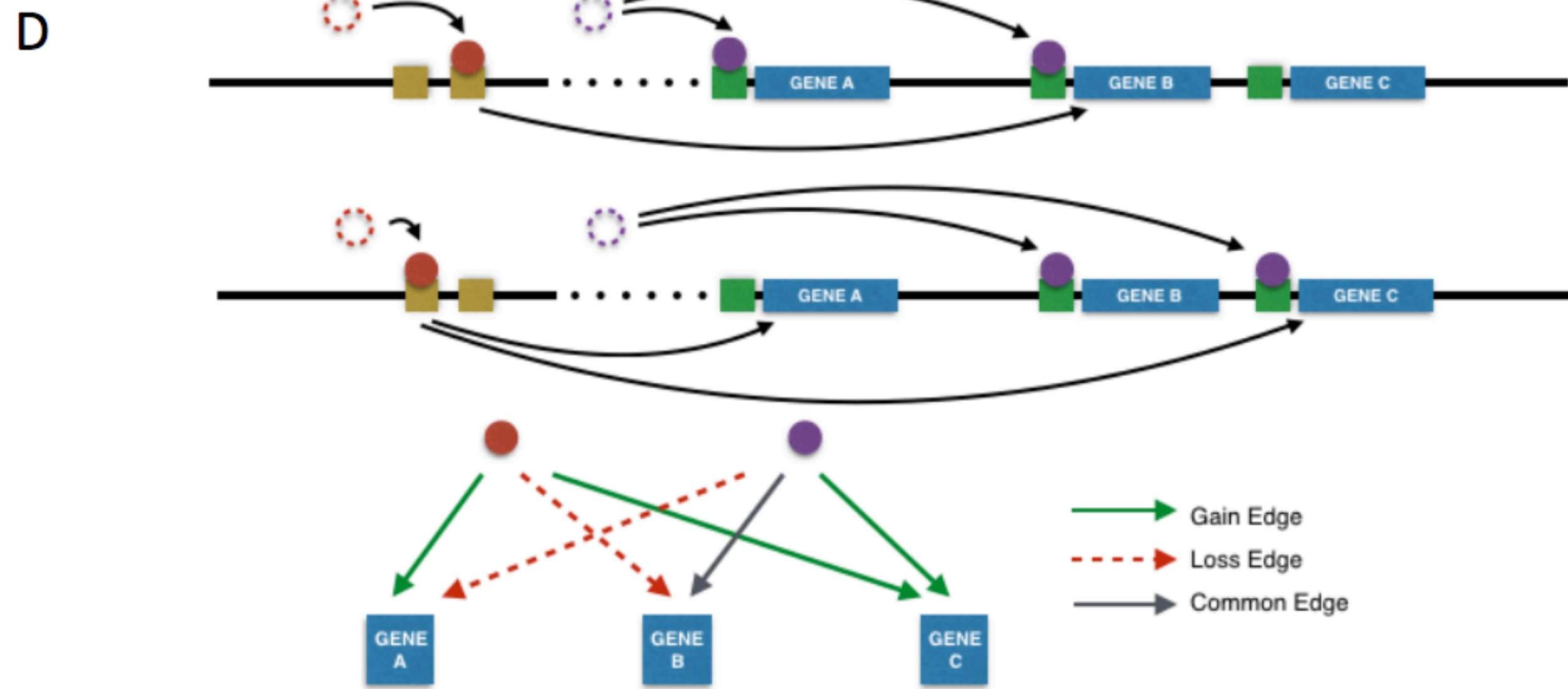
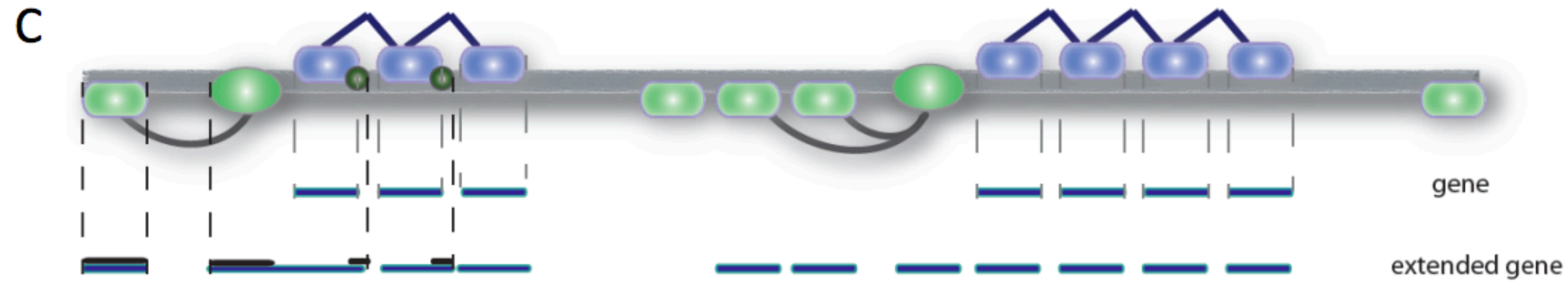
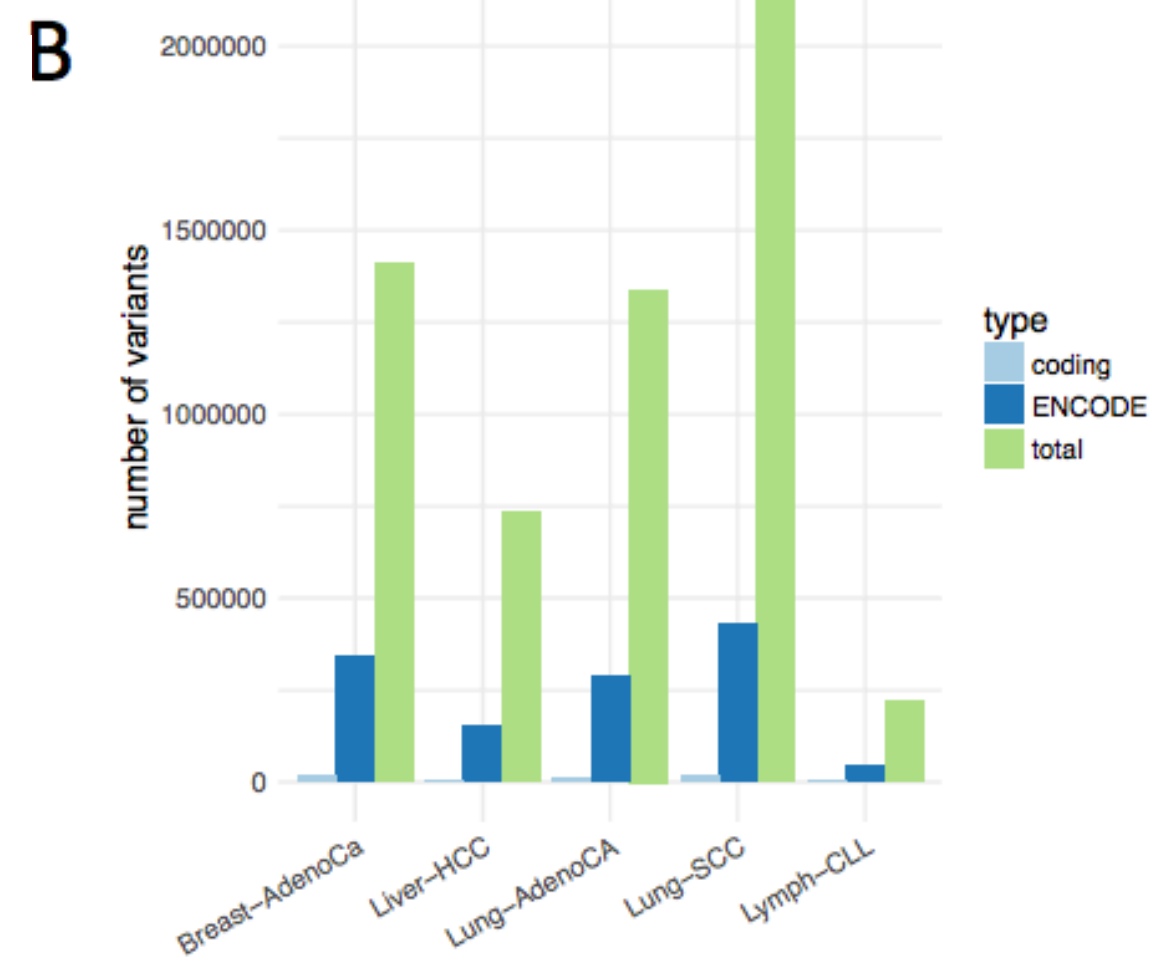


Figure 1

A

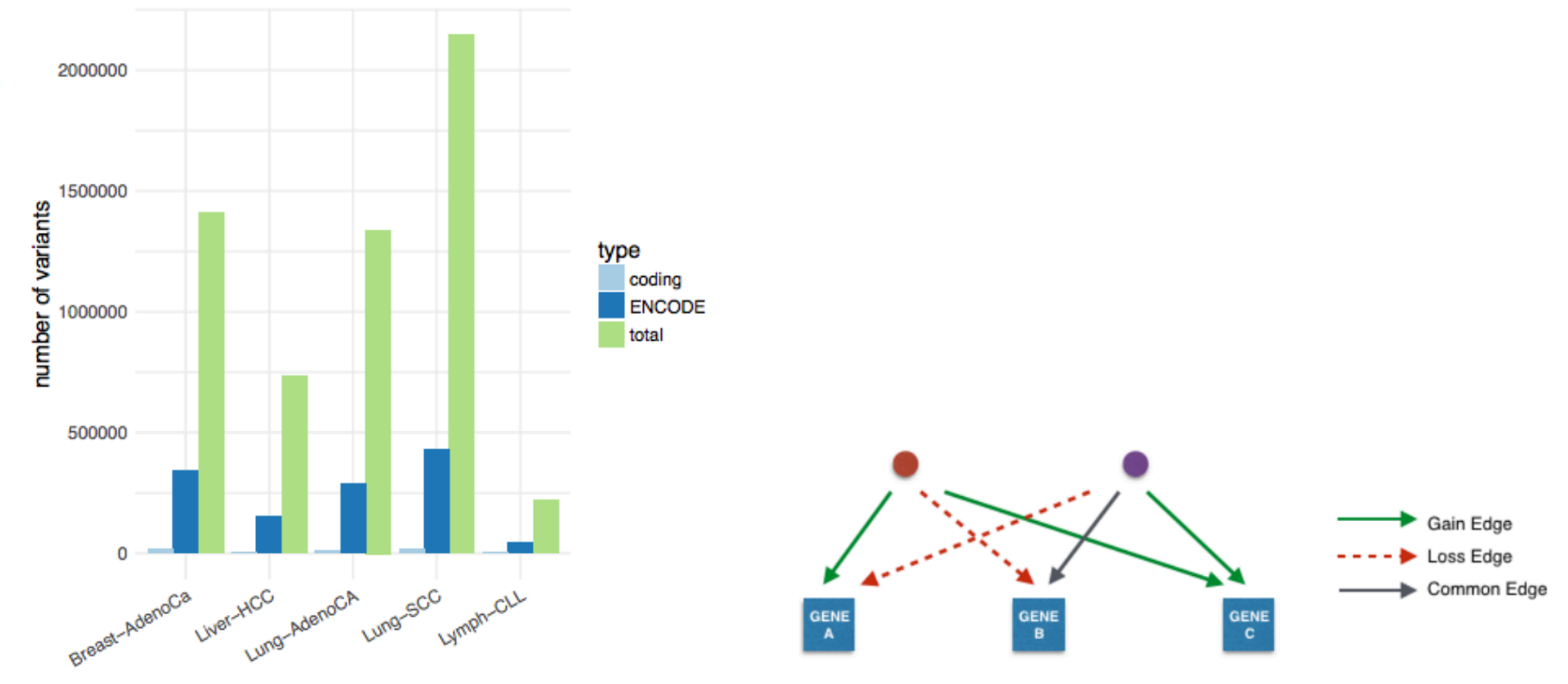
Data Matrix

		K562	GM12878	HepG2	Liver	A549	IMR-90	MCF-7	MCF-10A	HeLa-S3
Cis-regulatory Elements	DNase-seq	1	1	1	0	1	1	0	0	1
	EnhancerSeq	1	1	0	0	0	0	0	0	0
DNA-binding Proteins (ChIP-seq)	TF	209	101	97	7	32	9	52	4	60
	TFSS	64	50	48	5	21	6	15	3	29
	Chromatin	17	6	7	0	3	1	3	1	4
	Histone	12	11	11	7	11	28	5	0	11
Methylation	WGBS	1	1	1	1	0	1	0	0	0
	RRBS	1	1	1	1	1	1	1	1	1
Transcription	RNA-seq	1	1	1	1	1	1	1	0	1
	RAMPAGE	1	1	0	0	0	0	0	0	0
Replication Timing	Repli-seq	1	1	1	0	0	0	1	0	1
	Repli-chip	0	0	0	0	0	1	0	0	1
Knockdown	siRNA	29	0	0	0	0	0	2	0	0
	shRNA	219	0	221	0	0	0	0	0	0
3D Chromatin Structure	ChIA-PET	3	1	1	0	0	0	4	0	1
	Hi-C	1	1	0	0	1	0	1	0	0
WGS	SNV	1	1	0	0	0	0	1	0	1
	SV	1	1	0	0	0	0	1	0	1
Cohort		95	0	327	0	38	0	198	0	2
		T	N	T	N	T	N	T	N	T
		Blood	Liver	Liver	Lung	Lung	Breast	Breast		Cervix

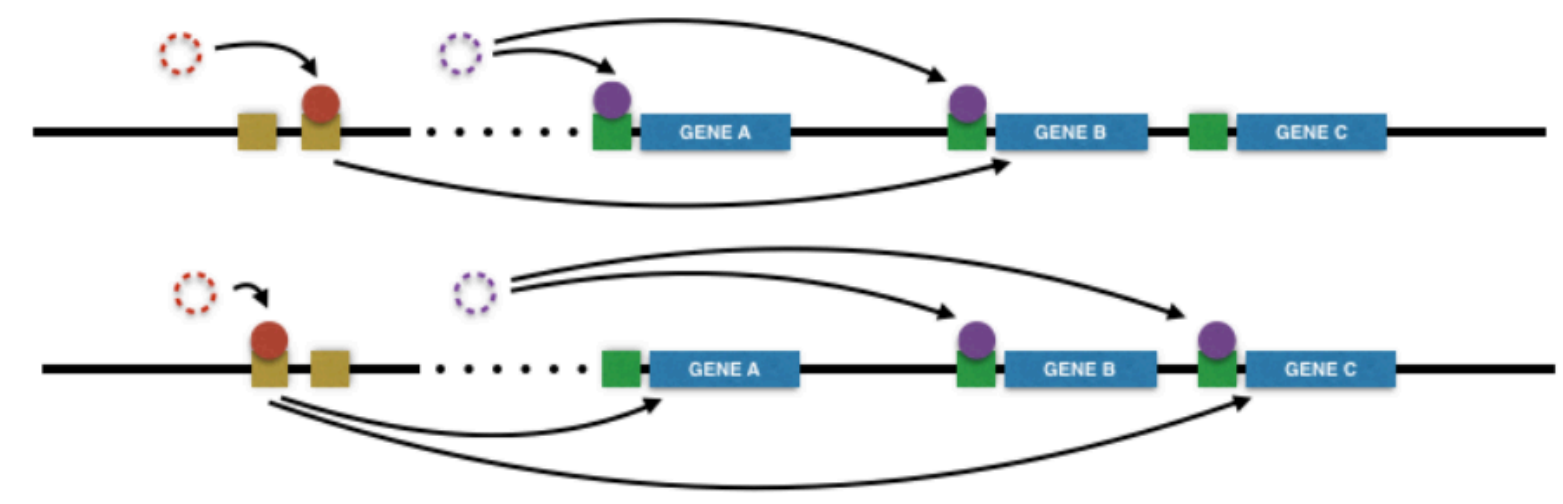
***Cohort:**
 K562::CLLE, HepG2::LIHC, A549::LUAD, MCF-7::BRCA, HeLa-S3::CESC

