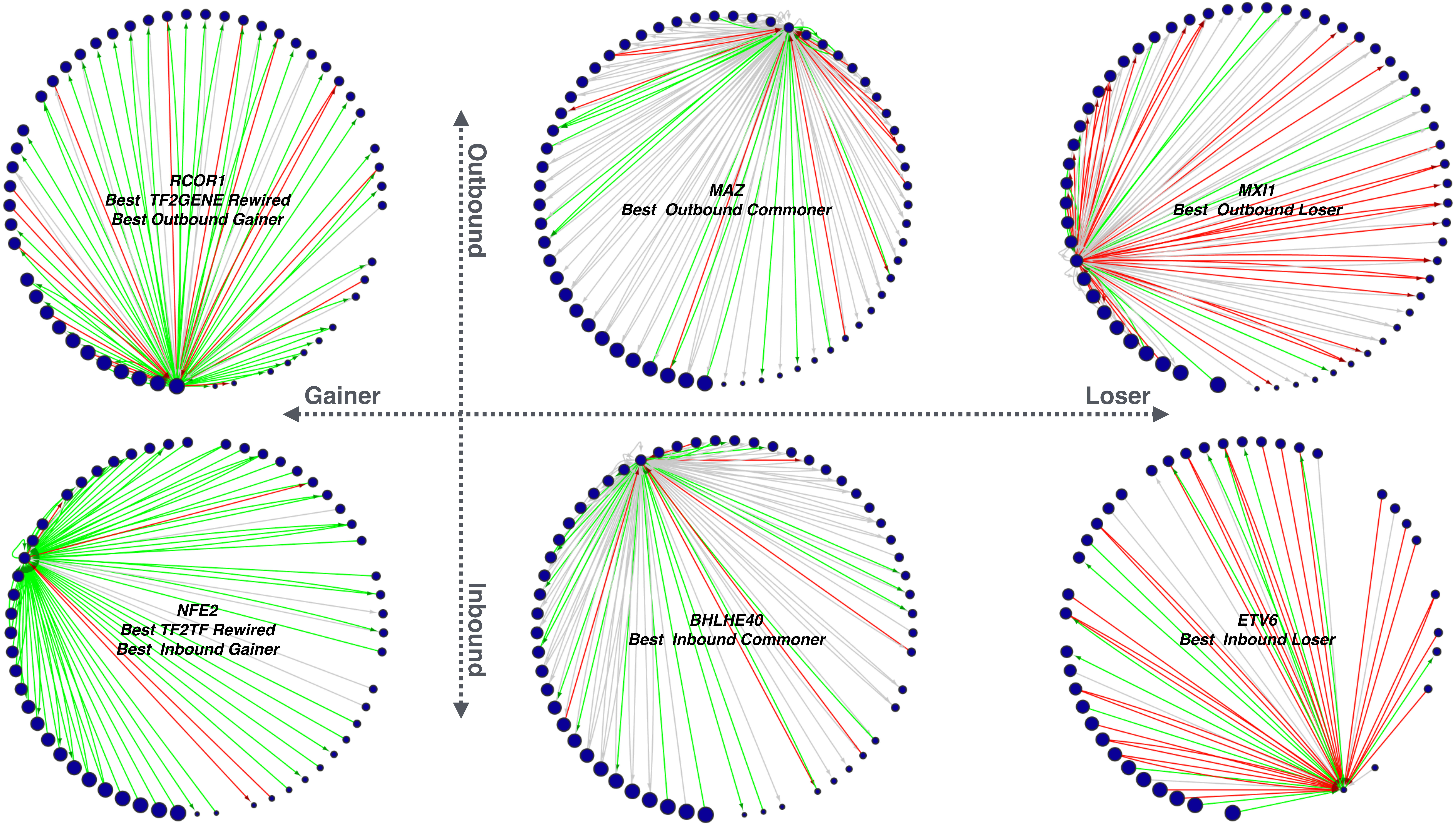
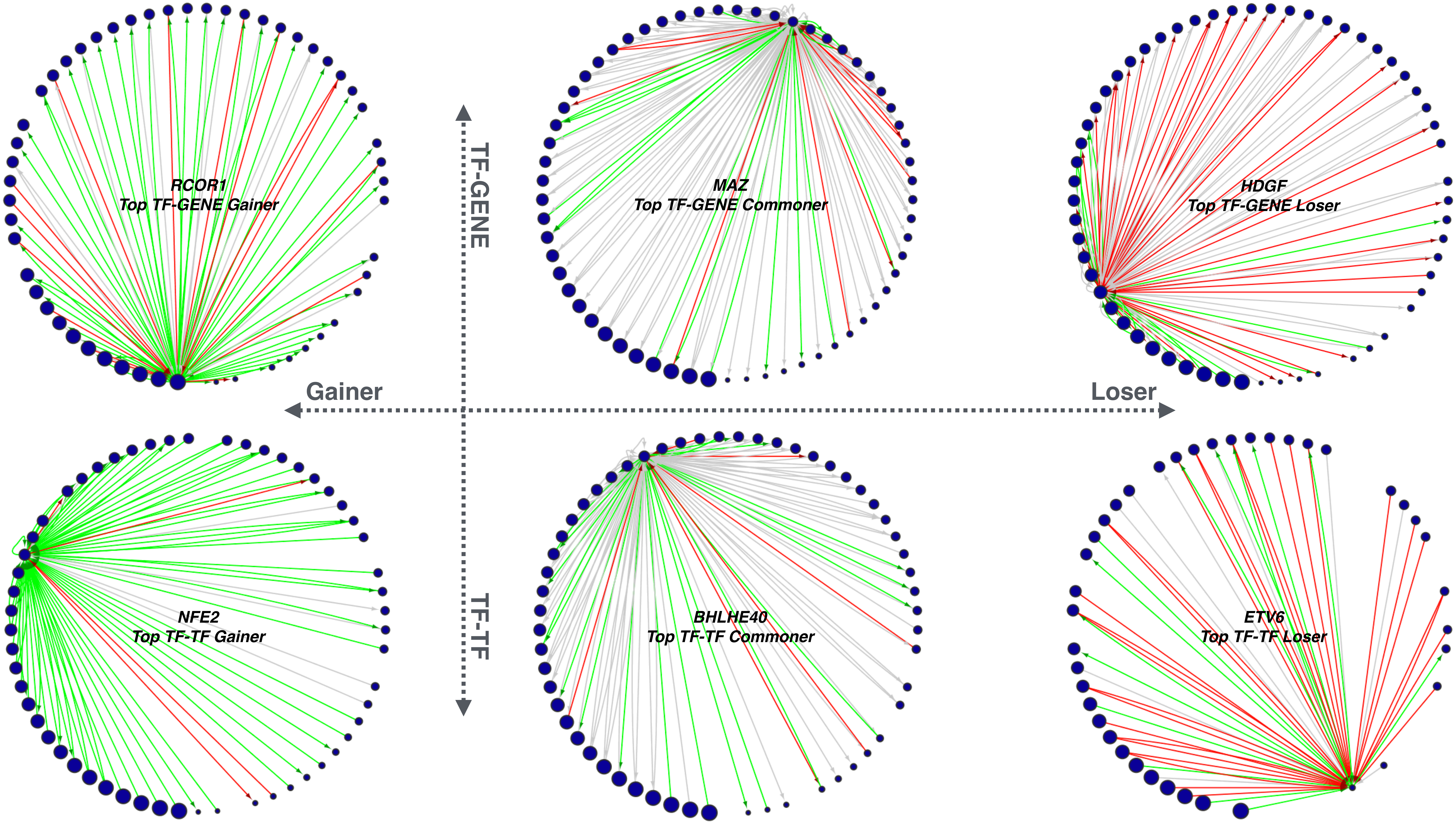
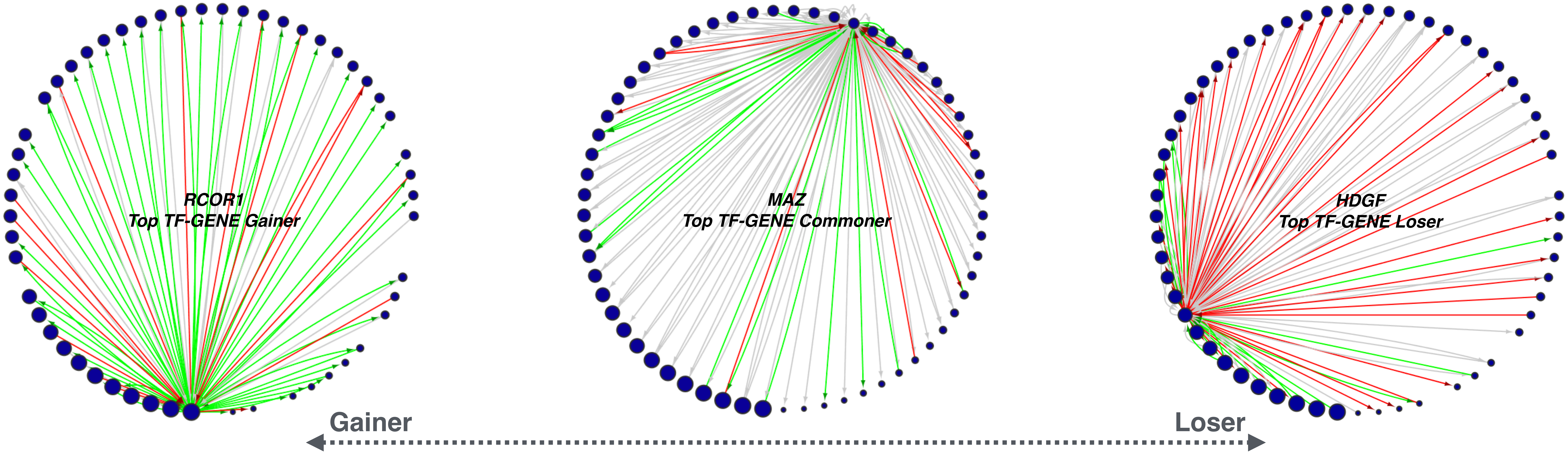
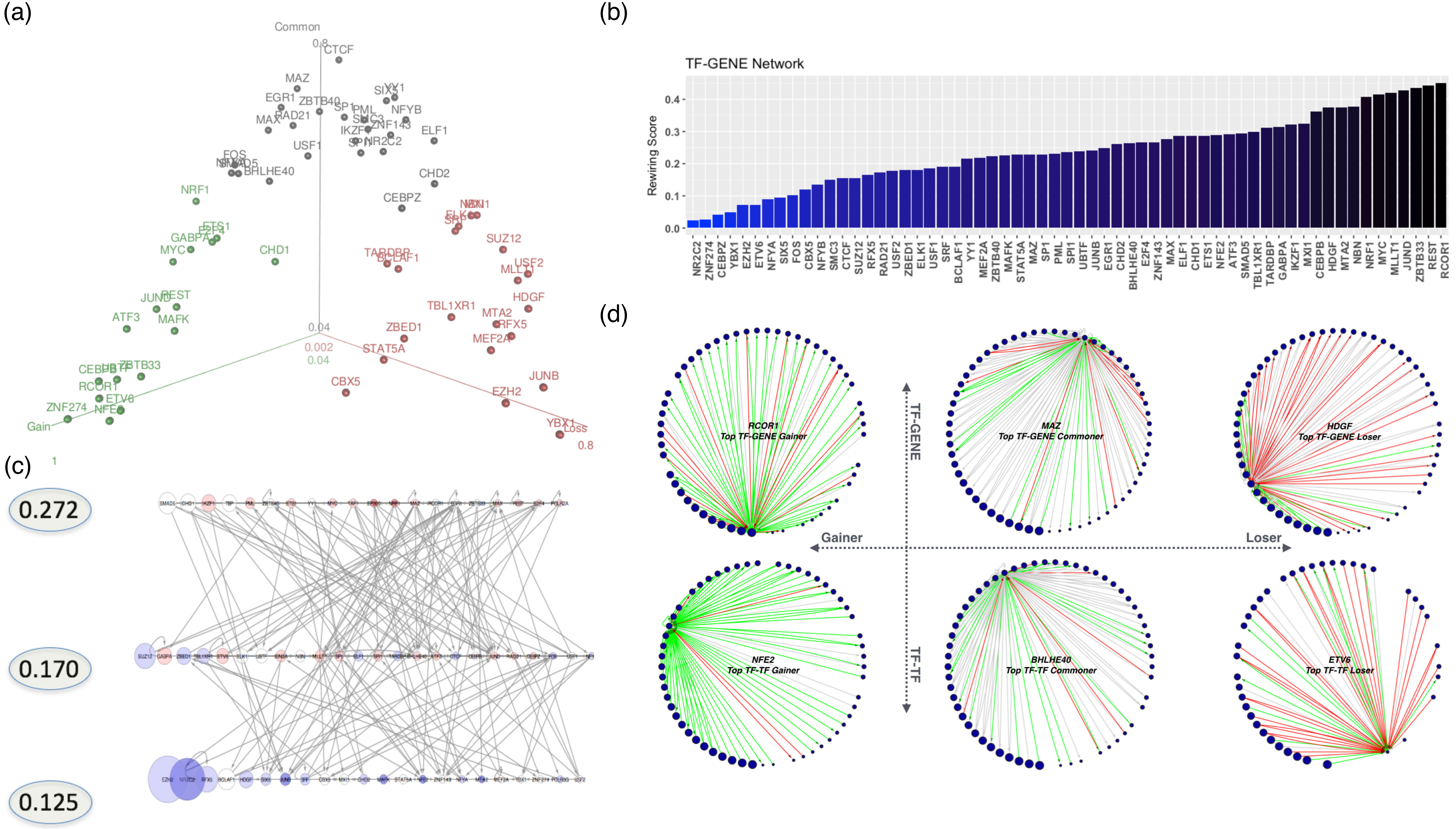
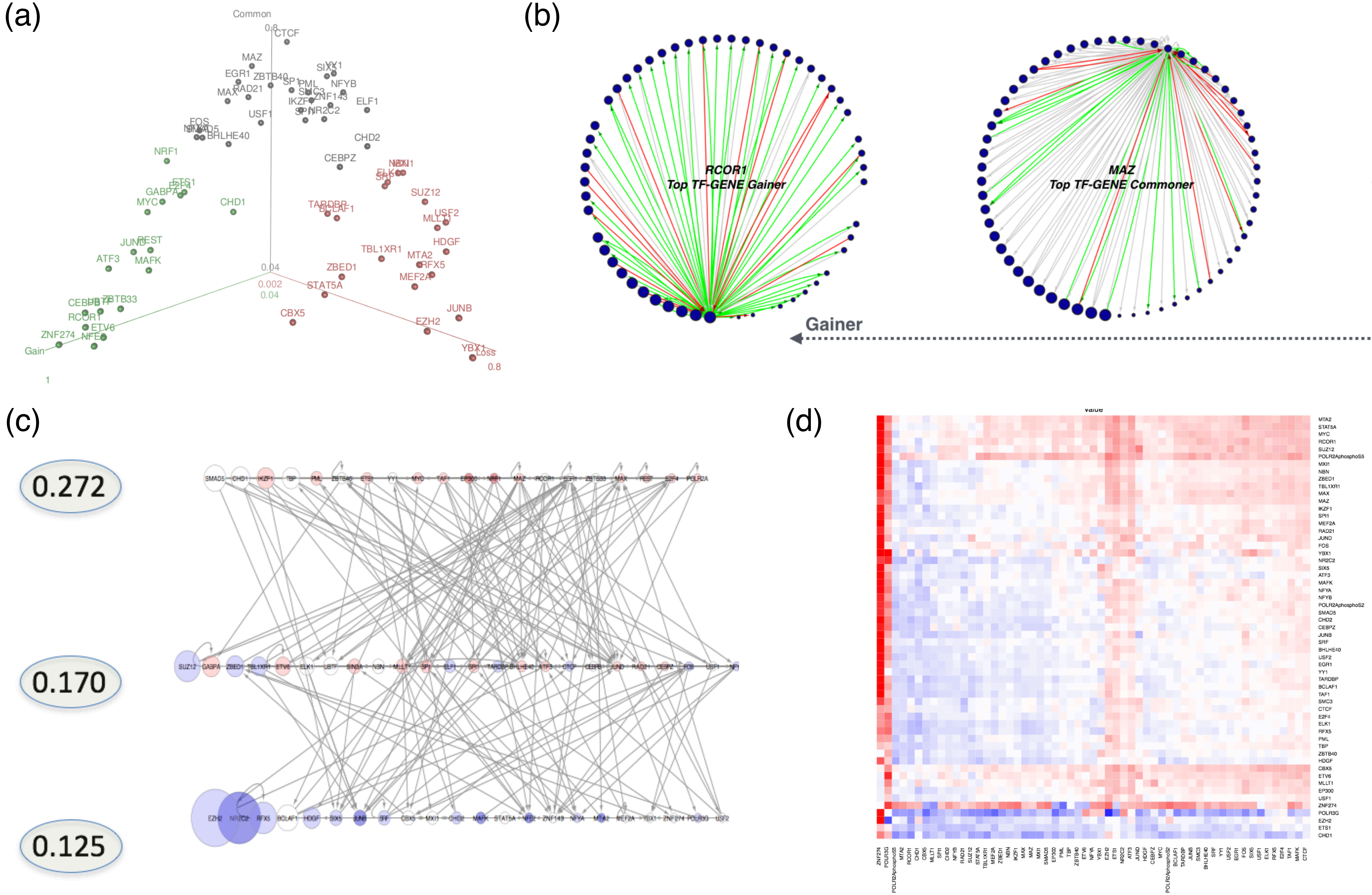

RCOR1
Best TF2GENE Rewired
Best Outbound Gainer
MAZ
Best Outbound Commoner
MXI1
Best Outbound Loser
Outbound
Gainer
Loser
Inbound
NFE2
Best TF2TF Rewired
Best Inbound Gainer
BHLHE40
Best Inbound Commoner
ETV6
Best Inbound Loser

