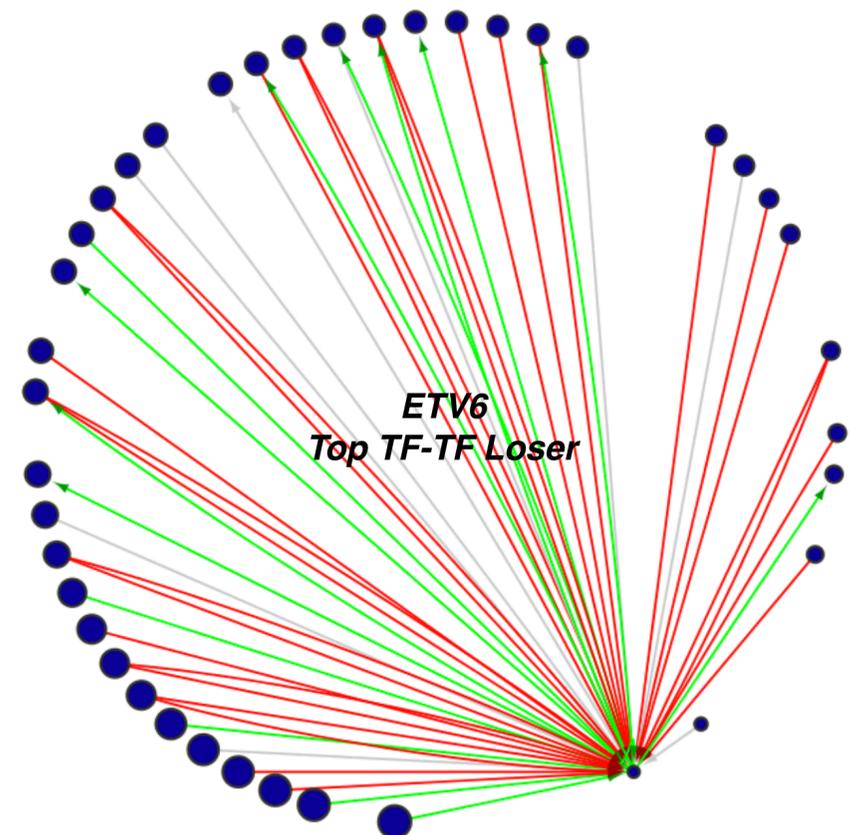
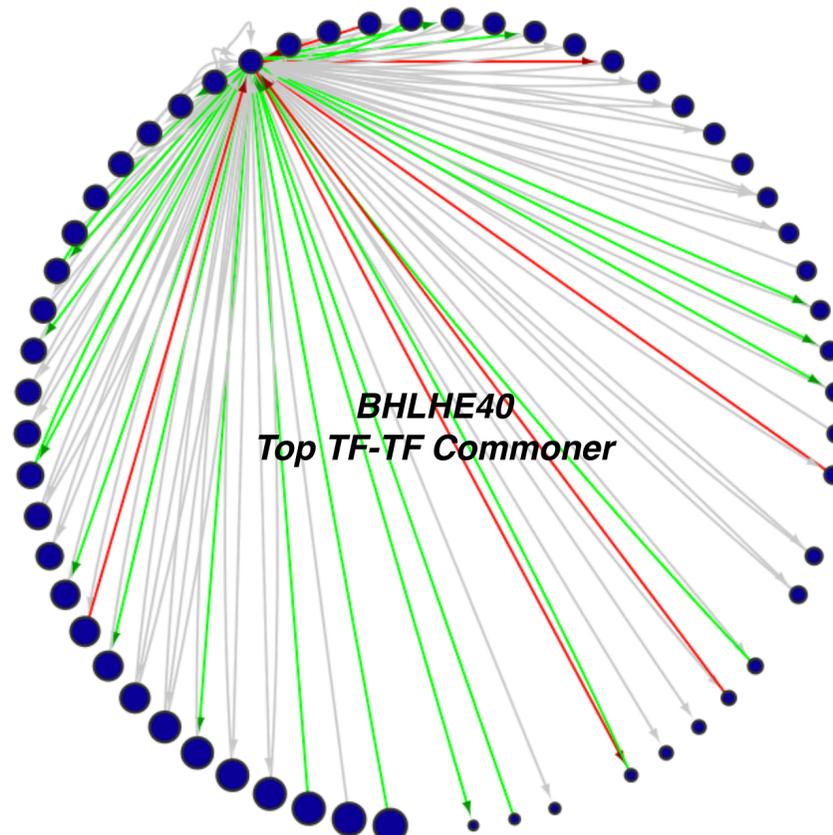
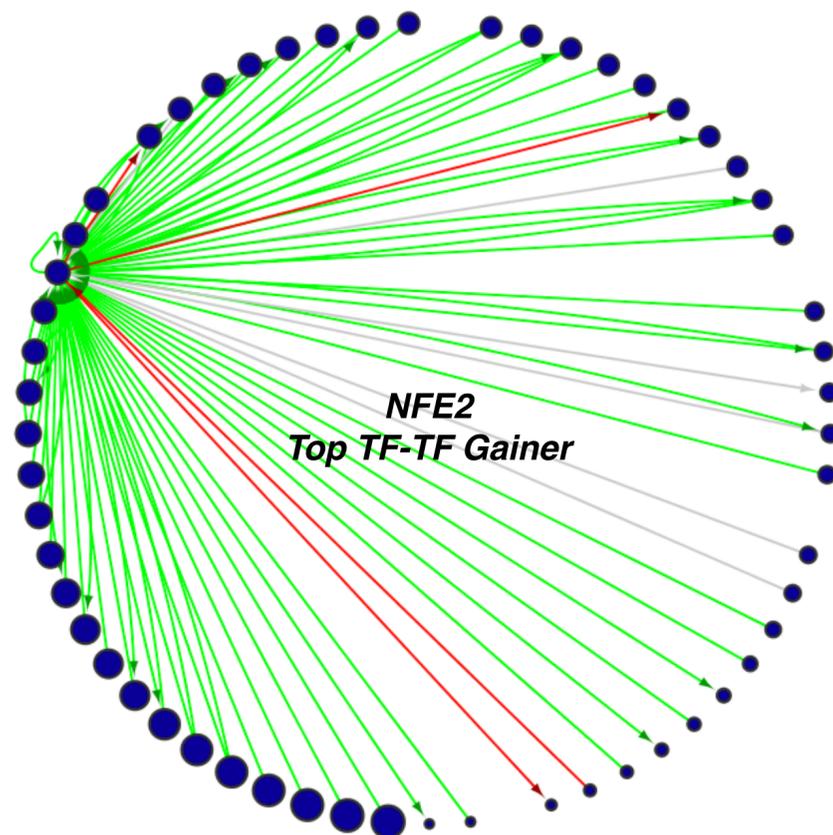
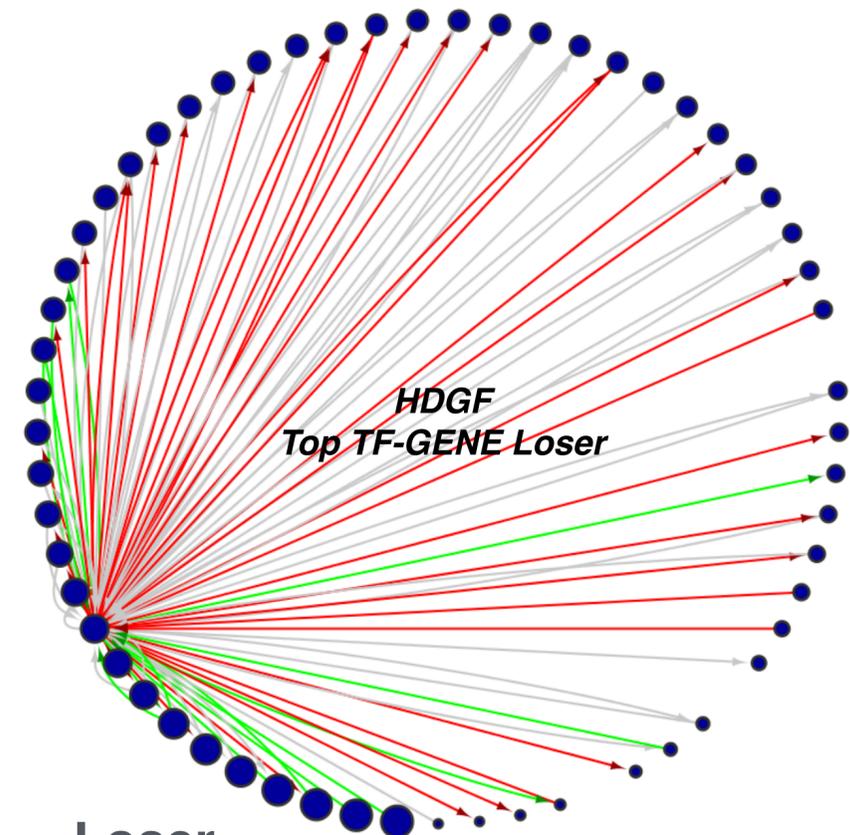
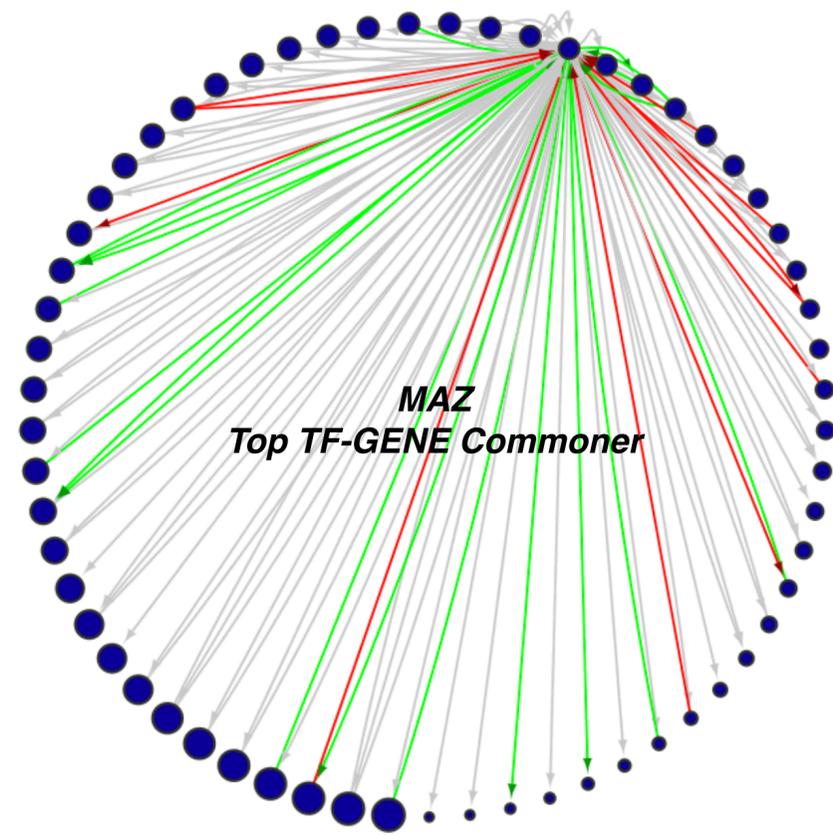
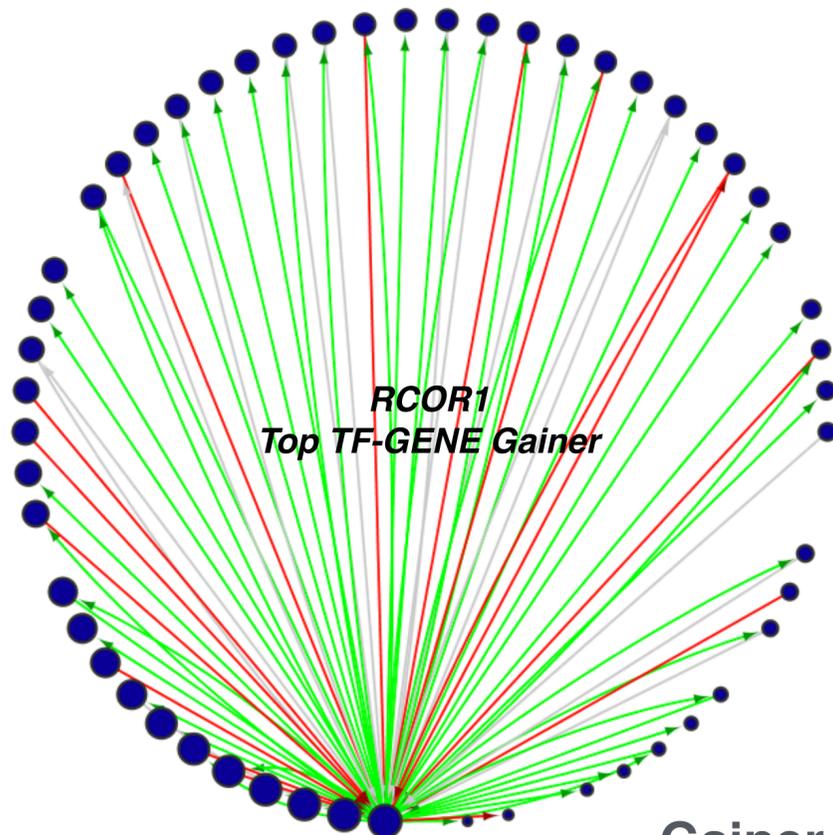


Outbound  
 Inbound

Gainer Loser

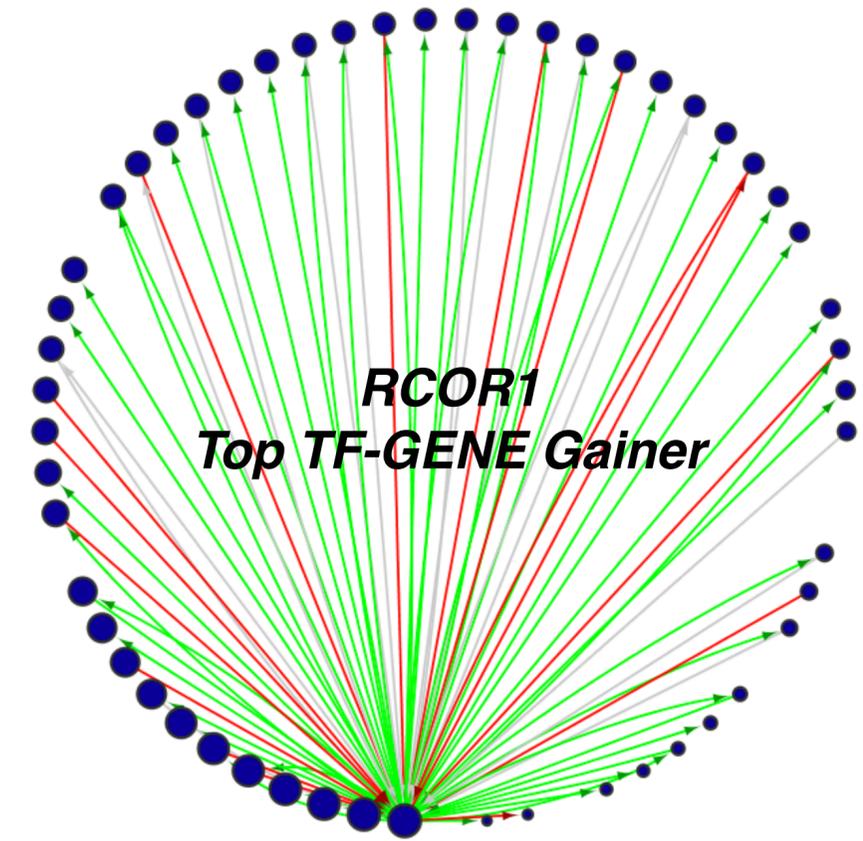
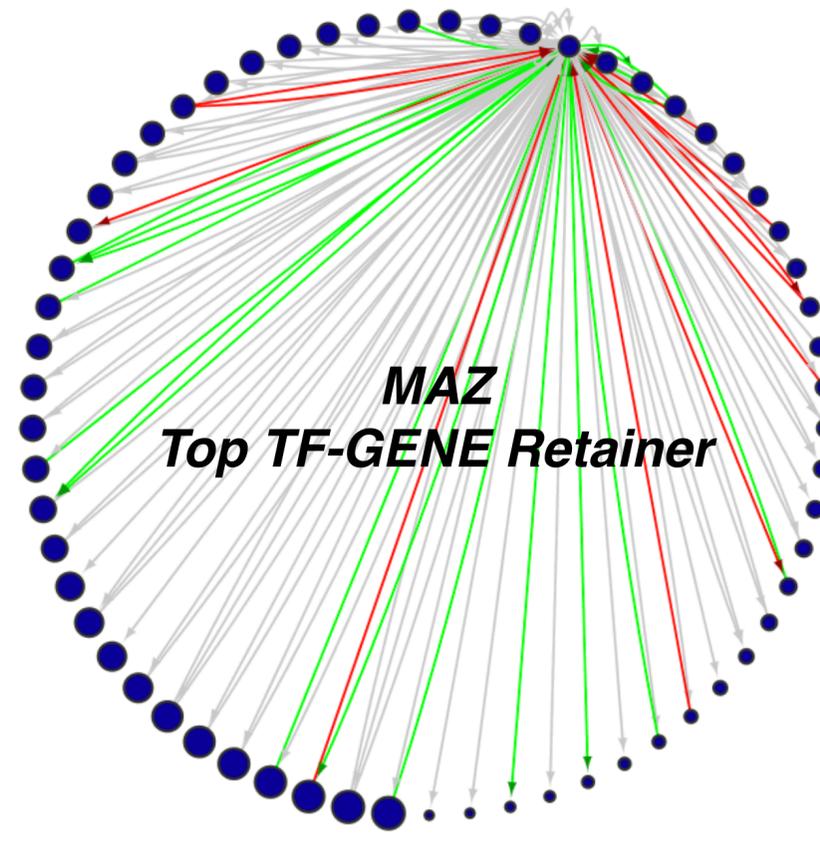
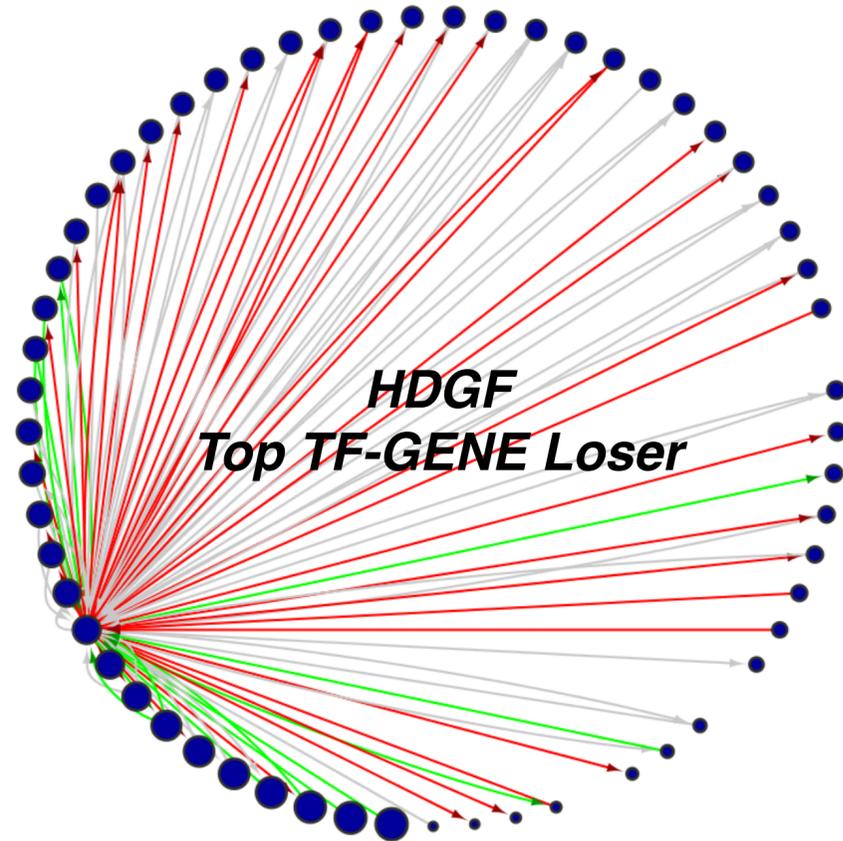


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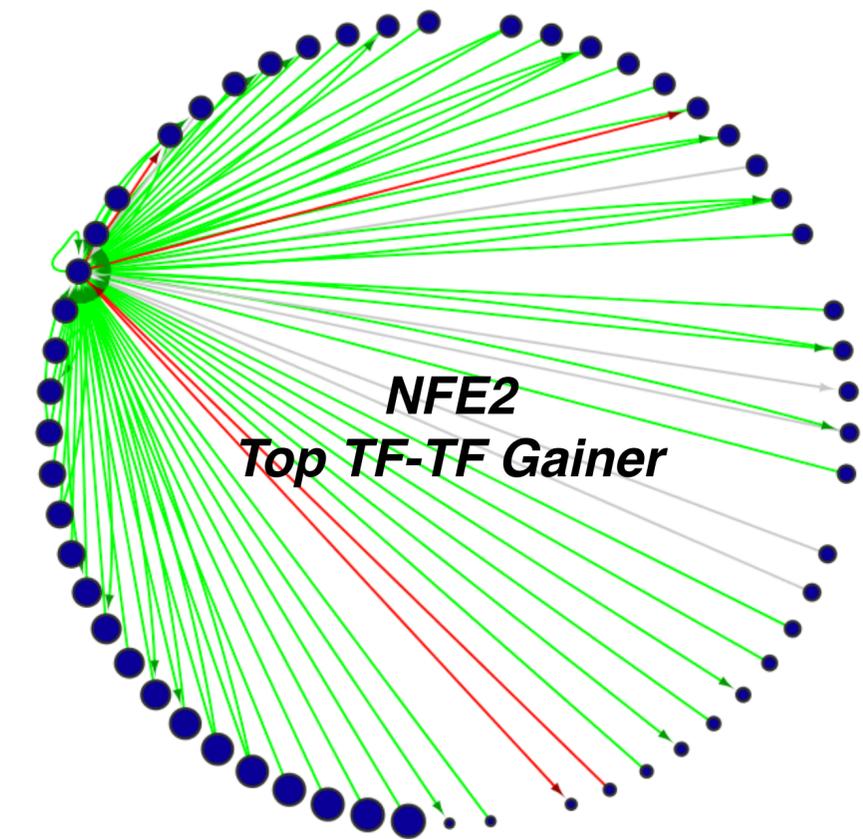
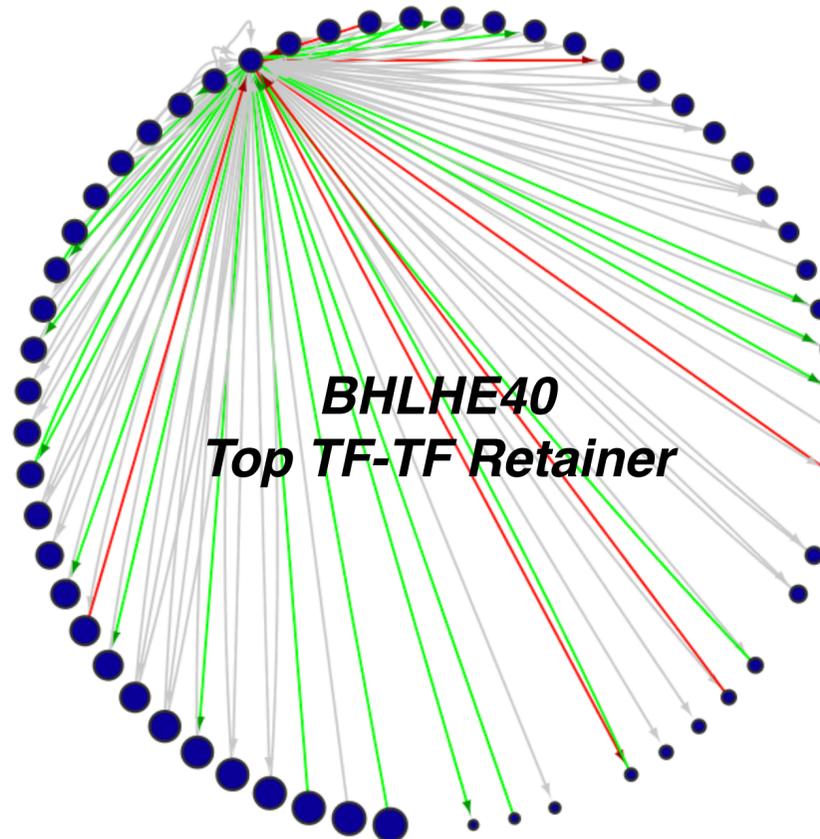
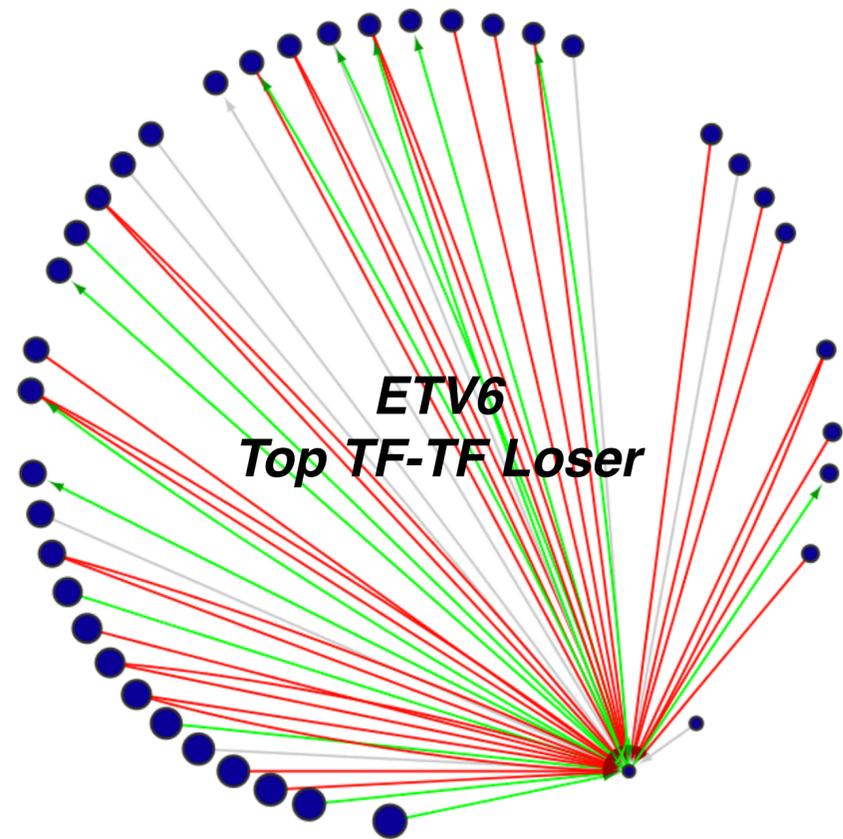
TF-TF

