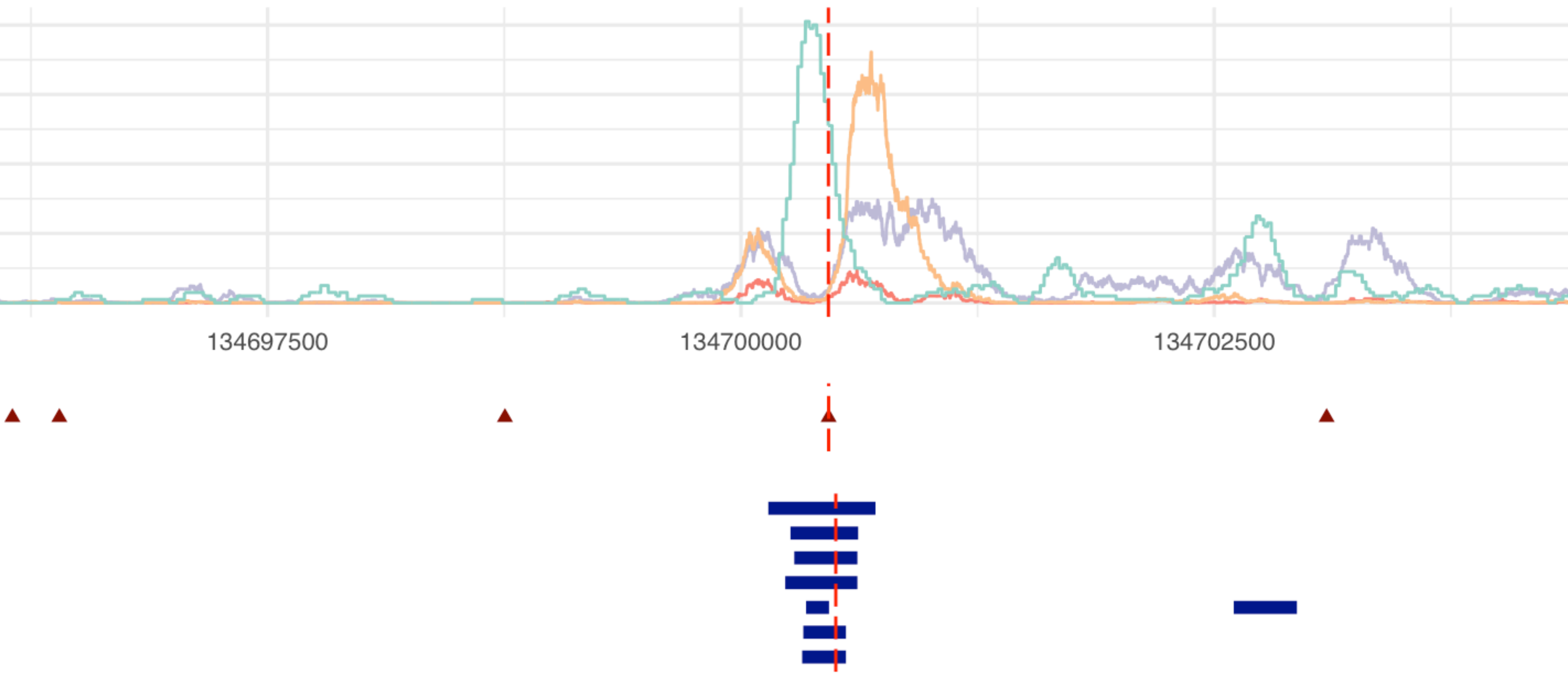


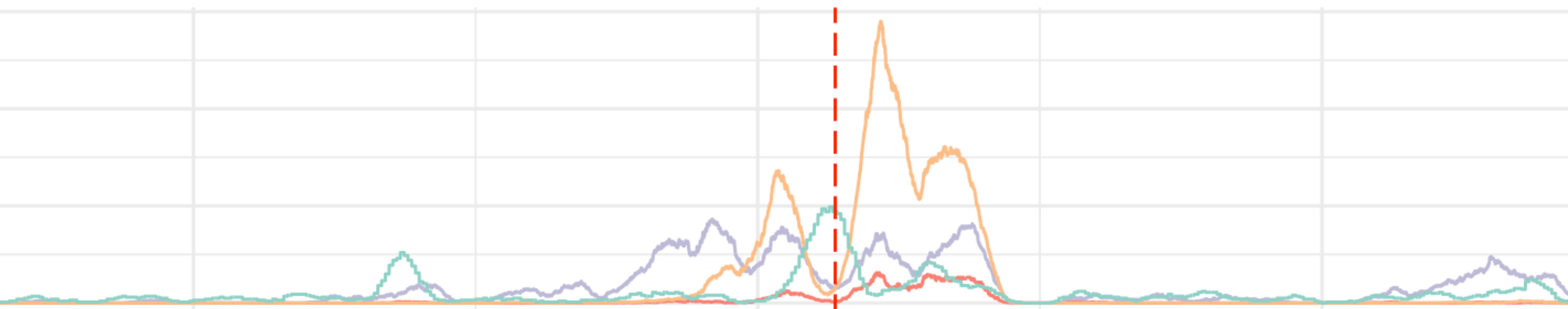
Type

- DNase
- H3K27ac
- H3K4me1
- H3K4me3



Type

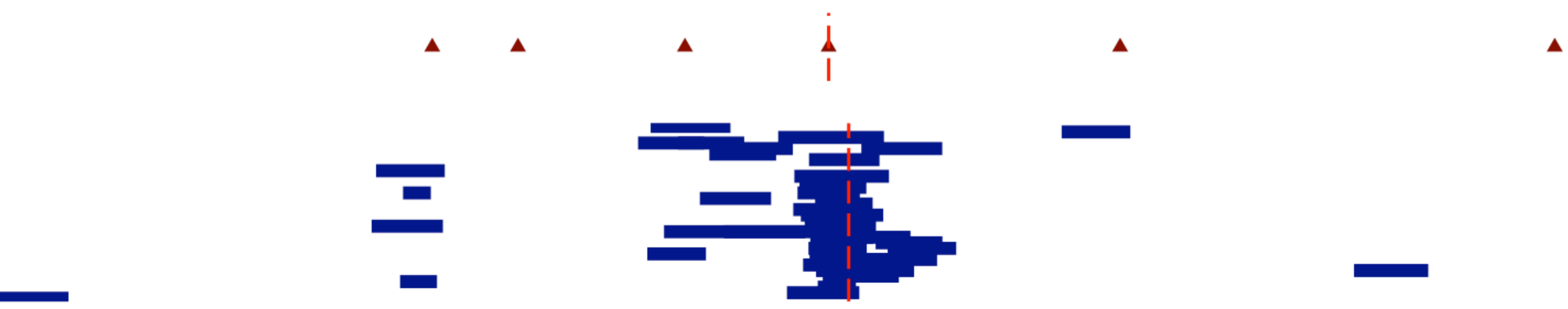
- DNase
- H3K27ac
- H3K4me1
- H3K4me3



58560000

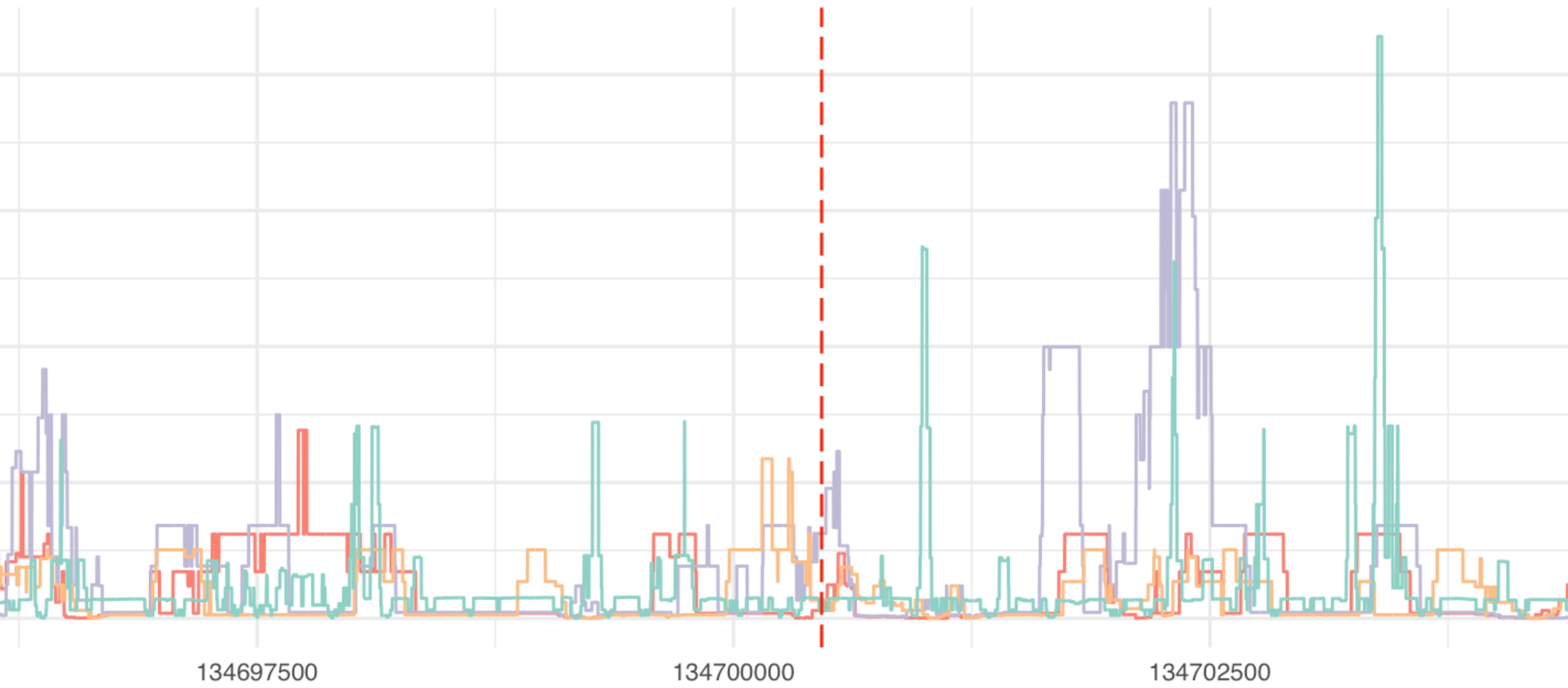
58563000

58566000



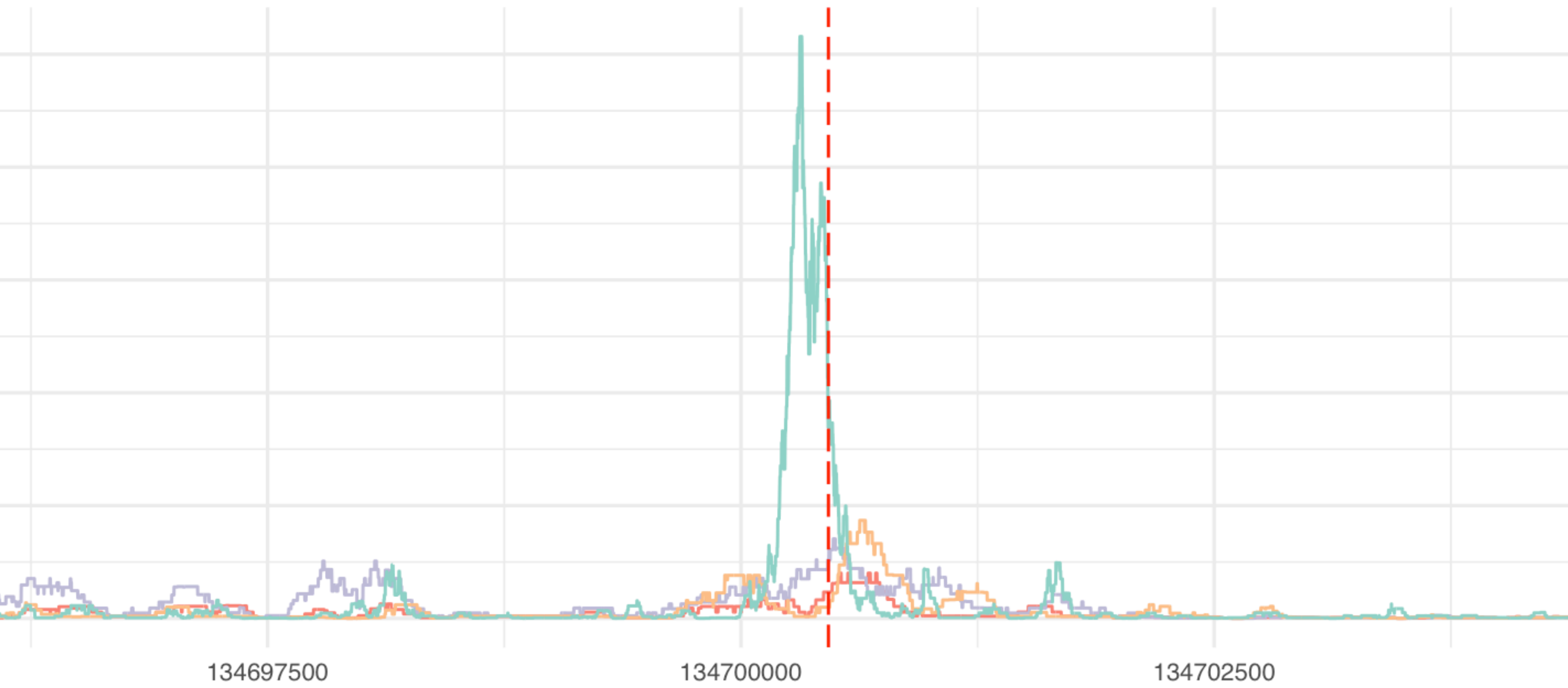
Type

DNase	H3K4me1
H3K27ac	H3K4me3



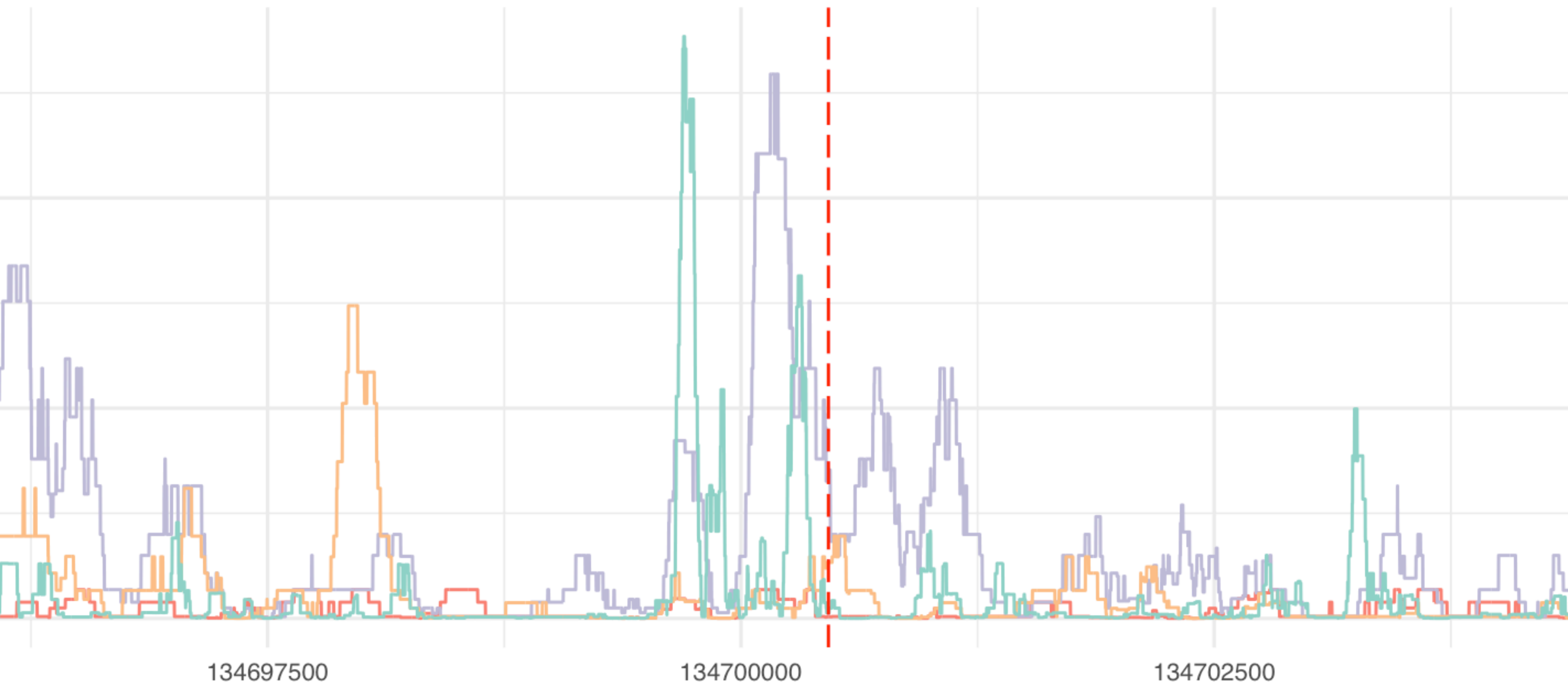
Type

- DNase
- H3K27ac
- H3K4me1
- H3K4me3



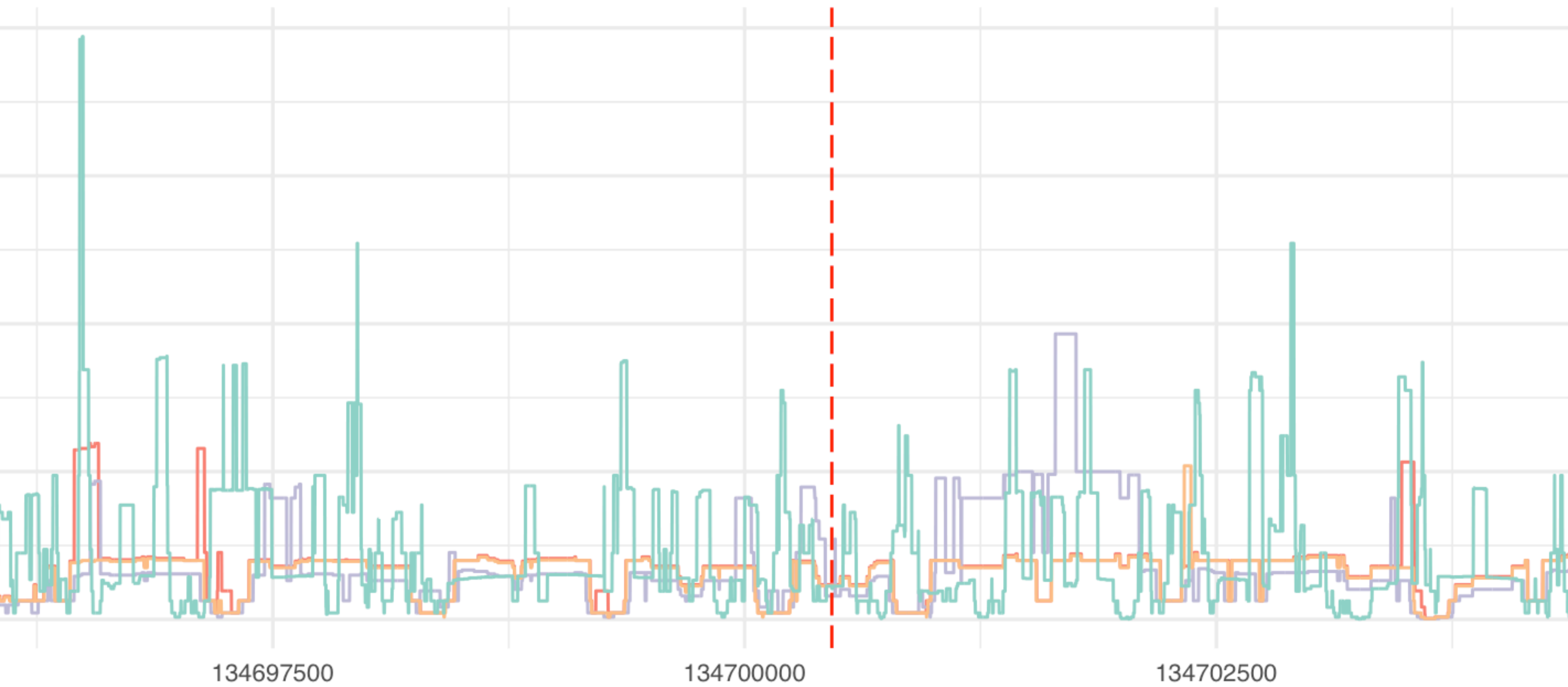
Type

- DNase
- H3K27ac
- H3K4me1
- H3K4me3



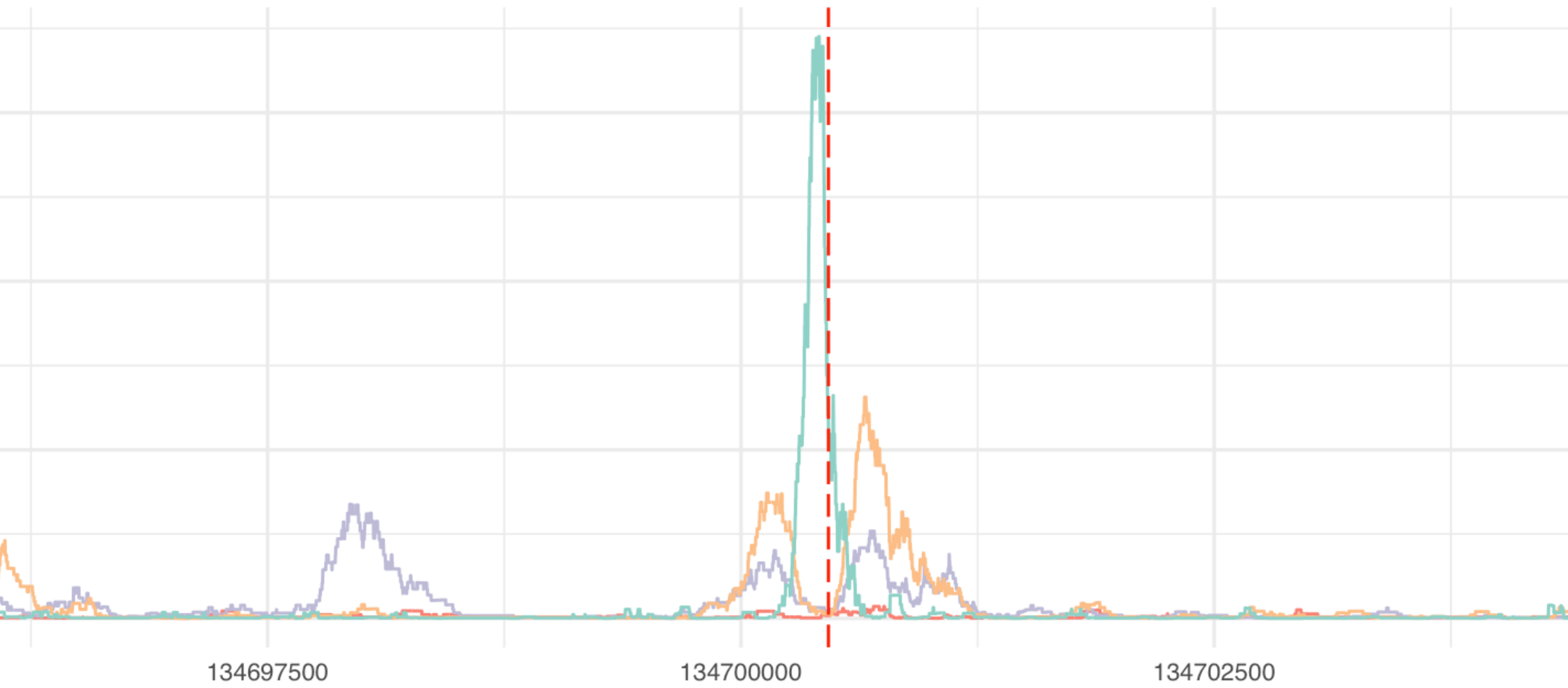
Type

— DNase	— H3K4me1
— H3K27ac	— H3K4me3



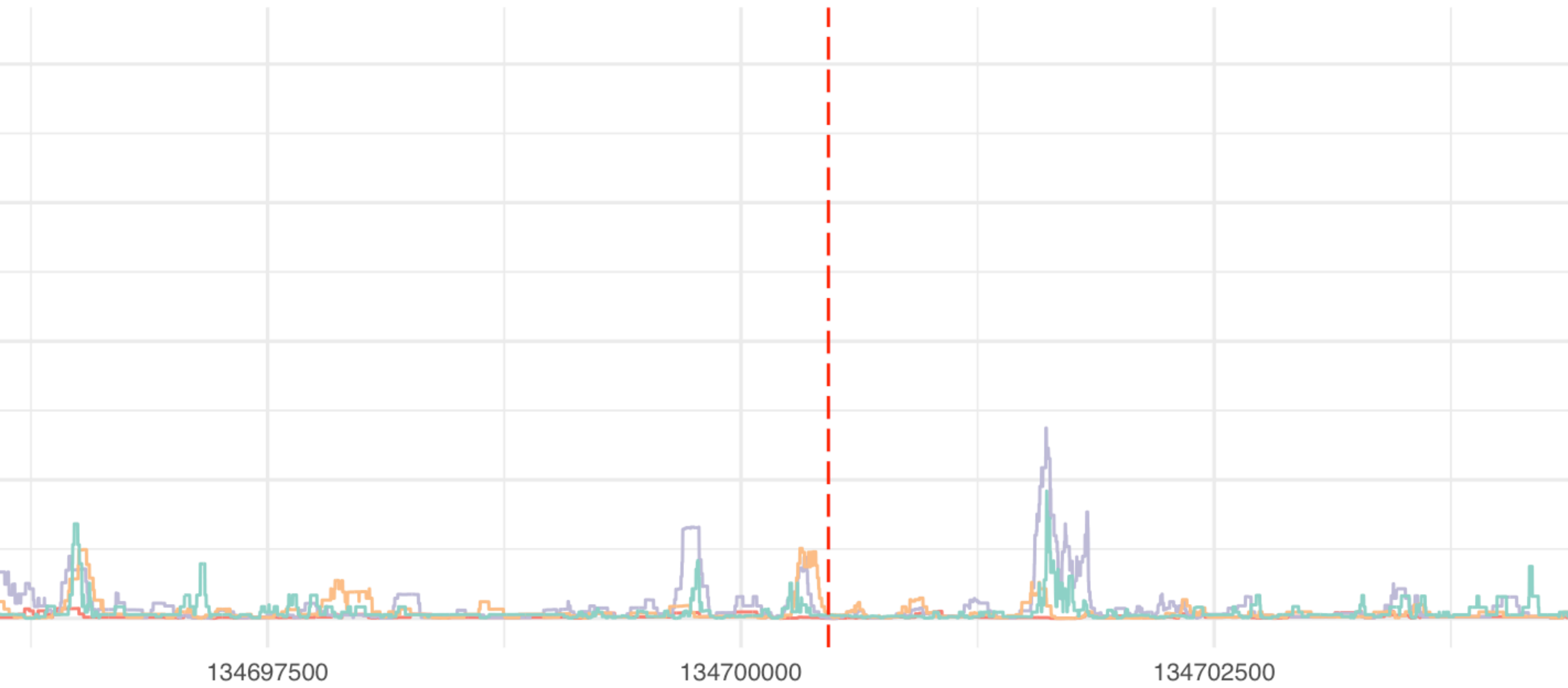
Type

- DNase
- H3K27ac
- H3K4me1
- H3K4me3