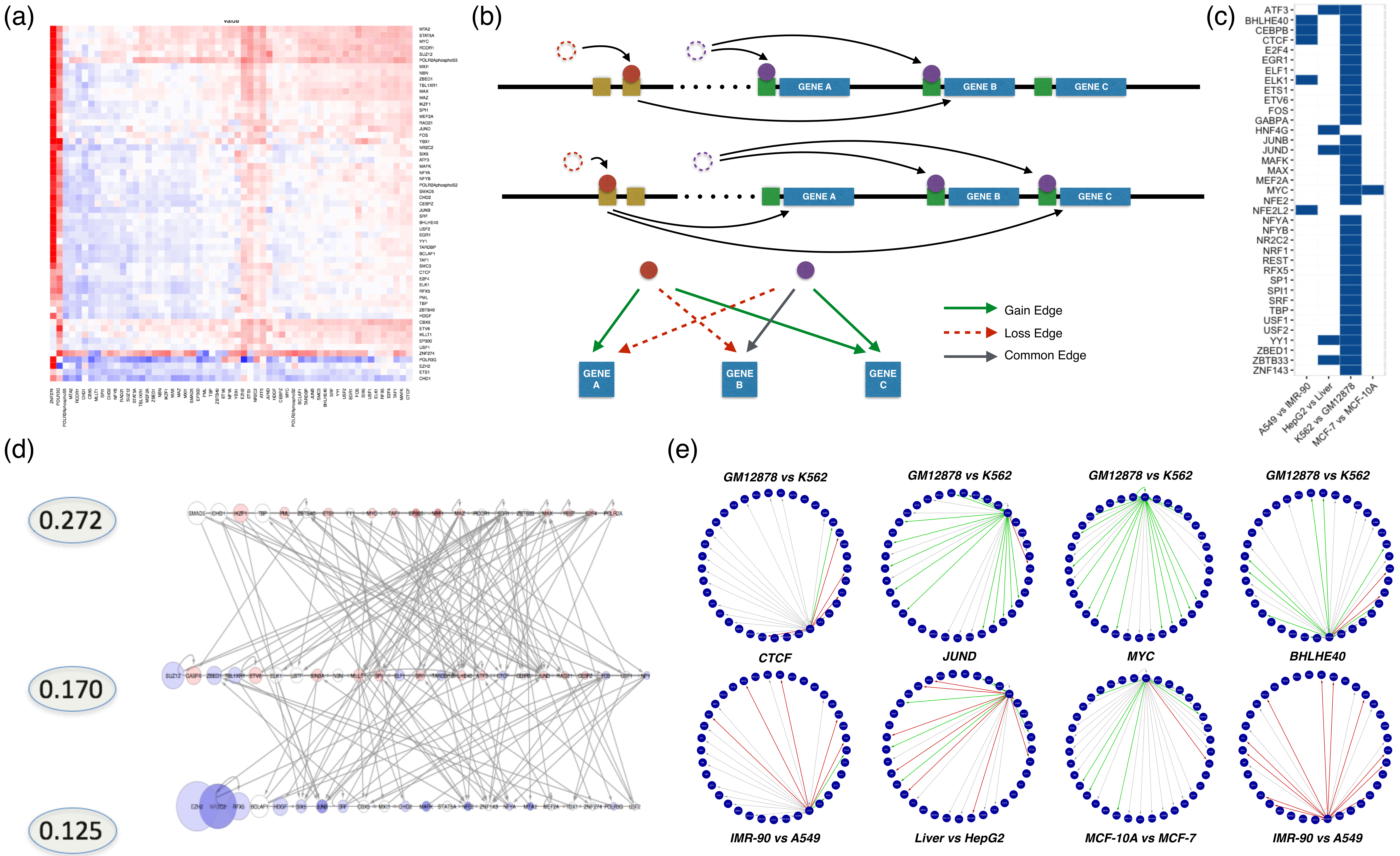

RCOR1
Top TF-GENE Gainer
MAZ
Top TF-GENE Commoner
HDGF
Top TF-GENE Loser
TF-GENE
Gainer
Loser
TF-TF
NFE2
Top TF-TF Gainer
BHLHE40
Top TF-TF Commoner
ETV6
Top TF-TF Loser


RCOR1
Top TF-GENE Gainer
MAZ
Top TF-GENE Commoner
HDGF
Top TF-GENE Loser
Gainer
Loser


(a)
Common
0.8
CTCF
MAZ
YY1
SIX5
EGR1
ZBTB40
SP1
PML
NFYB
MAX
RAD21
SMC3
ZNF143
IKZF1
ELF1
USF1
SPI1
NR2C2
FOS
SMAD5
BHLHE40
CHD2
NRF1
CEBPZ
NBN
MXI1
ETS1
E2F4
GABPA
ELK1
SRF
SUZ12
MYC
CHD1
TARDBP
BCLAF1
USF2
MLLT1
JUND
REST
HDGF
TBL1XR1
ATF3
MAFK
MTA2
RFX5
0.04
ZBED1
MEF2A
0.002
0.04
STAT5A
CEBPB
TBP
ZBTB33
JUNB
CBX5
RCOR1
ETV6
EZH2
ZNF274
NFE2
Gain
YBX1
Loss
0.8
1
(b)
TF-GENE Network
Rewiring Score
0.4
0.3
0.2
0.1
0.0
NR2C2
ZNF274
CEBPZ
YBX1
EZH2
ETV6
NFYA
SIX5
FOS
CBX5
NFYB
SMC3
CTCF
SUZ12
RFX5
RAD21
USF2
ZBED1
ELK1
USF1
SRF
BCLAF1
YY1
MEF2A
ZBTB40
MAFK
STAT5A
MAZ
SP1
PML
SPI1
UBTF
JUNB
EGR1
CHD2
BHLHE40
E2F4
ZNF143
MAX
ELF1
CHD1
ETS1
NFE2
ATF3
SMAD5
TBL1XR1
TARDBP
GABPA
IKZF1
MXI1
CEBPB
HDGF
MTA2
NBN
NRF1
MYC
MLLT1
JUND
ZBTB33
REST
RCOR1
(c)
0.272
0.170
0.125
(d)
RCOR1
Top TF-GENE Gainer
MAZ
Top TF-GENE Commoner
HDGF
Top TF-GENE Loser
TF-GENE
Gainer
Loser
TF-TF
NFE2
Top TF-TF Gainer
BHLHE40
Top TF-TF Commoner
ETV6
Top TF-TF Loser

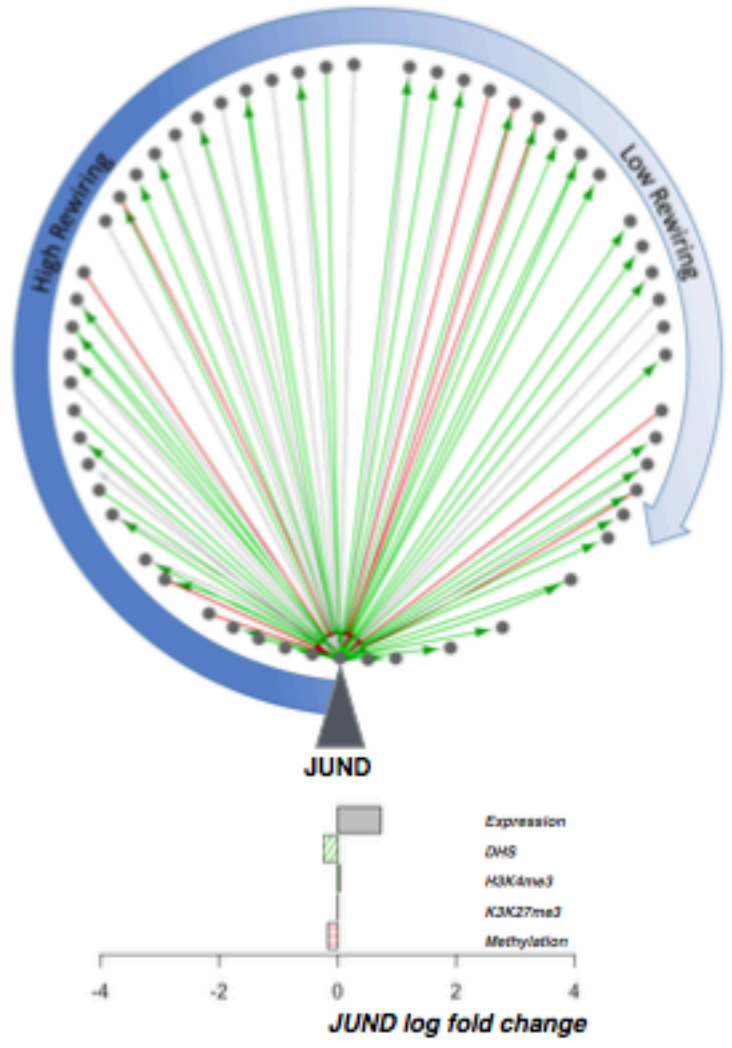

(a)
Common
Gain
Loss
0.8
0.04
0.002
0.04
0.8
1
CTCF
MAZ
SIX5
YY1
EGR1
ZBTB40
SP1
PML
NFYB
MAX
RAD21
SMC3
ZNF143
IKZF1
ELF1
USF1
SPI1
NR2C2
FOS
NBN
SMAD5
BHLHE40
CHD2
NRF1
CEBPZ
MXI1
ELK1
SRF
ETS1
E2F4
GABPA
MYC
CHD1
SUZ12
TARDBP
BCLAF1
USF2
MLLT1
JUND
REST
HDGF
TBL1XR1
MTA2
ATF3
MAFK
RFX5
ZBED1
MEF2A
STAT5A
CEBPB
TBP
ZBTB33
RCOR1
CBX5
JUNB
EZH2
ZNF274
ETV6
NFE2
YBX1
(b)
K562-GM12878 Network
Rewiring Score (%)
Cooperativity (AU)
0.50
0.25
0.00
-0.25
🟥 rScore_TF2GENE
🟩 rScore_TF2TF
🟦 Cooperativity
RCOR1
REST
ZBTB33
JUND
MLLT1
MYC
NRF1
NBN
MTA2
HDGF
CEBPB
MXI1
IKZF1
GABPA
TARDBP
TBL1XR1
SMAD5
ATF3
NFE2
ETS1
CHD1
ELF1
MAX
ZNF143
E2F4
BHLHE40
CHD2
EGR1
JUNB
UBTF
SPI1
PML
MAZ
SP1
STAT5A
MAFK
ZBTB40
MEF2A
YY1
BCLAF1
SRF
USF1
ELK1
ZBED1
USF2
RAD21
RFX5
SUZ12
CTCF
SMC3
NFYB
CBX5
FOS
SIX5
NFYA
ETV6
EZH2
YBX1
CEBPZ
ZNF274
NR2C2
(c)
0.272
0.170
0.125
SMAD5
CHD1
IKZF1
TBP
PML
ZBTB40
ETS1
YY1
MYC
TAF1
EP300
NRF1
MAZ
RCOR1
EGR1
ZBTB33
MAX
REST
E2F4
POLR2A
SUZ12
GABPA
ZBED1
TBL1XR1
ETV6
ELK1
UBTF
SIN3A
NBN
MLLT1
SP1
ELF1
SP1
TARDBP
BHLHE40
ATF3
CTCF
CEBPB
JUND
RAD21
CEBPZ
FOS
USF1
EZH2
NR2C2
RFX5
BCLAF1
HDGF
SIX5
JUNB
SRF
CBX5
MXI1
CHD2
MAFK
STAT5A
NFE2
ZNF143
NFYA
MTA2
MEF2A
YBX1
ZNF274
POLR3G
USF2
(d)
RCOR1
Top TF-GENE Gainer
MAZ
Top TF-GENE Commoner
HDGF
Top TF-GENE Loser
TF-GENE
Gainer
Loser
TF-TF
NFE2
Top TF-TF Gainer
BHLHE40
Top TF-TF Commoner
ETV6
Top TF-TF Loser

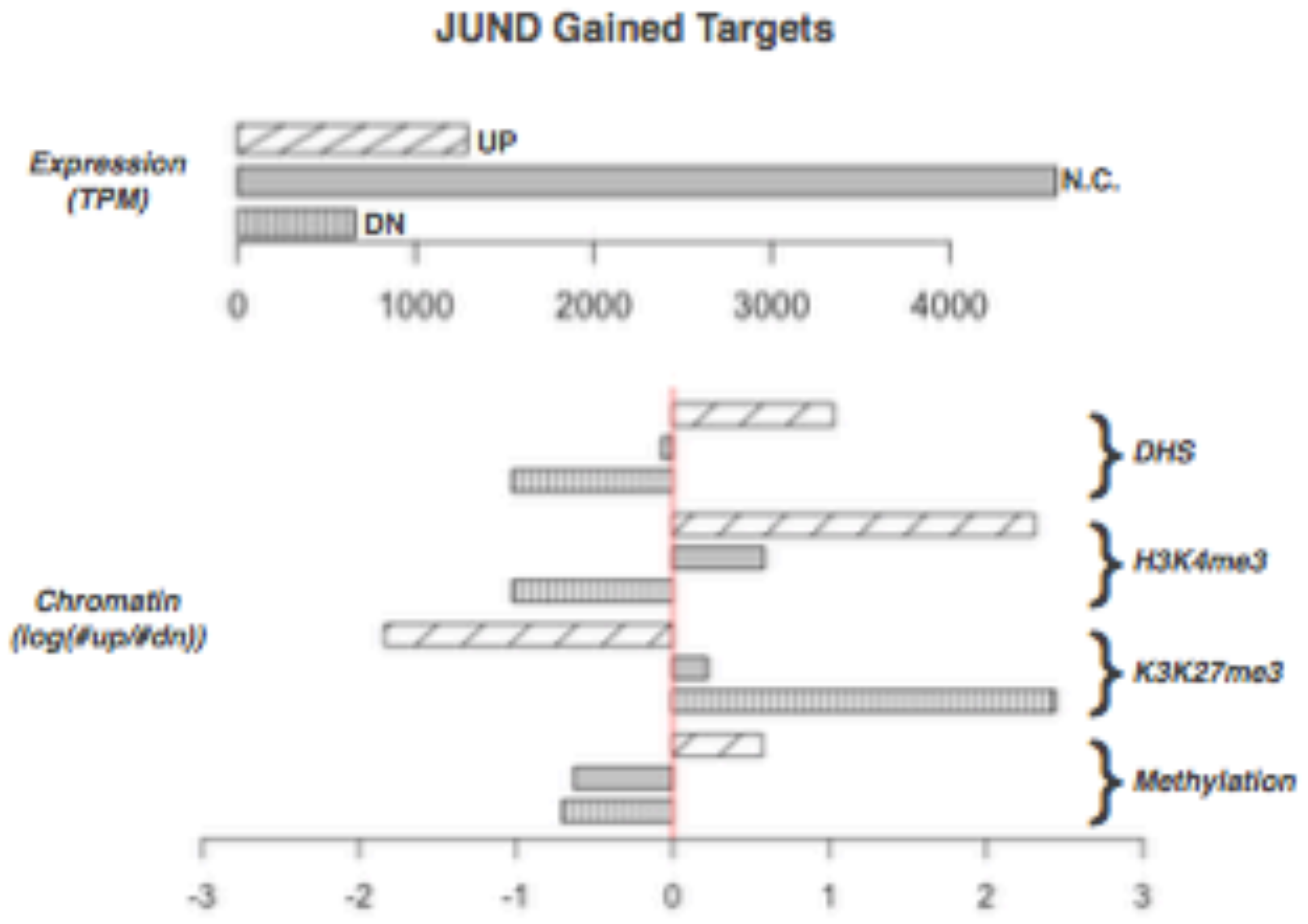

(a)
Common
Gain
Loss
CTCF
MAZ
EGR1
ZBTB40
SIX5
YY1
NFYB
MAX
RAD21
SP1
PML
SMC3
ZNF143
IKZF1
NR2C2
ELF1
USF1
FOS
BHLHE40
CHD2
CEBPZ
NRF1
ETS1
GABPA
MYC
CHD1
JUND
REST
ATF3
MAFK
CEBPB
ZBTB33
RCOR1
ETV6
ZNF274
NFE2
NBN
ELK1
SRF
SUZ12
TARDBP
BCLAF1
USF2
MLLT1
HDGF
TBL1XR1
ZBED1
MTA2
RFX5
STAT5A
MEF2A
CBX5
JUNB
EZH2
YBX1
(b)
RCOR1
Top TF-GENE Gainer
MAZ
Top TF-GENE Commoner
HDGF
Top TF-GENE Loser
Gainer
Loser
(c)
0.272
0.170
0.125
(d)
value

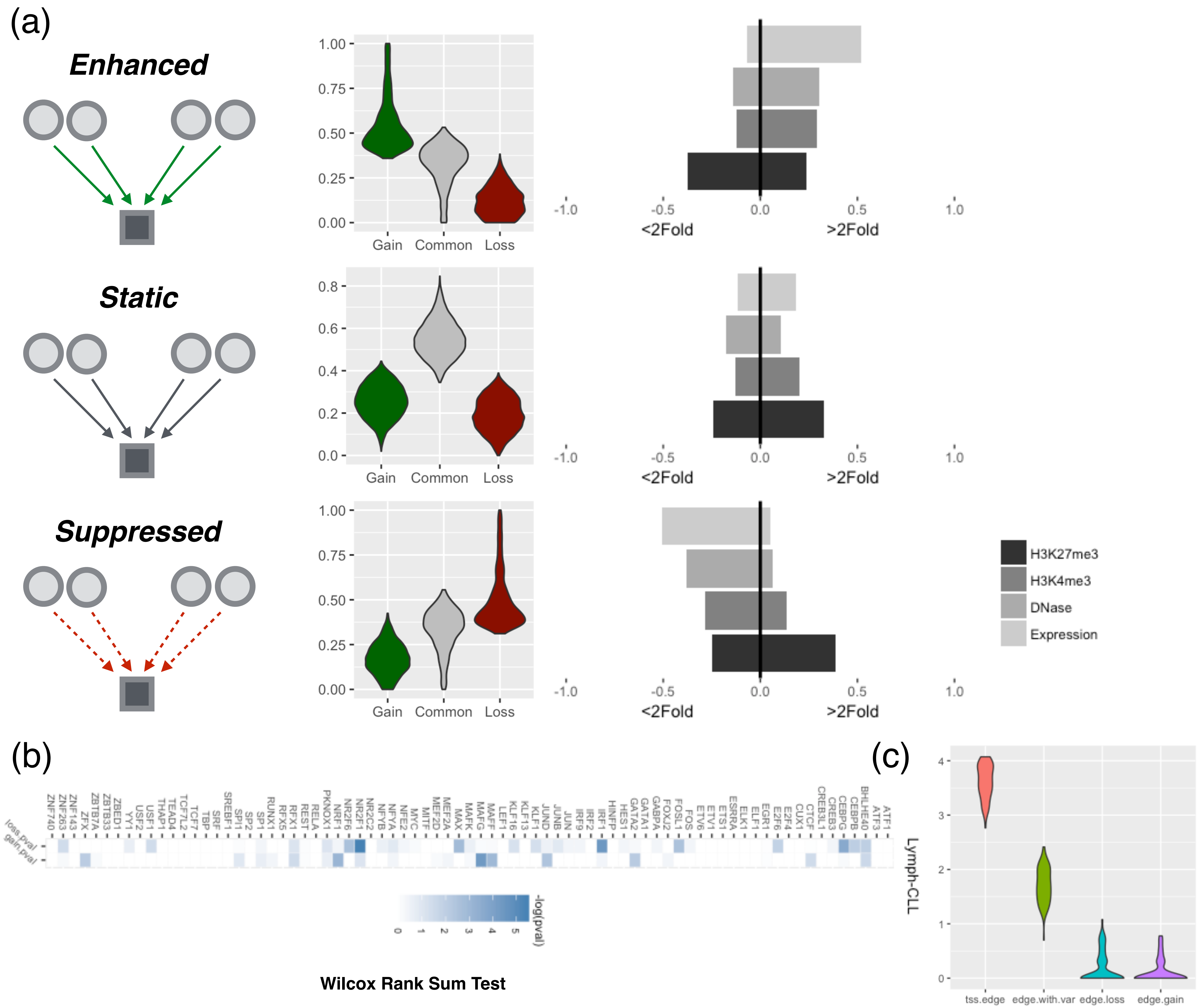

(a)
Value
(b)
GENE A
GENE B
GENE C
Gain Edge
Loss Edge
Common Edge
(c)
ATF3
BHLHE40
CEBPB
CTCF
E2F4
EGR1
ELF1
ELK1
ETS1
ETV6
FOS
GABPA
HNF4G
JUNB
JUND
MAFK
MAX
MEF2A
MYC
NFE2
NFE2L2
NFYA
NFYB
NR2C2
NRF1
REST
RFX5
SP1
SPI1
SRF
TBP
USF1
USF2
YY1
ZBED1
ZBTB33
ZNF143
A549 vs IMR-90
HepG2 vs Liver
K562 vs GM12878
MCF-7 vs MCF-10A
(d)
0.272
0.170
0.125
(e)
GM12878 vs K562
GM12878 vs K562
GM12878 vs K562
GM12878 vs K562
CTCF
JUND
MYC
BHLHE40
IMR-90 vs A549
Liver vs HepG2
MCF-10A vs MCF-7
IMR-90 vs A549