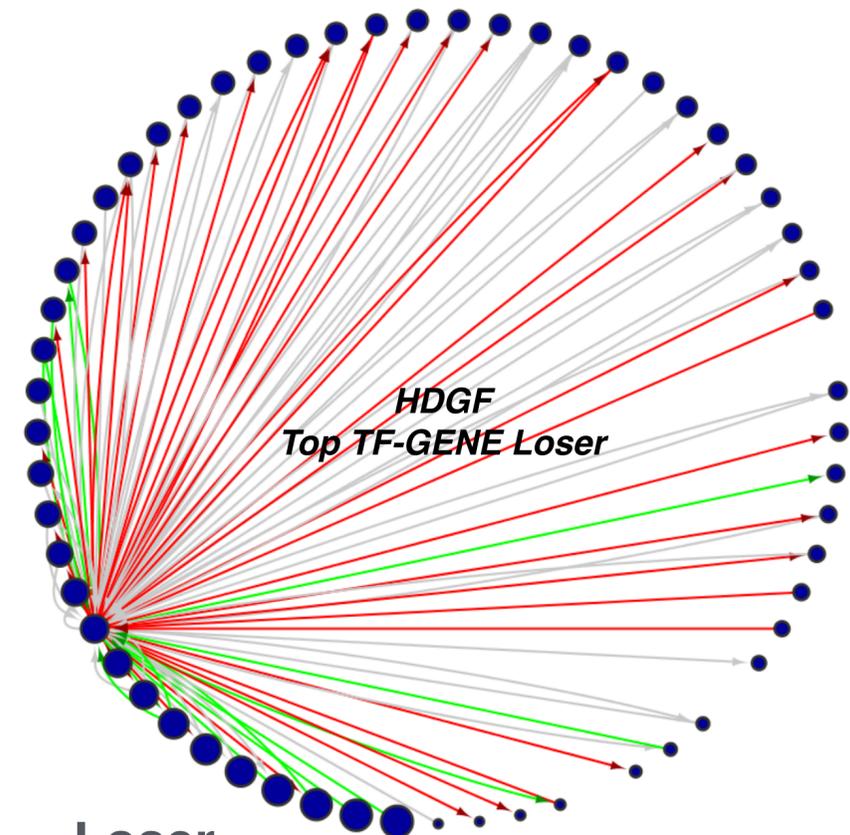
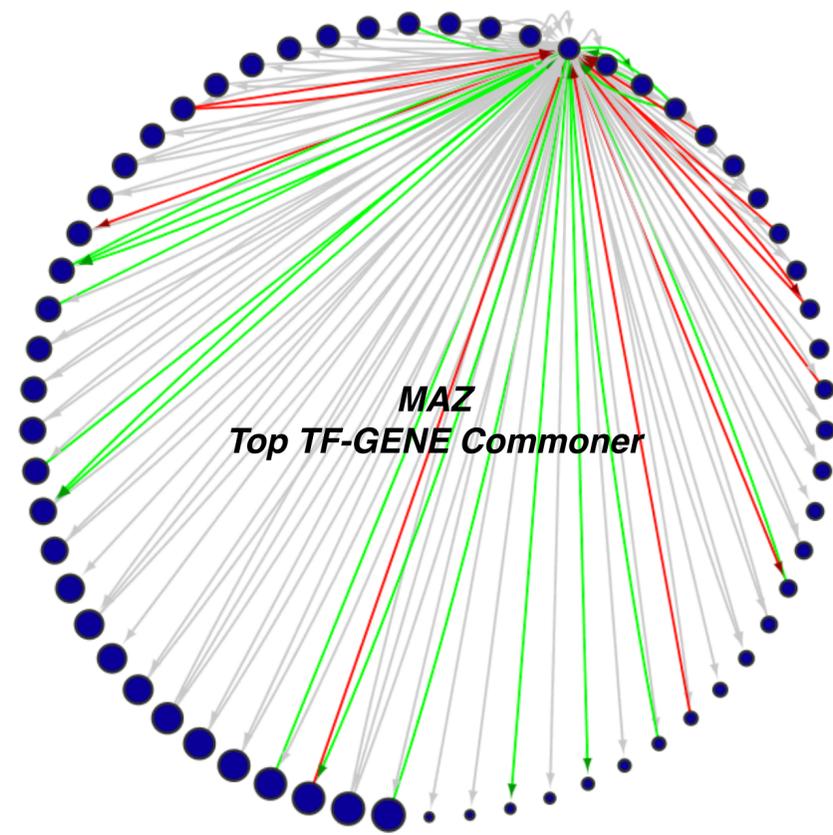
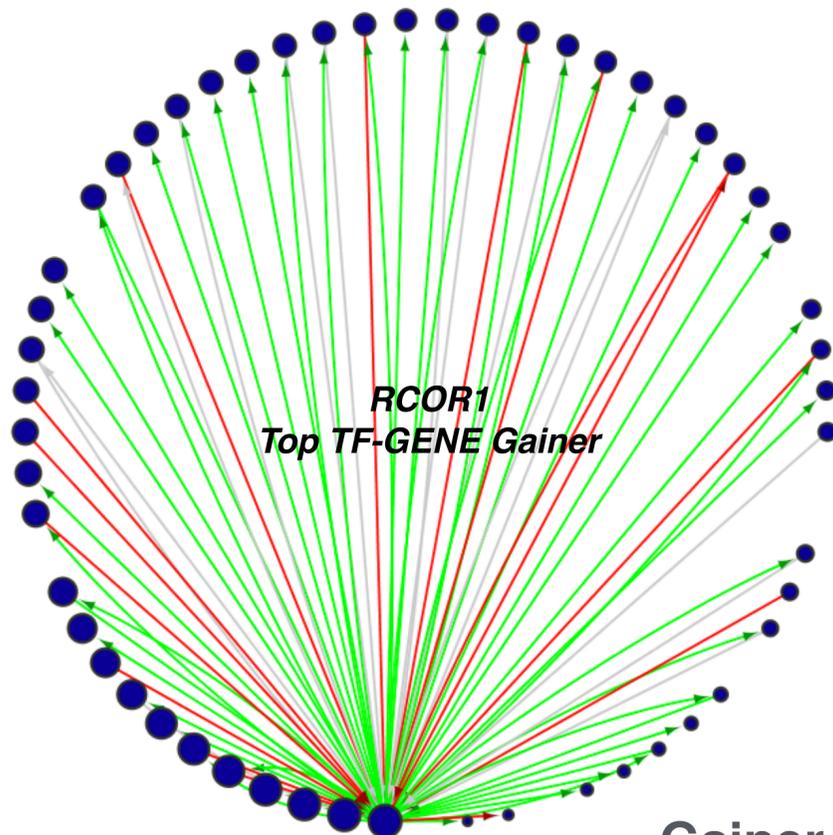
Gainer

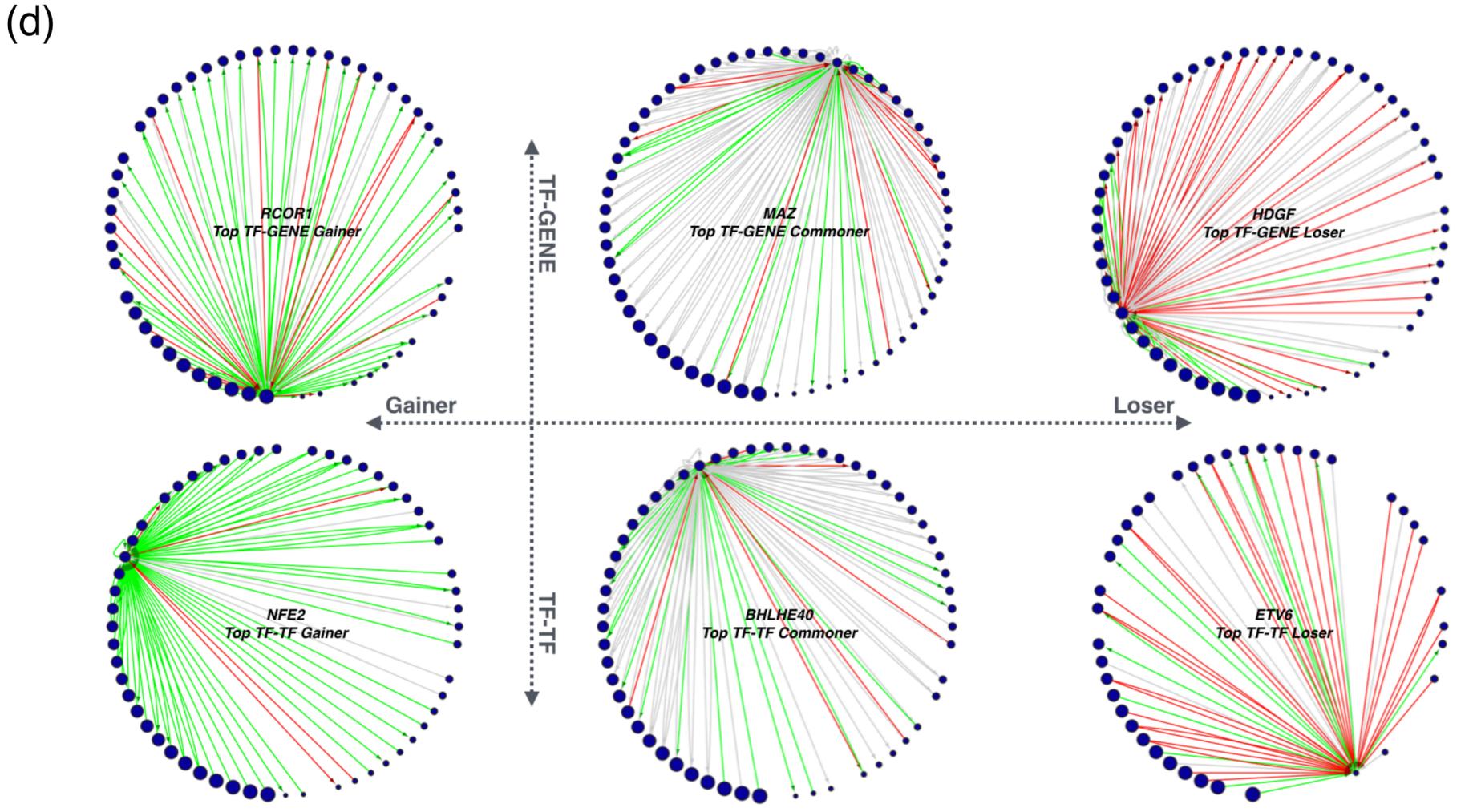
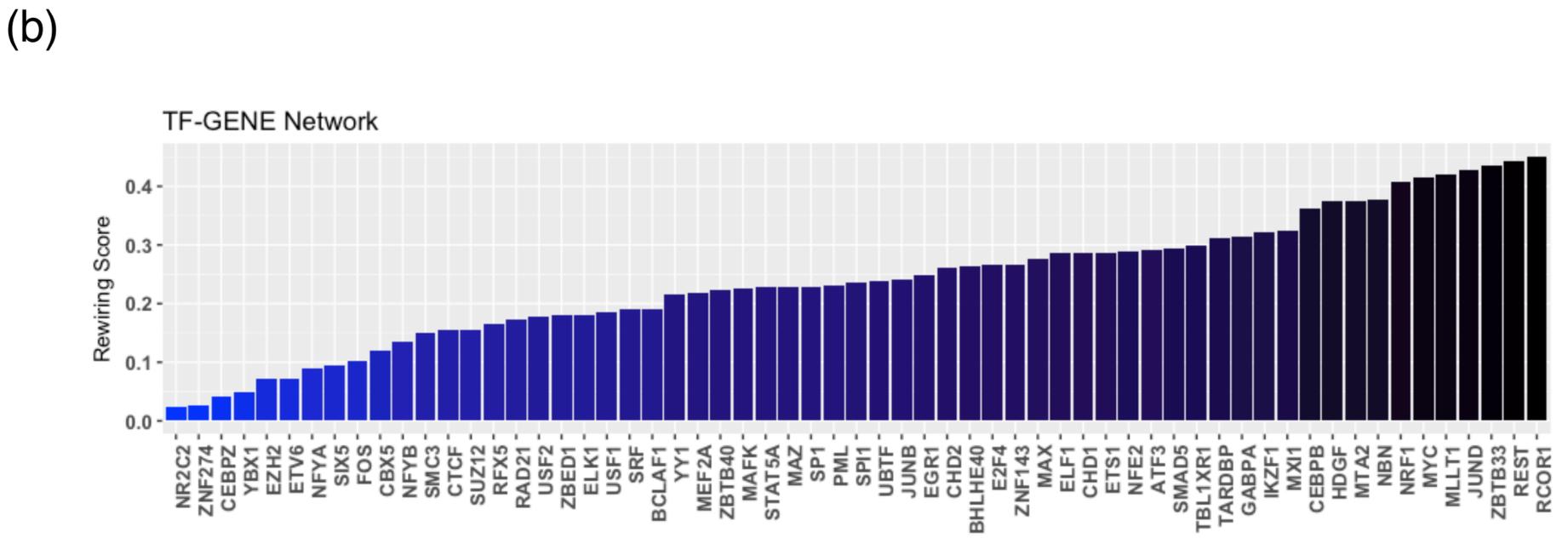
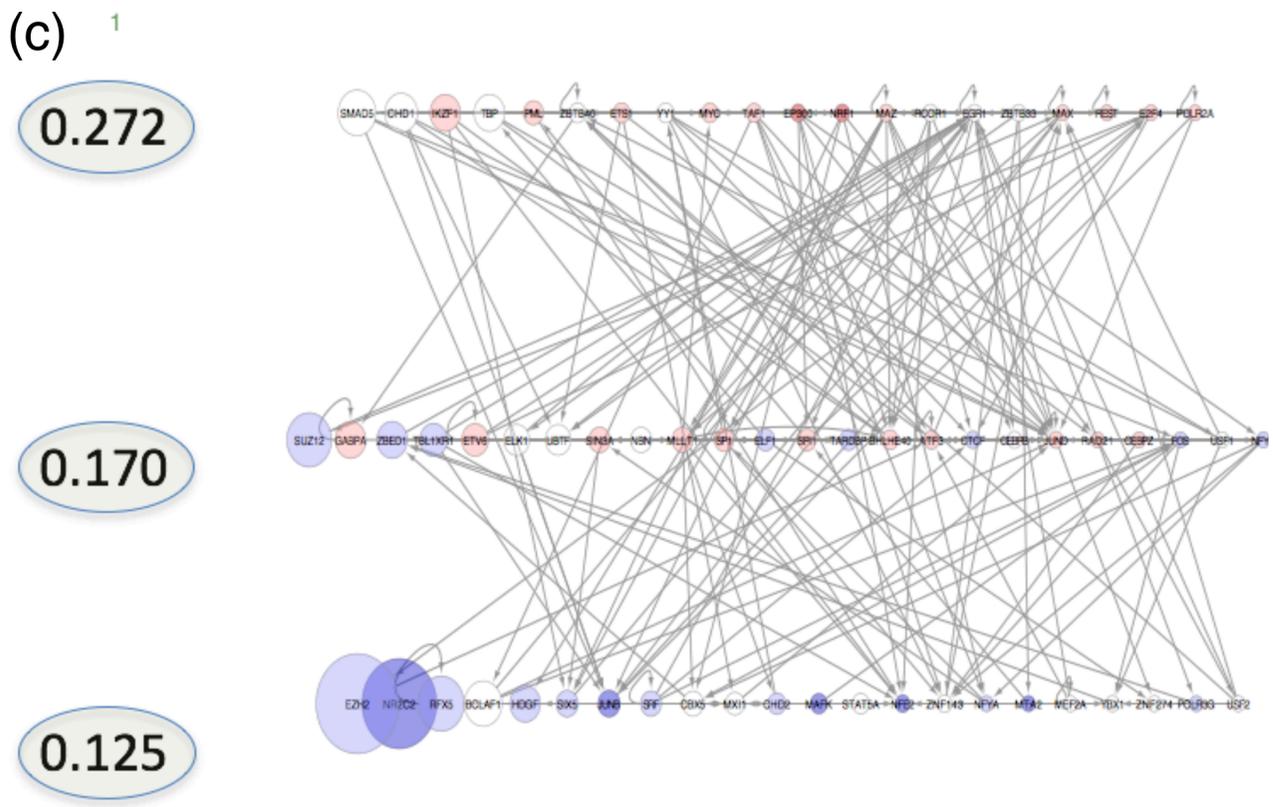
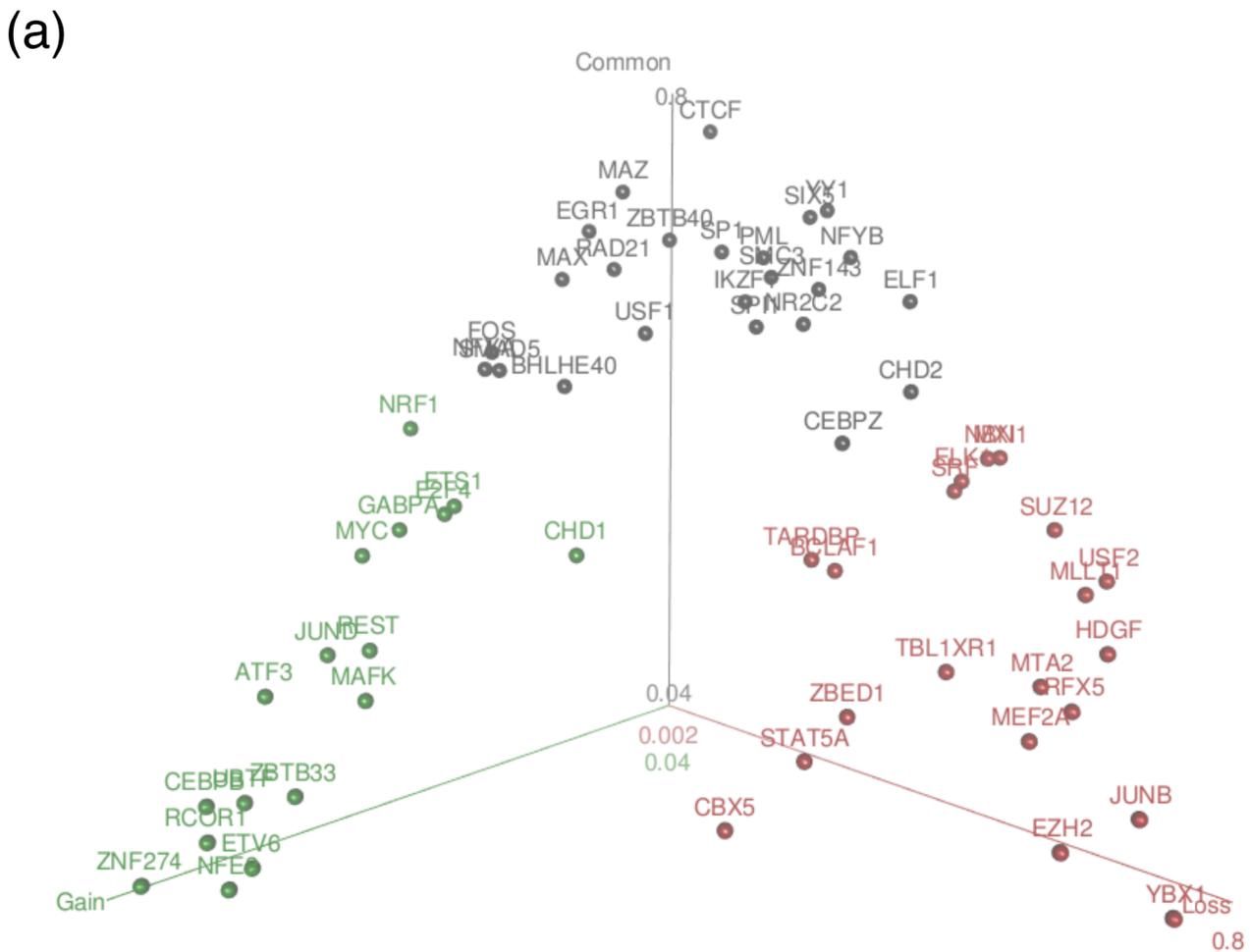
Loser

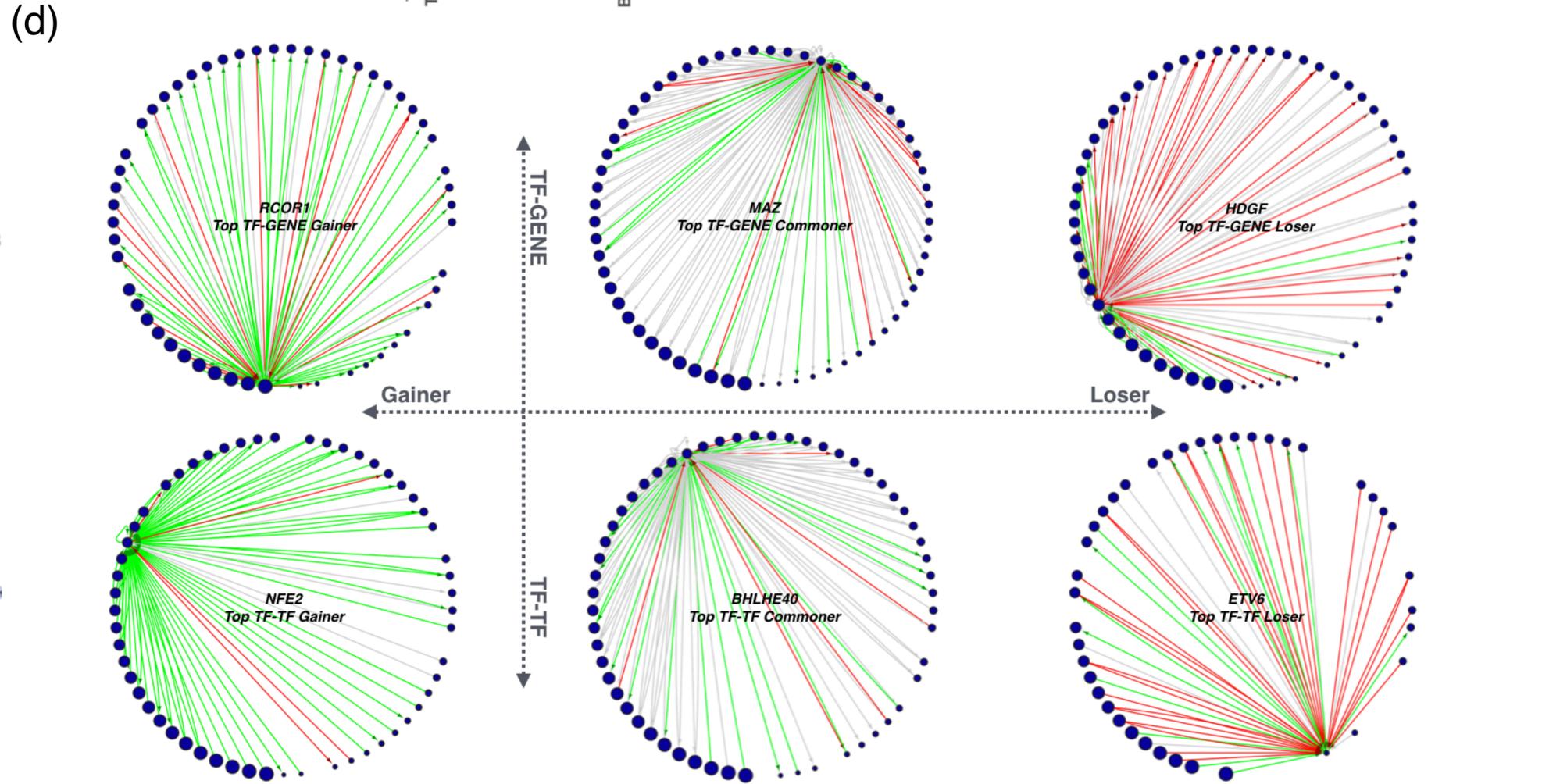
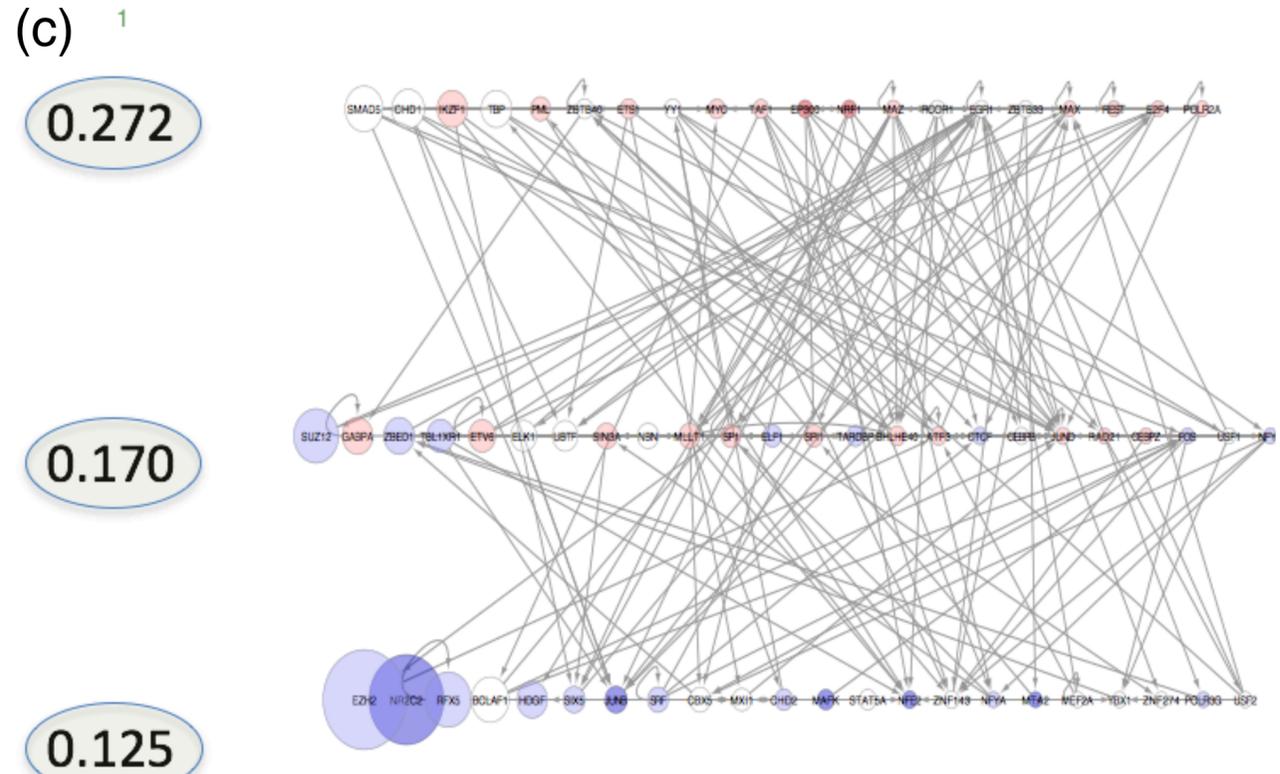
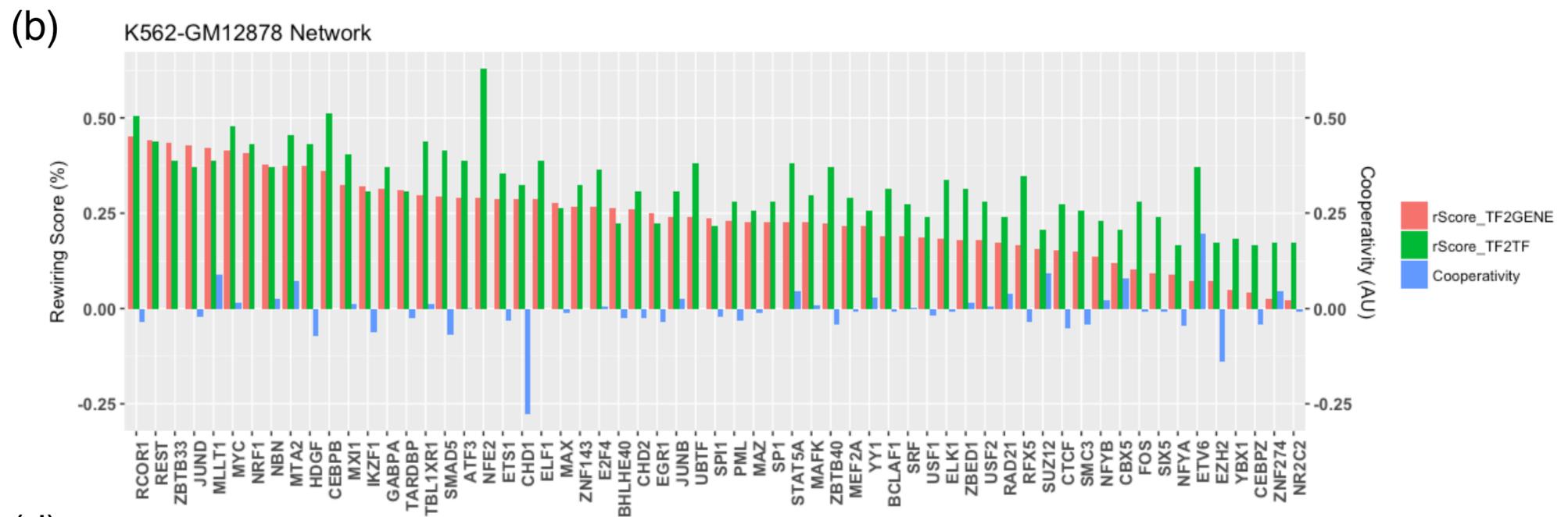
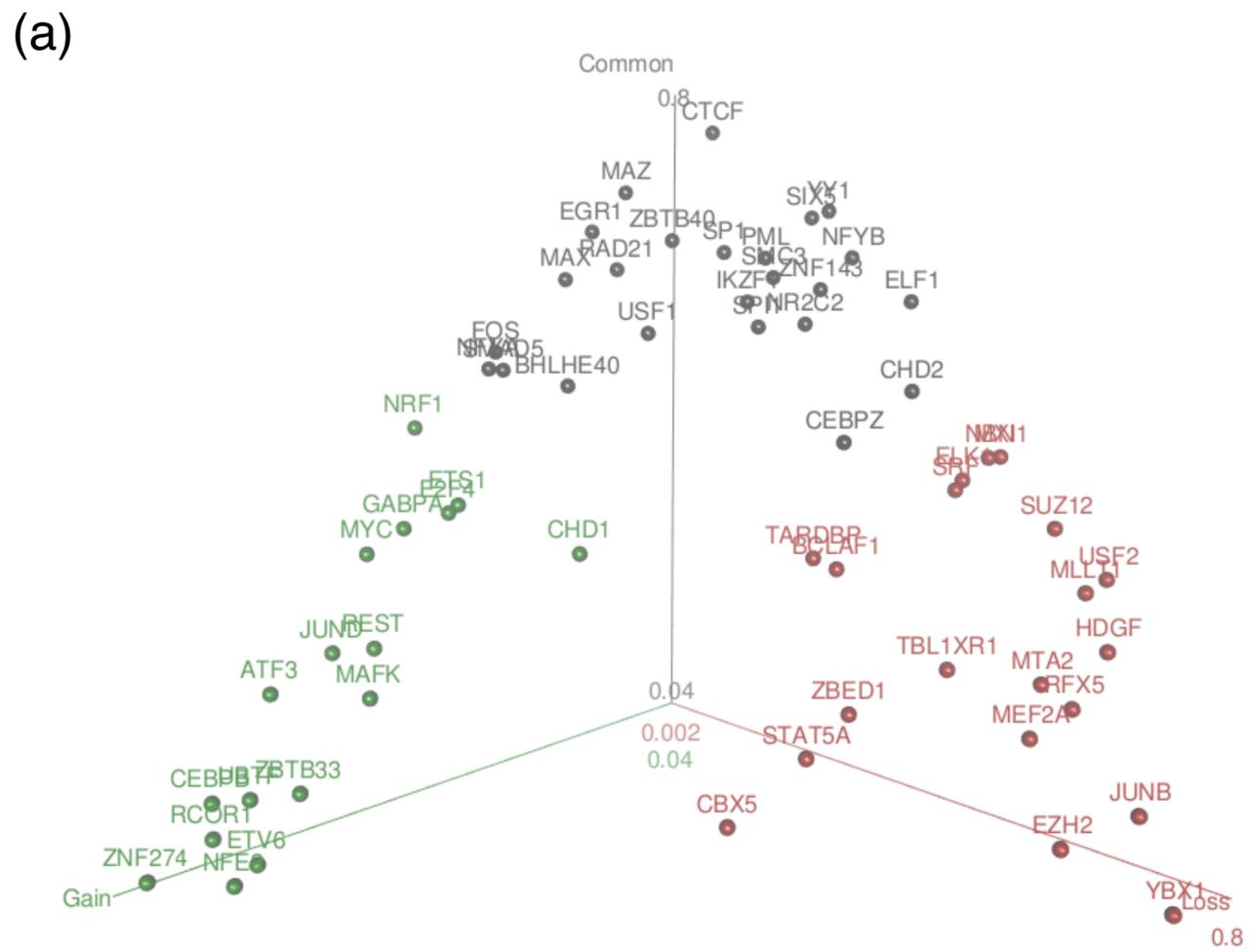