Type

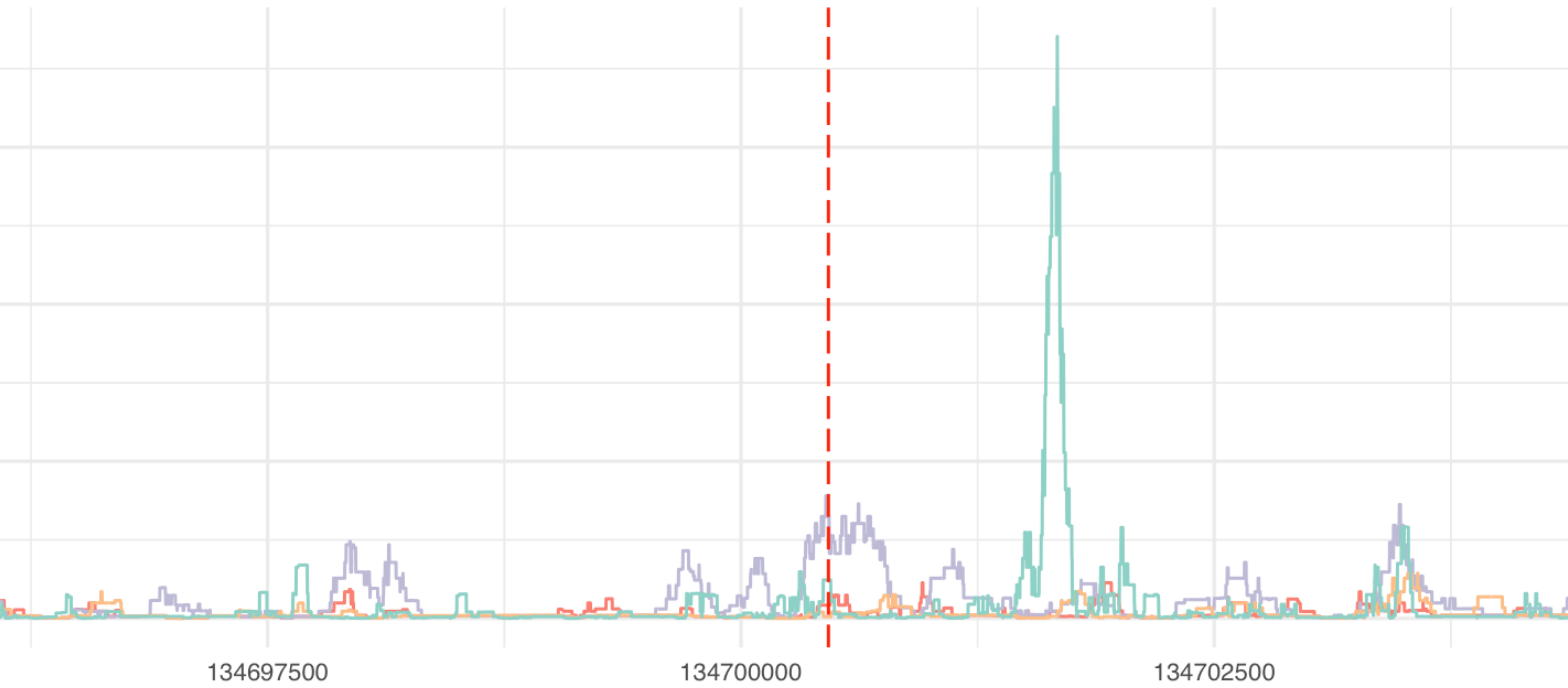
- DNase
- H3K27ac
- H3K4me1
- H3K4me3





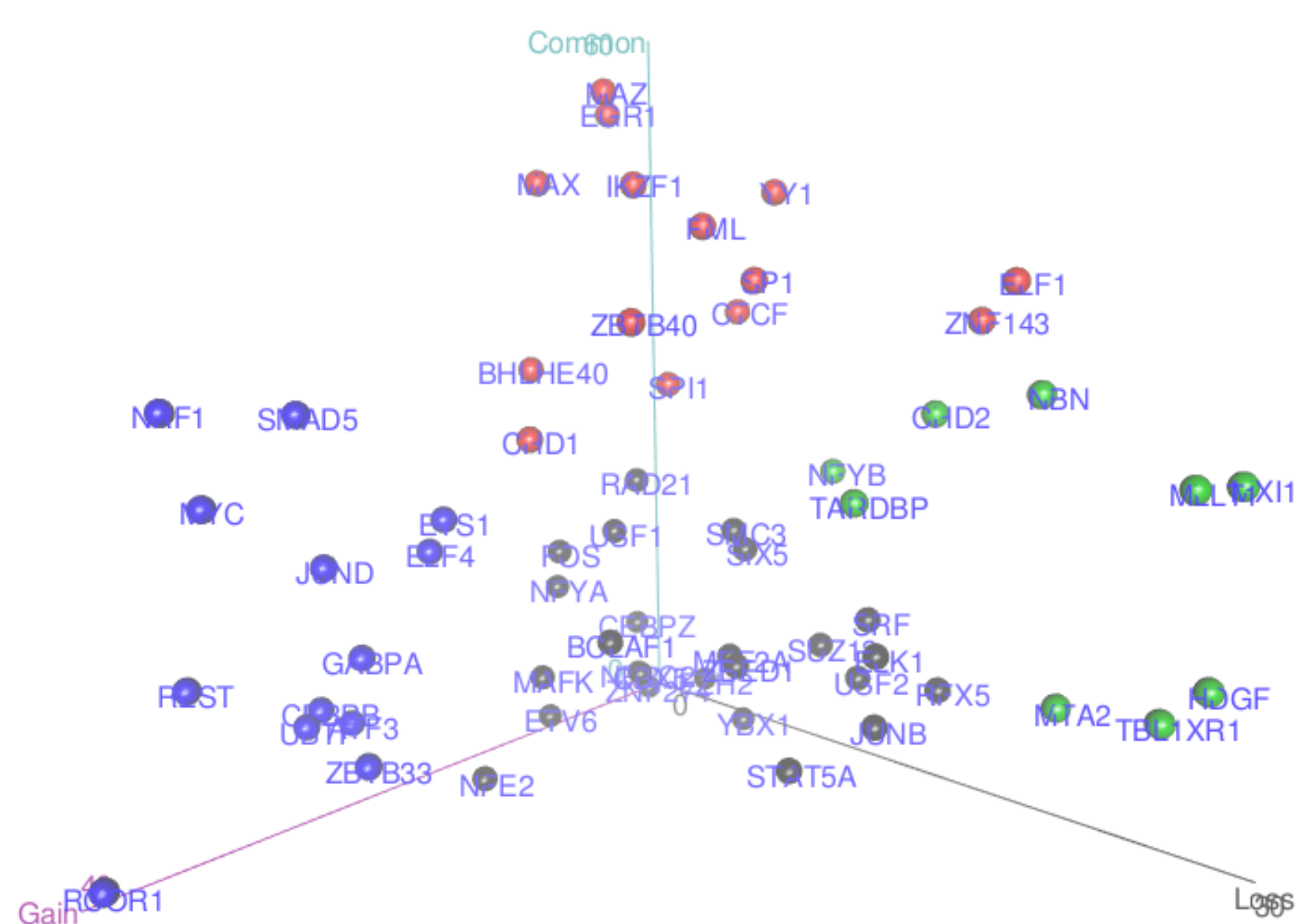
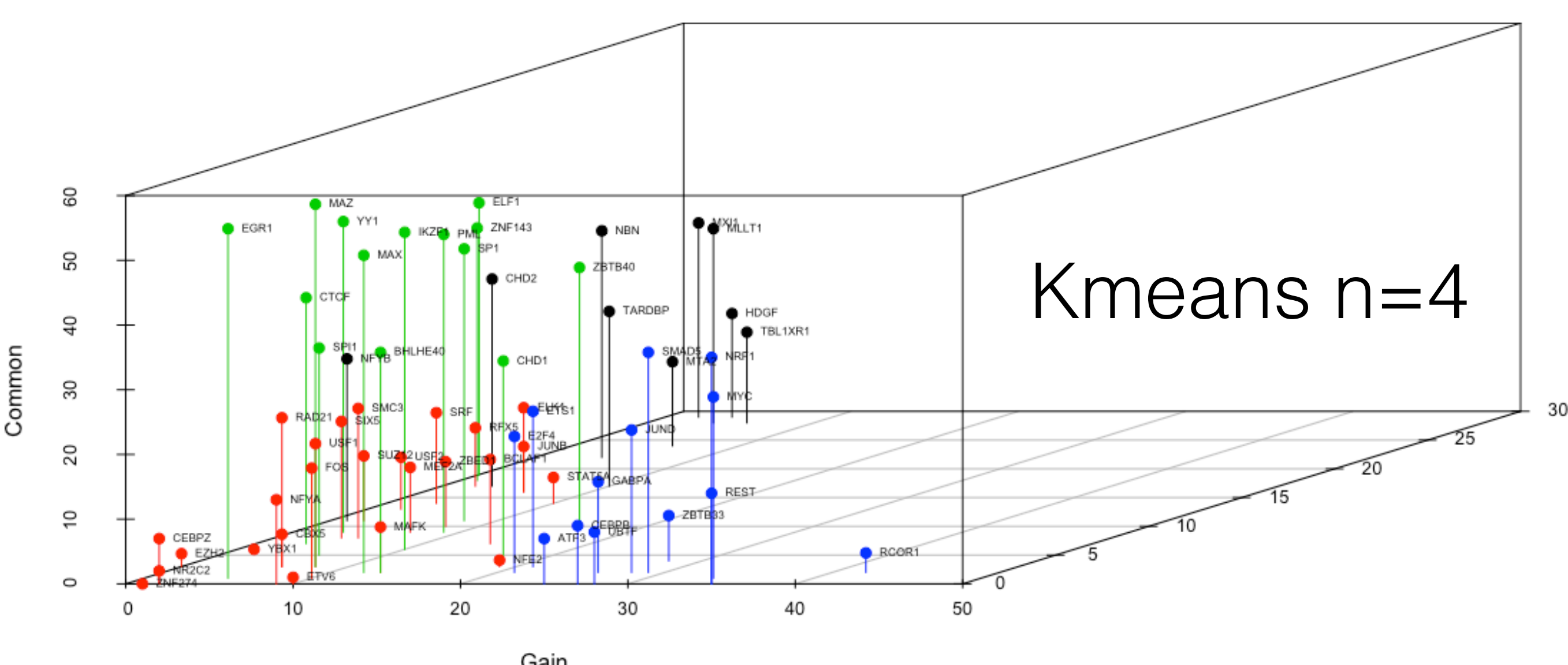
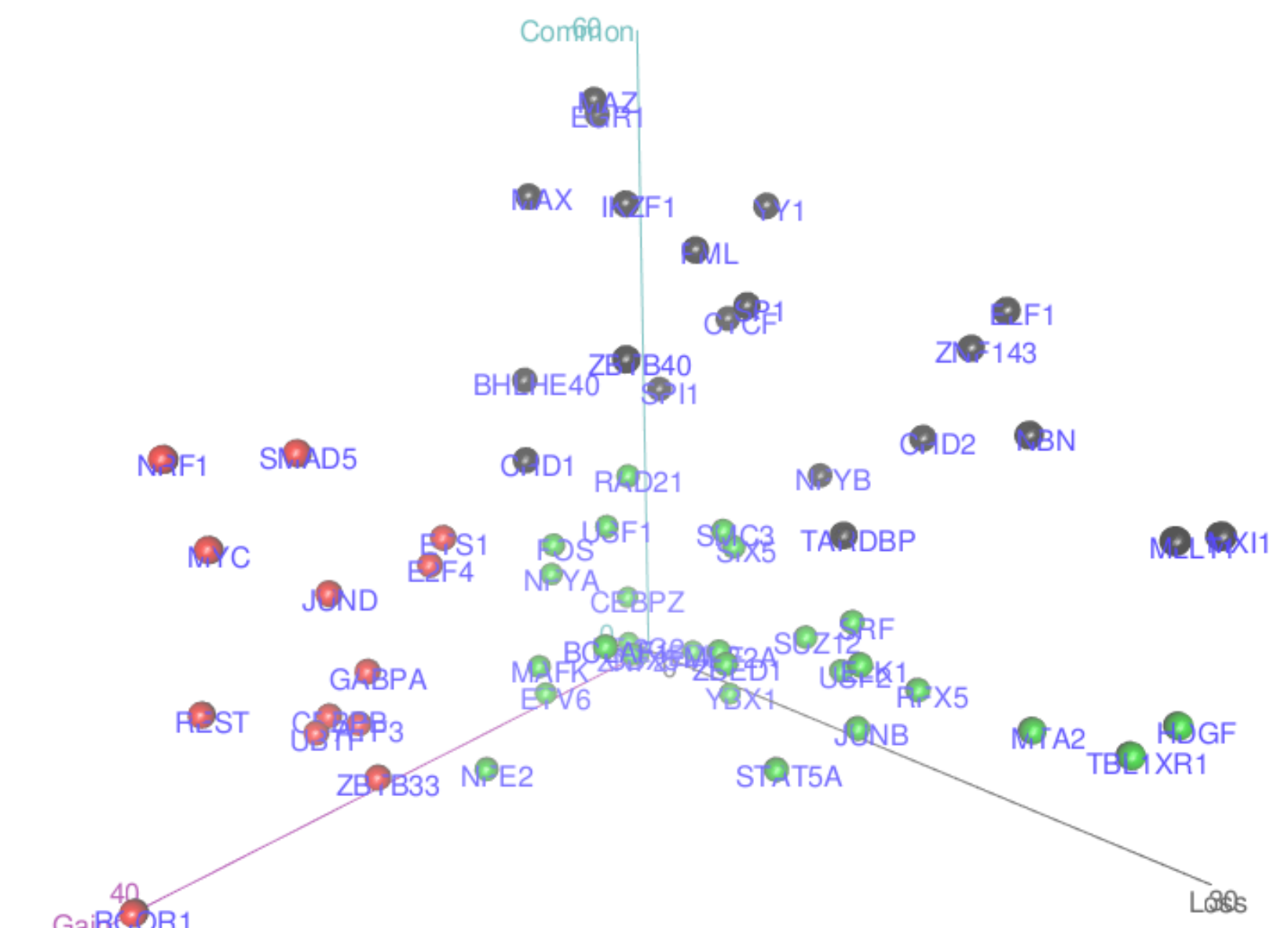
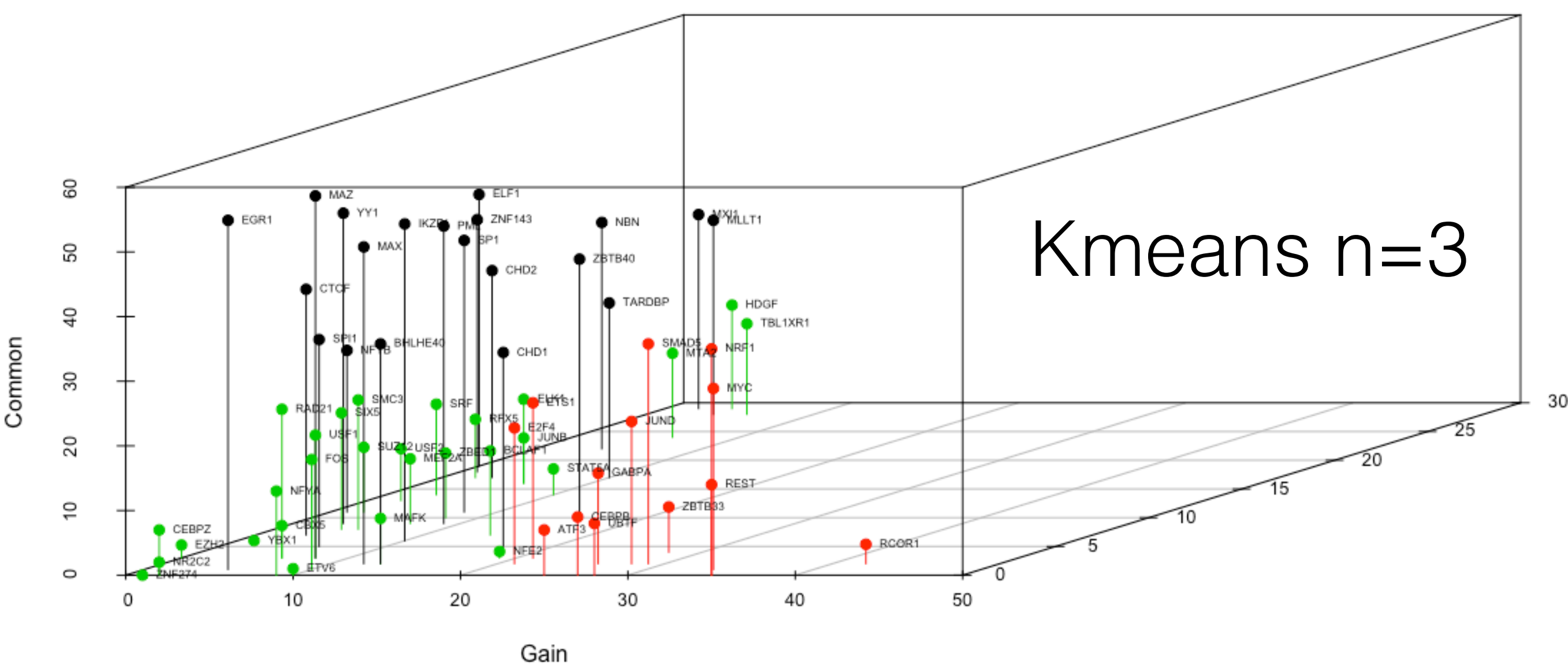
Type

- DNase
- H3K27ac
- H3K4me1
- H3K4me3

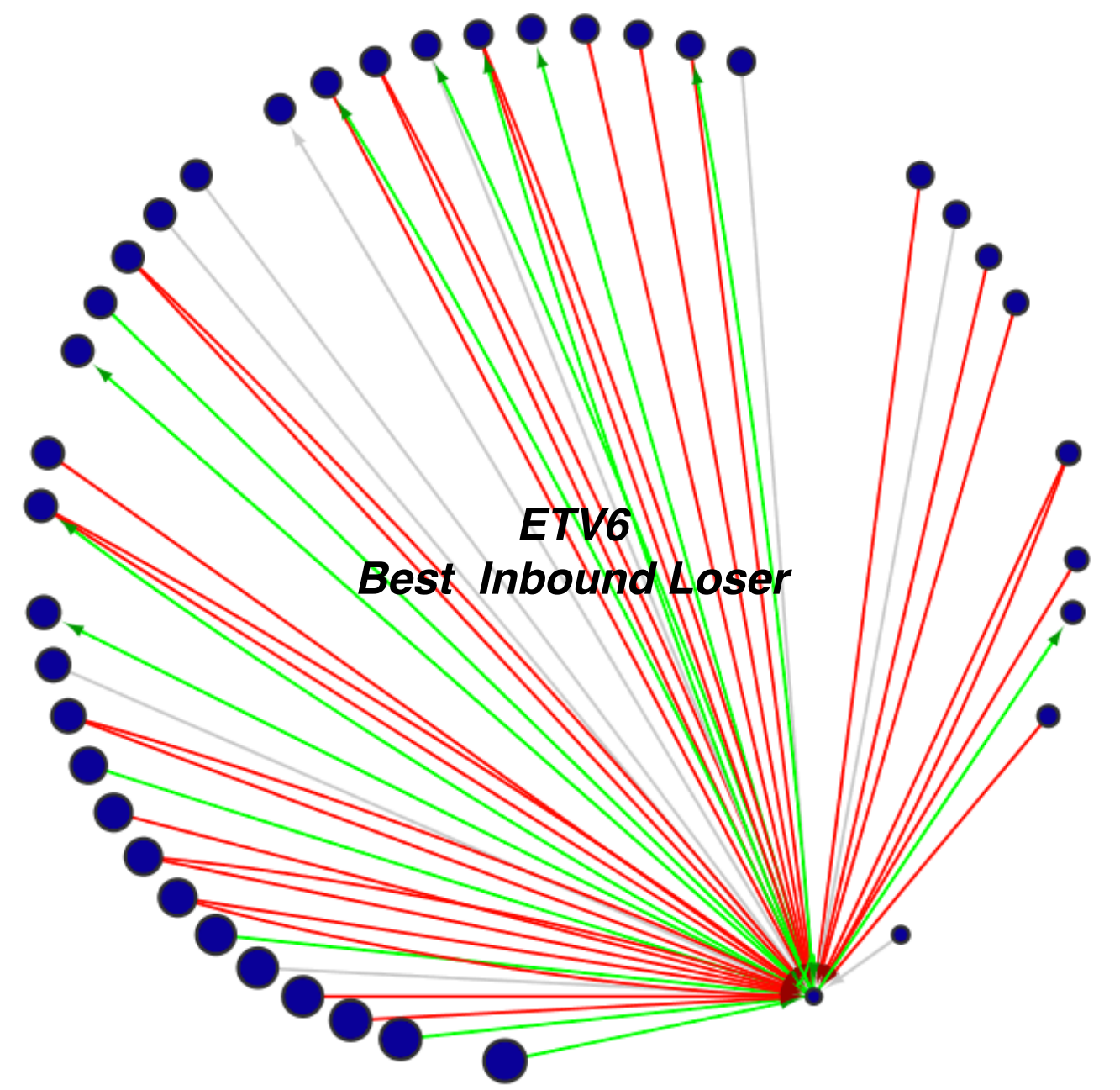
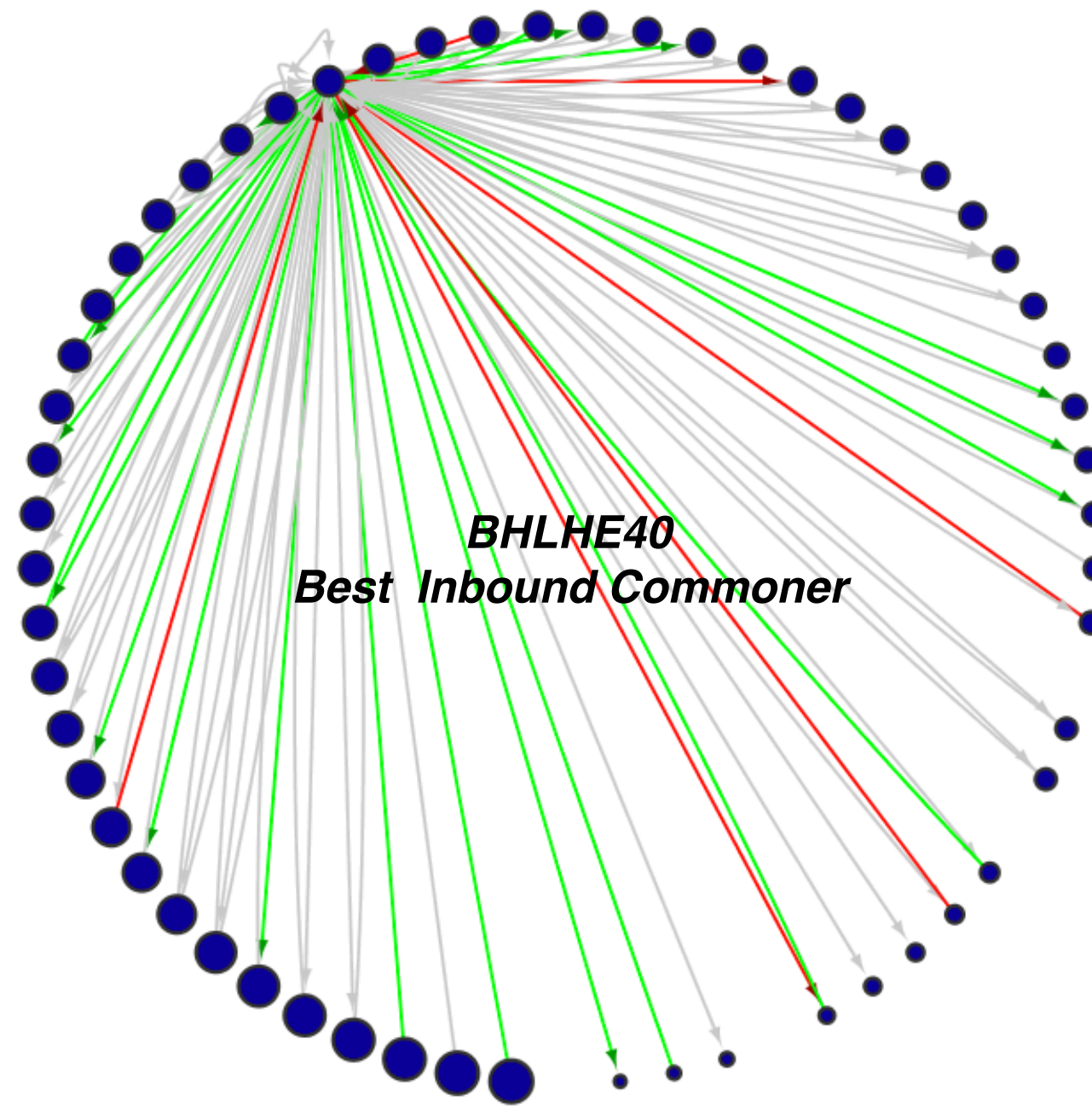
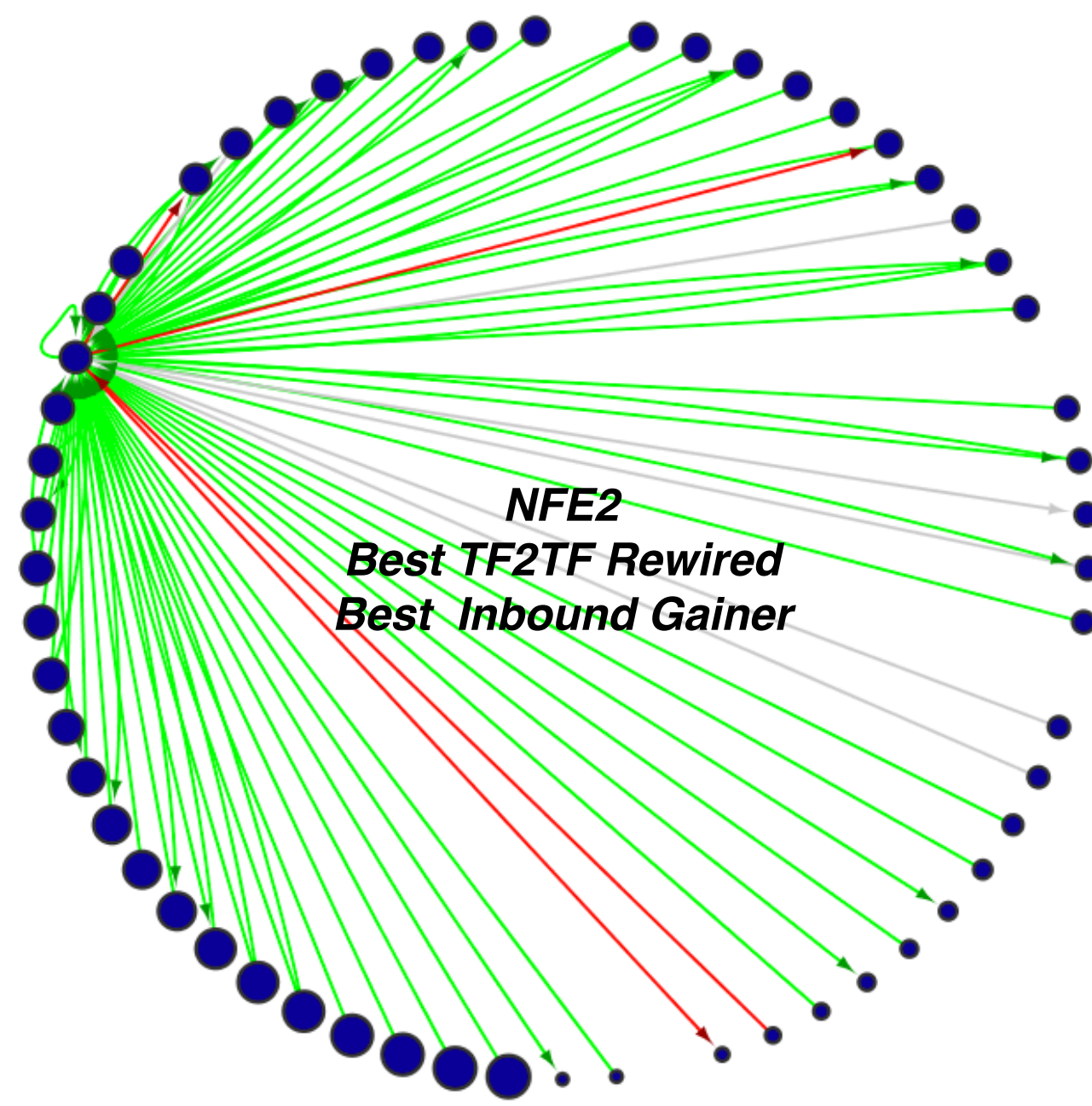
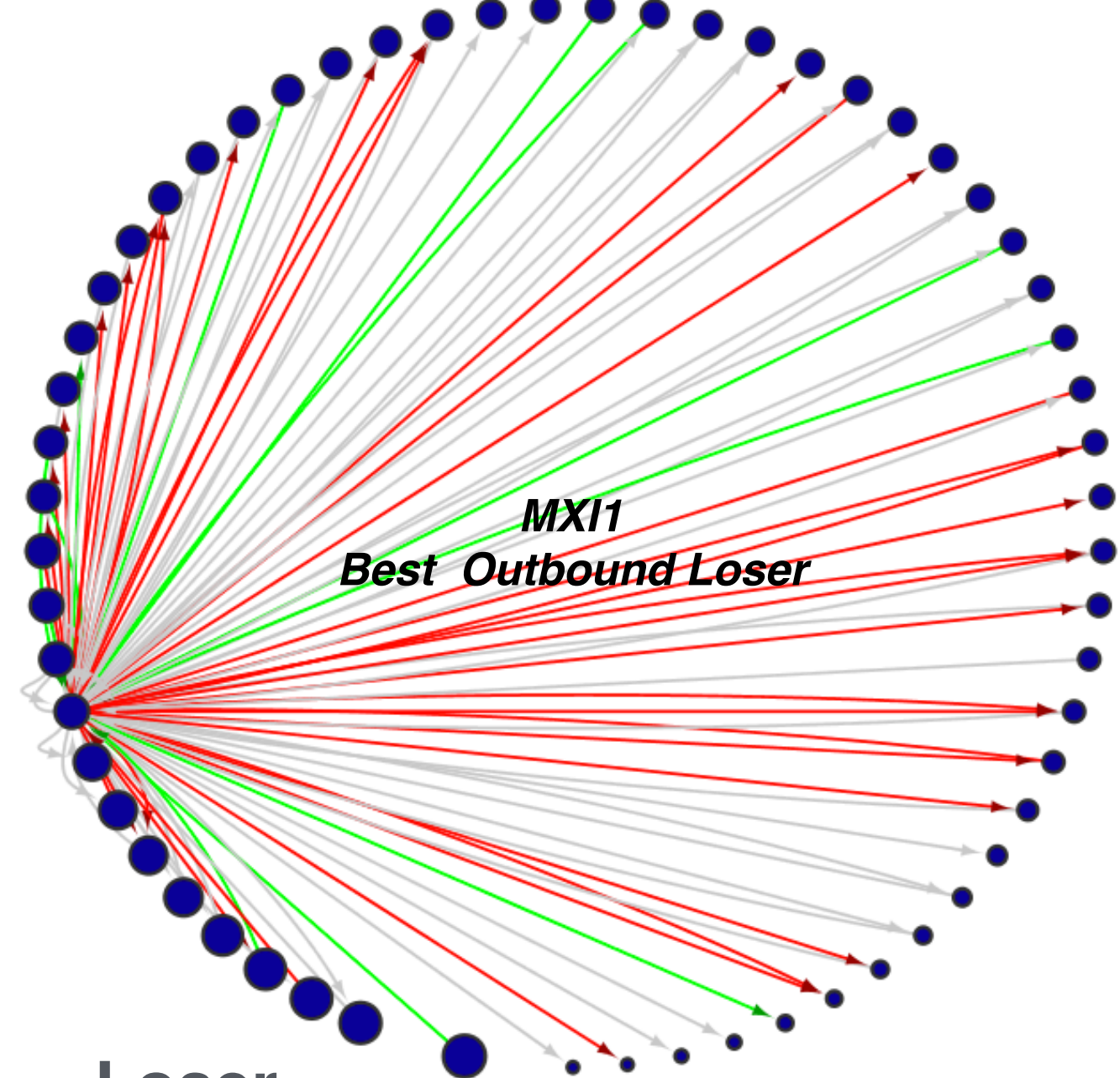
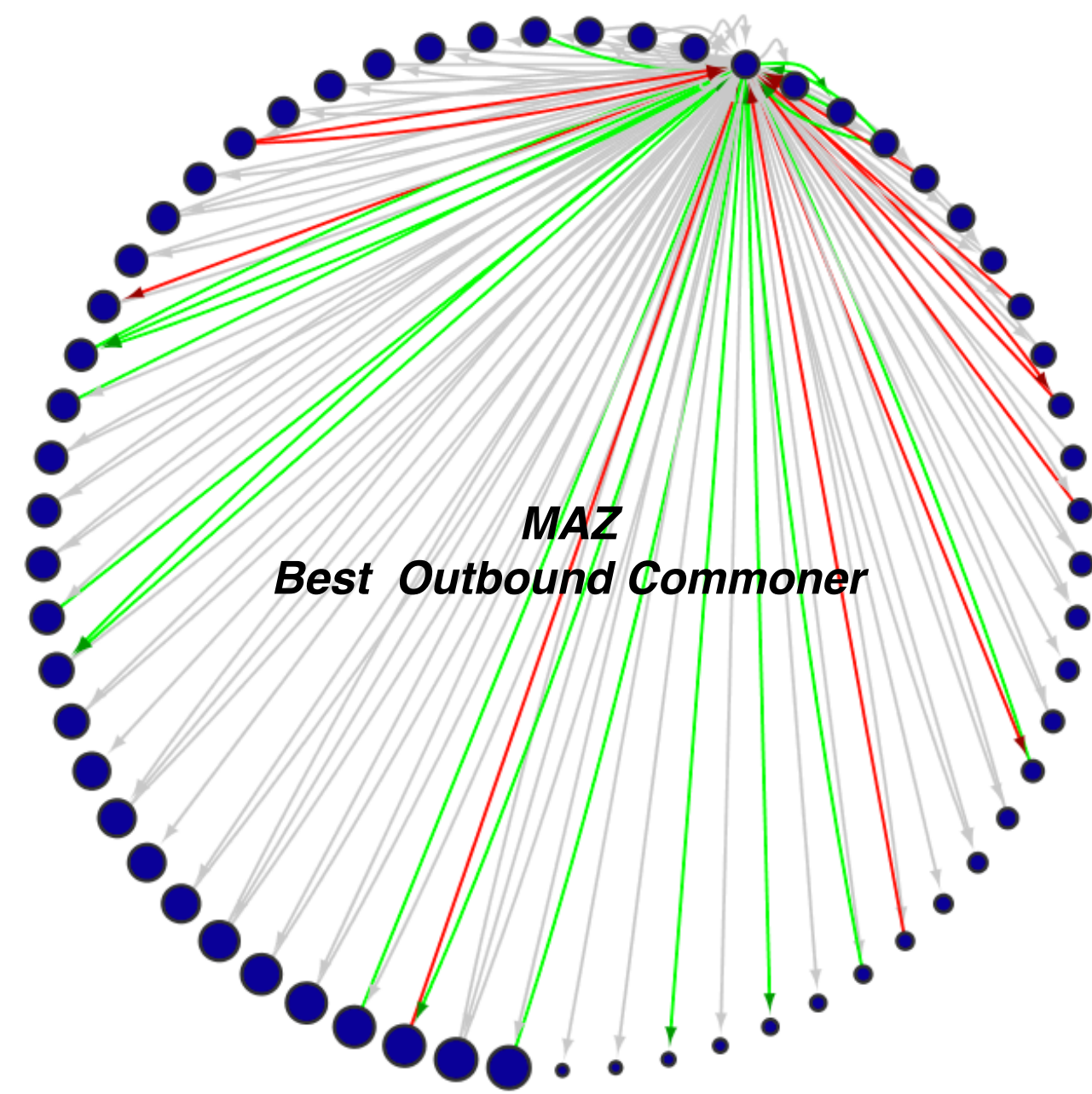
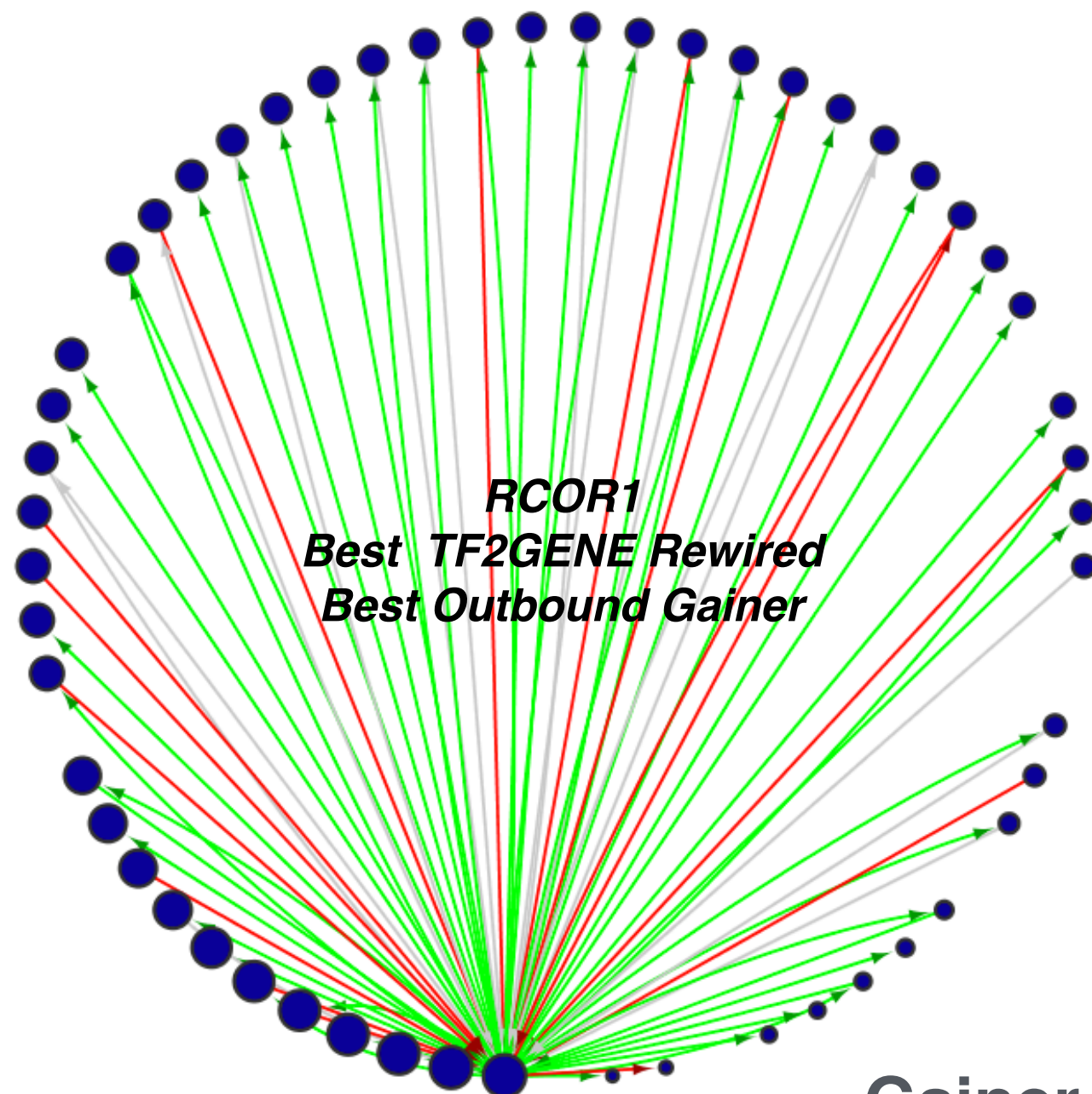


# Using count of interaction, instead of %gain, %loss, and %comm

Clustering



clustering with 4 categories work better, gain(blue)/loss(green)/common(red)/inactive(black)