Overall Gene Target (n=15,189)

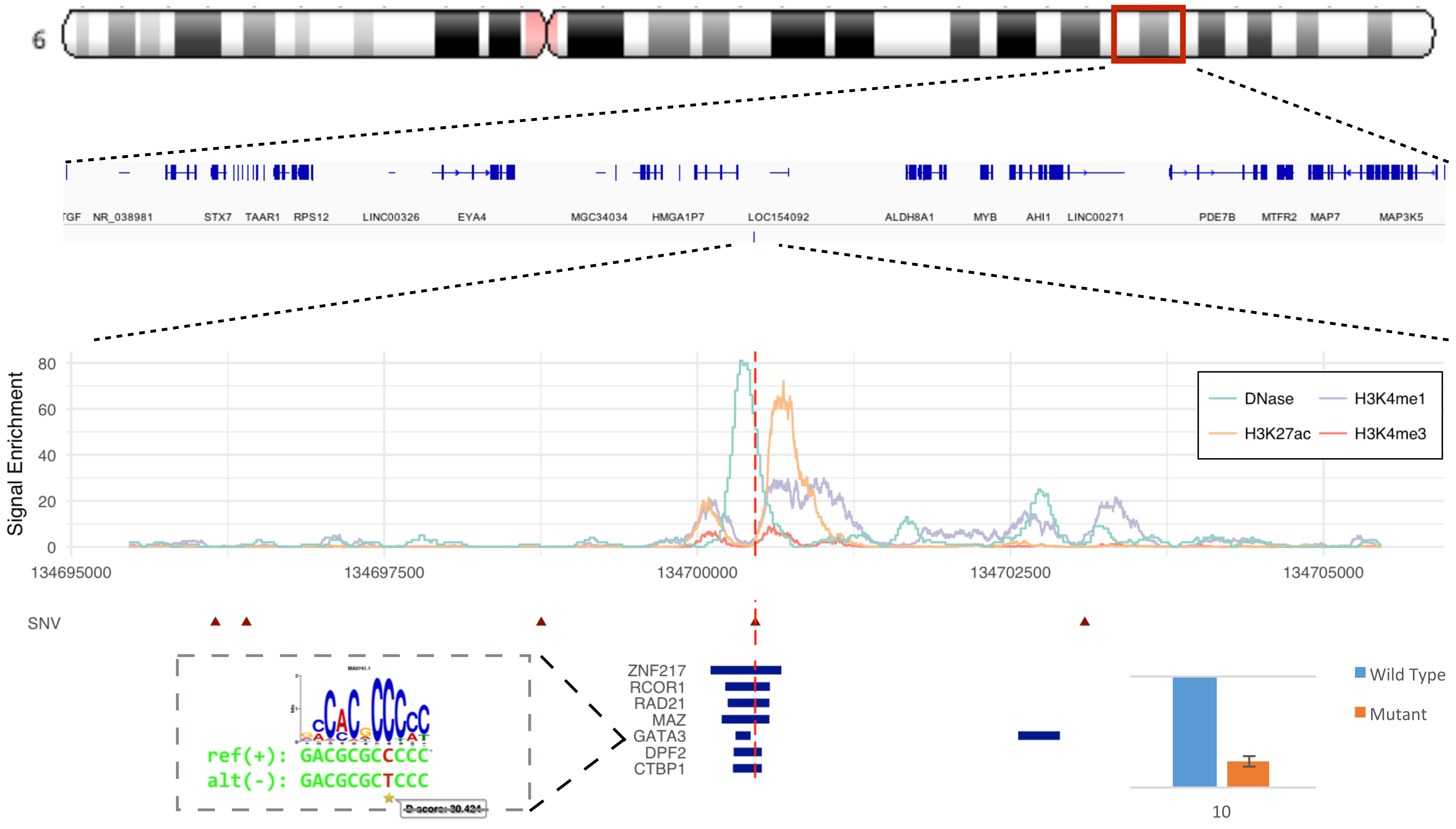
Expression (TPM)	UP			NC			DN		
n	2442			10294			2453		
%	16.1%			67.8%			16.1%		
DHS (TSS Cov) active	UP	NC	DN	UP	NC	DN	UP	NC	DN
n	622	1622	198	1280	7723	1291	108	1430	915
%	25.5%	66.4%	8.1%	12.4%	75.0%	12.5%	4.4%	58.3%	37.3%
H3K4me3 (TSS Cov) active promoter	UP	NC	DN	UP	NC	DN	UP	NC	DN
n	569	1817	56	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%		



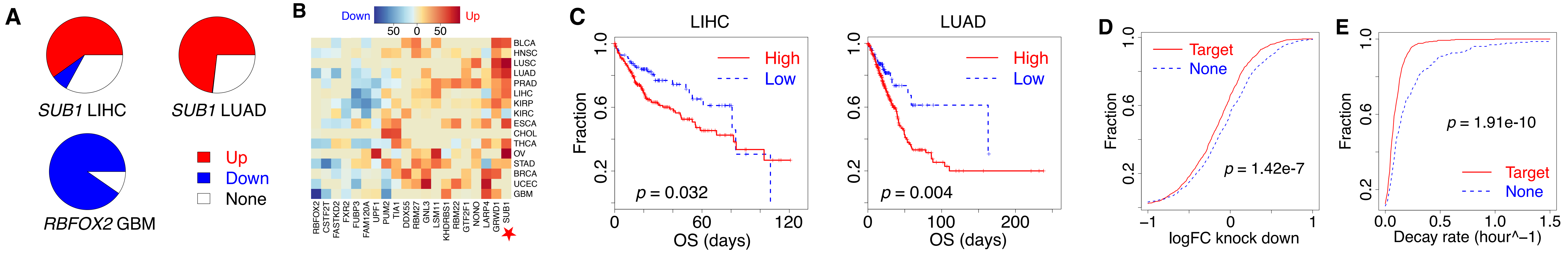



(a)
Enhanced
Static
Suppressed
1.00
0.75
0.50
0.25
0.00
0.8
0.6
0.4
0.2
0.0
Gain
Common
Loss
-1.0
-0.5
0.0
0.5
1.0
<2Fold
>2Fold
H3K27me3
H3K4me3
DNase
Expression
(b)
loss.pval
gain.pval
ZNF740
ZNF263
ZNF143
ZFX
ZBTB7A
ZBTB33
ZBED1
YY1
USF2
USF1
THAP1
TEAD4
TCF7L2
TCF7
TBP
SRF
SREBF1
SPI1
SP2
SP1
RUNX1
RFX5
RFX1
REST
RELA
PKNOX1
NRF1
NR2F6
NR2F1
NR2C2
NFYB
NFYA
NFE2
MYC
MITF
MEF2D
MEF2A
MAX
MAFK
MAFG
MAFF
LEF1
KLF16
KLF13
KLF1
JUND
JUNB
JUN
IRF9
IRF2
IRF1
HINFP
HES1
GATA2
GATA1
GABPA
FOXJ2
FOSL1
FOS
ETV6
ETV1
ETS1
ESRRA
ELK1
ELF1
EGR1
E2F6
E2F4
CUX1
CTCF
CREB3L1
CREB3
CEBPG
CEBPB
BHLHE40
ATF3
ATF1
-log(pval)
0
1
2
3
4
5
Wilcox Rank Sum Test
(c)
Lymph-CLL
4
3
2
1
0
tss.edge
edge.with.var
edge.loss
edge.gain

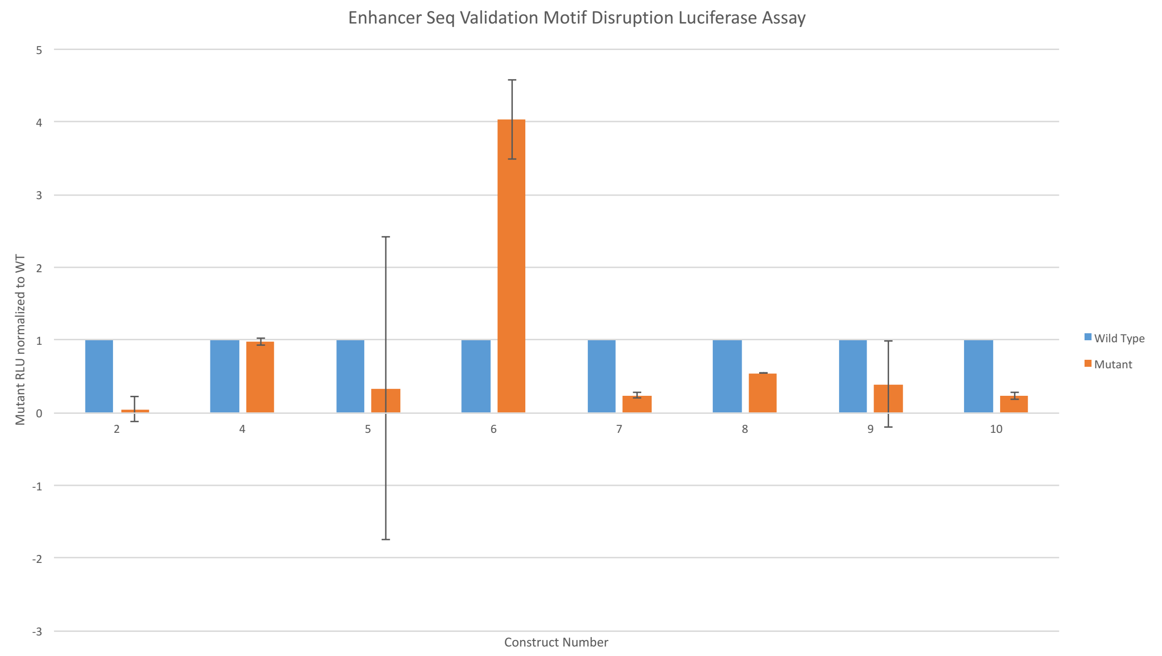
(a)



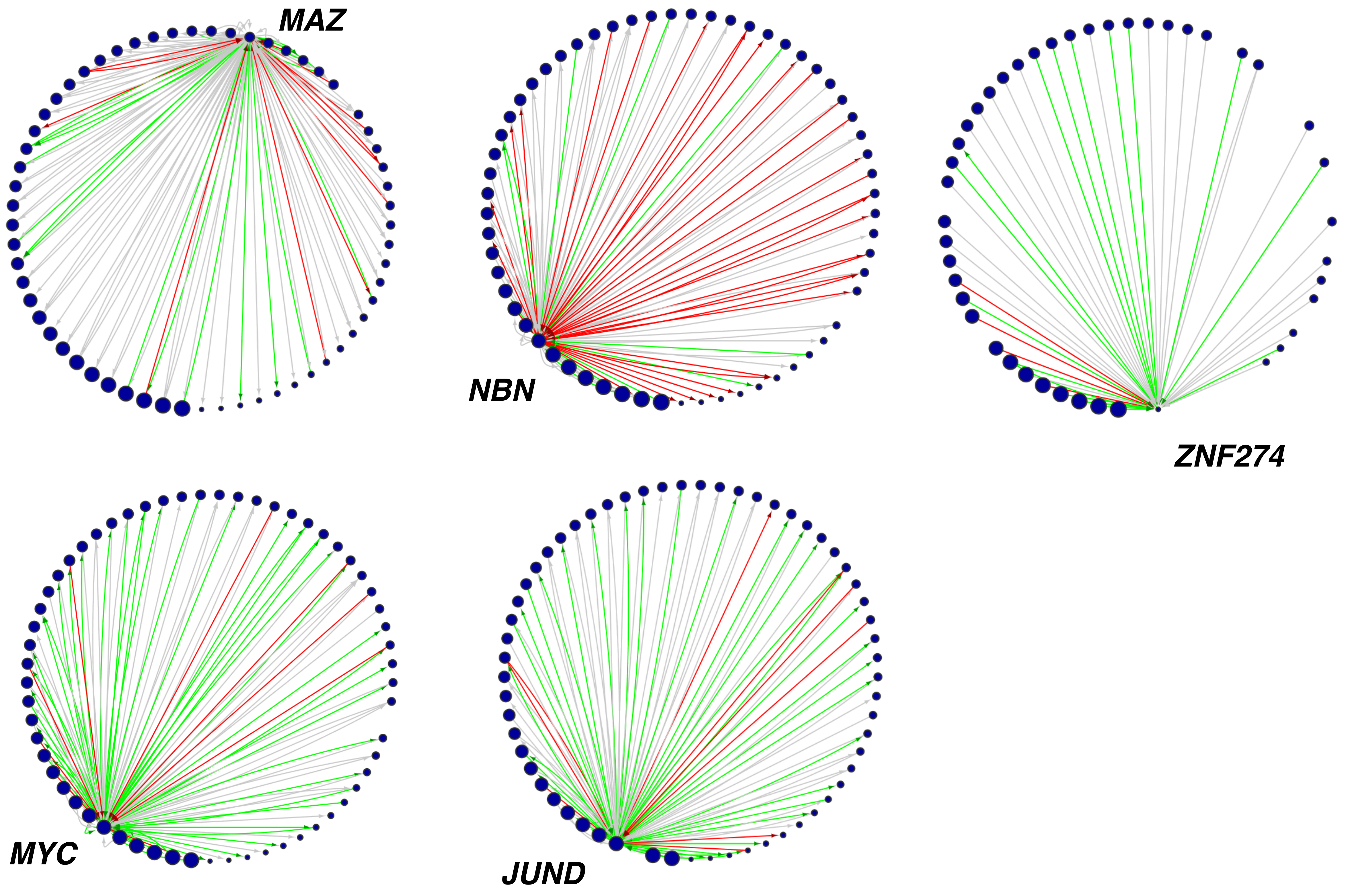
6
TGF
NR_038981
STX7
TAAR1
RPS12
LINC00326
EYA4
MGC34034
HMGA1P7
LOC154092
ALDH8A1
MYB
AHI1
LINC00271
PDE7B
MTFR2
MAP7
MAP3K5
Signal Enrichment
80
60
40
20
0
DNase
H3K4me1
H3K27ac
H3K4me3
134695000
134697500
134700000
134702500
134705000
SNV
ref(+): GACGCGCCCCC
alt(-): GACGCGCTCCC
D-score: 30.424
ZNF217
RCOR1
RAD21
MAZ
GATA3
DPF2
CTBP1
Wild Type
Mutant
10

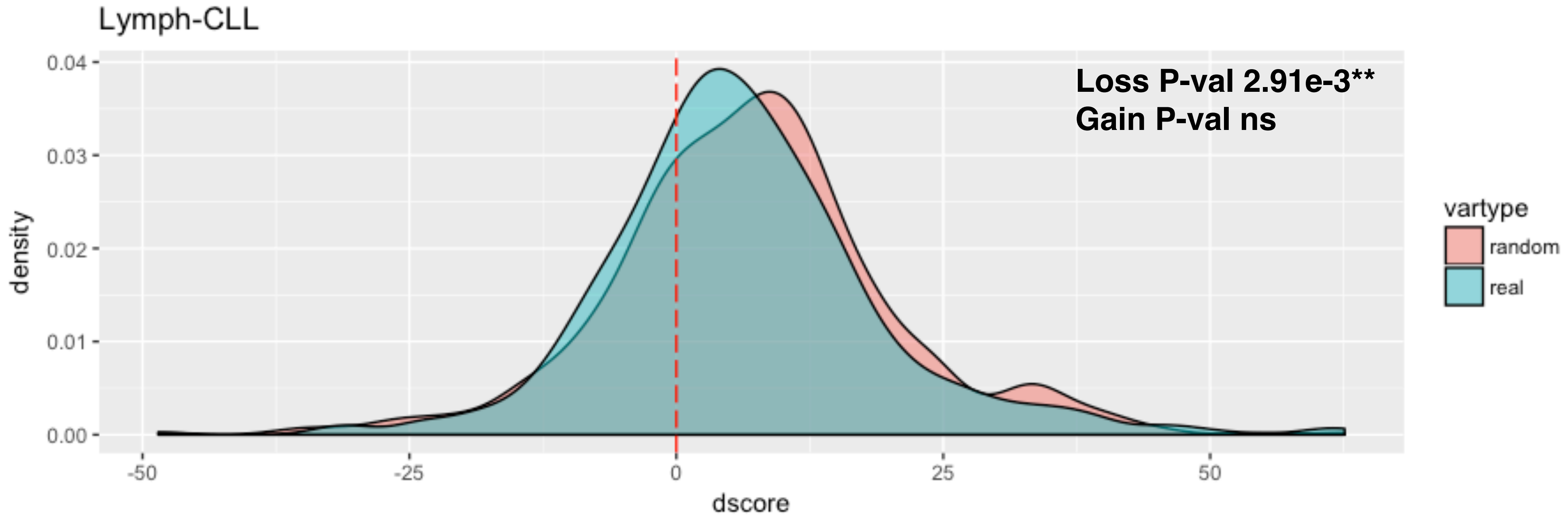


A
SUB1 LIHC
SUB1 LUAD
RBFOX2 GBM
Up
Down
None
B
Down
Up
50
0
50
BLCA
HNSC
LUSC
LUAD
PRAD
LIHC
KIRP
KIRC
ESCA
CHOL
THCA
OV
STAD
BRCA
UCEC
GBM
RBFOX2
CSTF2T
FASTKD2
FXR2
FUBP3
FAM120A
UPF1
PUM2
TIA1
DDX55
RBM27
GNL3
LSM11
KHDRBS1
RBM22
GTF2F1
NONO
LARP4
GRWD1
SUB1
C
LIHC
High
Low
Fraction
1.0
0.6
0.2
p = 0.032
0
60
120
OS (days)
LUAD
High
Low
1.0
0.6
0.2
p = 0.004
0
100
200
OS (days)
D
Target
None
Fraction
1.0
0.6
0.2
p = 1.42e-7
−1
0
1
logFC knock down
E
Fraction
1.0
0.6
0.2
p = 1.91e-10
Target
None
0.0
0.5
1.0
1.5
Decay rate (hour^−1)