**Loser** ← TF-GENE Network TF-TF Network → **Gainer**

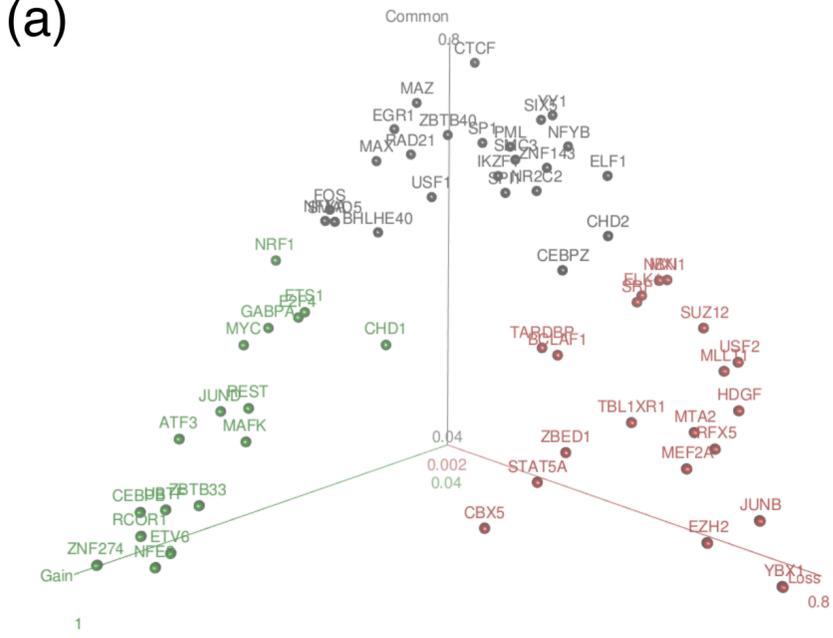




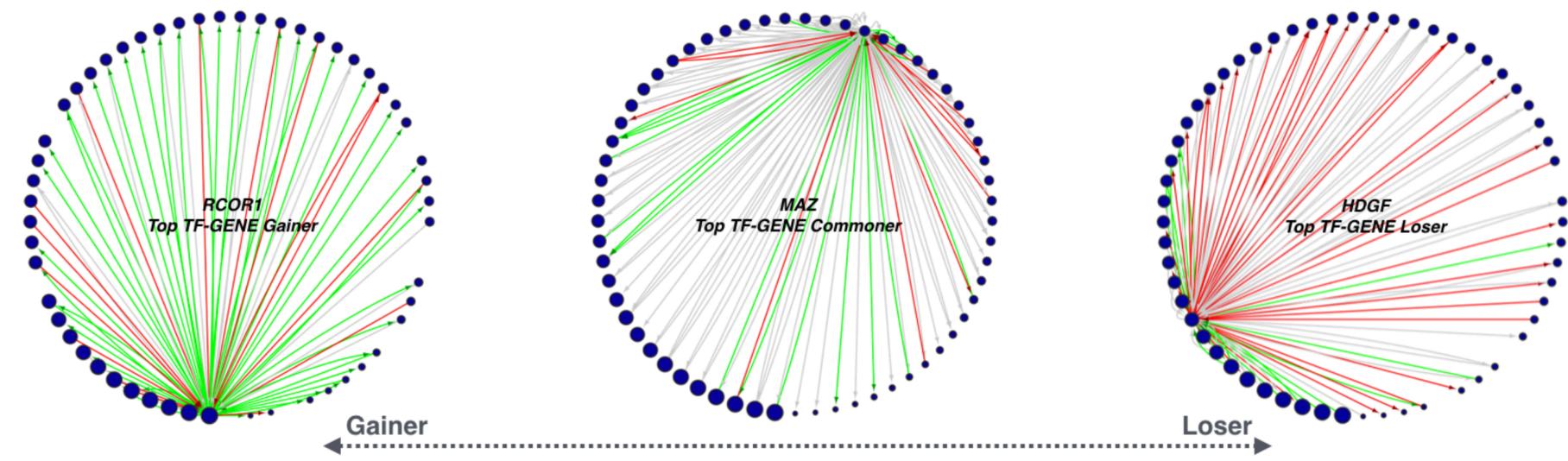




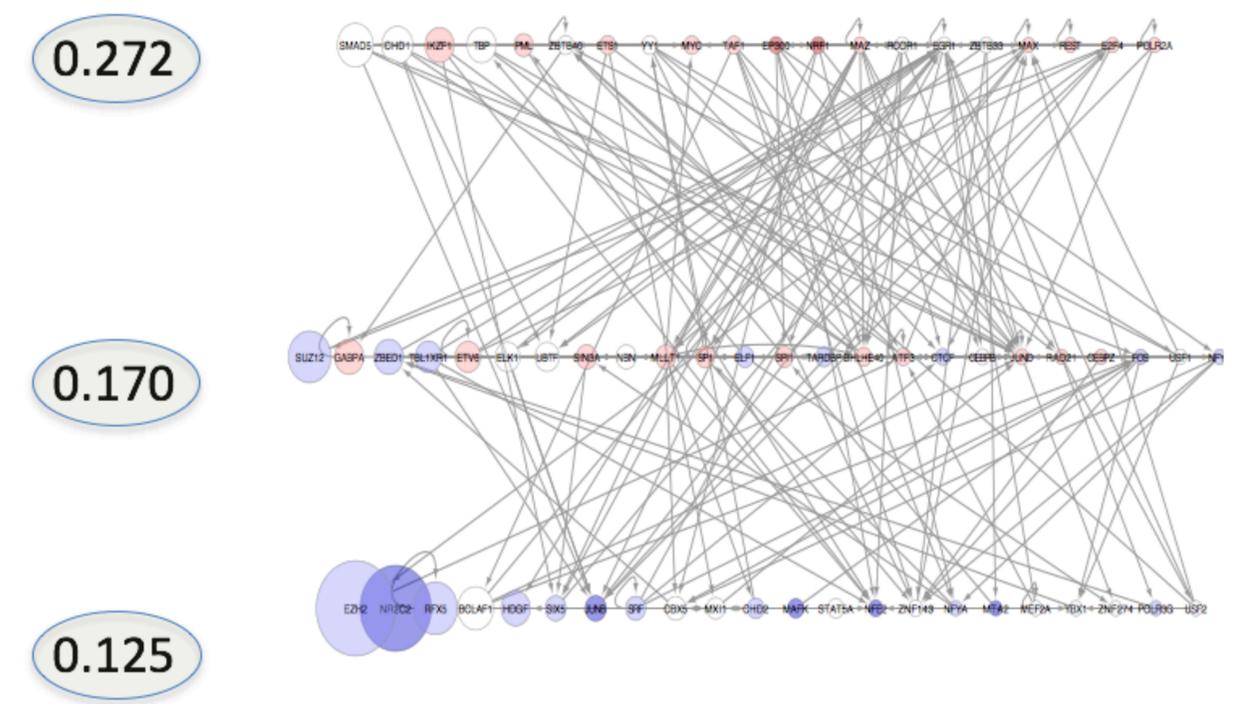
(a)



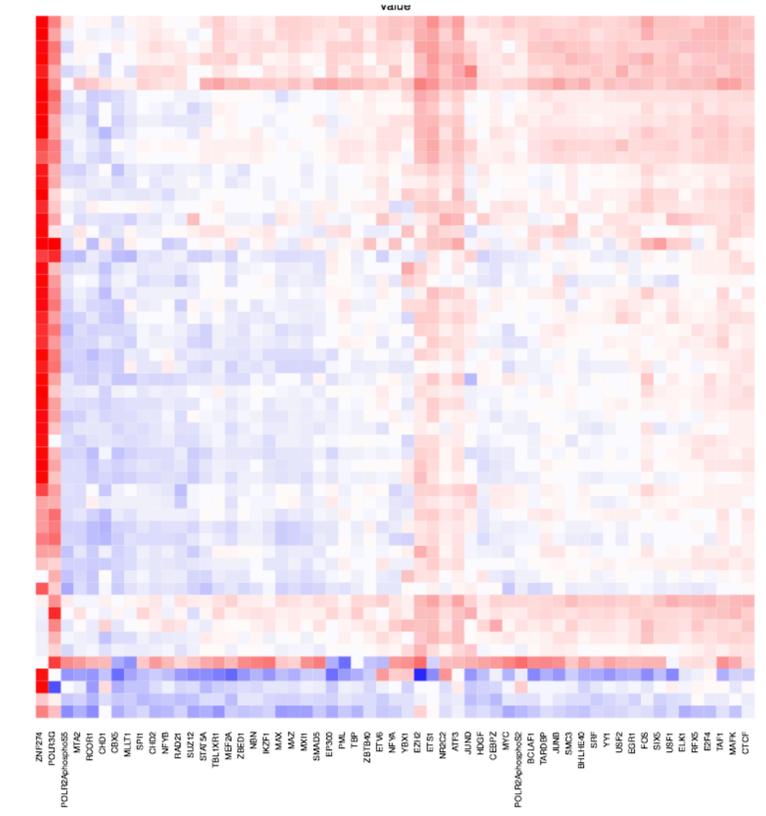
(b)



(c)



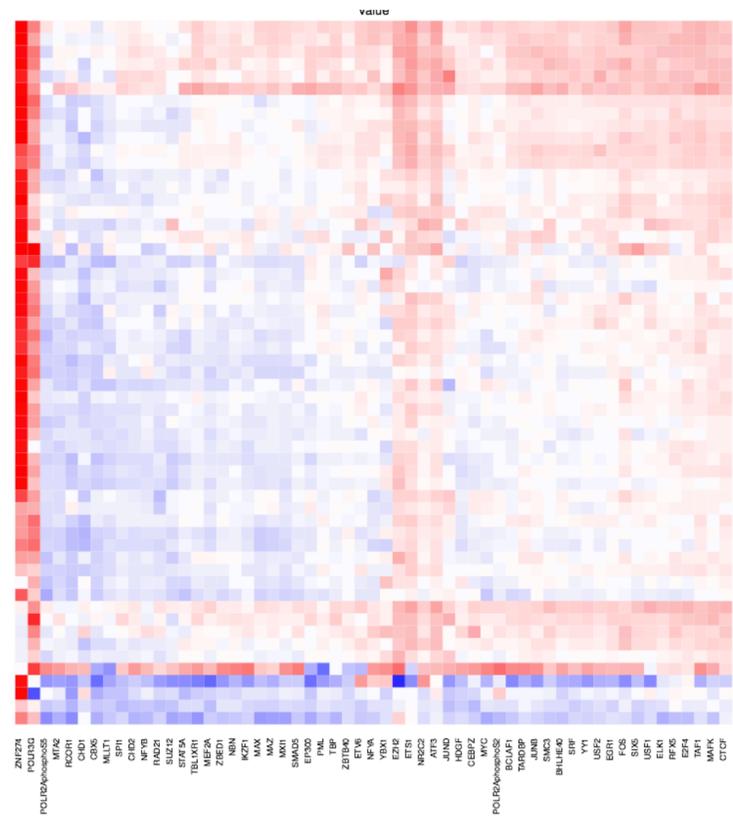
(d)



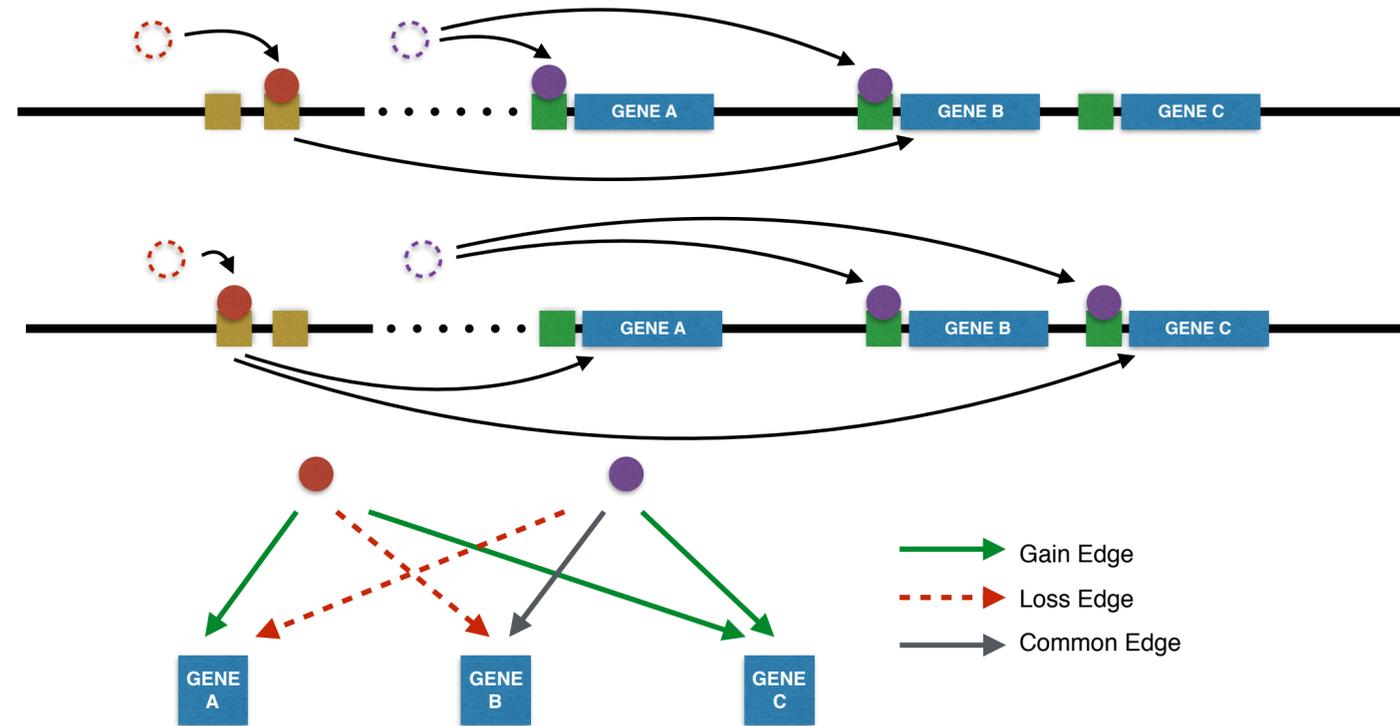
value

MTA2  
STAT5A  
MYC  
RCOR1  
SUZ12  
POLR2AphosphoS5  
SMAD3  
NFN  
ZBED1  
TBL1XR1  
MAX  
MAZ  
RFX5  
SPI1  
MEF2A  
RAD21  
JUN  
FOS  
YBX1  
NR1H5  
SIN3  
ATF3  
MAFK  
NFYA  
NFYB  
POLR2AphosphoS2  
SMAD3  
CHD2  
CEBP2  
JUNB  
SRF  
BHLHE40  
USF2  
EGR1  
YY1  
TARDBP  
BCLAF1  
TAF1  
SMC3  
CTCF  
E2F4  
ELK1  
RFX5  
PML  
TBP  
ZBTB40  
HDGF  
CBX5  
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MLL1  
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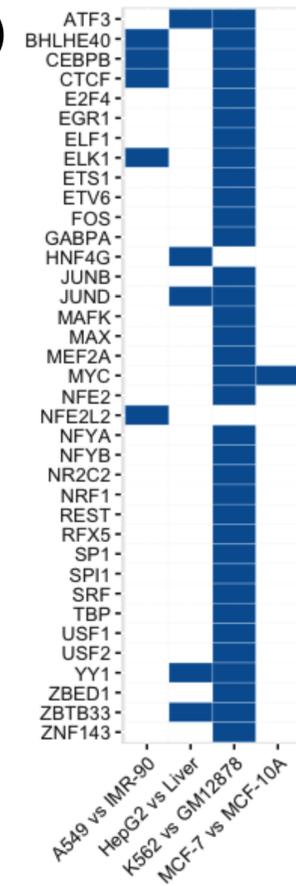
(a)



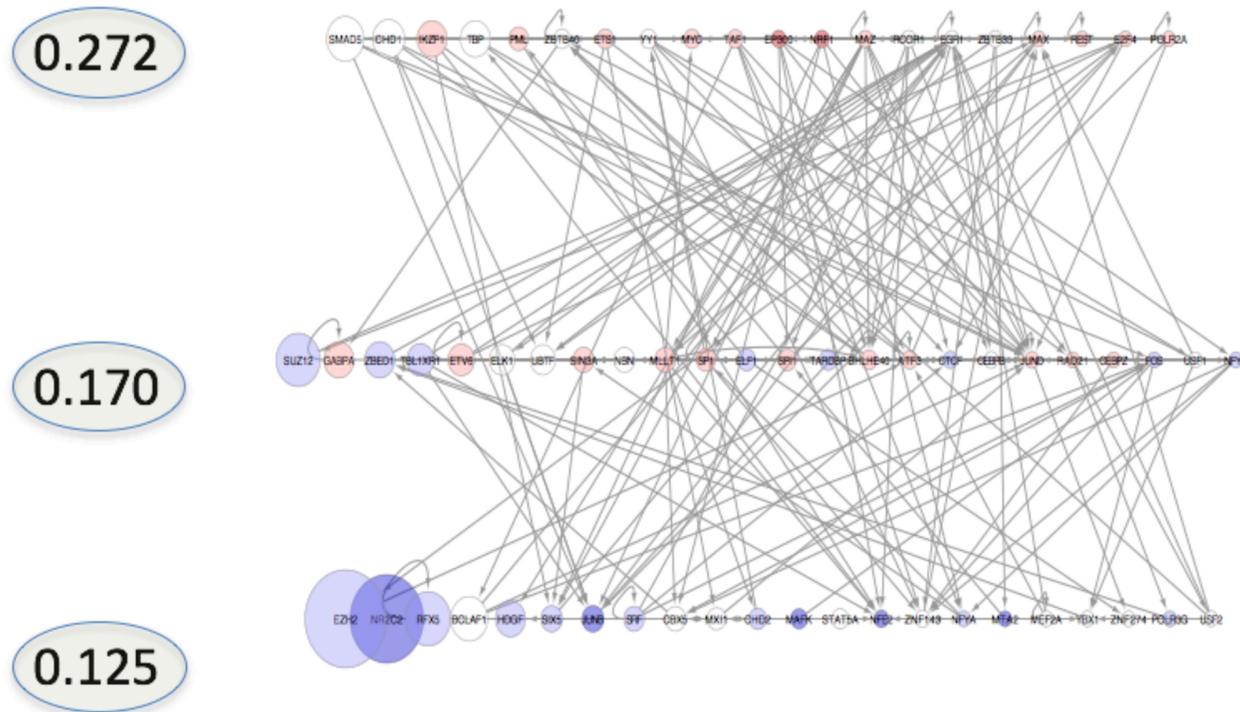
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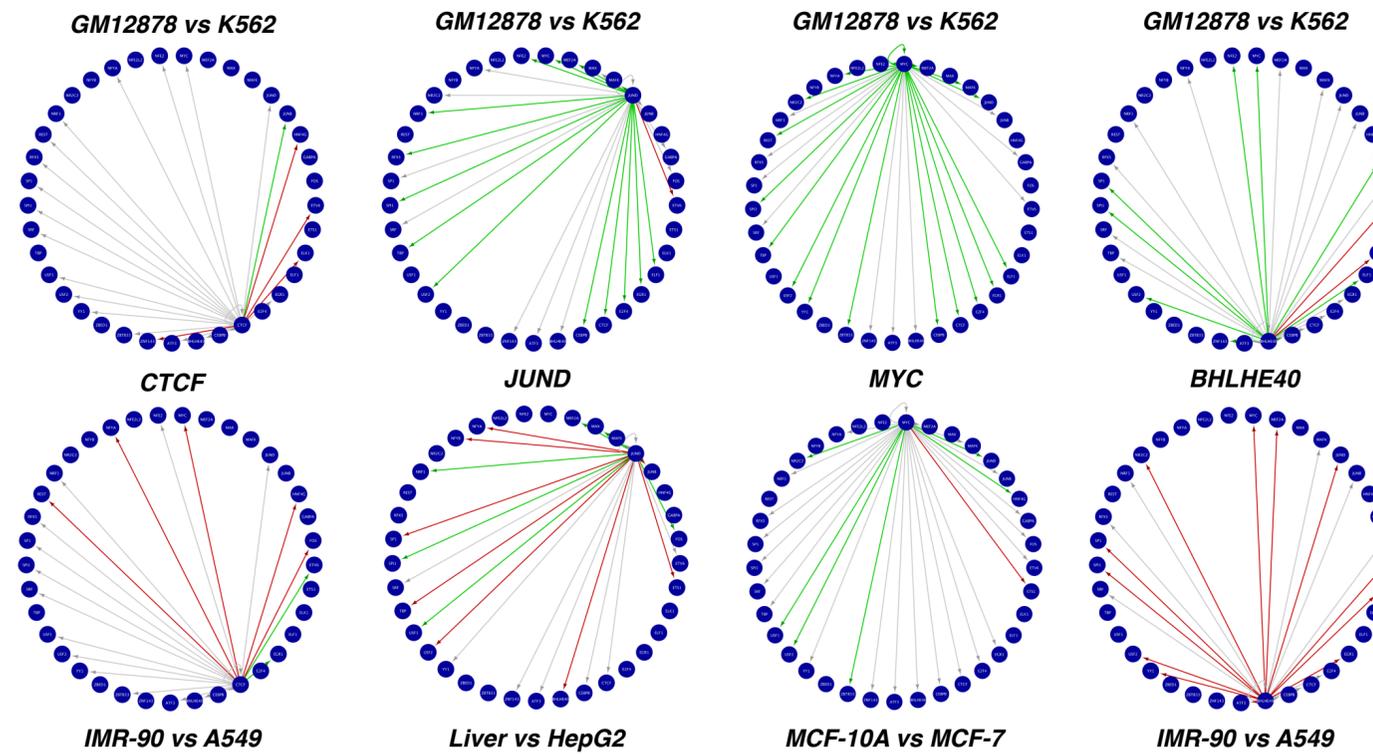
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(d)

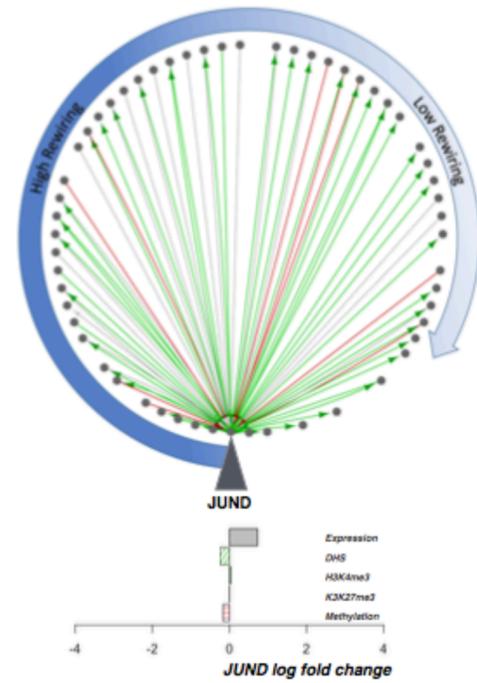


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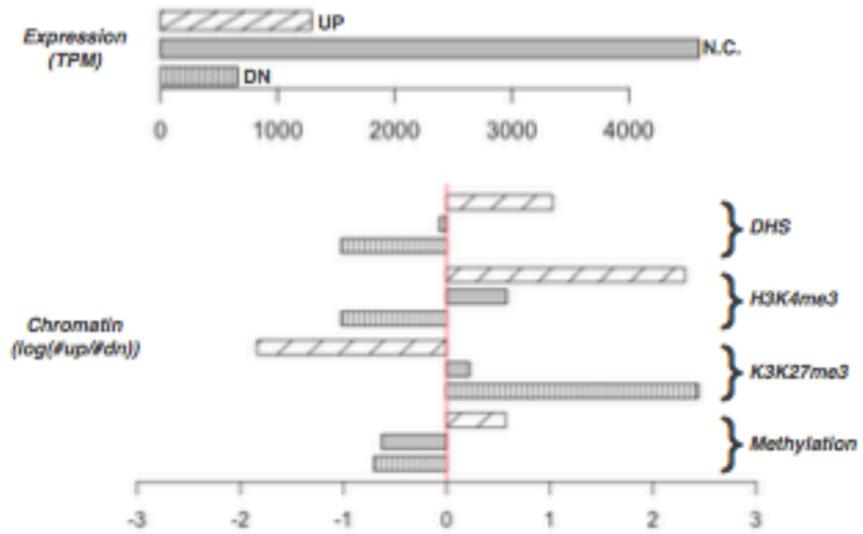