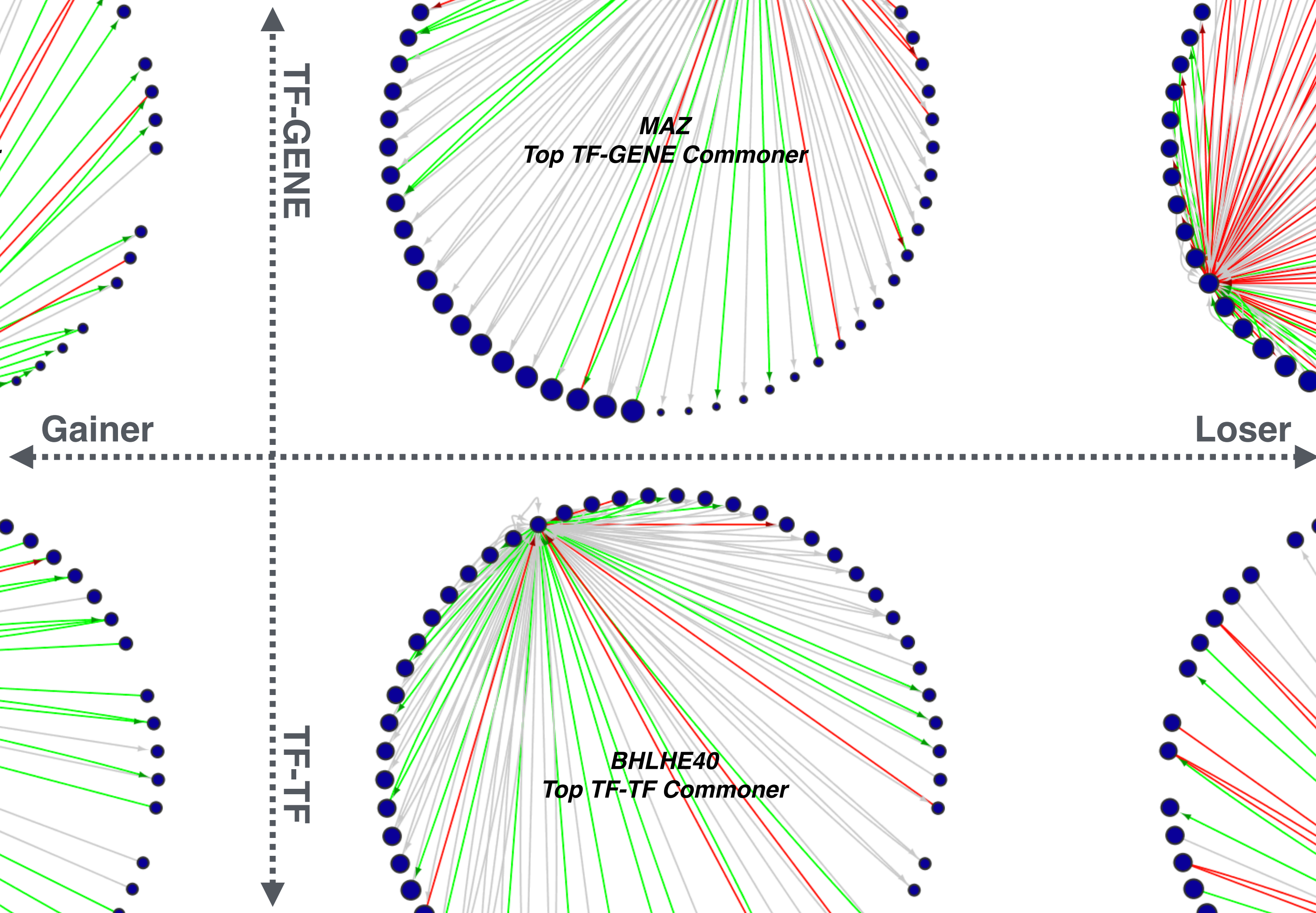
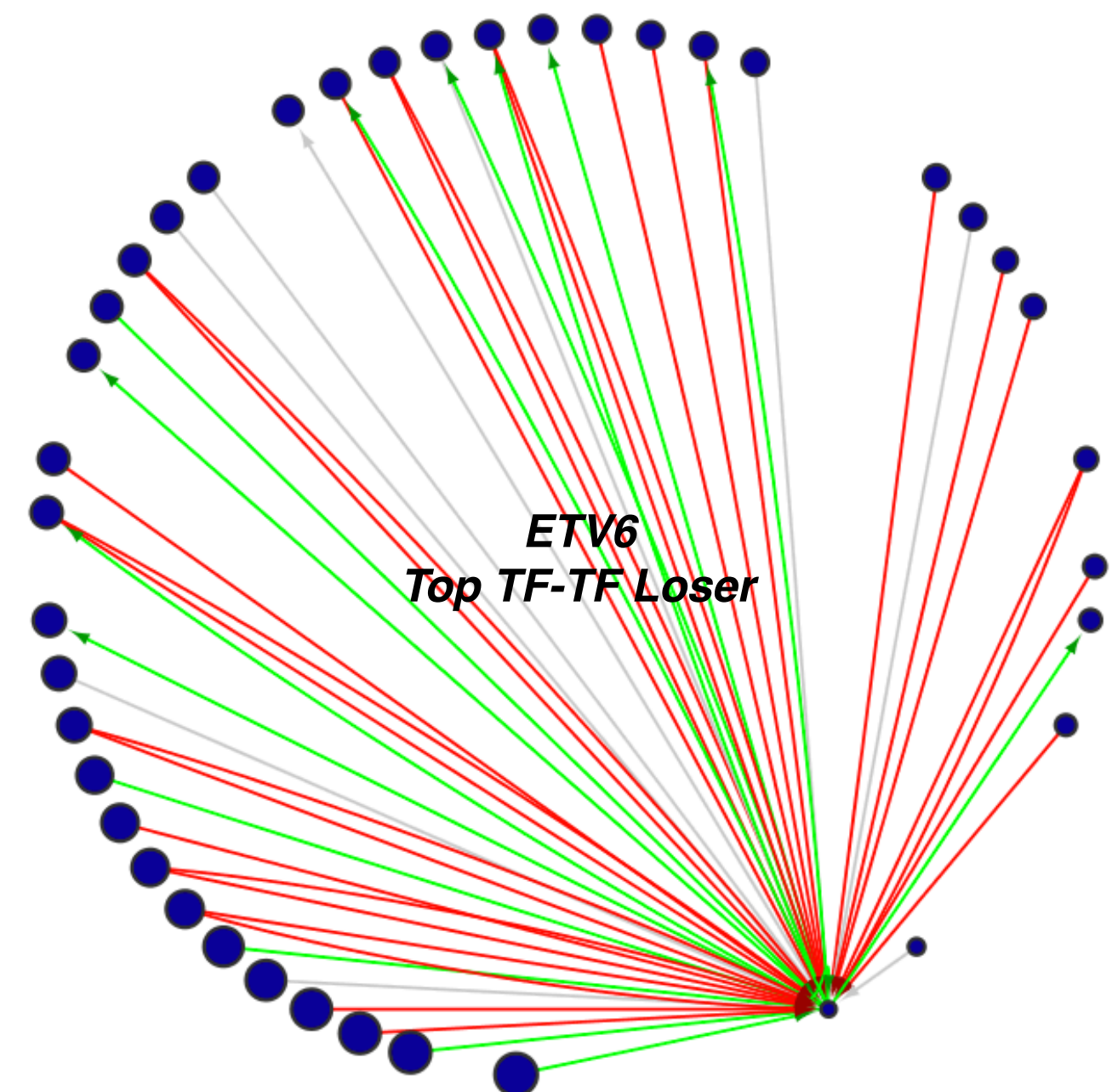
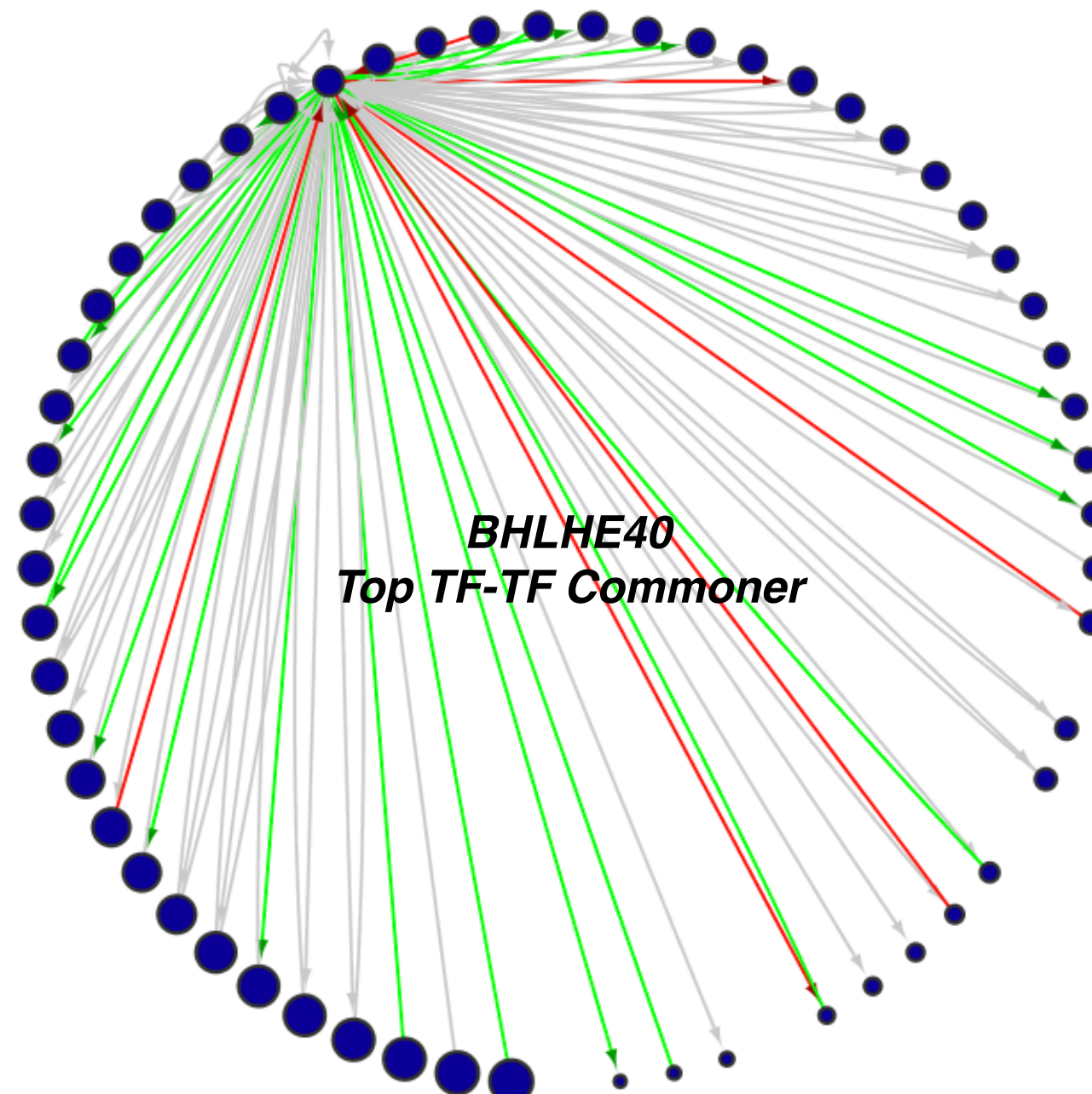
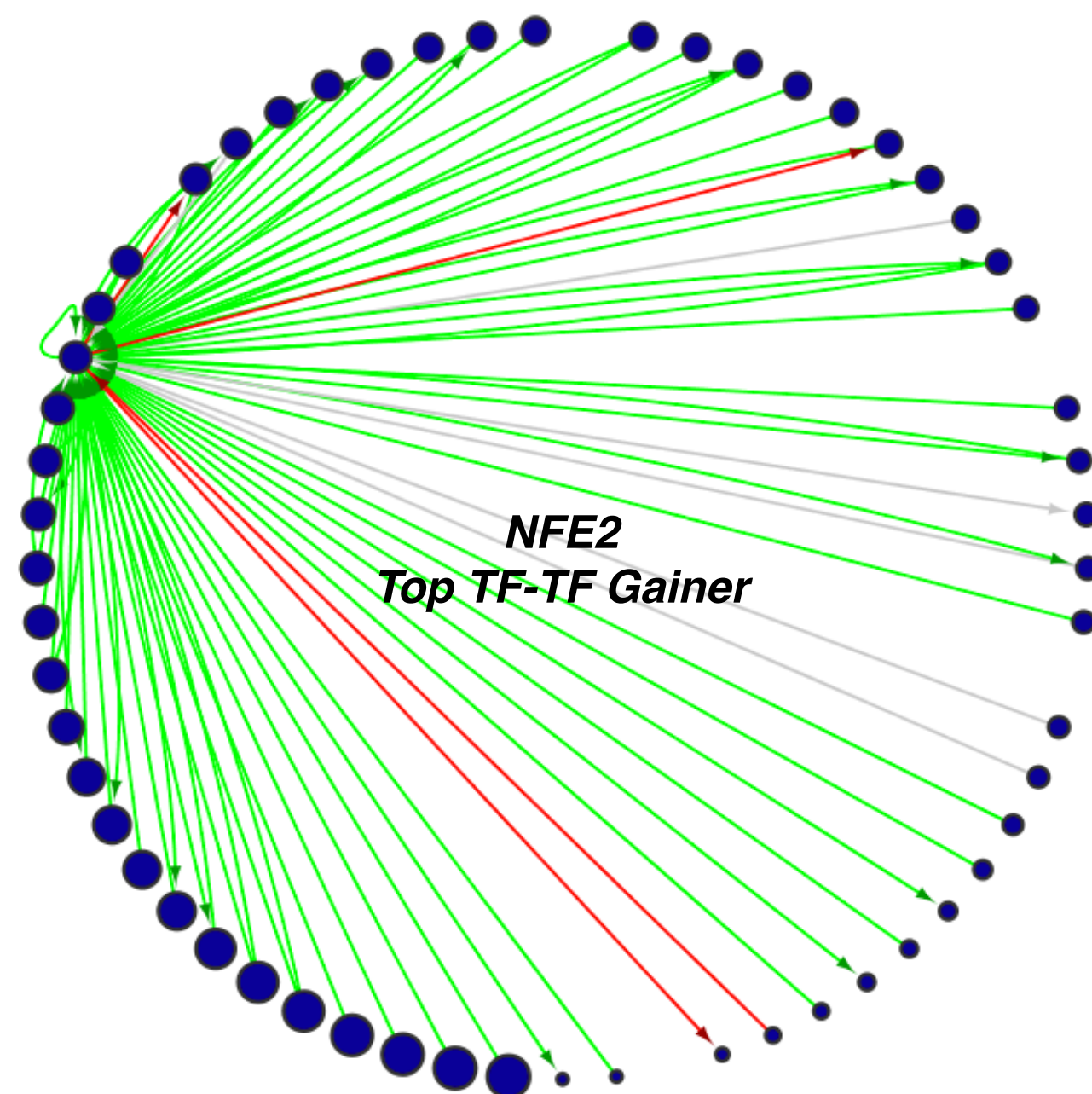
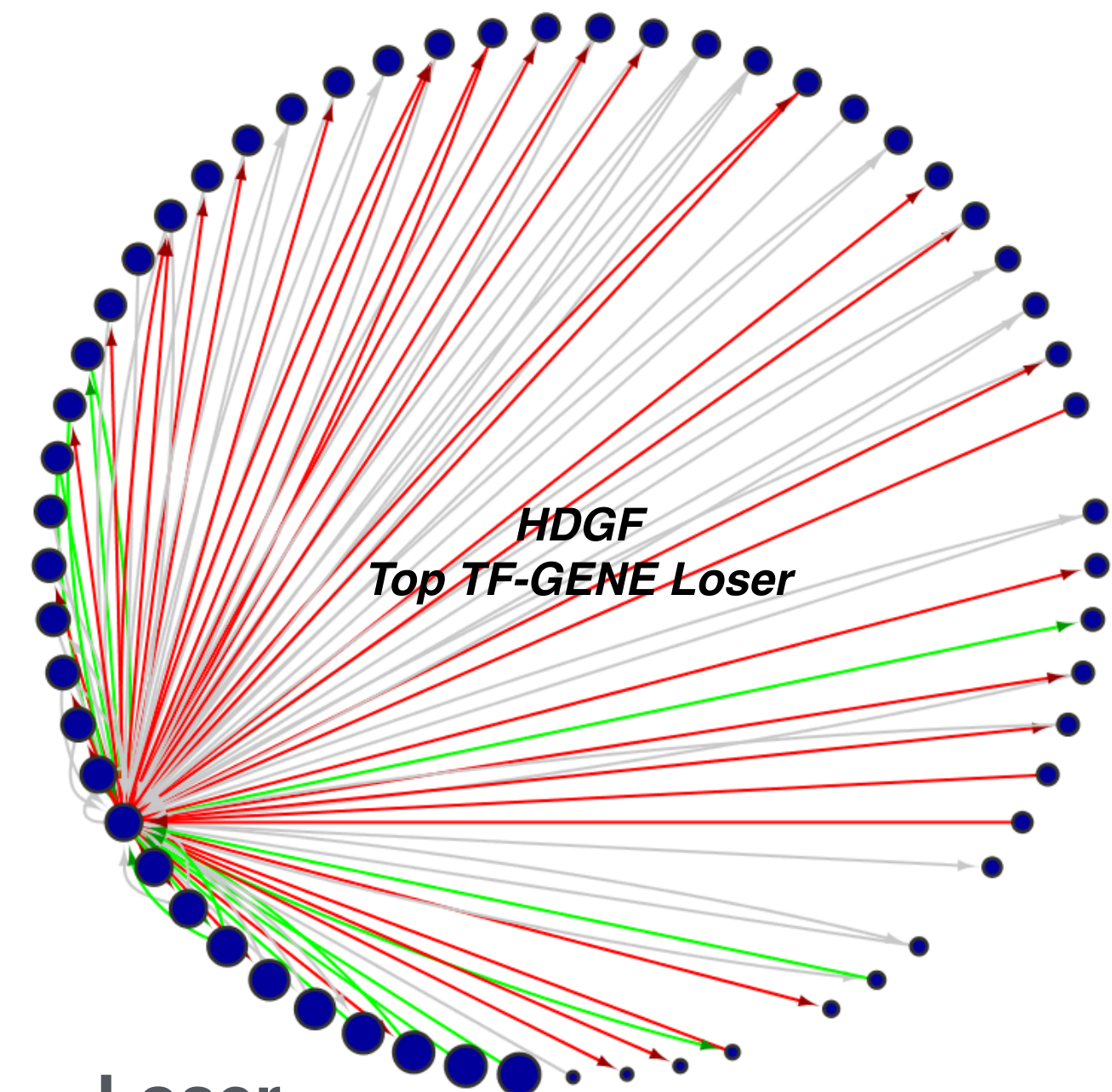
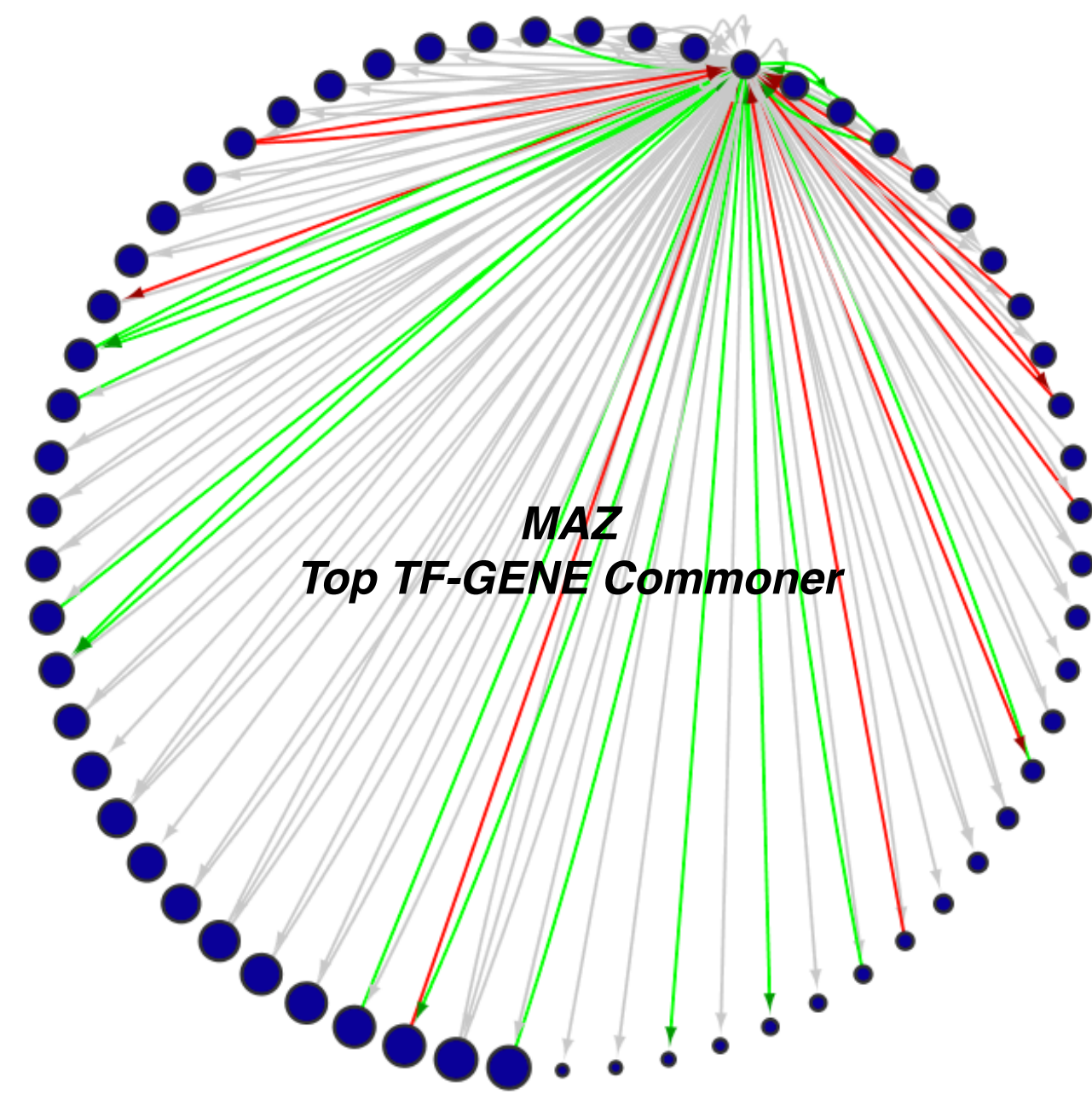
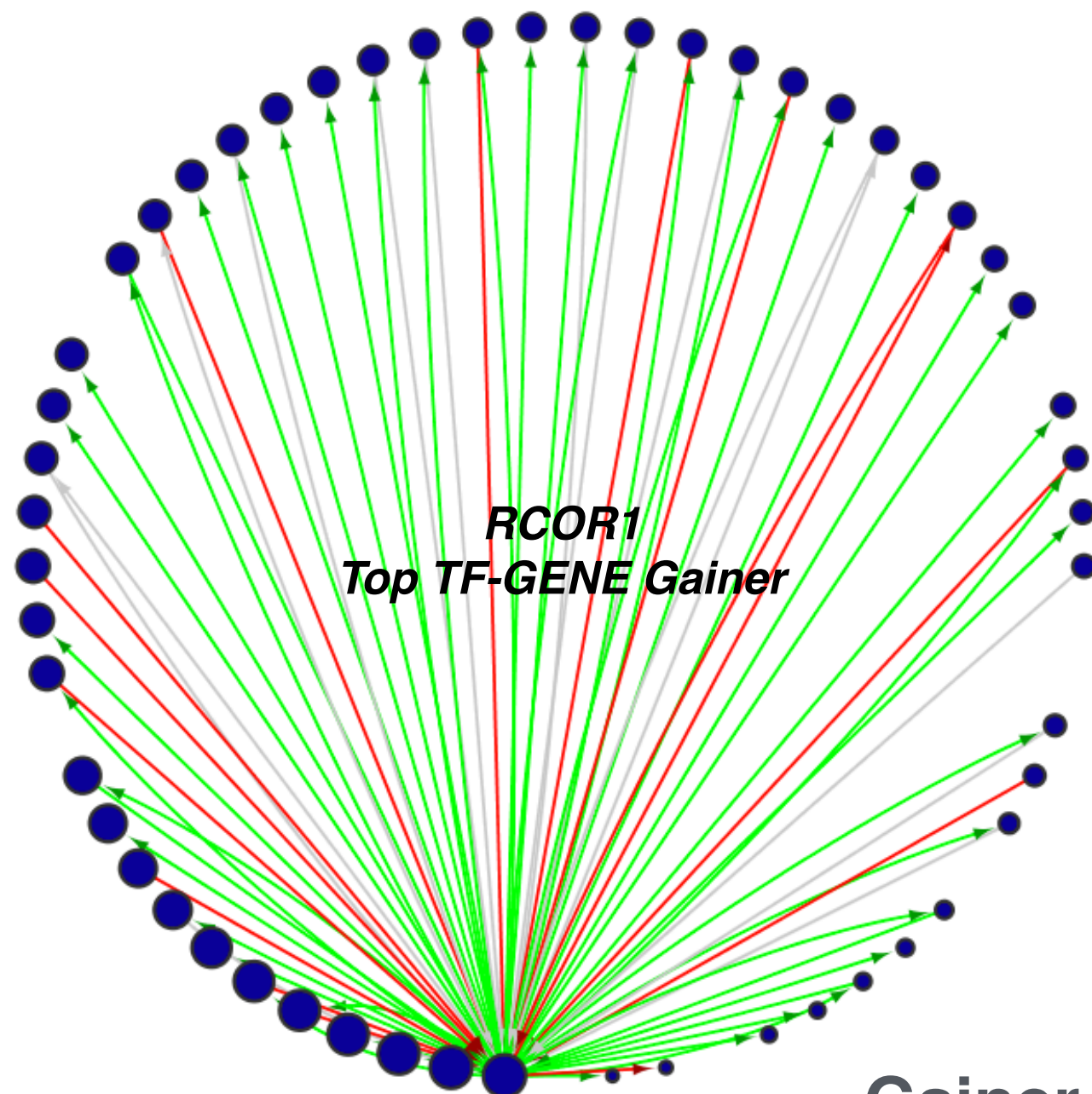


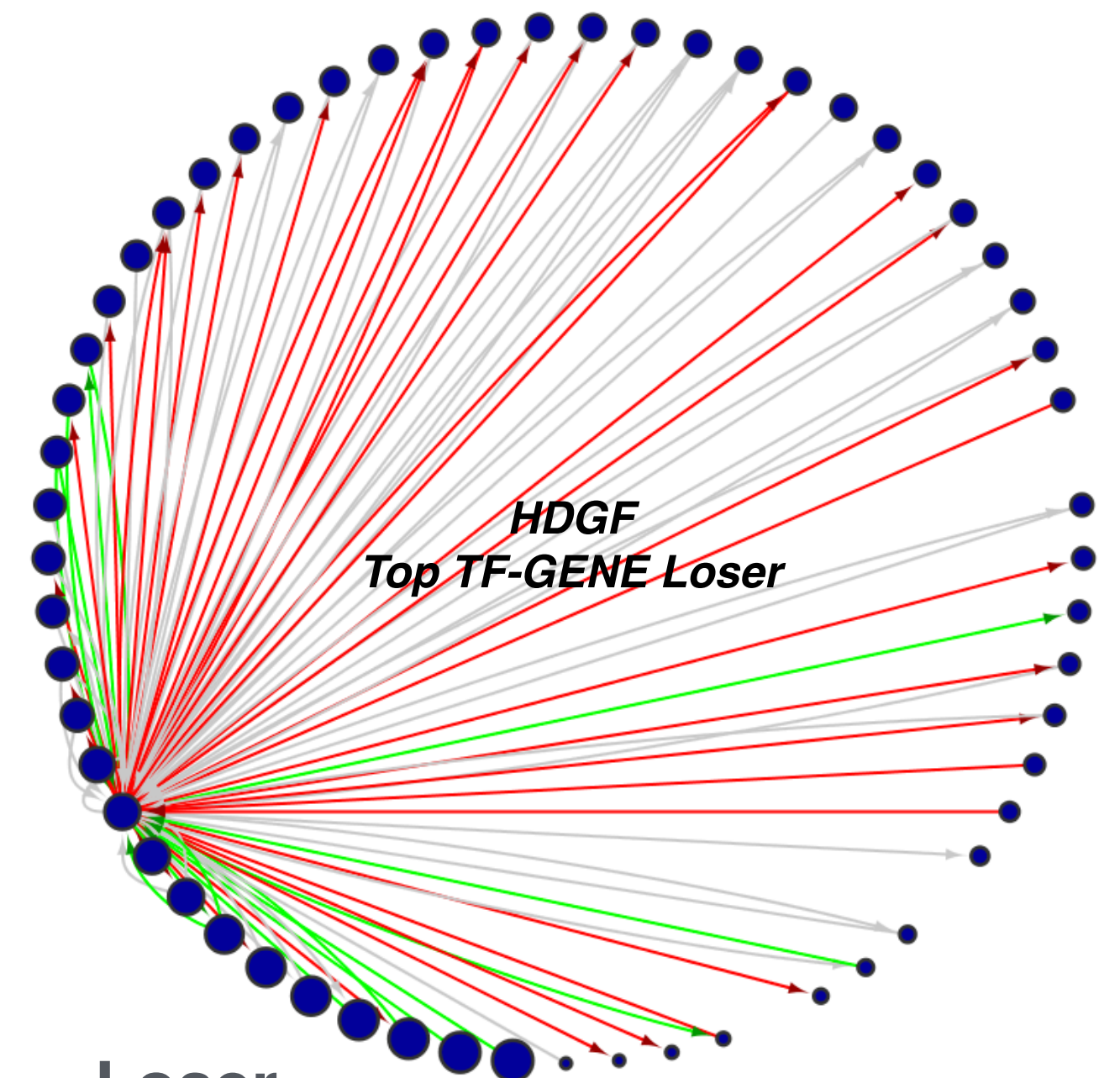
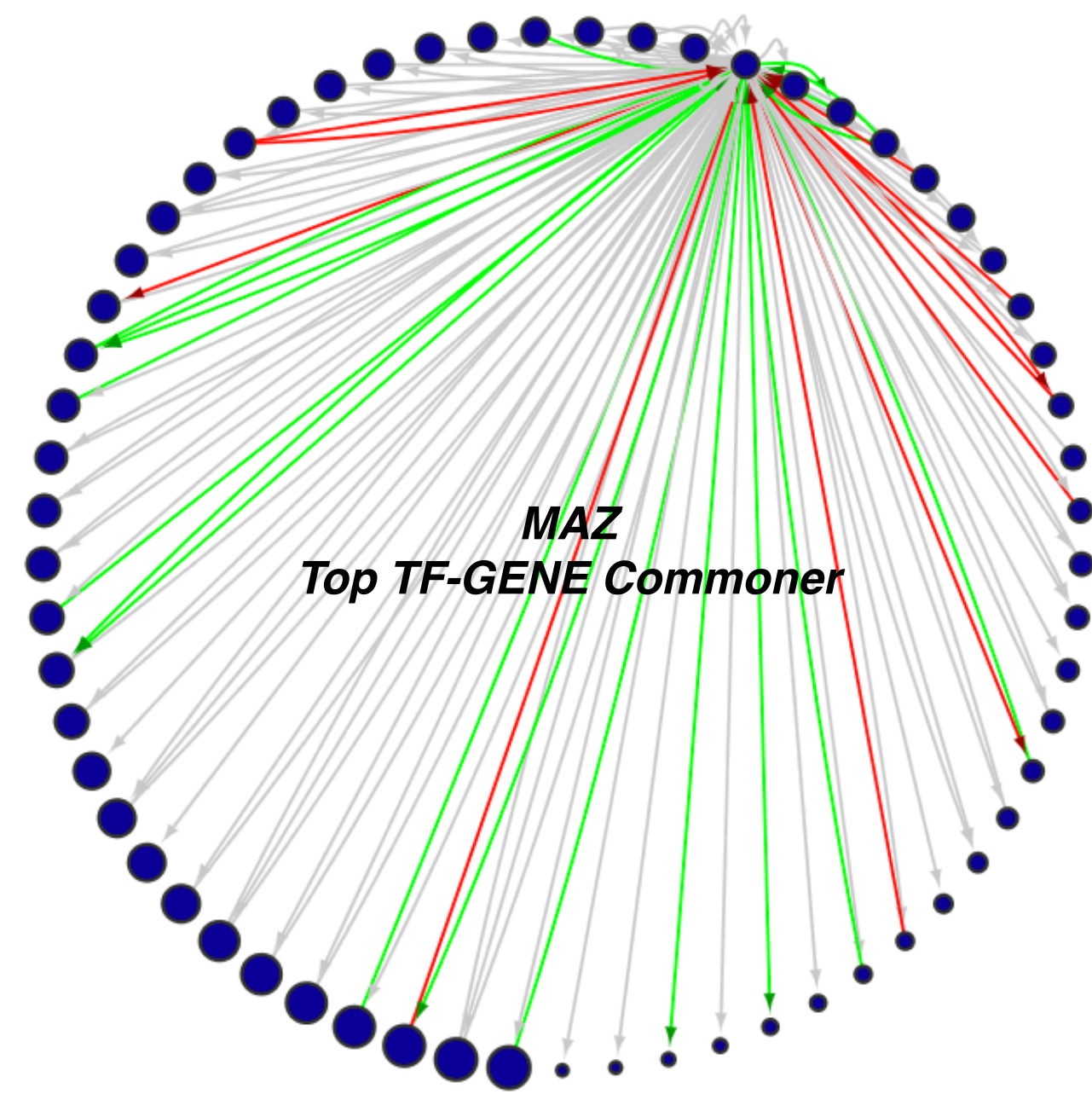
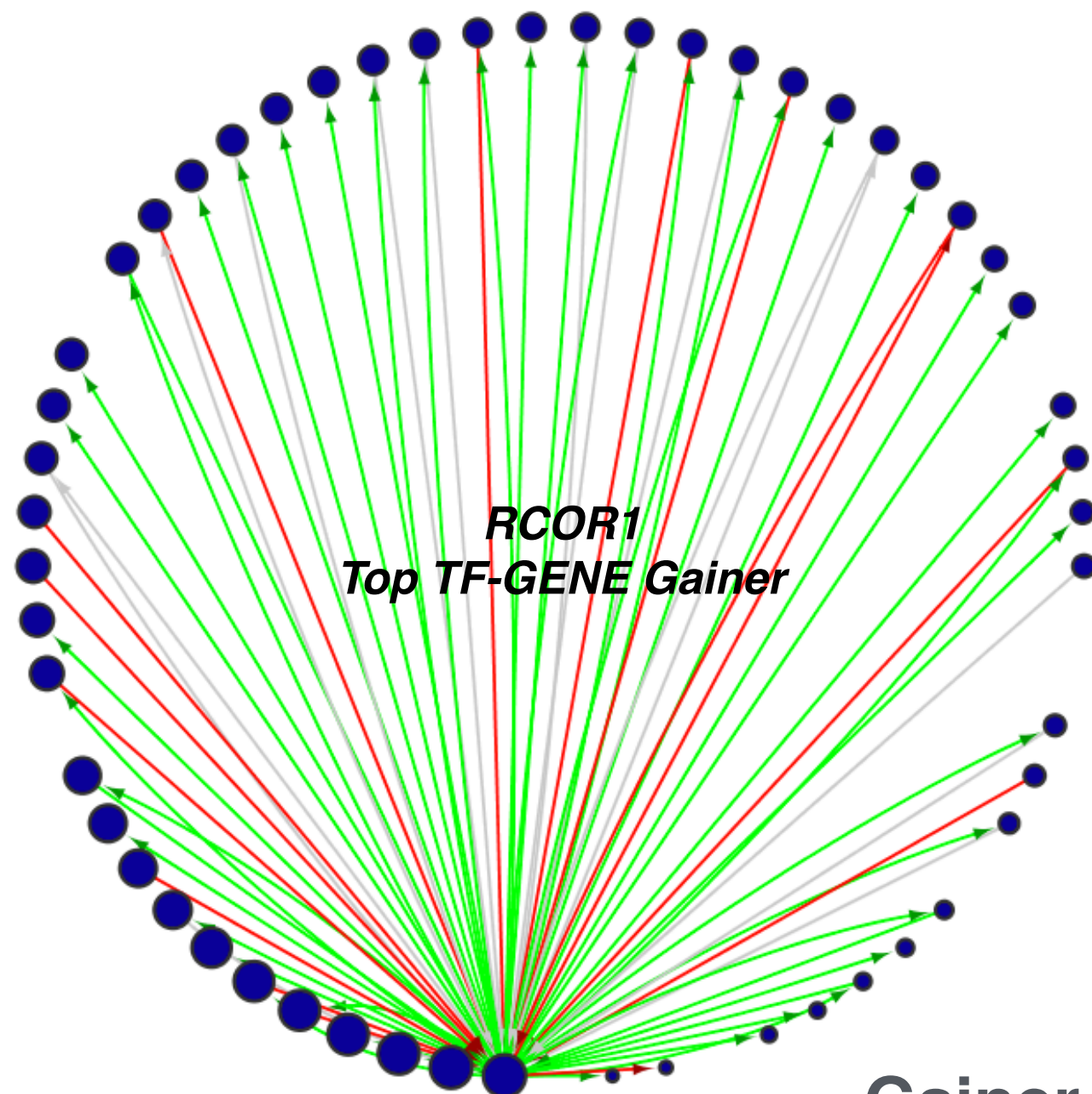
Outbound