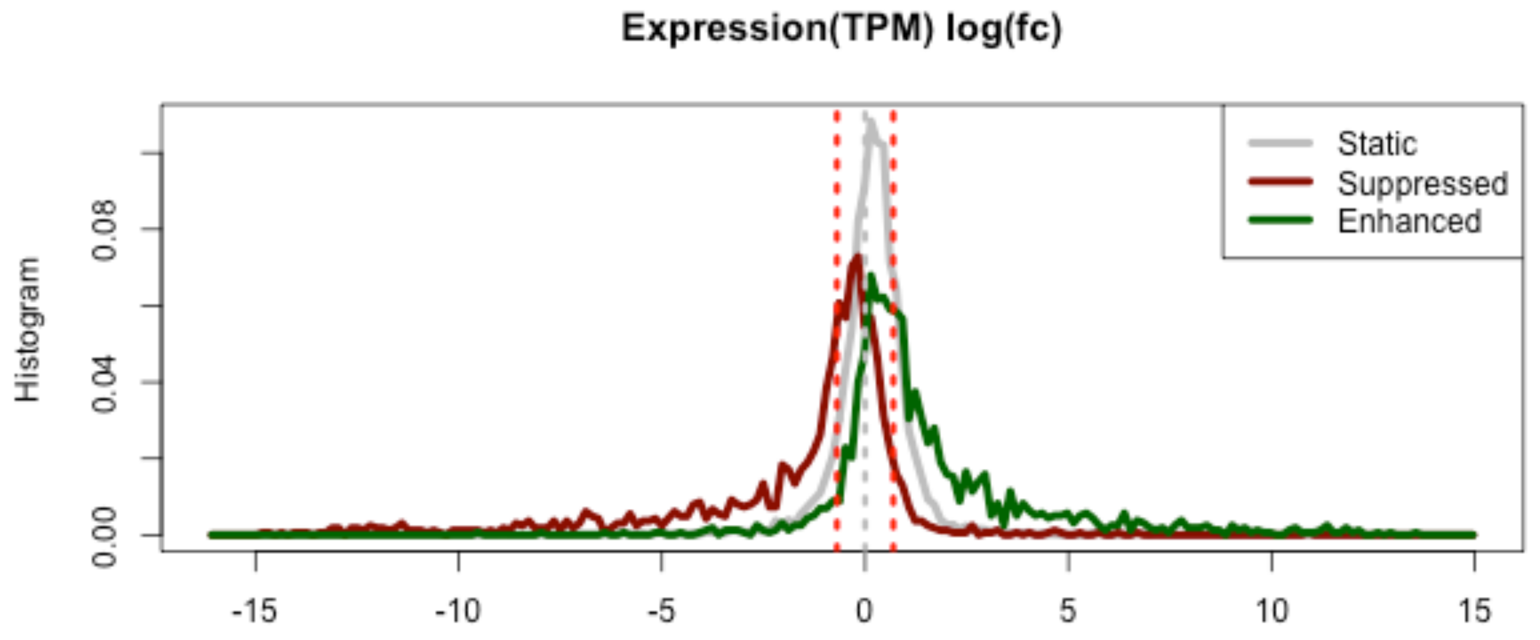


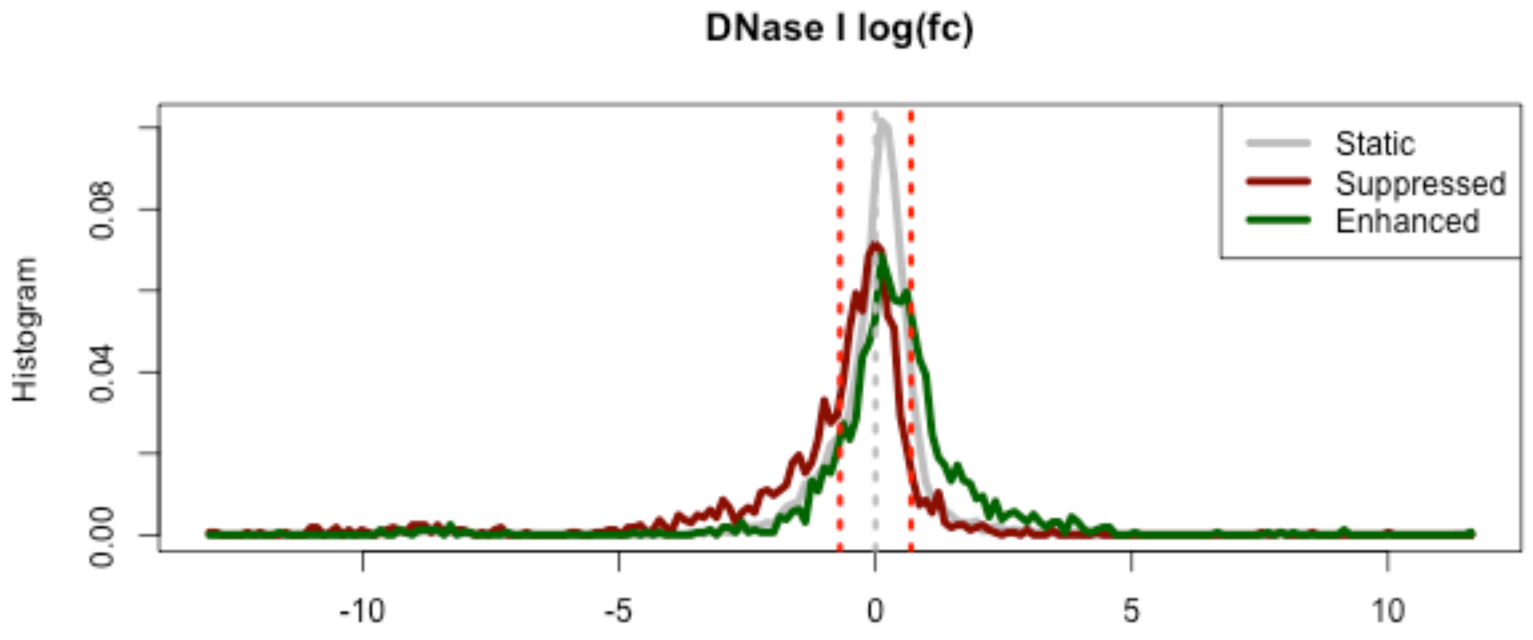
	Sample02	Sample04	Sample05	Sample06	Sample07	Sample08	Sample09	Sample10
chr	chr21	chr17	chr20	chr7	chr20	chr7	chr7	chr6
pos	27,541,982	38,474,408	43,971,343	1,598,567	58,563,412	150,759,483	5,596,005	134,700,462
ref	G	C	G	C	C	C	T	G
alt	A	G	C	T	T	G	G	T
D-score_min	20.361	16.910	3.665	15.746	7.217	13.959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

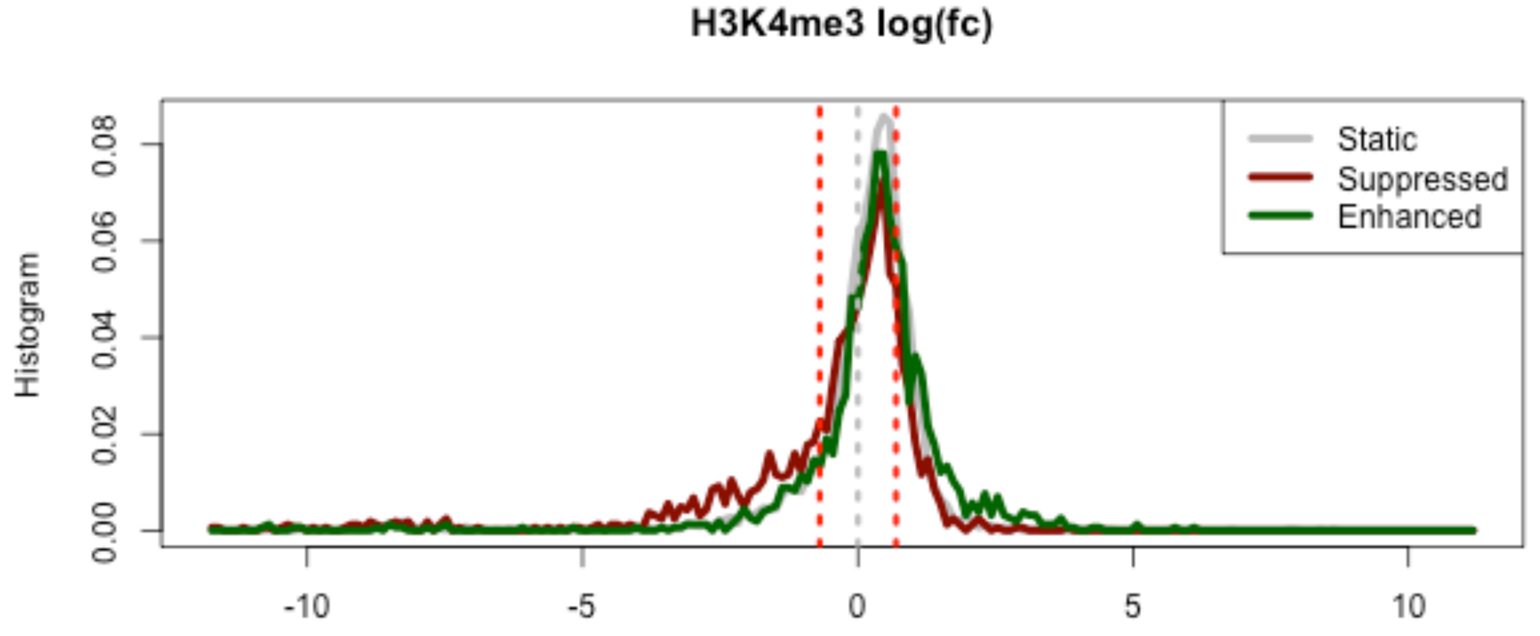

MAZ
NBN
ZNF274
MYC
JUND

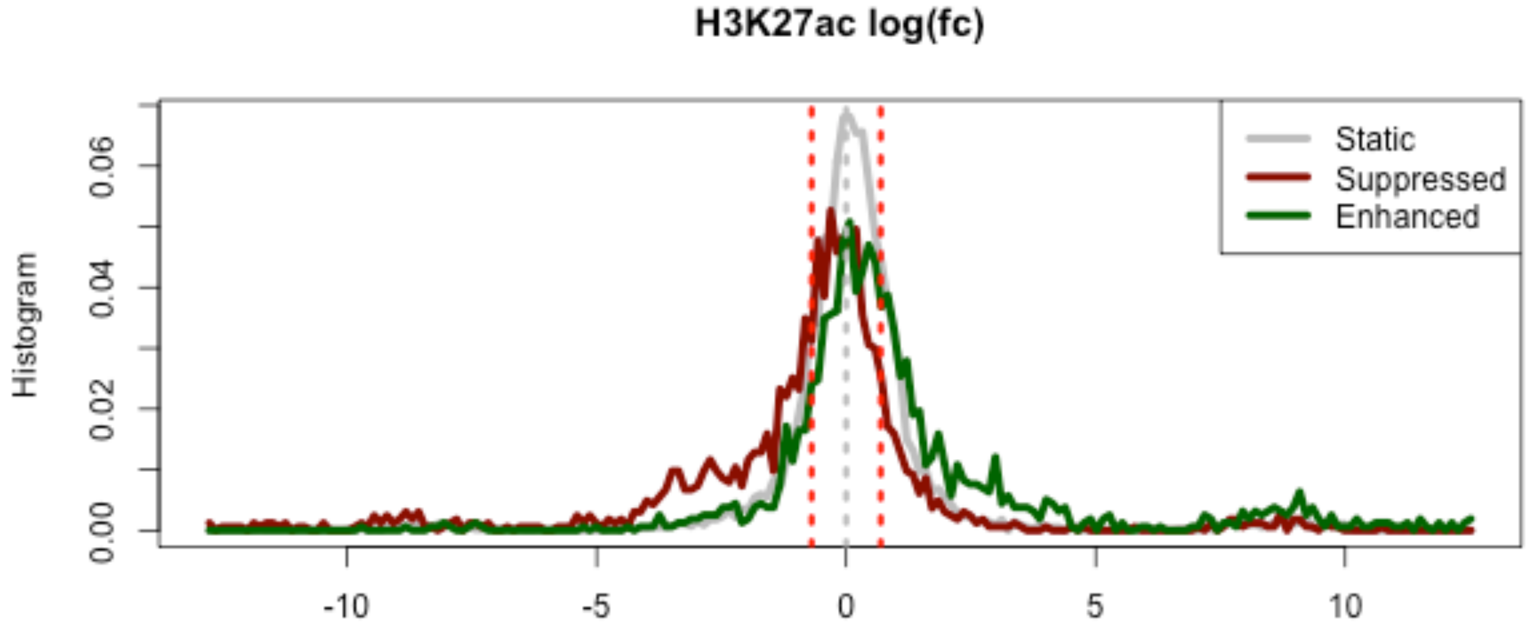


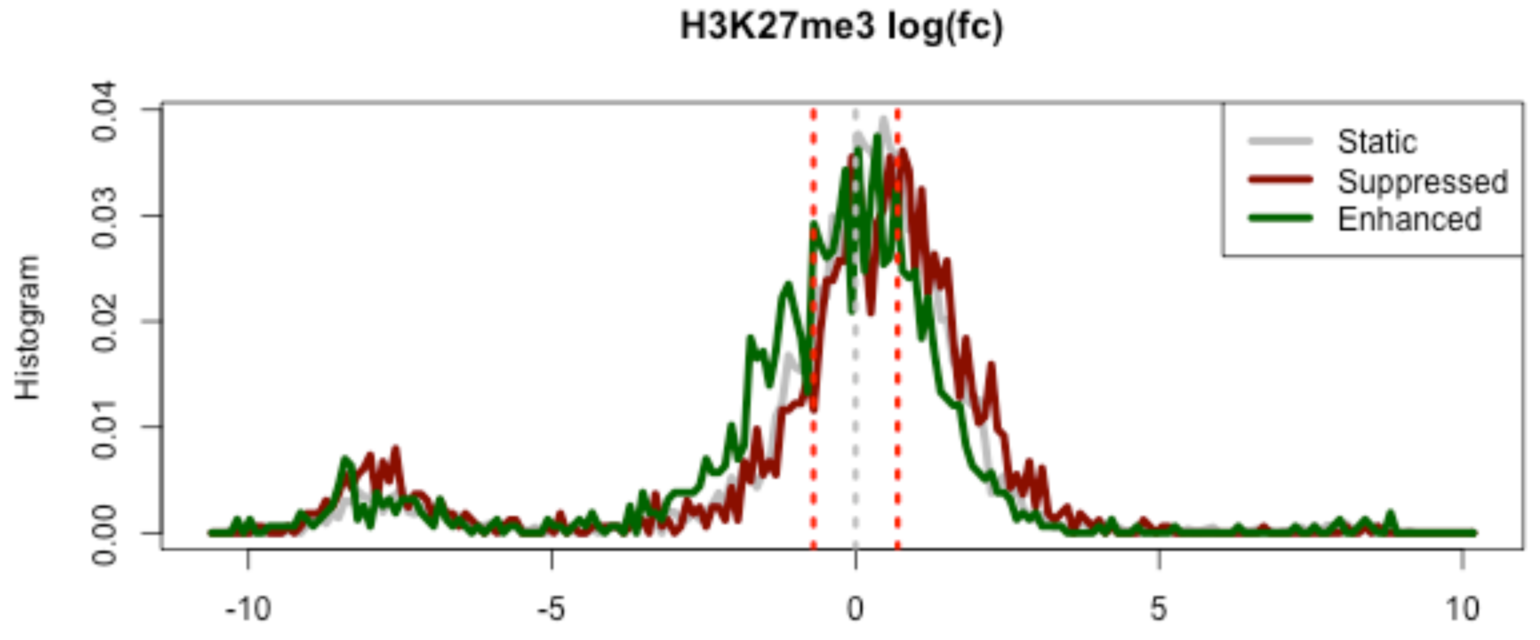
Fisher's Exact Test
ns P > 0.05, * P ≤ 0.05, ** P ≤ 0.01, *** P ≤ 0.001, **** P ≤ 0.0001

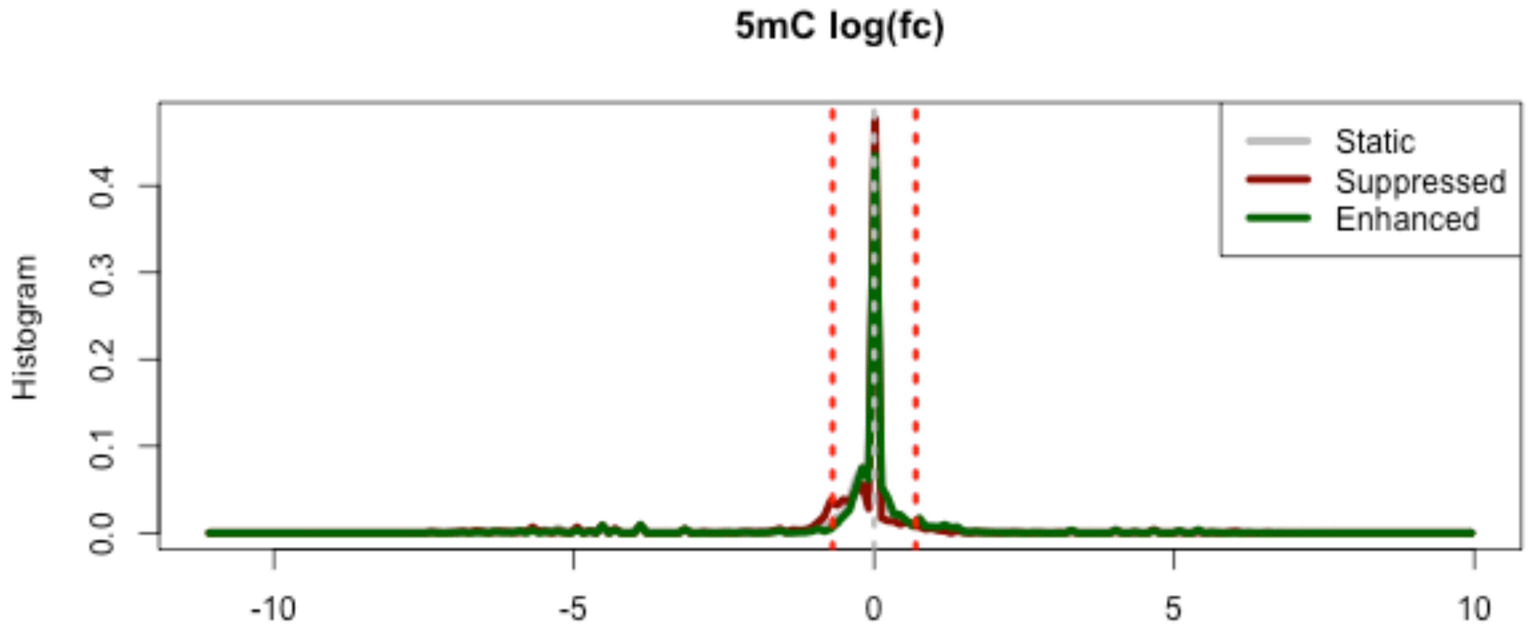

Expression(TPM) log(fc)