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

B



D



C

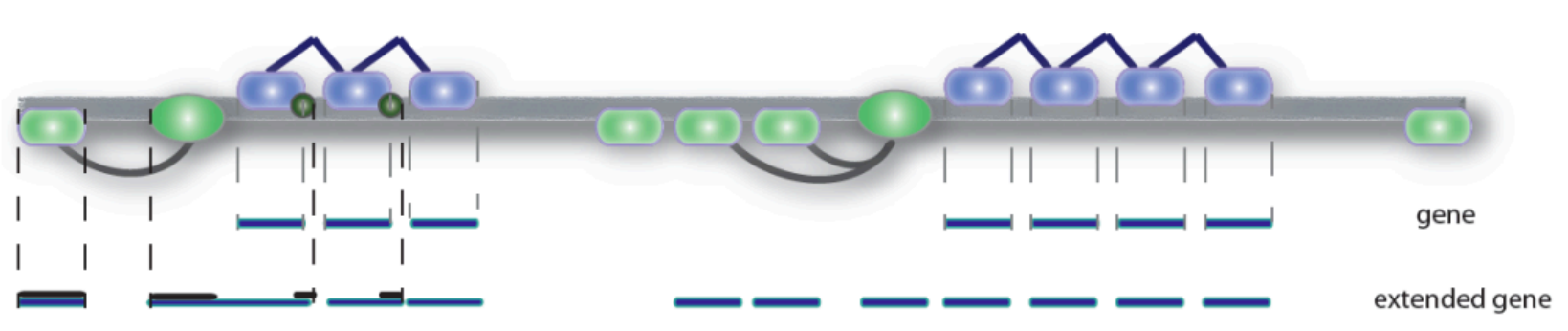


Figure 1

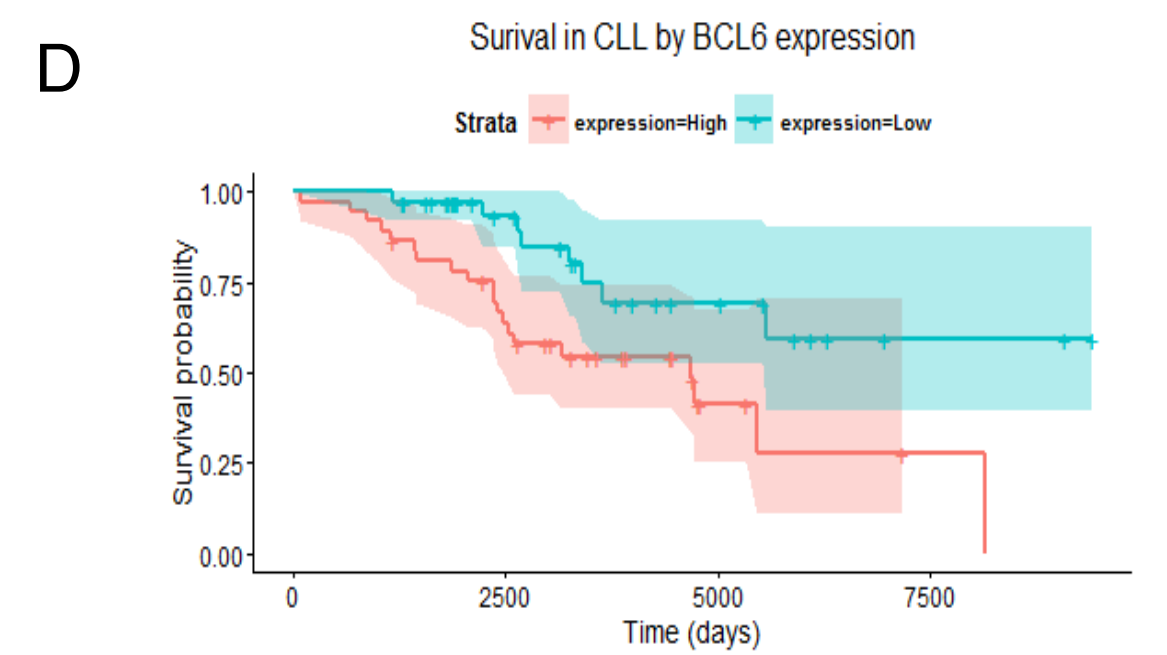
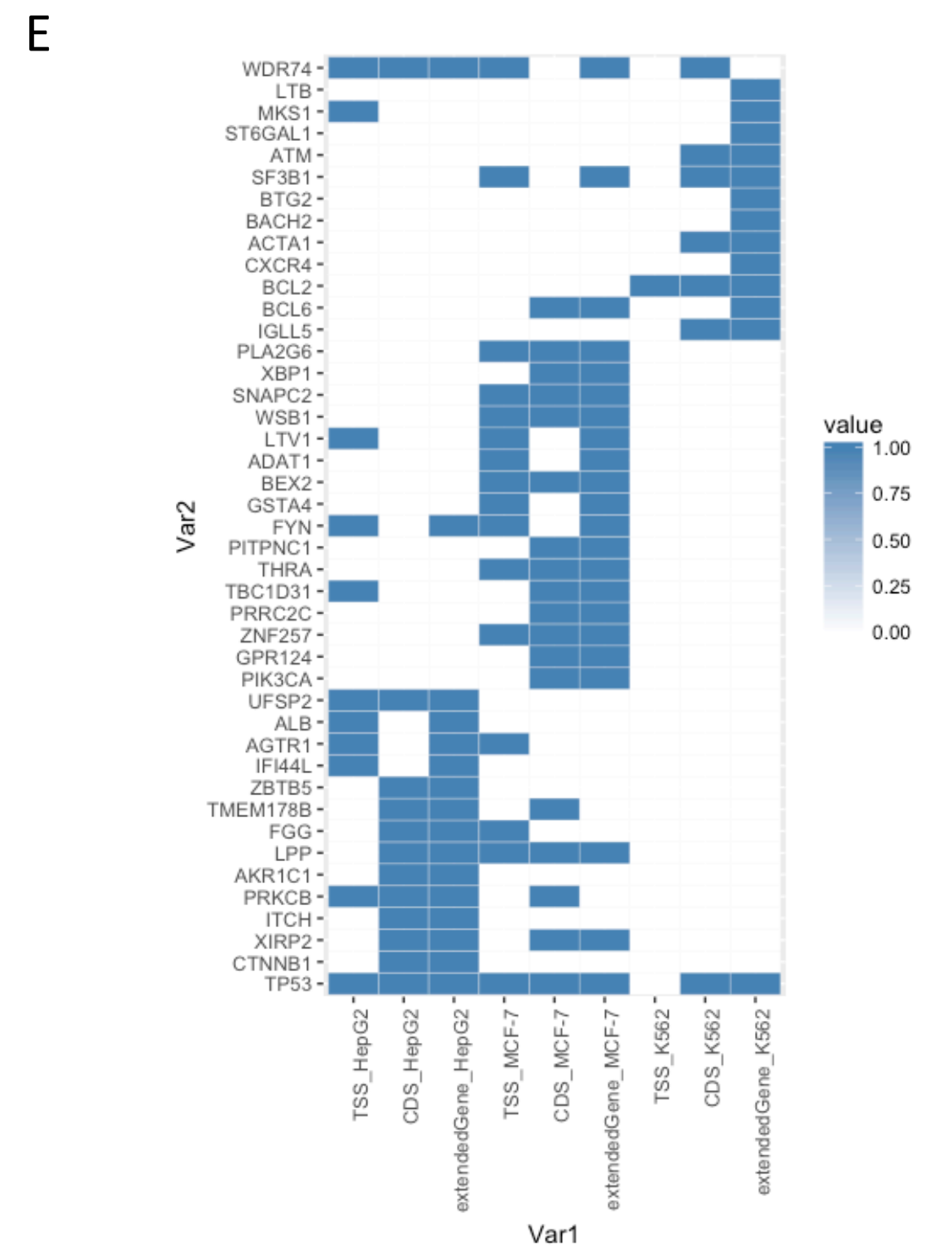
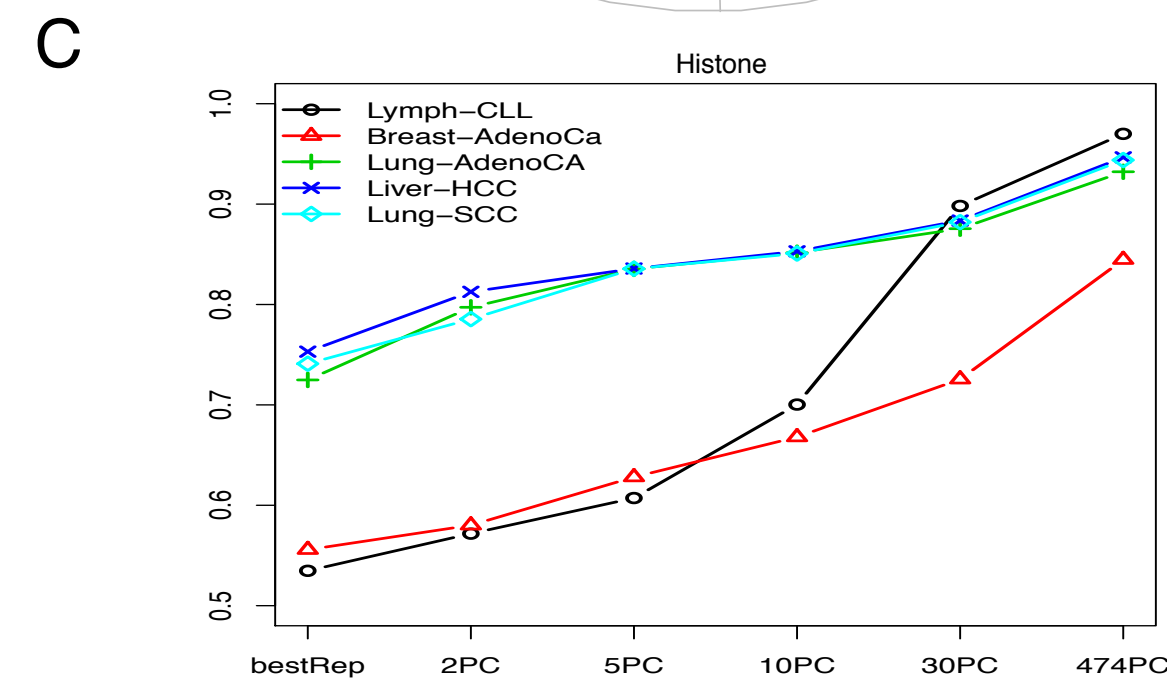
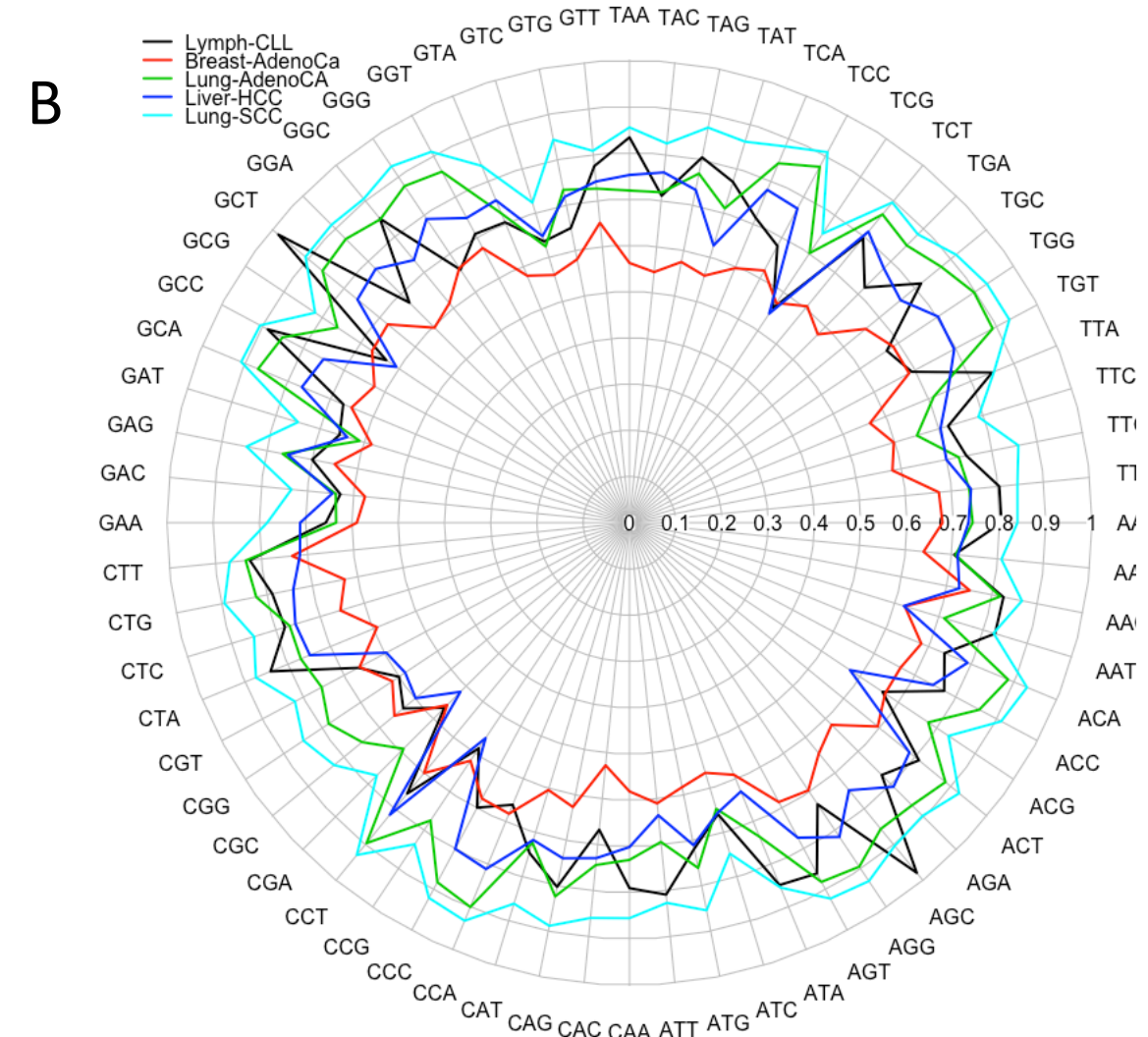