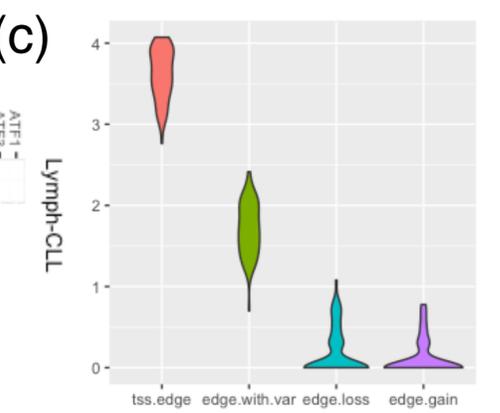
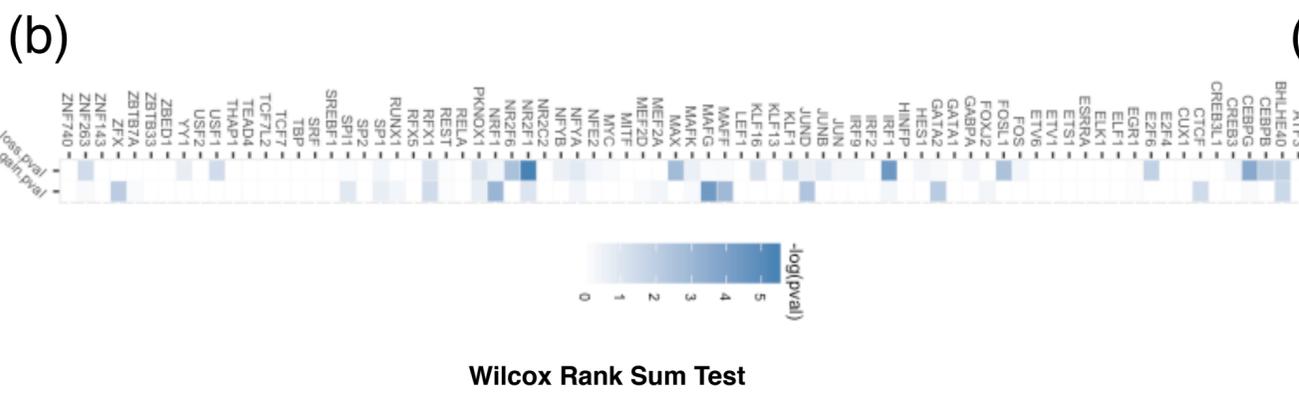
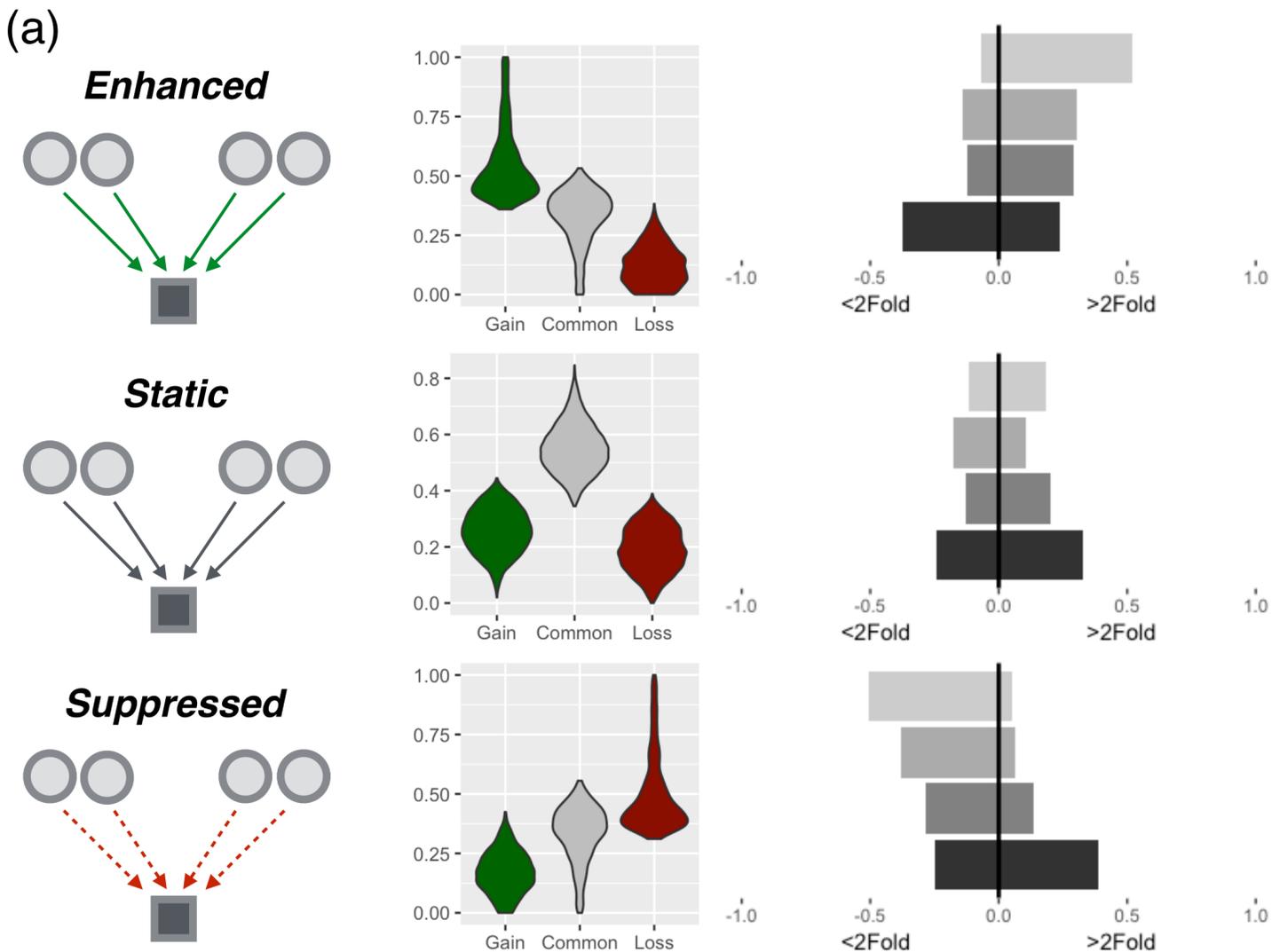
Overall Gene Target (n=15,189)

Expression (TPM)	UP			NC			DN		
n	2442			10294			2453		
%	16.1%			67.8%			16.1%		
<b>DHS (TSS Cov) active</b>	<b>UP</b>	<b>NC</b>	<b>DN</b>	<b>UP</b>	<b>NC</b>	<b>DN</b>	<b>UP</b>	<b>NC</b>	<b>DN</b>
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%
<b>H3K4me3 (TSS Cov) active promoter</b>	<b>UP</b>	<b>NC</b>	<b>DN</b>	<b>UP</b>	<b>NC</b>	<b>DN</b>	<b>UP</b>	<b>NC</b>	<b>DN</b>
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%
<b>H3K27me3 (TSS Cov) inactive promoter</b>	<b>UP</b>	<b>NC</b>	<b>DN</b>	<b>UP</b>	<b>NC</b>	<b>DN</b>	<b>UP</b>	<b>NC</b>	<b>DN</b>
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%
<b>Methylation (Sig Avg) repressive</b>	<b>UP</b>	<b>NC</b>	<b>DN</b>	<b>UP</b>	<b>NC</b>	<b>DN</b>	<b>UP</b>	<b>NC</b>	<b>DN</b>
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%
<b>Mutation ext.gene count</b>	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%
<b>Mutation ext.gene pval &lt; 0.05</b>	29			138			57		
	1.2%			1.3%			2.3%		

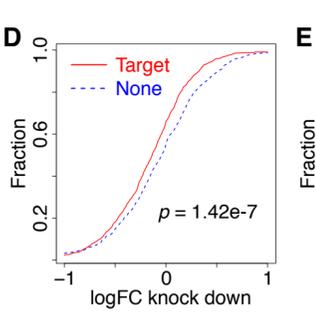
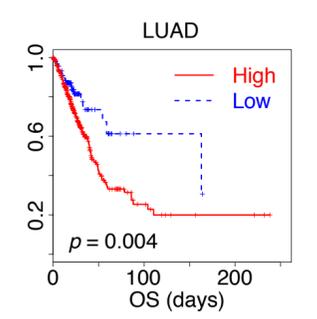
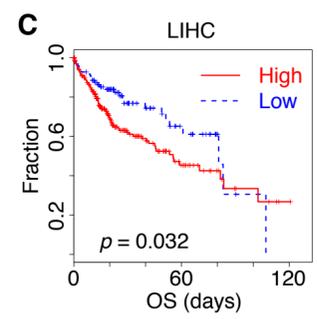
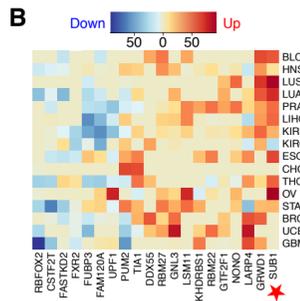
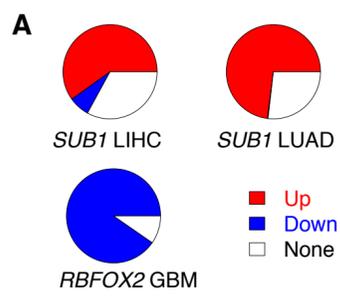
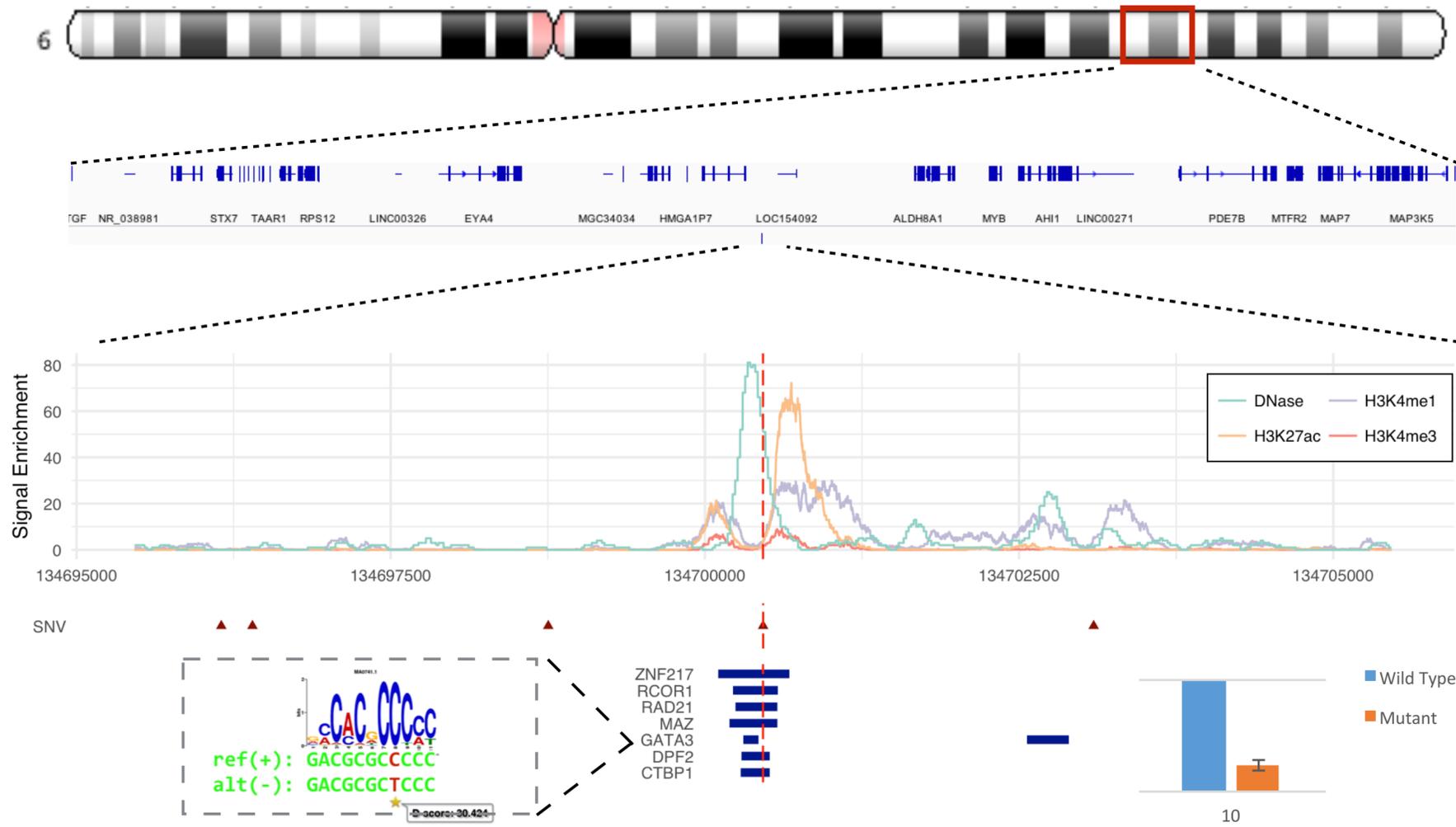


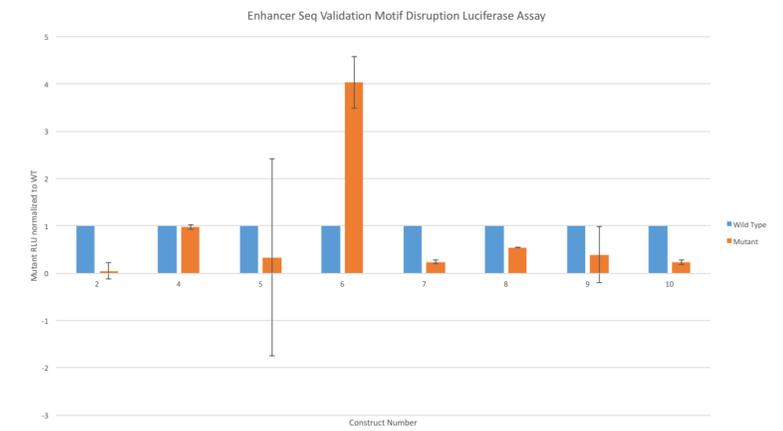
JUND Gained Targets



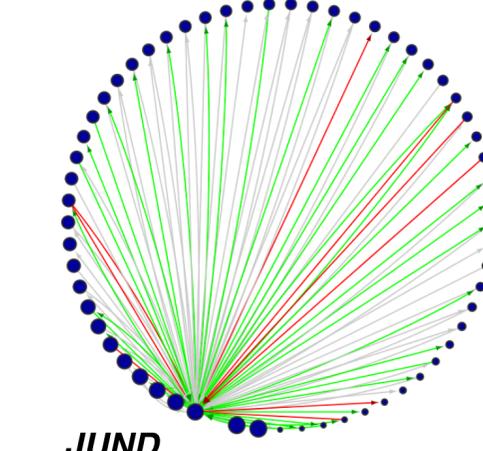
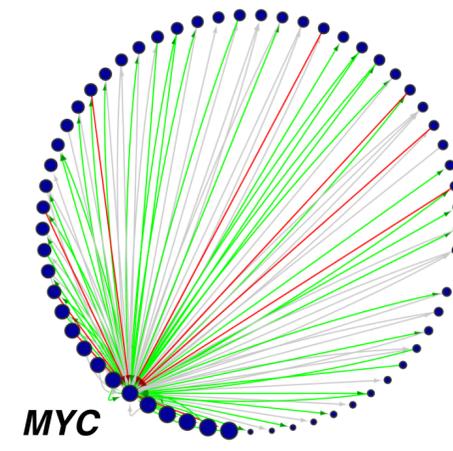
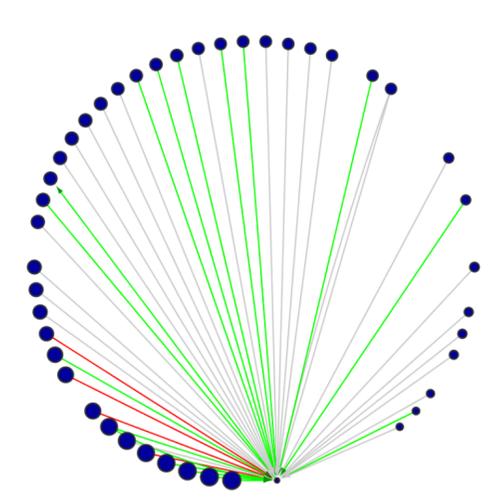
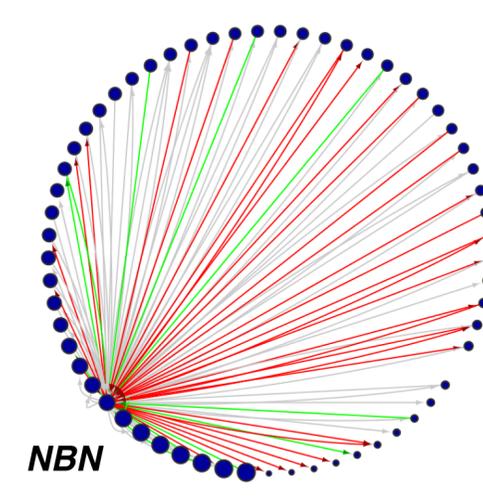
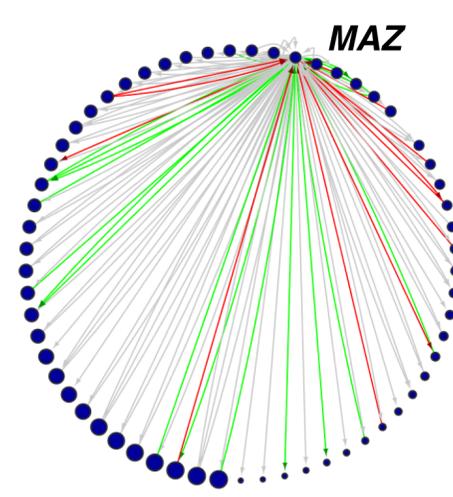


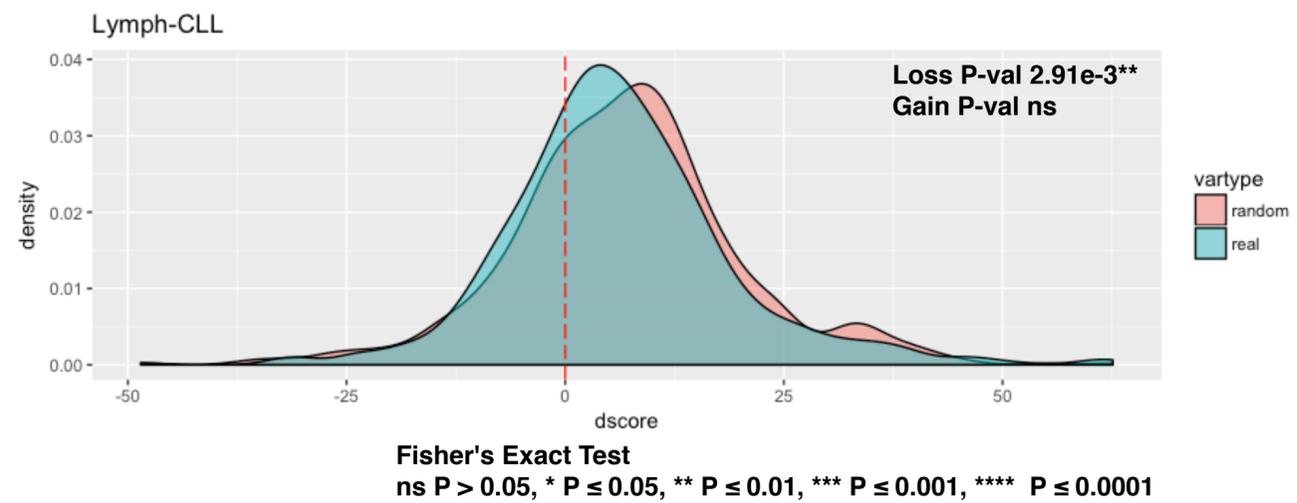
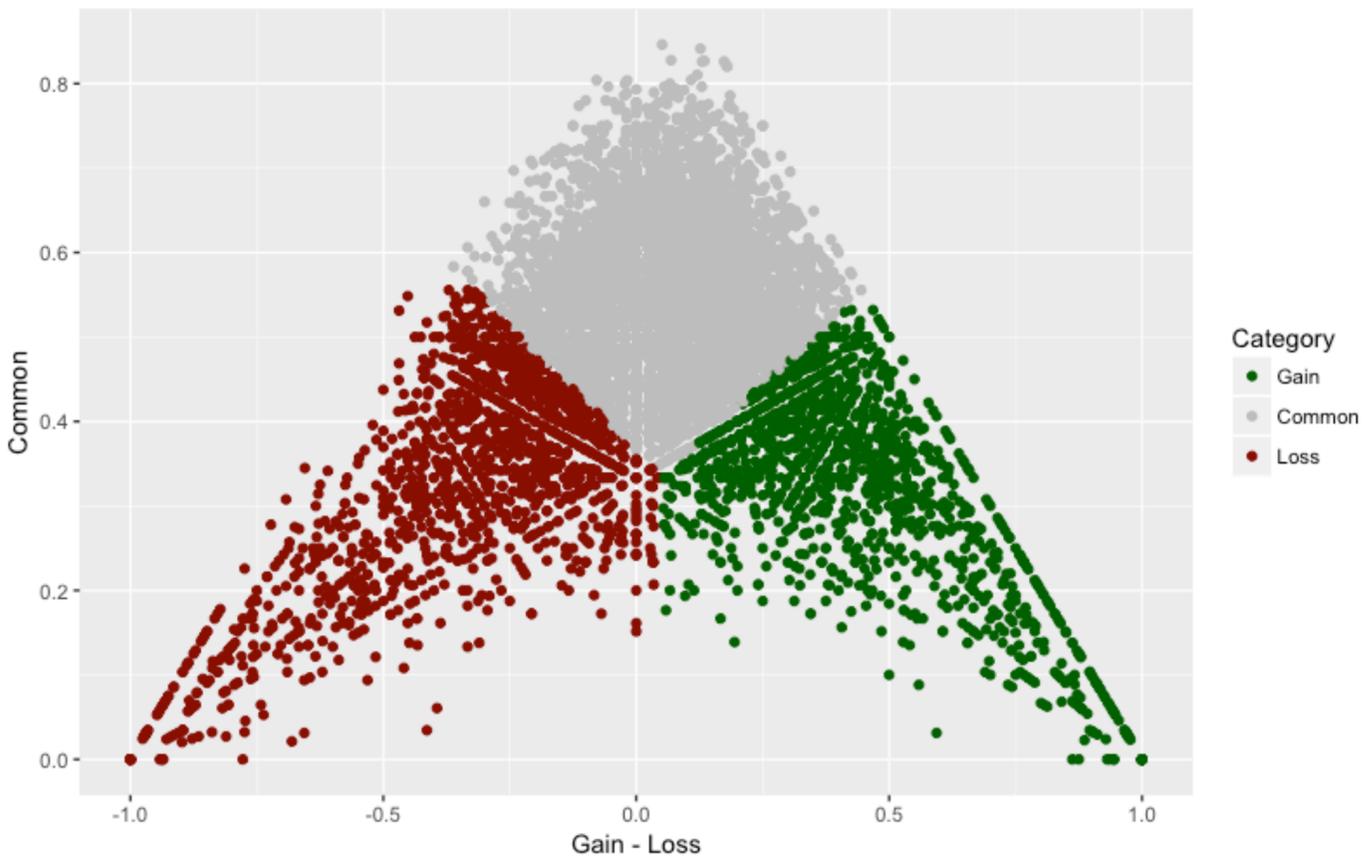
(a)



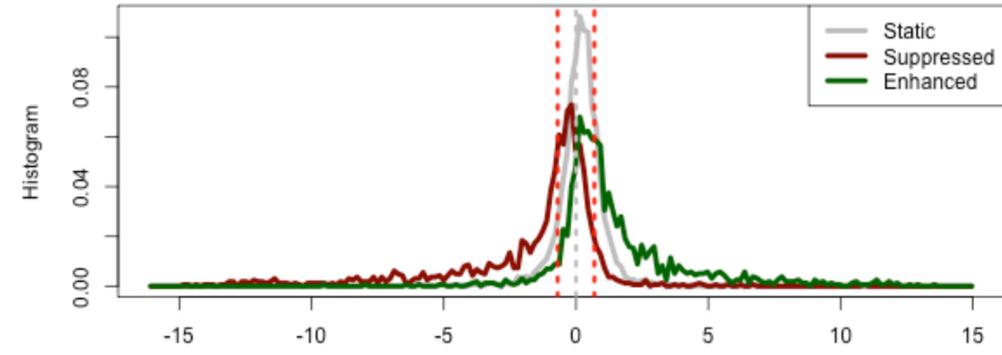


	Sample02	Sample04	Sample05	Sample06	Sample07	Sample08	Sample09	Sample10
chr	chr21	chr17	chr20	chr7	chr20	chr7	chr7	chr6
pos	27,541,982	38,474,408	43,971,343	1,598,567	58,563,412	150,759,483	5,596,005	134,700,462
ref	G	C	G	C	C	C	T	G
alt	A	G	C	T	T	G	G	T
D-score_min	20.361	16.910	3.665	15.746	7.217	13.959	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

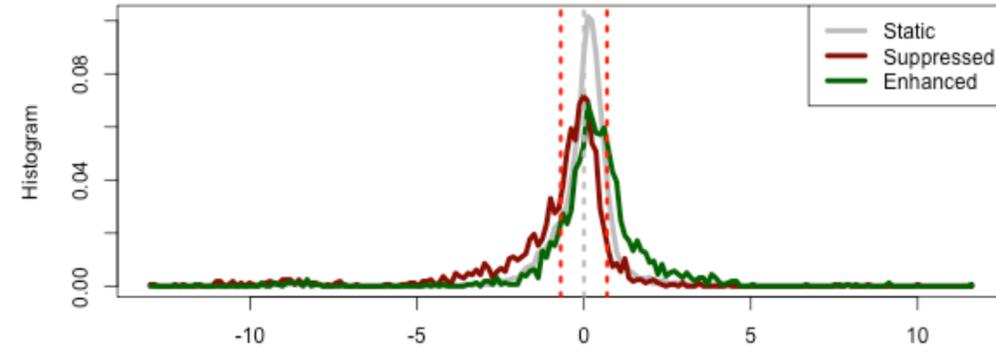




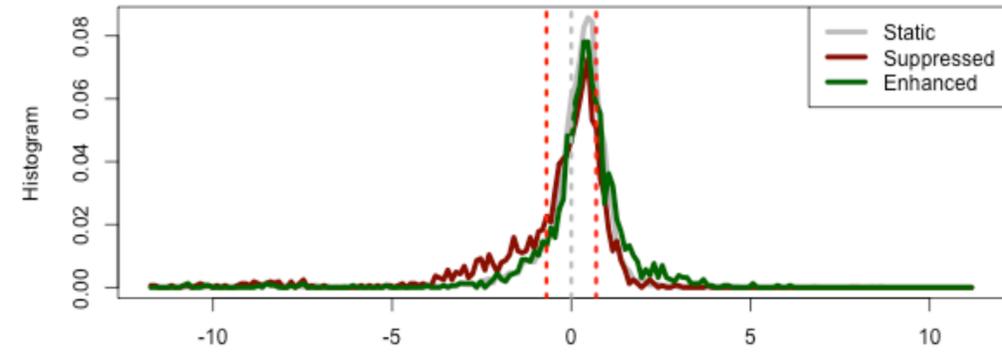
Expression(TPM) log(fc)