DNase I log(fc)

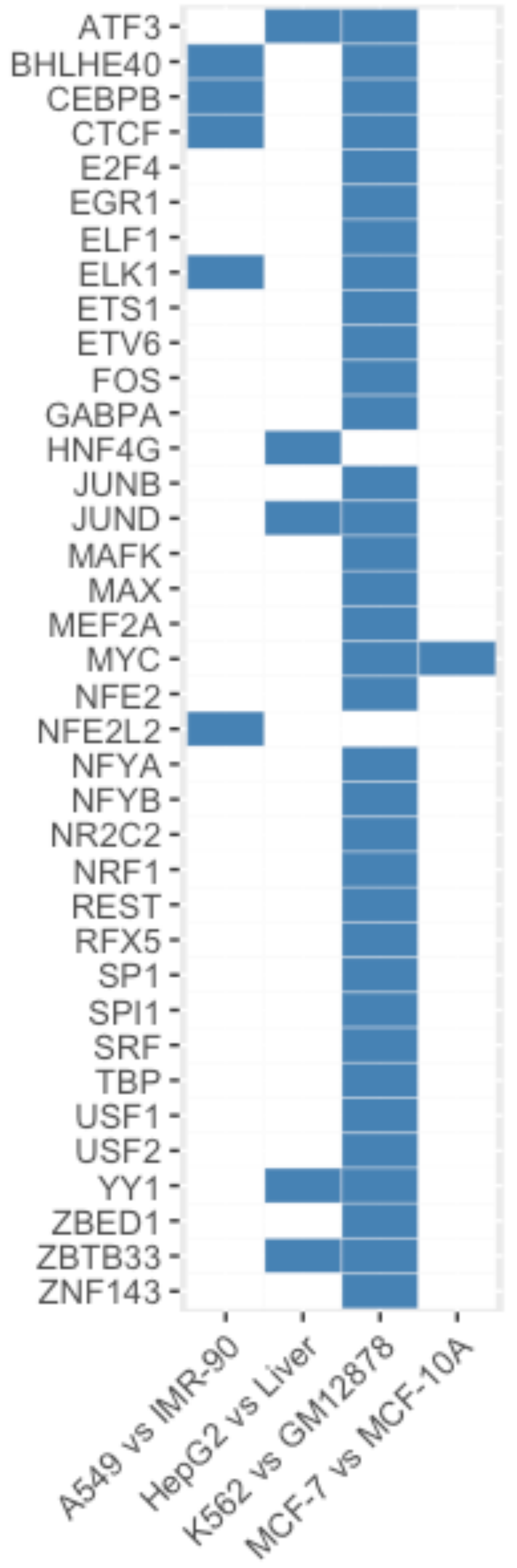

H3K4me3 log(fc)

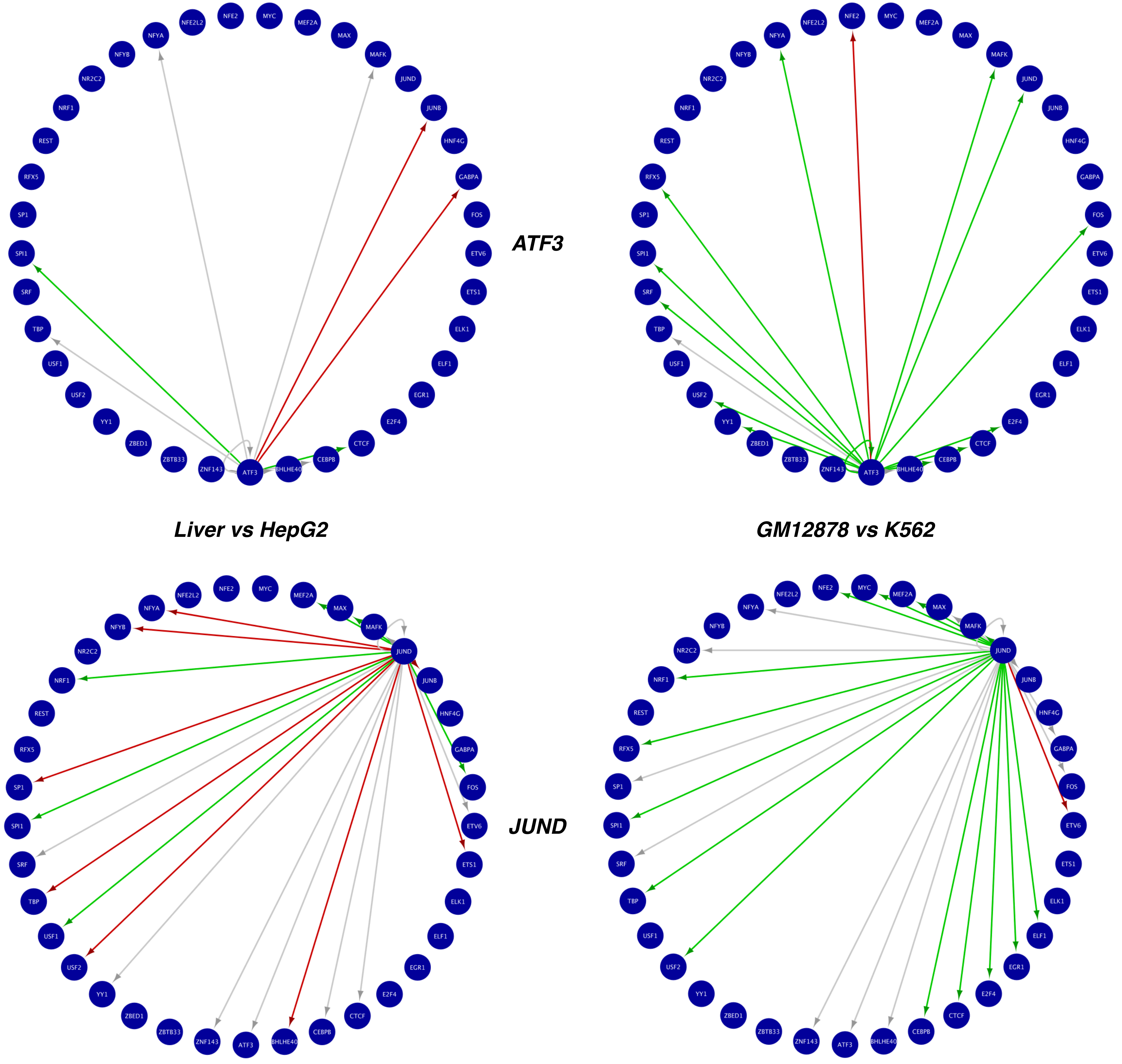

H3K27ac log(fc)

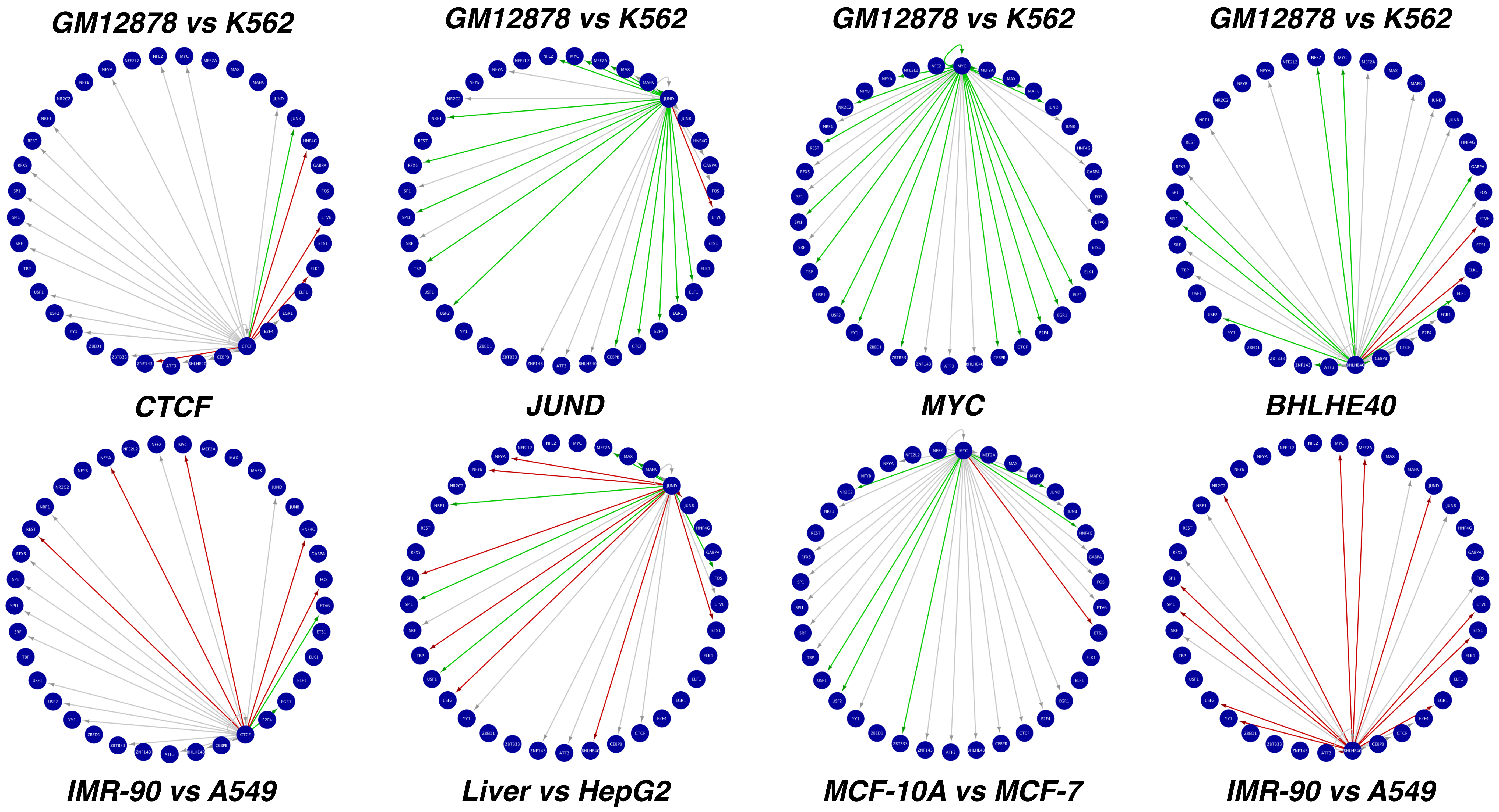

H3K27me3 log(fc)

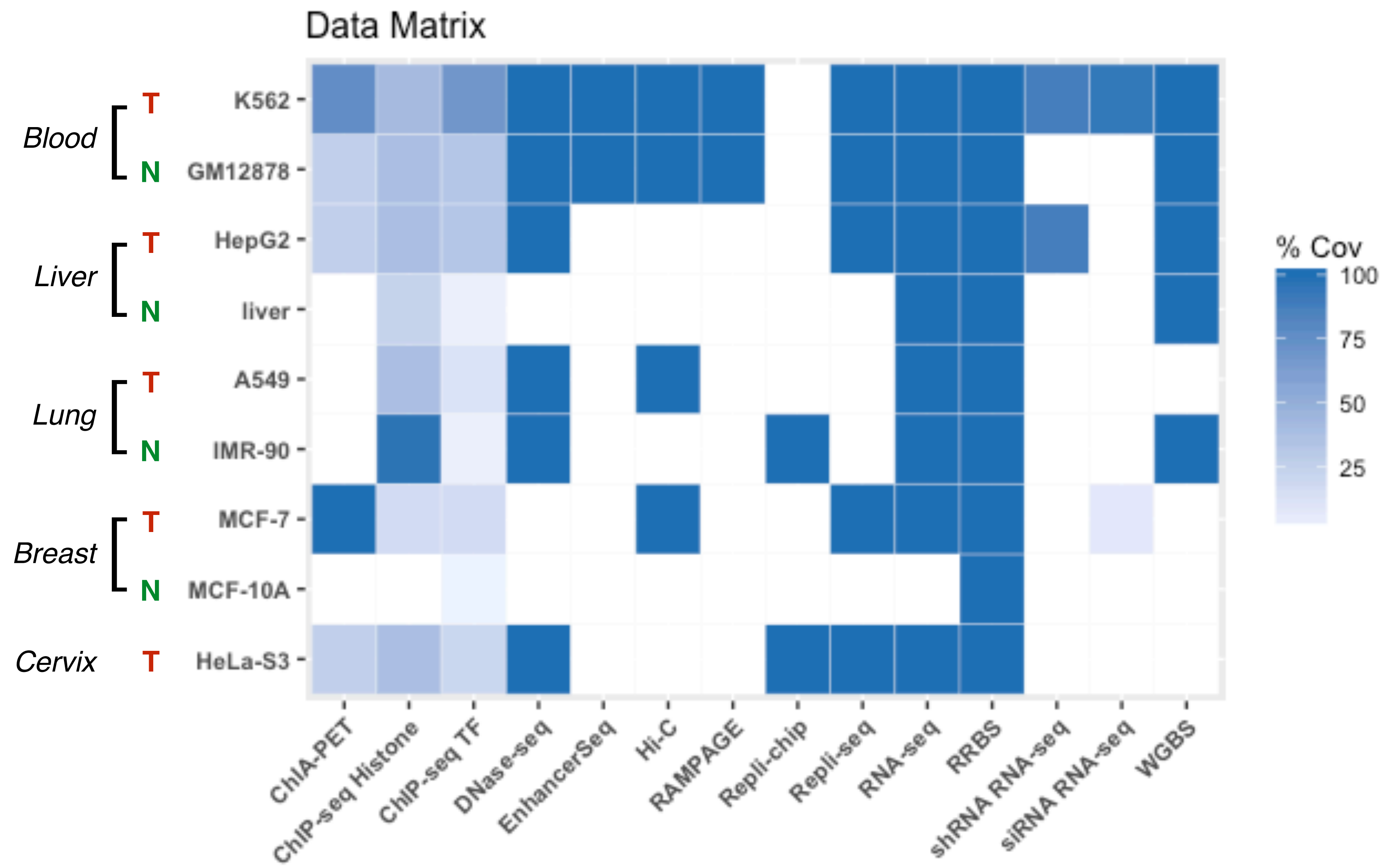

5mC log(fc)

Cross-Cancer TFSS Matrix

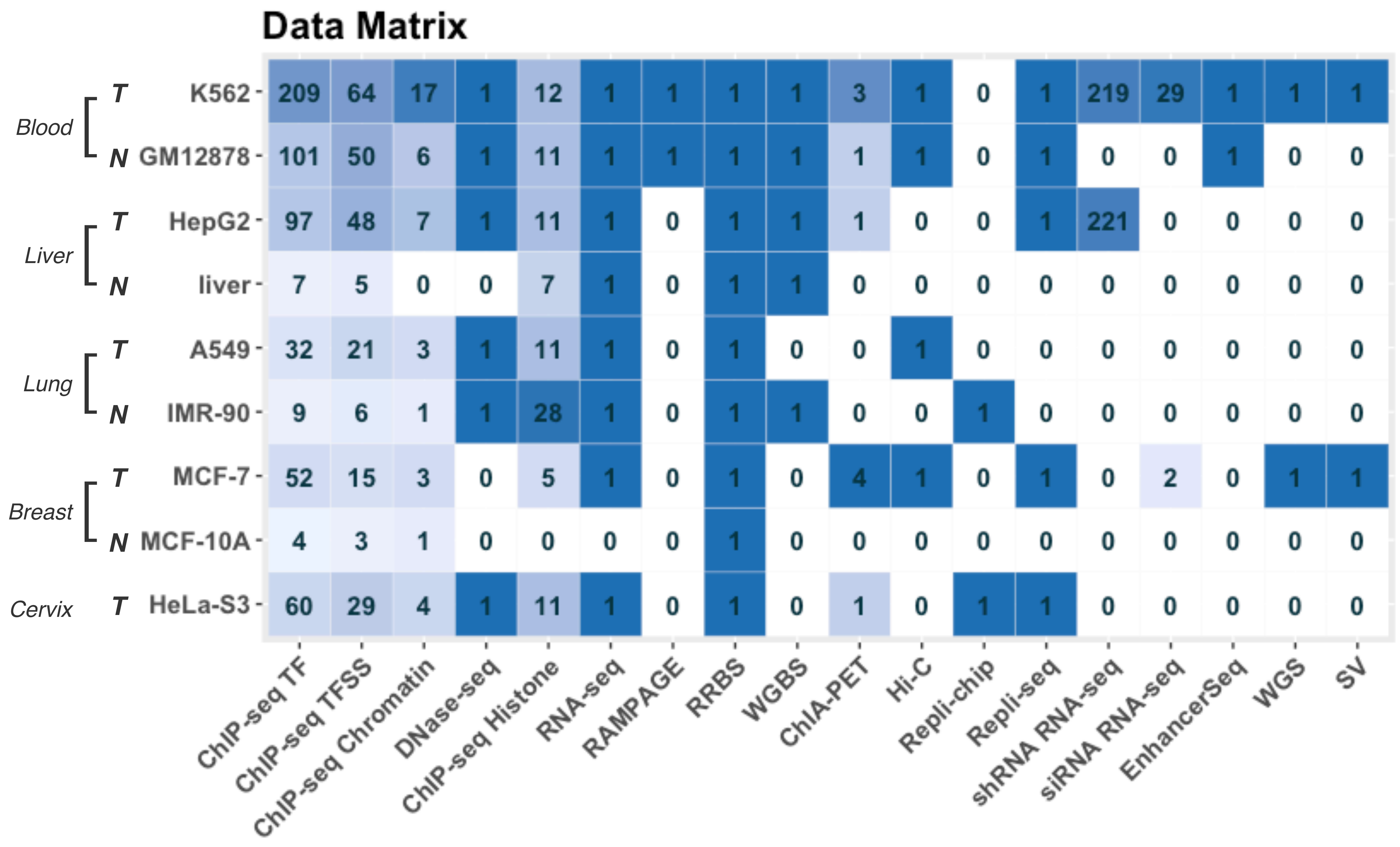





GM12878 vs K562
GM12878 vs K562
GM12878 vs K562
GM12878 vs K562
CTCF
JUND
MYC
BHLHE40
IMR-90 vs A549
Liver vs HepG2
MCF-10A vs MCF-7
IMR-90 vs A549