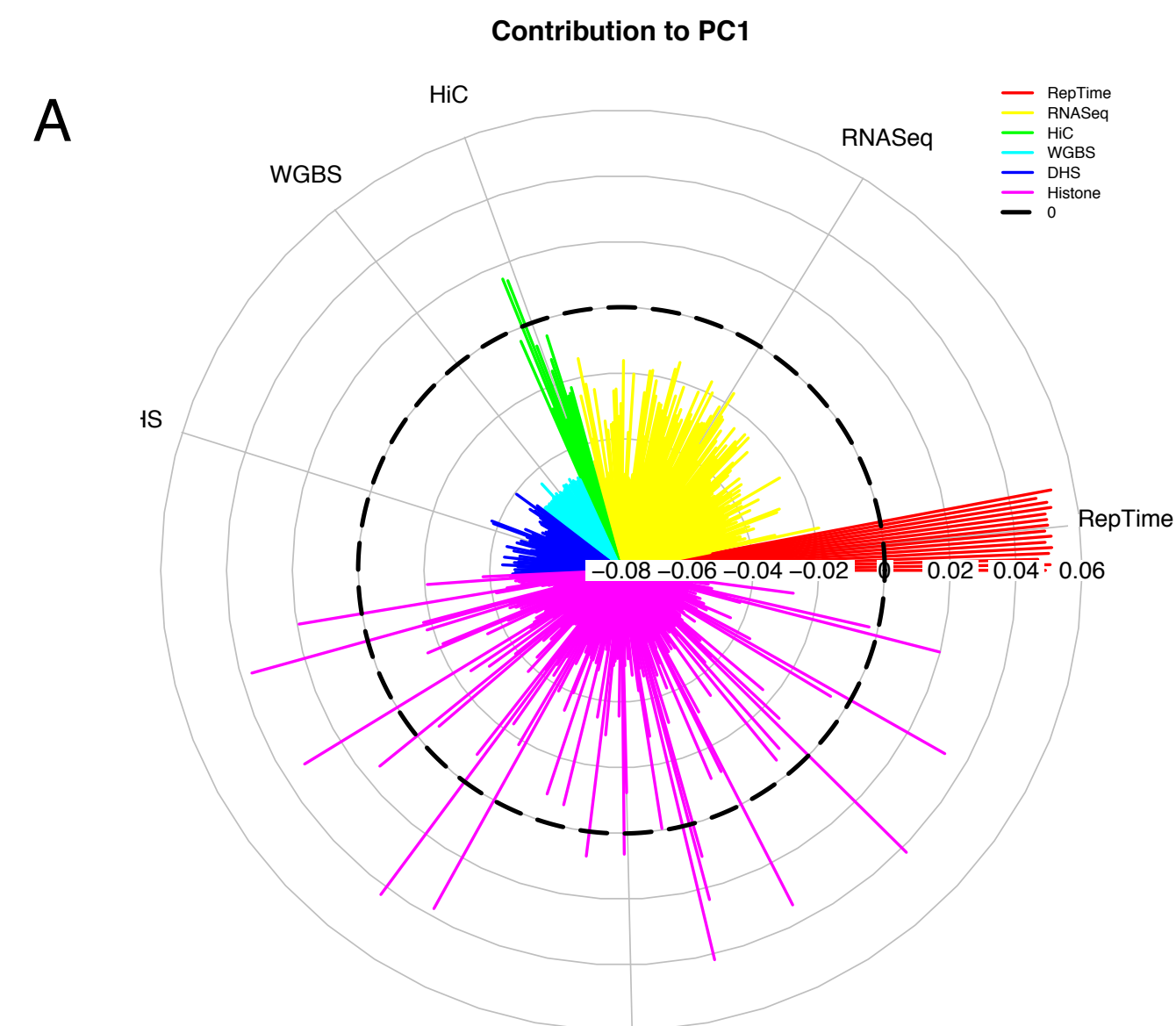


Figure 2

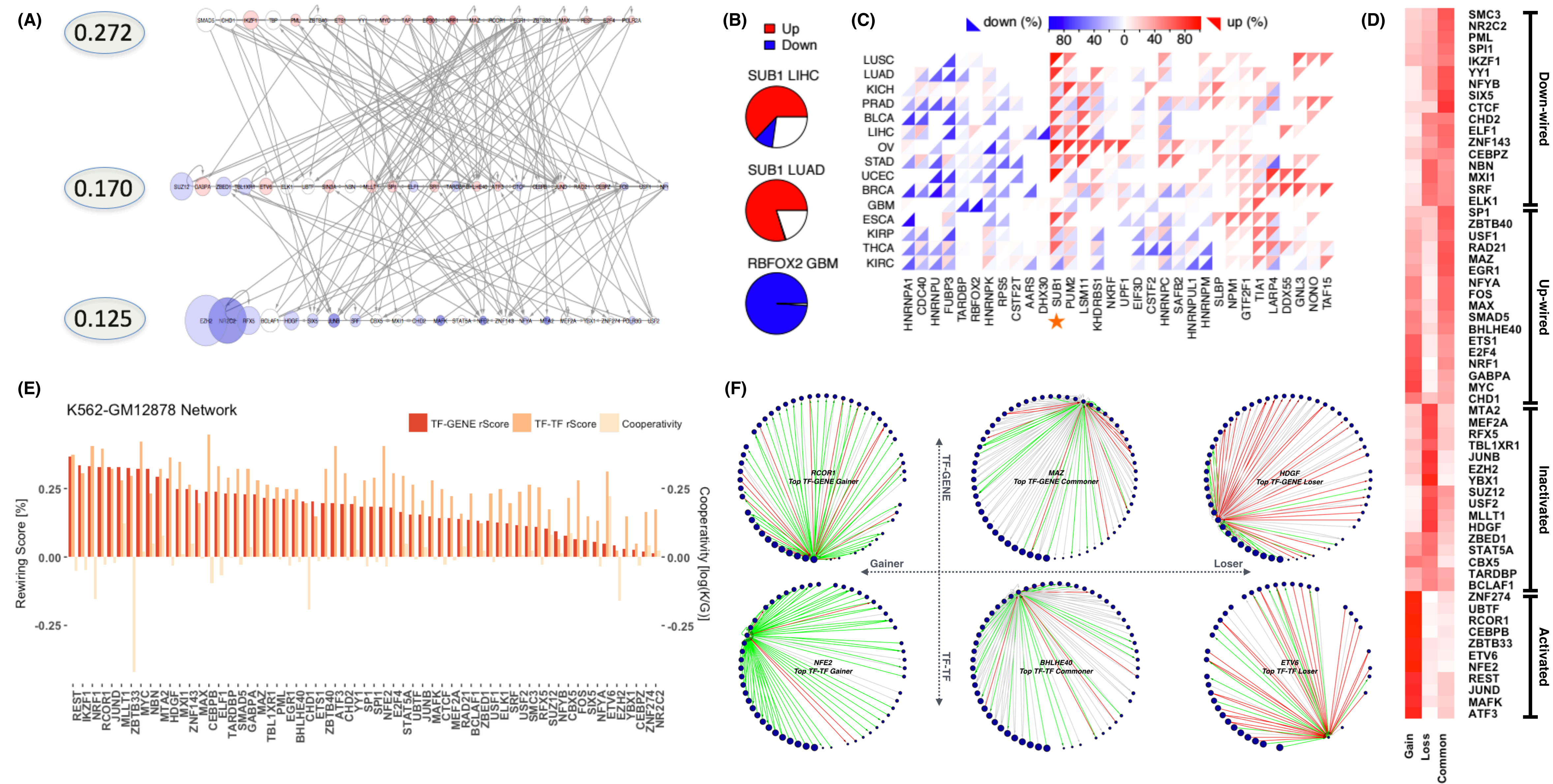


Figure 3

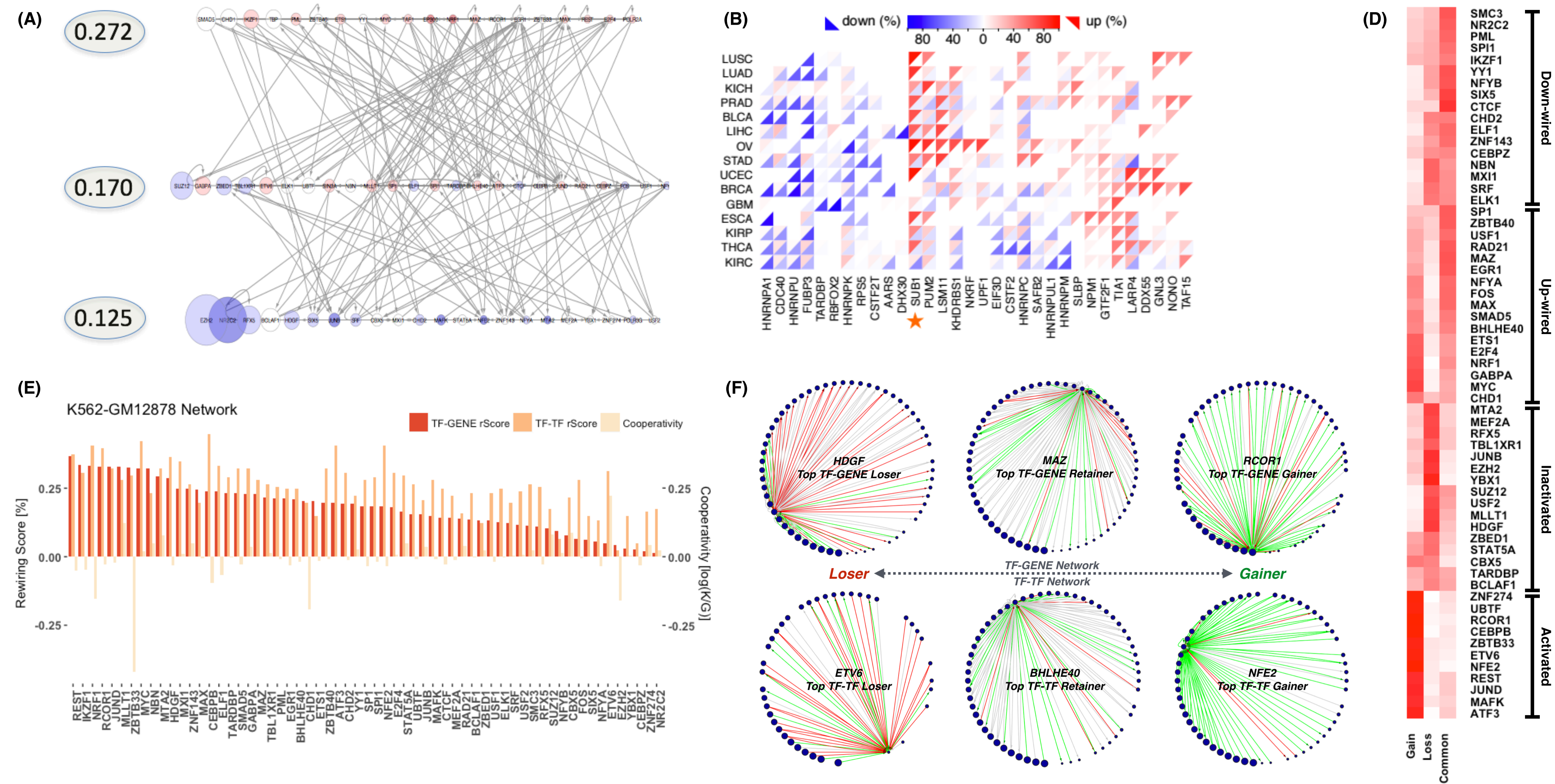
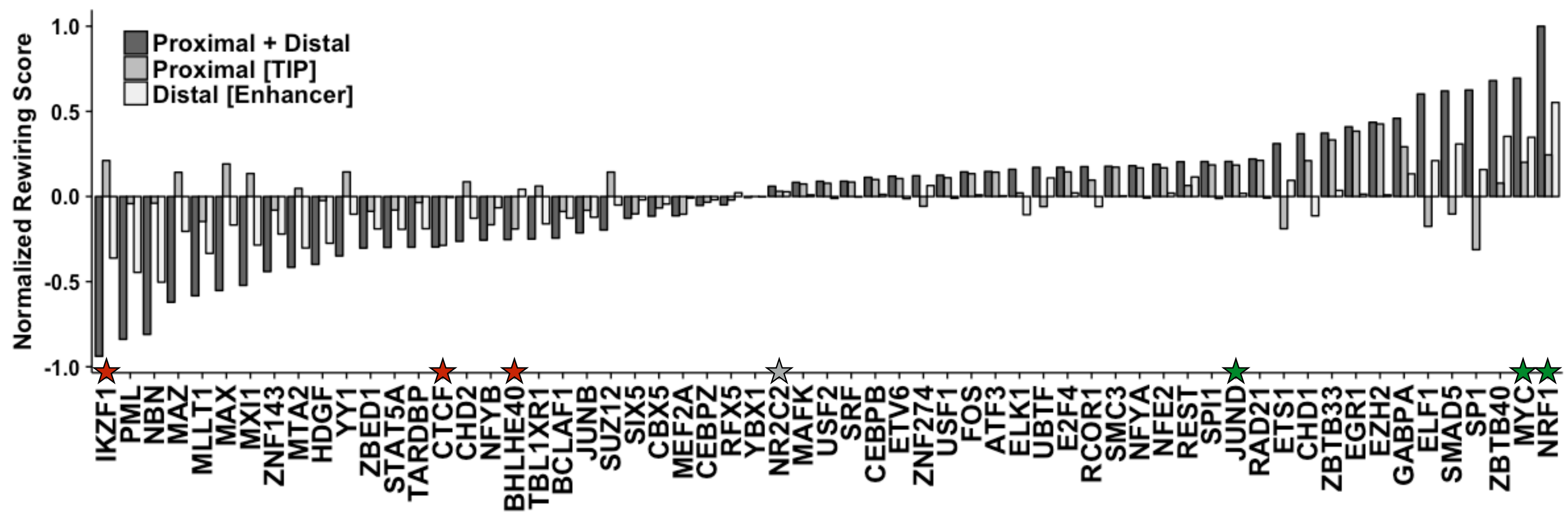
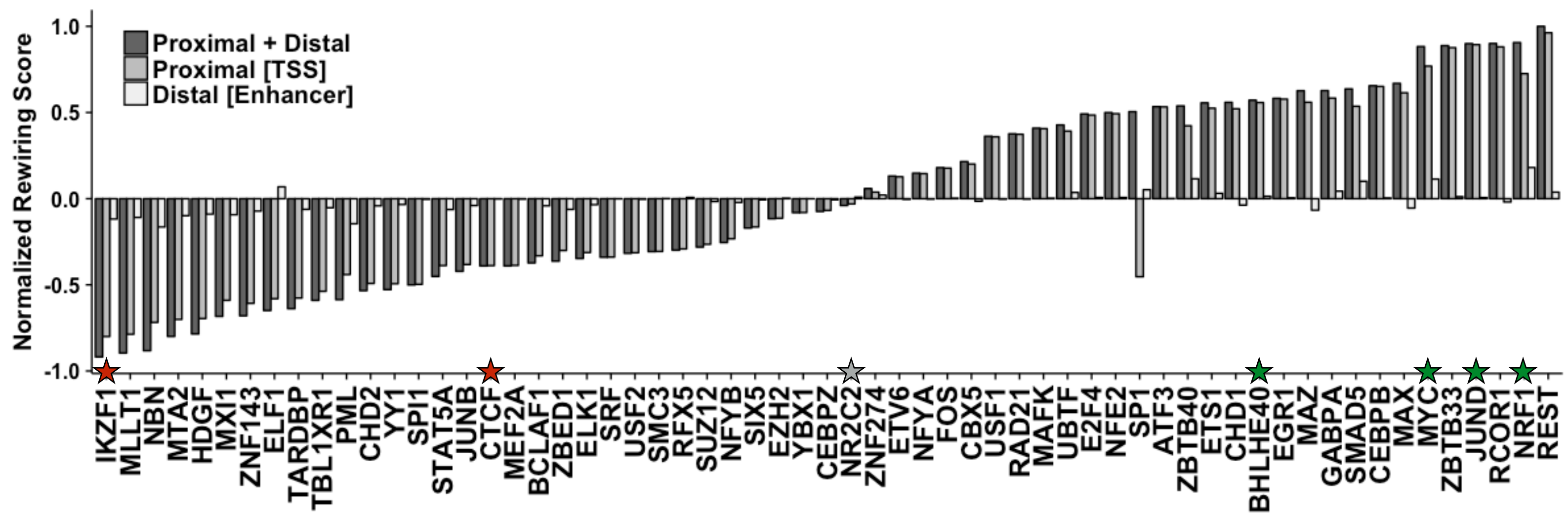
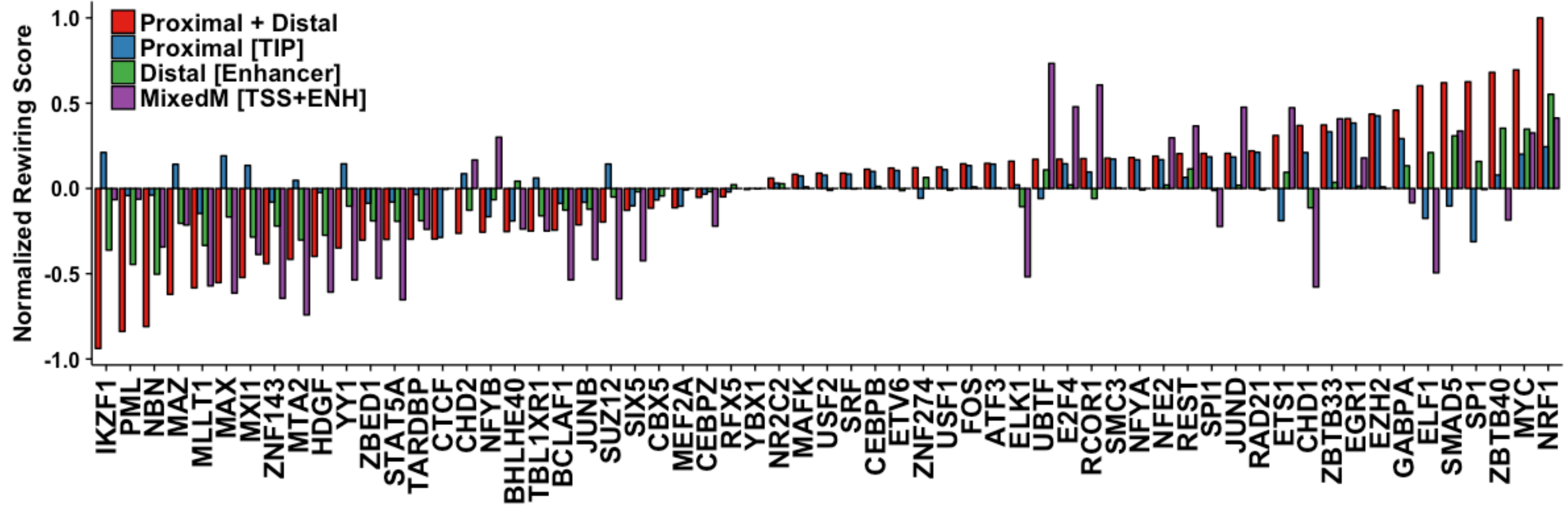
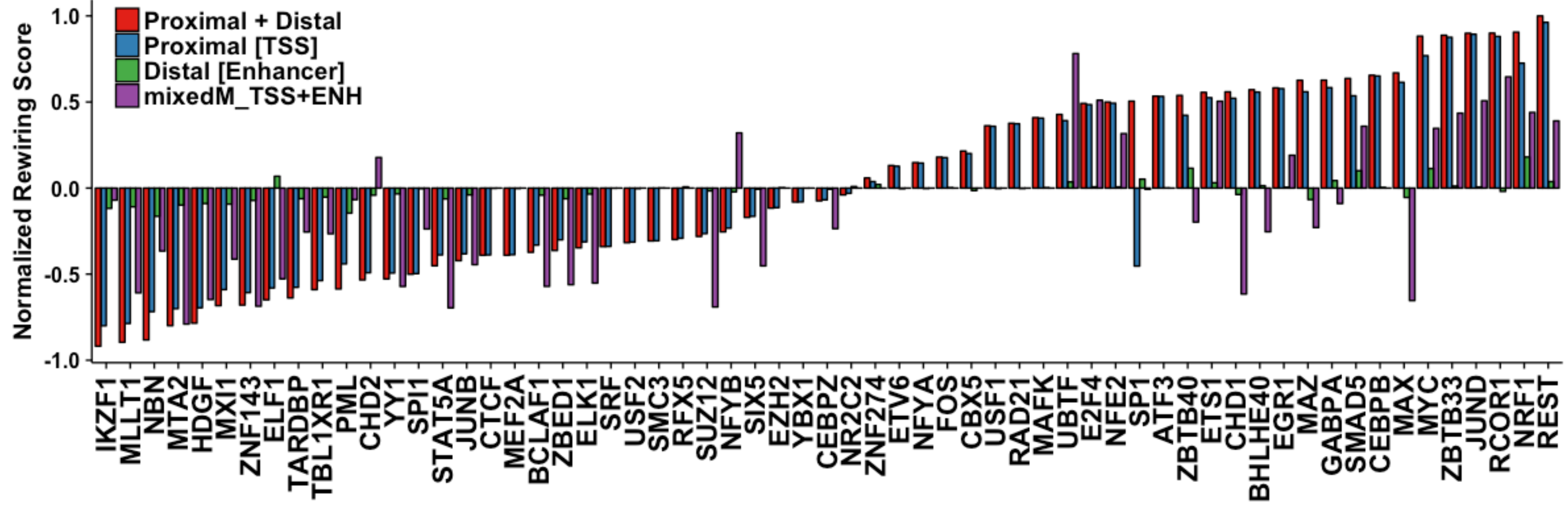