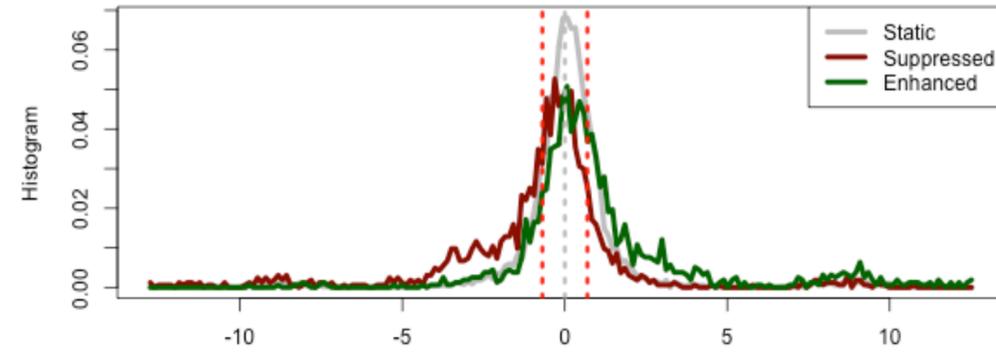
DNase I log(fc)



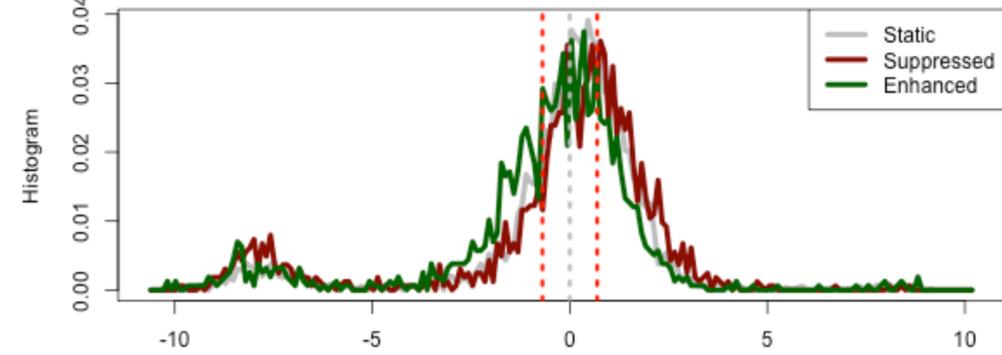
H3K4me3 log(fc)



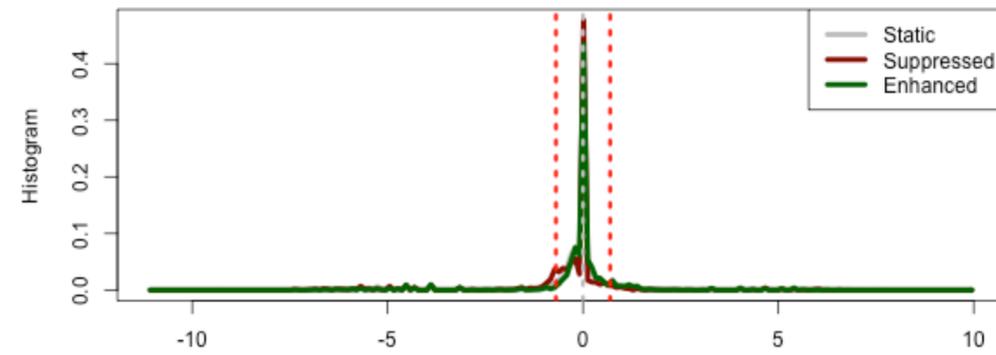
H3K27ac log(fc)



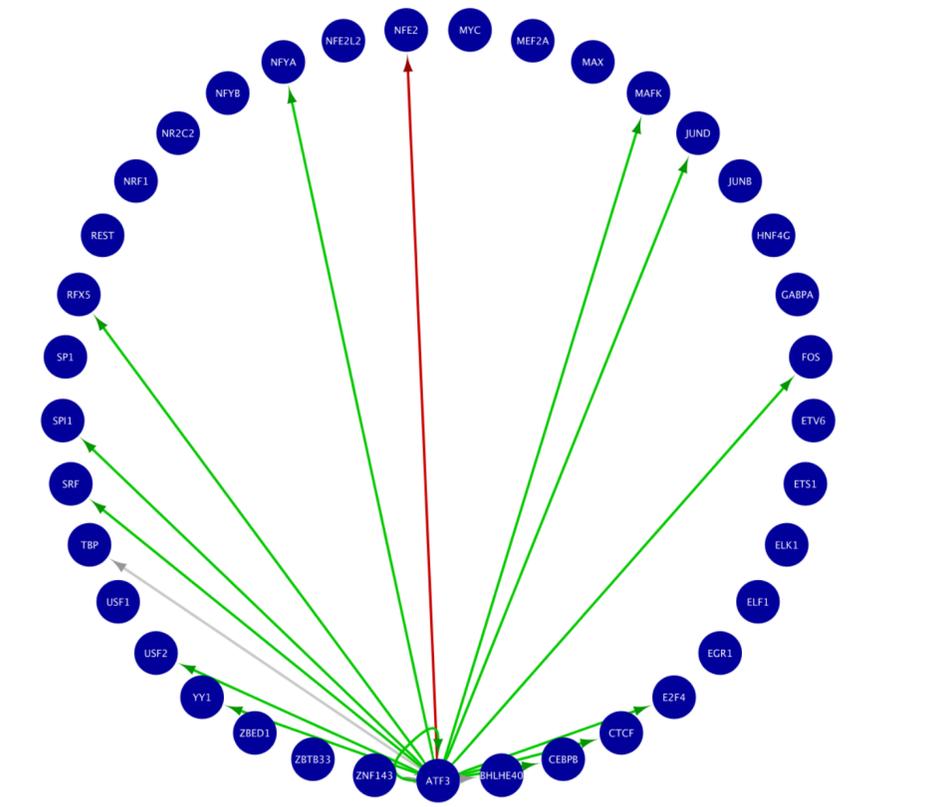
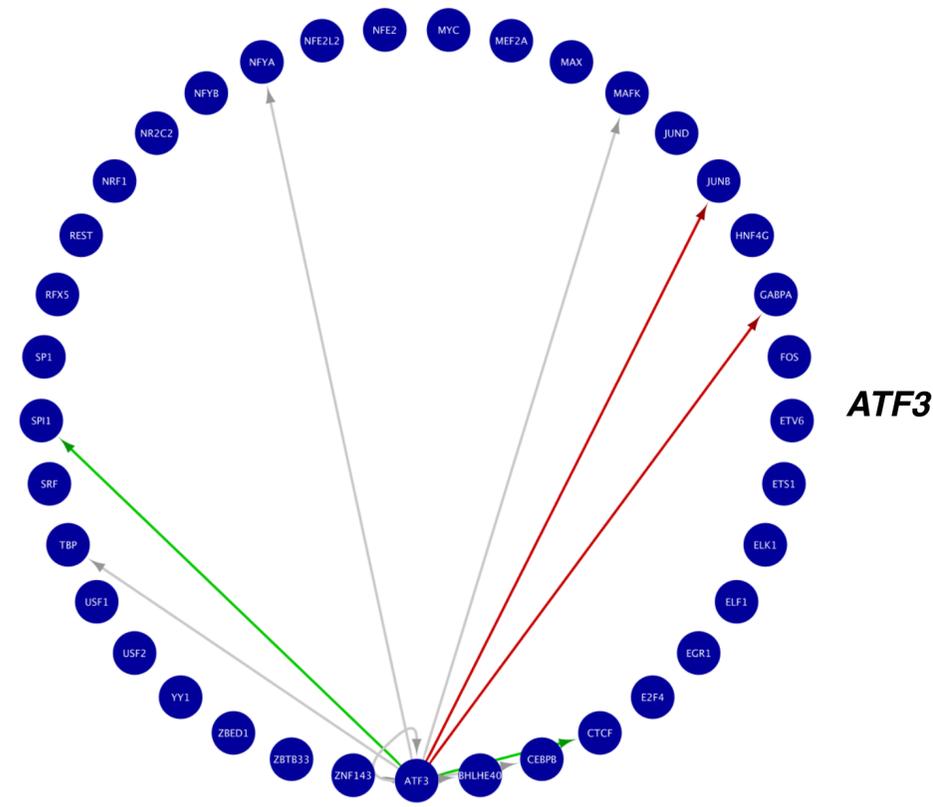
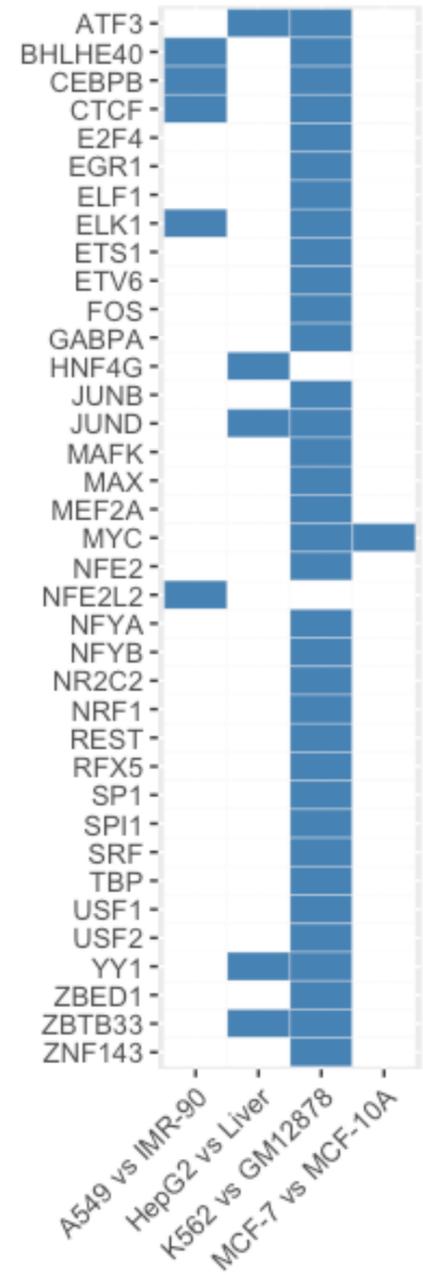
H3K27me3 log(fc)



5mC log(fc)

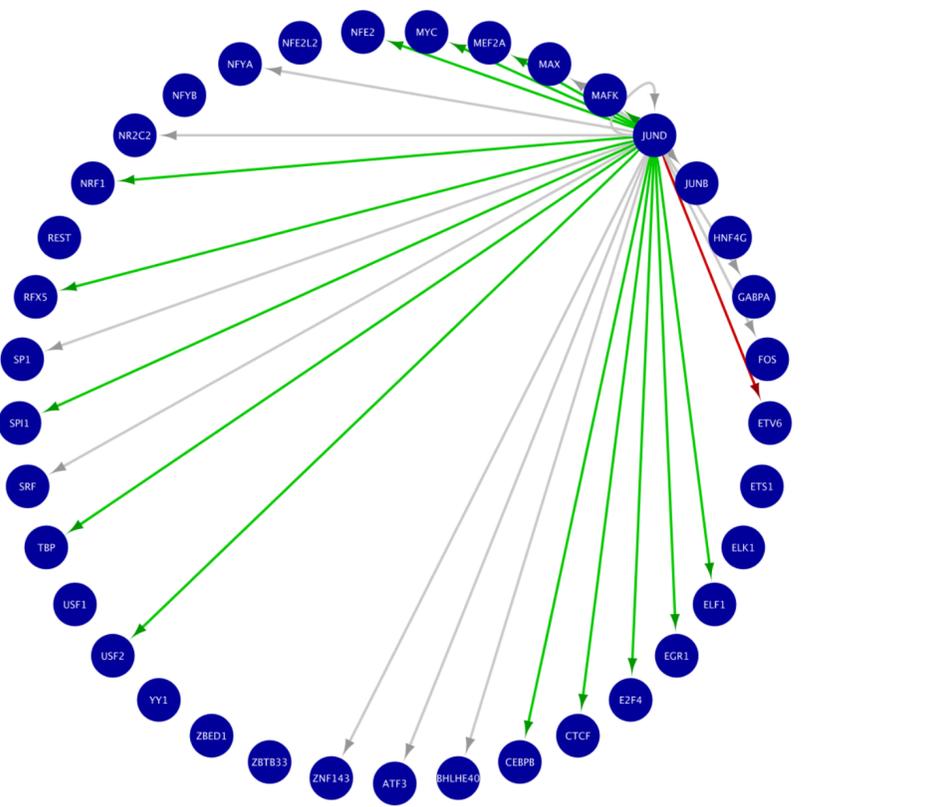
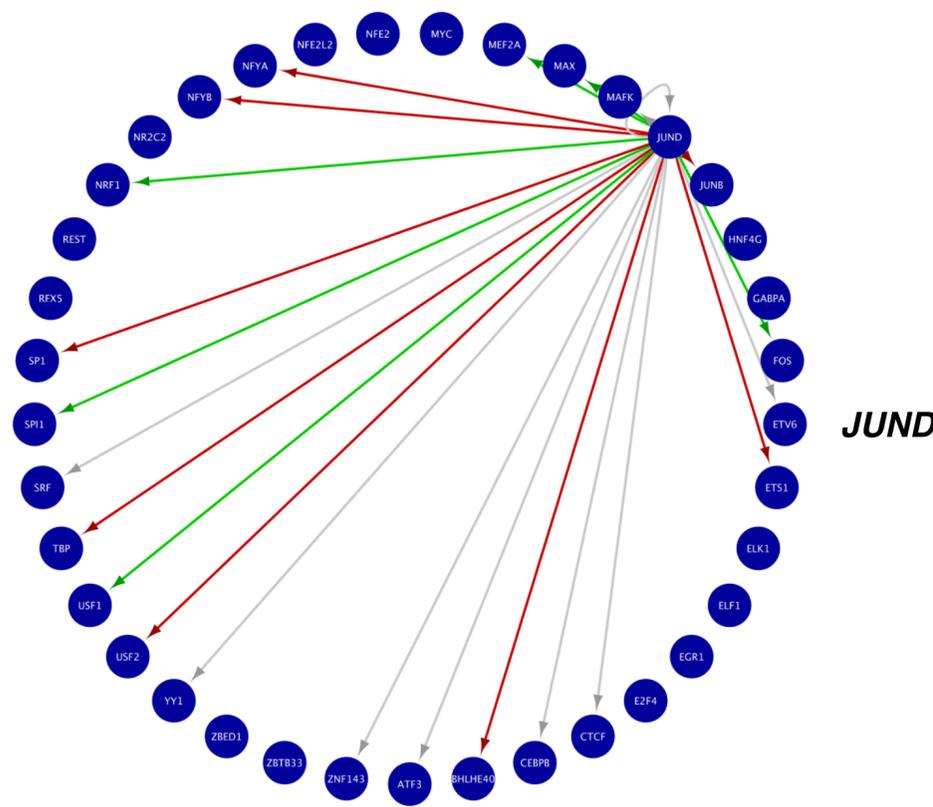


# Cross-Cancer TFSS Matrix



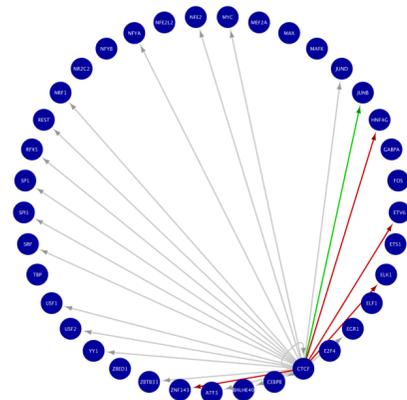
*Liver vs HepG2*

*GM12878 vs K562*



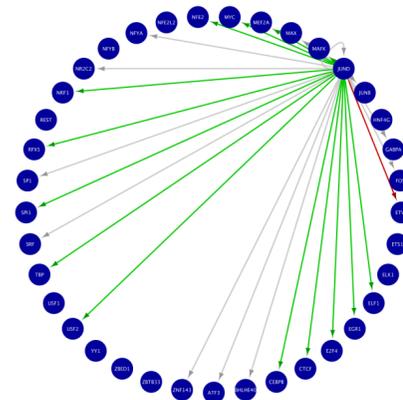
**JUND**

**GM12878 vs K562**



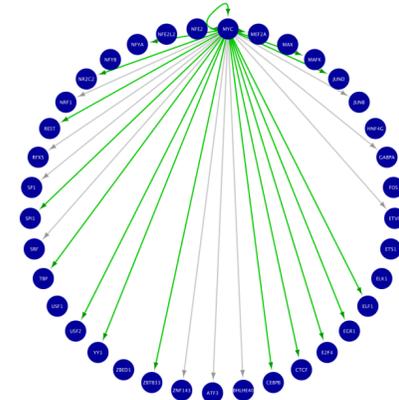
**CTCF**

**GM12878 vs K562**



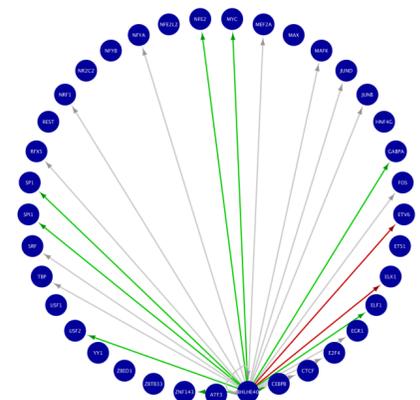
**JUND**

**GM12878 vs K562**

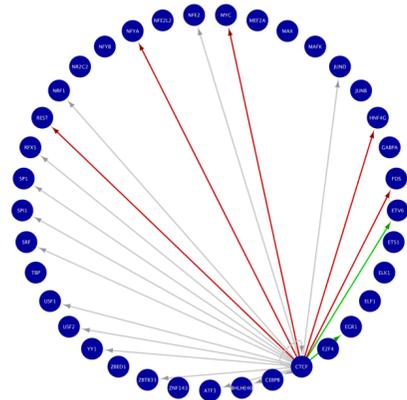


**MYC**

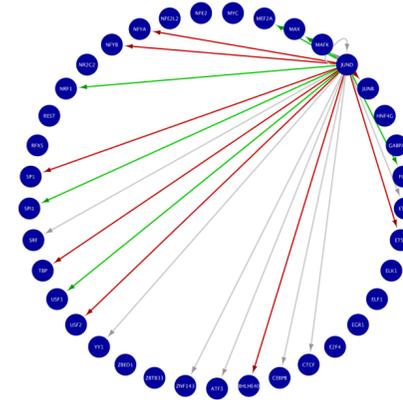
**GM12878 vs K562**



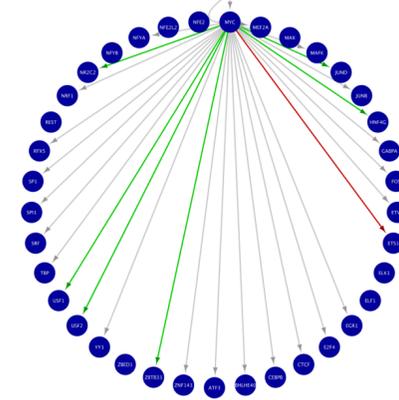
**BHLHE40**



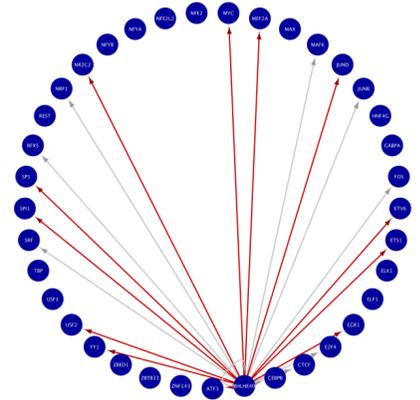
**IMR-90 vs A549**



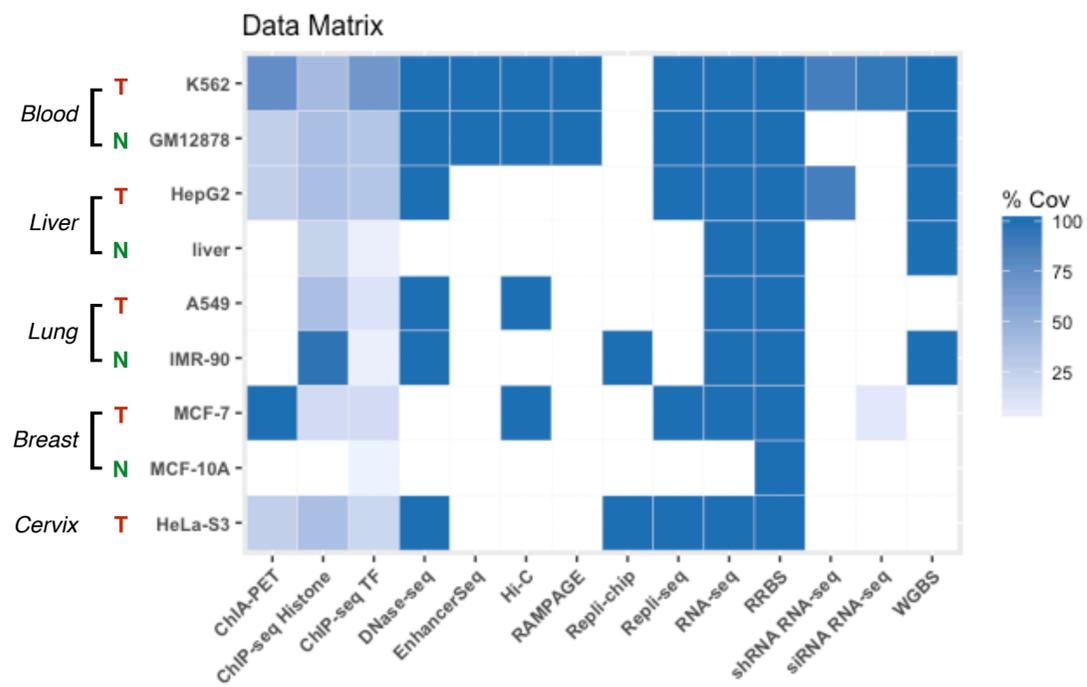
**Liver vs HepG2**



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



**IMR-90 vs A549**



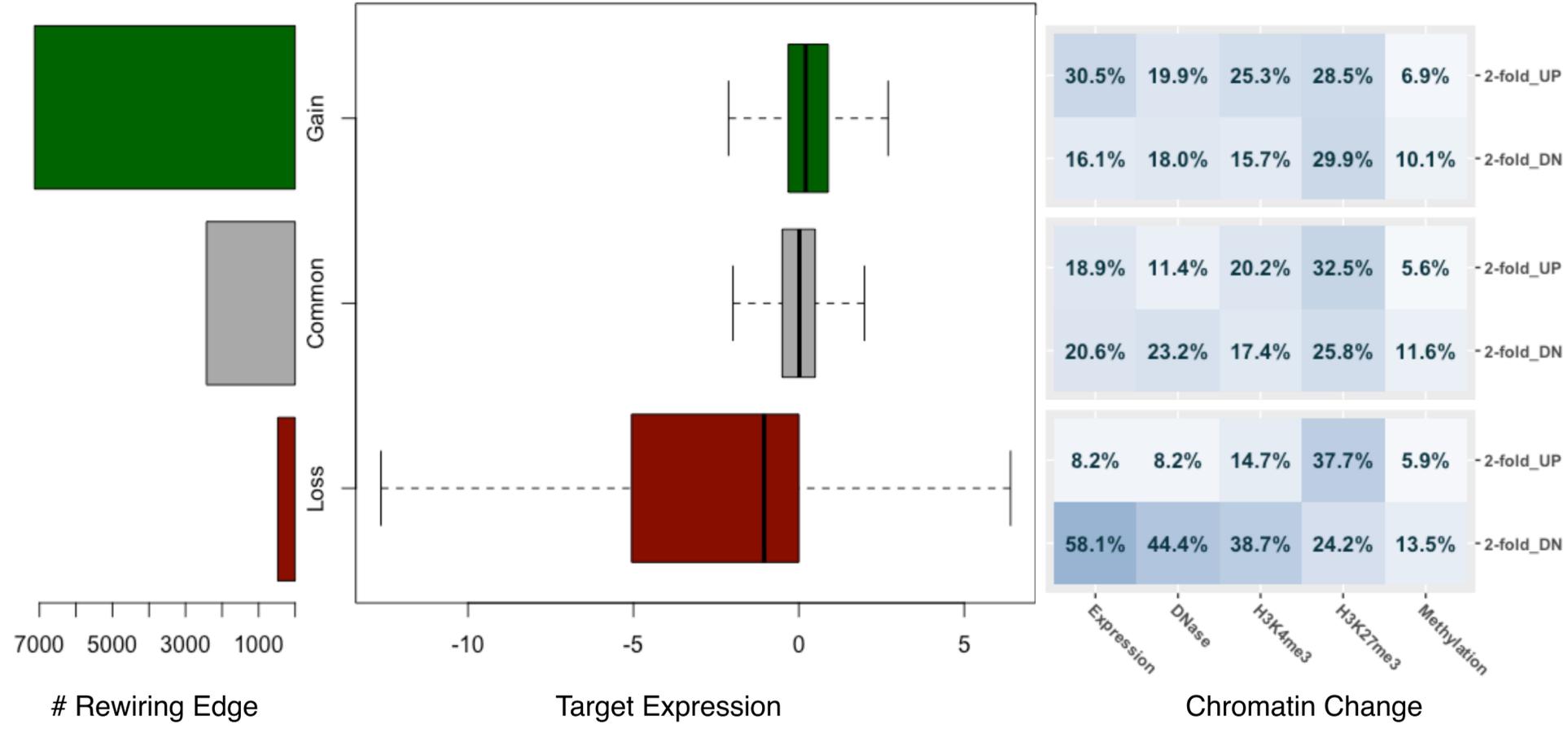
### Data Matrix

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	0	0	0	0	0	0

### Data Matrix

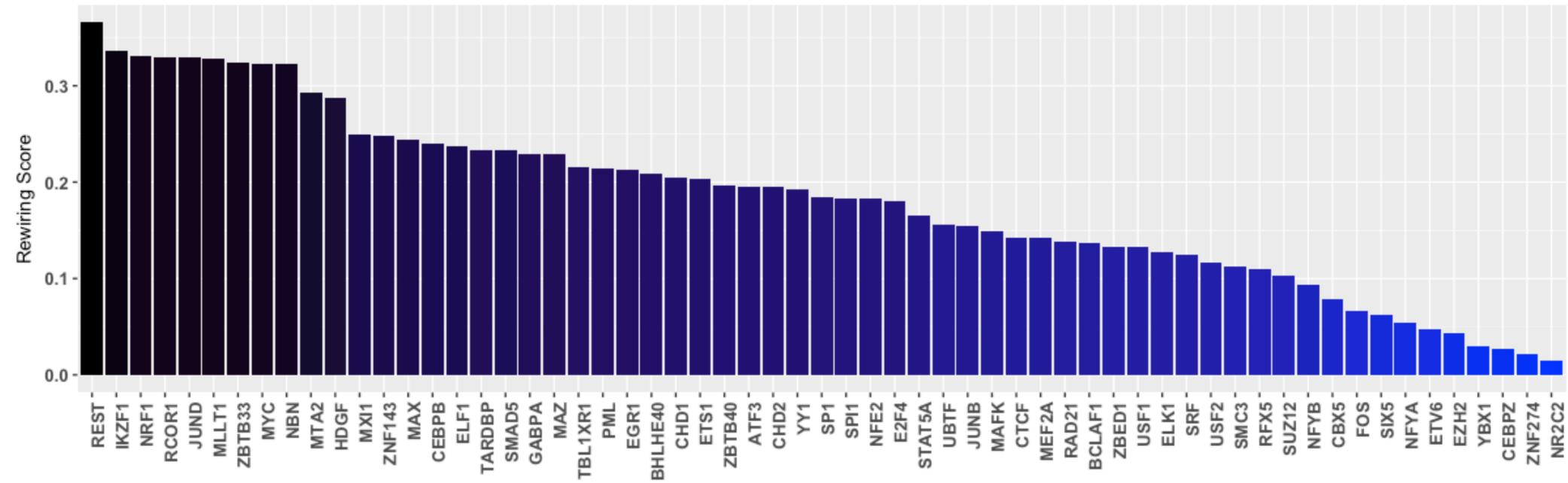
Blood	T K562	209	64	17	1	12	1	1	1	1	3	1	0	1	219	29	1	1	1	95
	N GM12878	101	50	6	1	11	1	1	1	1	1	1	0	1	0	0	1	1	1	0
Liver	T HepG2	97	48	7	1	11	1	0	1	1	1	0	0	1	221	0	0	0	0	327
	N liver	7	5	0	0	7	1	0	1	1	0	0	0	0	0	0	0	0	0	0
Lung	T A549	32	21	3	1	11	1	0	1	0	0	1	0	0	0	0	0	0	0	38
	N IMR-90	9	6	1	1	28	1	0	1	1	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	0	0	0	0	0	0	2