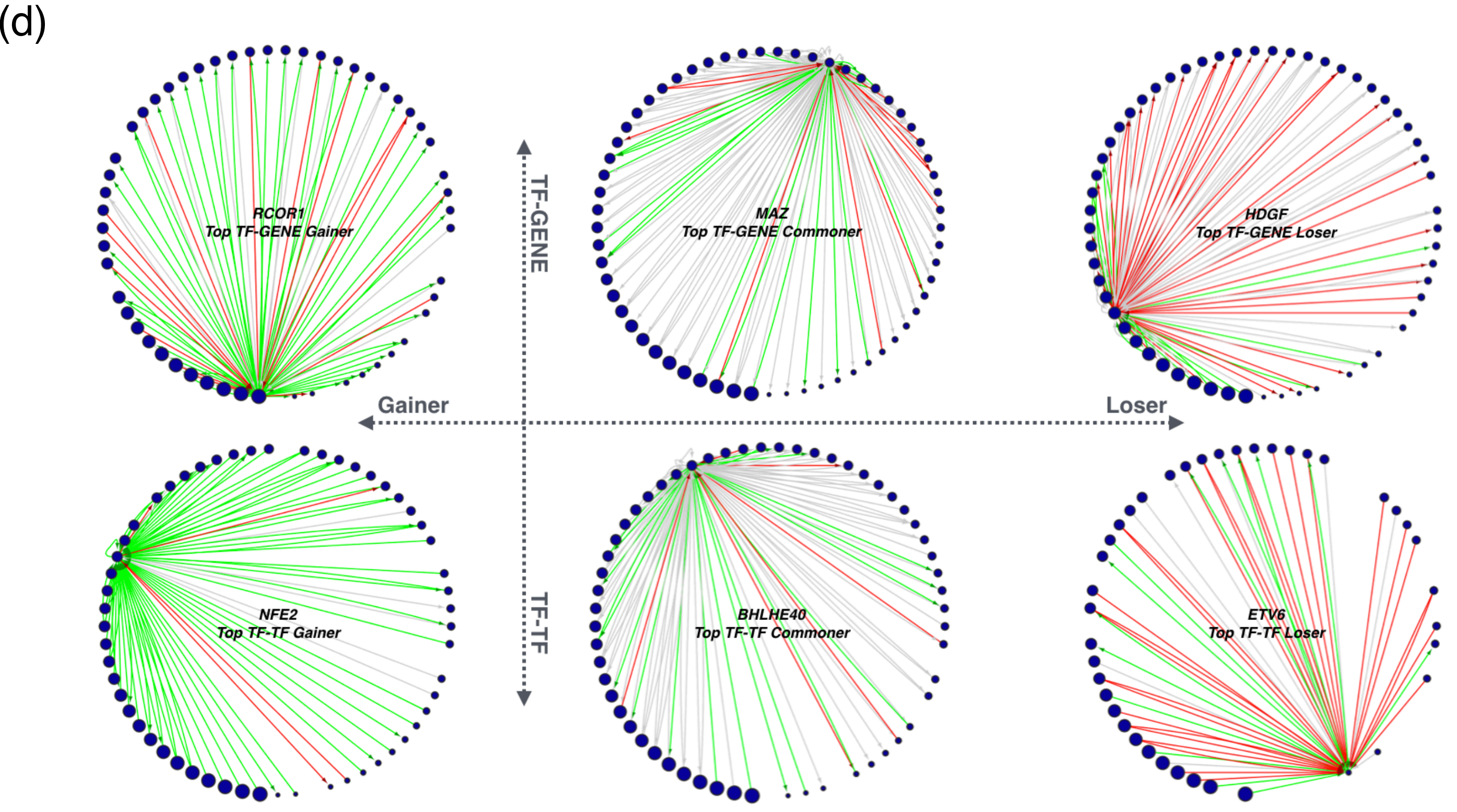
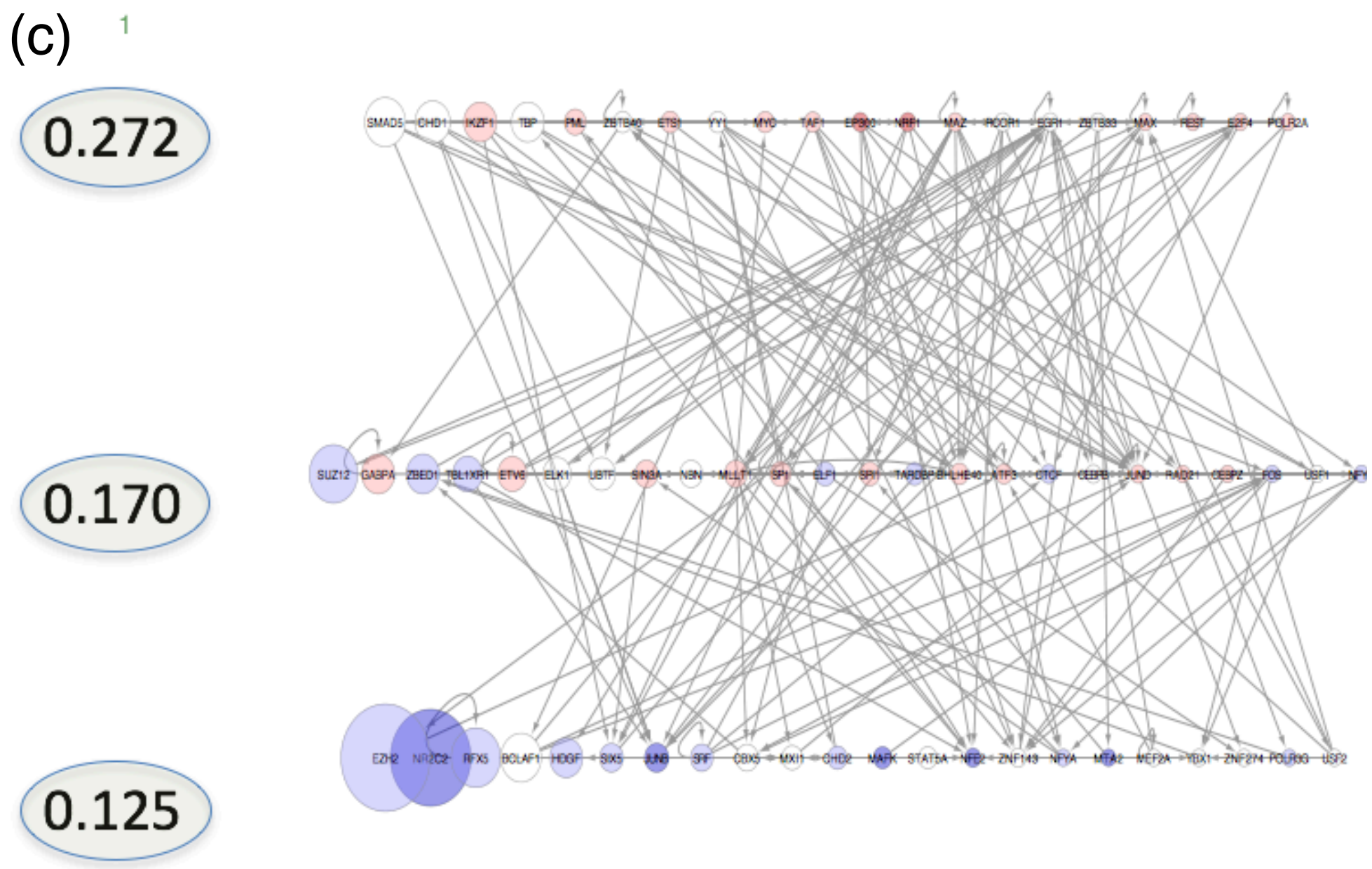
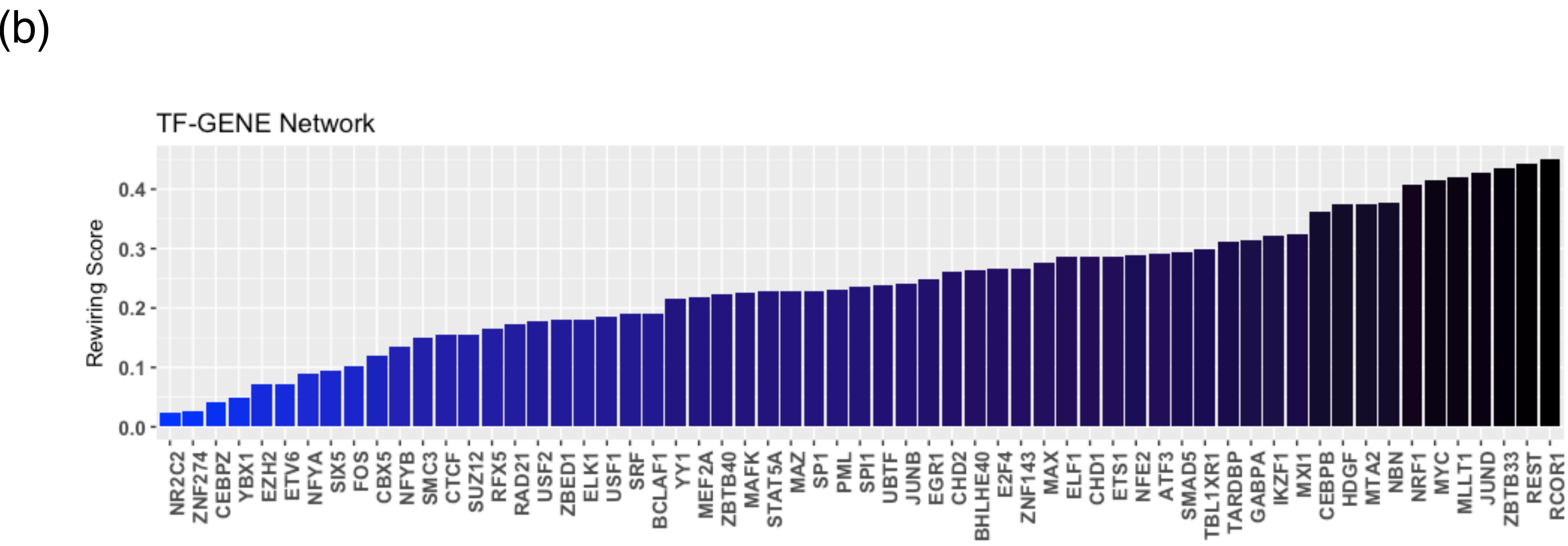
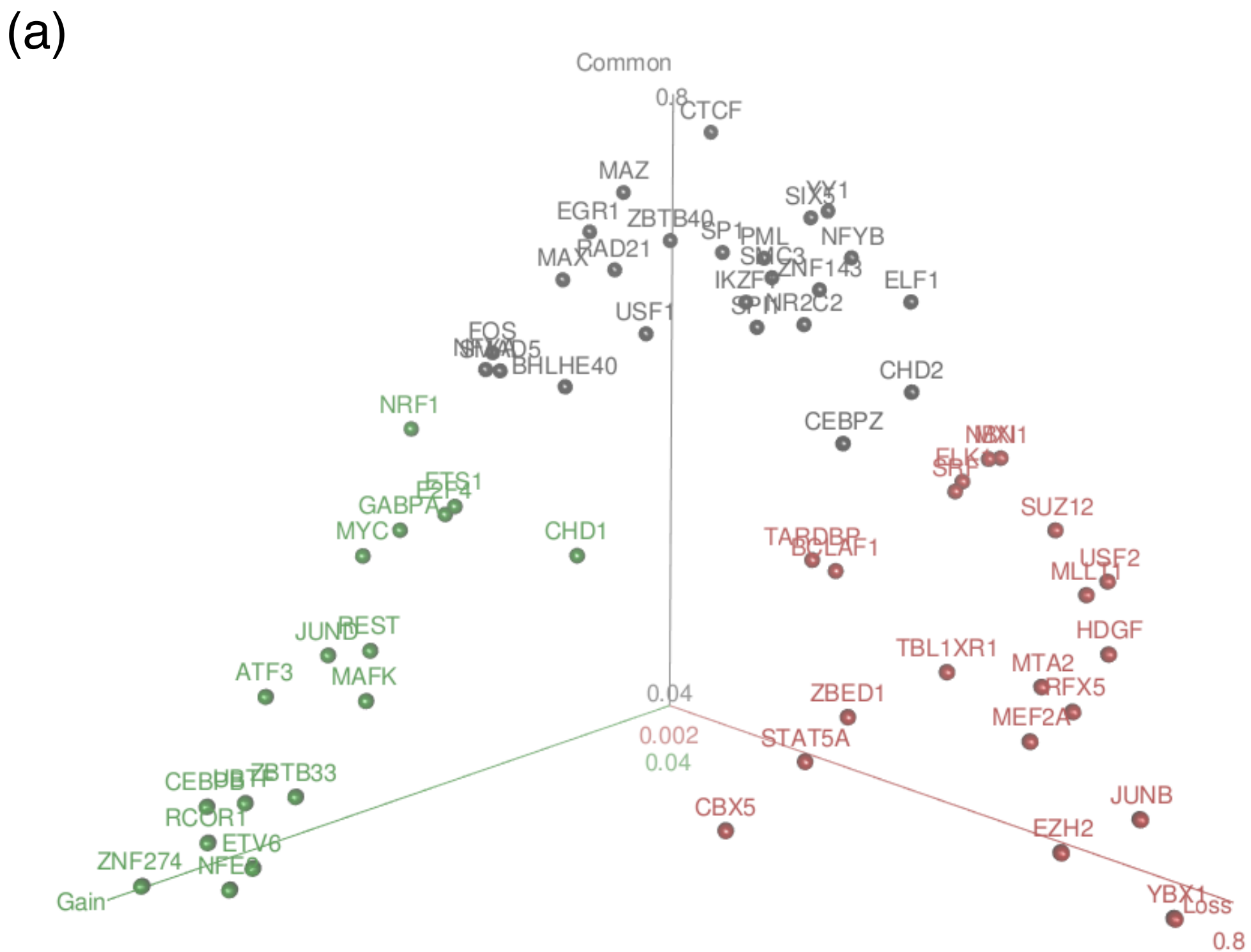
Inbound

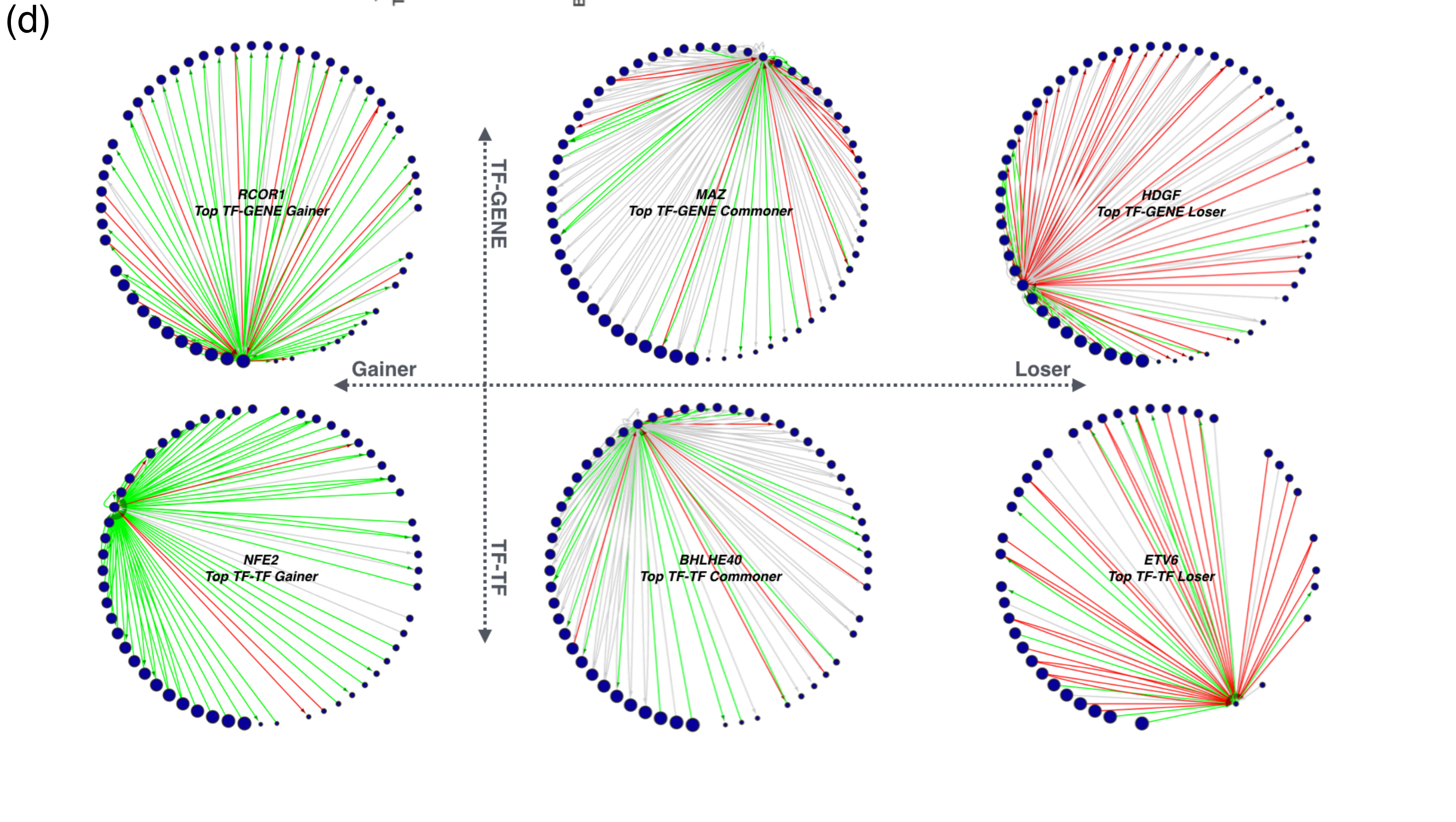
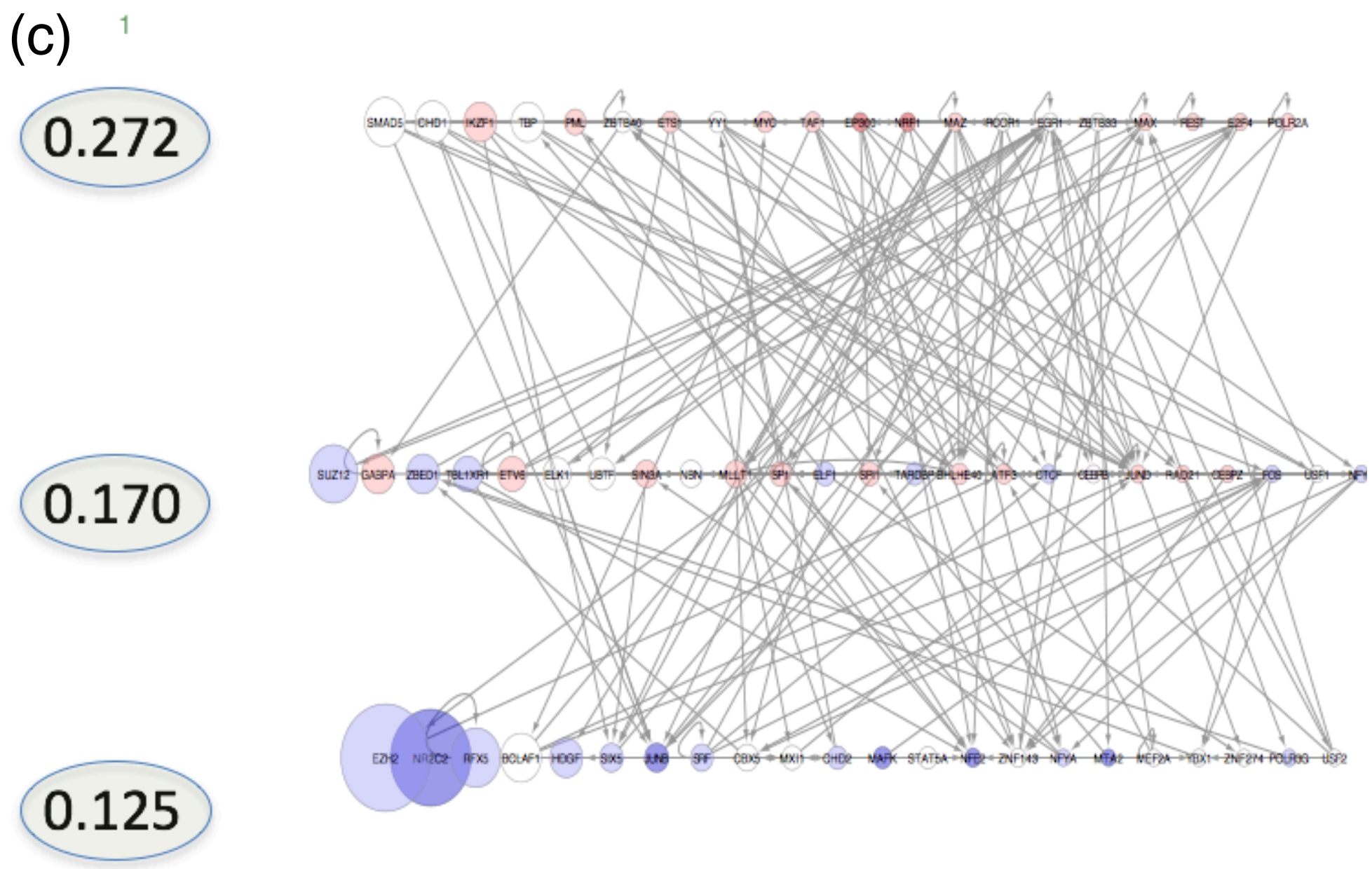
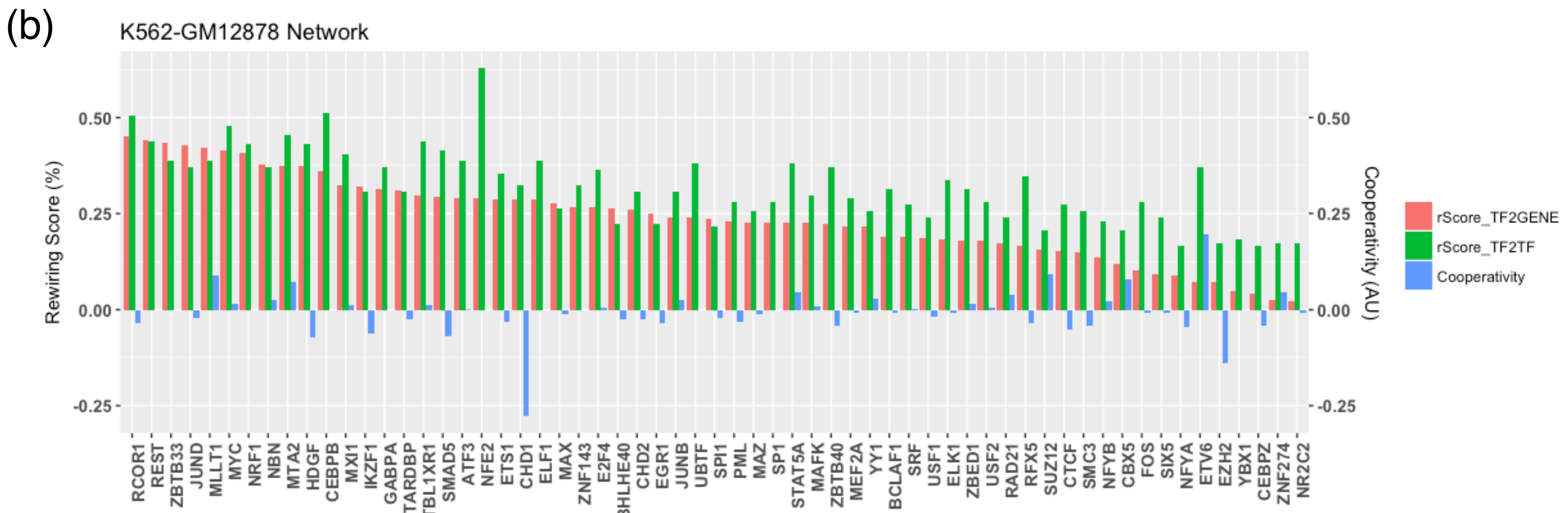
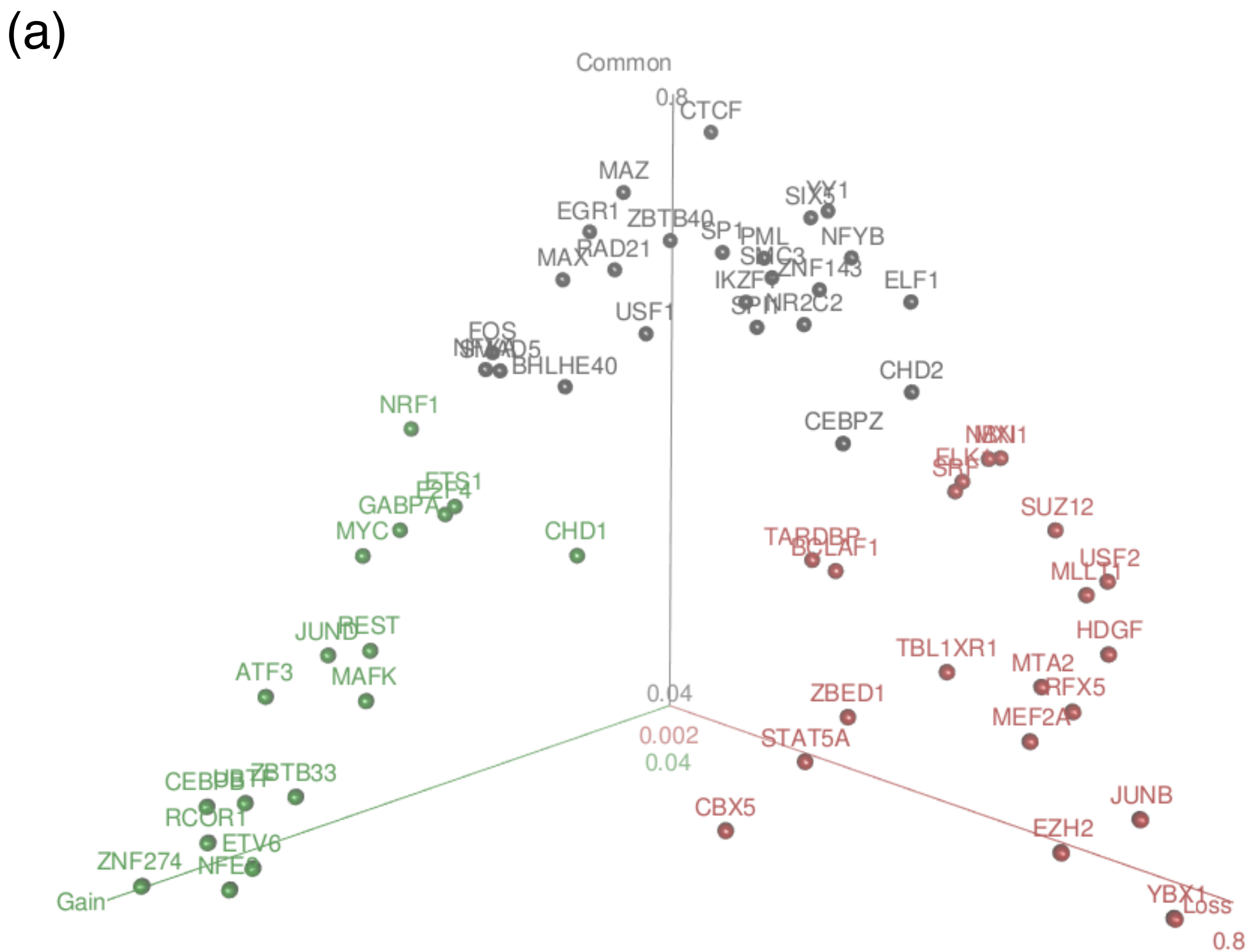
Gainer

Loser

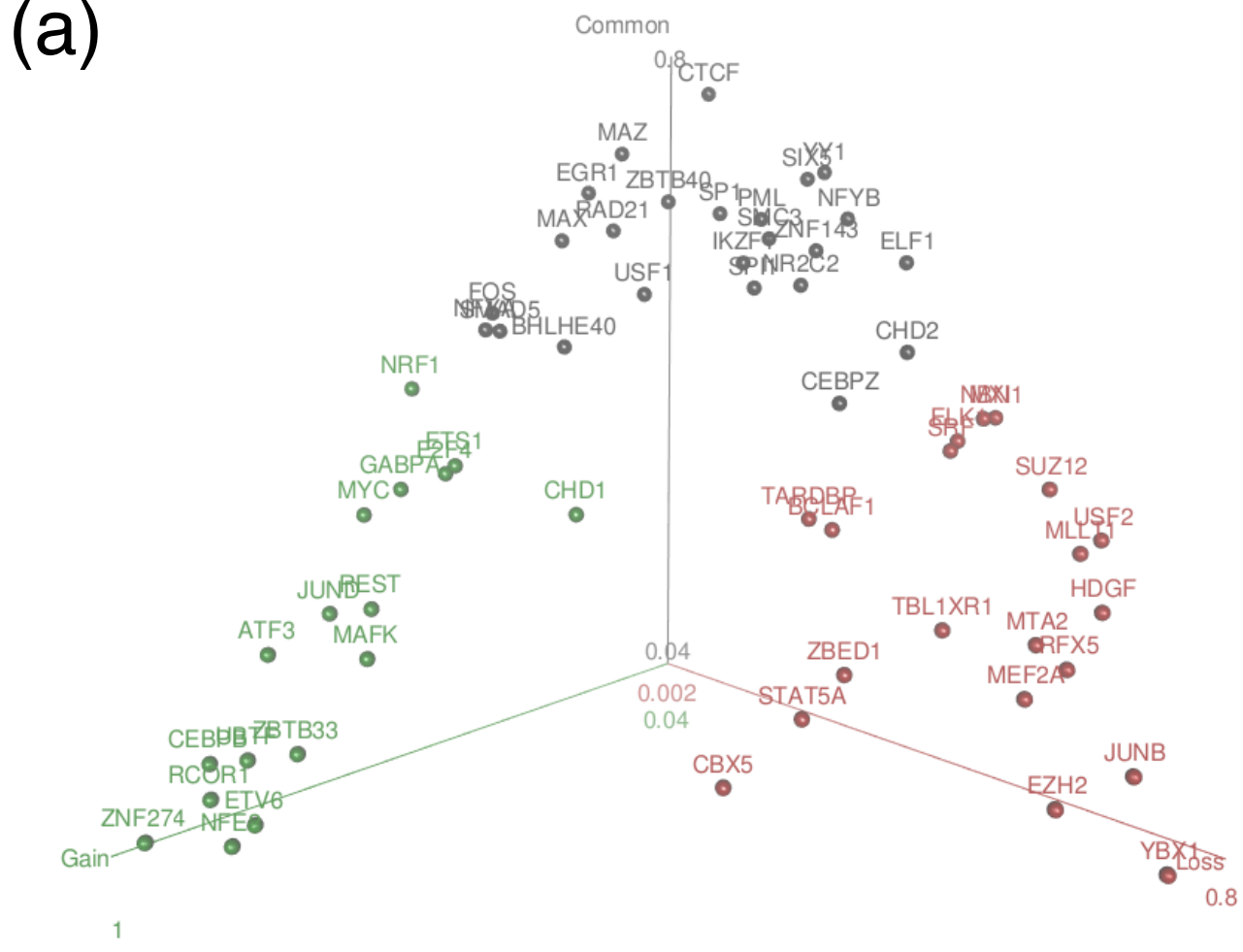




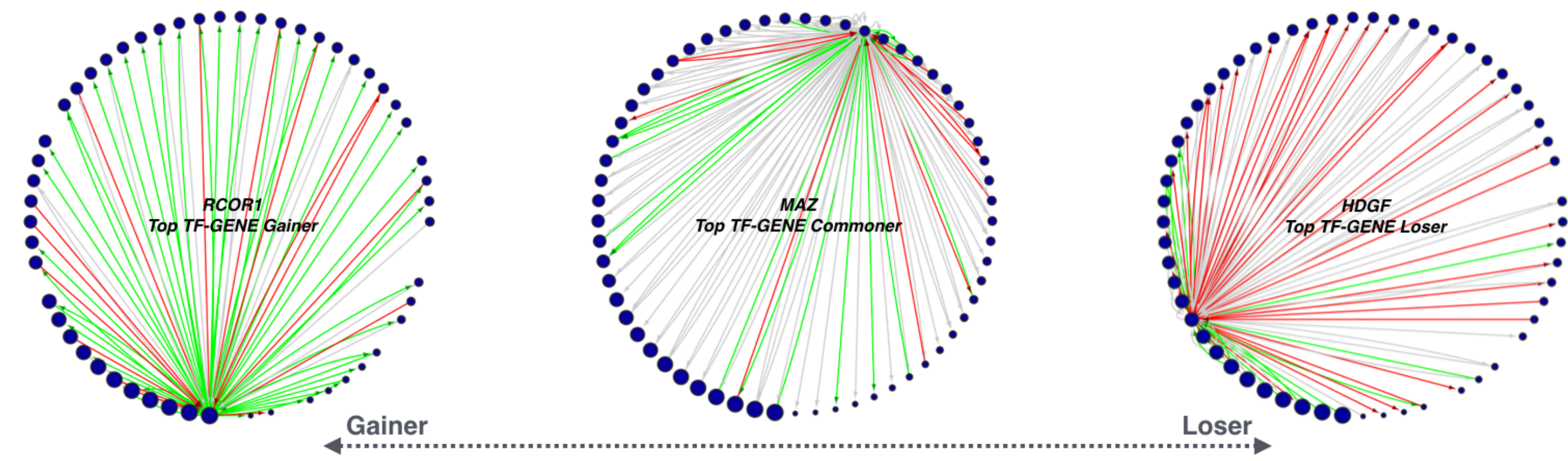




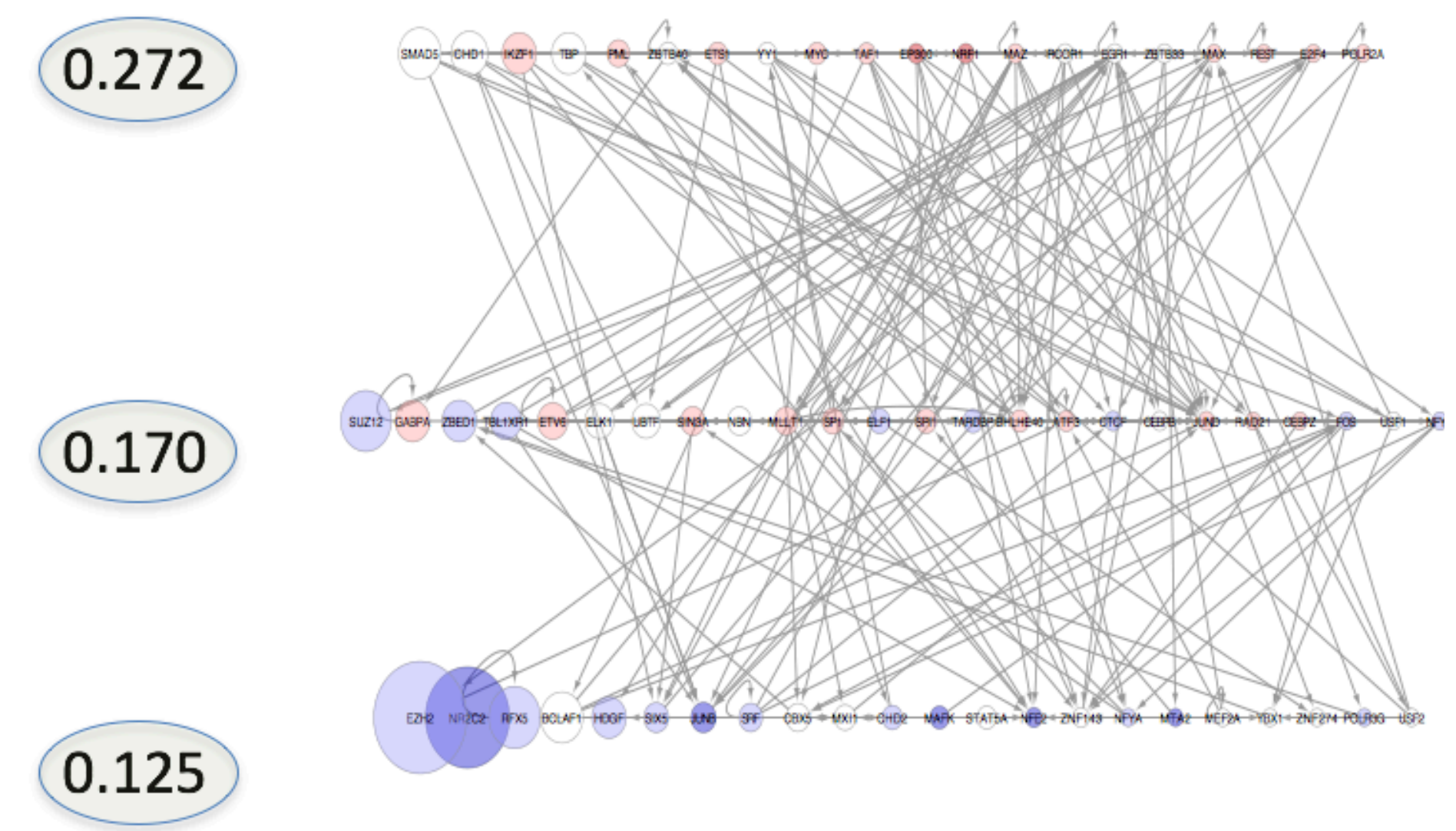
(a)