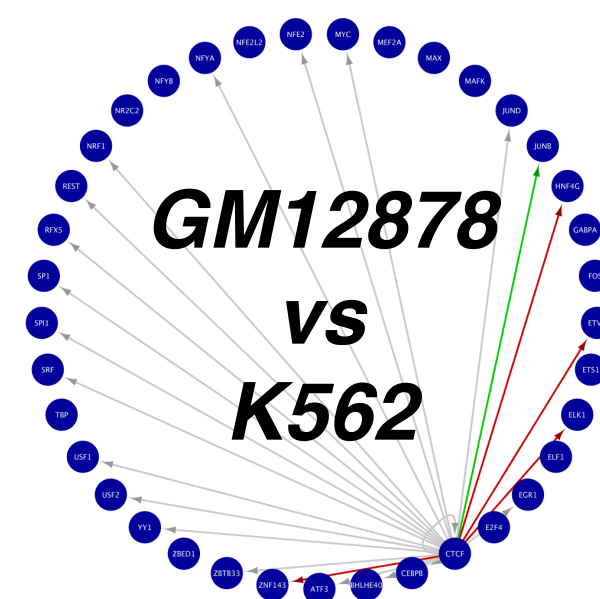
Figure 3



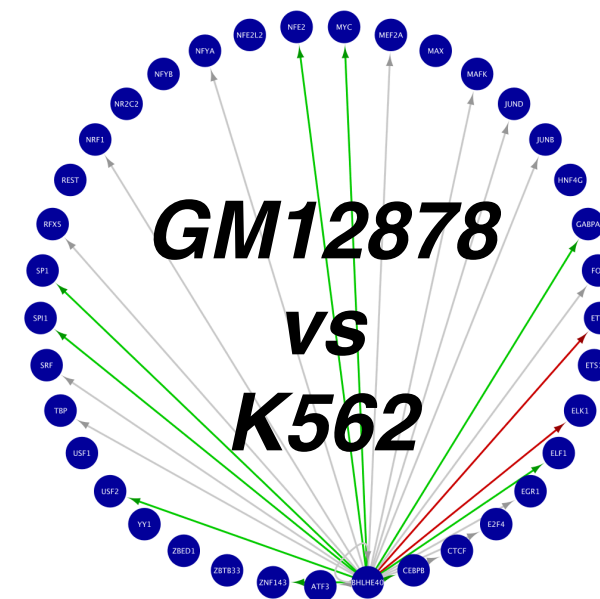
+ Shaoke's Mixed Membership Model



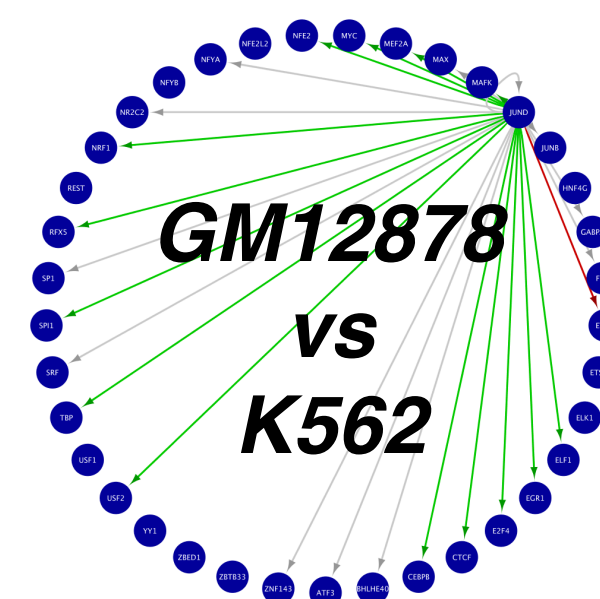
CTCF



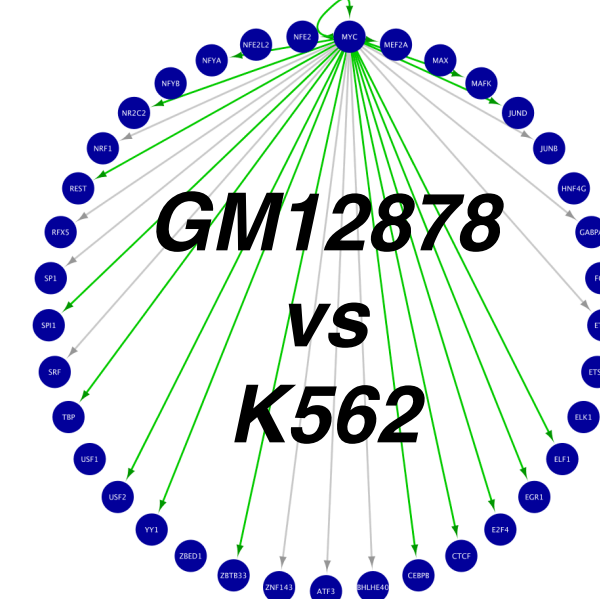
BHLHE40



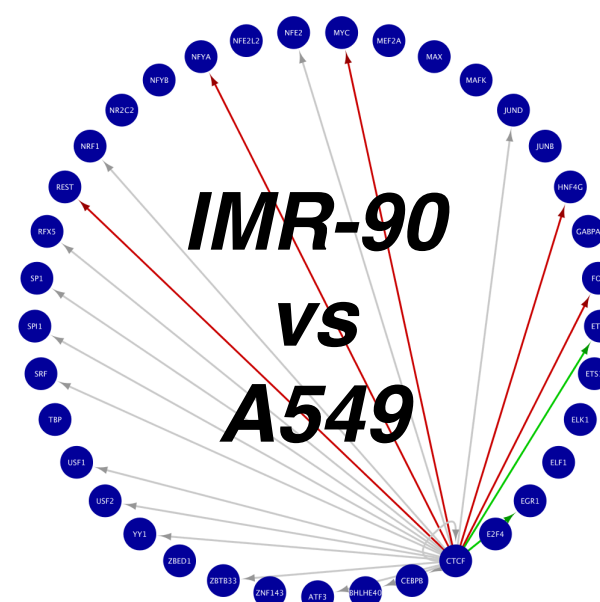
JUND



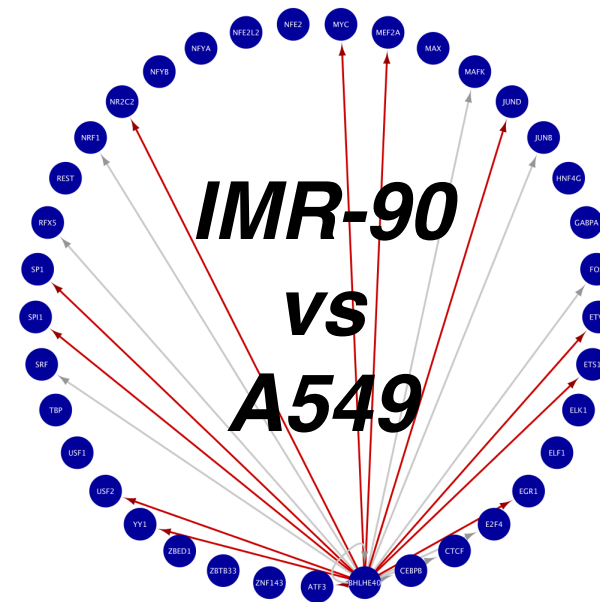
MYC



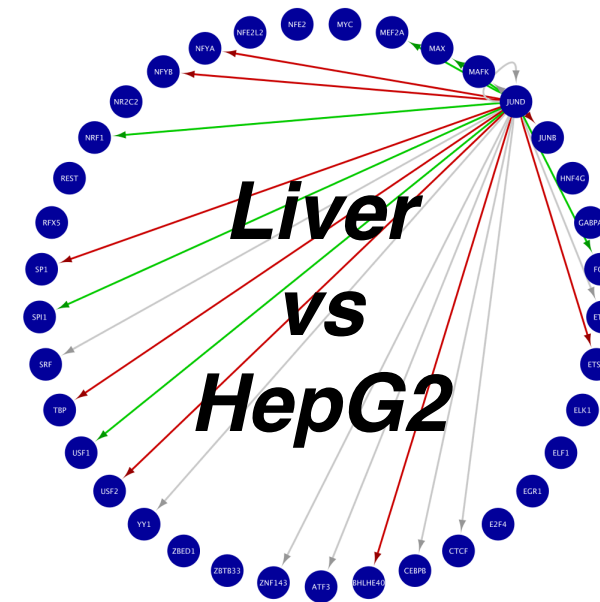
**IMR-90
vs
A549**



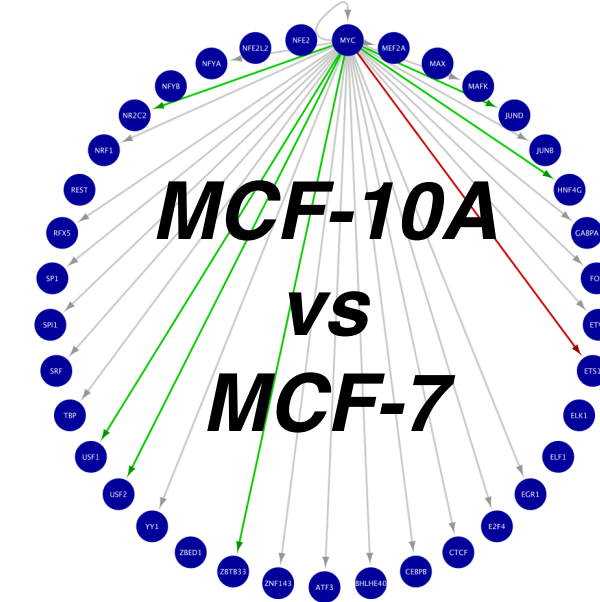
**IMR-90
vs
A549**



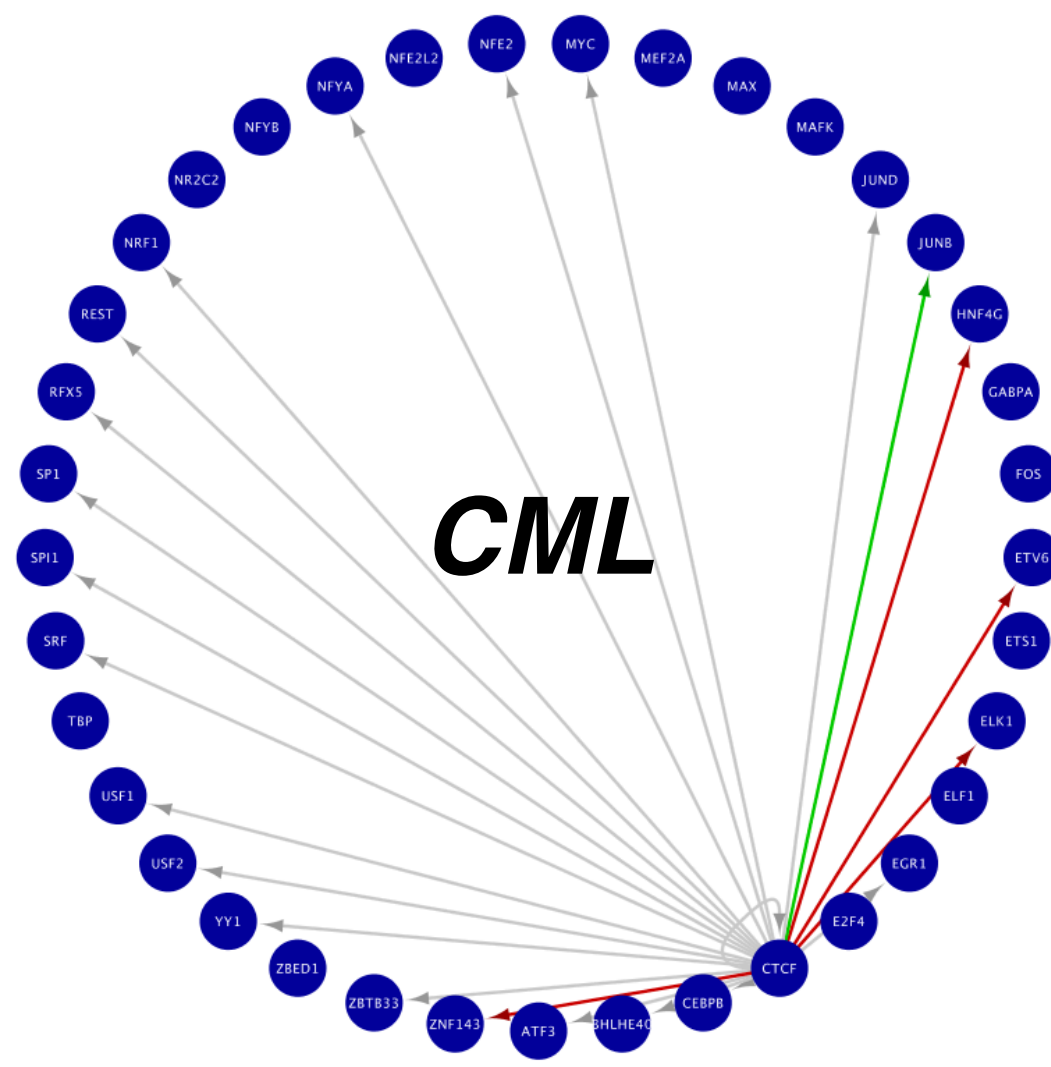
**Liver
vs
HepG2**



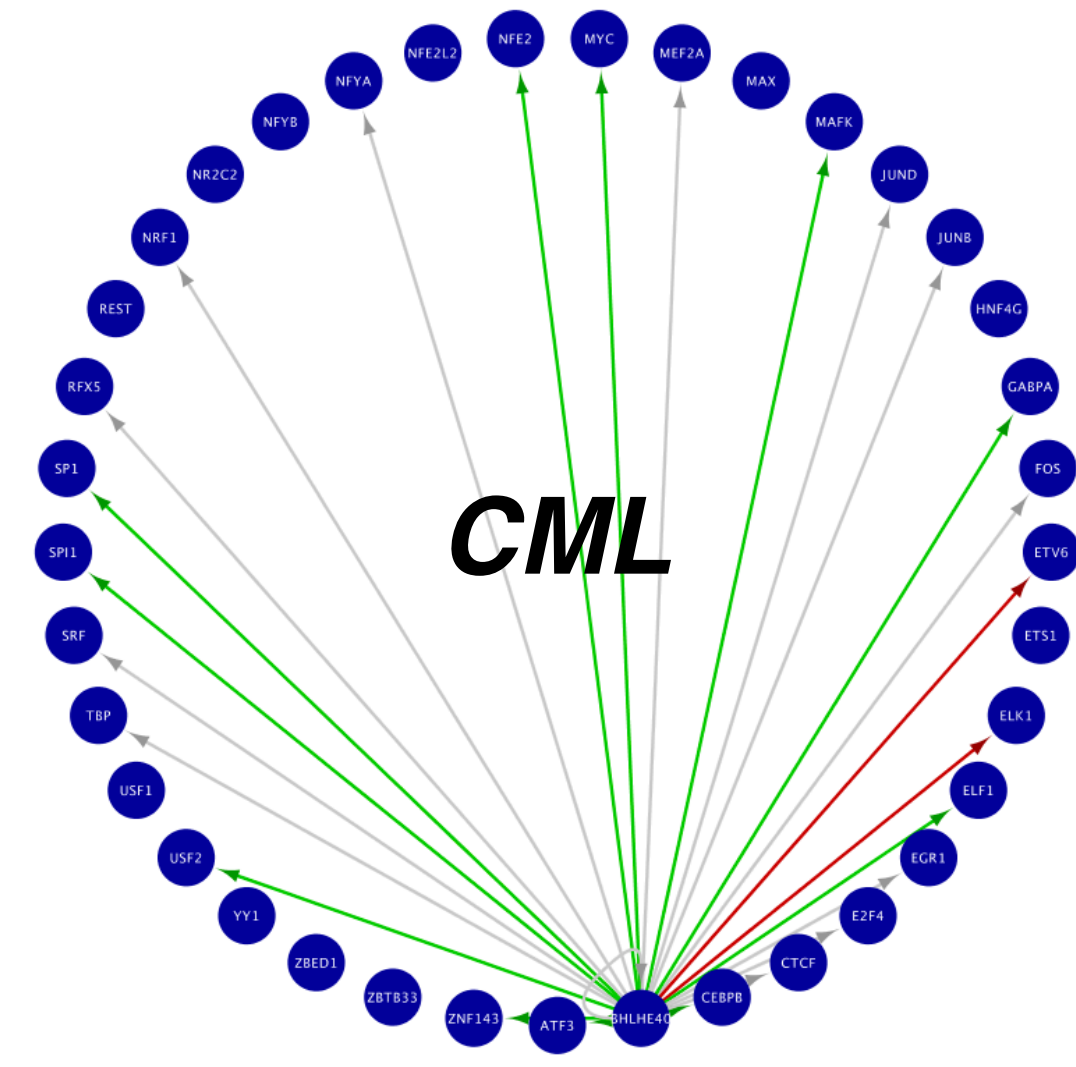