# JUND

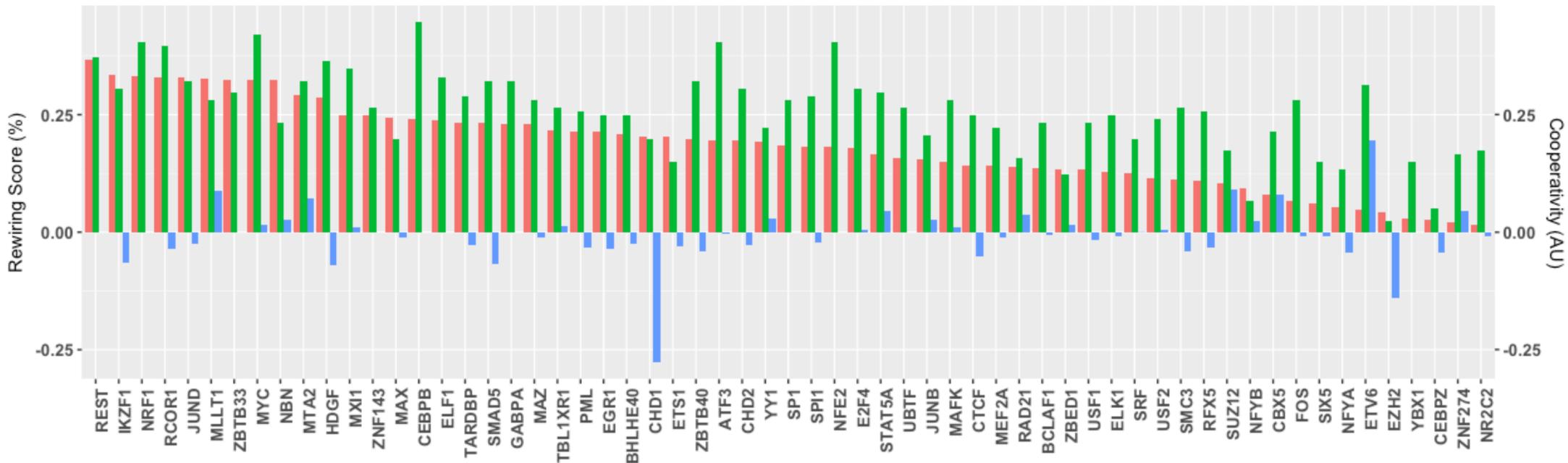


# new TSS network, one TSS per gene

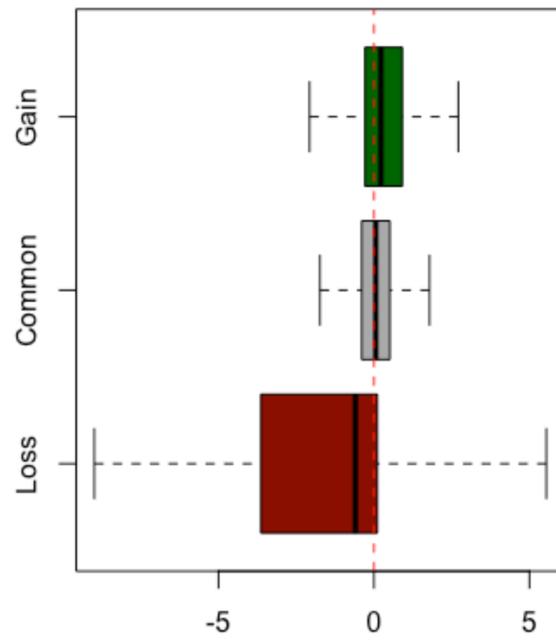
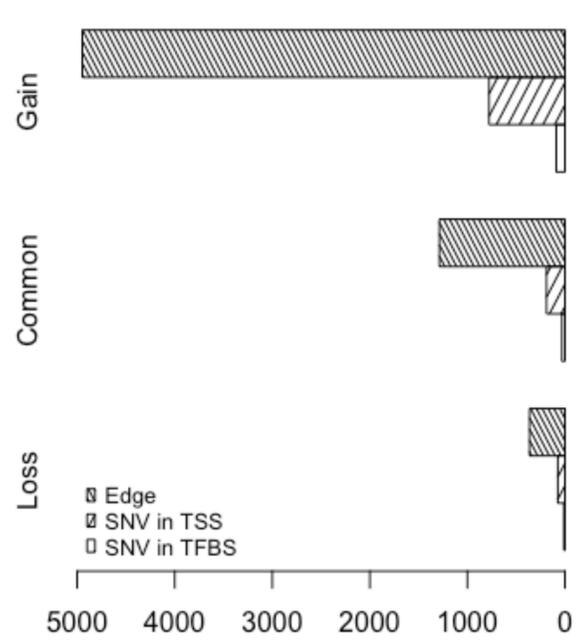
TF-GENE Network



K562-GM12878 Network

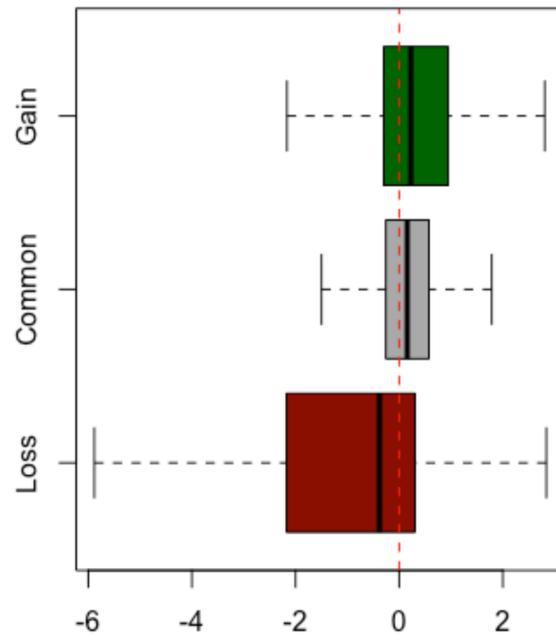
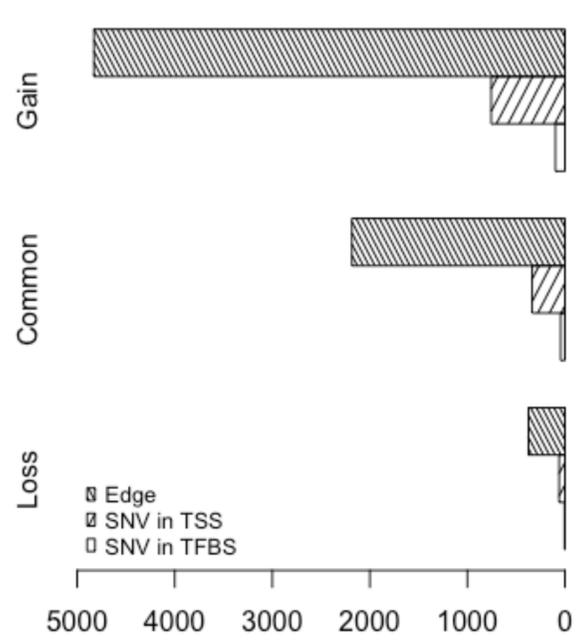


# JUND



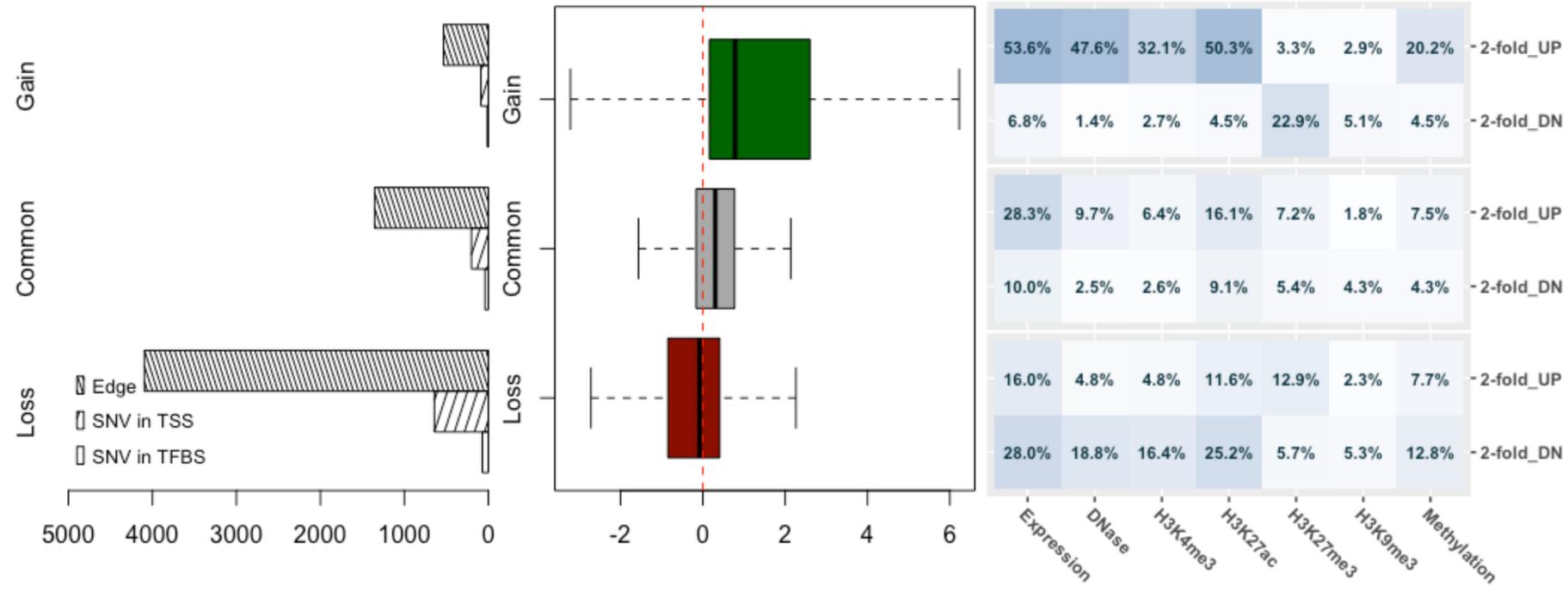
31.1%	24.8%	16.7%	29.7%	7.8%	3.2%	9.9%	-2-fold_UP
15.7%	2.9%	4.2%	9.1%	12.1%	5.3%	7.9%	-2-fold_DN
18.9%	7.0%	6.3%	13.9%	8.3%	0.8%	3.6%	-2-fold_UP
16.7%	6.2%	4.3%	12.4%	5.1%	4.3%	9.8%	-2-fold_DN
11.8%	2.5%	2.8%	5.8%	22.6%	2.2%	8.0%	-2-fold_UP
47.1%	54.8%	49.0%	57.3%	7.4%	10.5%	11.6%	-2-fold_DN
Expression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

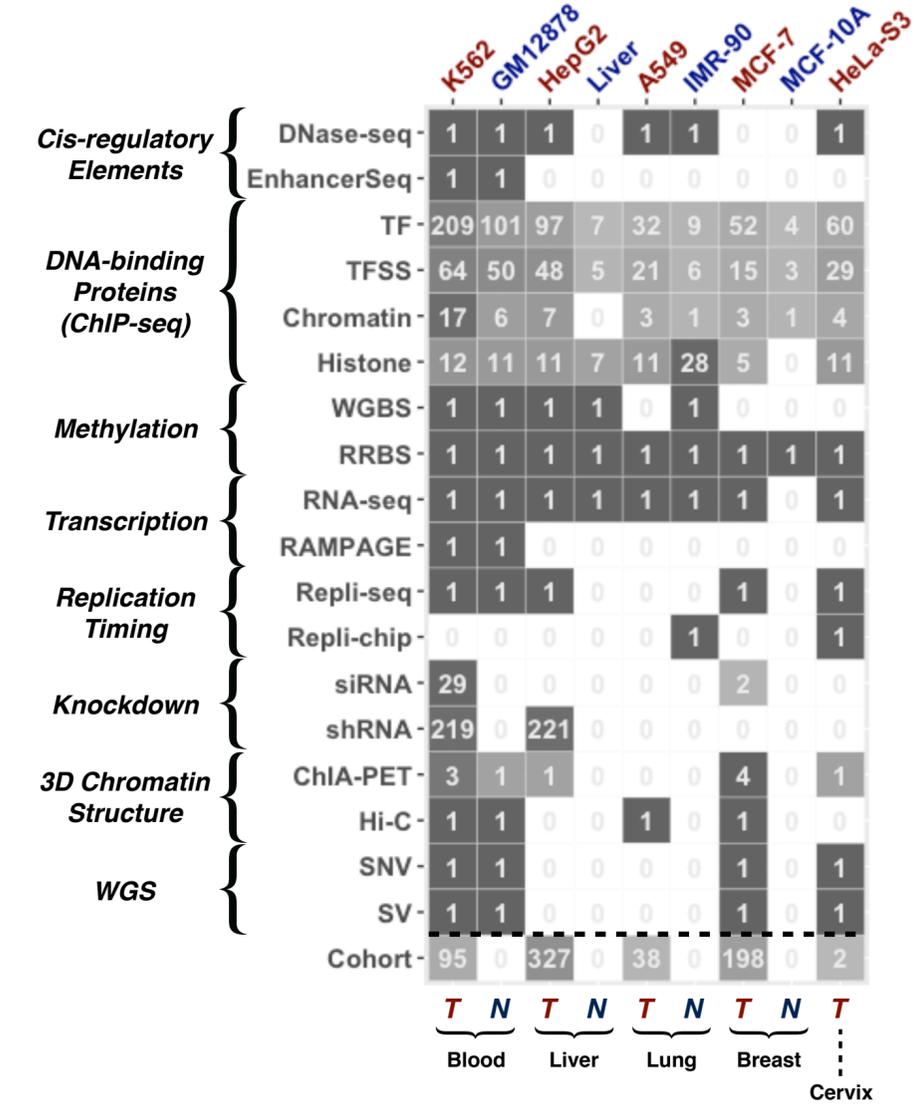
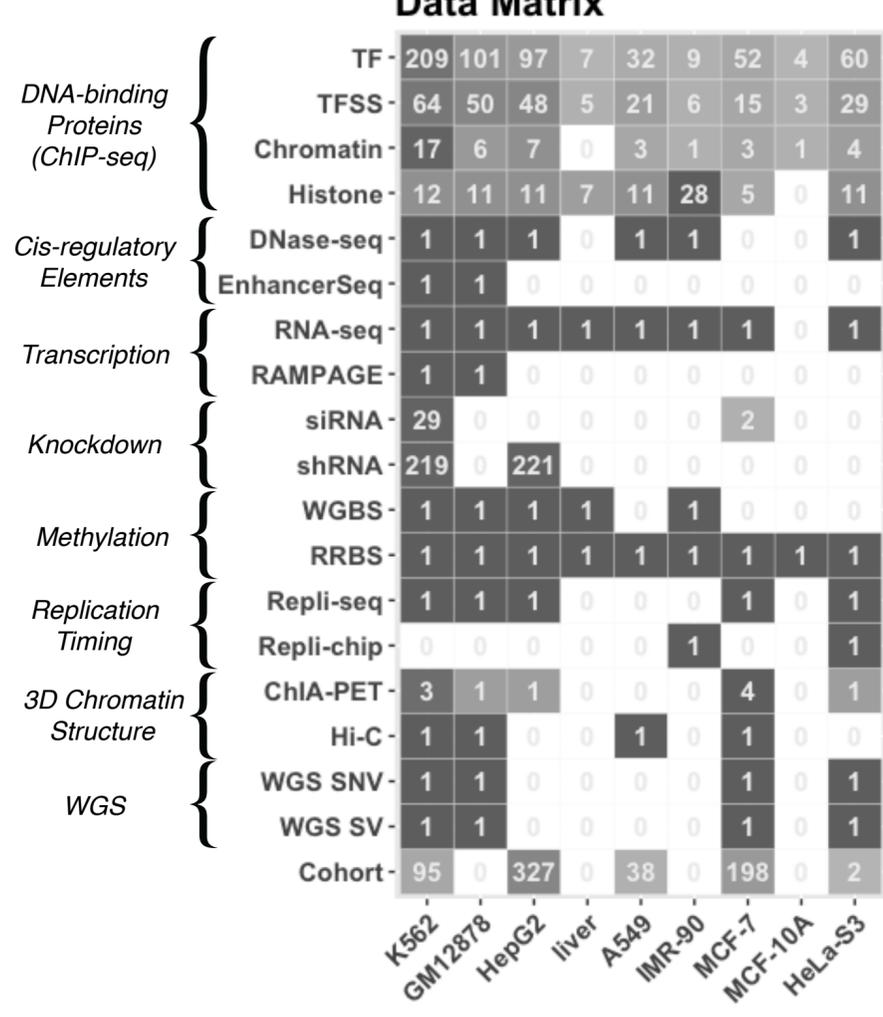
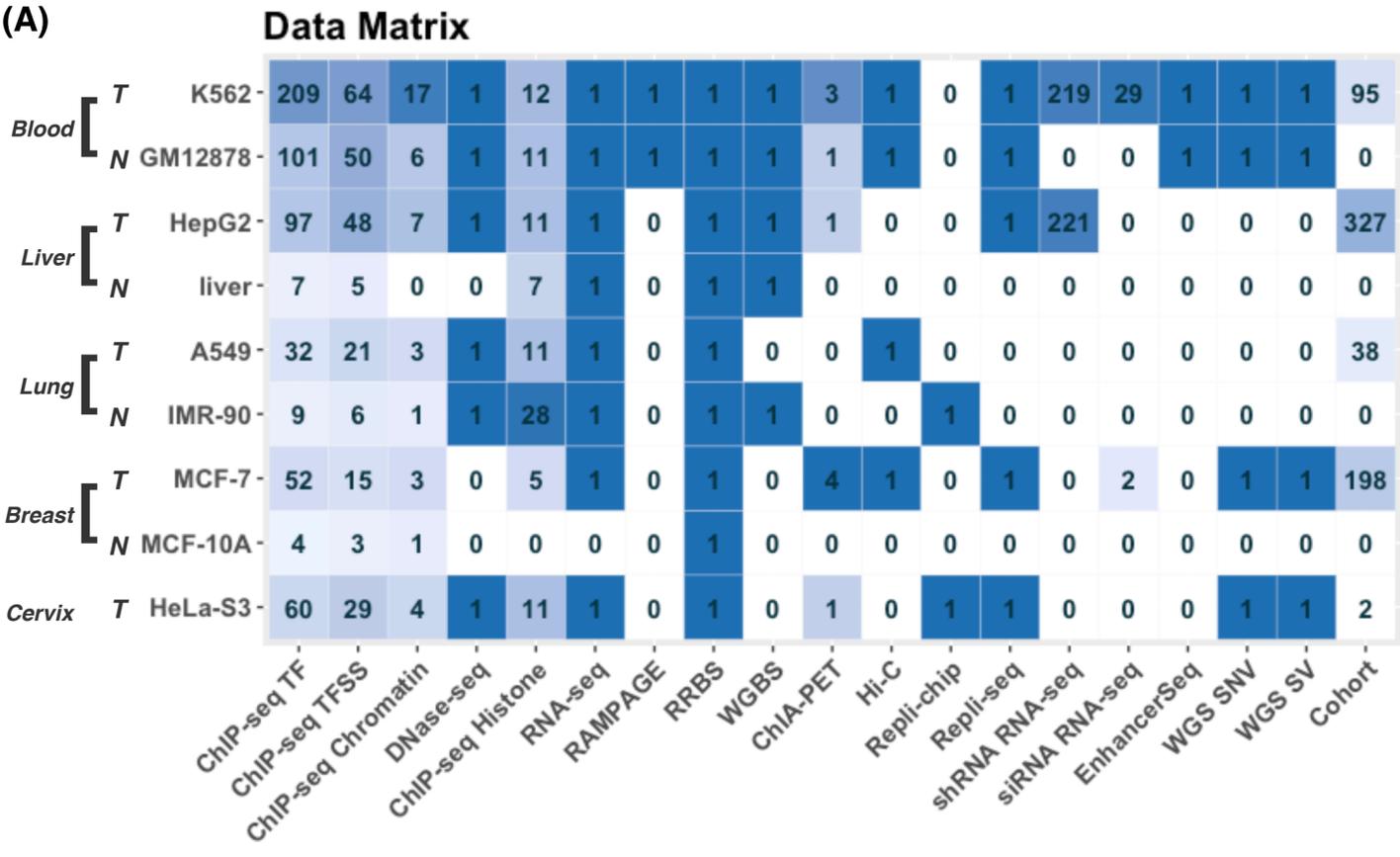
# MYC



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



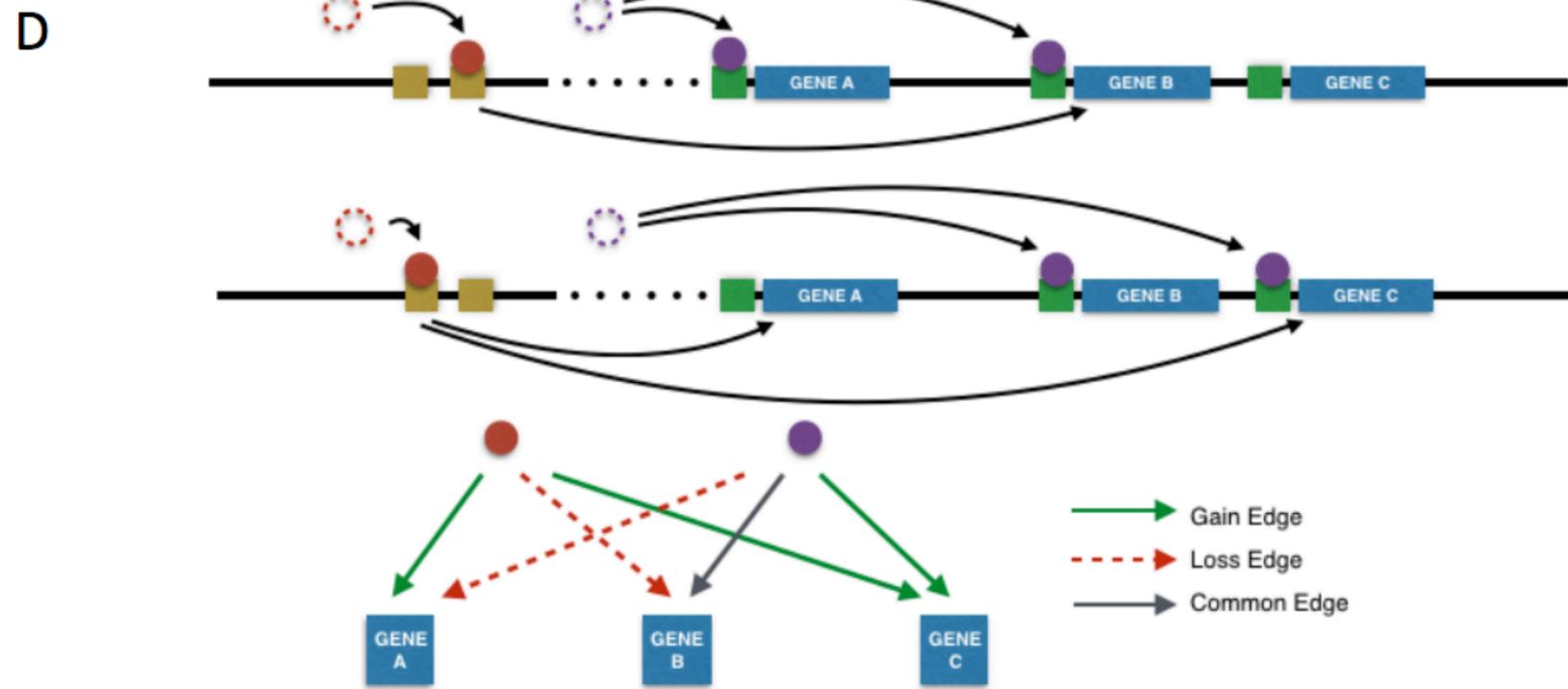
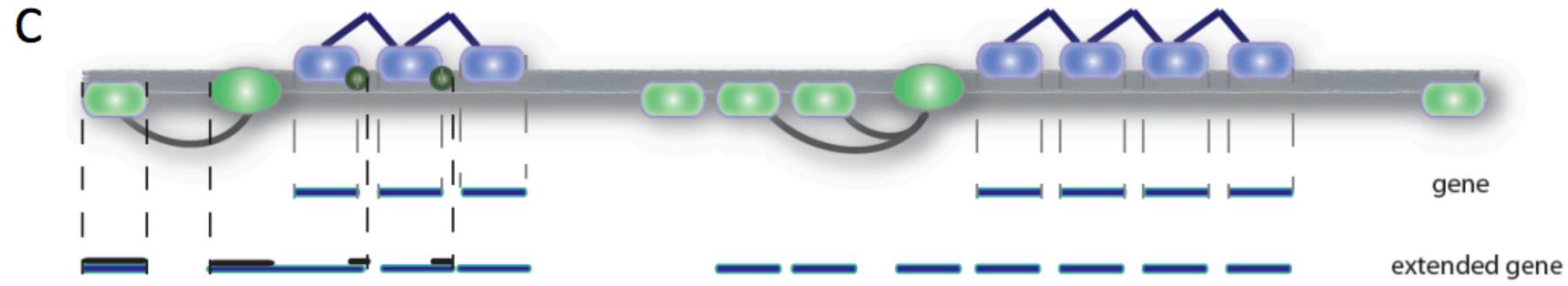
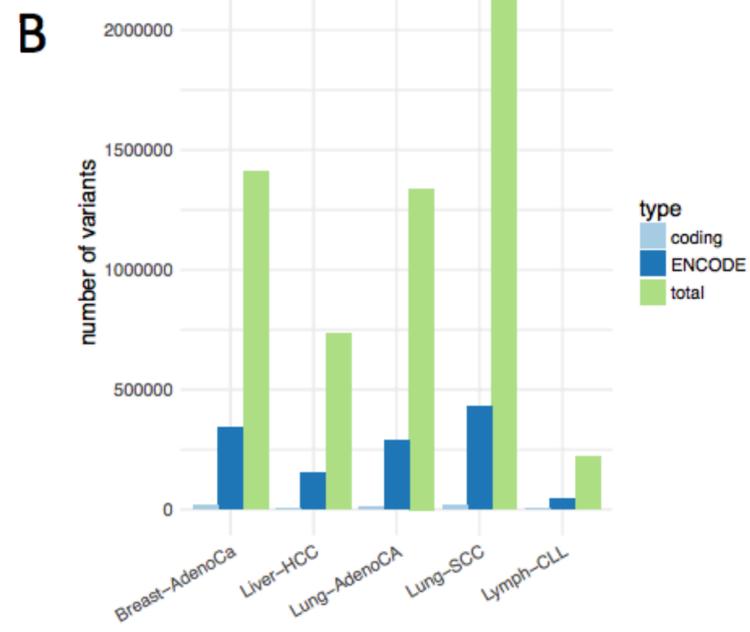