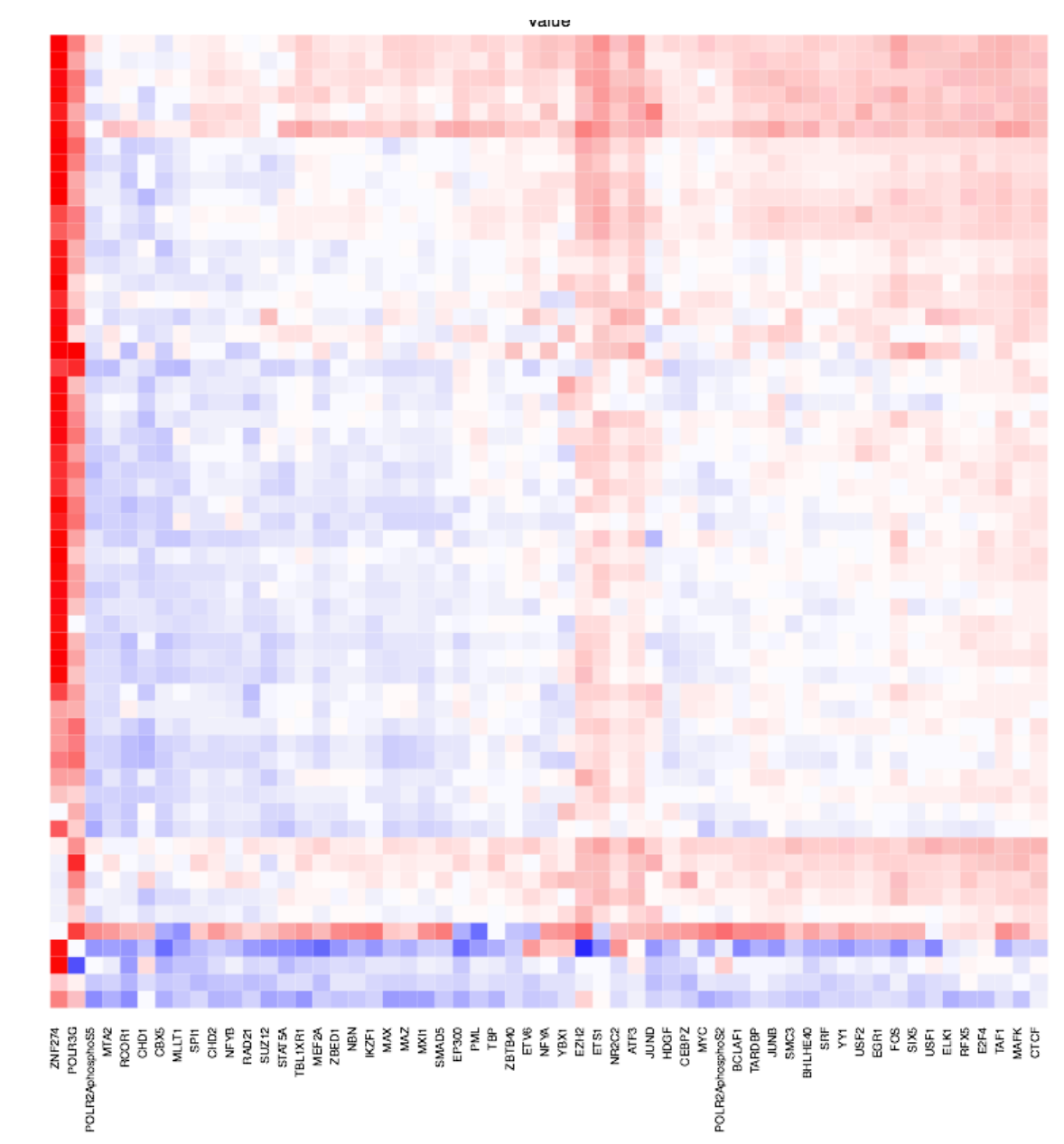
(b)



(c)



(d)

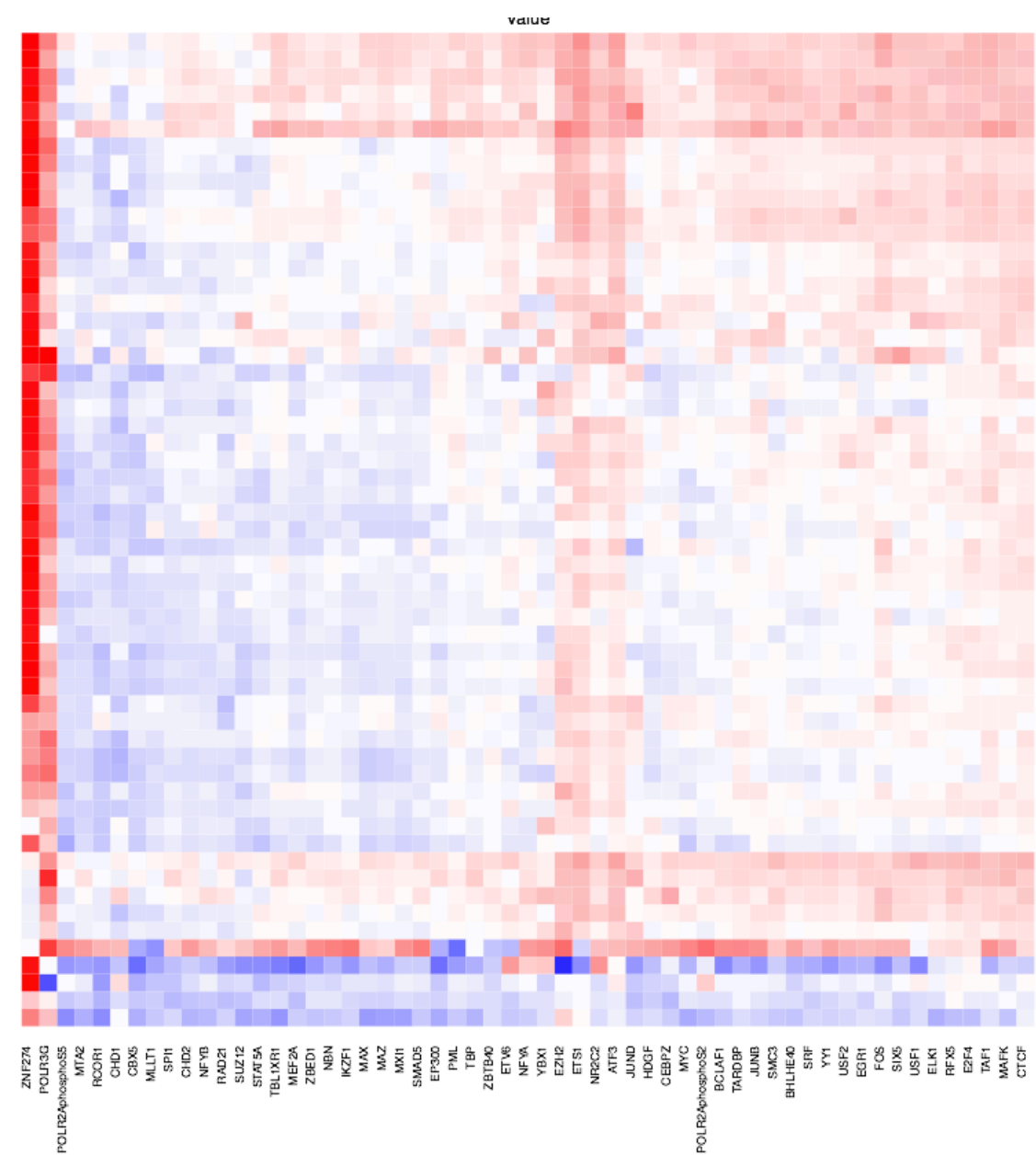


MTA2  
STAT5A  
MYC  
RCOR1  
SUZ12  
POLR2AphosphoS5  
SMI1  
NBN  
ZBED1  
TBL1XR1  
MAX  
MAZ  
IKZF1  
SPI1  
MEF2A  
RAD21  
JUNO  
FOS  
YBX1  
NRXG2  
SIX5  
ATF3  
MAFK  
NFYA  
NFYB  
POLR2AphosphoS2  
SMAD3  
CHD2  
CEBPZ  
JUNB  
SRF  
BHLHE40  
USP2  
EGRI1  
YY1  
TARDBP  
BCLAF1  
TAF1  
SMC3  
CTCF  
E2F4  
ELK1  
RFX5  
PML  
TBP  
ZBTB40  
HDGF  
CBX5  
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MLL1  
EP300  
USP1  
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POLR3G  
EZH2  
ETS1  
CHD1

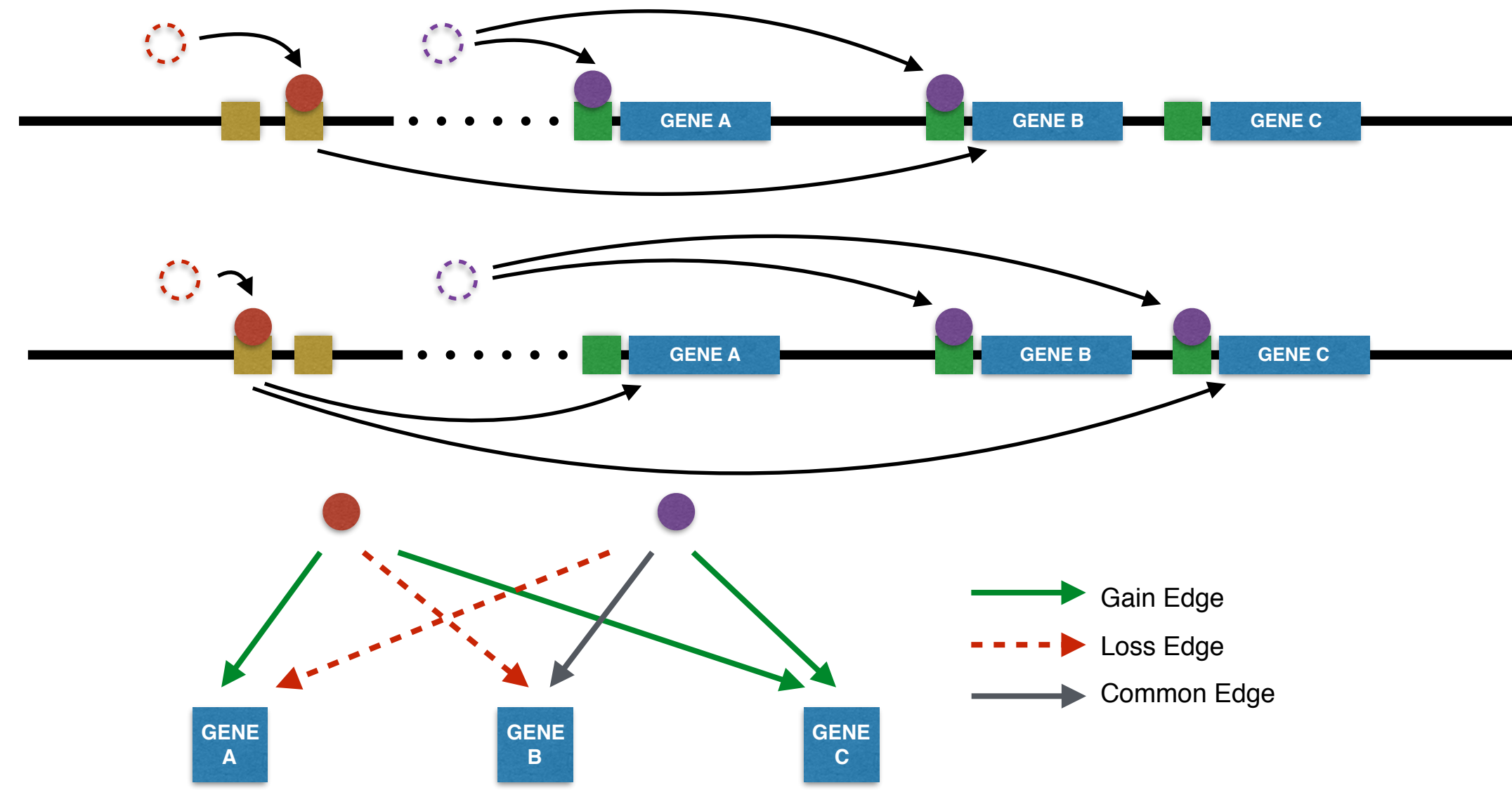
ZNF274  
POLR3G  
POLR2AphosphoS5  
MAZ  
MYC  
SMI1  
ODI1  
CBX5  
MLL1  
SPI1  
NFYB  
RAD21  
SUZ12  
TBL1XR1  
TAF1  
MEF2A  
NBN  
NFX1  
MAX  
MOT1  
SMAD3  
EZH2  
EP300  
PML  
TBP  
ZBTB40  
HDGF  
MYC  
YBX1  
E2F4  
ETS1  
JUNO  
HDGF  
CEBPZ  
POLR2AphosphoS2  
BCLAF1  
TARDBP  
JUNB  
NBN  
BHLHE40  
SRF  
YY1  
EGRI1  
EDR1  
FOS  
SIX5  
USP1  
NFYB  
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E2F4  
TAF1  
MAFK  
CTCF



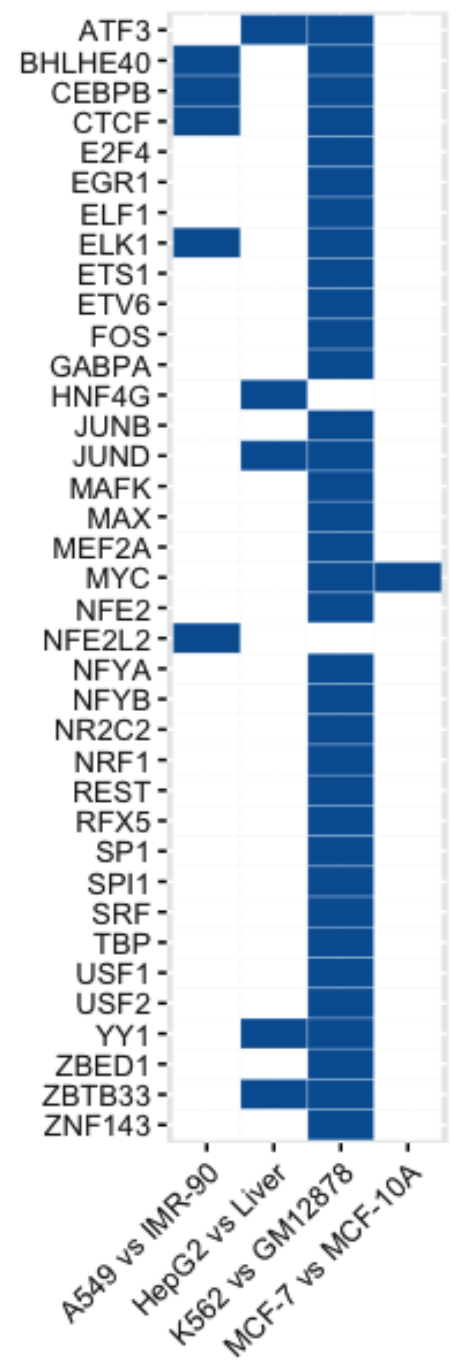
(a)



(b)



(c)

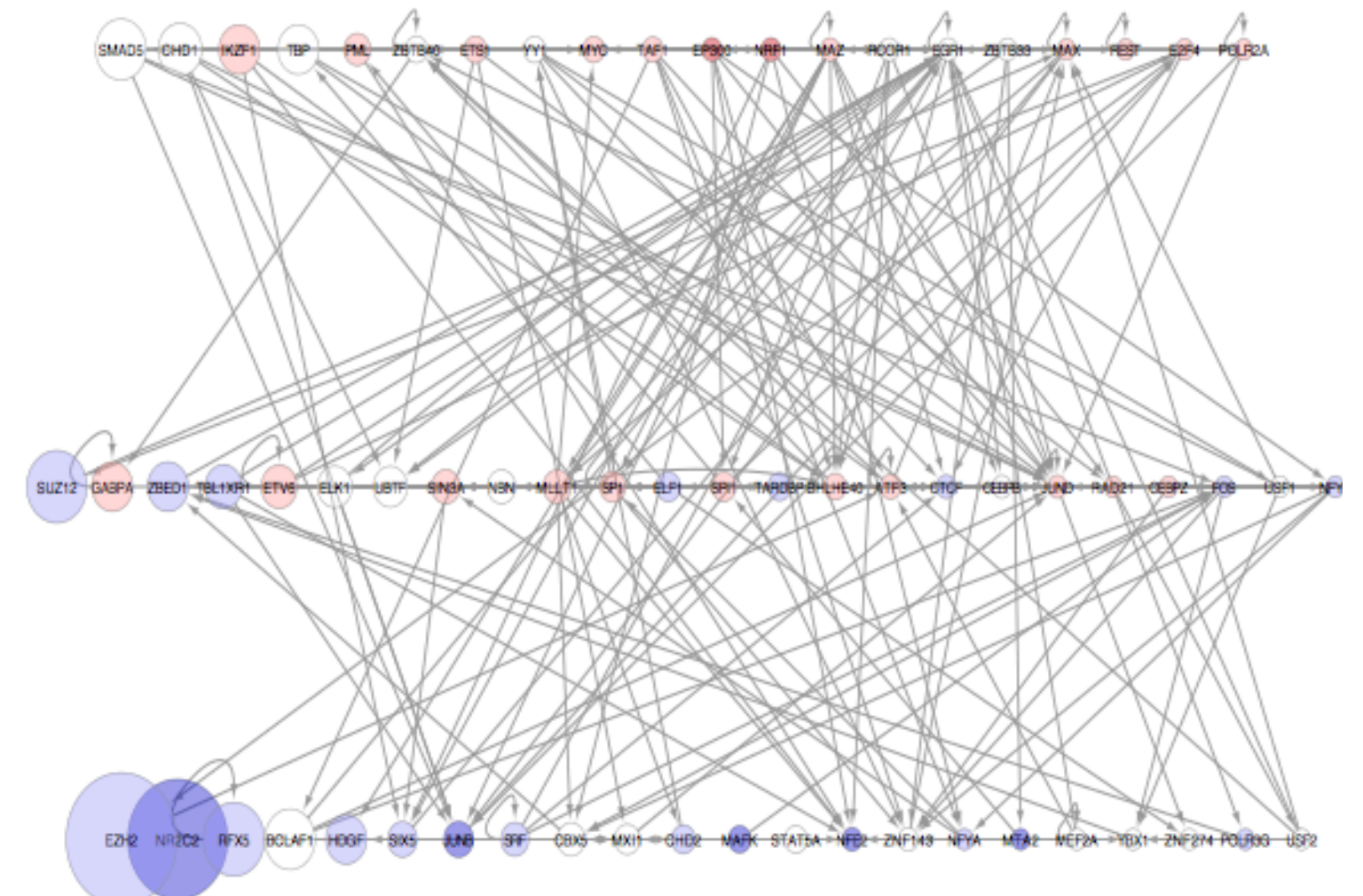


(d)

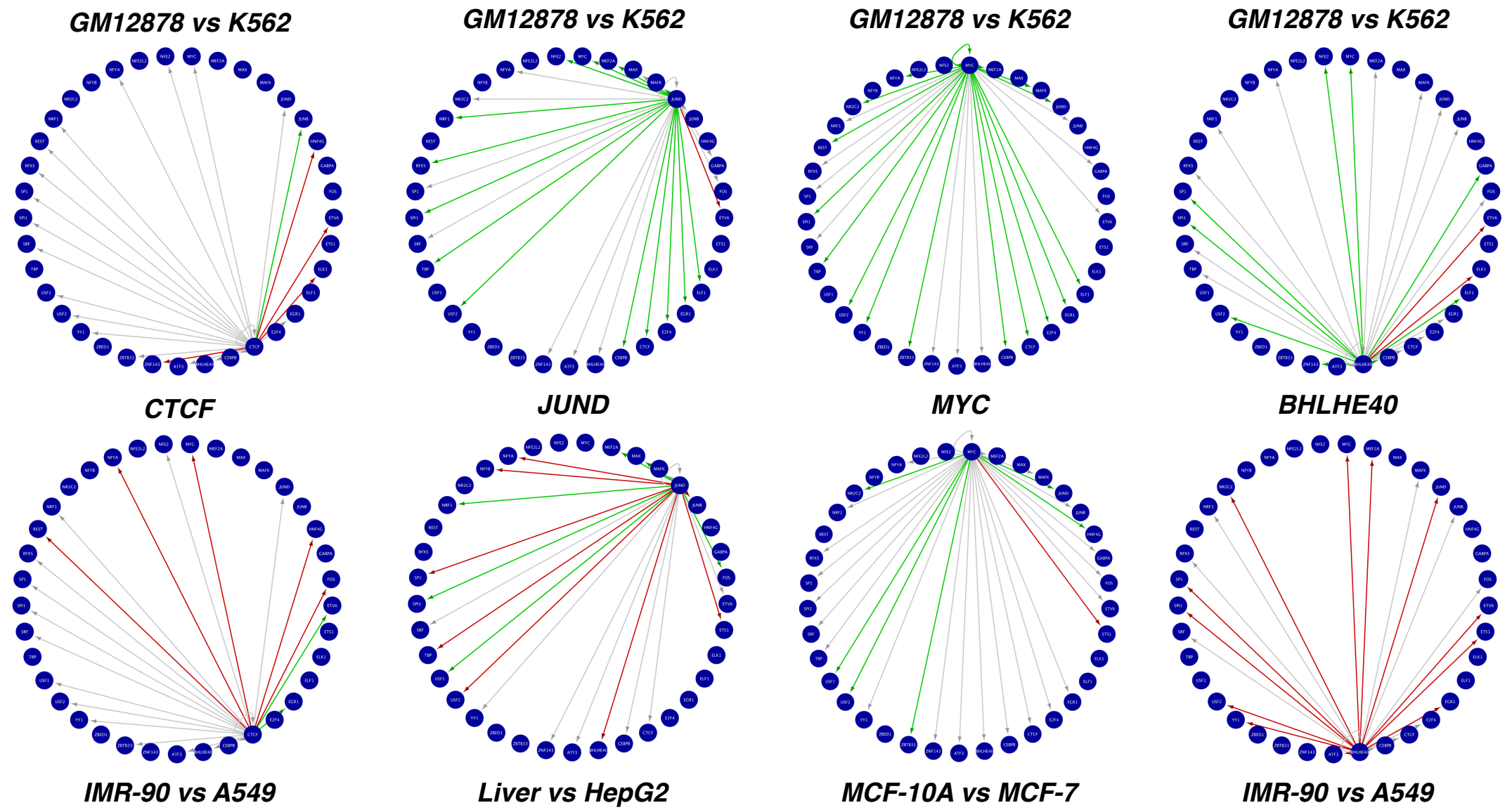
0.272

0.170

0.125

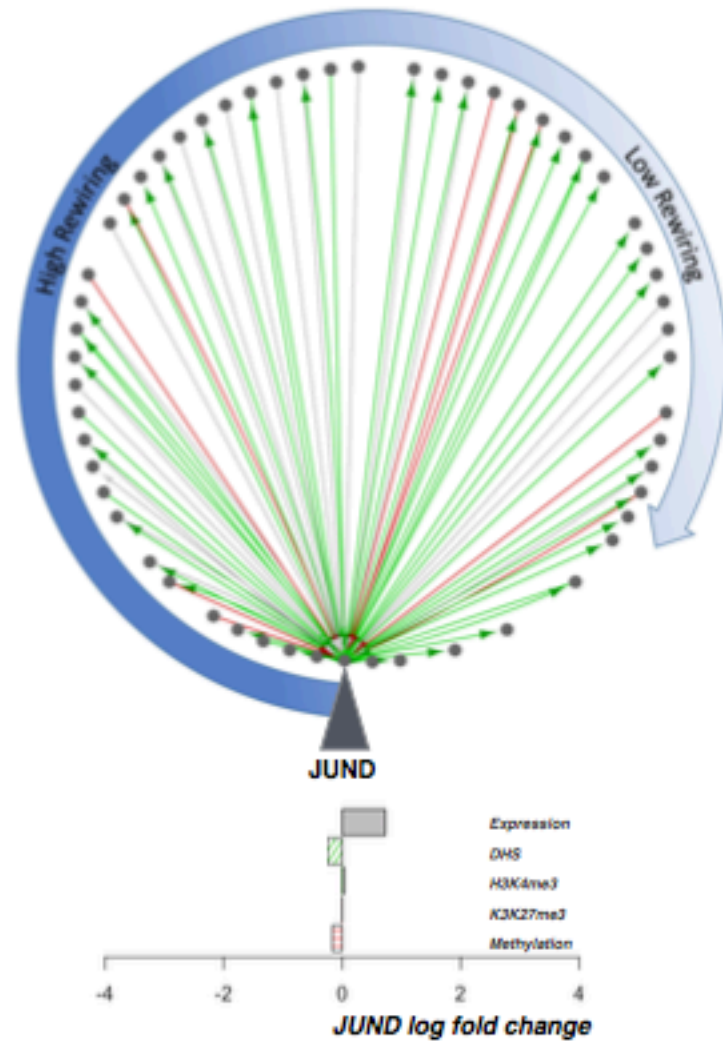


(e)

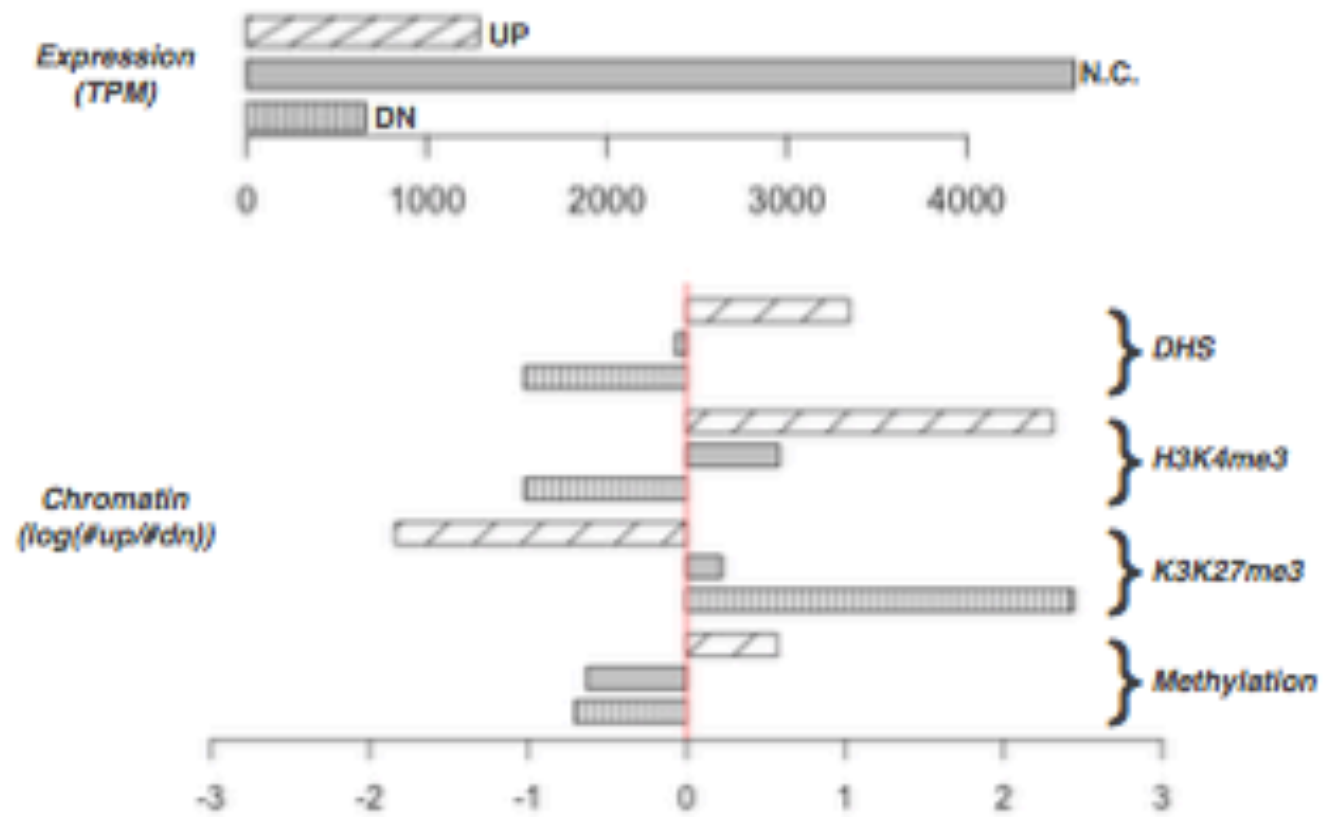


Overall Gene Target (n=15,189)

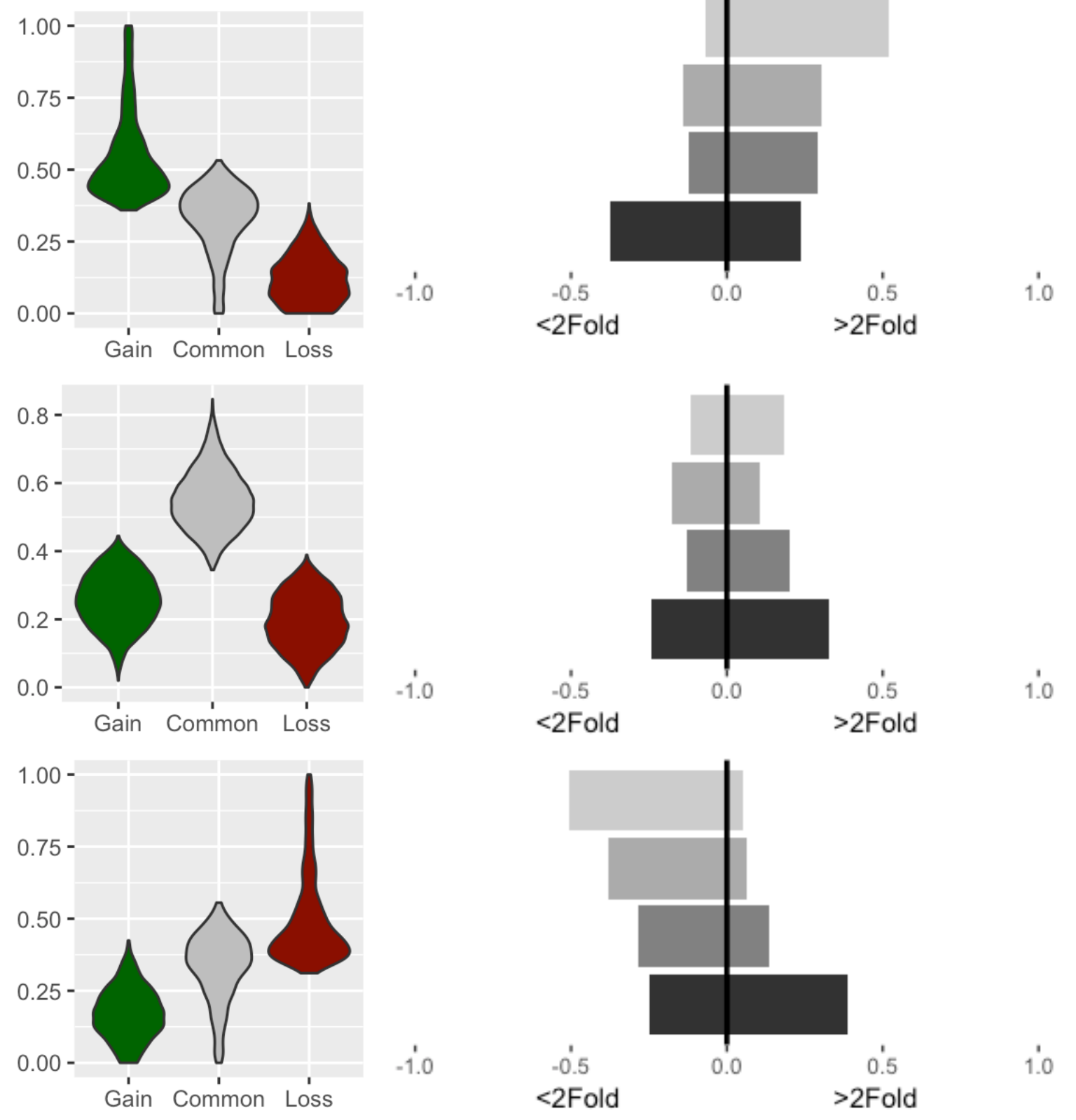
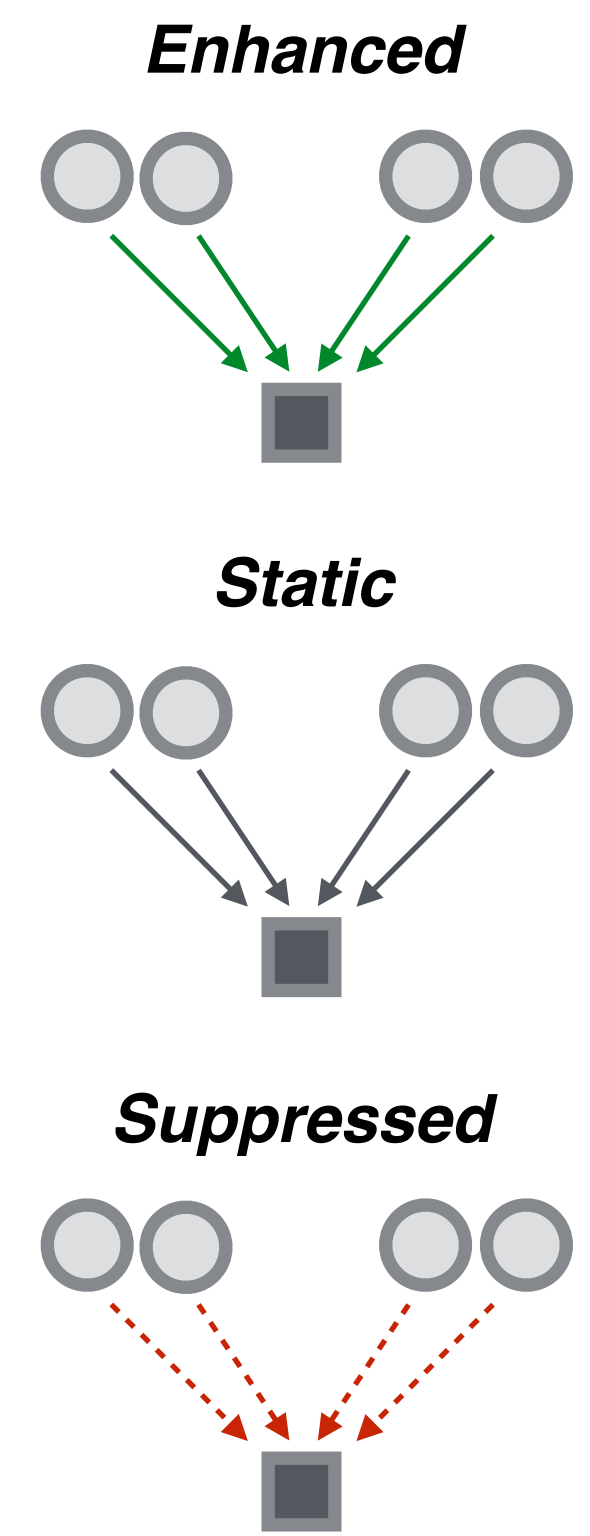
Expression (TPM)	UP			NC			DN		
n	2442			10294			2453		
%	16.1%			67.8%			16.1%		
<b>DHS (TSS Cov) active</b>	<b>UP</b>	<b>NC</b>	<b>DN</b>	<b>UP</b>	<b>NC</b>	<b>DN</b>	<b>UP</b>	<b>NC</b>	<b>DN</b>
n	622	1622	198	1280	7723	1291	108	1430	915
%	25.5%	66.4%	8.1%	12.4%	75.0%	12.5%	4.4%	58.3%	37.3%
<b>H3K4me3 (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%		