**MCF-10A
vs
MCF-7**



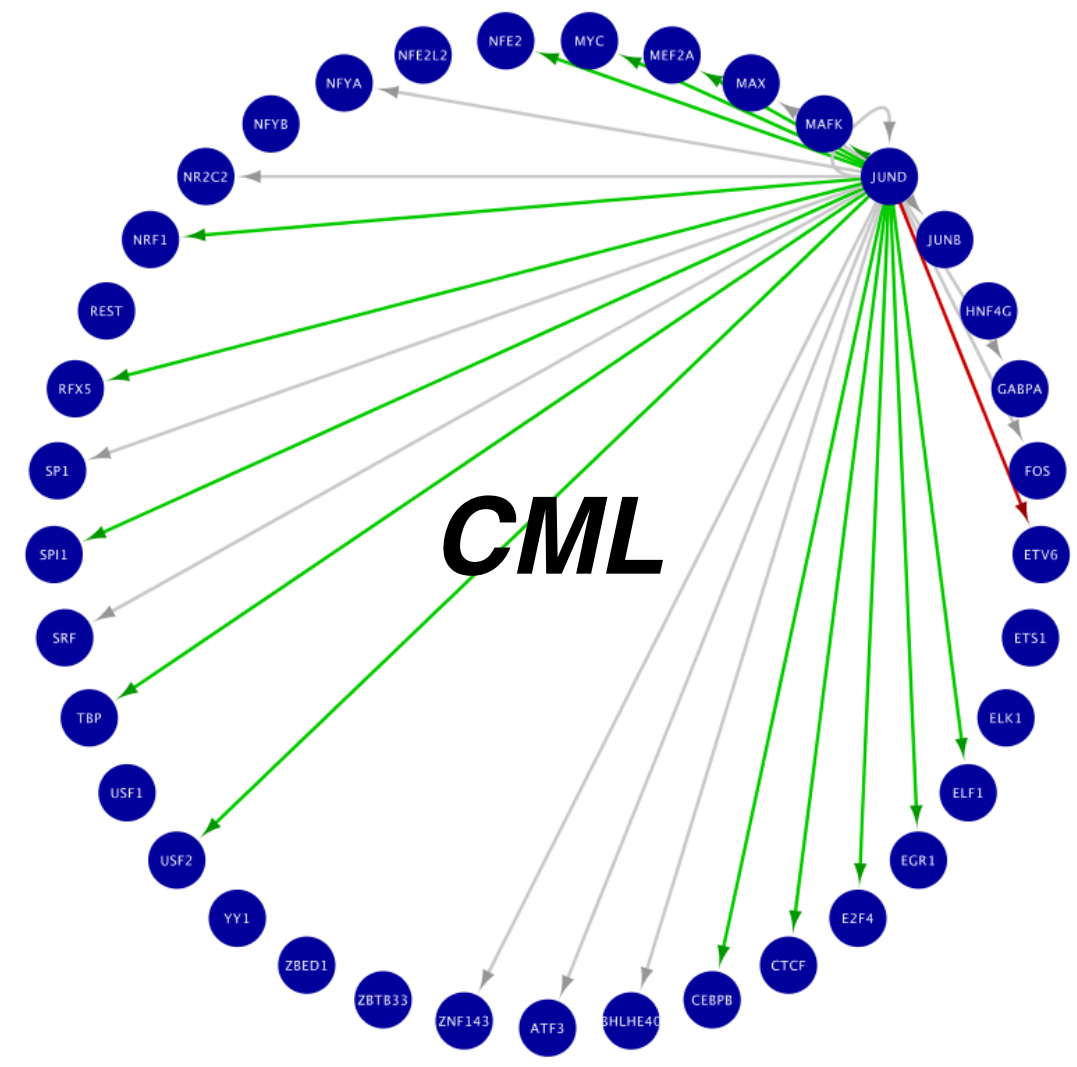
CTCF



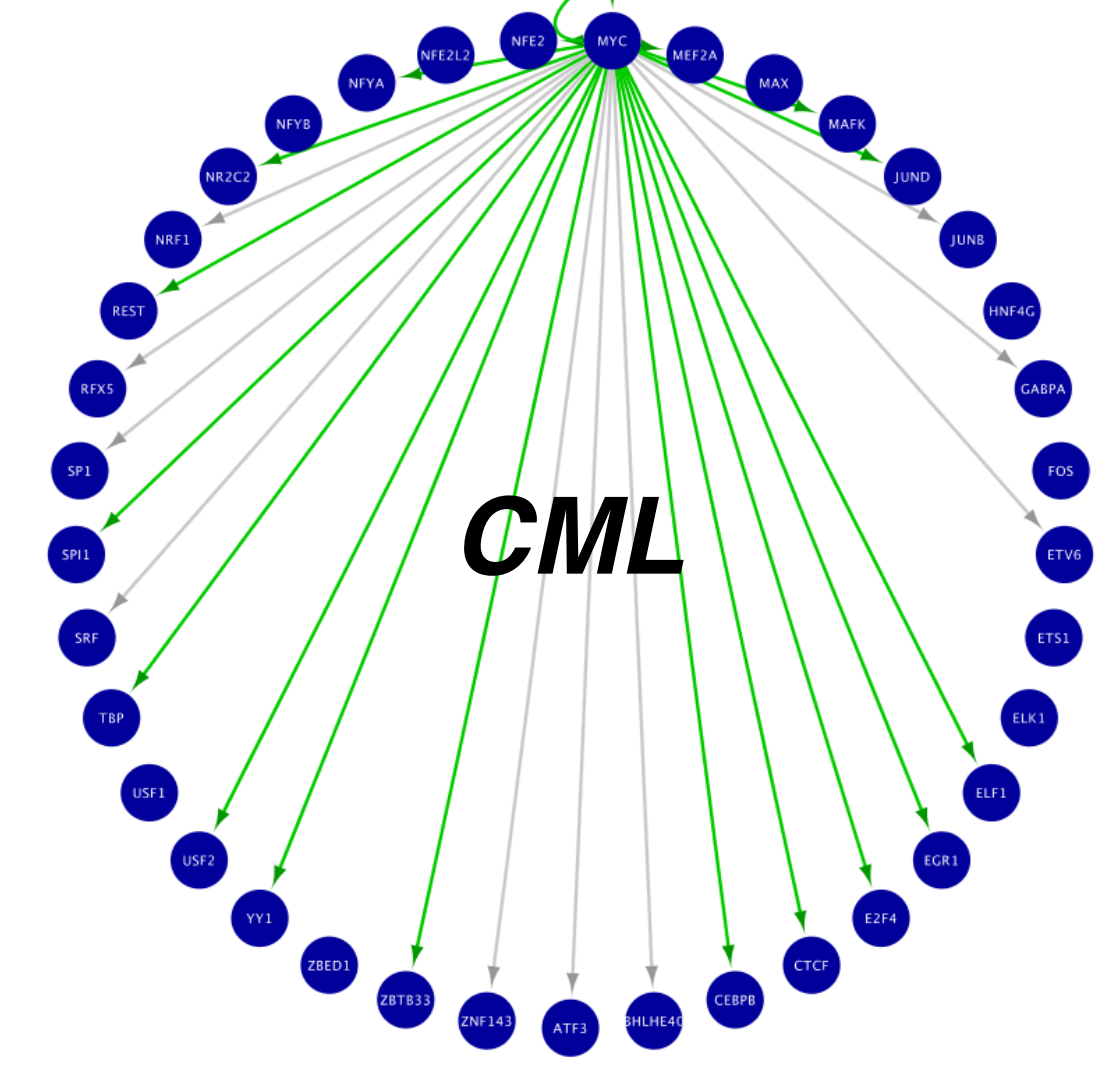
BHLHE40



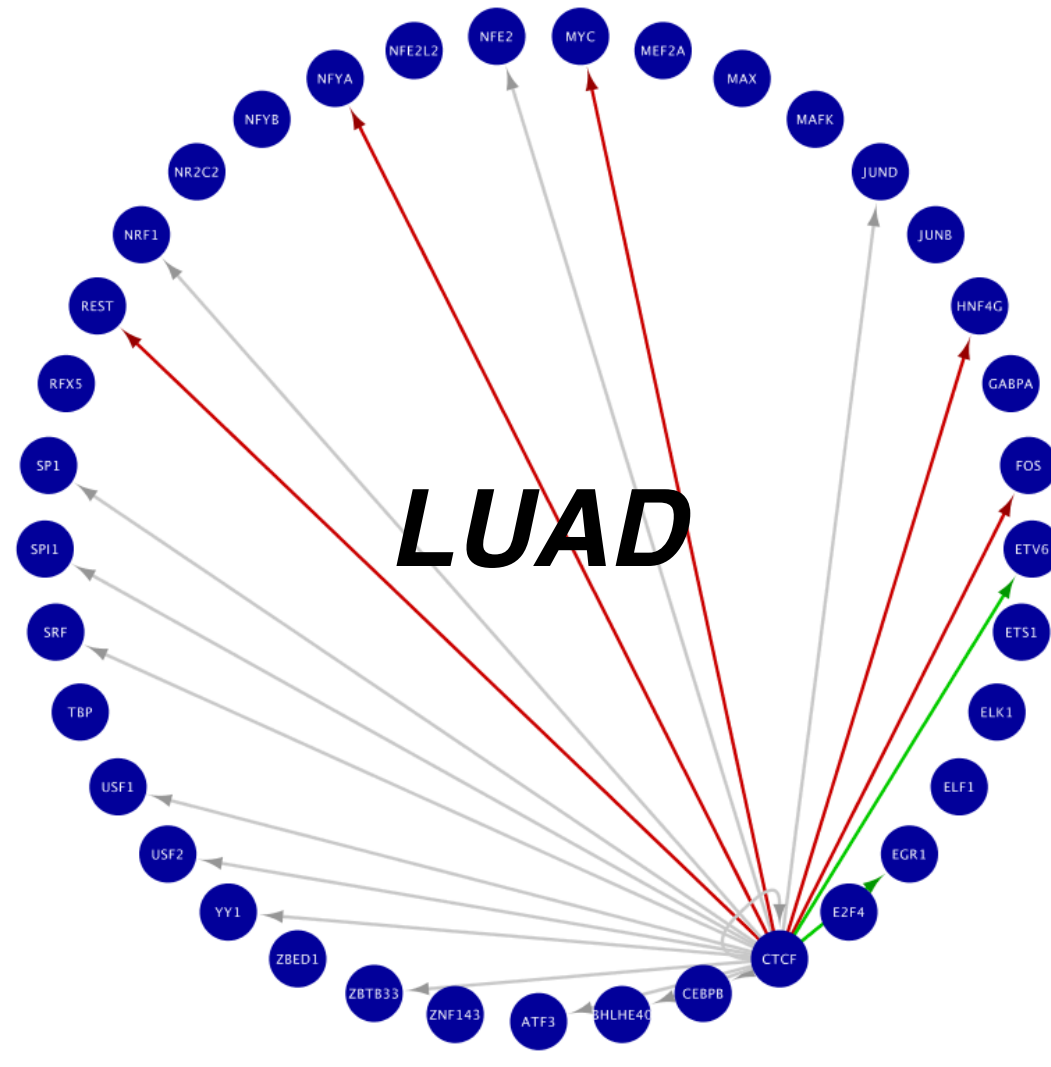
JUND



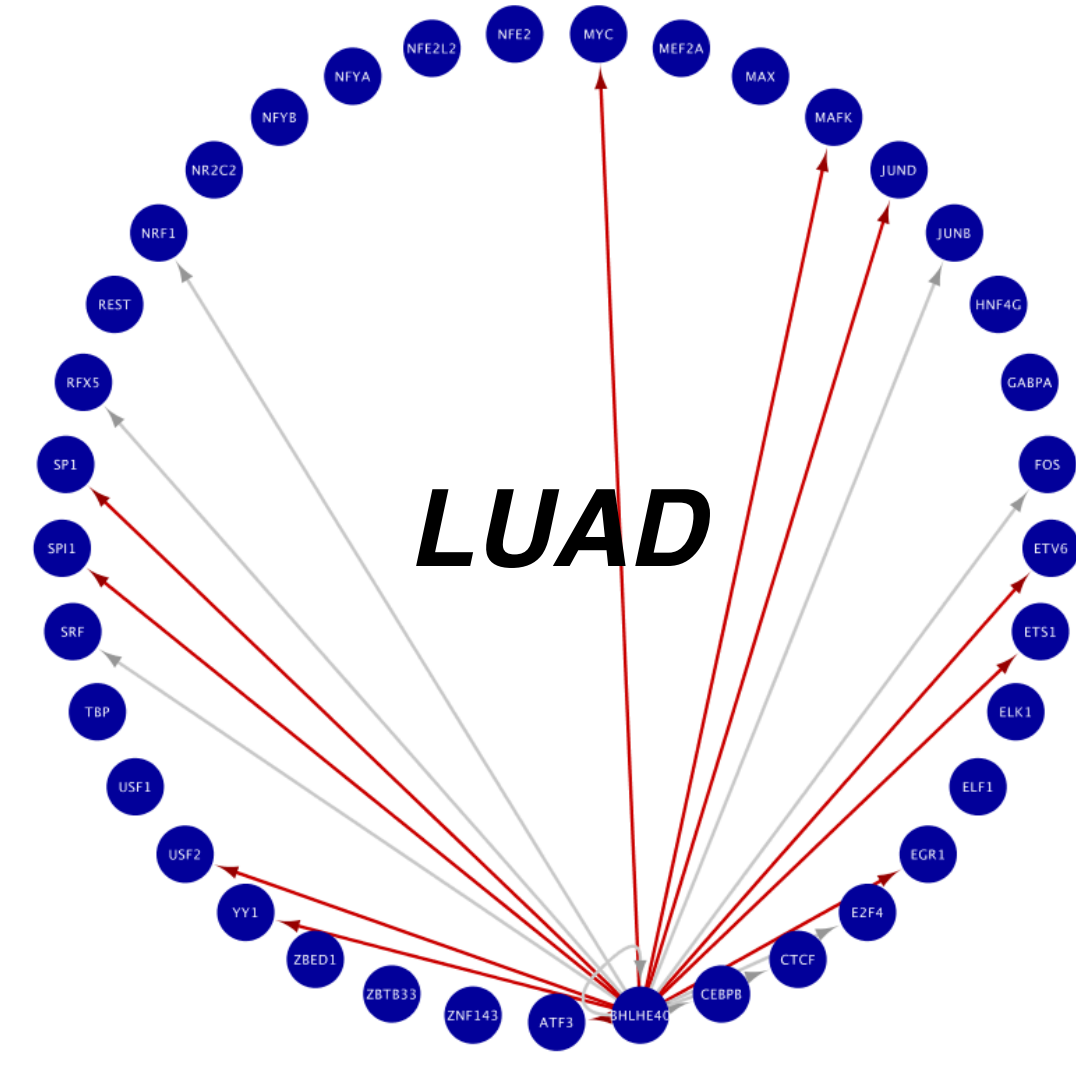
MYC



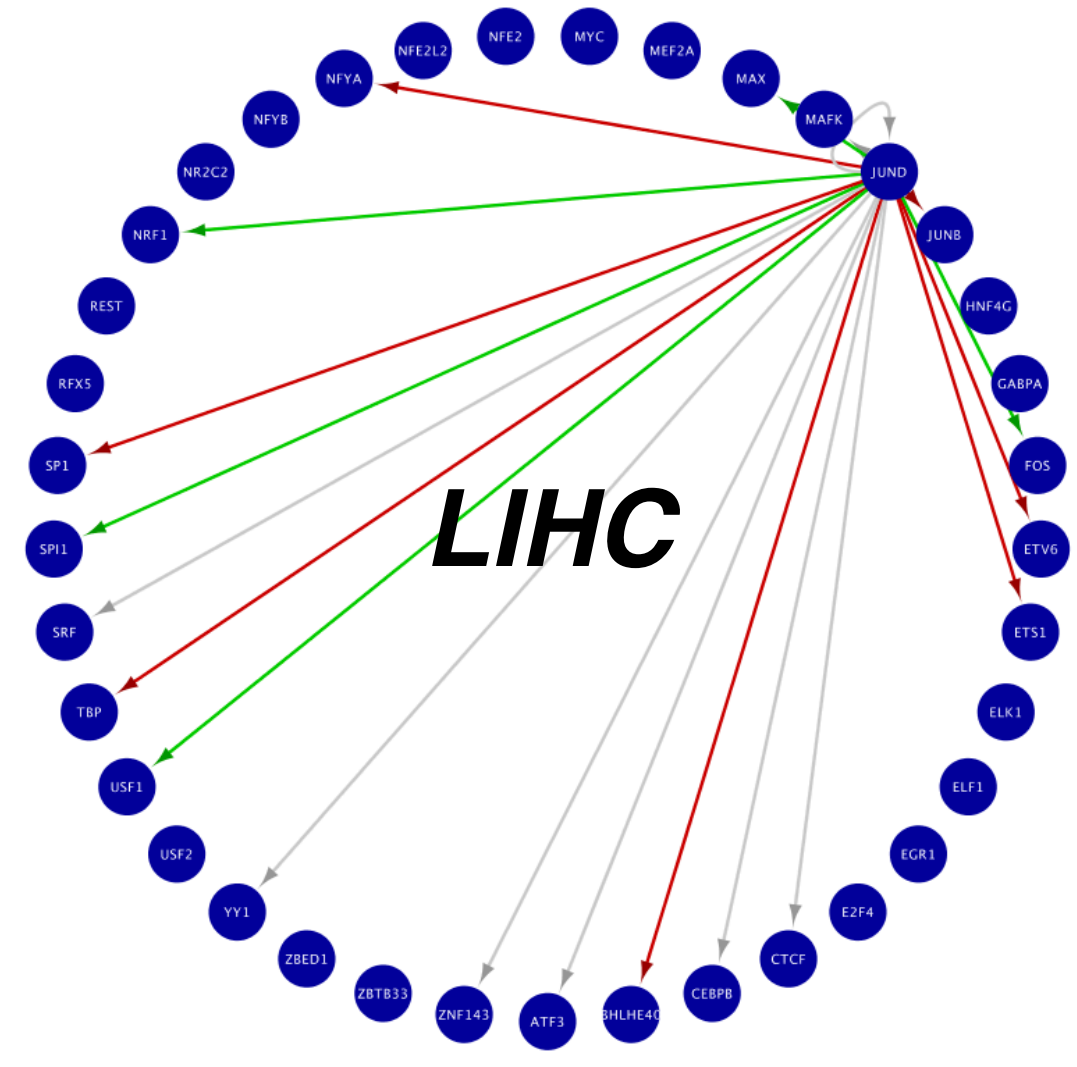
LUAD



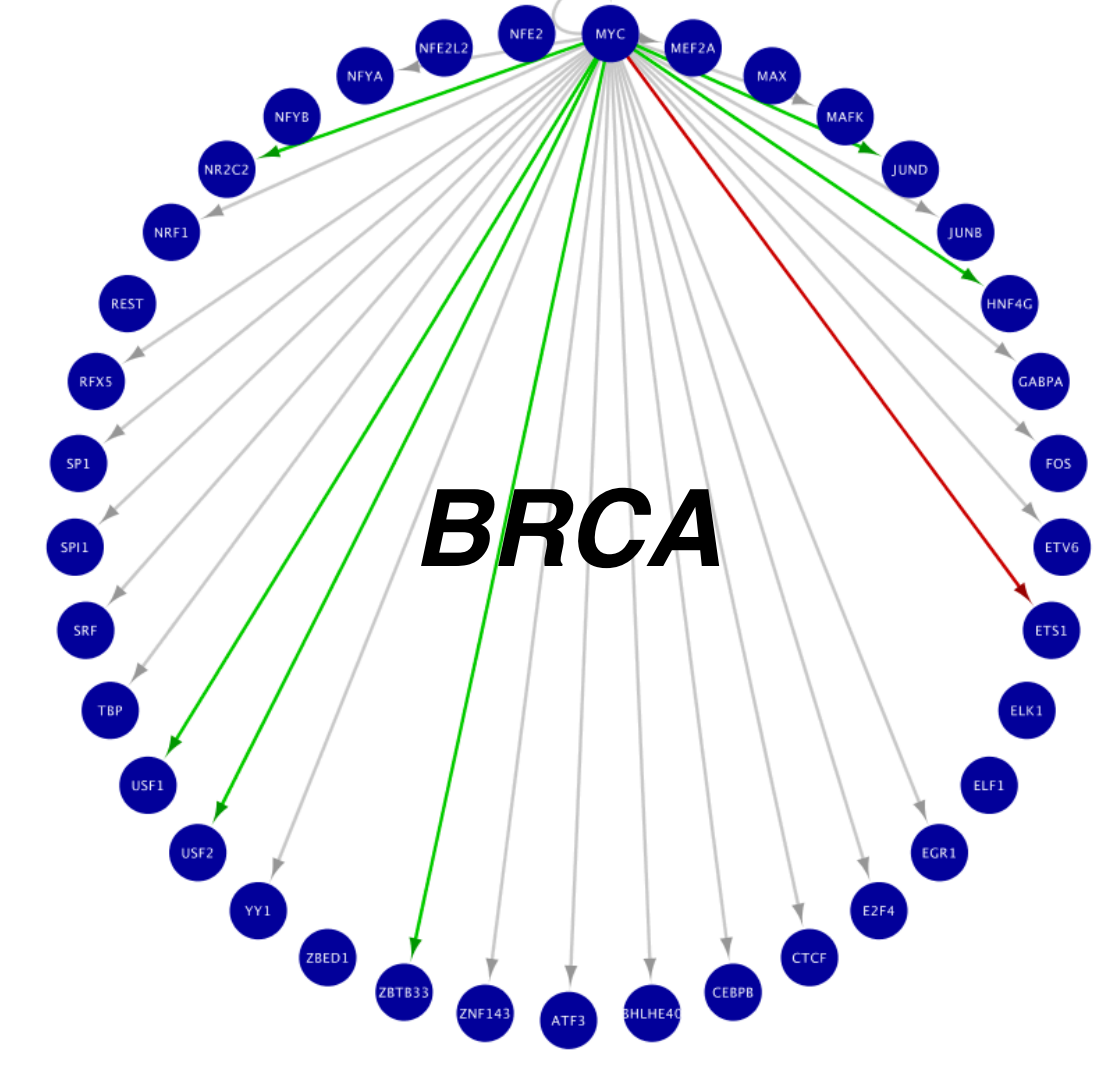
LUAD



LIHC



BRCA



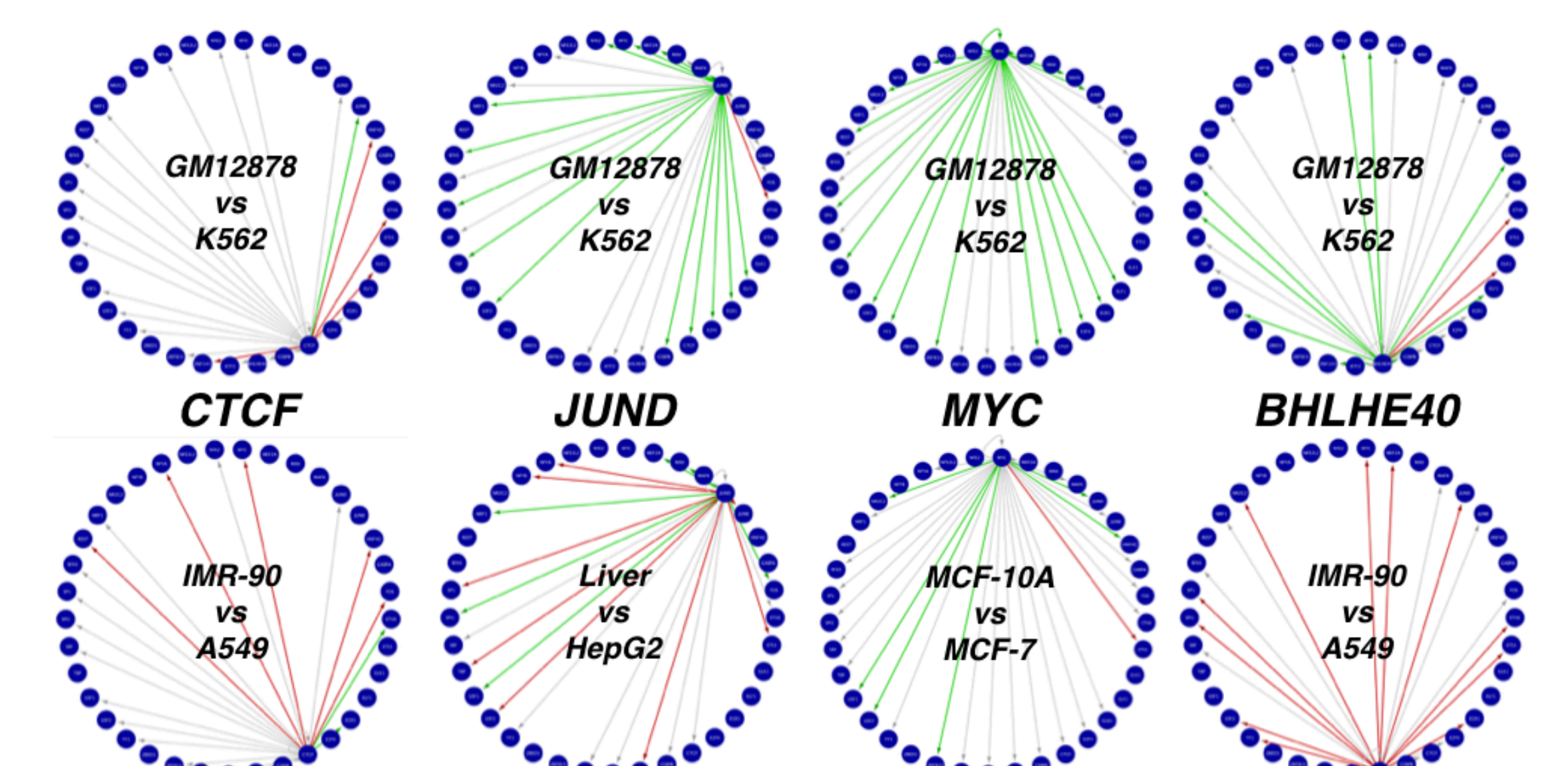
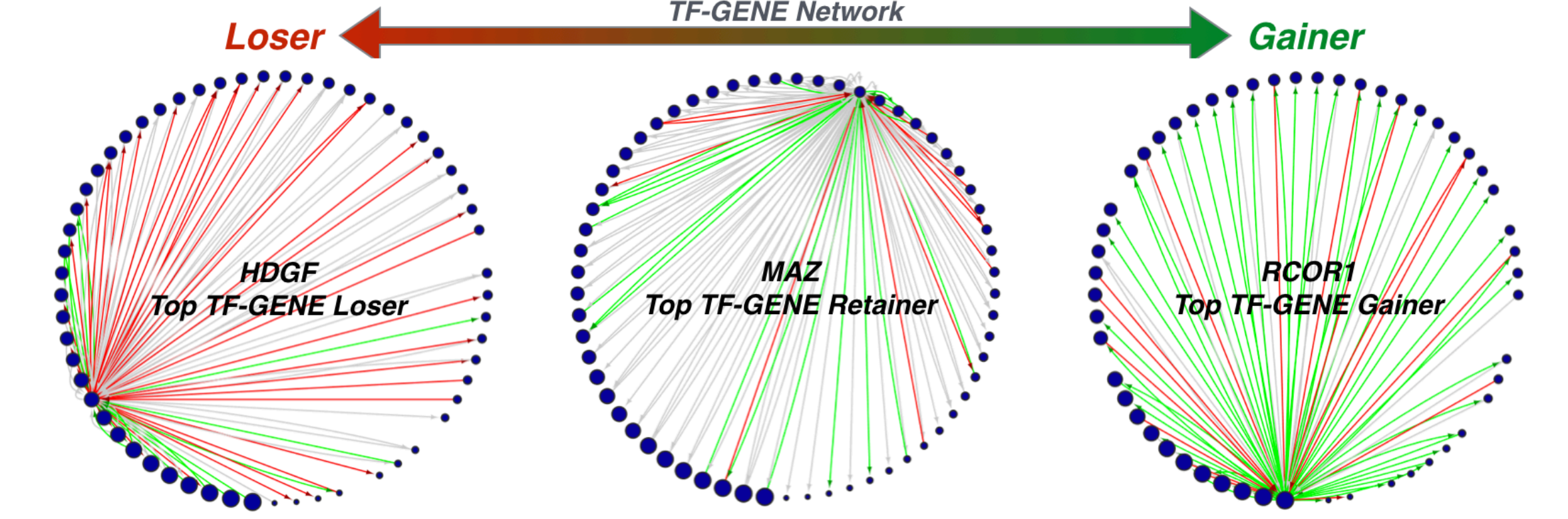
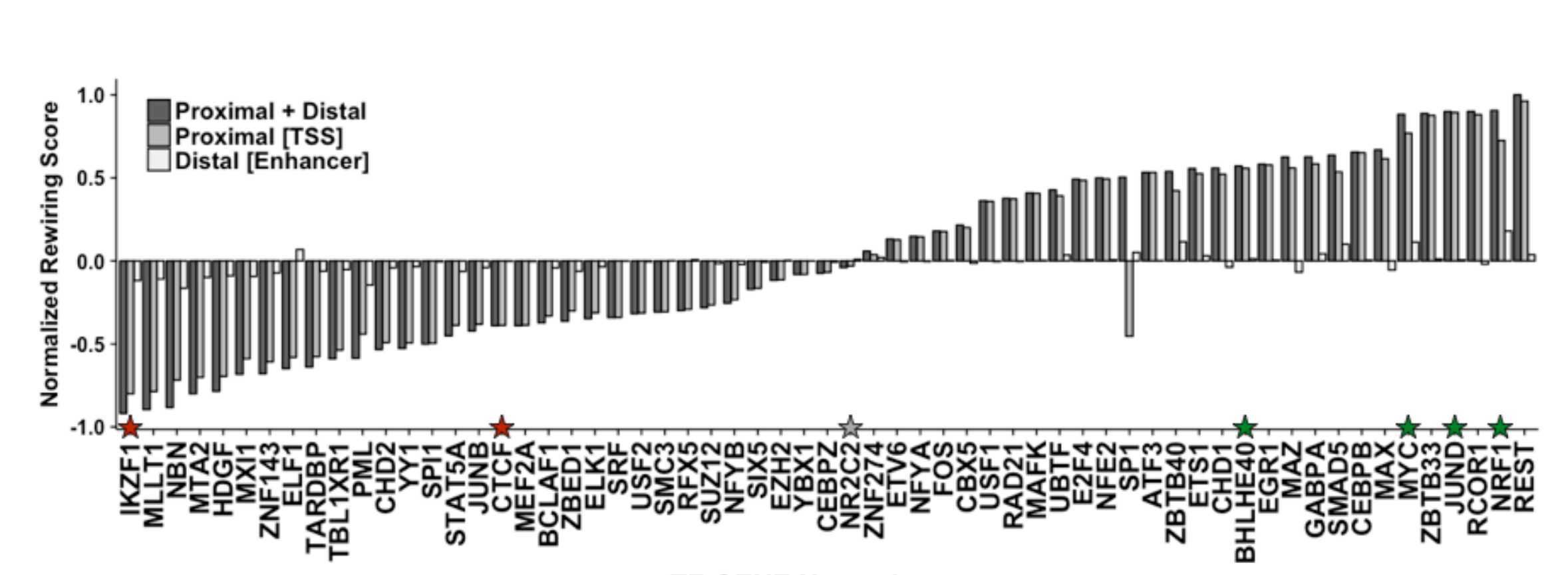
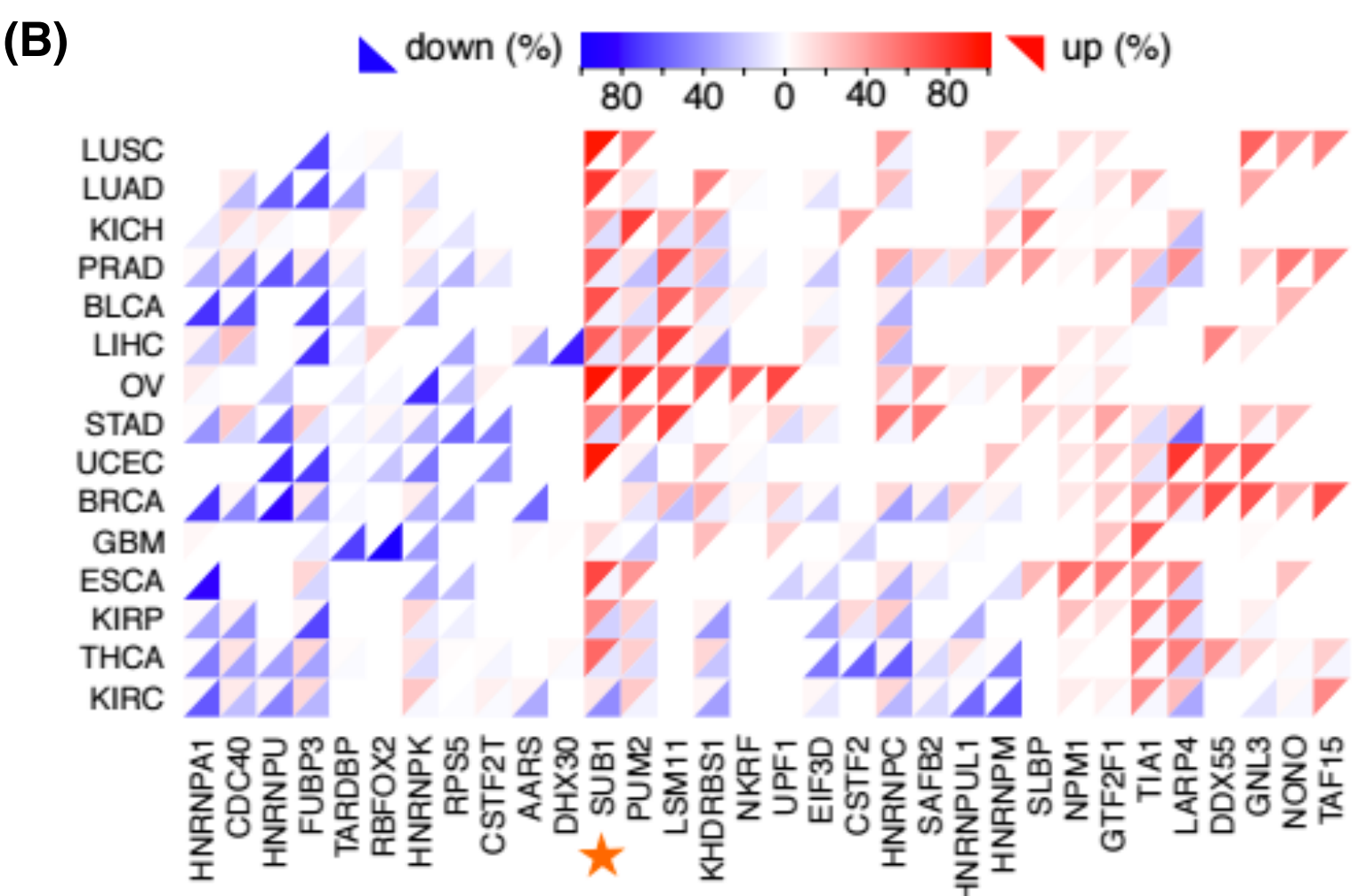
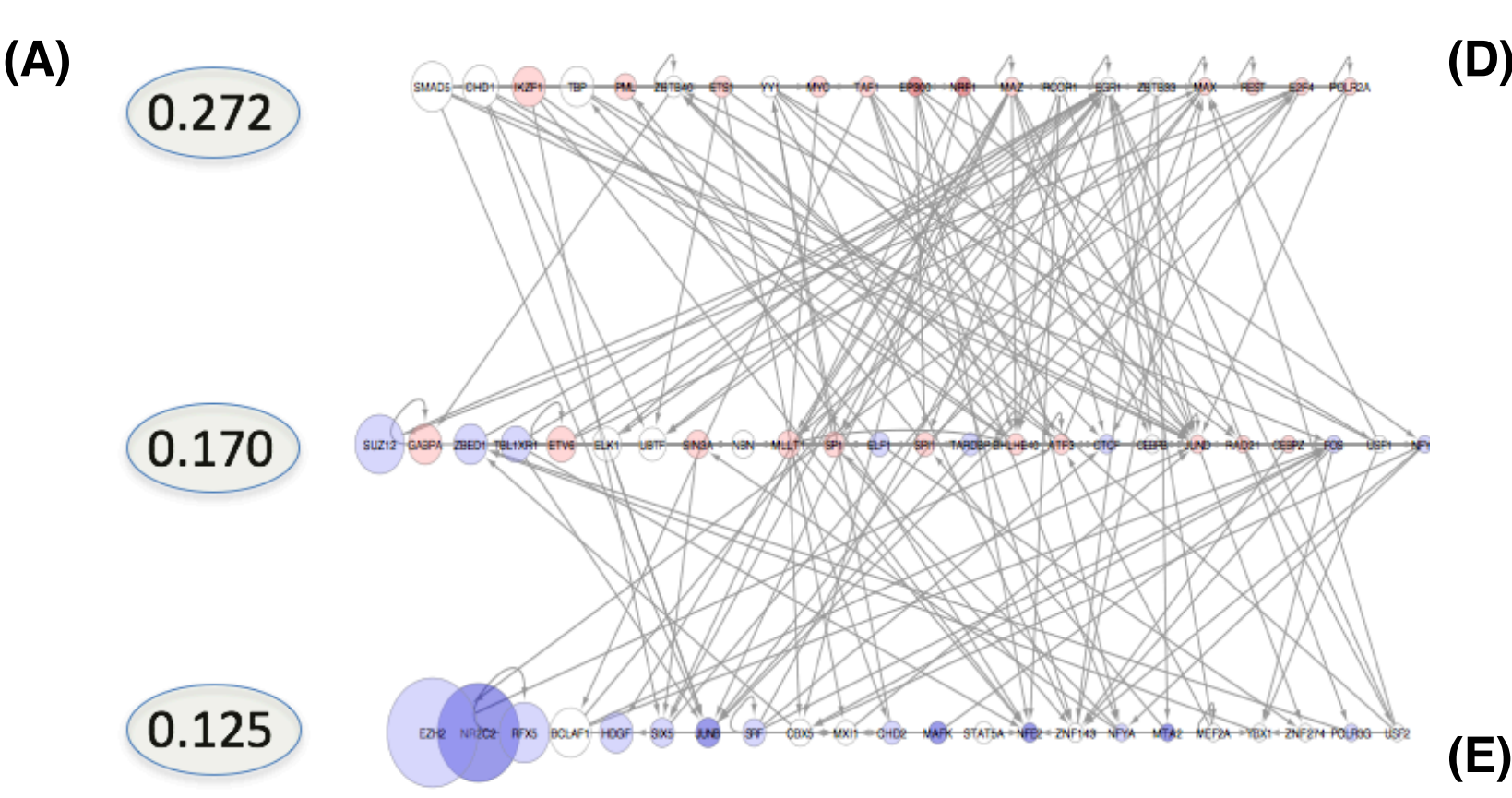