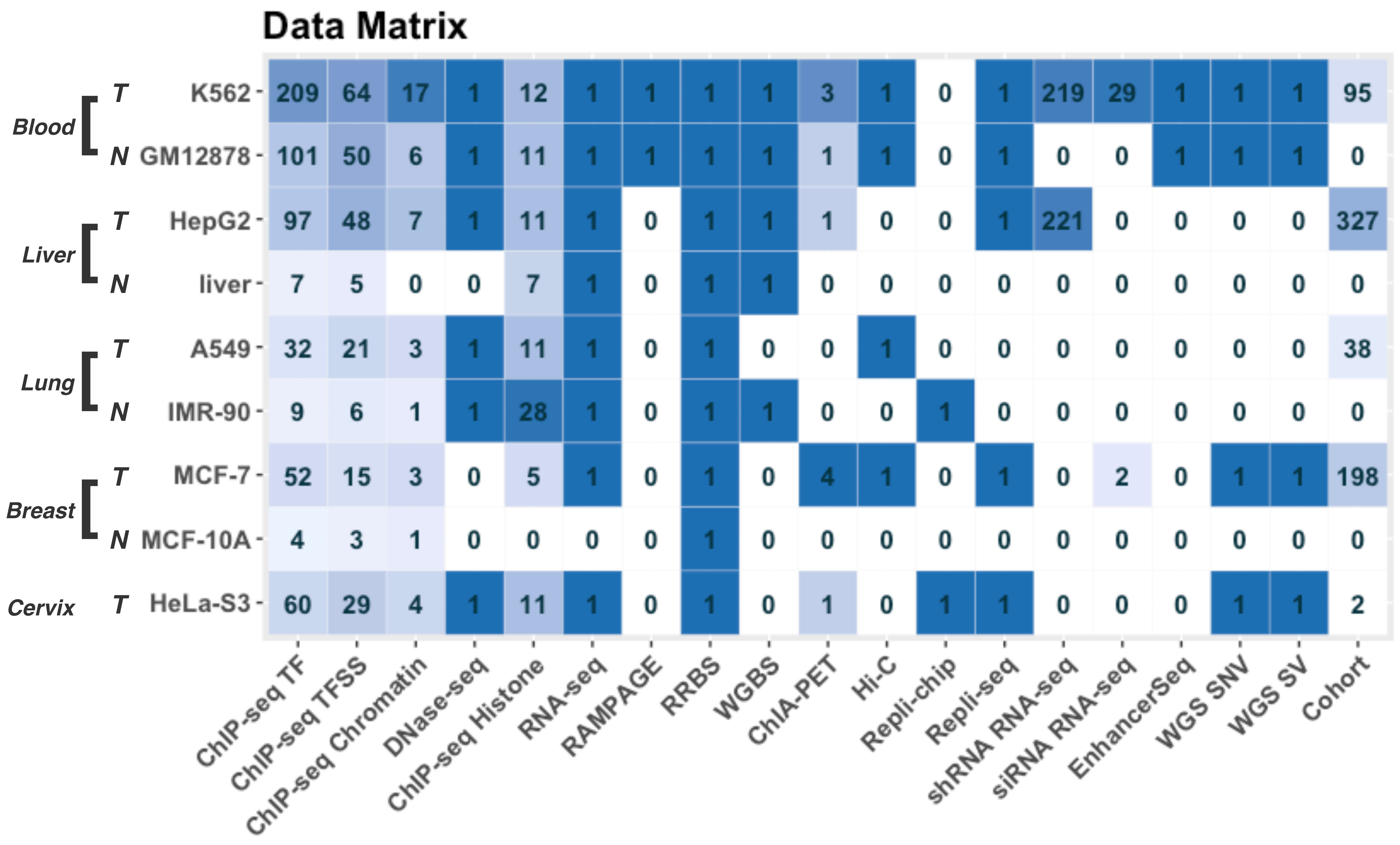


Data Matrix



Data Matrix

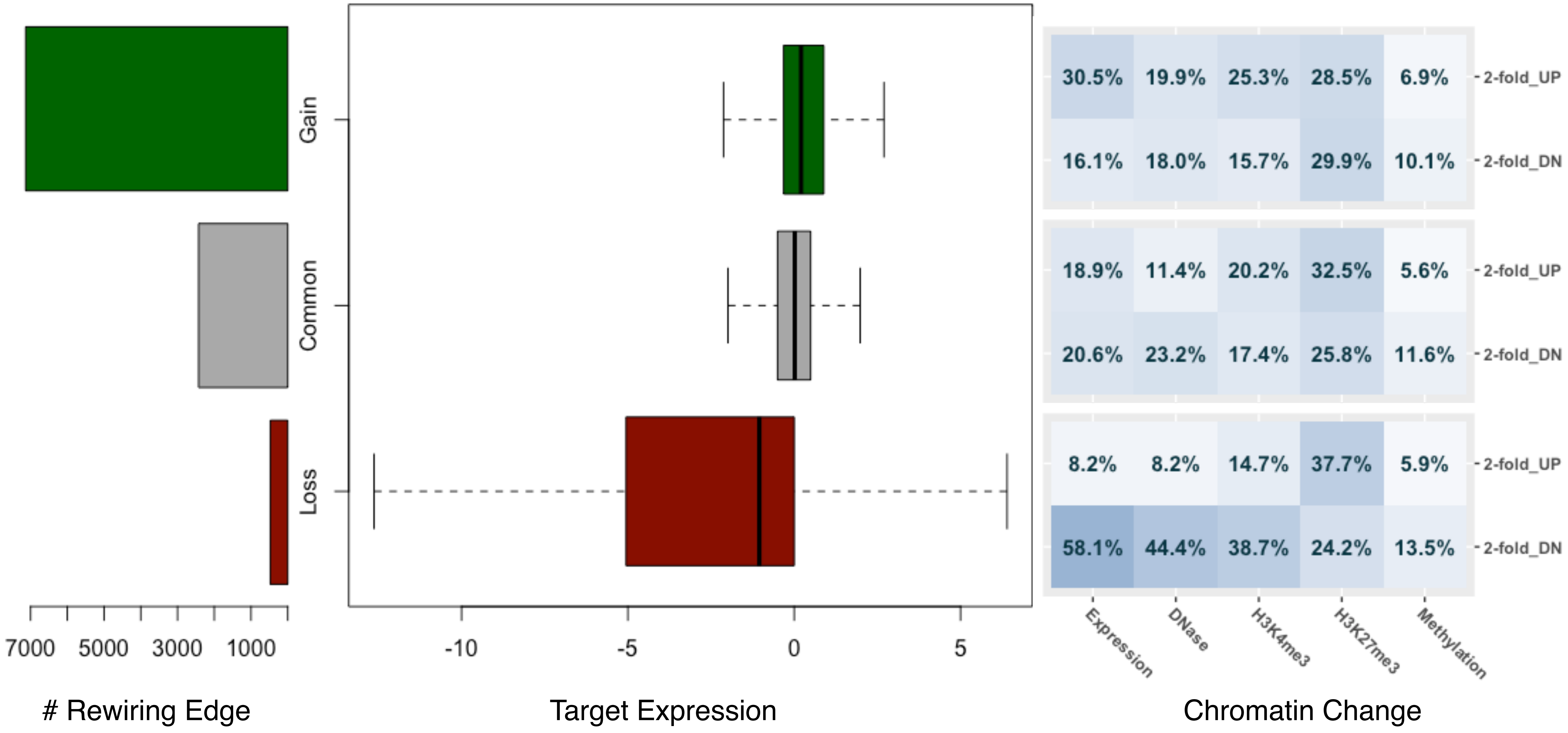
			ChIP-seq TF	ChIP-seq TFSS	ChIP-seq Chromatin	DNase-seq	ChIP-seq Histone	RNA-seq	RAMPAGE	RRBS	WGBS	ChIA-PET	Hi-C	Repli-chip	Repli-seq	shRNA RNA-seq	siRNA RNA-seq	EnhancerSeq	WGS	SV
Blood	T	K562	209	64	17	1	12	1	1	1	1	3	1	0	1	219	29	1	1	1
	N	GM12878	101	50	6	1	11	1	1	1	1	1	1	0	1	0	0	1	0	0
Liver	T	HepG2	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

			ChIP-seq TF	ChIP-seq TFSS	ChIP-seq Chromatin	DNase-seq	ChIP-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	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	1	1	2

JUND

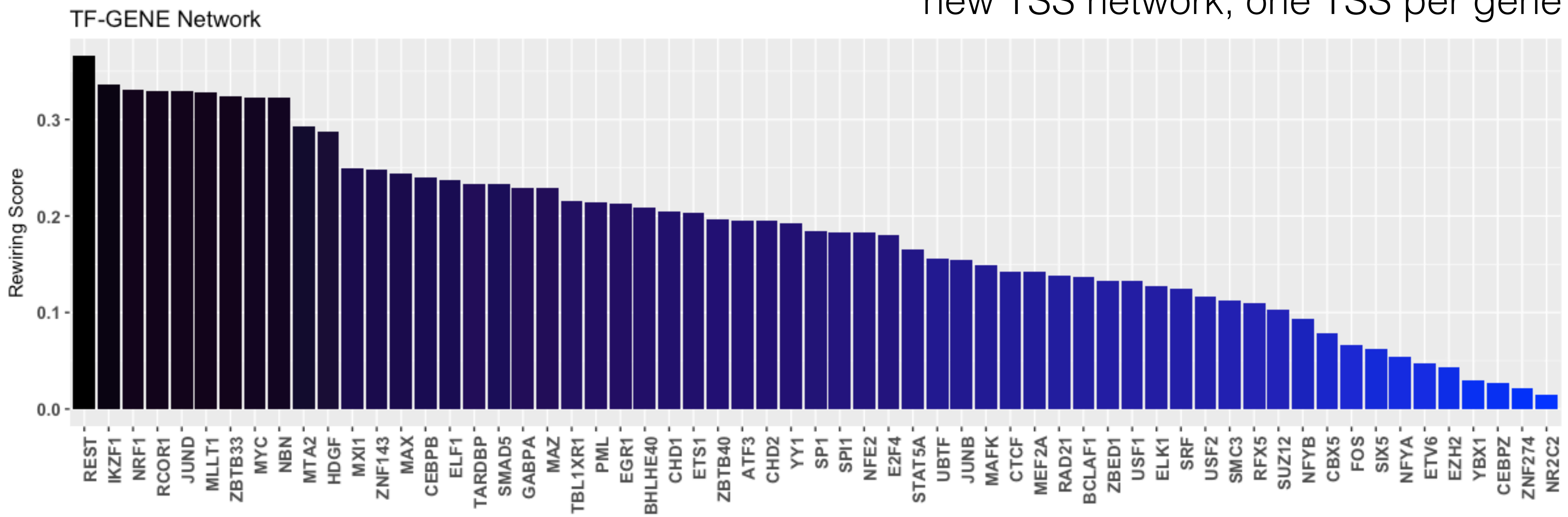


	Expression	DNase	H3K4me3	H3K27me3	Methylation
2-fold_UP	30.5%	19.9%	25.3%	28.5%	6.9%
2-fold_DN	16.1%	18.0%	15.7%	29.9%	10.1%

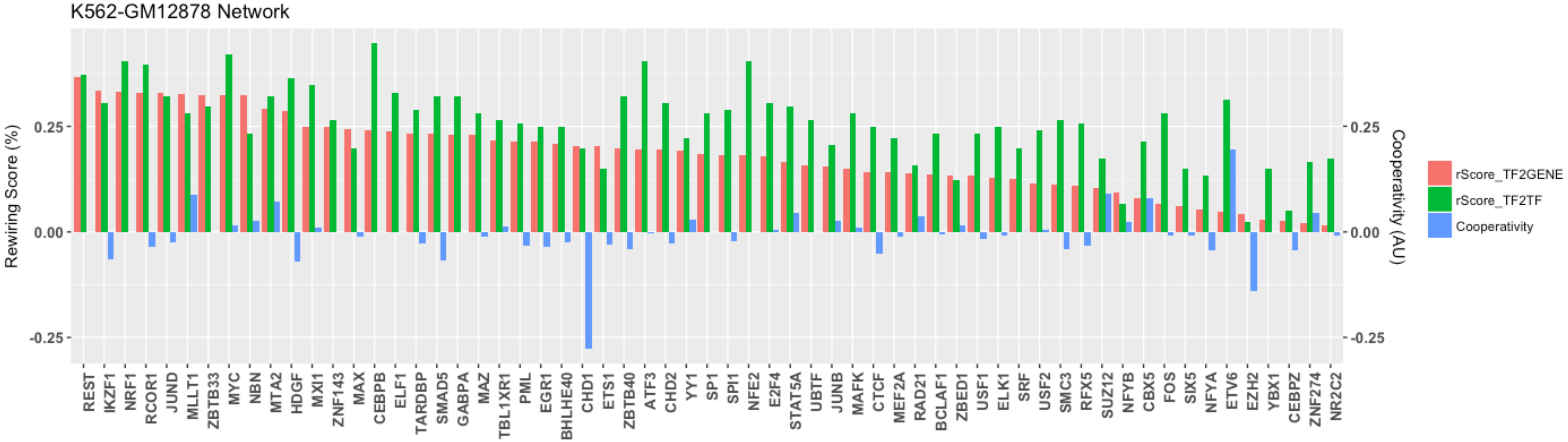
	Expression	DNase	H3K4me3	H3K27me3	Methylation
2-fold_UP	18.9%	11.4%	20.2%	32.5%	5.6%
2-fold_DN	20.6%	23.2%	17.4%	25.8%	11.6%

	Expression	DNase	H3K4me3	H3K27me3	Methylation
2-fold_UP	8.2%	8.2%	14.7%	37.7%	5.9%
2-fold_DN	58.1%	44.4%	38.7%	24.2%	13.5%