**Figure 1**

**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



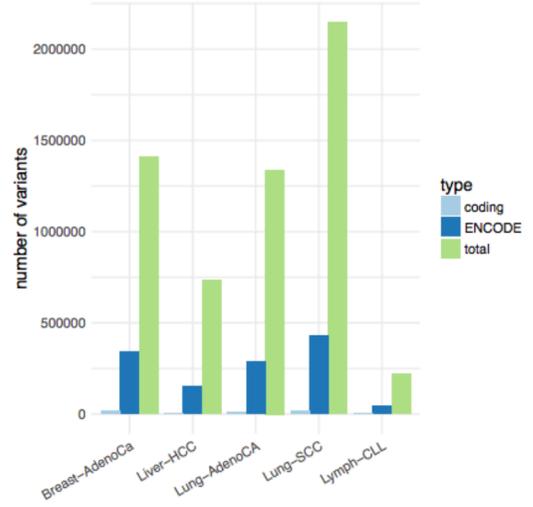
**Figure 1**

**Data Matrix**

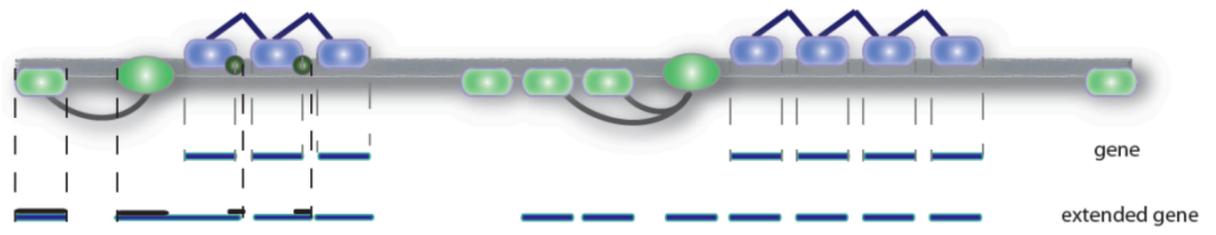
		K562		GM12878		HepG2		Liver		A549		IMR-90		MCF-7		MCF-10A		HeLa-S3		
Cis-regulatory Elements	DNase-seq	1	1	1	0	1	1	0	0	1	0	0	0	1						
	EnhancerSeq	1	1	0	0	0	0	0	0	0	0	0	0	0						
DNA-binding Proteins (ChIP-seq)	TF	209	101	97	7	32	9	52	4	60										
	TFSS	64	50	48	5	21	6	15	3	29										
	Chromatin	17	6	7	0	3	1	3	1	4										
Methylation	Histone	12	11	11	7	11	28	5	0	11										
	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										
	SNV	1	1	0	0	0	0	1	0	1										
WGS	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 Lung Breast Cervix

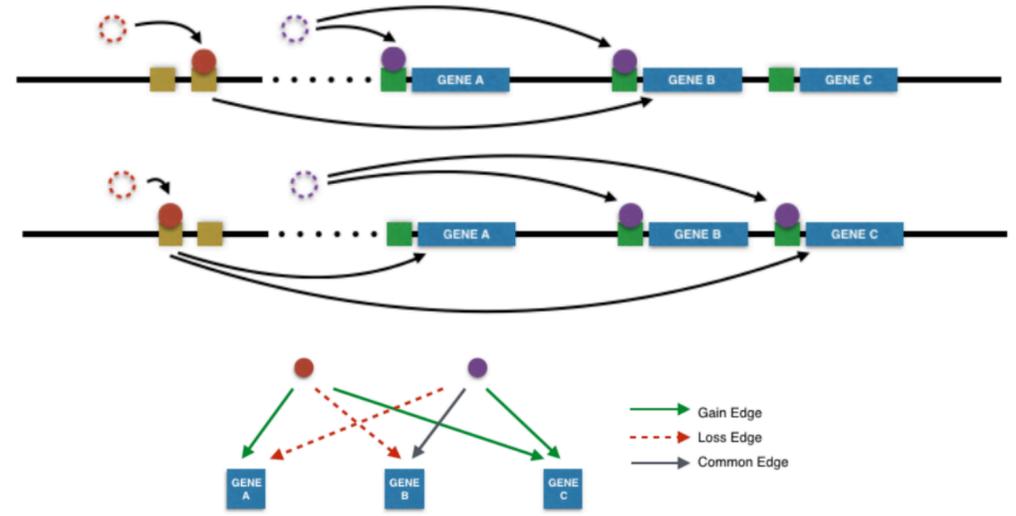
**B**



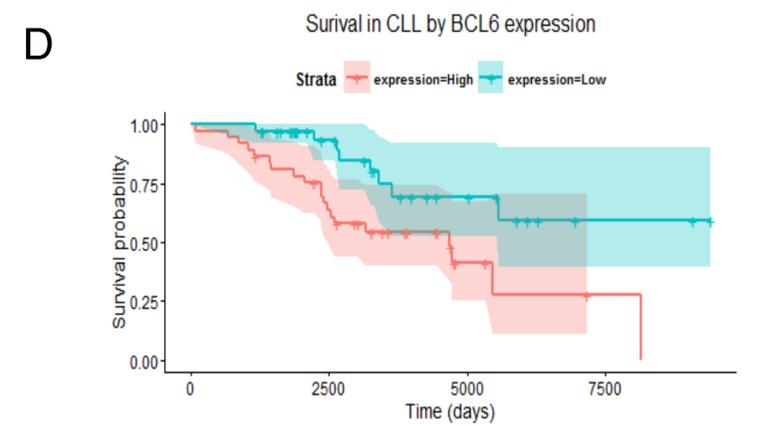
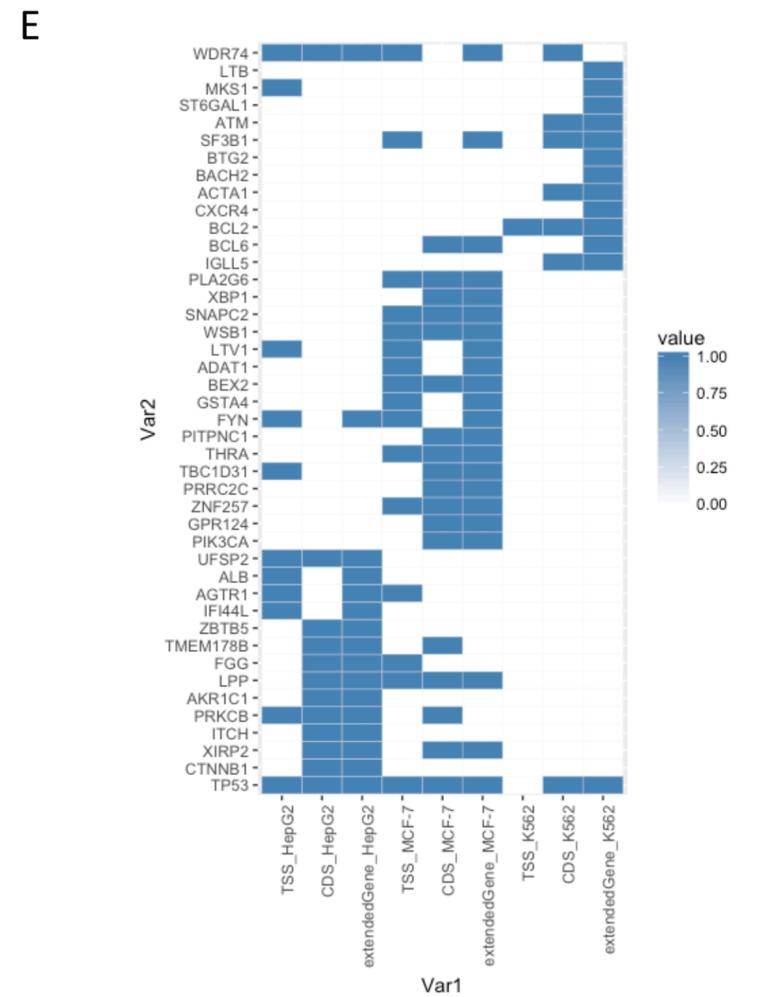
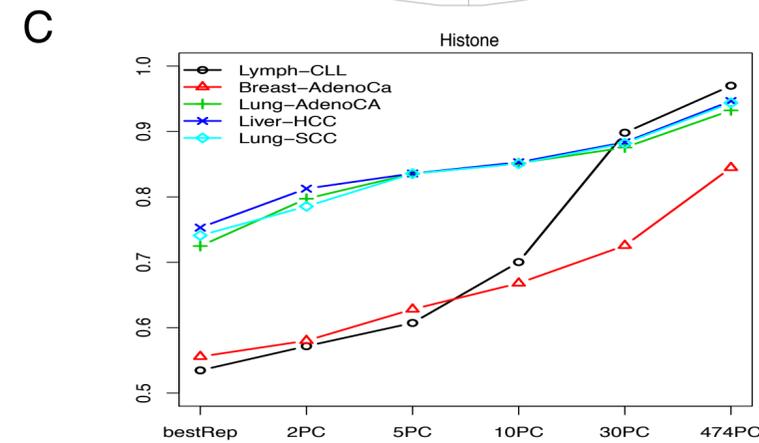
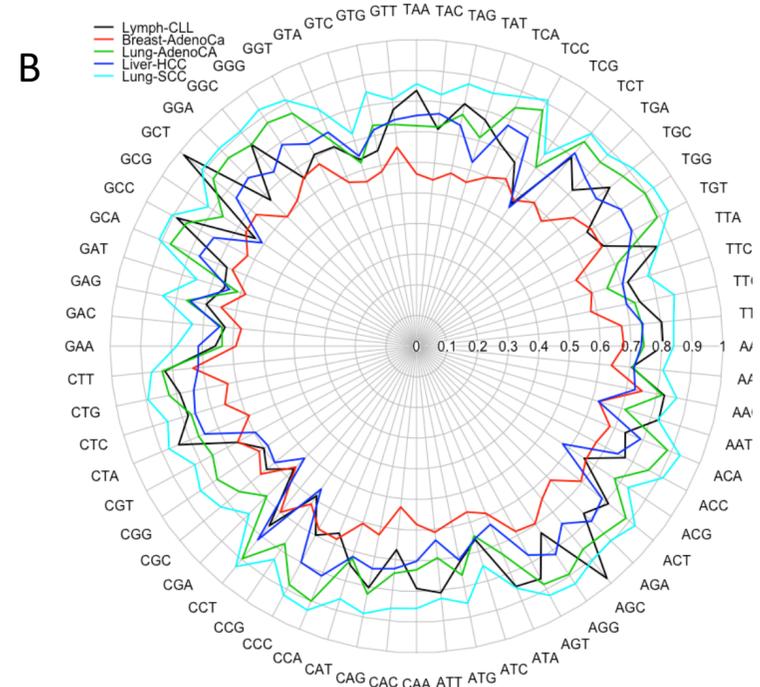
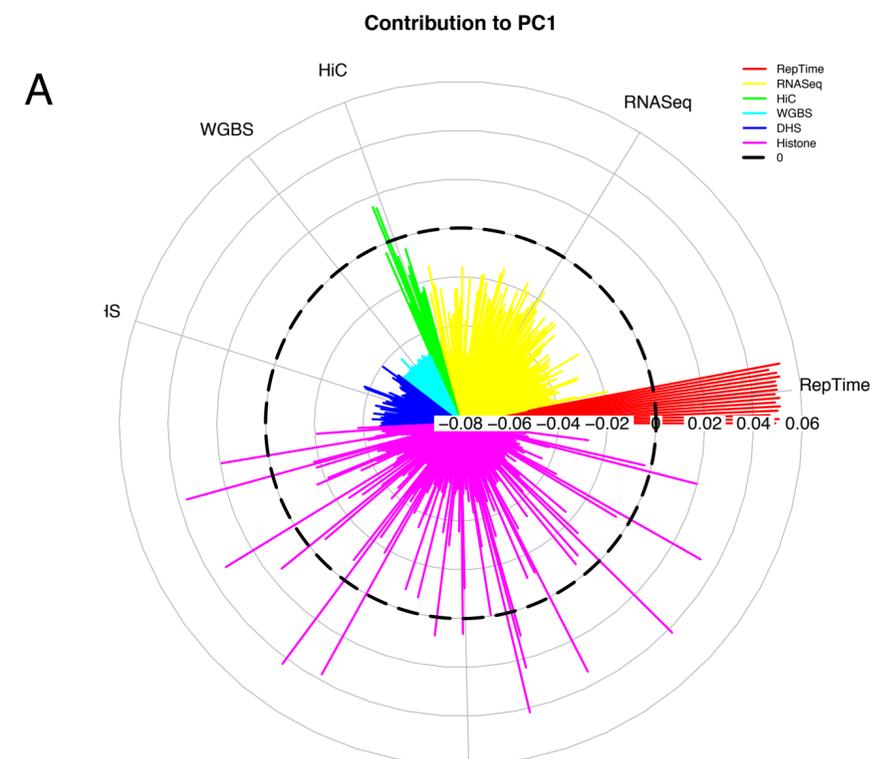
**C**