Figure 3

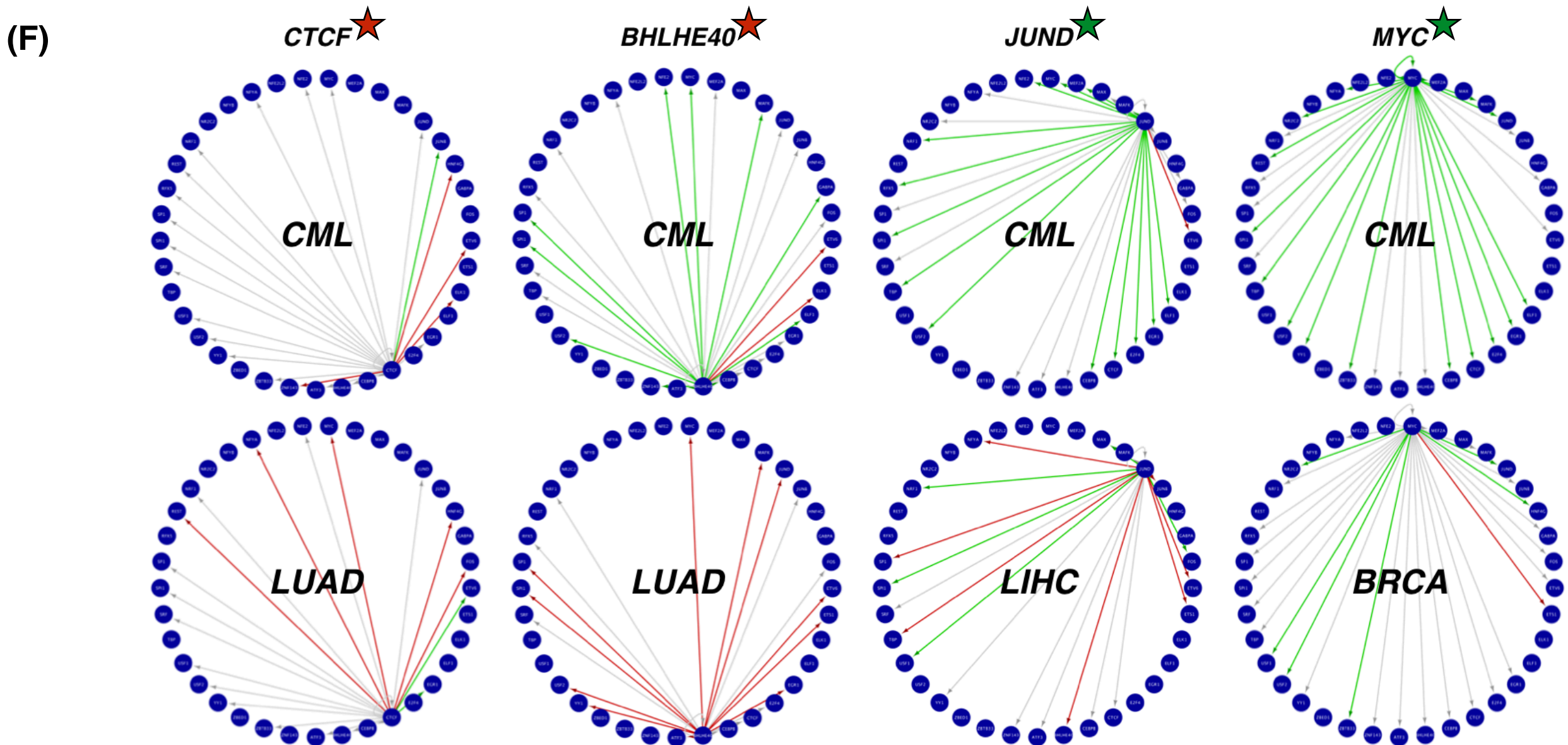
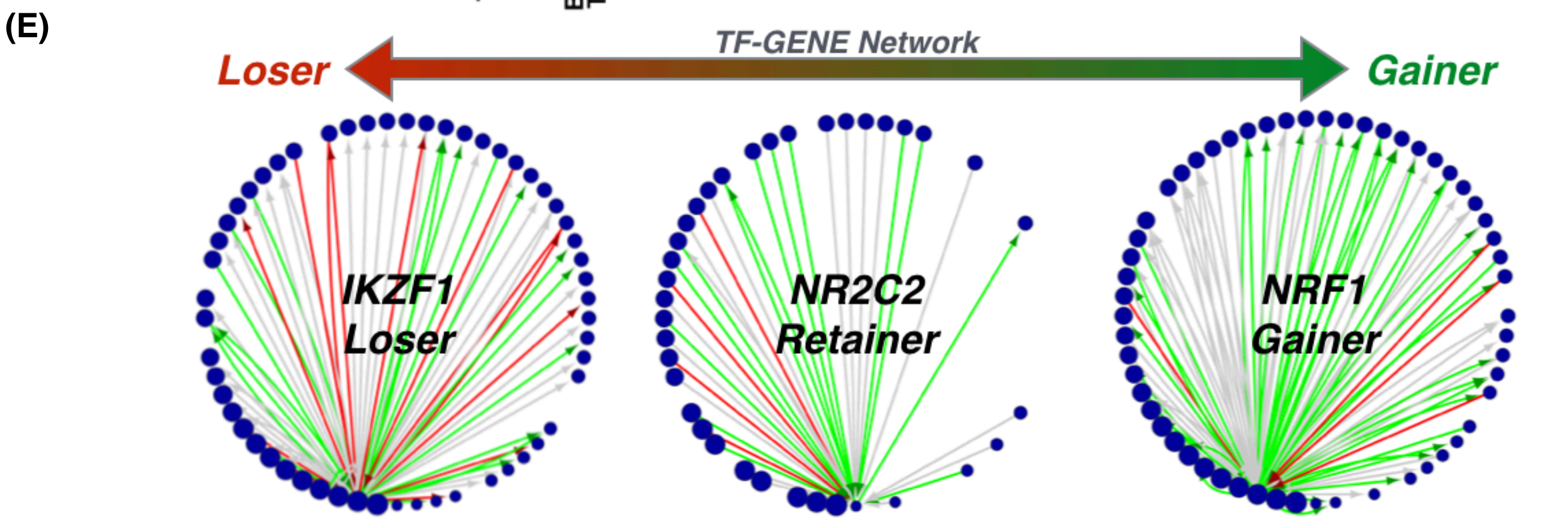
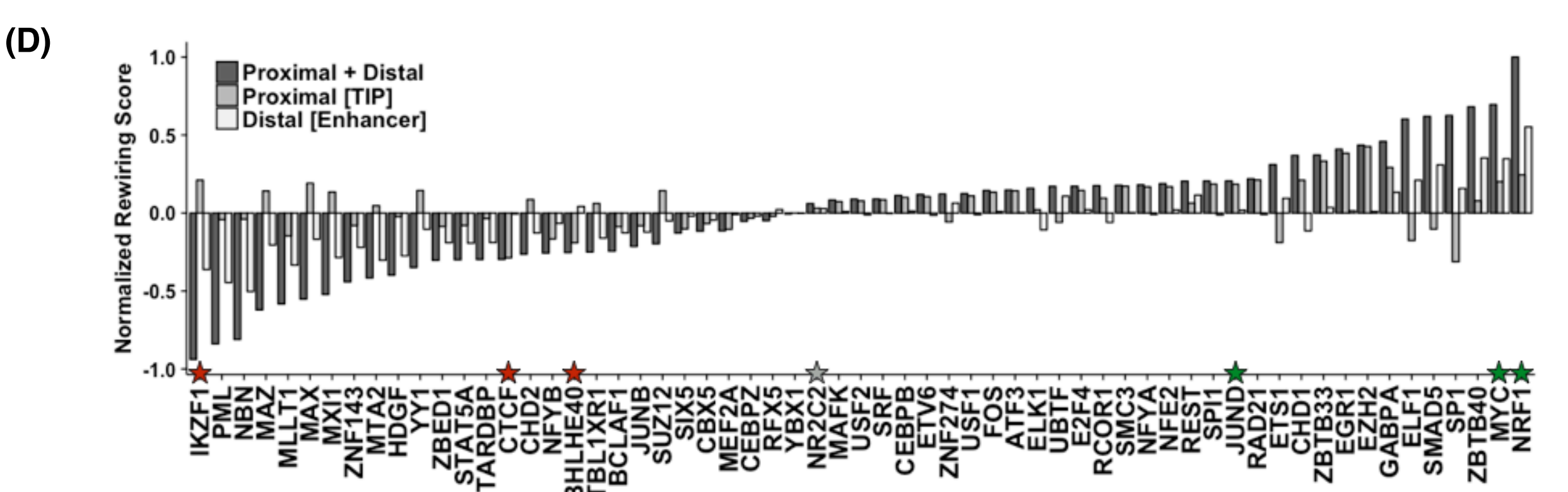
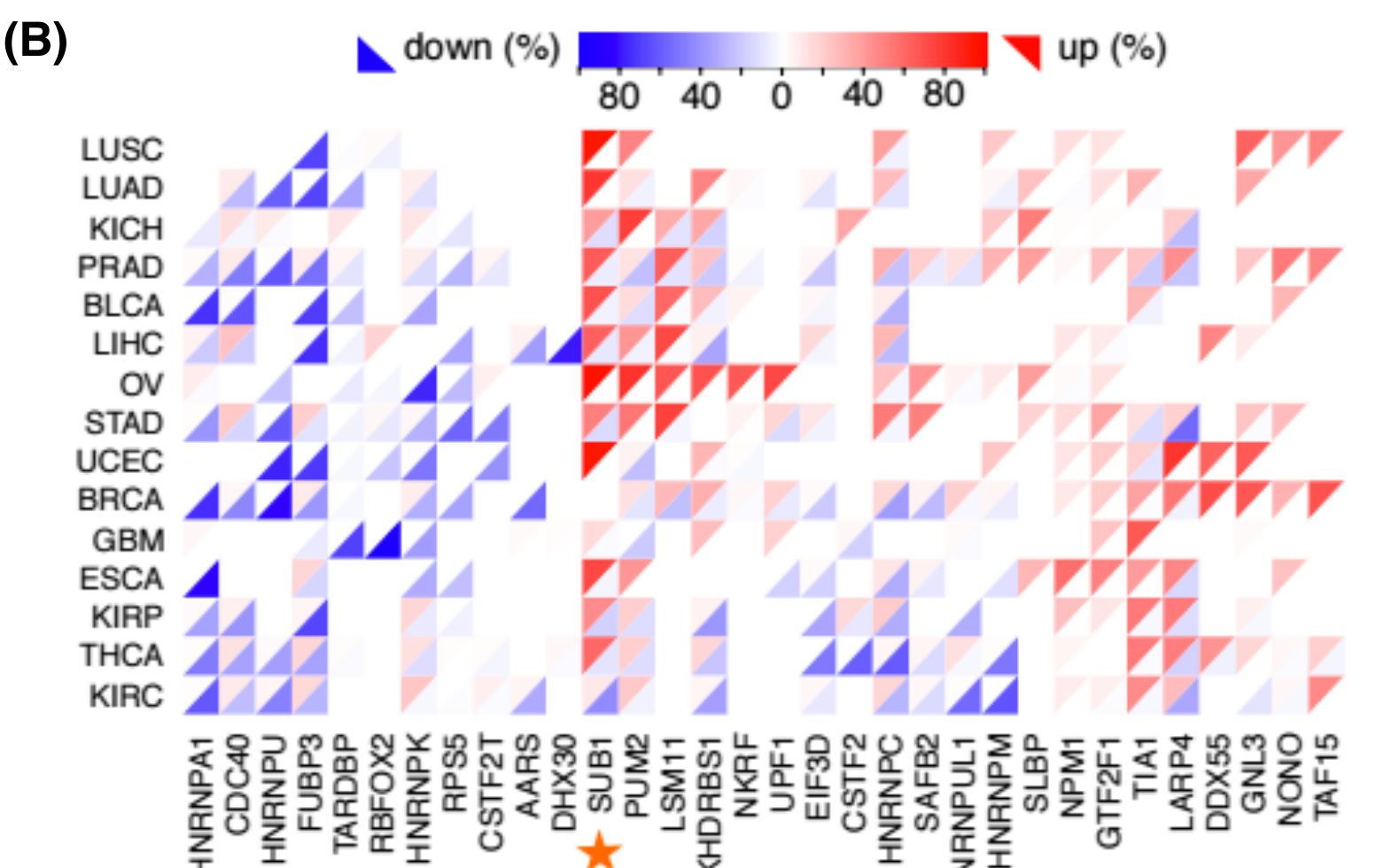
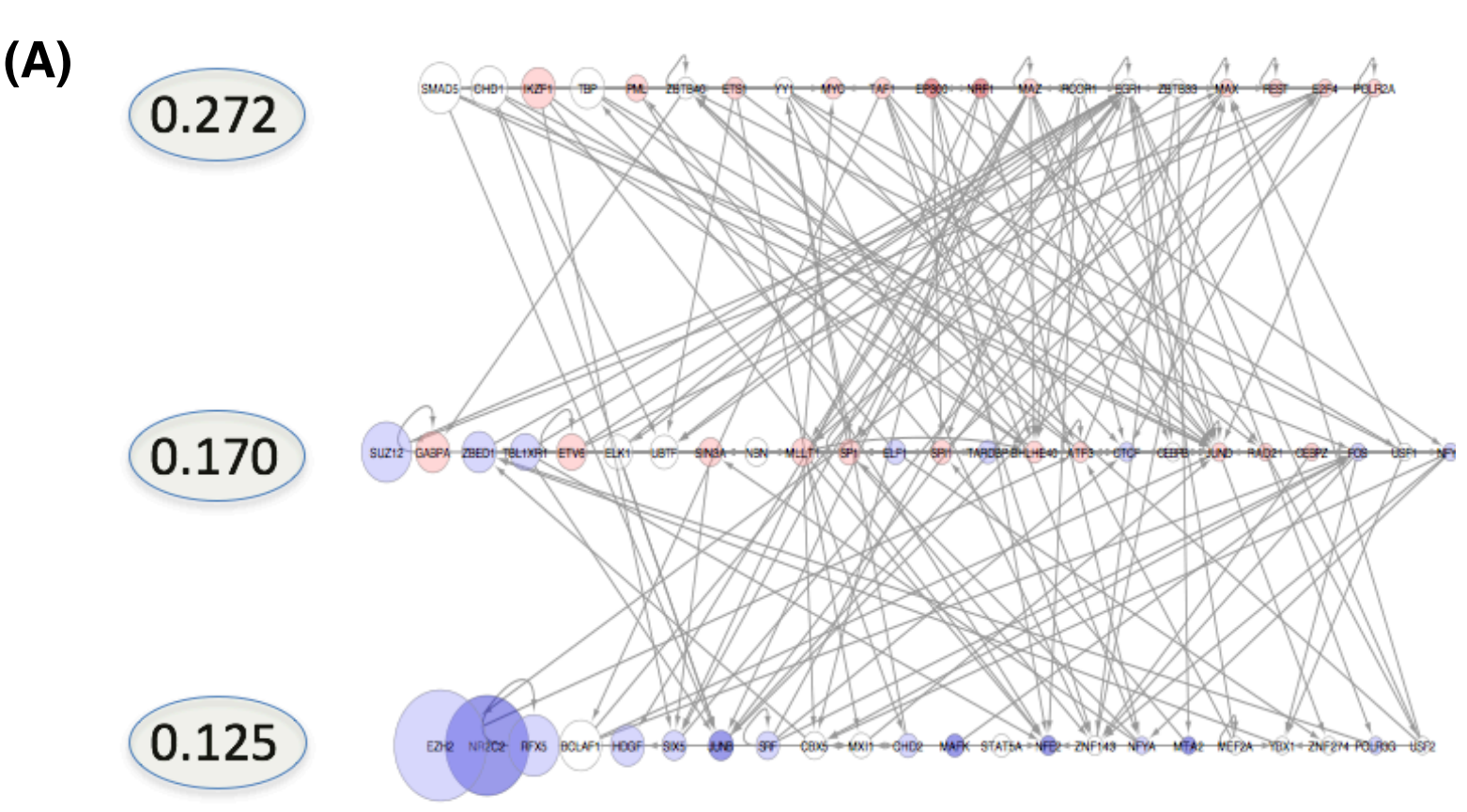
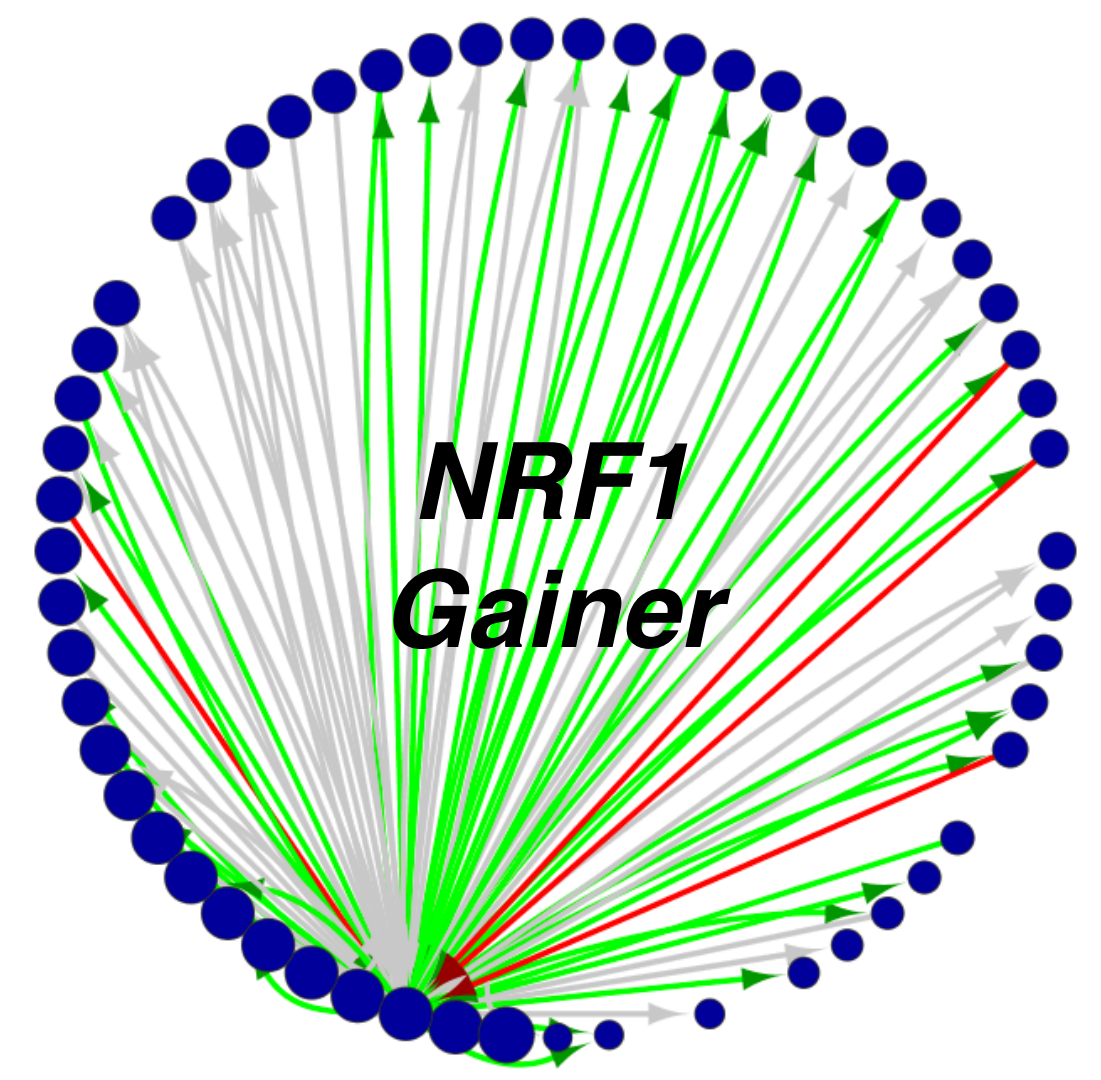
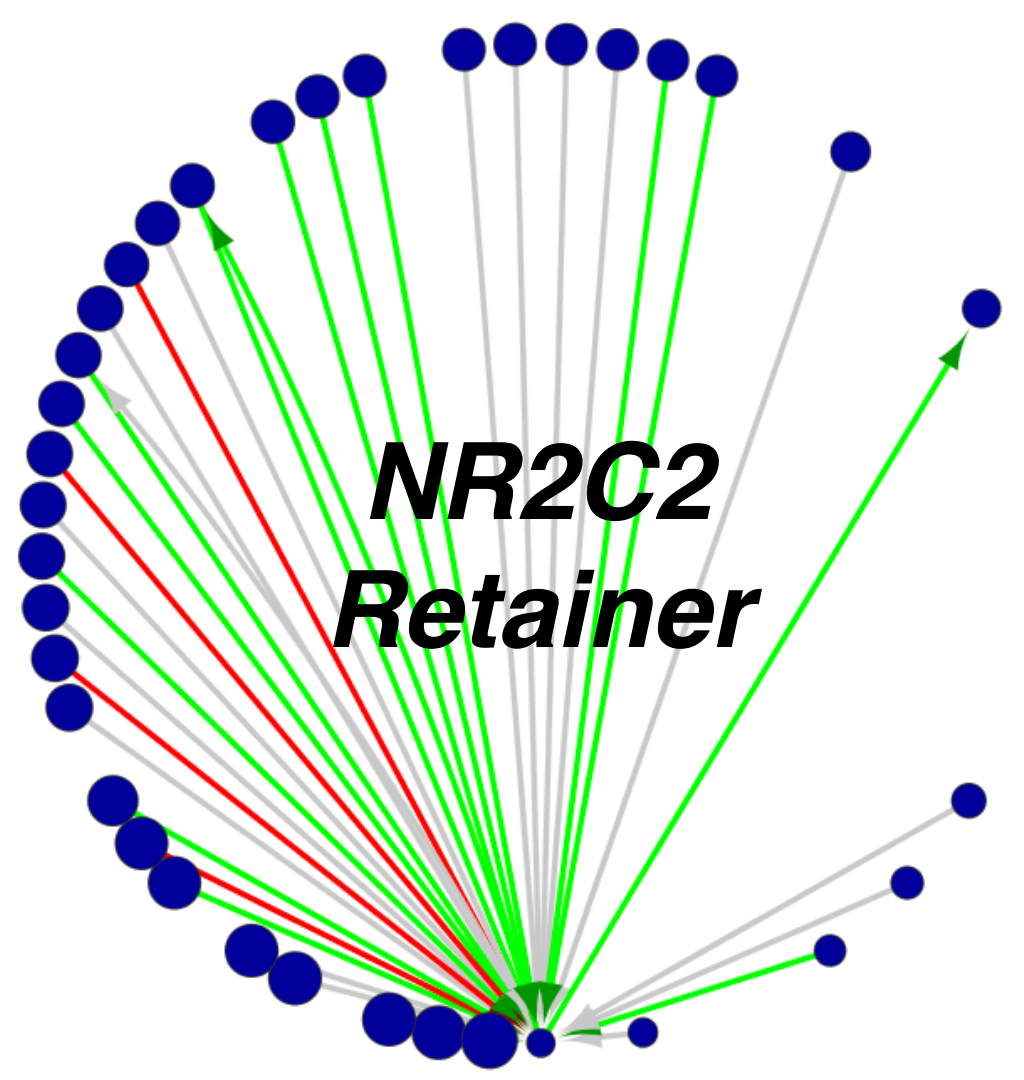
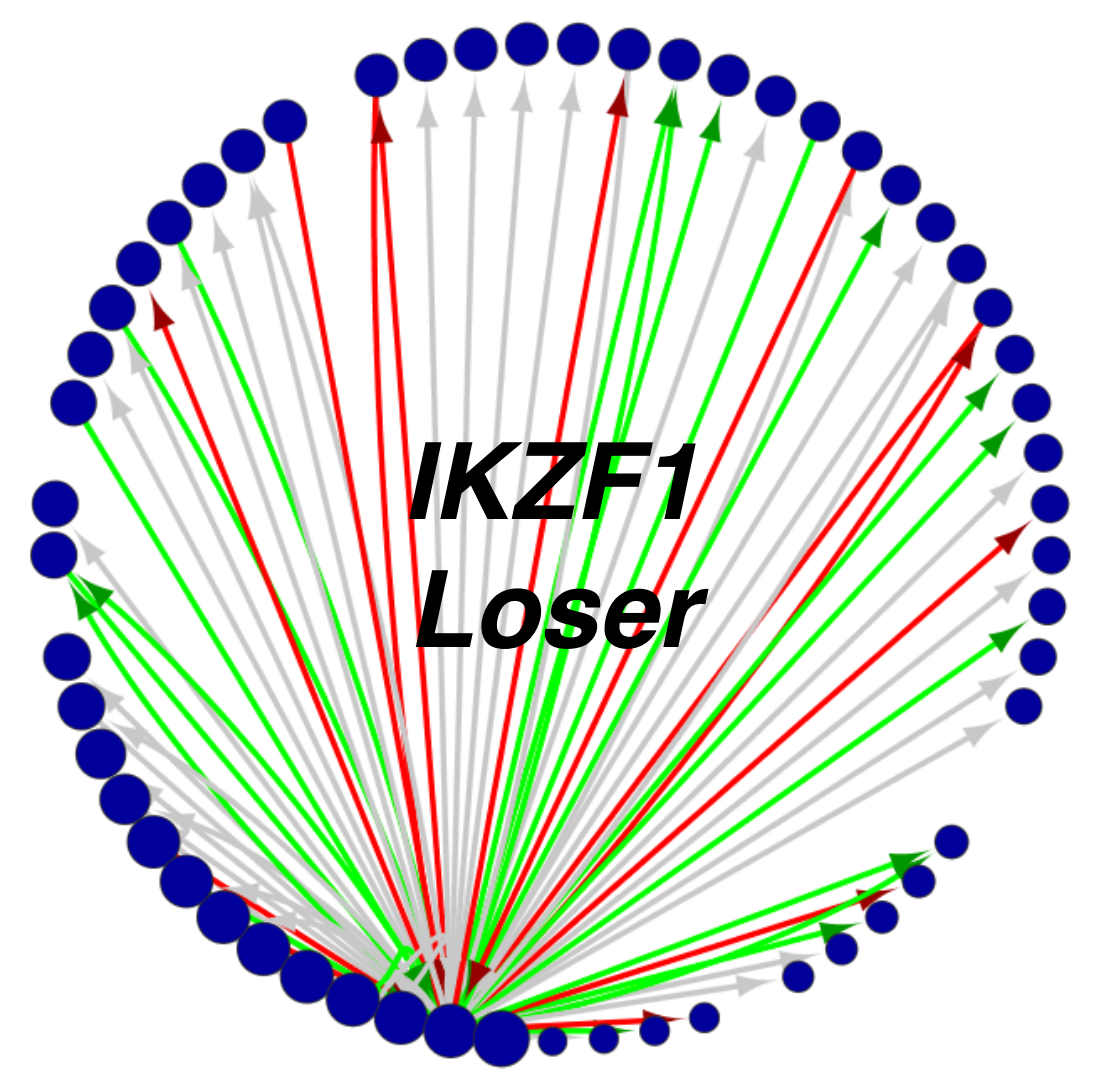