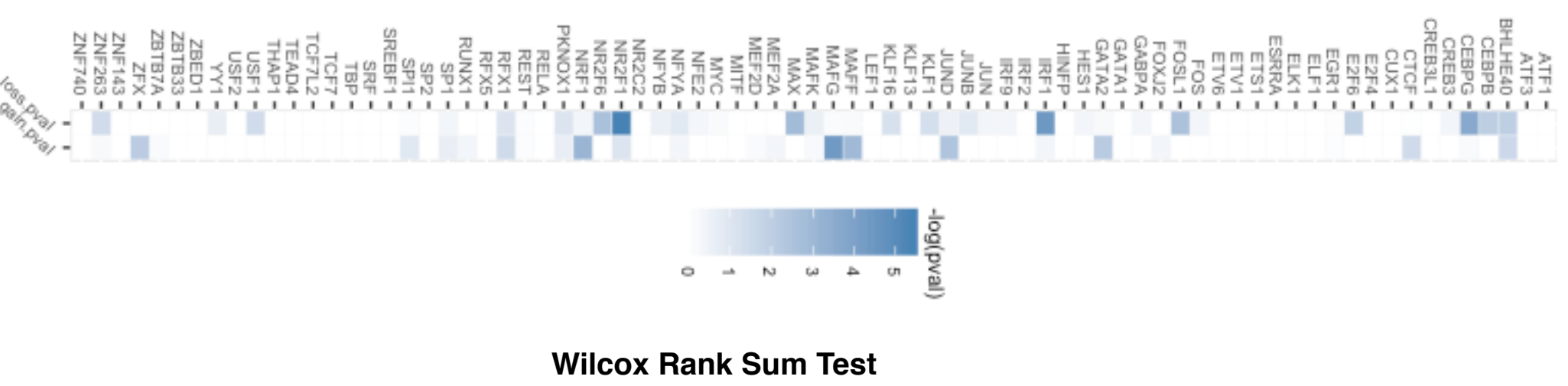
JUND Gained Targets



(a)

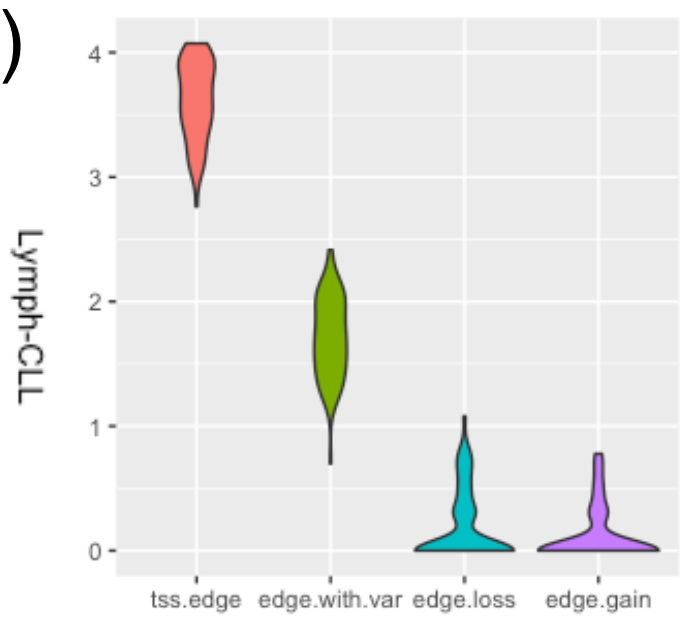


(b)

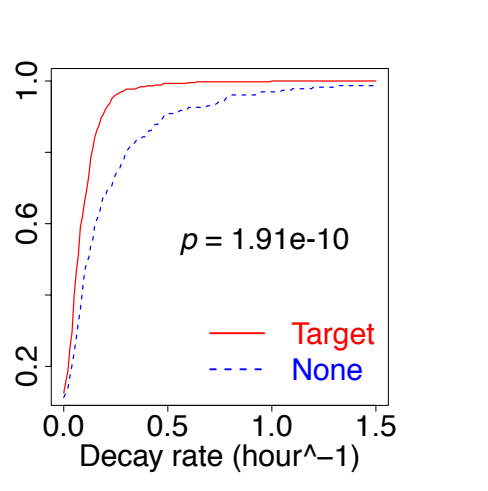
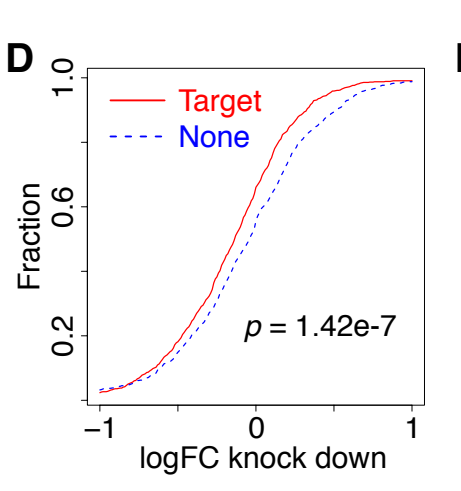
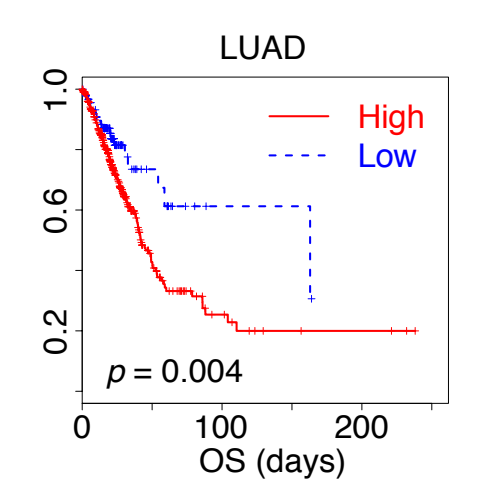
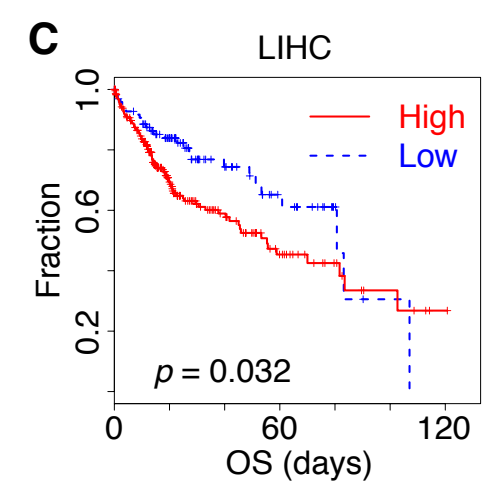
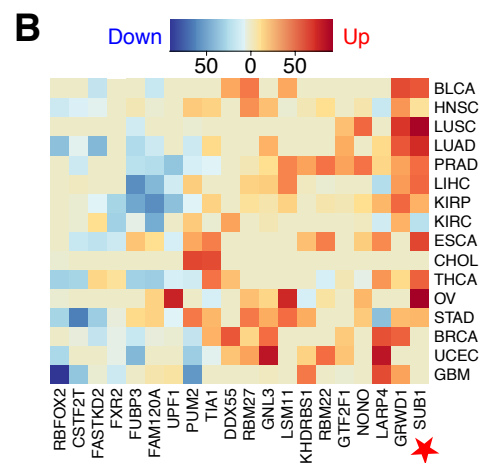
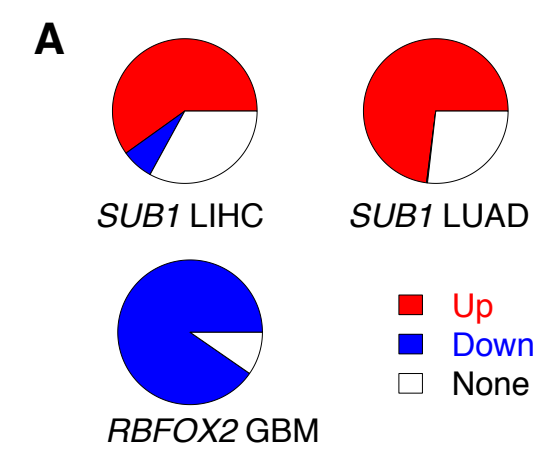
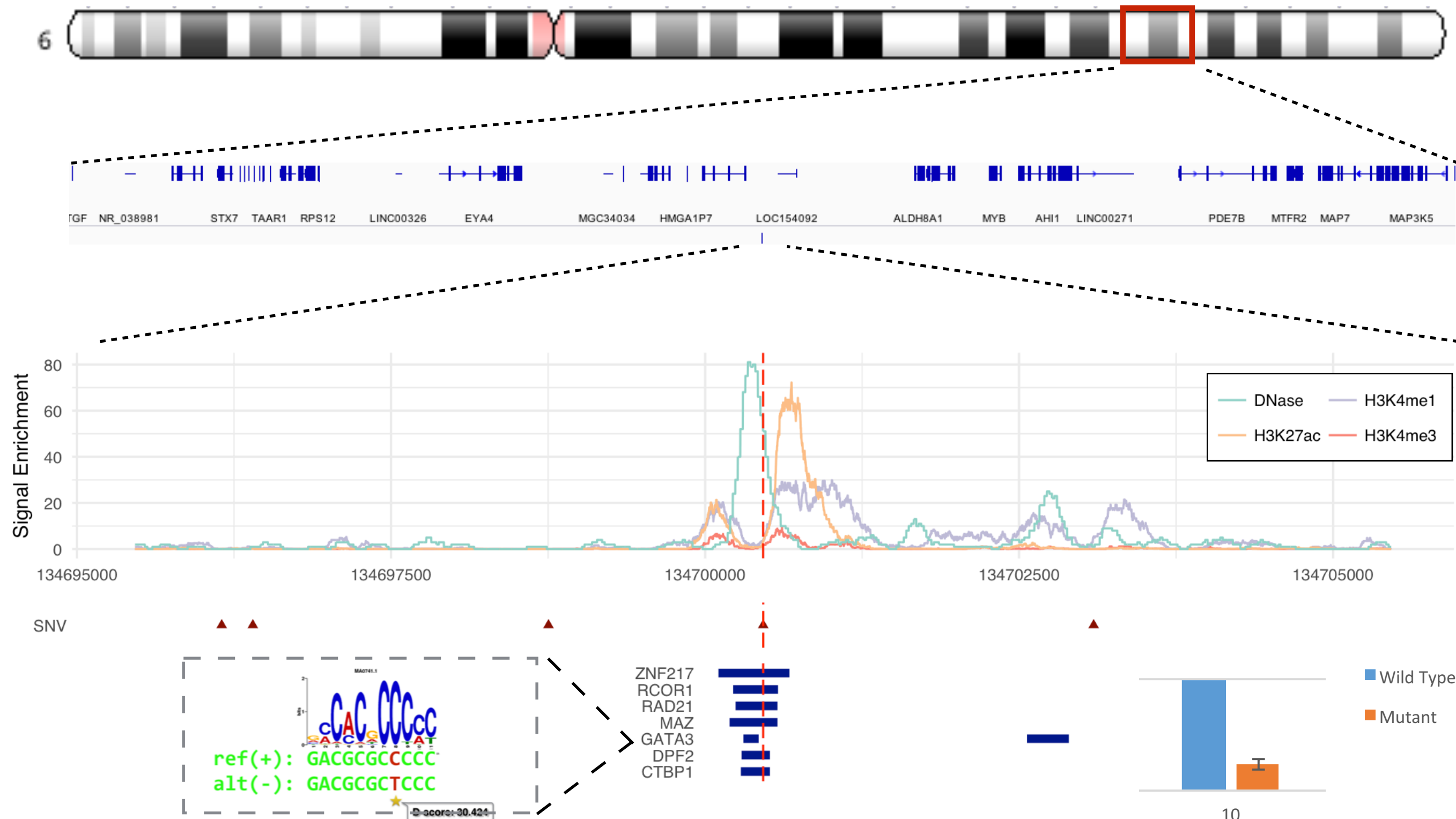


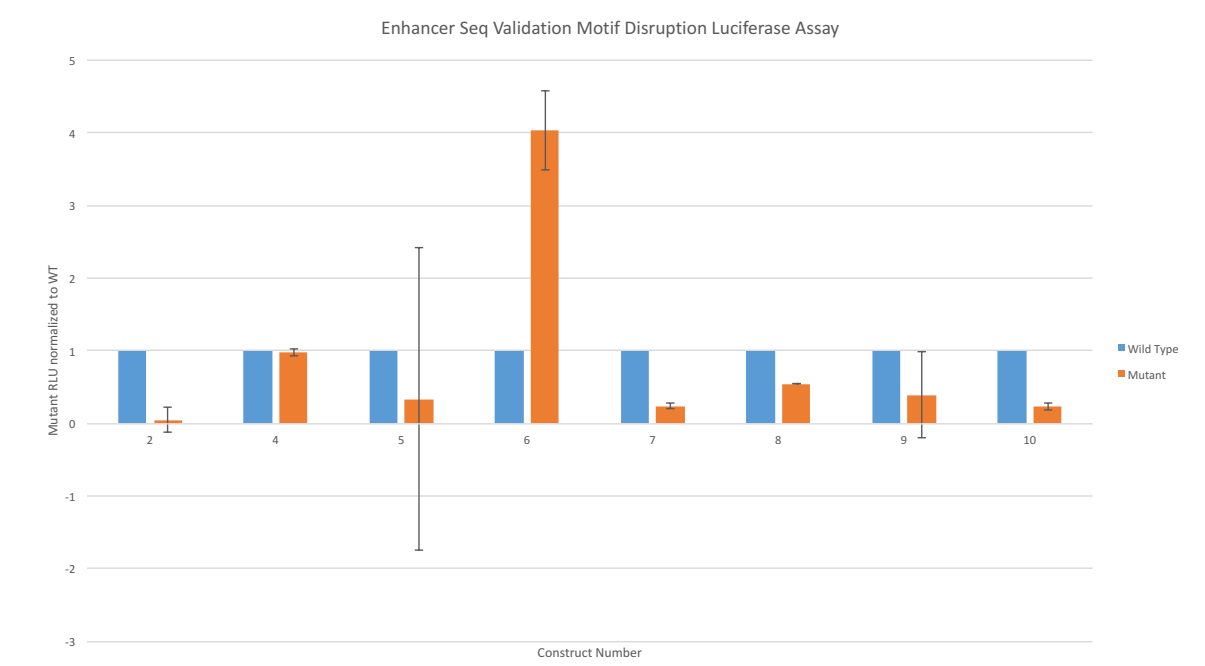
Wilcoxon Rank Sum Test

(c)

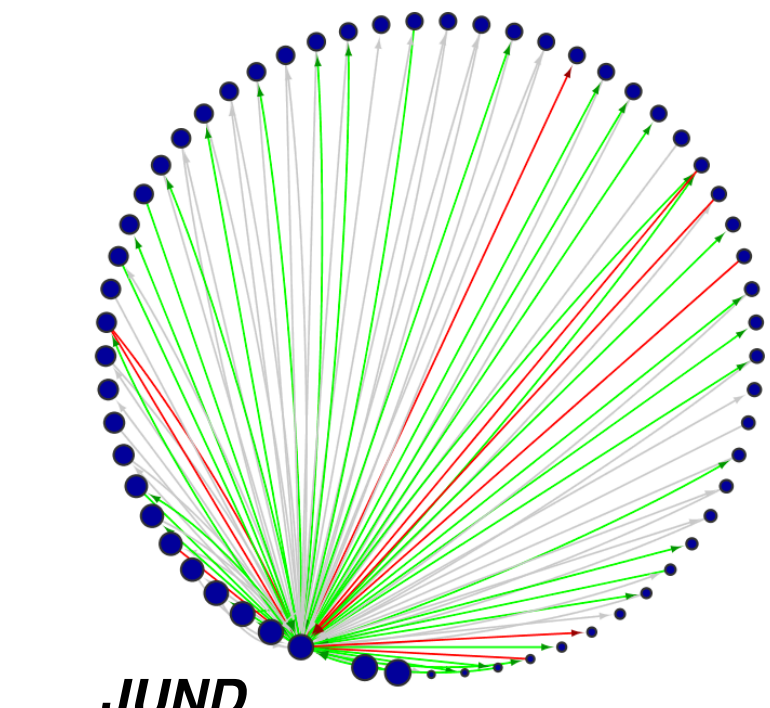
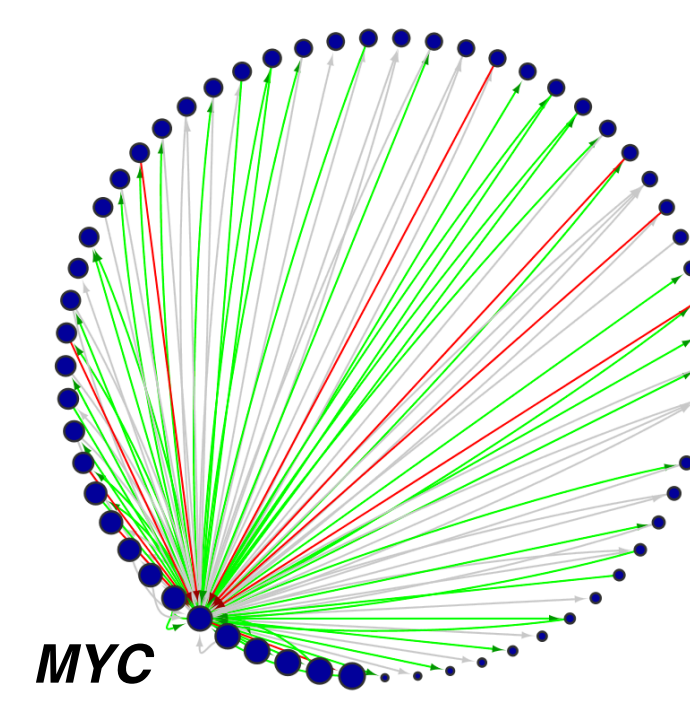
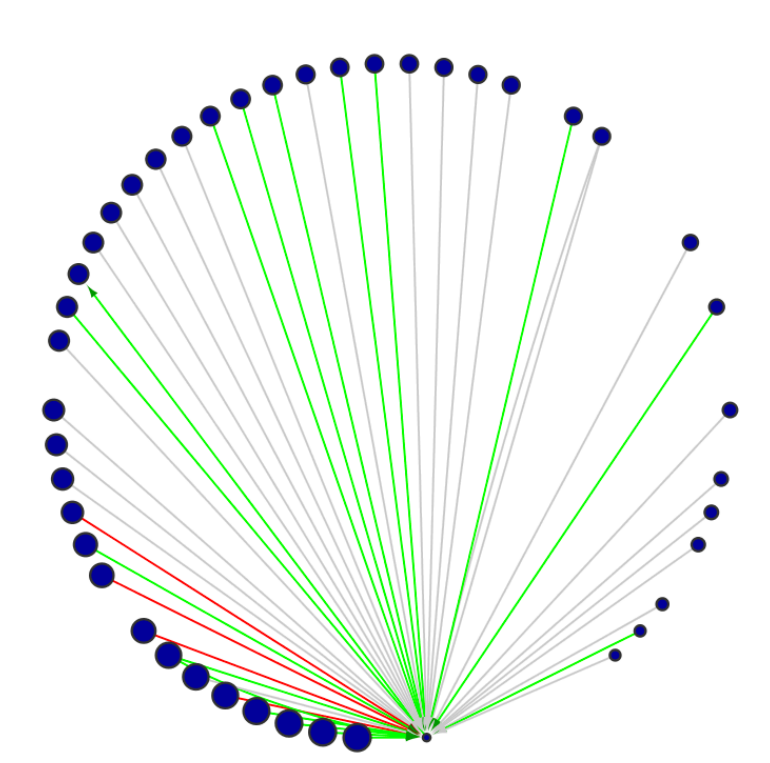
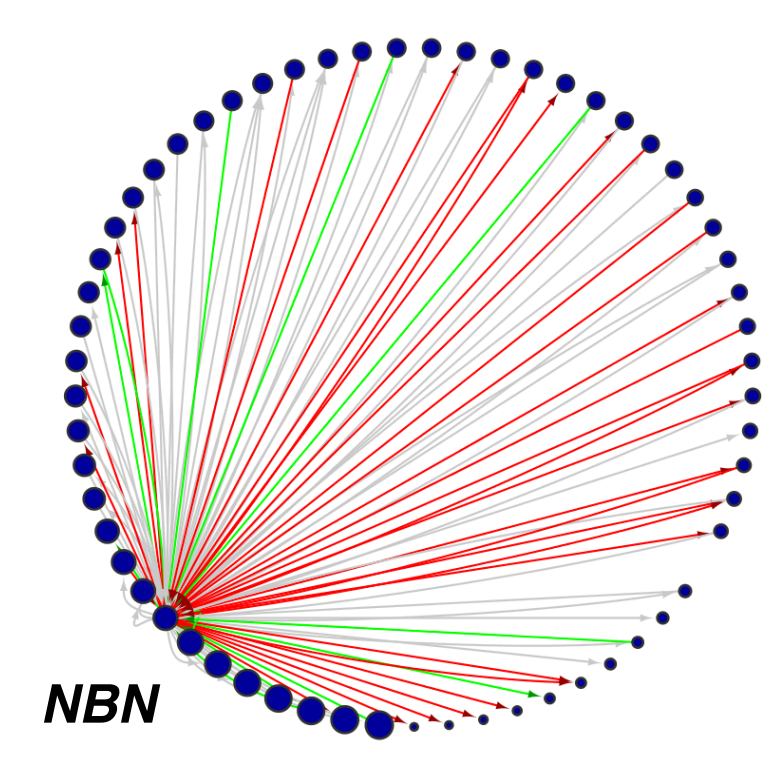
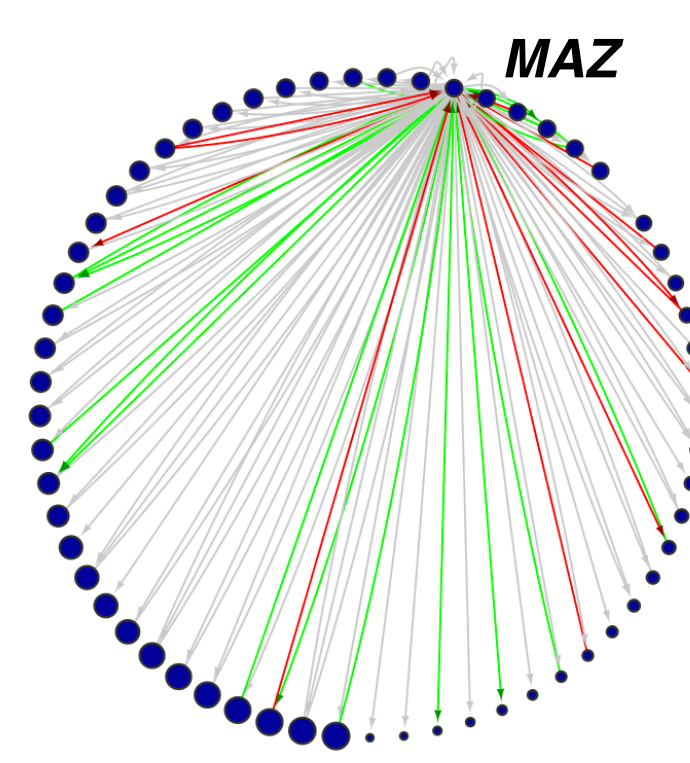


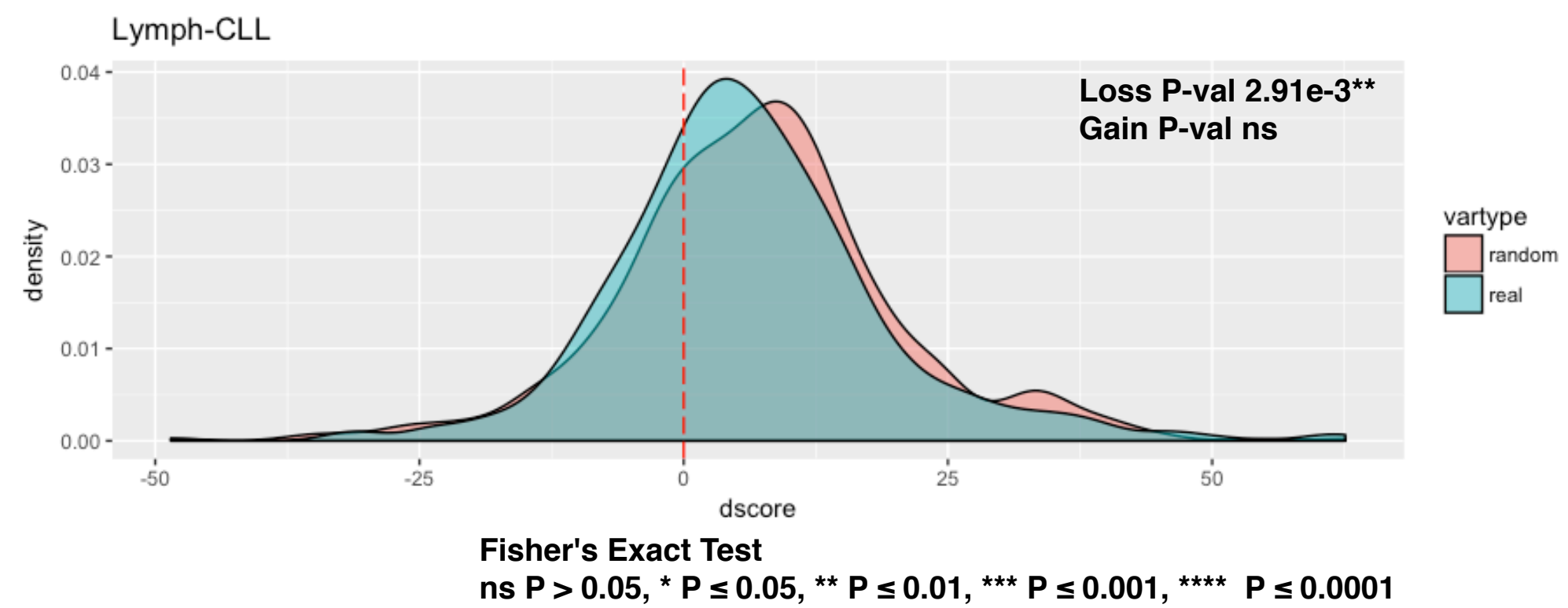
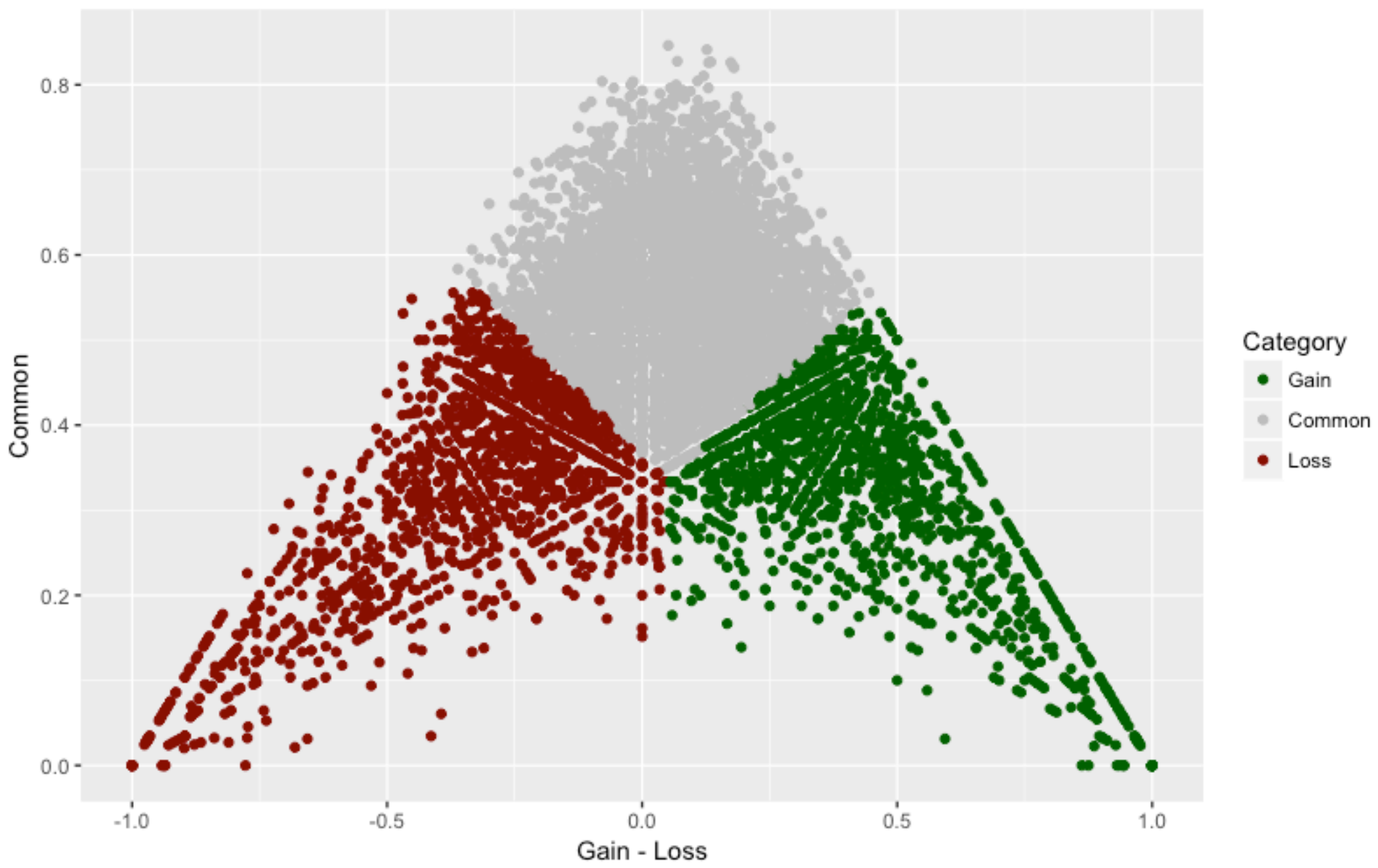
(a)



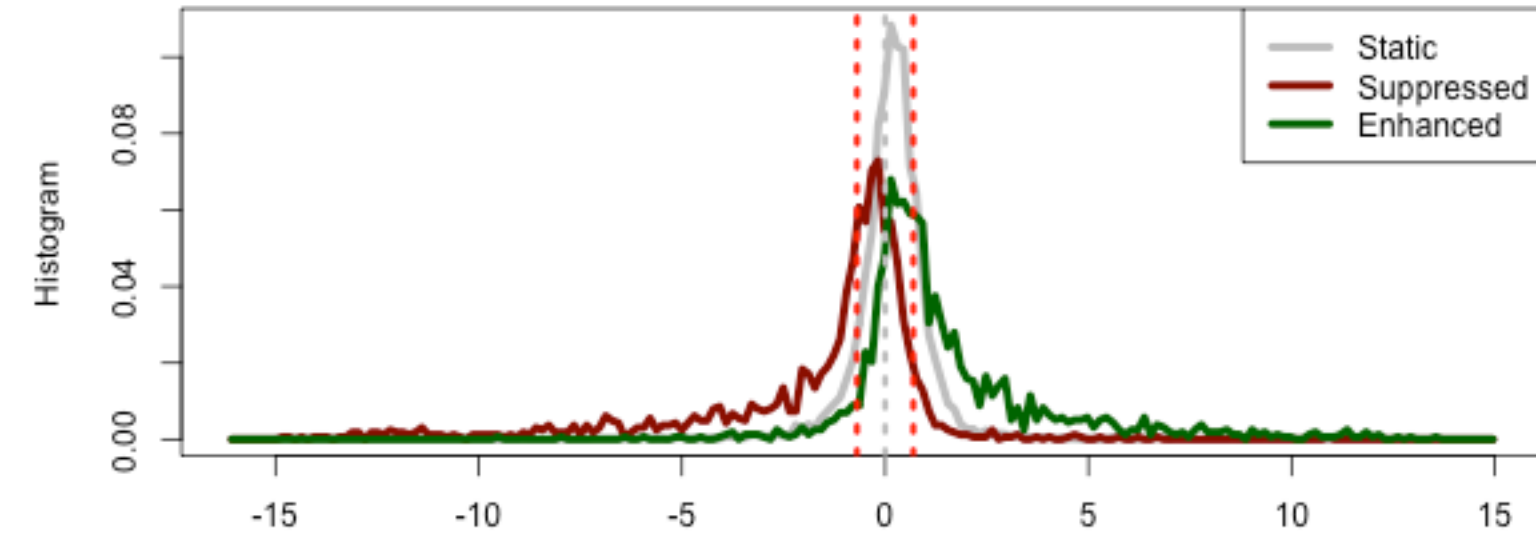


	Sample02	Sample04	Sample05	Sample06	Sample07	Sample08	Sample09	Sample10
chr	chr21	chr17	chr20	chr7	chr20	chr7	chr7	chr6
pos	27,541,982	38,474,408	43,971,343	1,598,567	58,563,412	150,759,483	5,596,005	134,700,462
ref	G	C	G	C	C	C	T	G
alt	A	G	C	T	T	G	G	T
D-score_min	20.361	16.910	3.665	15.746	7.217	13.959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

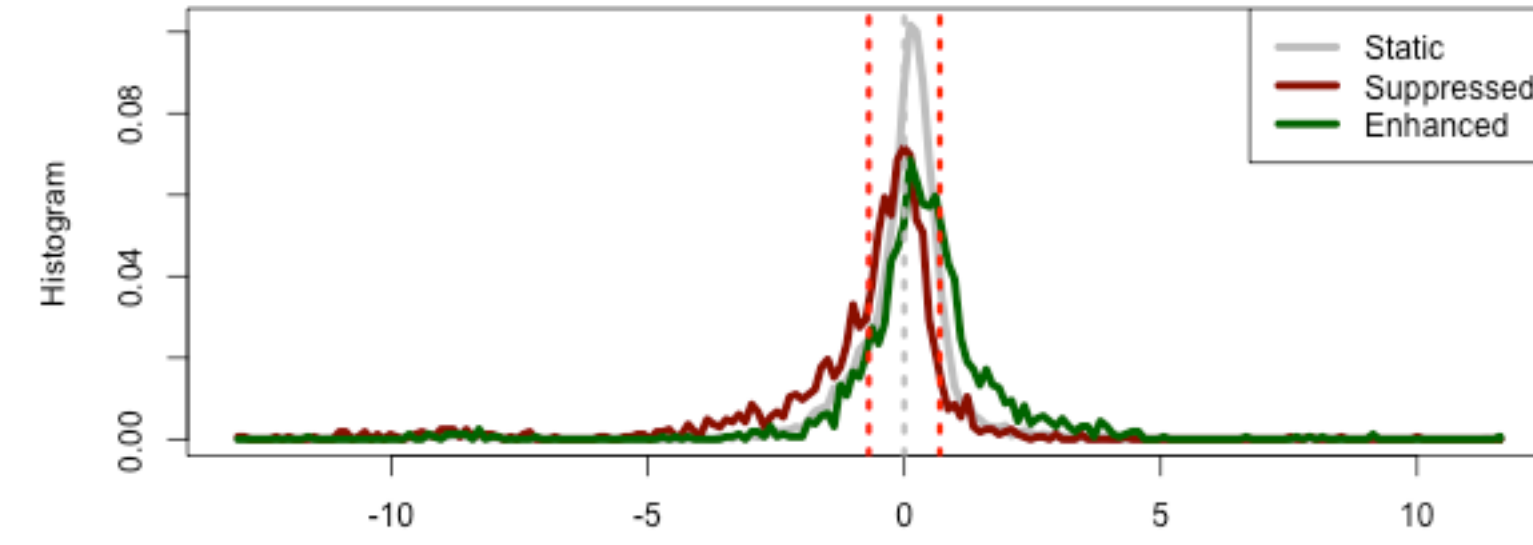




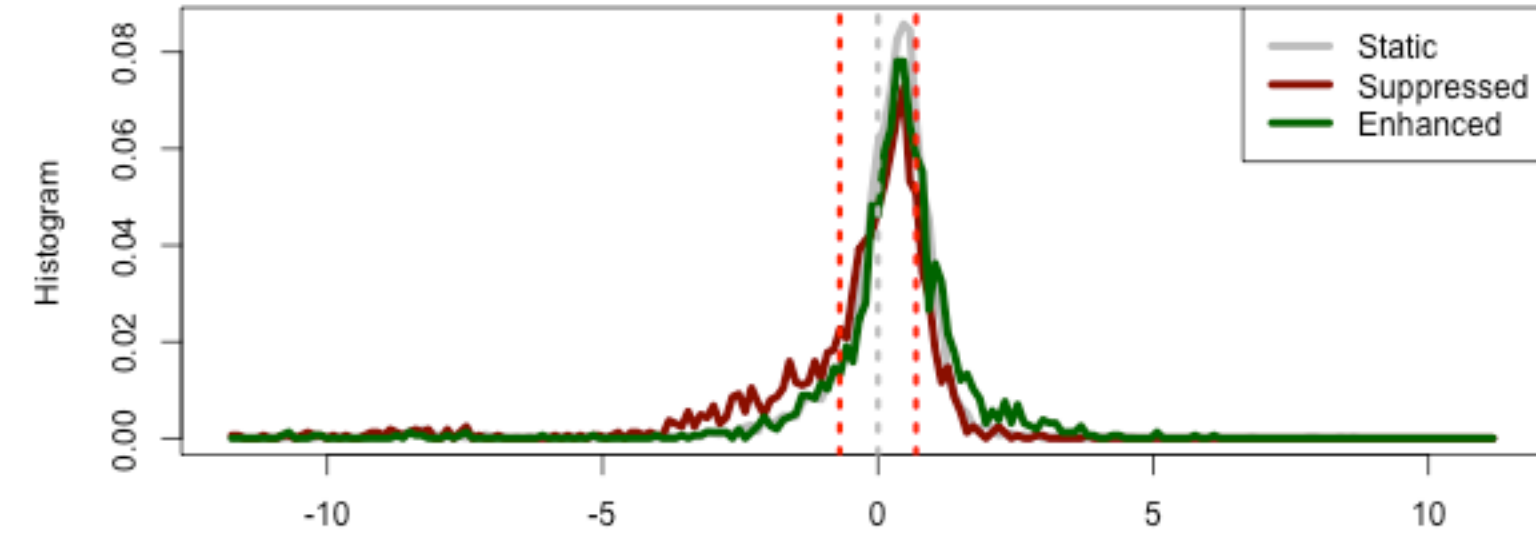
Expression(TPM) log(fc)