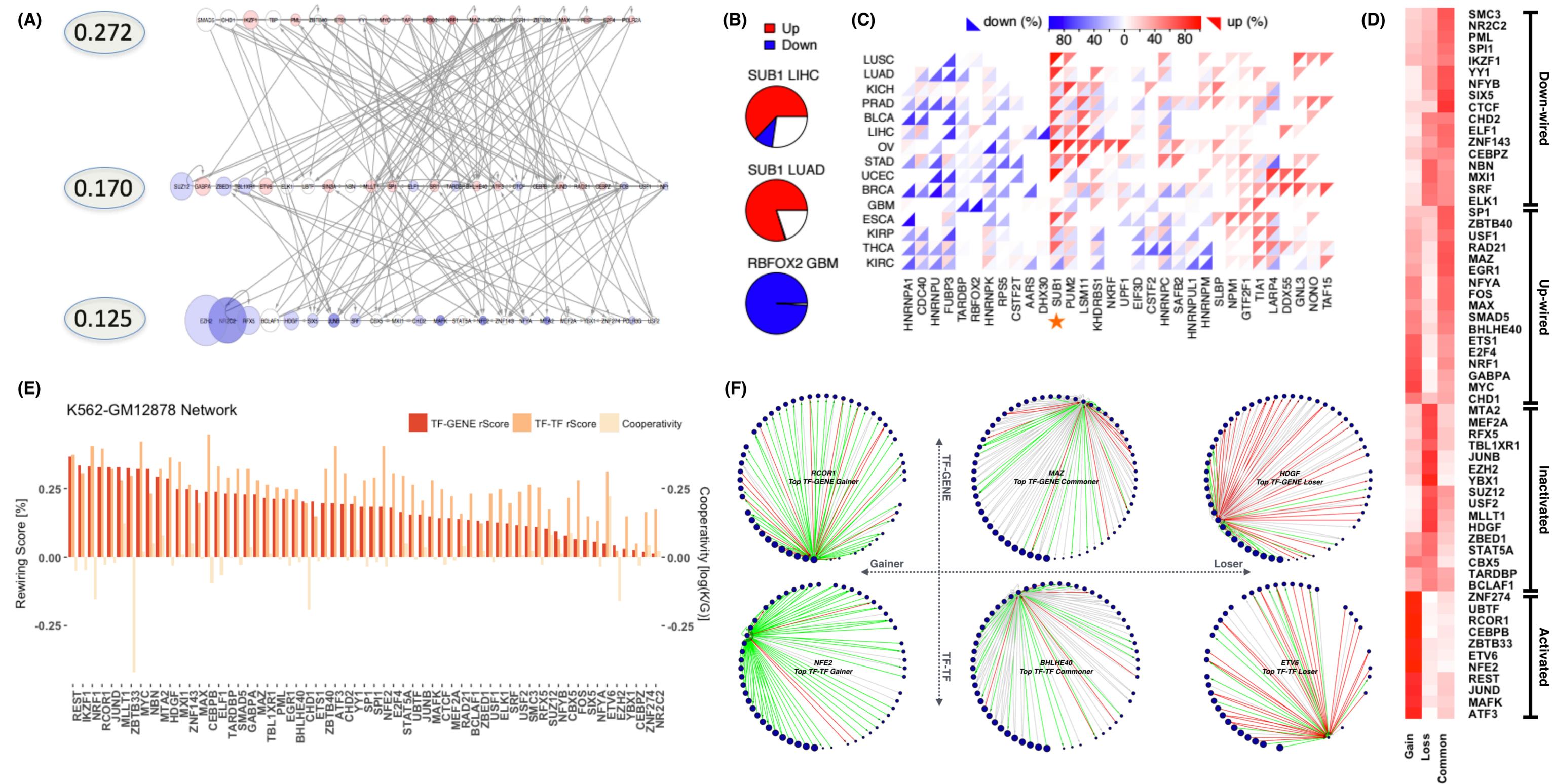
**D**



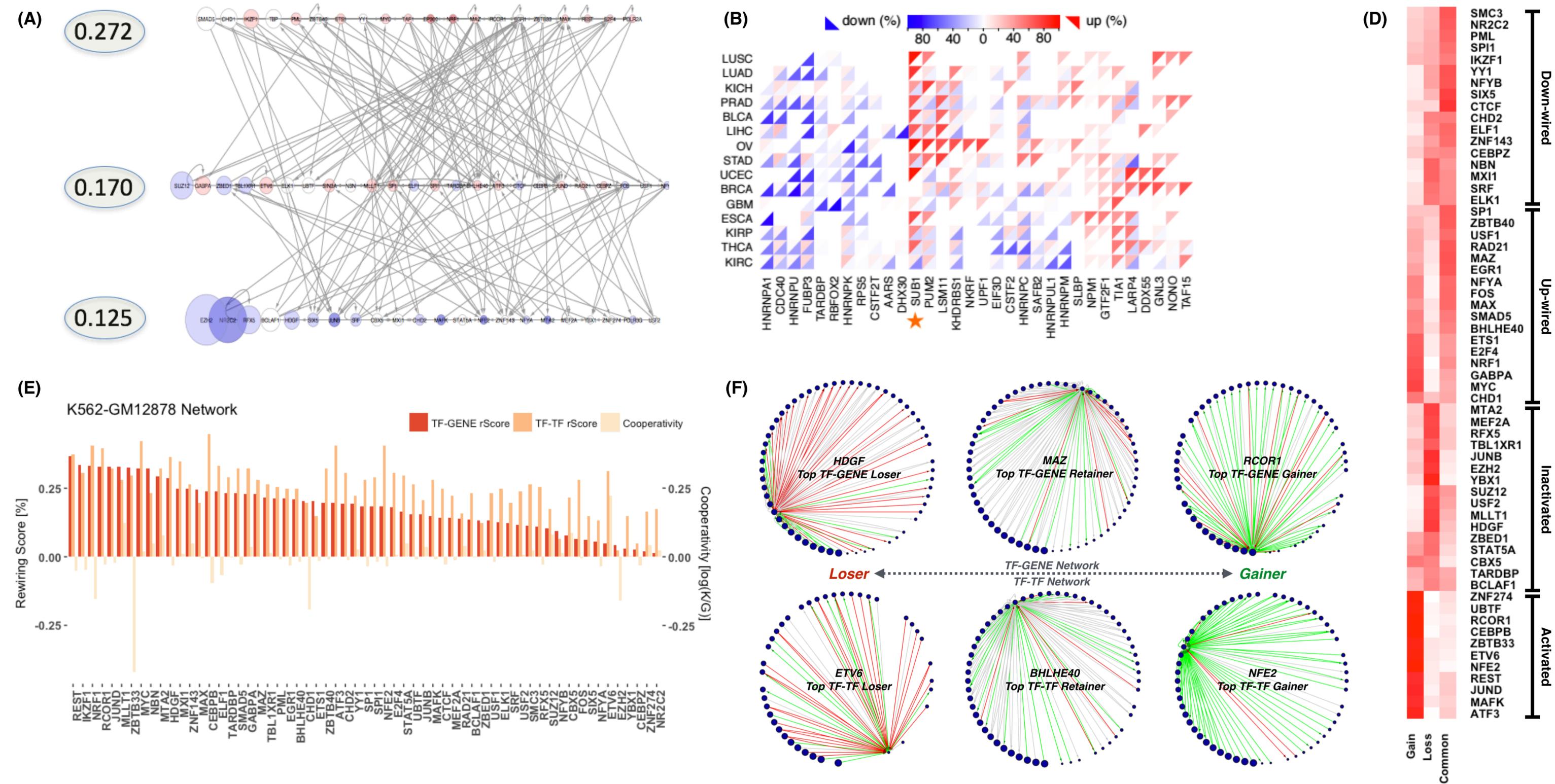
**Figure 1**



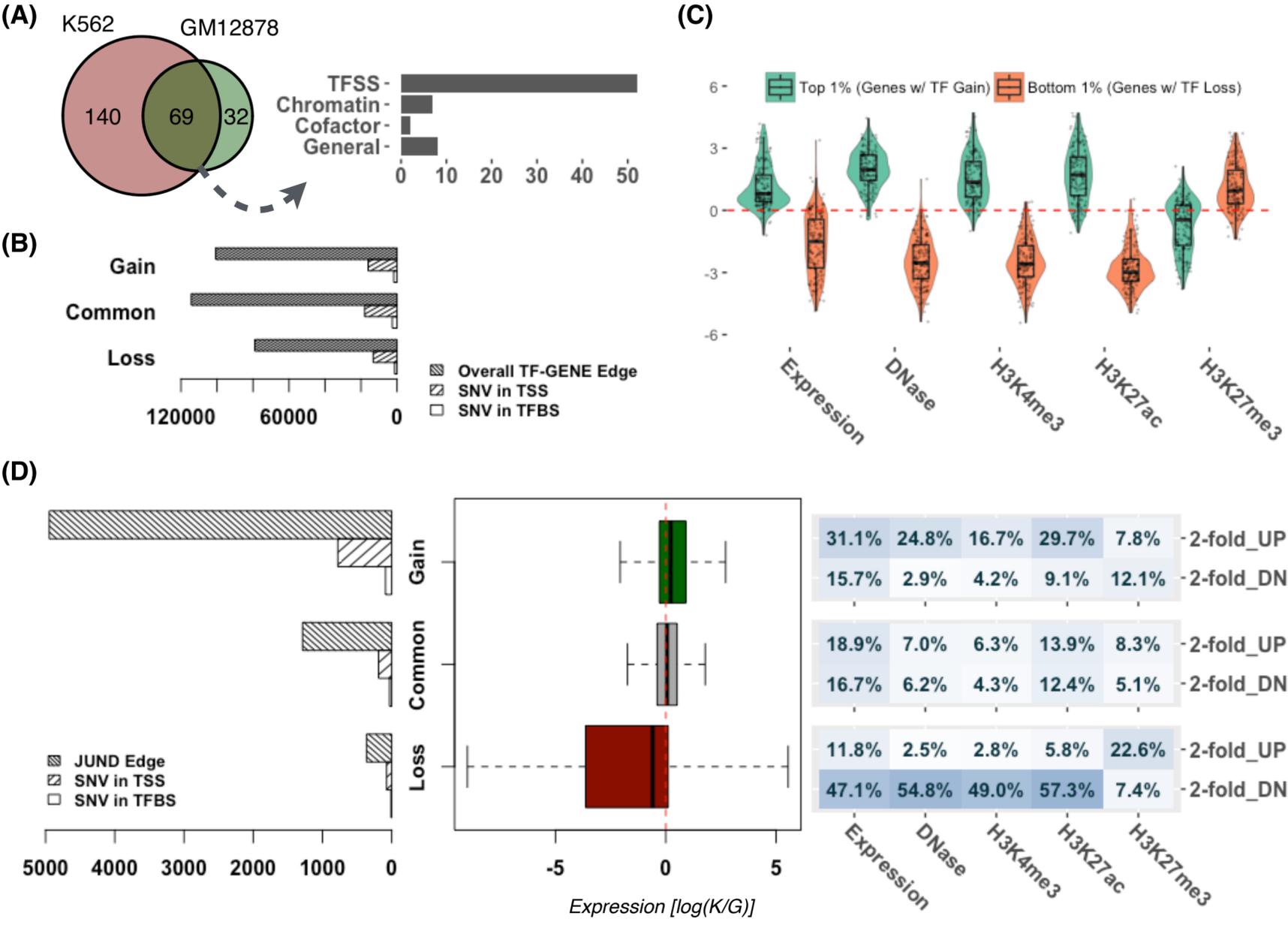
**Figure 2**



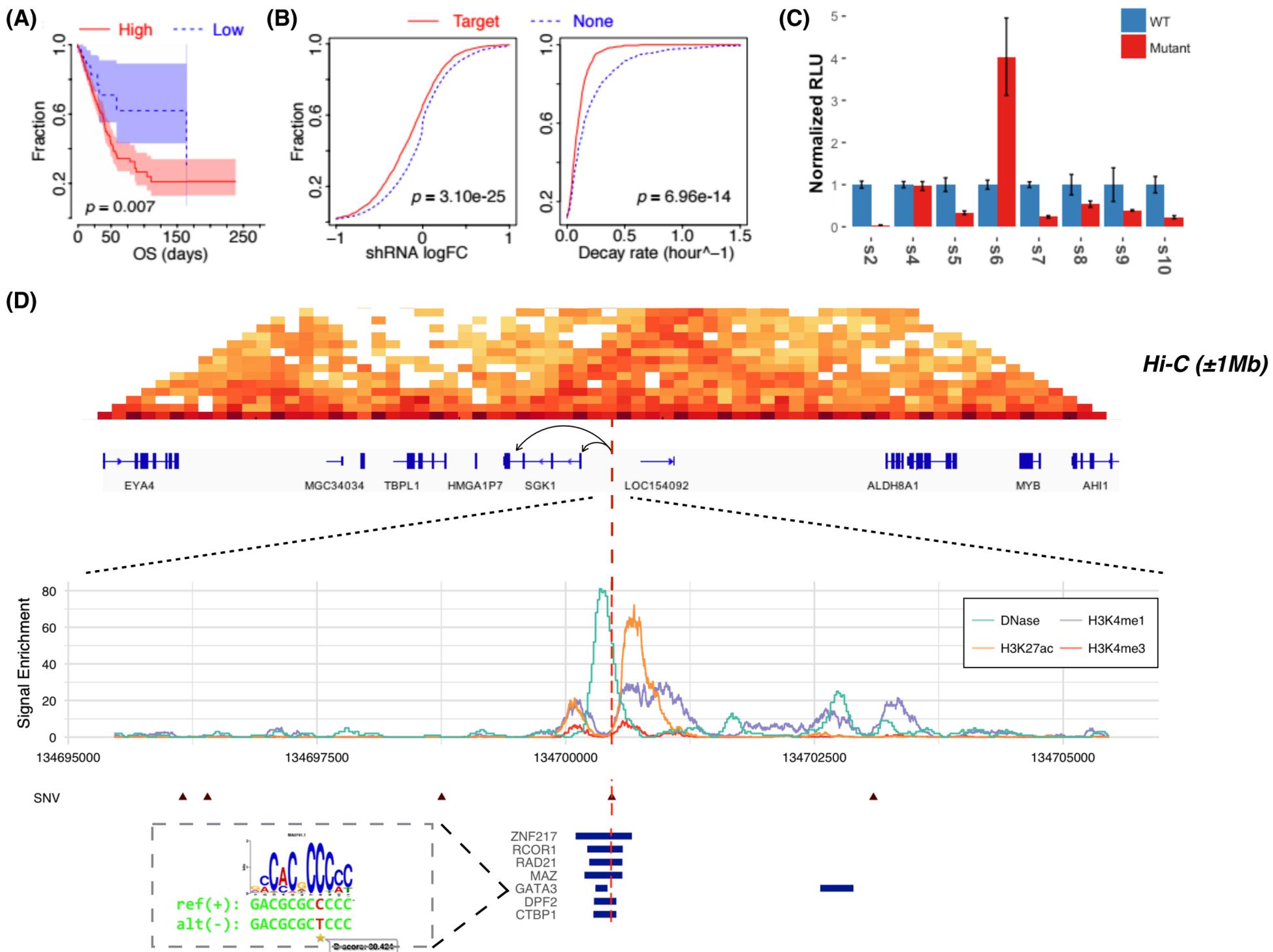
**Figure 3**



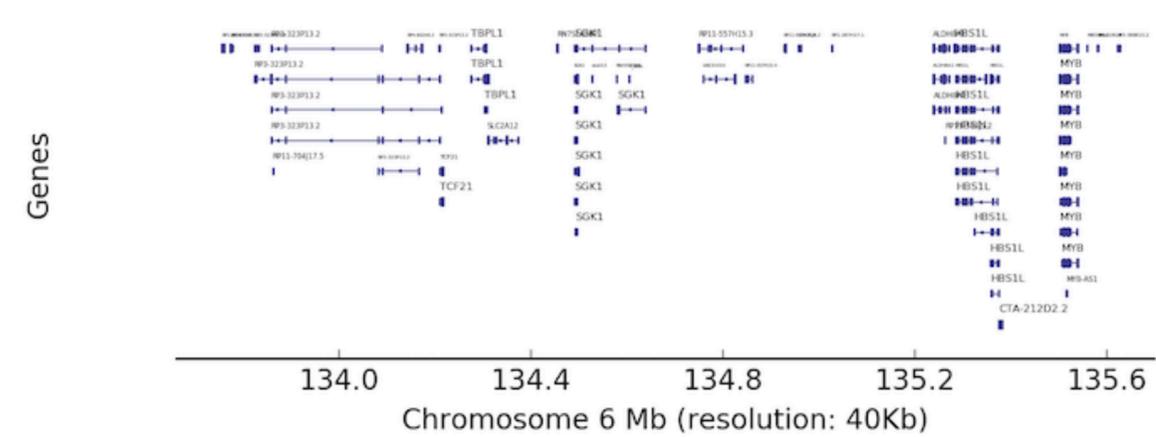
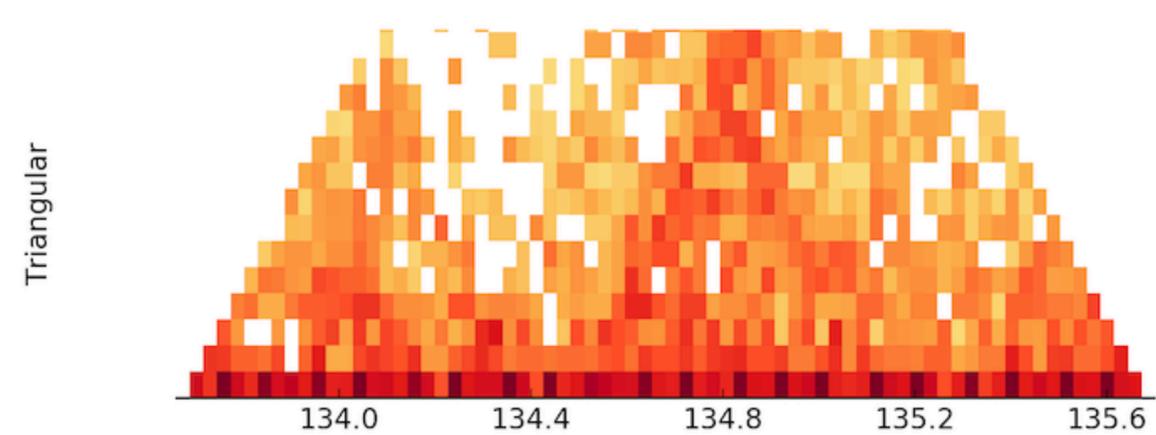
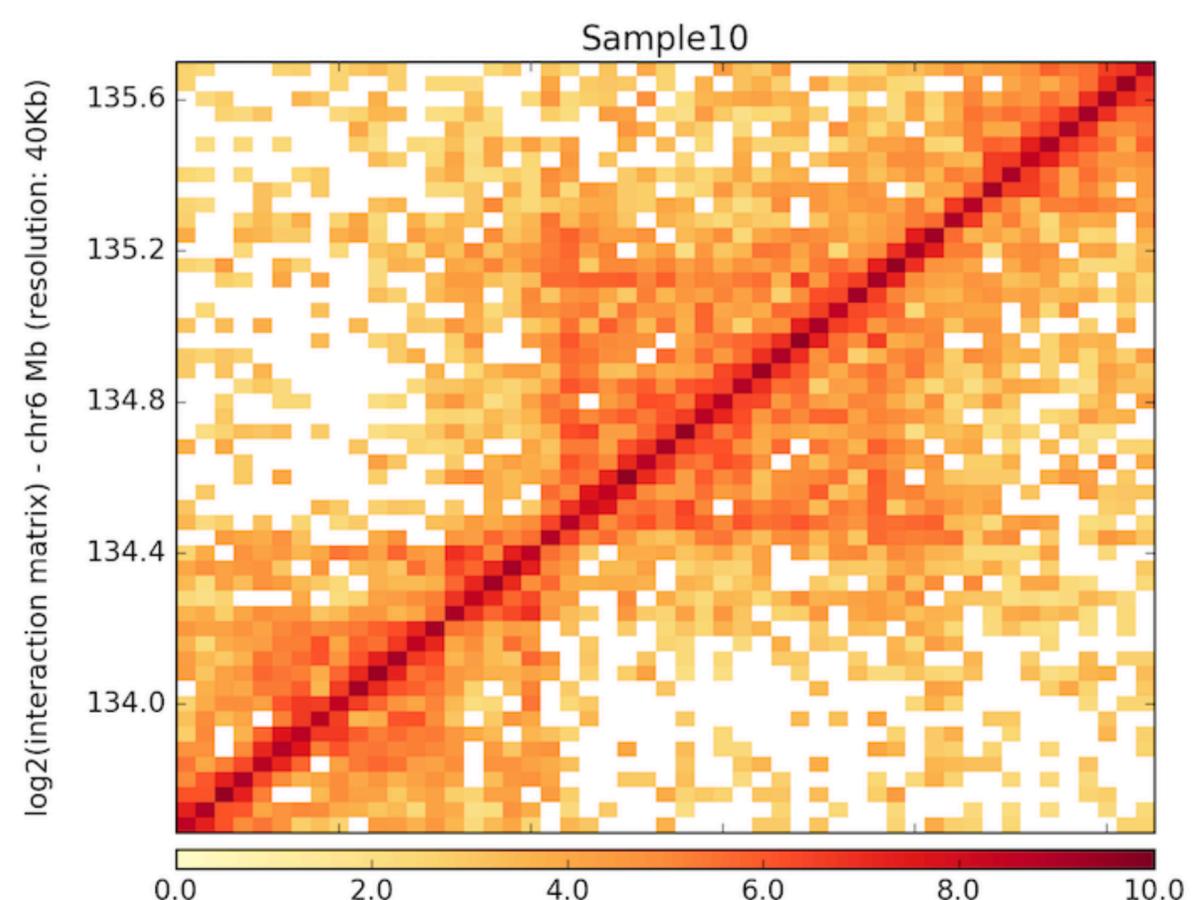
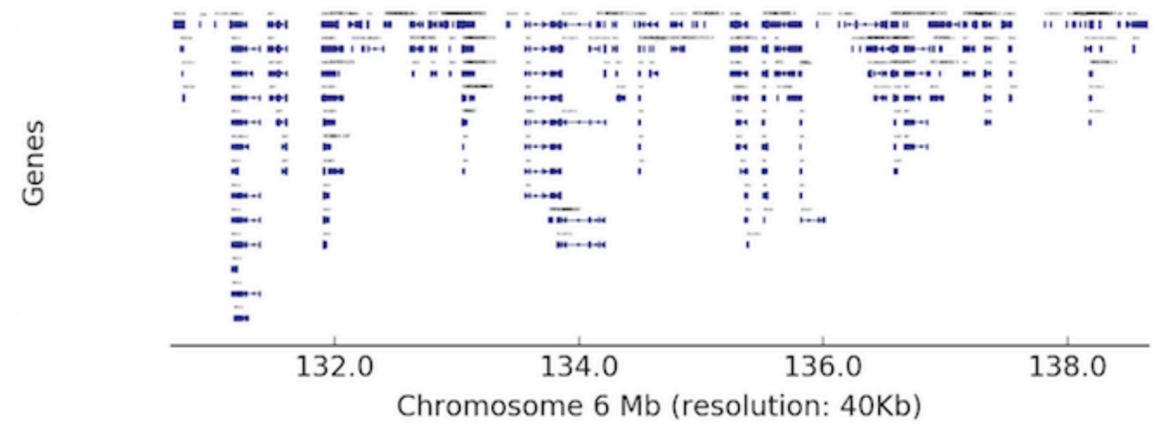
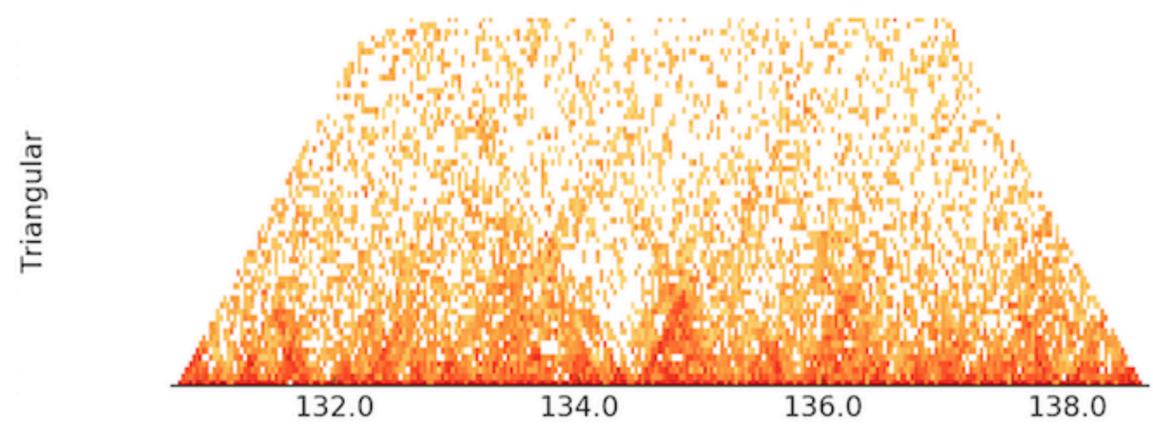
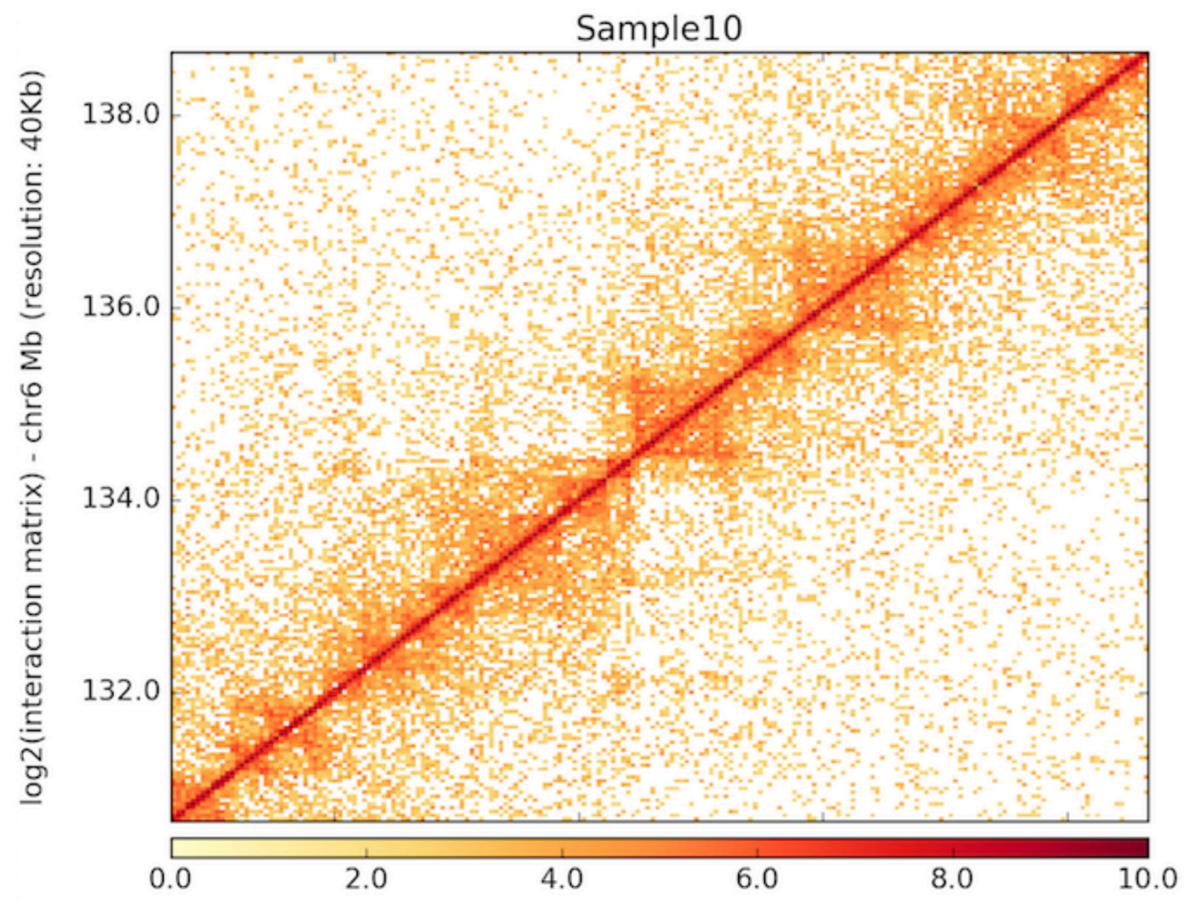
**Figure 3**



**Figure 4**

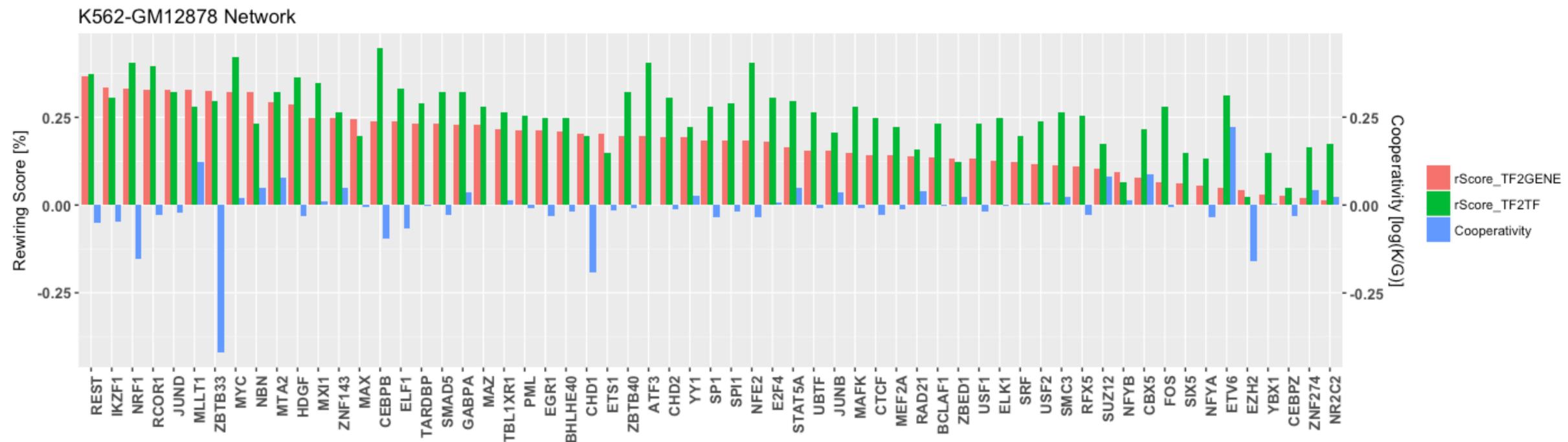


**Figure 5**



# GG's new cooperativity logR of K/G

+ve means it's more cooperative in K, vice versa



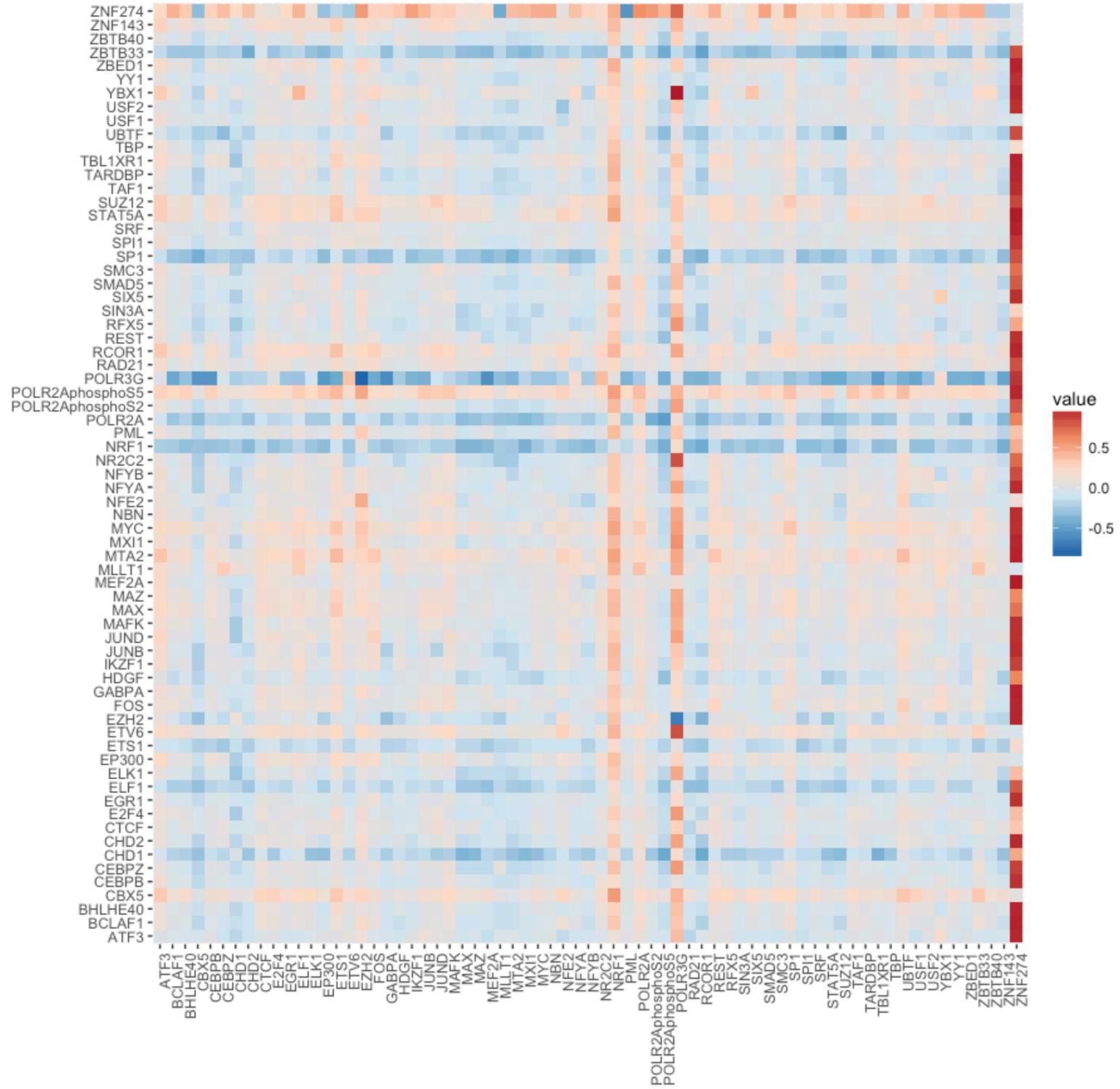
ZBTB33 becomes less cooperative in K

it “could” mean that its targets are unique in K

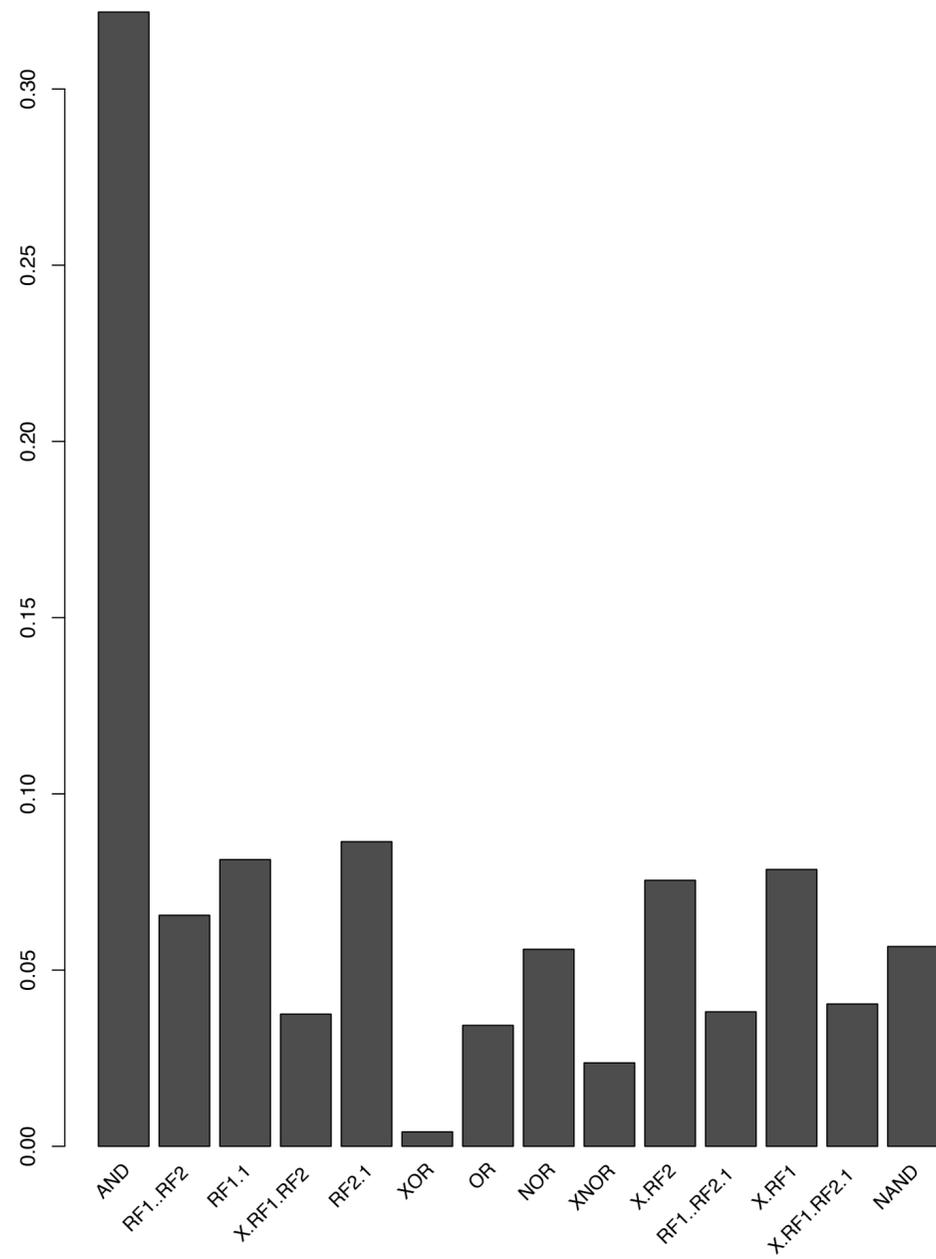
ETV6 becomes more cooperative in K

this “could” mean they become more ubiquitous

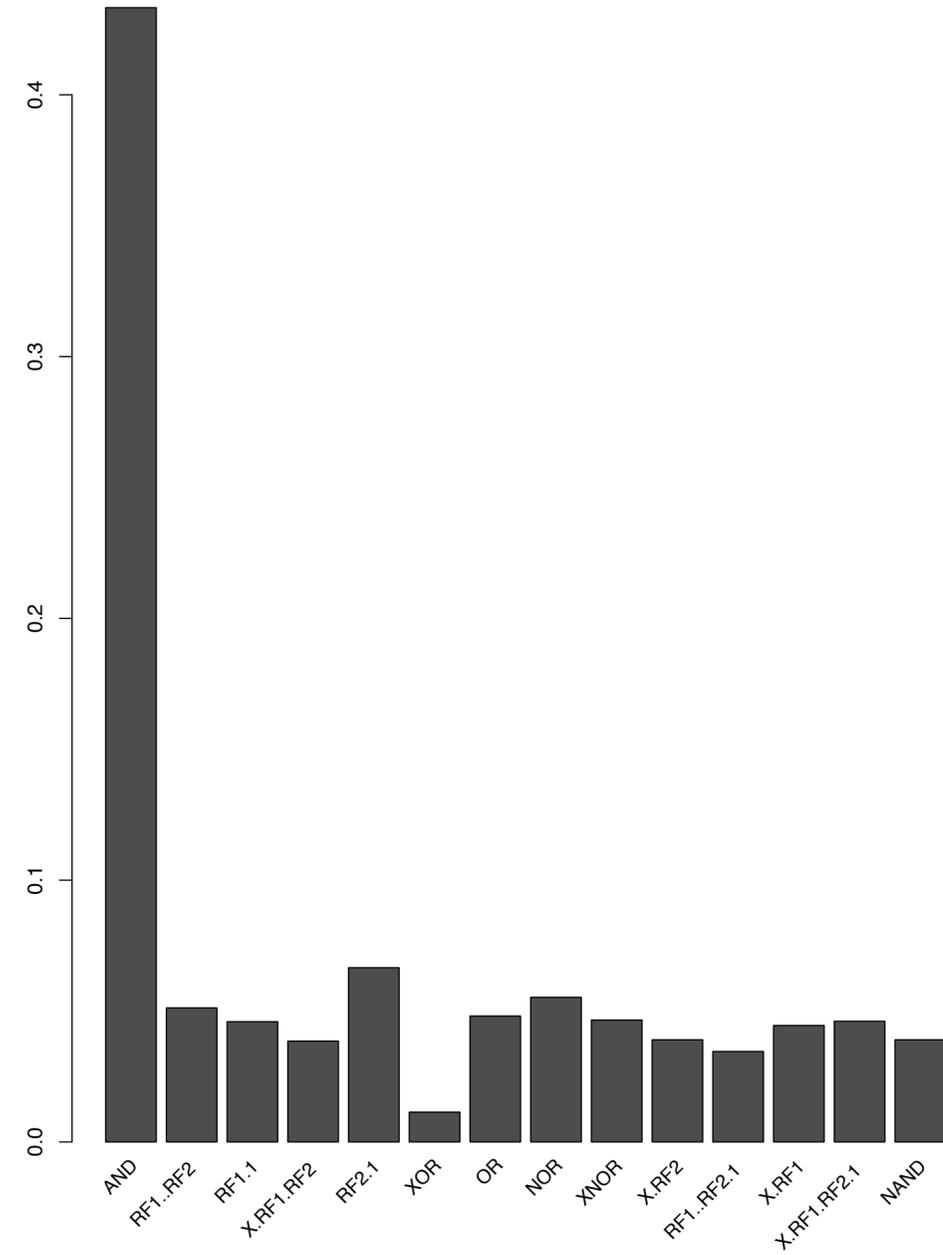
### K-G Co-binding



Logic results WITHOUT permutation tests, TIP TF-gene, K&G common TF (without general)



GM12878



K562