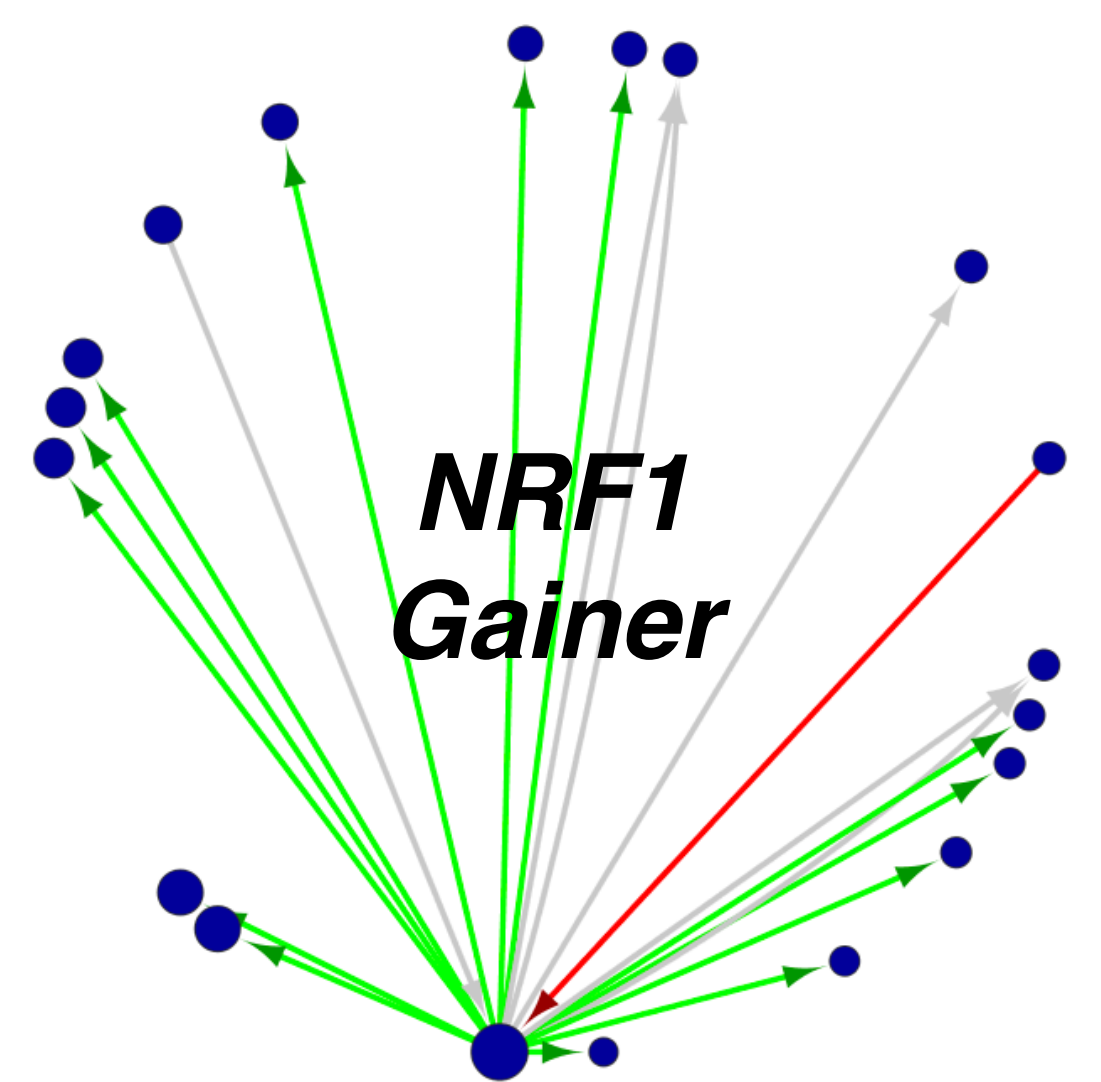
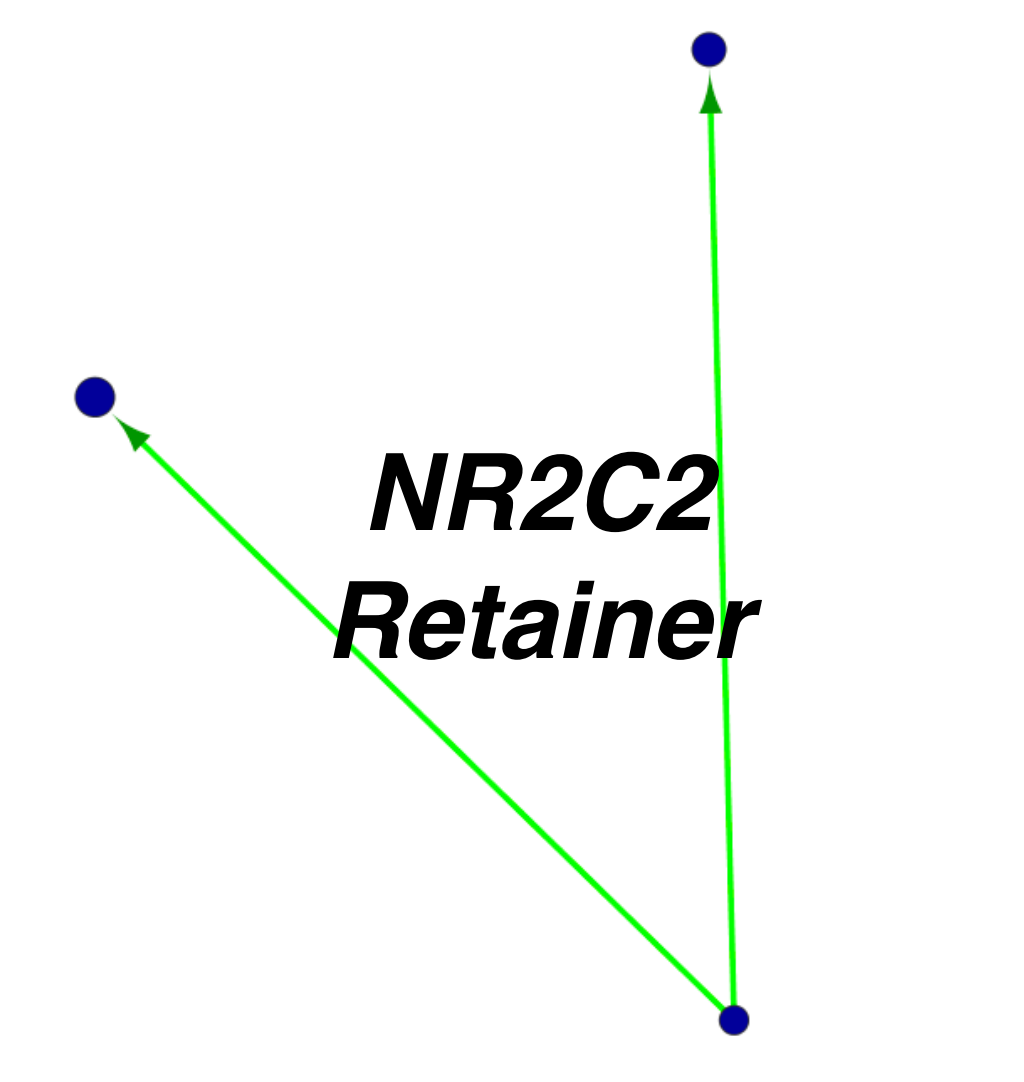
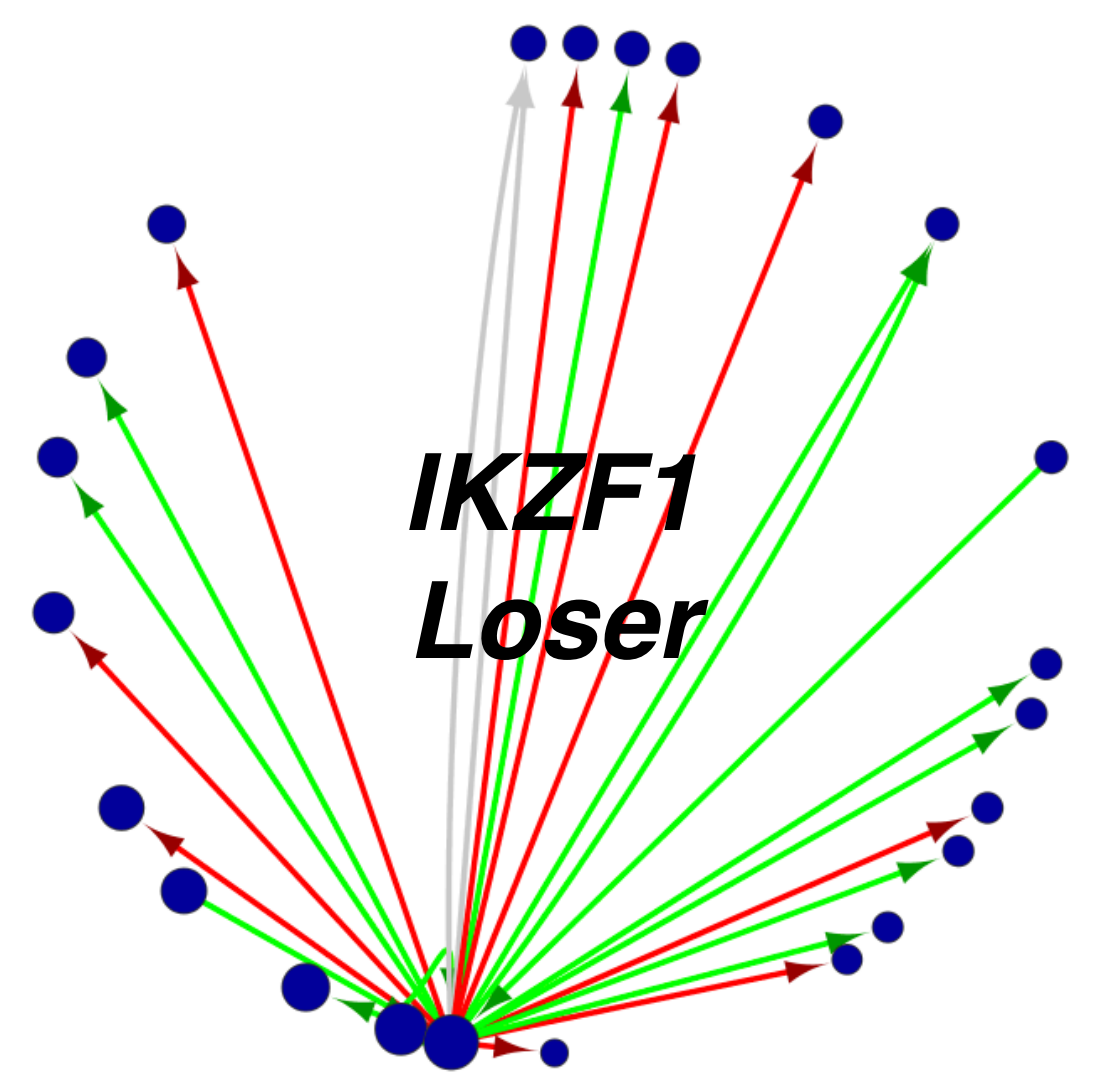
Figure 3

Loser ← **TF-GENE Network** → *Gainer*

TSS+ENH



TIP+ENH



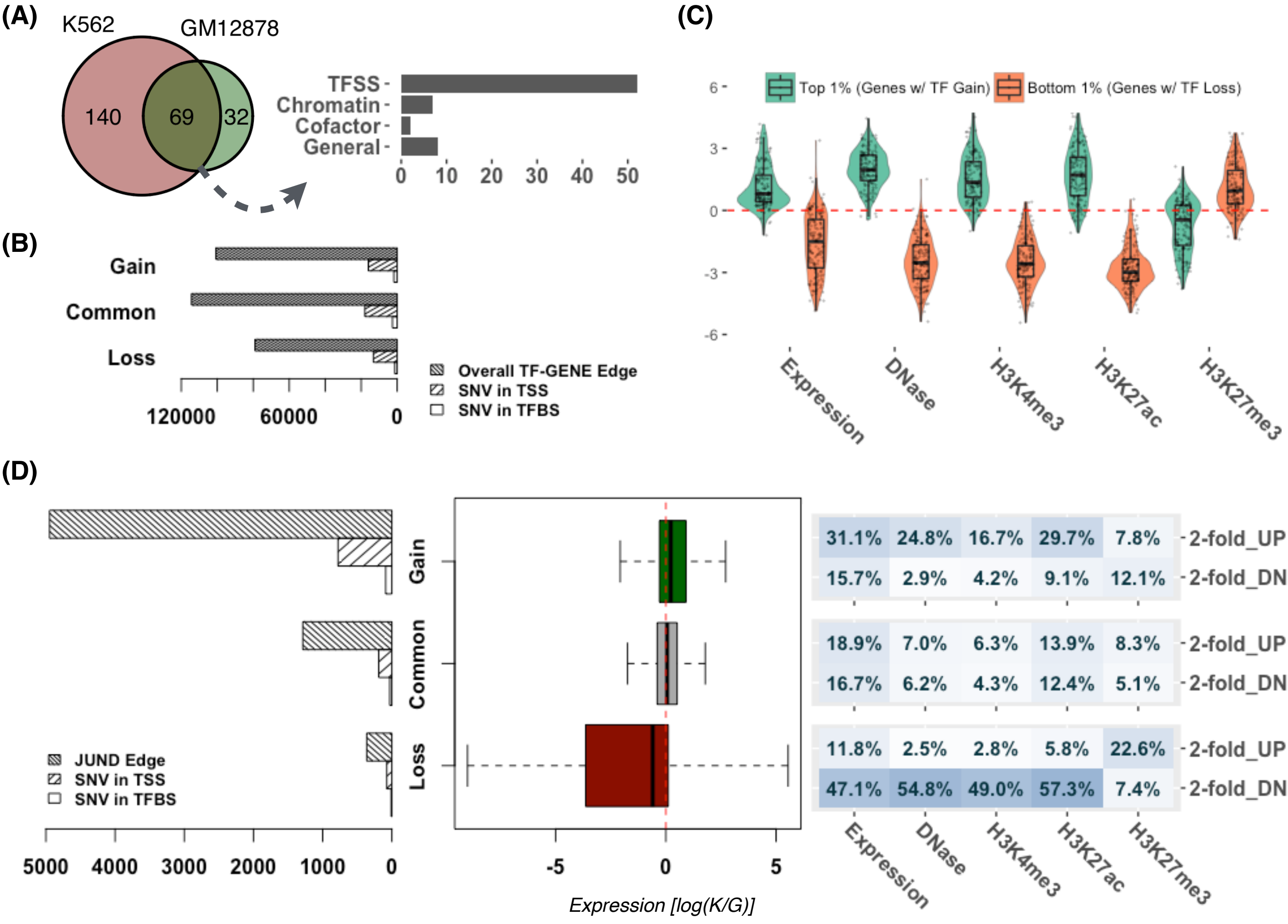


Figure 4

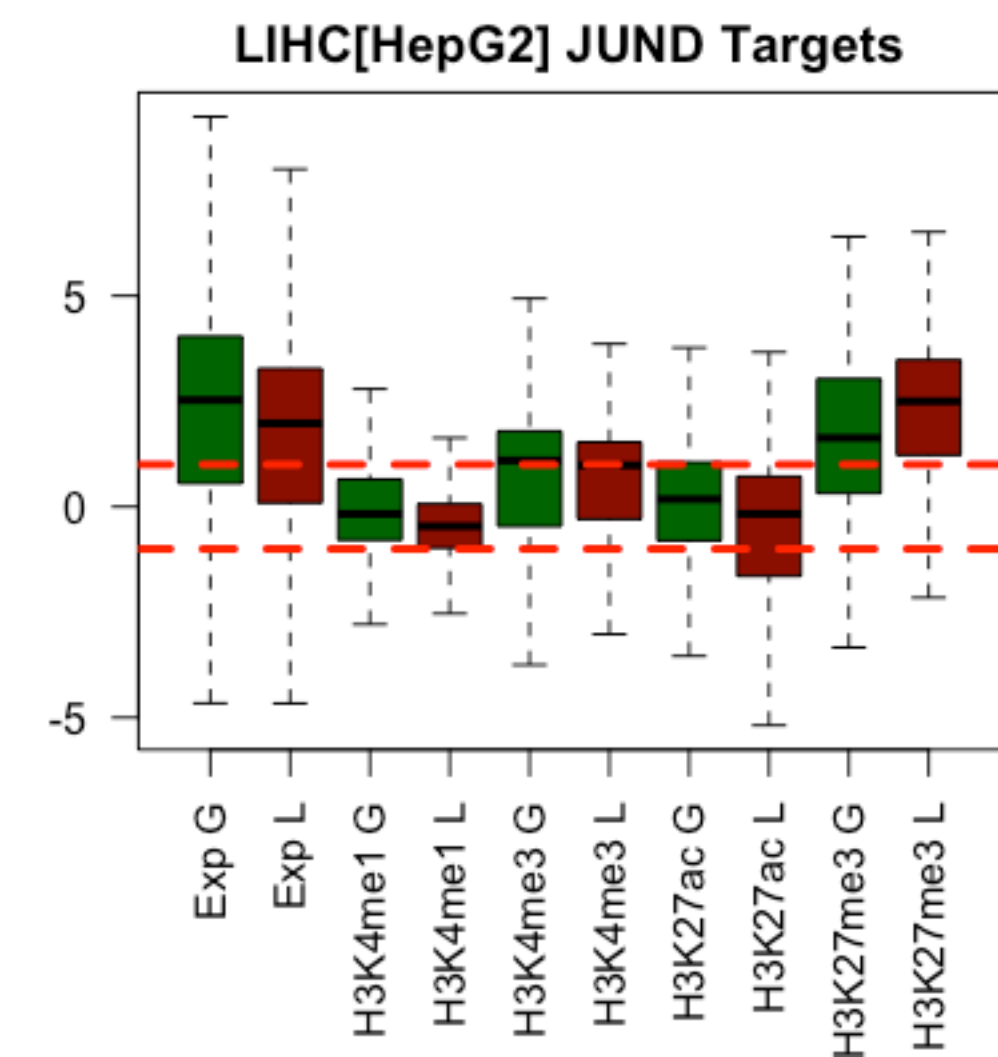
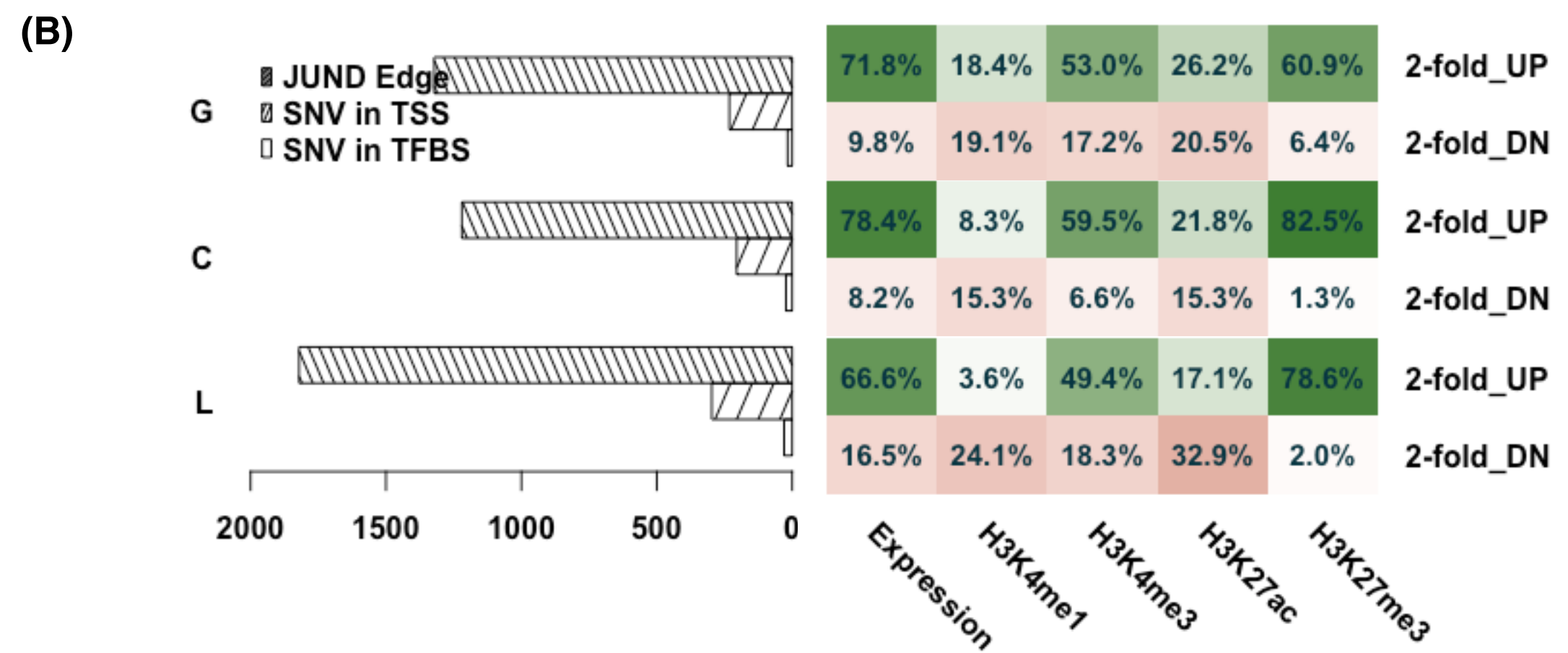
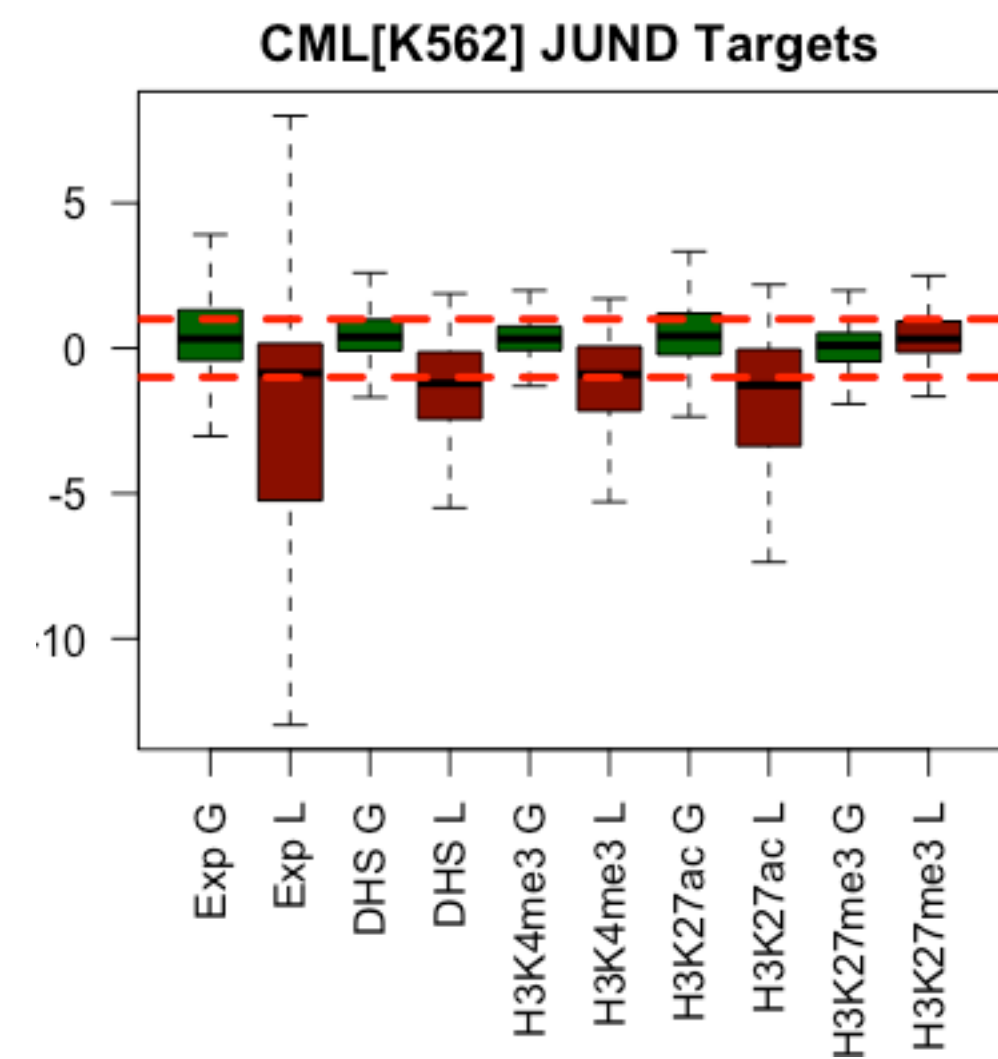
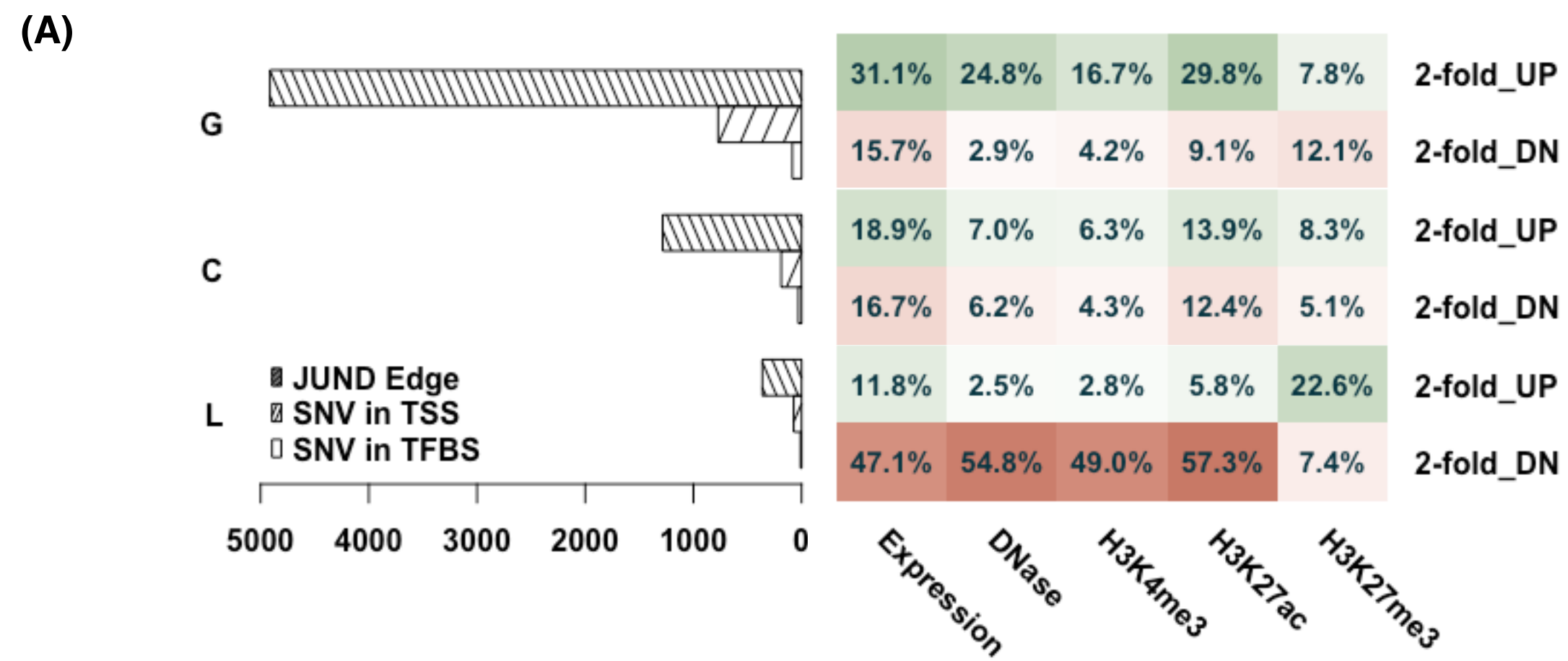