new TSS network, one TSS per gene

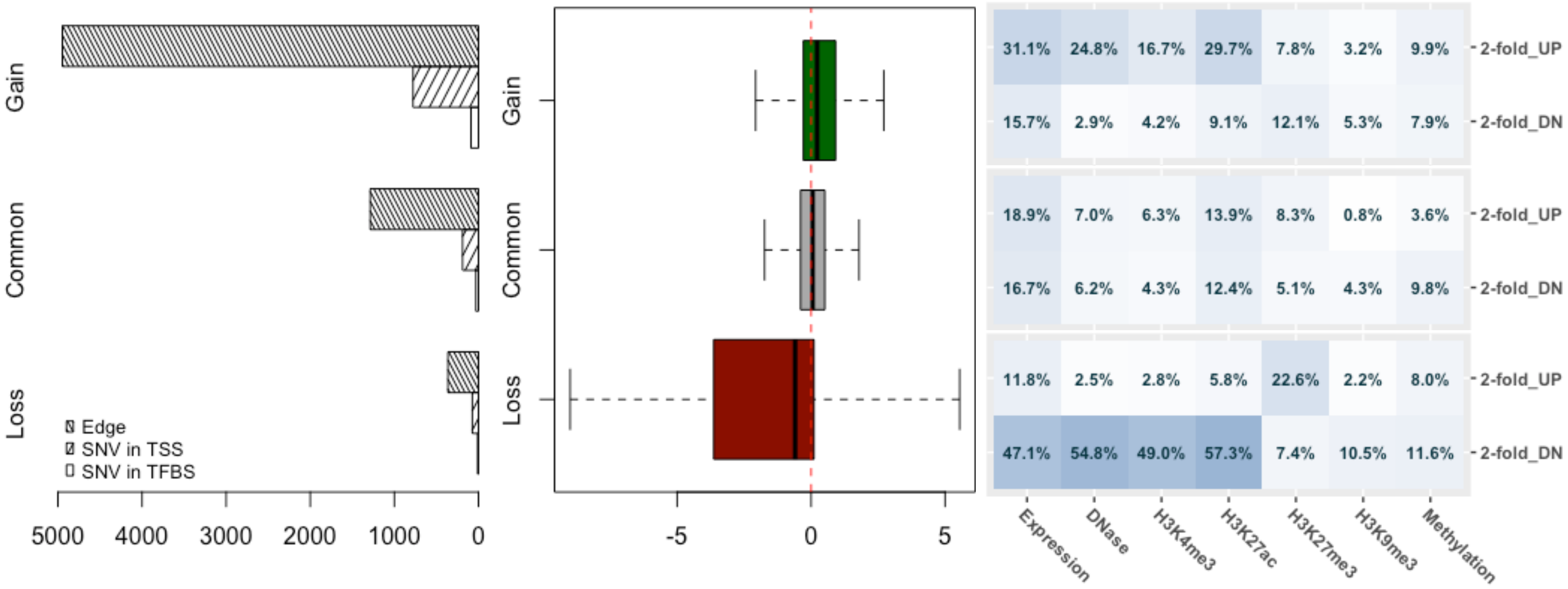


TF-GENE Network

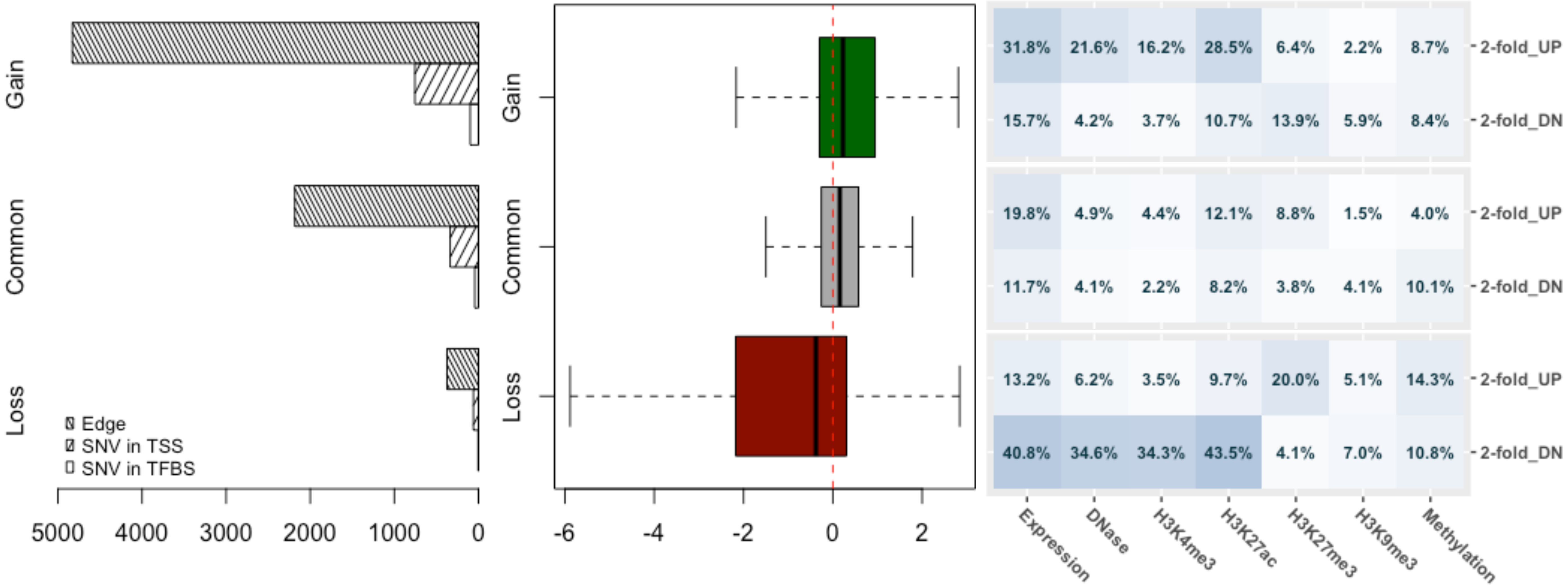


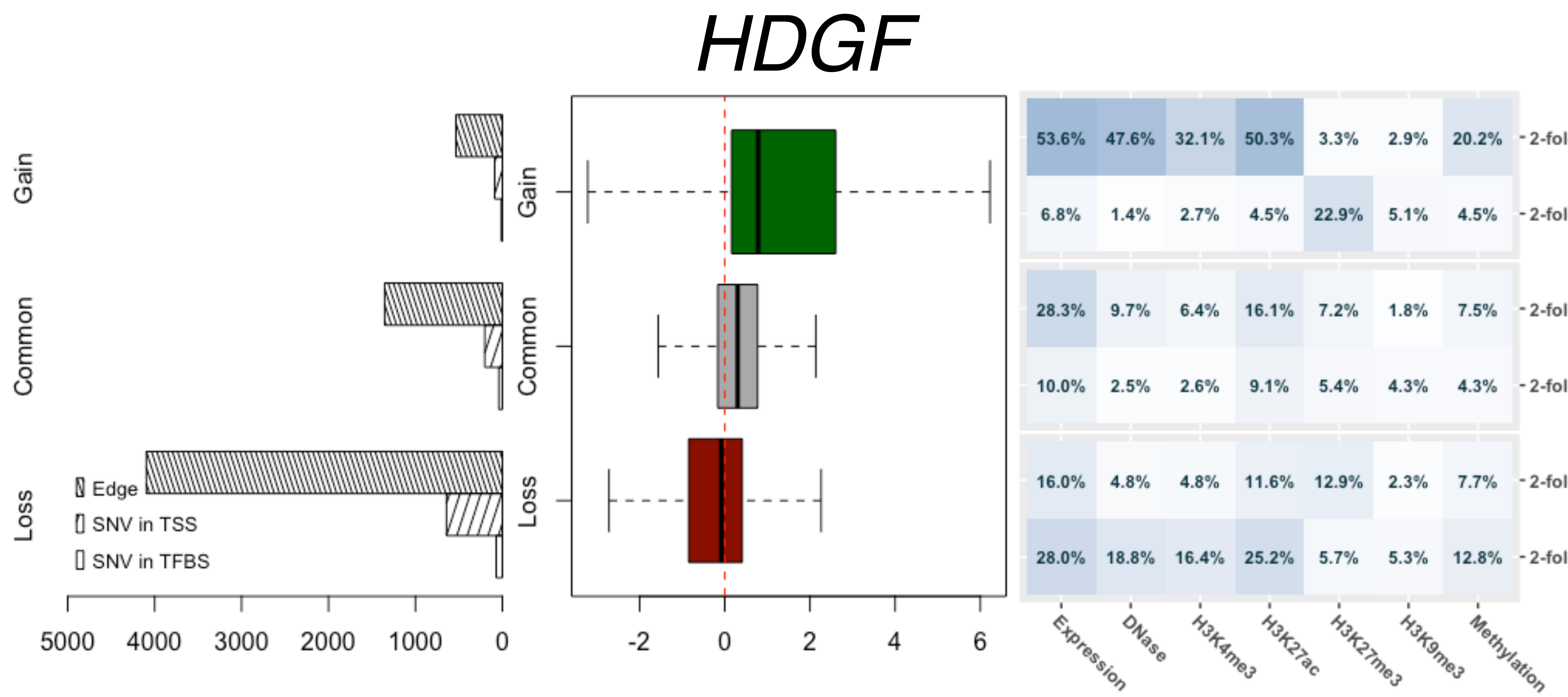
K562-GM12878 Network

JUND


Gain
Common
Loss
Edge
SNV in TSS
SNV in TFBS
5000
4000
3000
2000
1000
0
-5
0
5
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

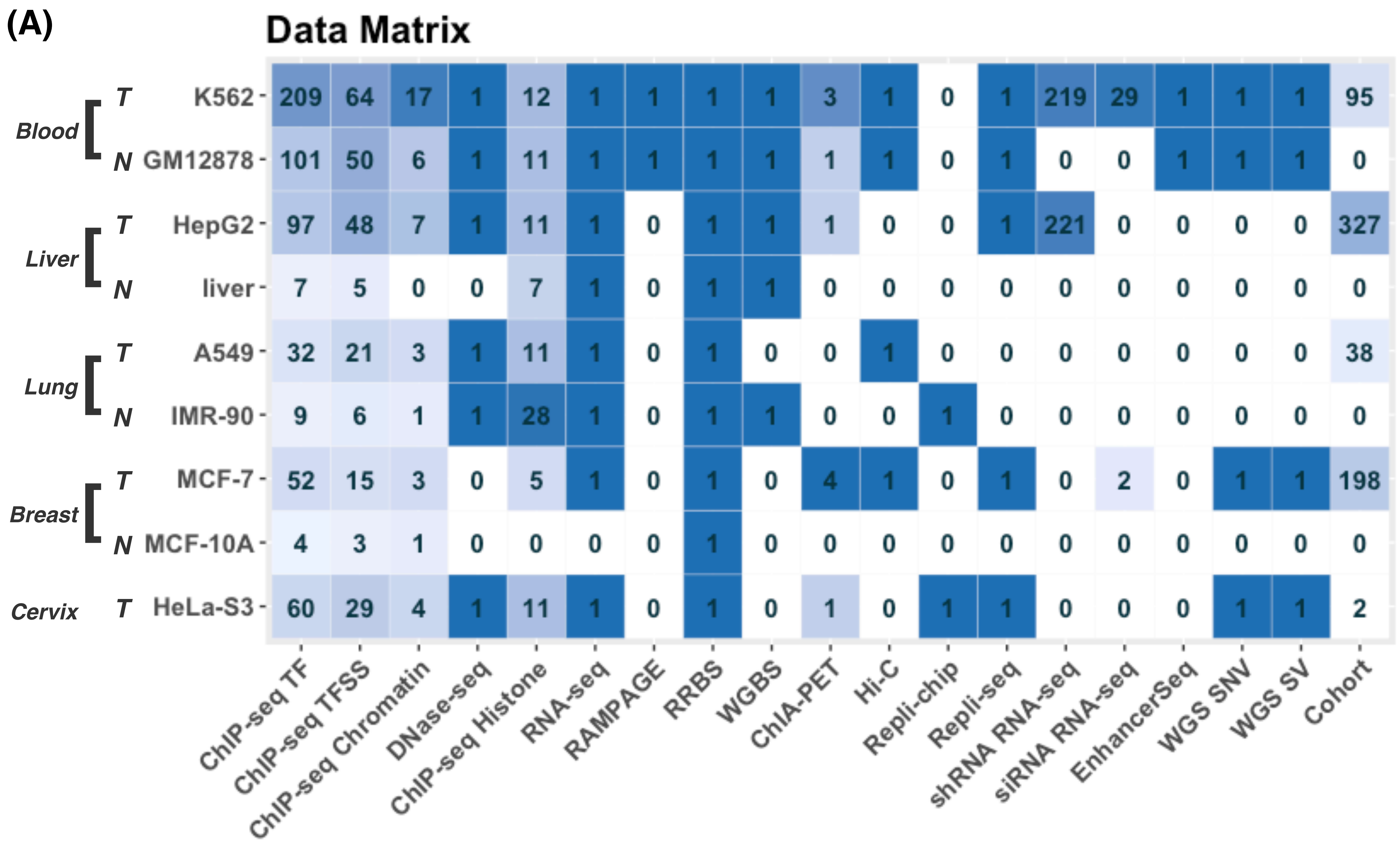
MYC


Gain
Common
Loss
Edge
SNV in TSS
SNV in TFBS
5000
4000
3000
2000
1000
0
-6
-4
-2
0
2
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

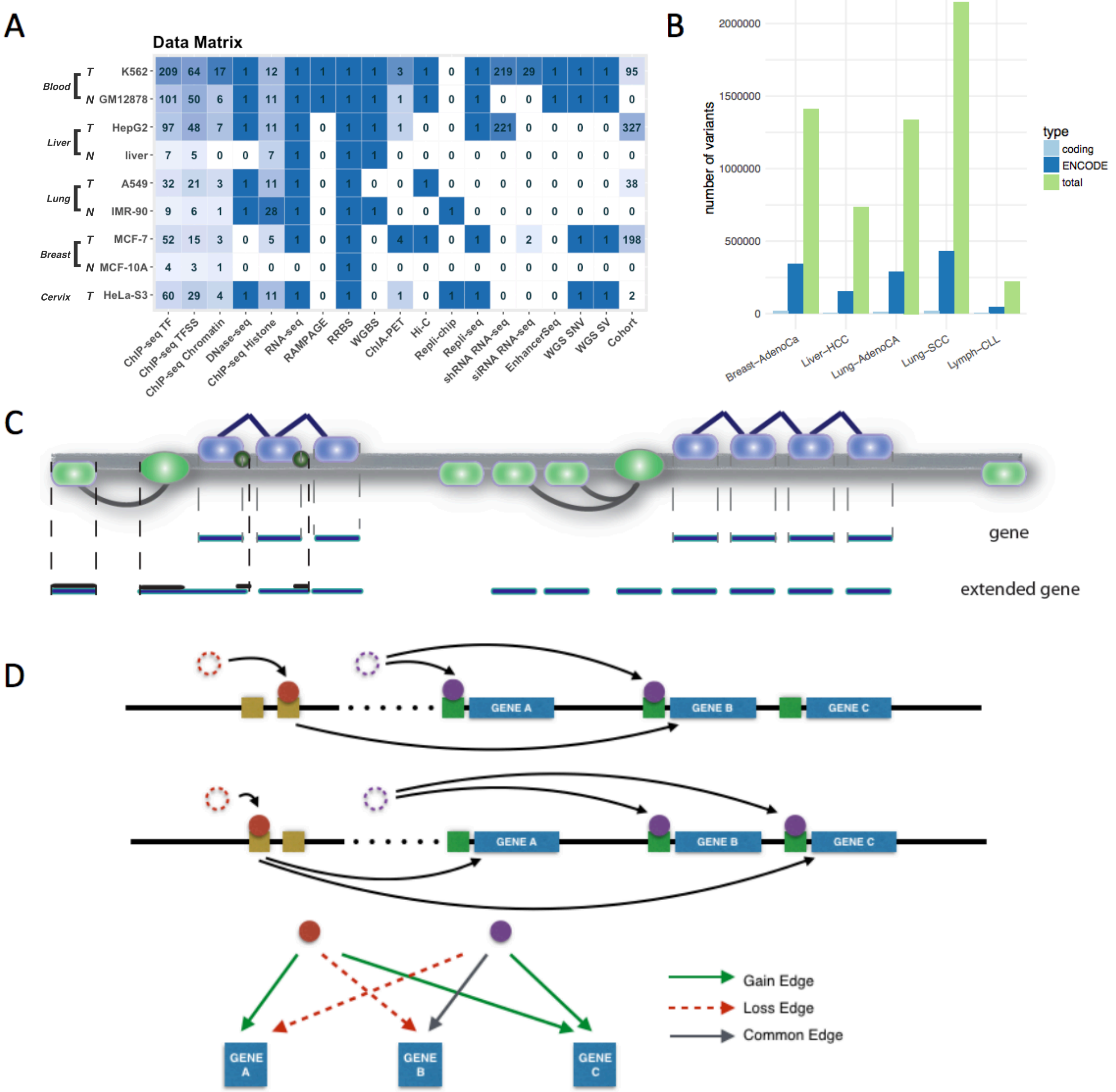
		Expression	DNase	H3K4me3	H3K27ac	H3K27me3	H3K9me3	Methylation
Gain	2-fold_UP	53.6%	47.6%	32.1%	50.3%	3.3%	2.9%	20.2%
	2-fold_DN	6.8%	1.4%	2.7%	4.5%	22.9%	5.1%	4.5%
Common	2-fold_UP	28.3%	9.7%	6.4%	16.1%	7.2%	1.8%	7.5%
	2-fold_DN	10.0%	2.5%	2.6%	9.1%	5.4%	4.3%	4.3%
Loss	2-fold_UP	16.0%	4.8%	4.8%	11.6%	12.9%	2.3%	7.7%
	2-fold_DN	28.0%	18.8%	16.4%	25.2%	5.7%	5.3%	12.8%



Data Matrix

			ChIP-seq TF	ChIP-seq TFSS	ChIP-seq Chromatin	DNase-seq	ChIP-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	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	1	1	2

Figure 1



			ChIP-seq TF	ChIP-seq TFSS	ChIP-seq Chromatin	DNase-seq	ChIP-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	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	1	1	2

Figure 1

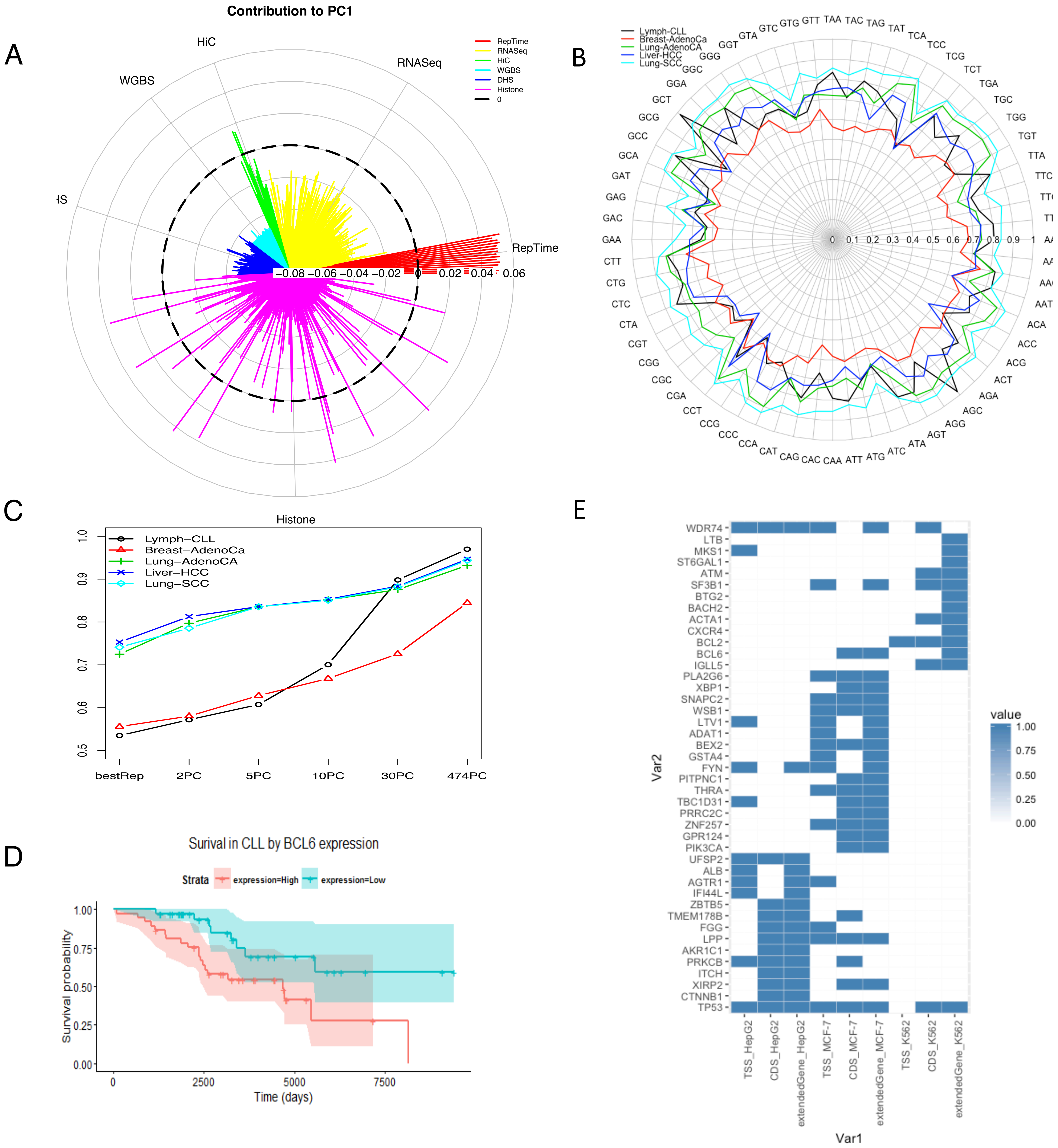

A
Contribution to PC1
HiC
WGBS
RNASeq
RepTime
Histone
RepTime
RNASeq
HiC
WGBS
DHS
Histone
0
−0.08 −0.06 −0.04 −0.02 0 0.02 0.04 0.06
B
Lymph-CLL
Breast-AdenoCa
Lung-AdenoCA
Liver-HCC
Lung-SCC
0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1
C
Histone
Lymph−CLL
Breast−AdenoCa
Lung−AdenoCA
Liver−HCC
Lung−SCC
bestRep
2PC
5PC
10PC
30PC
474PC
0.5
0.6
0.7
0.8
0.9
1.0
D
Surival in CLL by BCL6 expression
Strata
expression=High
expression=Low
Survival probability
Time (days)
0
2500
5000
7500
0.00
0.25
0.50
0.75
1.00
E
Var2
Var1
value
1.00
0.75
0.50
0.25
0.00
WDR74
LTB
MKS1
ST6GAL1
ATM
SF3B1
BTG2
BACH2
ACTA1
CXCR4
BCL2
BCL6
IGLL5
PLA2G6
XBP1
SNAPC2
WSB1
LTV1
ADAT1
BEX2
GSTA4
FYN
PITPNC1
THRA
TBC1D31
PRRC2C
ZNF257
GPR124
PIK3CA
UFSP2
ALB
AGTR1
IFI44L
ZBTB5
TMEM178B
FGG
LPP
AKR1C1
PRKCB
ITCH
XIRP2
CTNNB1
TP53
TSS_HepG2
CDS_HepG2
extendedGene_HepG2
TSS_MCF-7
CDS_MCF-7
extendedGene_MCF-7
TSS_K562
CDS_K562
extendedGene_K562