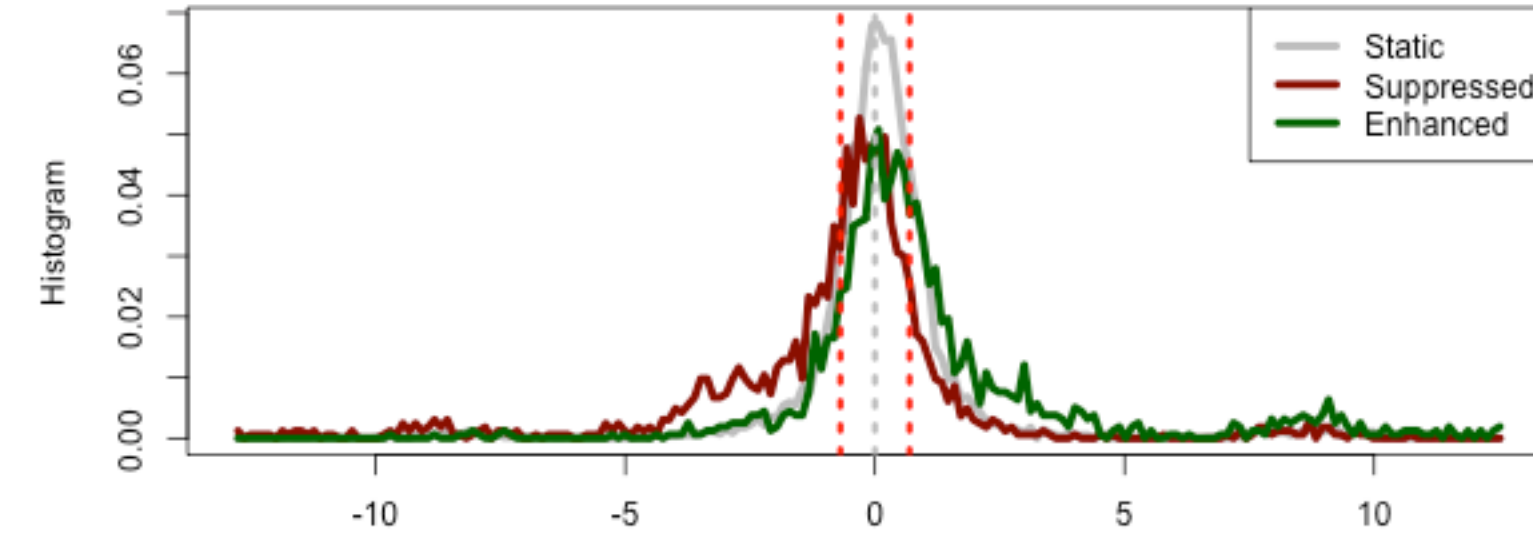
DNase I log(fc)



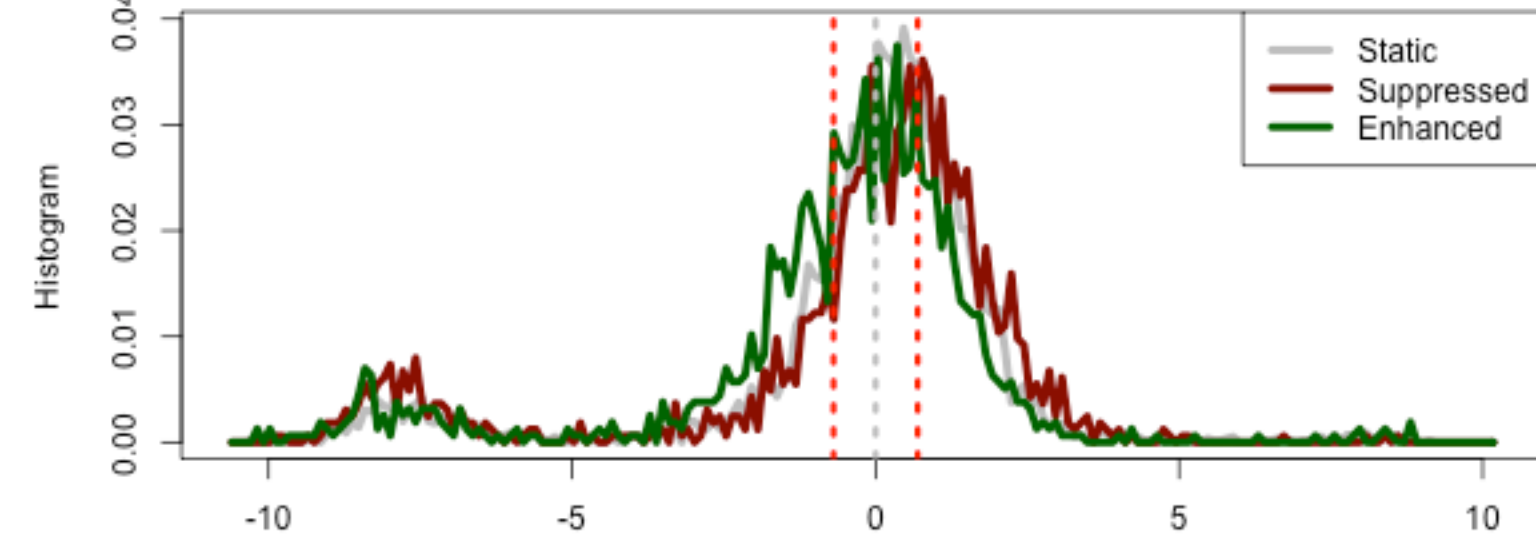
H3K4me3 log(fc)



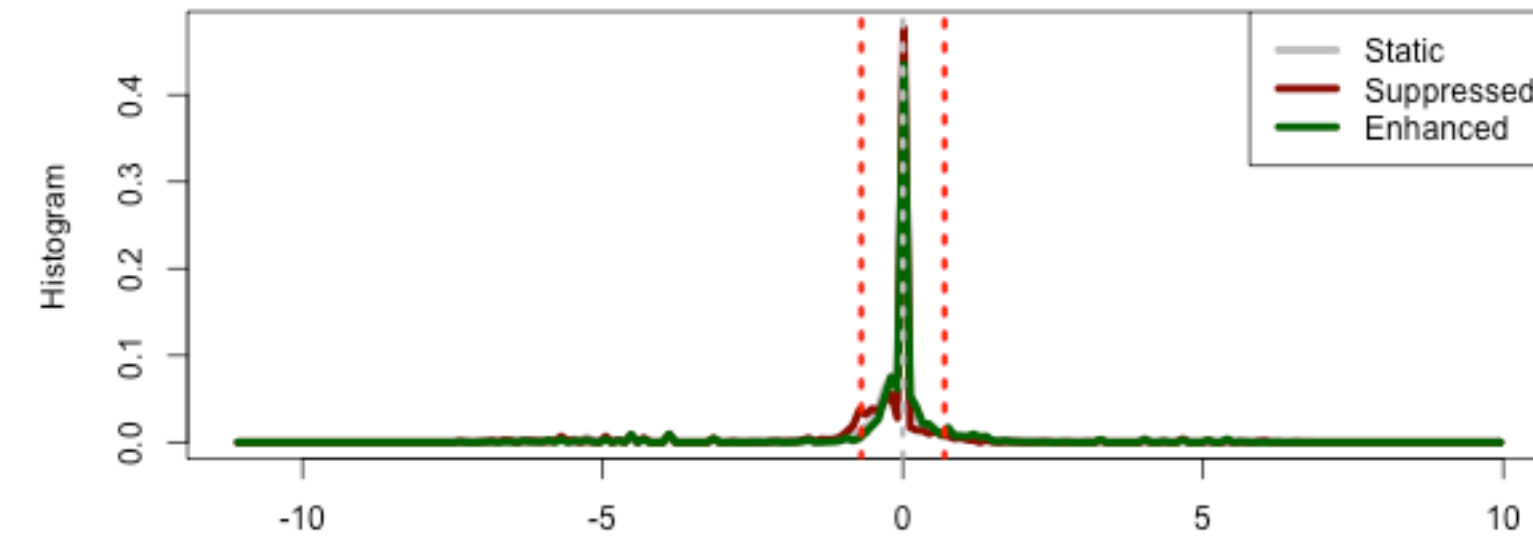
H3K27ac log(fc)



H3K27me3 log(fc)

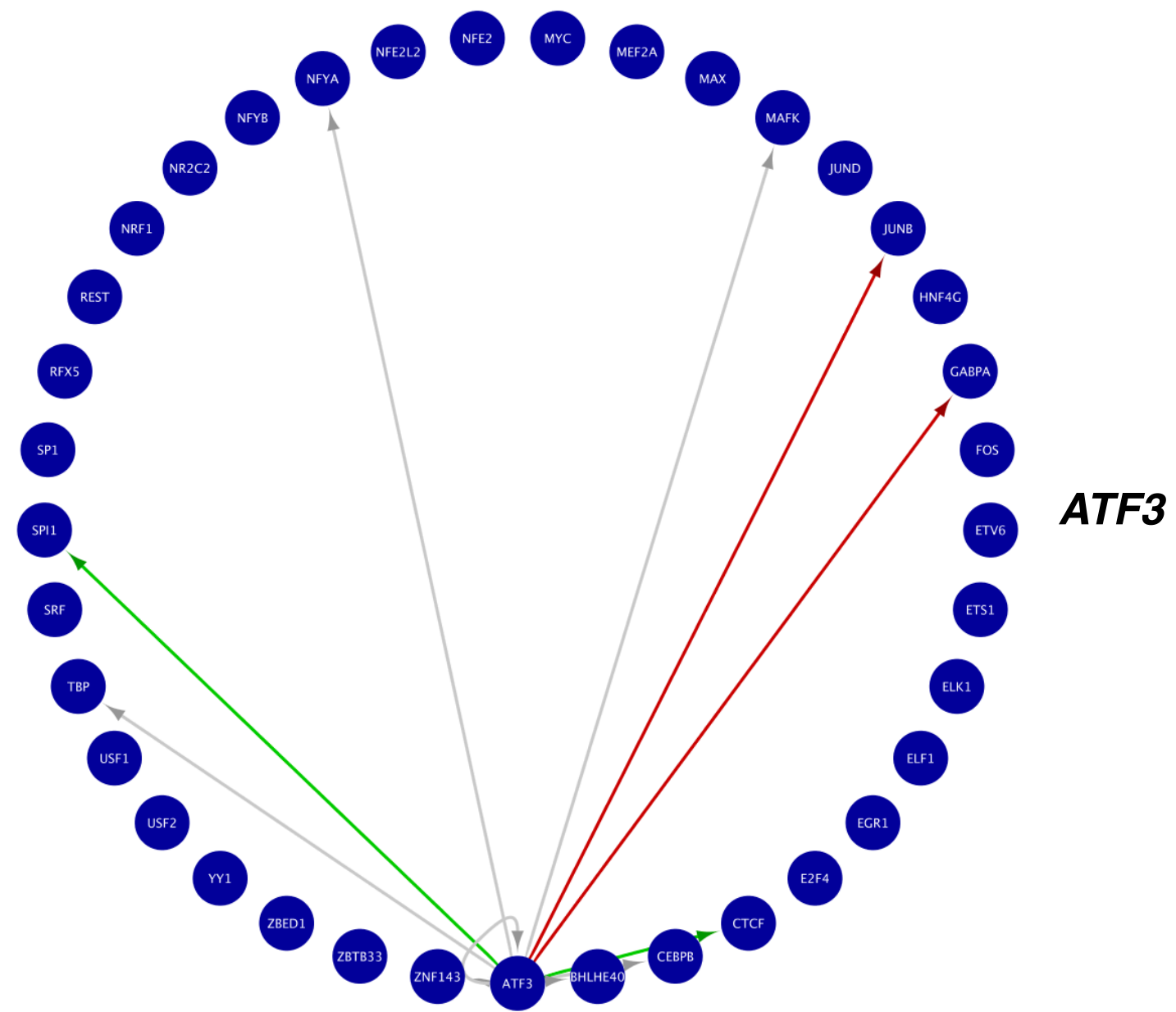
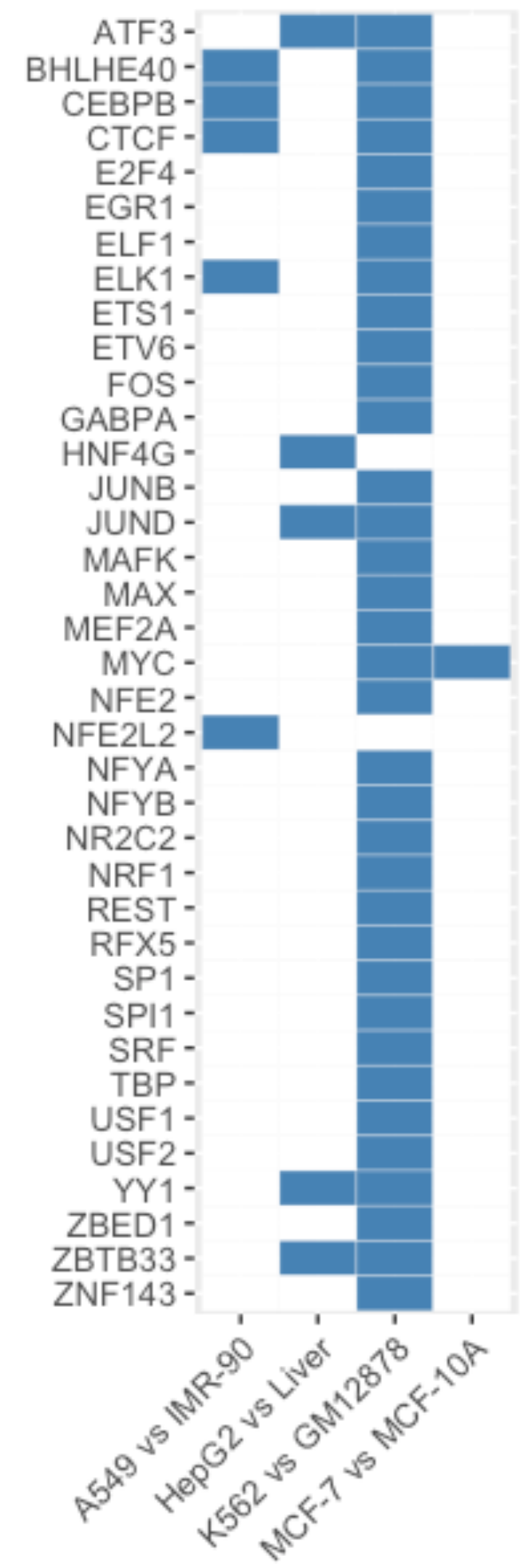


5mC log(fc)