Figure 4

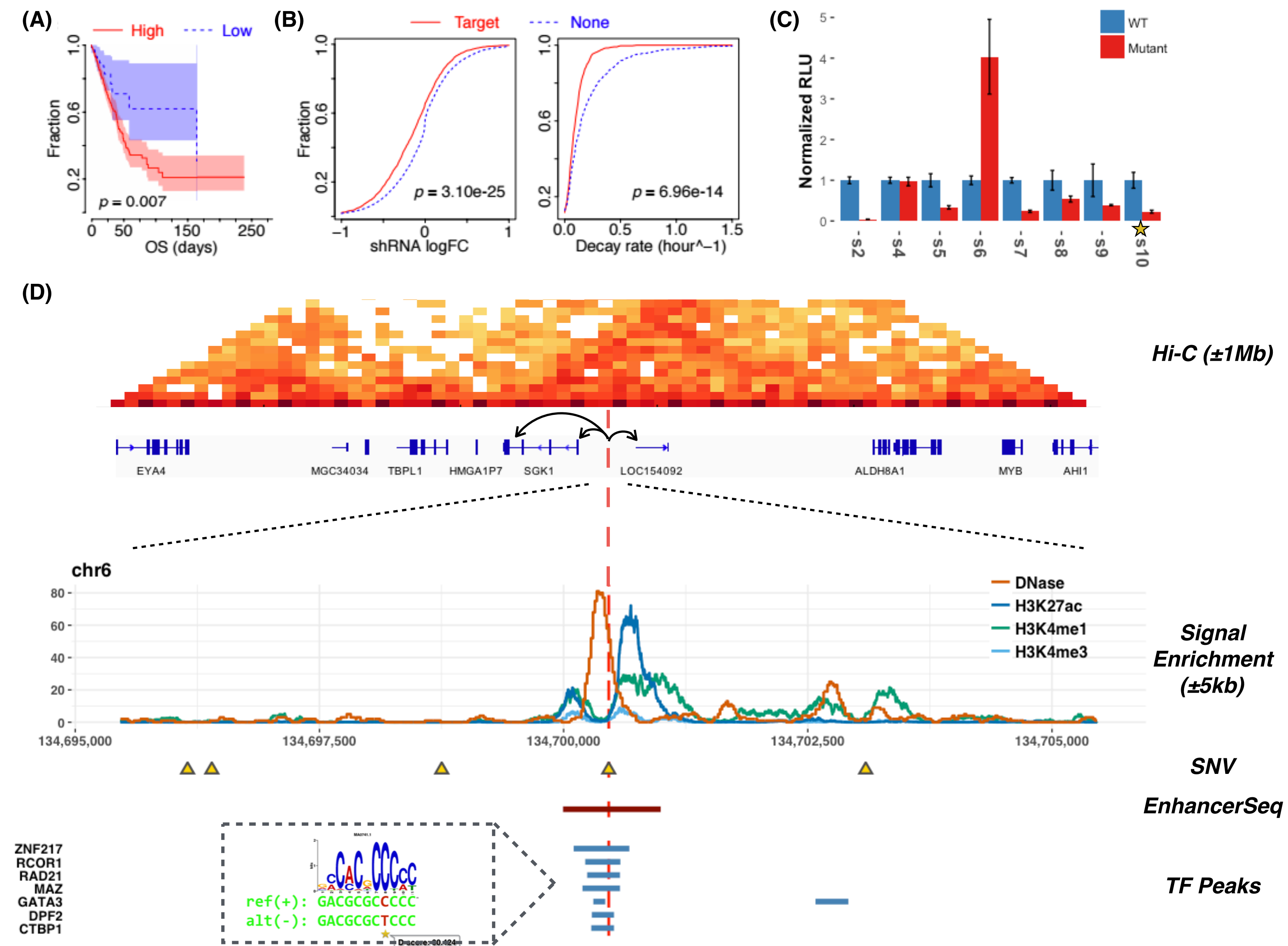
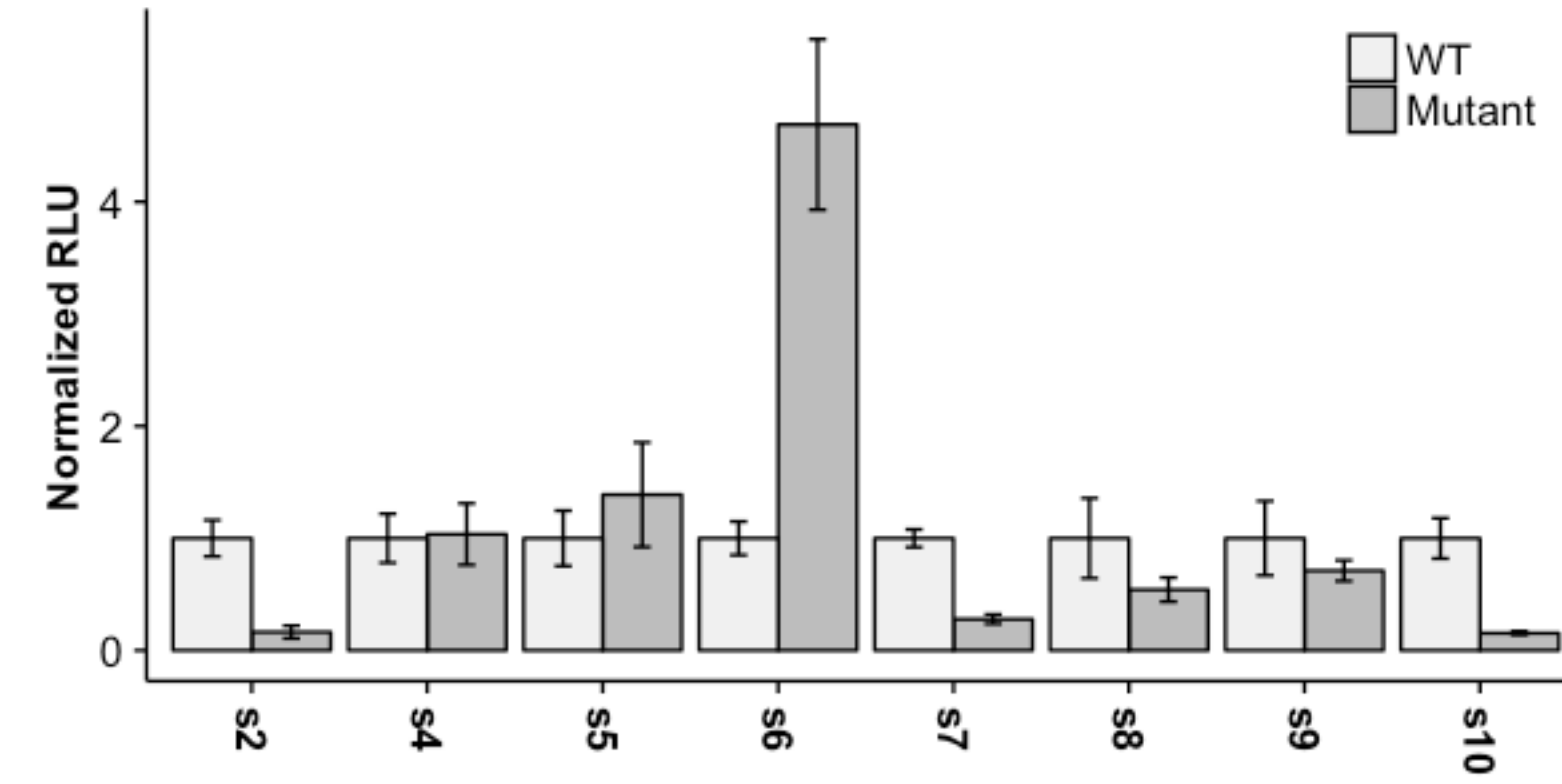
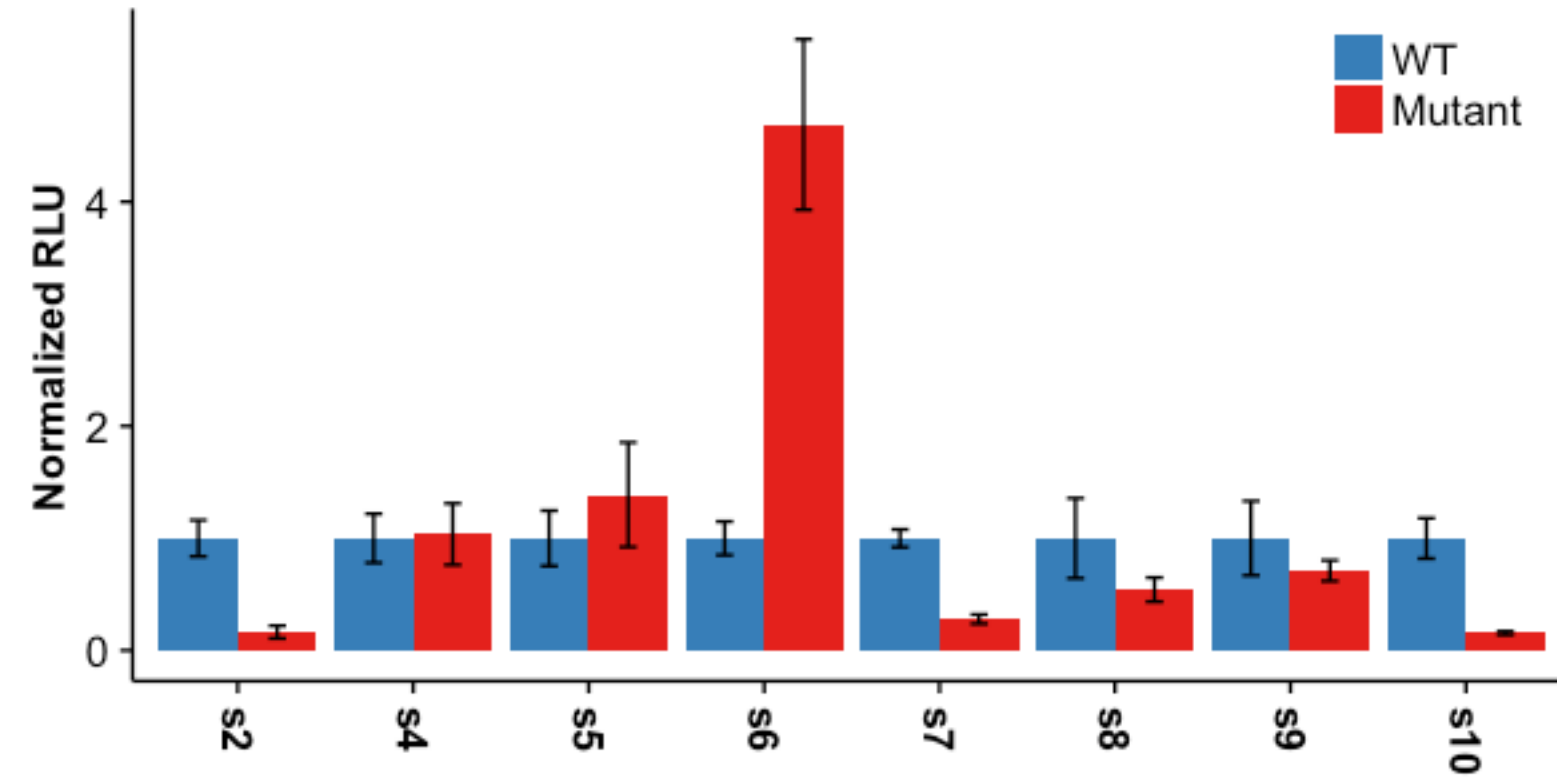
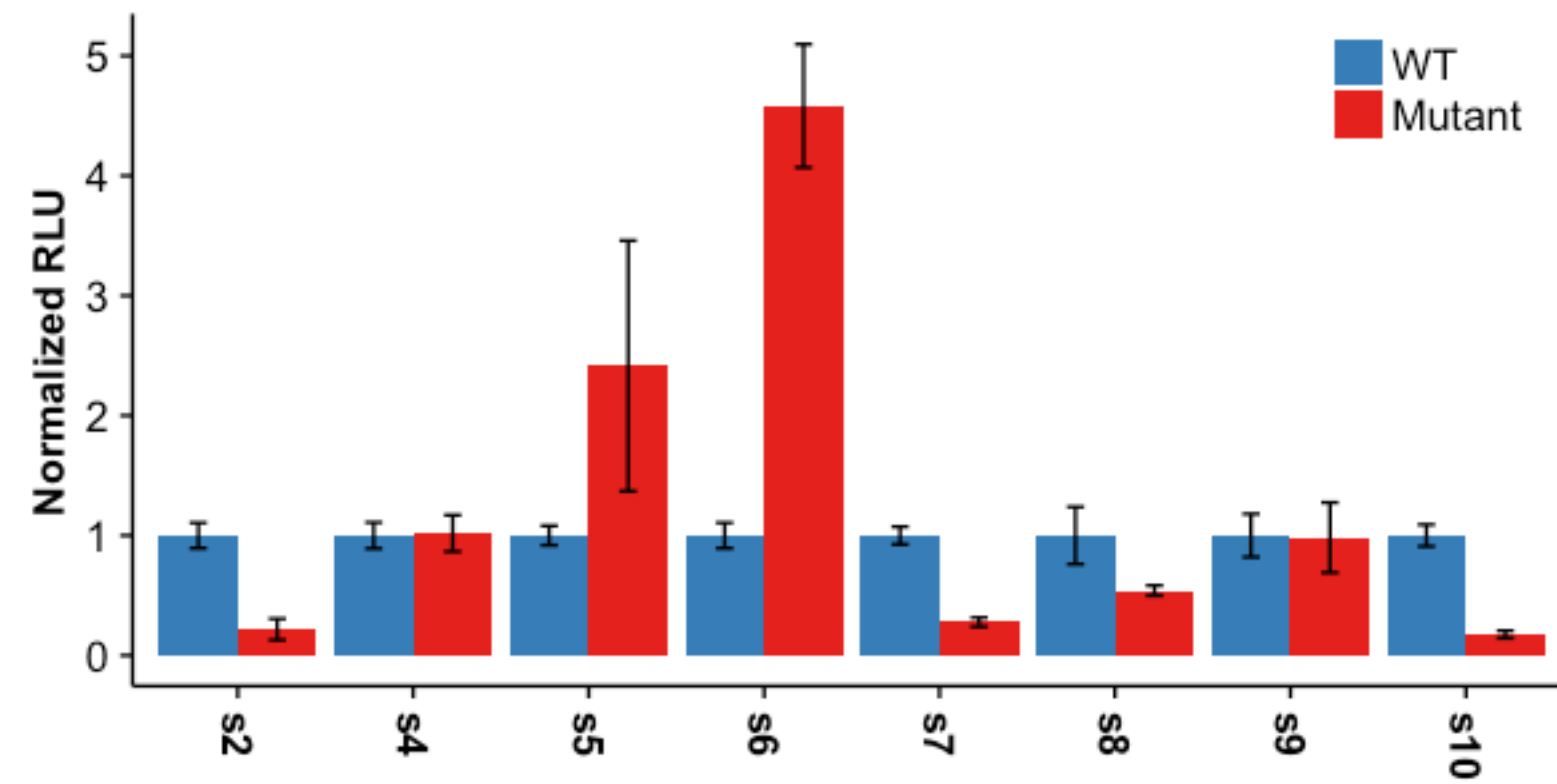


Figure 5

6 replicates (3 from Vineet and 3 from Mike)



3 reps from Vineet and 3 reps from Mike separately



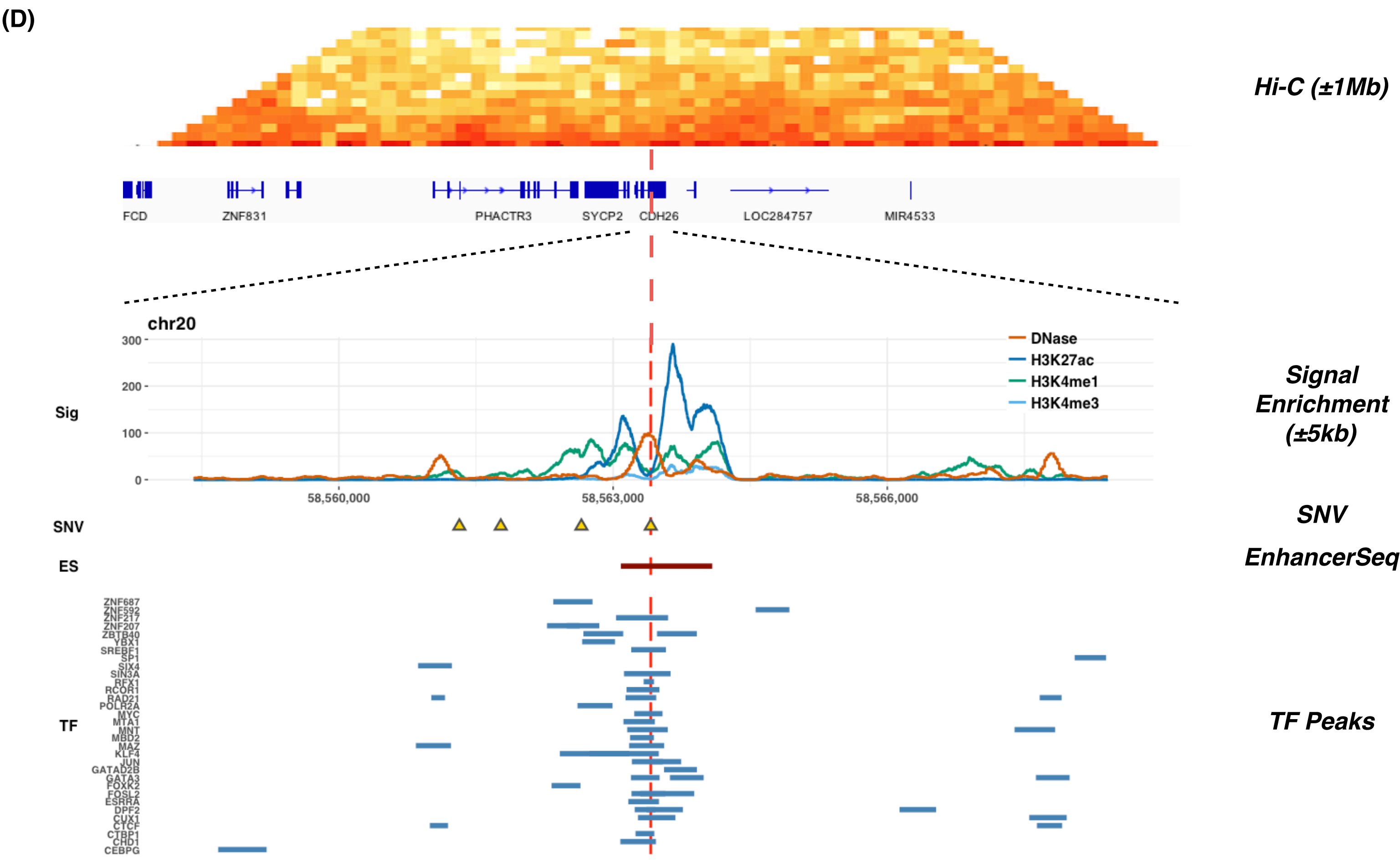
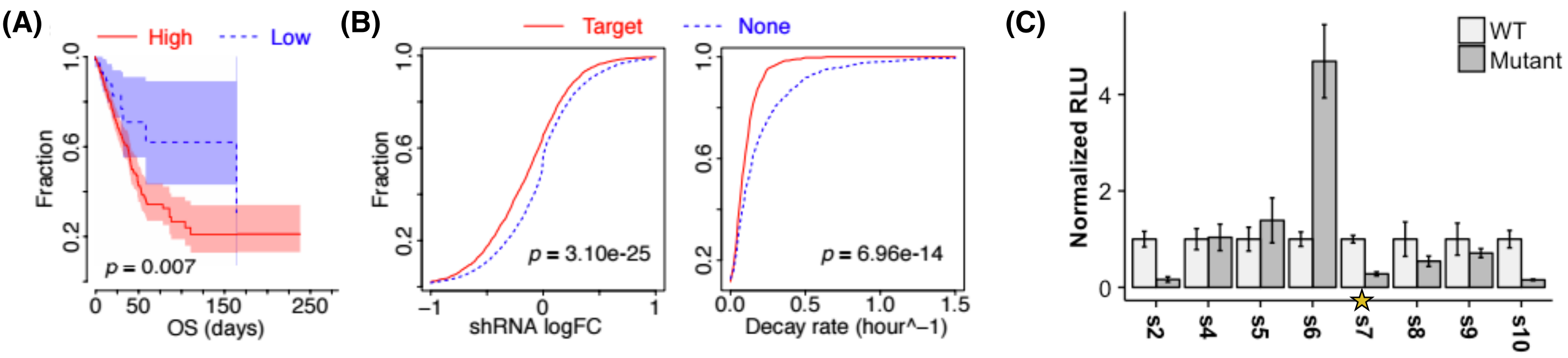


Figure 5