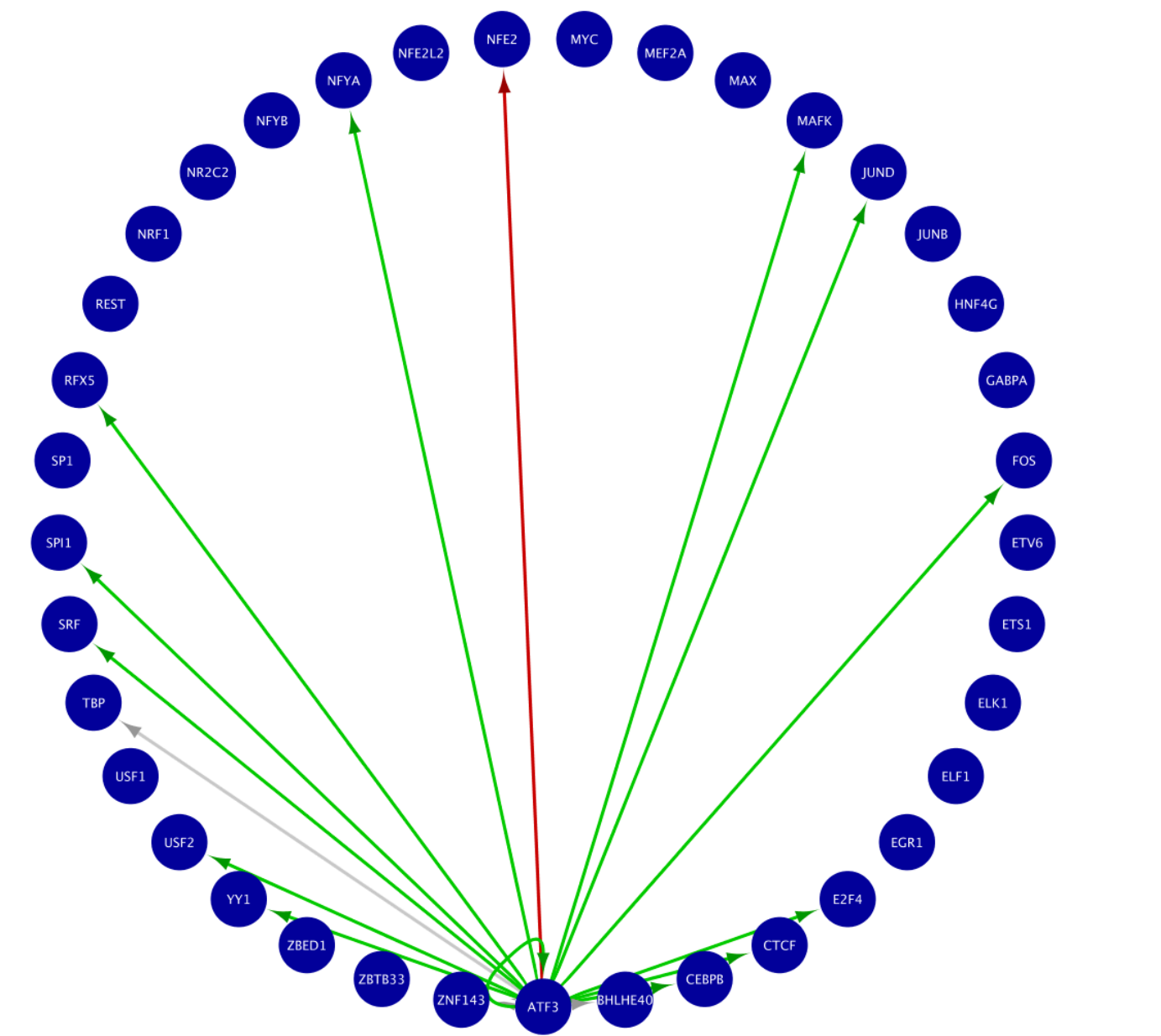


# Cross-Cancer TFSS Matrix

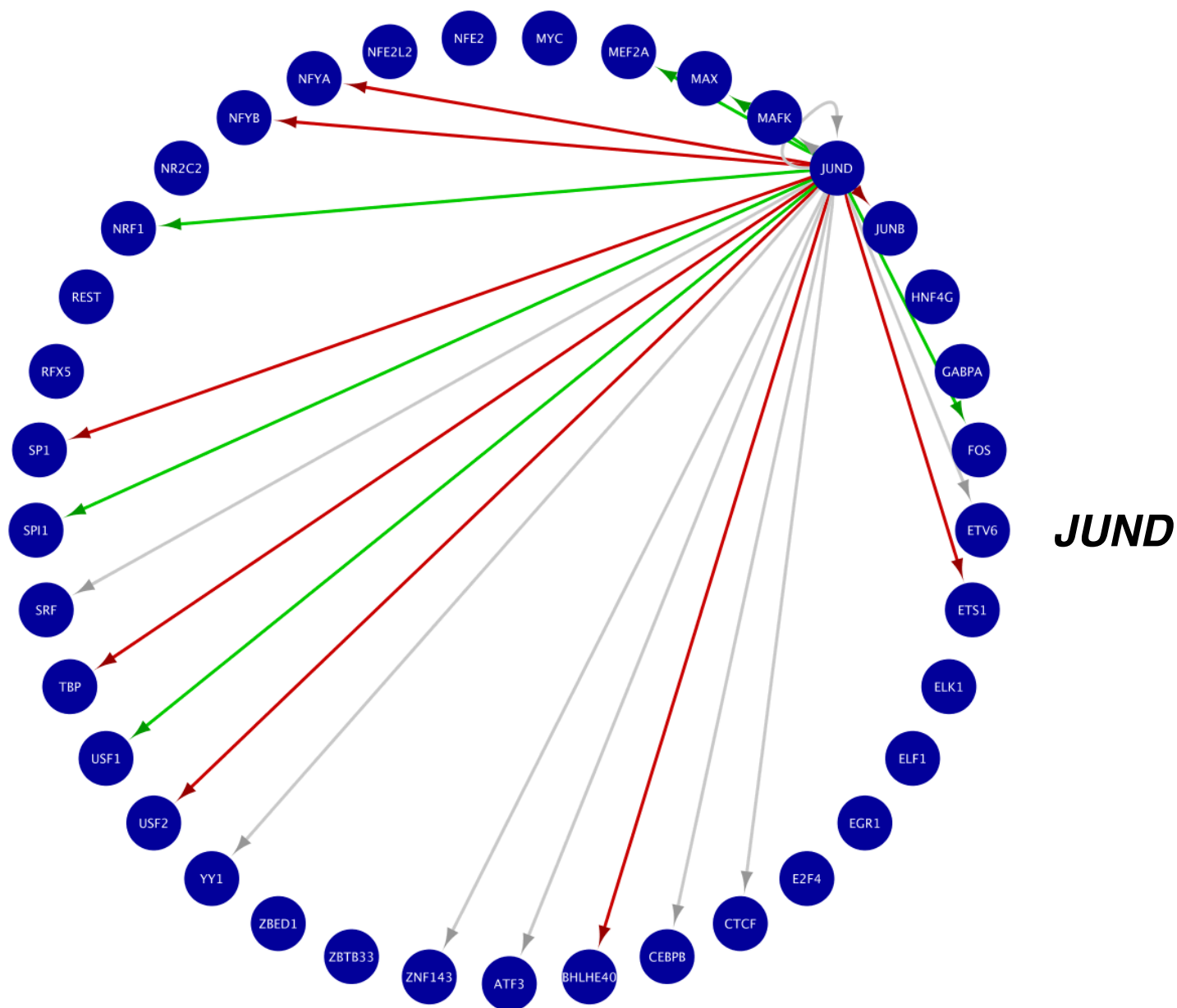


*Liver vs HepG2*

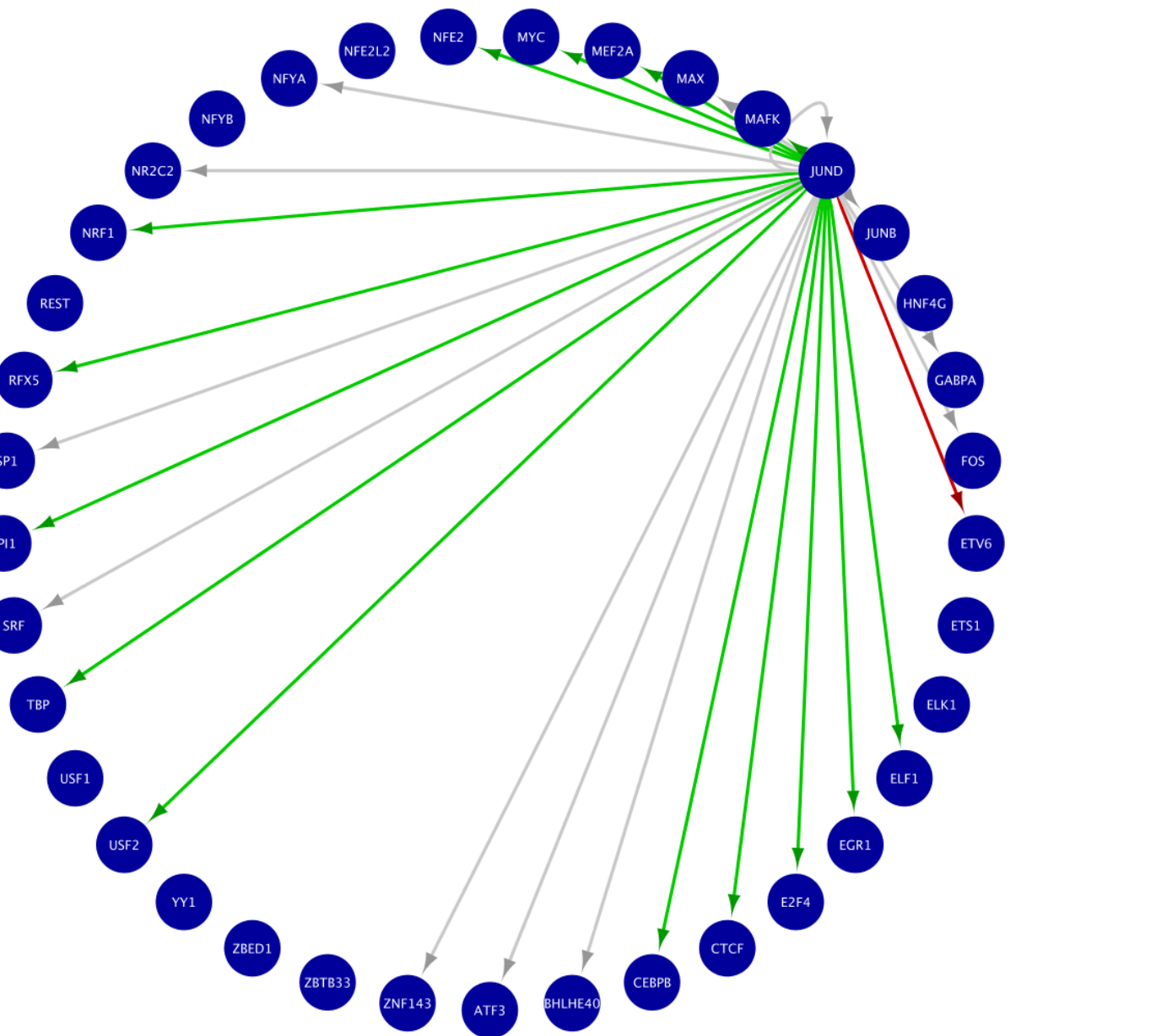
**ATF3**



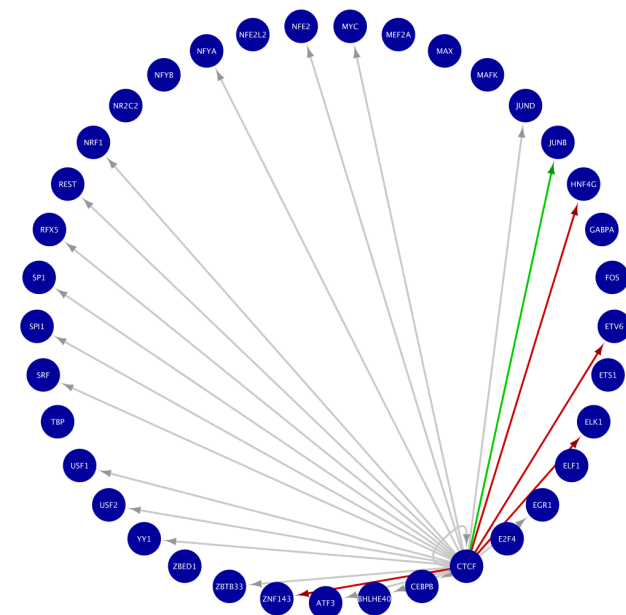
*GM12878 vs K562*



**JUND**

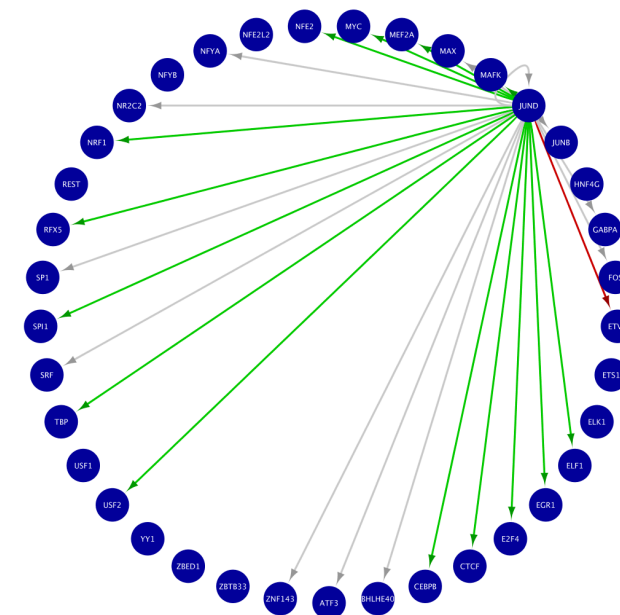


**GM12878 vs K562**



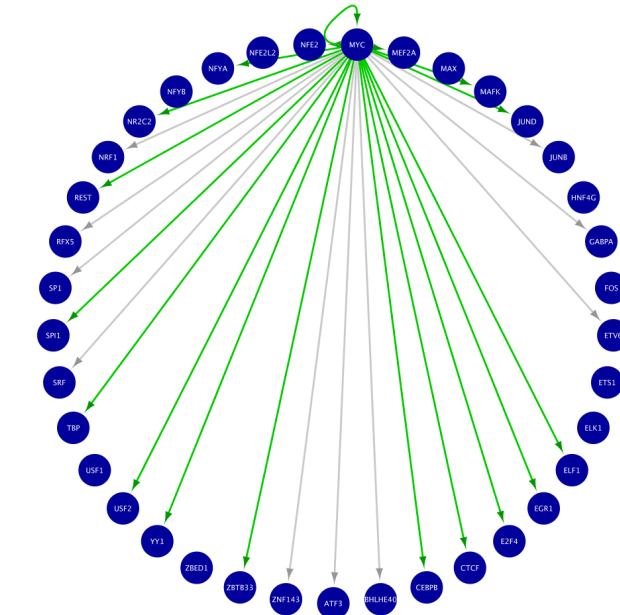
**CTCF**

**GM12878 vs K562**



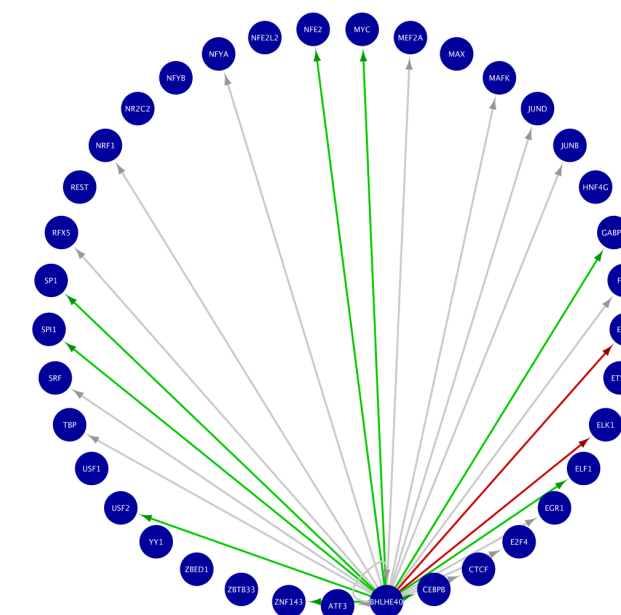
**JUND**

**GM12878 vs K562**



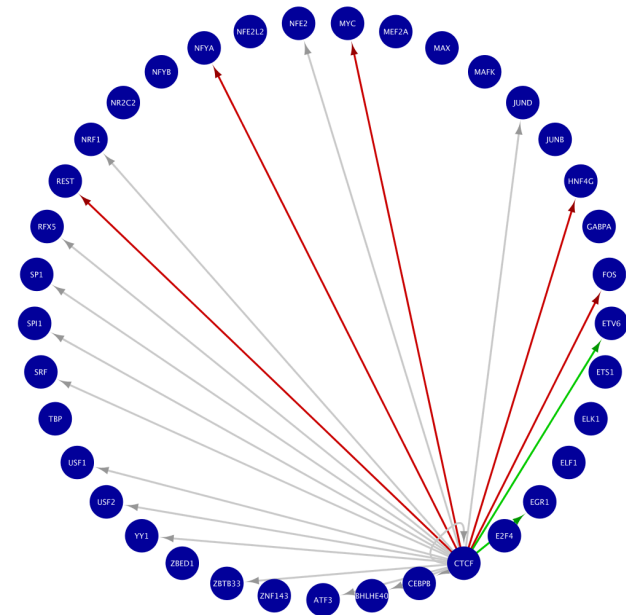
**MYC**

**GM12878 vs K562**



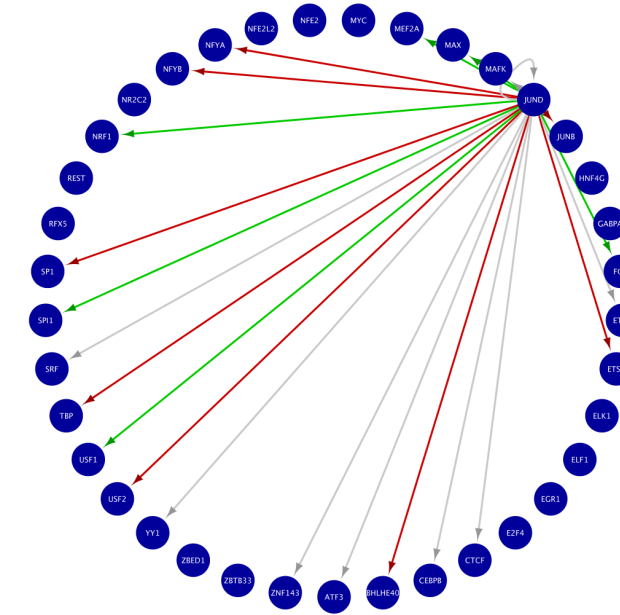
**BHLHE40**

**IMR-90 vs A549**



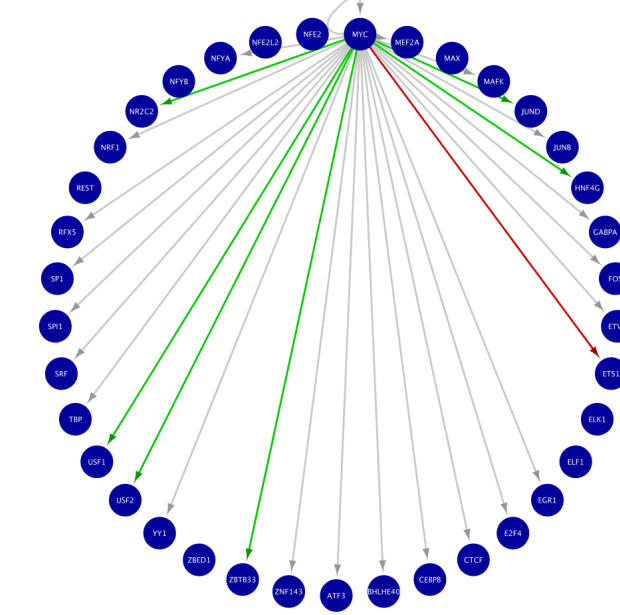
**CTCF**

**Liver vs HepG2**



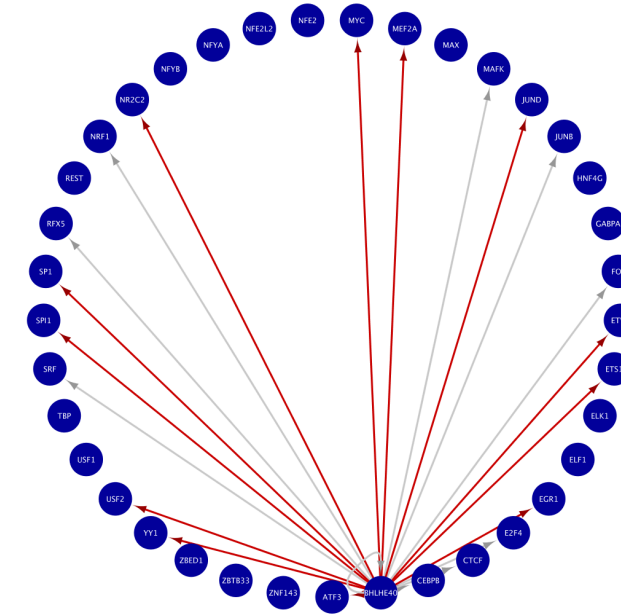
**JUND**

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

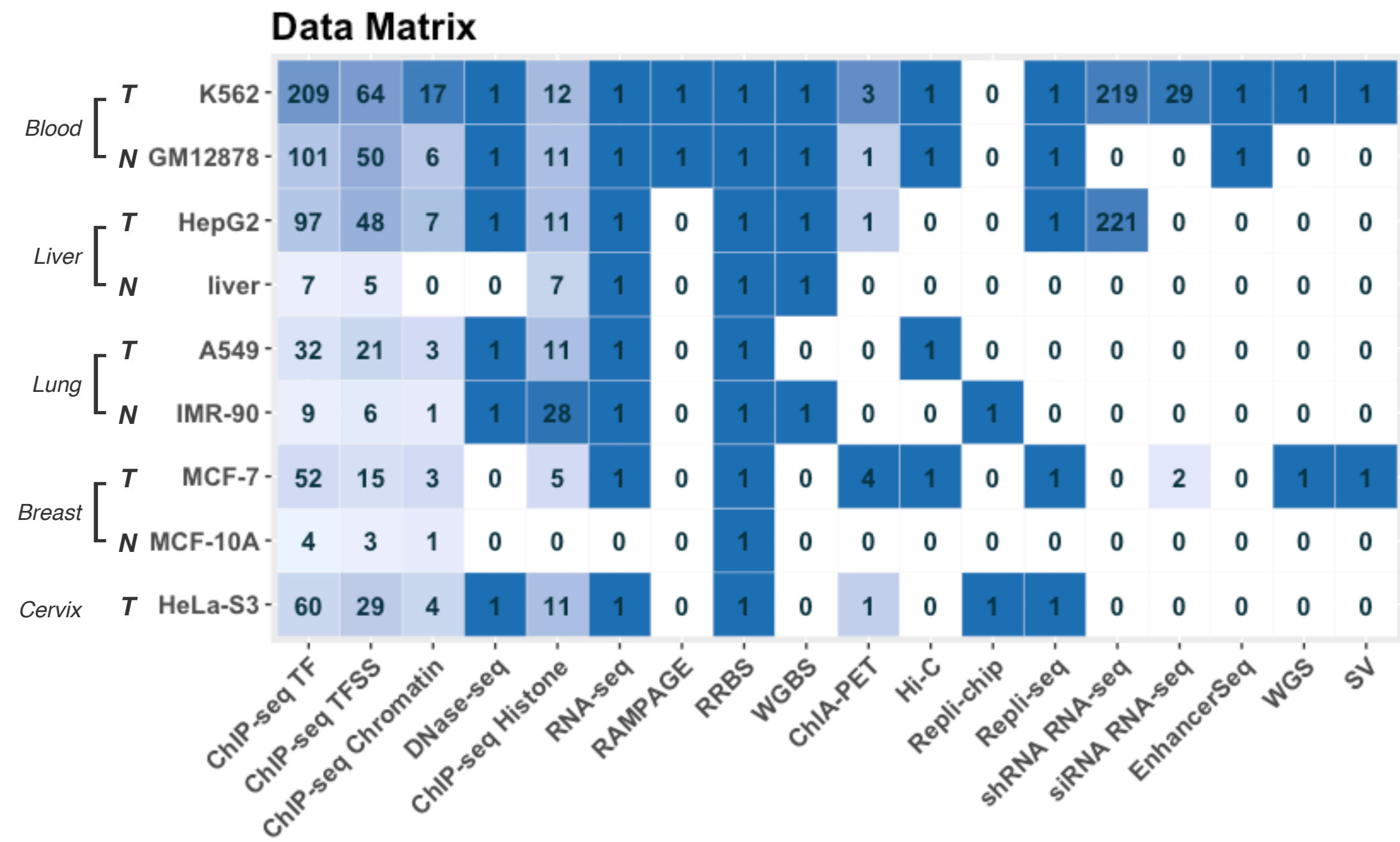
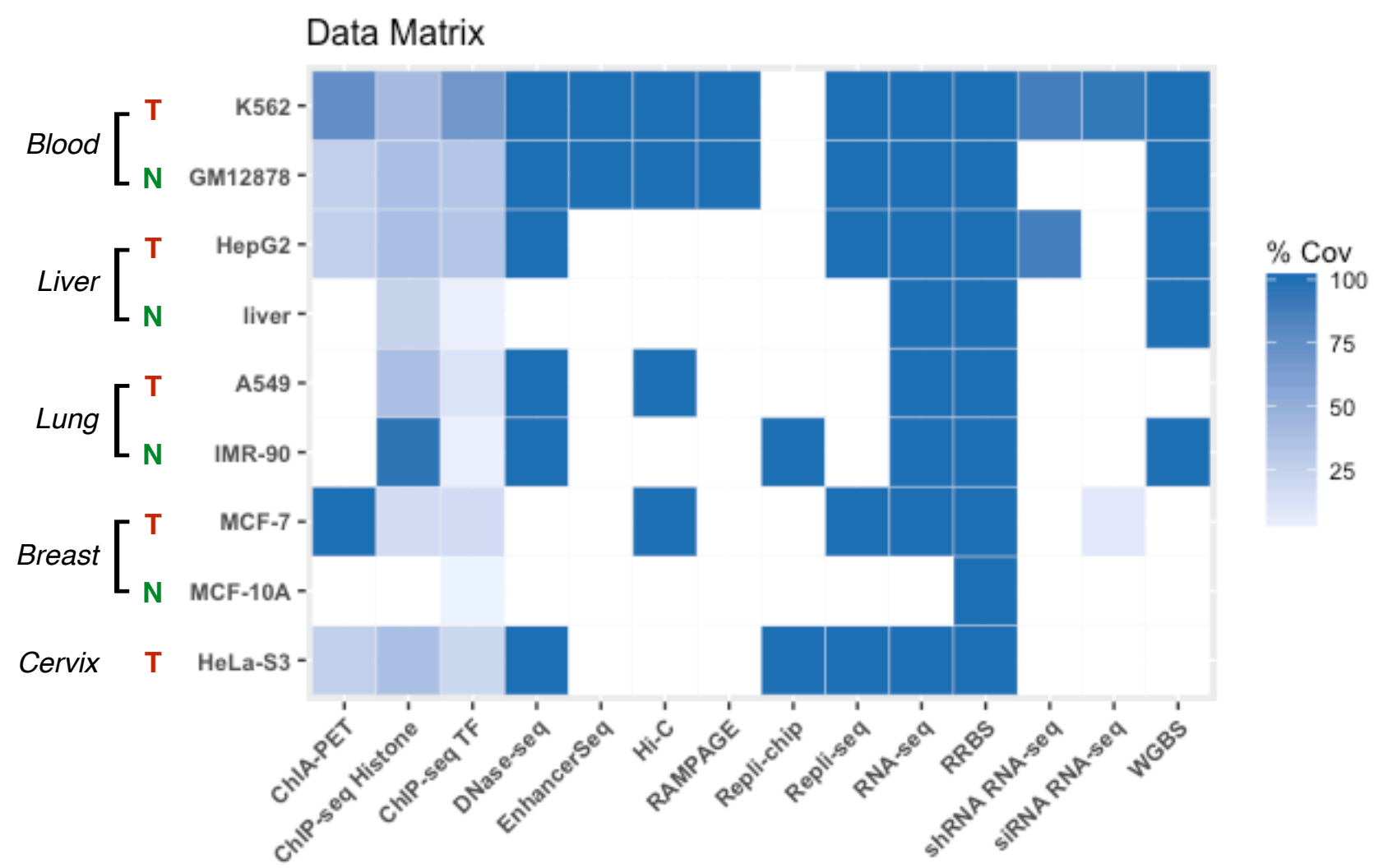


**MYC**

**IMR-90 vs A549**

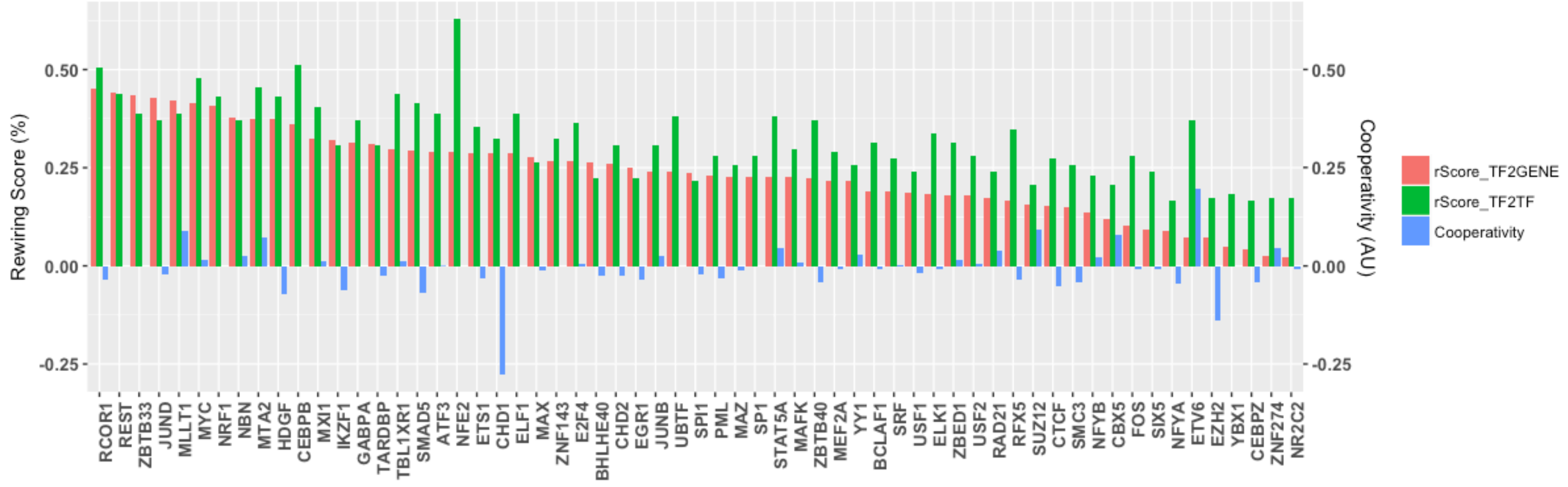


**BHLHE40**

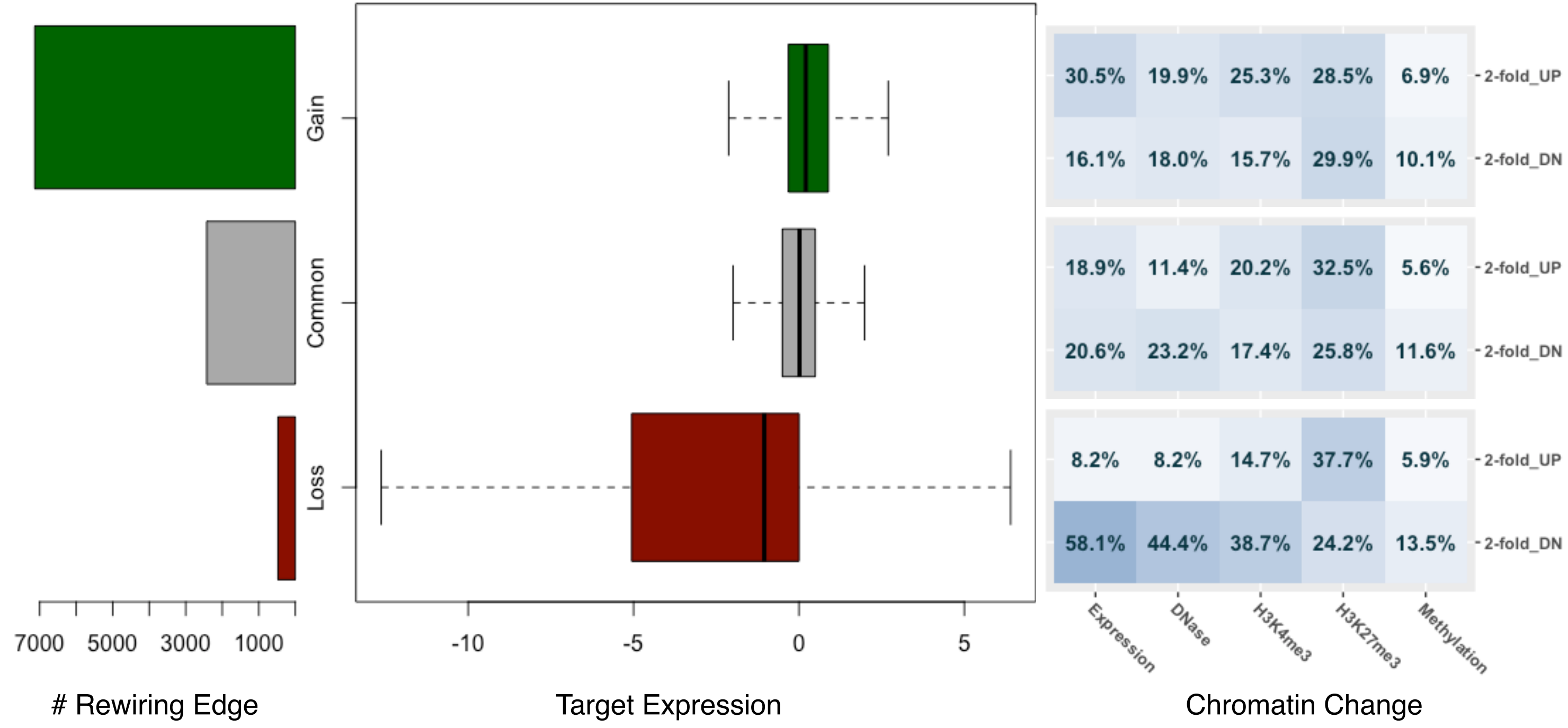




K562-GM12878 Network

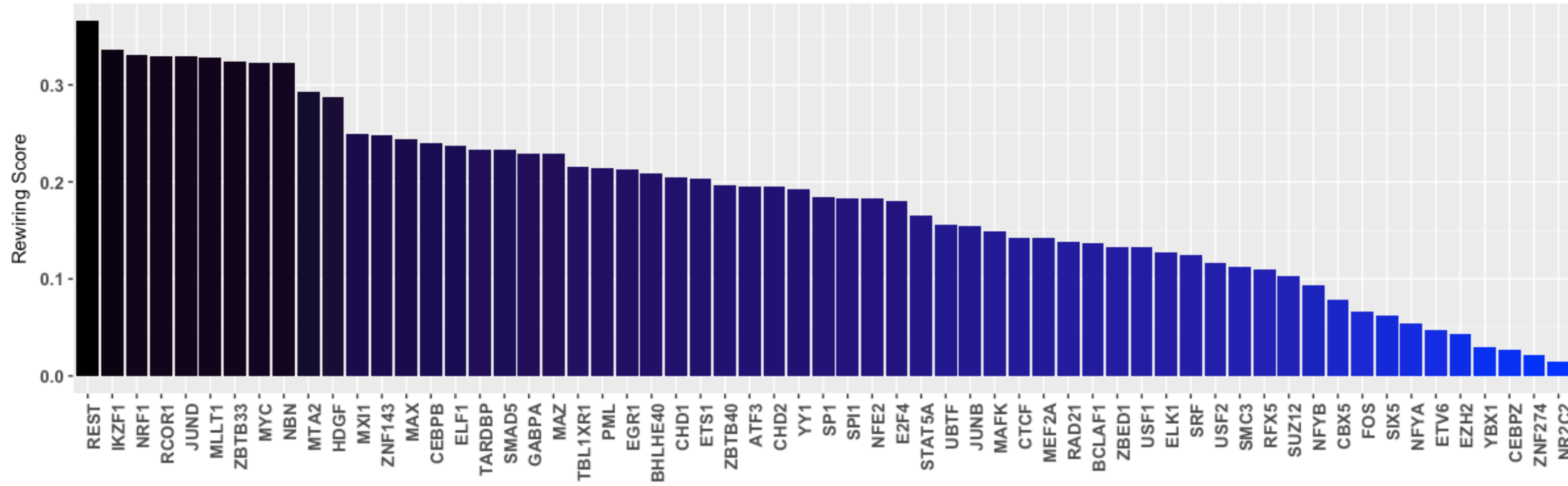


# JUND

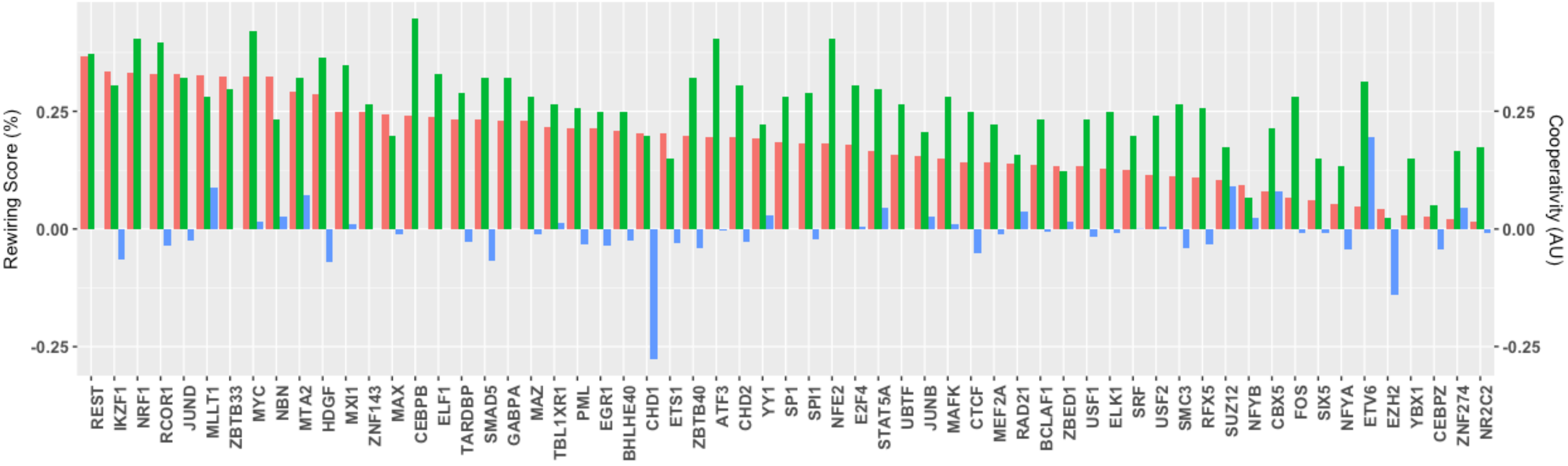


# new TSS network, one TSS per gene

TF-GENE Network

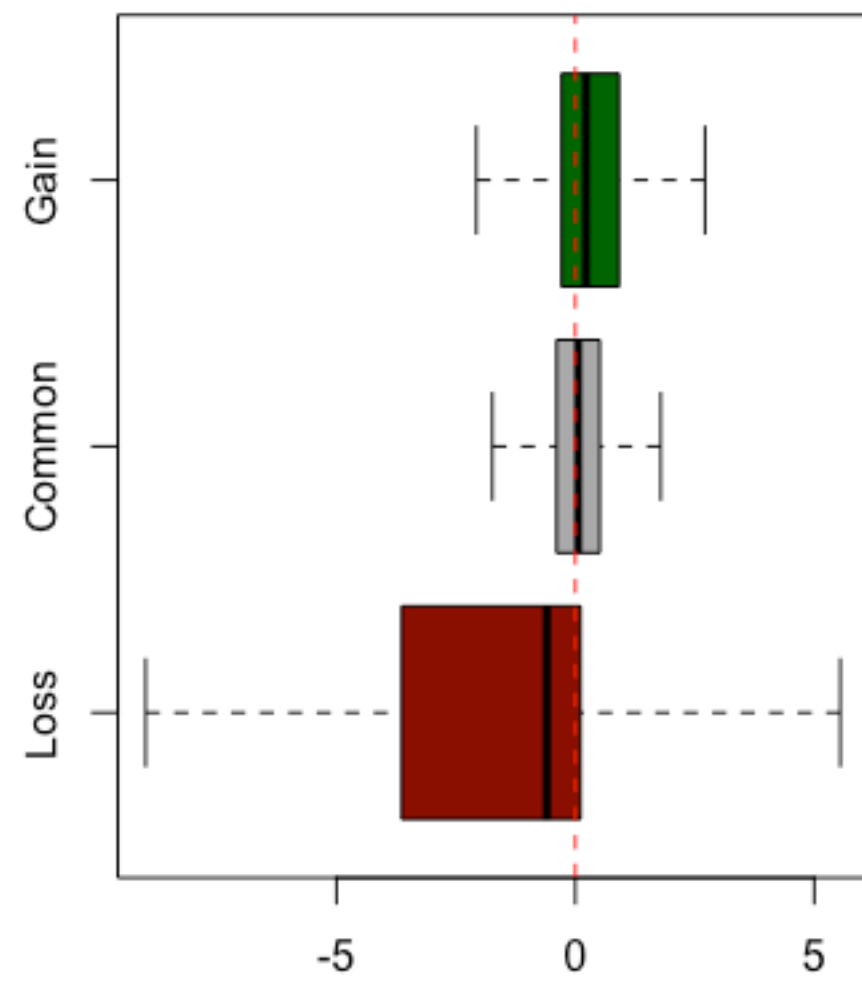
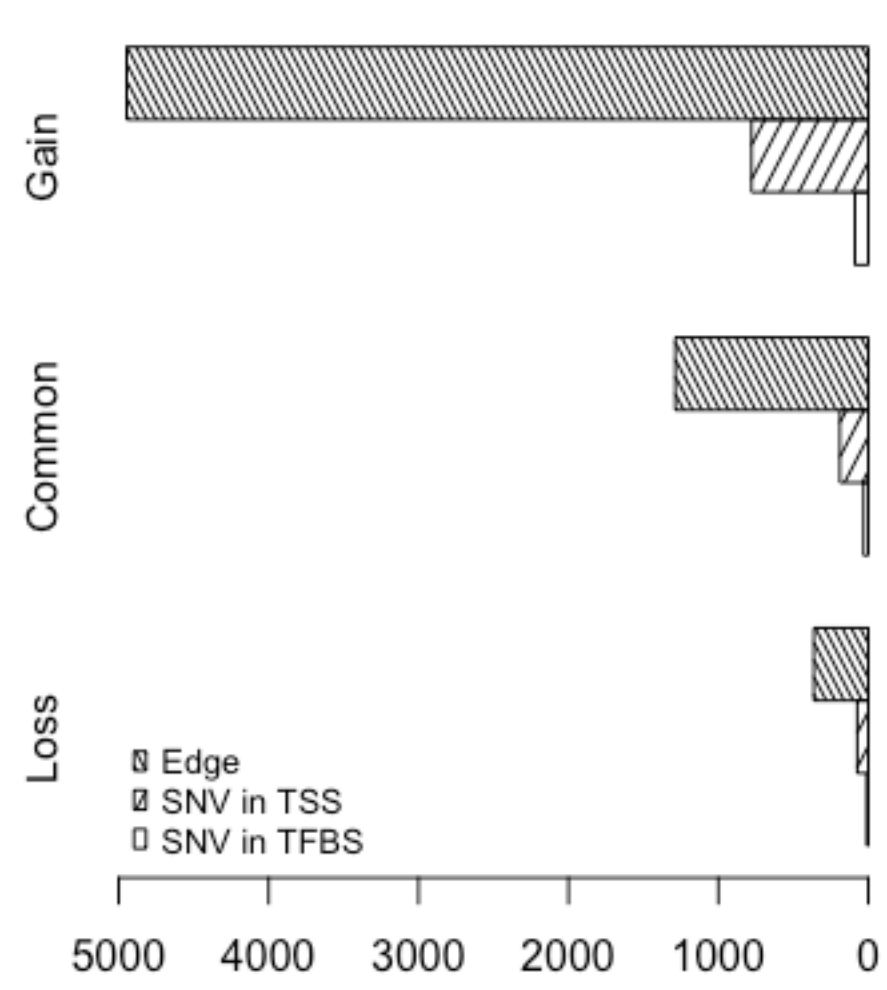


K562-GM12878 Network



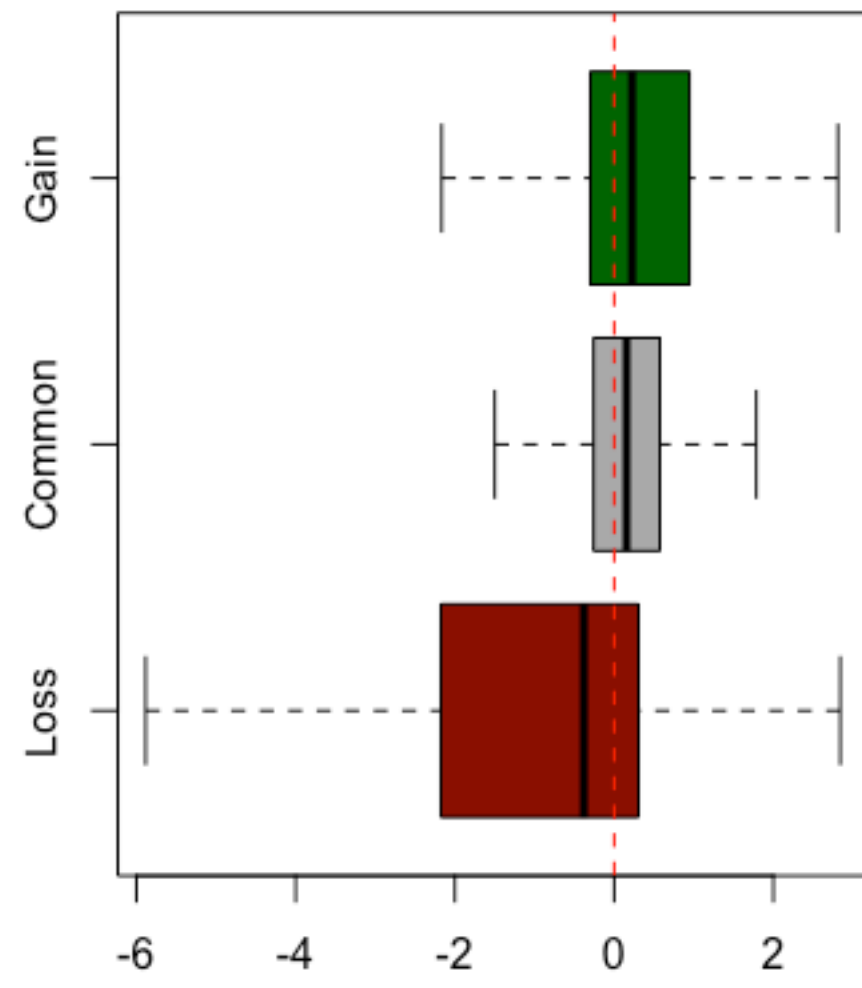
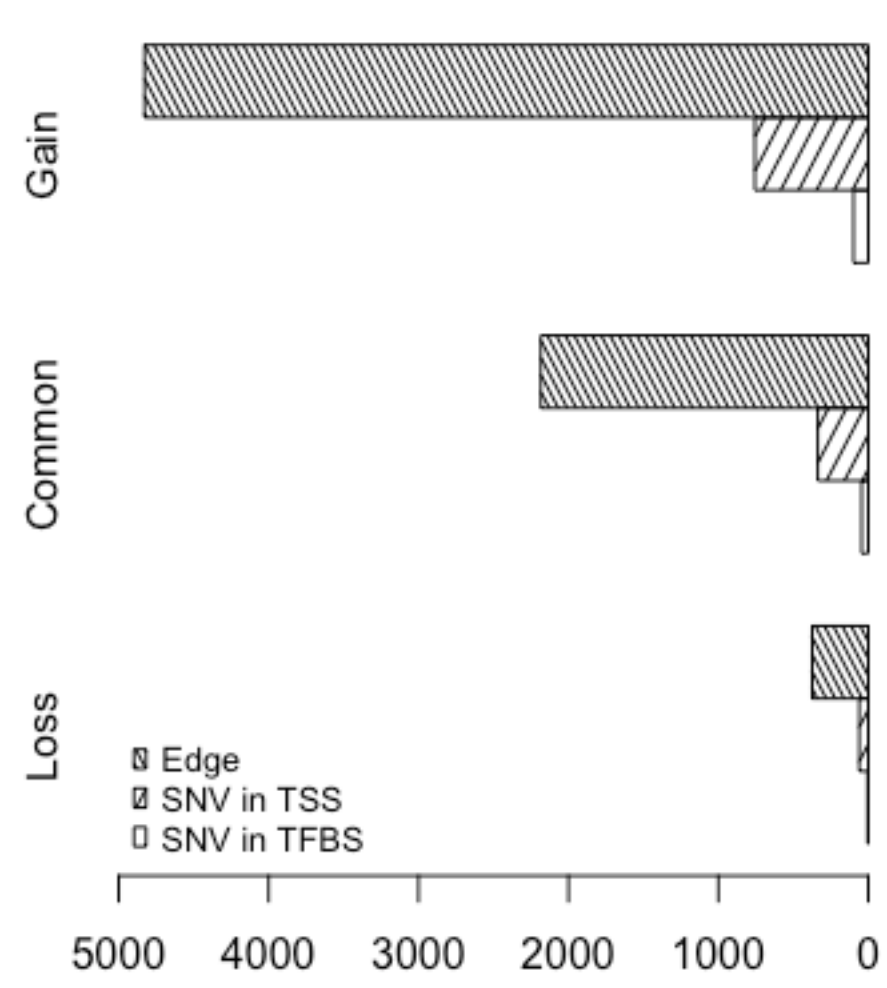
■ rScore\_TF2GENE  
■ rScore\_TF2TF  
■ Cooperativity

# 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	

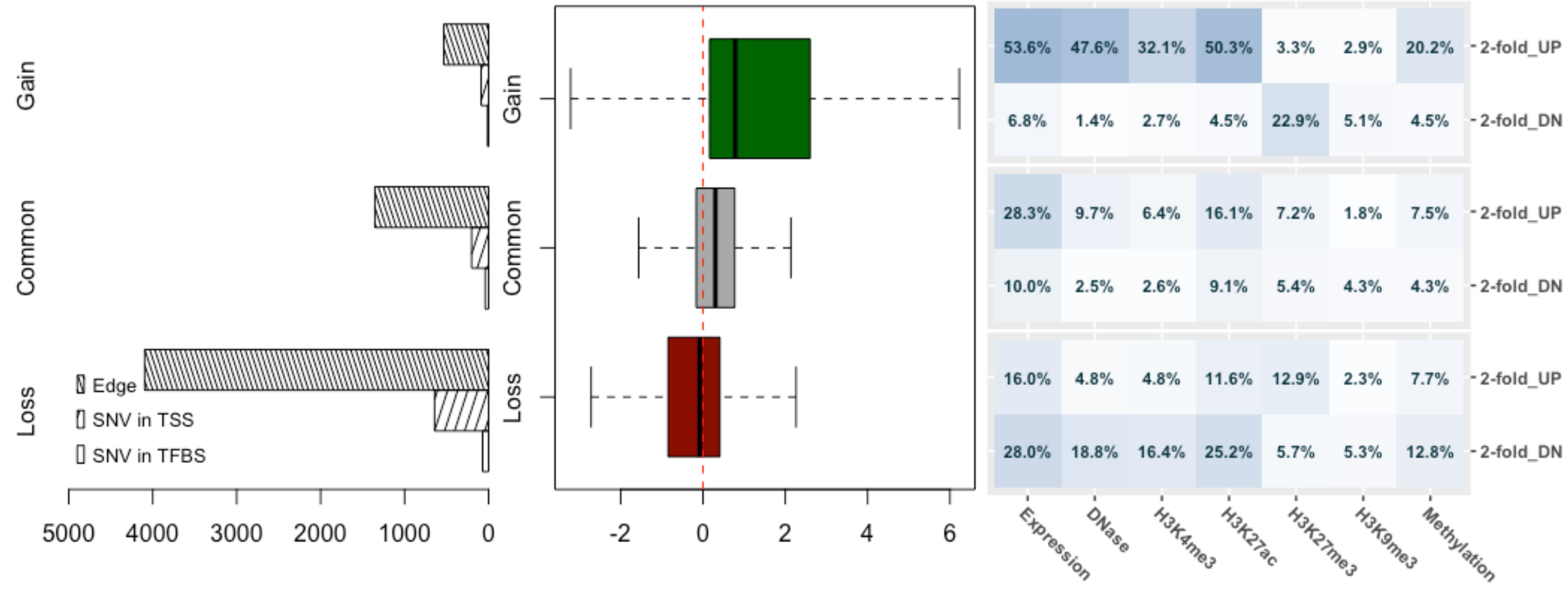
# MYC



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



53.6%	47.6%	32.1%	50.3%	3.3%	2.9%	20.2%	2-fold_UP
6.8%	1.4%	2.7%	4.5%	22.9%	5.1%	4.5%	2-fold_DN

28.3%	9.7%	6.4%	16.1%	7.2%	1.8%	7.5%	2-fold_UP
10.0%	2.5%	2.6%	9.1%	5.4%	4.3%	4.3%	2-fold_DN

16.0%	4.8%	4.8%	11.6%	12.9%	2.3%	7.7%	2-fold_UP
28.0%	18.8%	16.4%	25.2%	5.7%	5.3%	12.8%	2-fold_DN