Figure 2

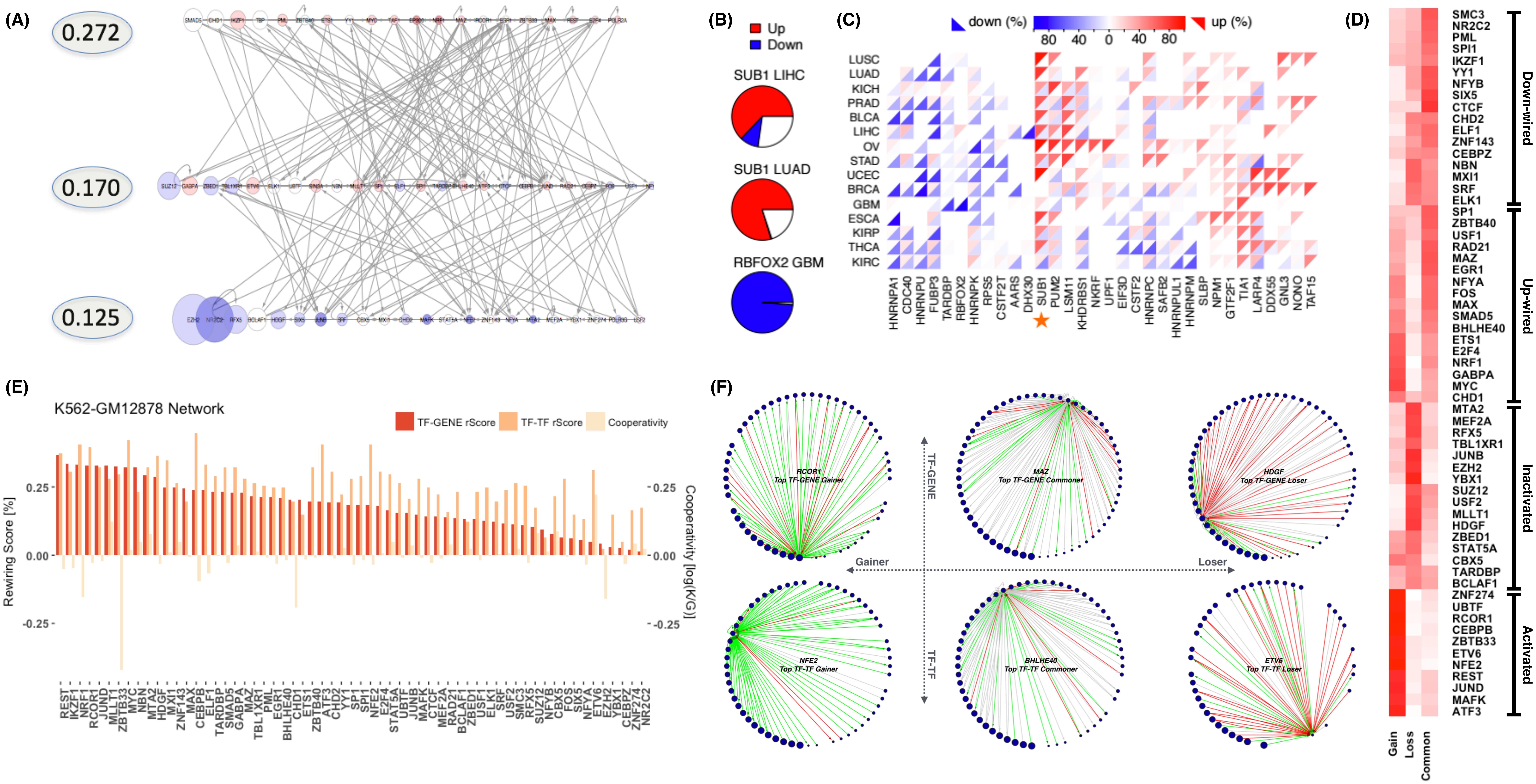

(A)
0.272
0.170
0.125
SMAD5
CHD1
IKZF1
TBP
PML
ZBTB40
ETS1
YY1
MYC
TAF1
EP300
NRF1
MAZ
RCOR1
EGR1
ZBTB33
MAX
REST
E2F4
POLR2A
SUZ12
GABPA
ZBED1
TBL1XR1
ETV6
ELK1
UBTF
SIN3A
NBN
MLLT1
SP1
ELF1
SPI1
TARDBP
BHLHE40
ATF3
CTCF
CEBPB
JUND
RAD21
CEBPZ
FOS
USF1
NFY
EZH2
NR2C2
RFX5
BCLAF1
HDGF
SIX5
JUNB
SRF
CBX5
MXI1
CHD2
MAFK
STAT5A
NFE2
ZNF143
NFYA
MTA2
MEF2A
YBX1
ZNF274
POLR3G
USF2
(B)
Up
Down
SUB1 LIHC
SUB1 LUAD
RBFOX2 GBM
(C)
down (%)
80
40
0
40
80
up (%)
LUSC
LUAD
KICH
PRAD
BLCA
LIHC
OV
STAD
UCEC
BRCA
GBM
ESCA
KIRP
THCA
KIRC
HNRNPA1
CDC40
HNRNPU
FUBP3
TARDBP
RBFOX2
HNRNPK
RPS5
CSTF2T
AARS
DHX30
SUB1
PUM2
LSM11
KHDRBS1
NKRF
UPF1
EIF3D
CSTF2
HNRNPC
SAFB2
HNRNPUL1
HNRNPM
SLBP
NPM1
GTF2F1
TIA1
LARP4
DDX55
GNL3
NONO
TAF15
(D)
SMC3
NR2C2
PML
SPI1
IKZF1
YY1
NFYB
SIX5
CTCF
CHD2
ELF1
ZNF143
CEBPZ
NBN
MXI1
SRF
ELK1
SP1
ZBTB40
USF1
RAD21
MAZ
EGR1
NFYA
FOS
MAX
SMAD5
BHLHE40
ETS1
E2F4
NRF1
GABPA
MYC
CHD1
MTA2
MEF2A
RFX5
TBL1XR1
JUNB
EZH2
YBX1
SUZ12
USF2
MLLT1
HDGF
ZBED1
STAT5A
CBX5
TARDBP
BCLAF1
ZNF274
UBTF
RCOR1
CEBPB
ZBTB33
ETV6
NFE2
REST
JUND
MAFK
ATF3
Down-wired
Up-wired
Inactivated
Activated
Gain
Loss
Common
(E)
K562-GM12878 Network
TF-GENE rScore
TF-TF rScore
Cooperativity
Rewiring Score [%]
0.25
0.00
-0.25
Cooperativity [log(K/G)]
0.25
0.00
-0.25
REST
IKZF1
NRF1
RCOR1
JUND
MLLT1
ZBTB33
MYC
NBN
MTA2
HDGF
MXI1
ZNF143
MAX
CEBPB
ELF1
TARDBP
SMAD5
GABPA
MAZ
TBL1XR1
PML
EGR1
BHLHE40
CHD1
ETS1
ZBTB40
ATF3
CHD2
YY1
SP1
SPI1
NFE2
E2F4
STAT5A
UBTF
JUNB
MAFK
CTCF
MEF2A
RAD21
BCLAF1
ZBED1
USF1
ELK1
SRF
USF2
SMC3
RFX5
SUZ12
NFYB
CBX5
FOS
SIX5
NFYA
ETV6
EZH2
YBX1
CEBPZ
ZNF274
NR2C2
(F)
RCOR1
Top TF-GENE Gainer
MAZ
Top TF-GENE Commoner
HDGF
Top TF-GENE Loser
NFE2
Top TF-TF Gainer
BHLHE40
Top TF-TF Commoner
ETV6
Top TF-TF Loser
TF-GENE
TF-TF
Gainer
Loser

Figure 3

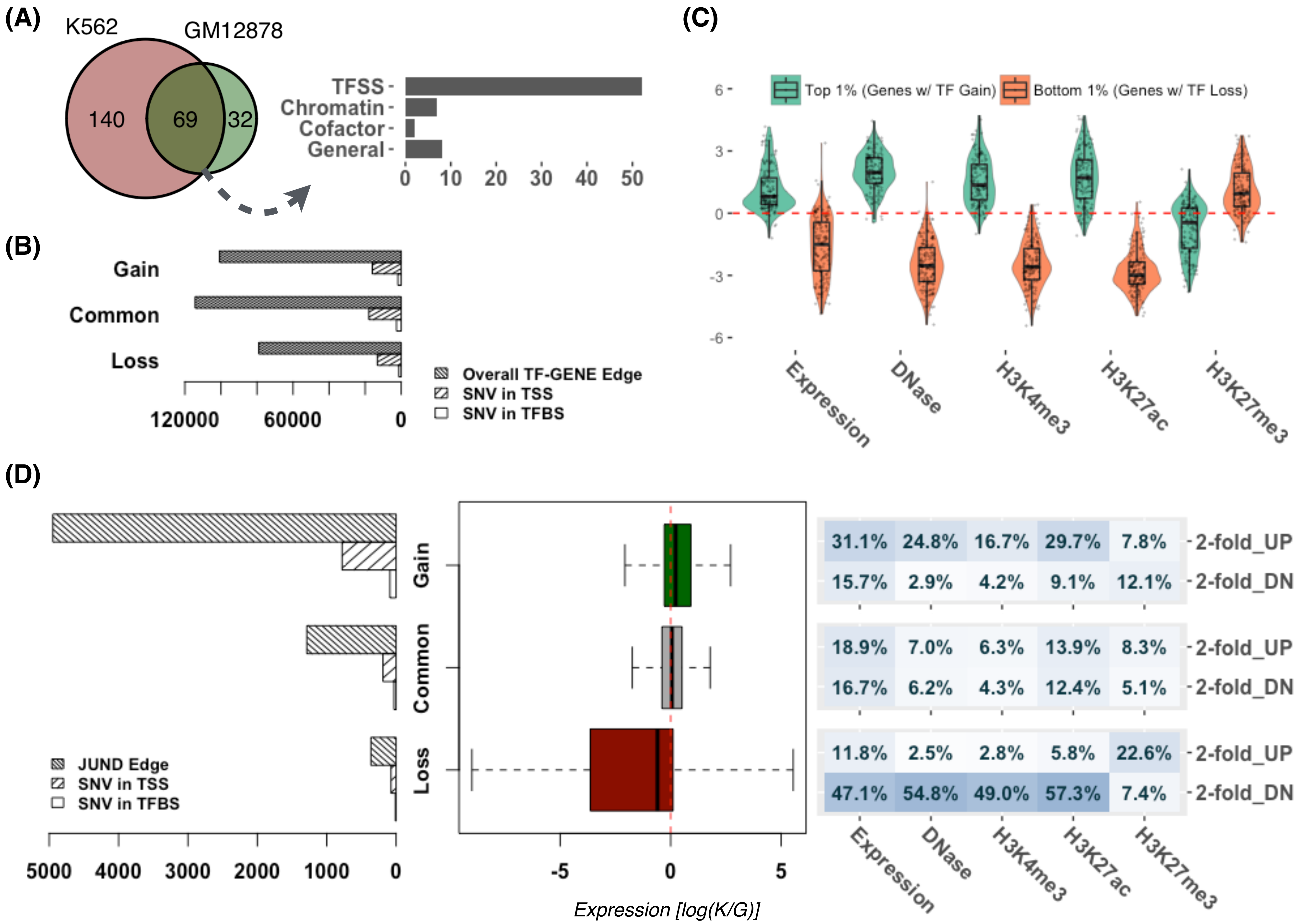

(A)
K562
GM12878
140
69
32
TFSS
Chromatin
Cofactor
General
0
10
20
30
40
50
(B)
Gain
Common
Loss
120000
60000
0
▧ Overall TF-GENE Edge
▨ SNV in TSS
☐ SNV in TFBS
(C)
Top 1% (Genes w/ TF Gain)
Bottom 1% (Genes w/ TF Loss)
6
3
0
-3
-6
Expression
DNase
H3K4me3
H3K27ac
H3K27me3
(D)
▧ JUND Edge
▨ SNV in TSS
☐ SNV in TFBS
5000
4000
3000
2000
1000
0
Gain
Common
Loss
-5
0
5
Expression [log(K/G)]
31.1% 24.8% 16.7% 29.7% 7.8% 2-fold_UP
15.7% 2.9% 4.2% 9.1% 12.1% 2-fold_DN
18.9% 7.0% 6.3% 13.9% 8.3% 2-fold_UP
16.7% 6.2% 4.3% 12.4% 5.1% 2-fold_DN
11.8% 2.5% 2.8% 5.8% 22.6% 2-fold_UP
47.1% 54.8% 49.0% 57.3% 7.4% 2-fold_DN
Expression
DNase
H3K4me3
H3K27ac
H3K27me3

Figure 4

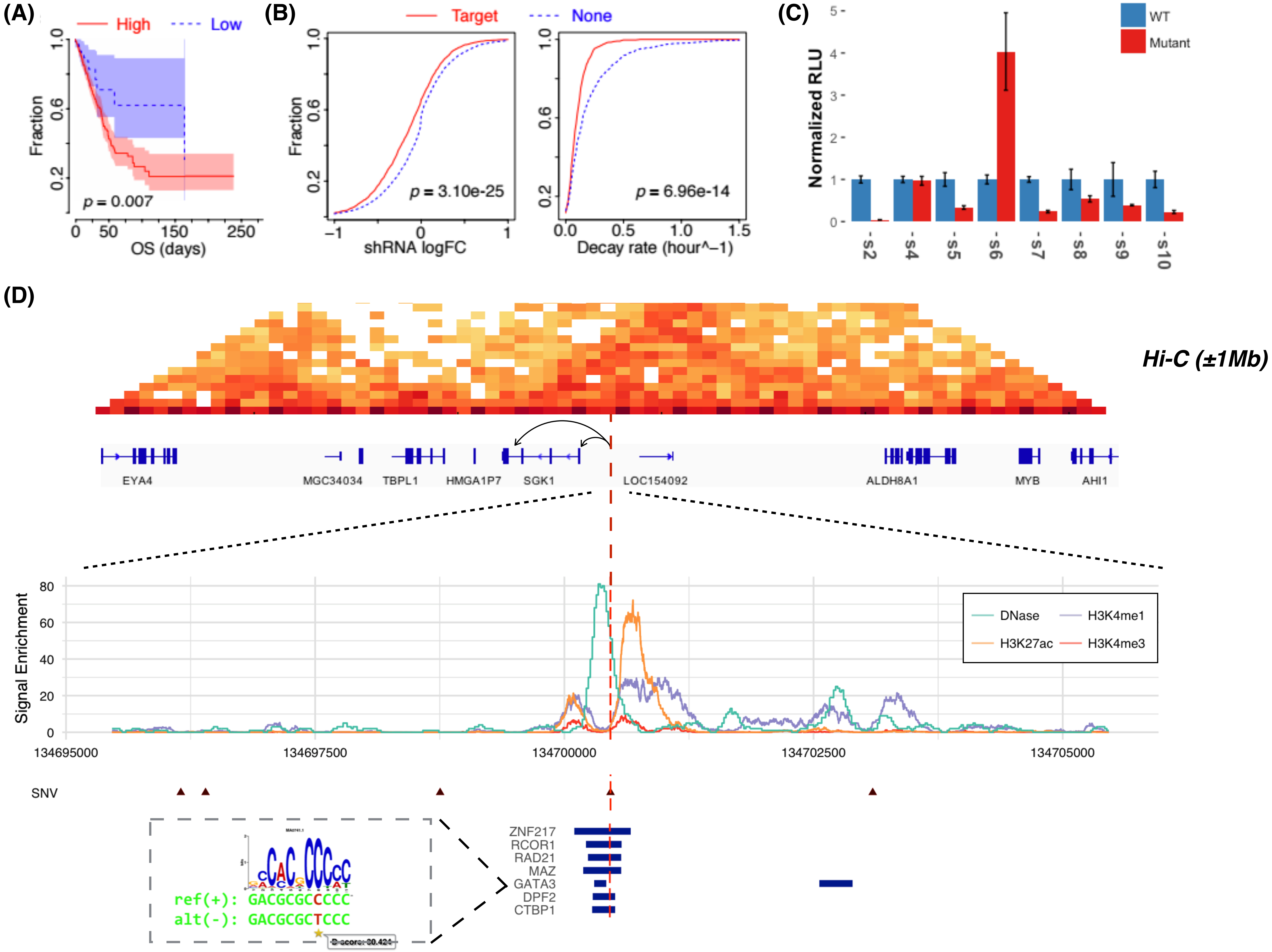
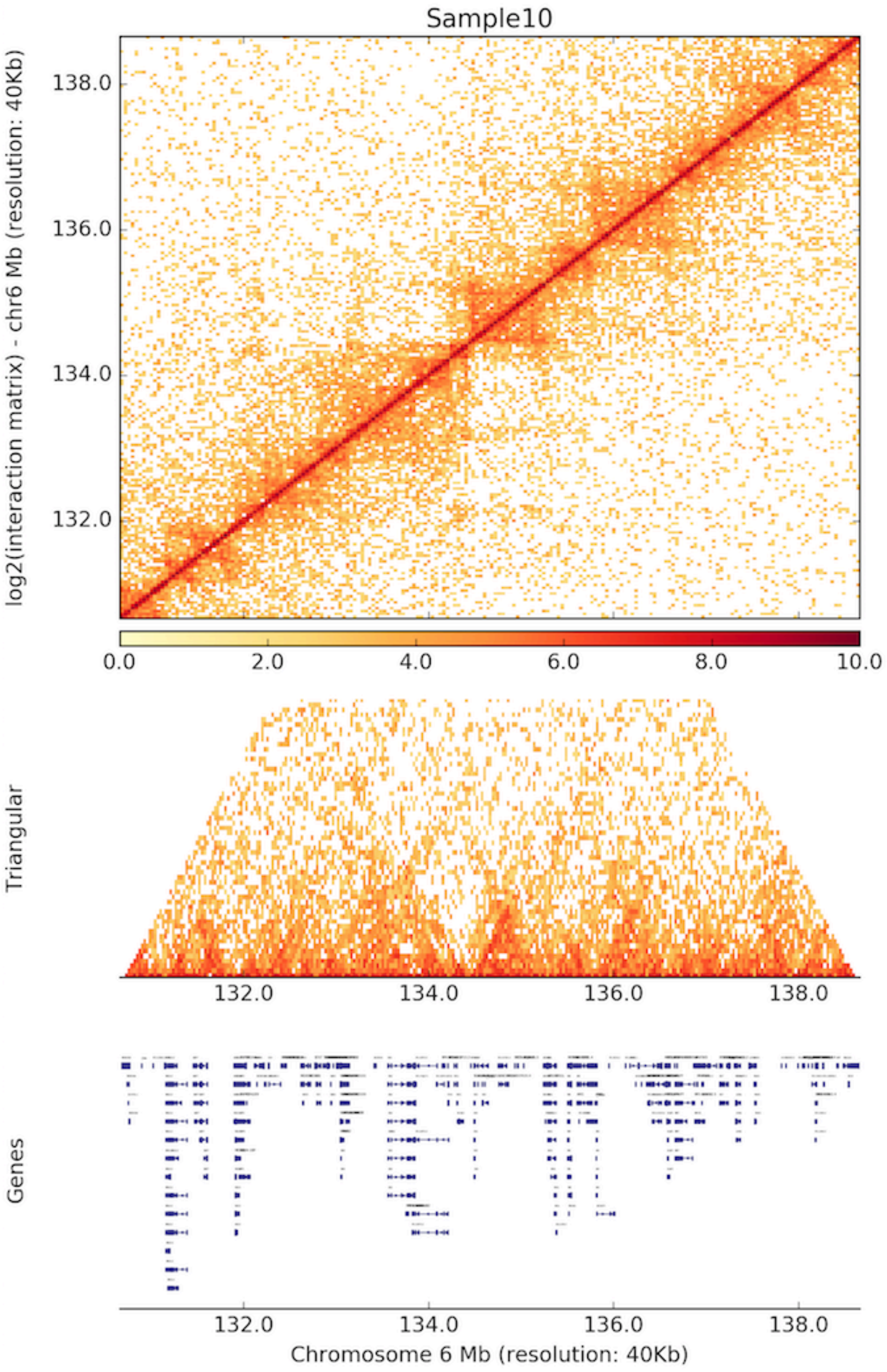
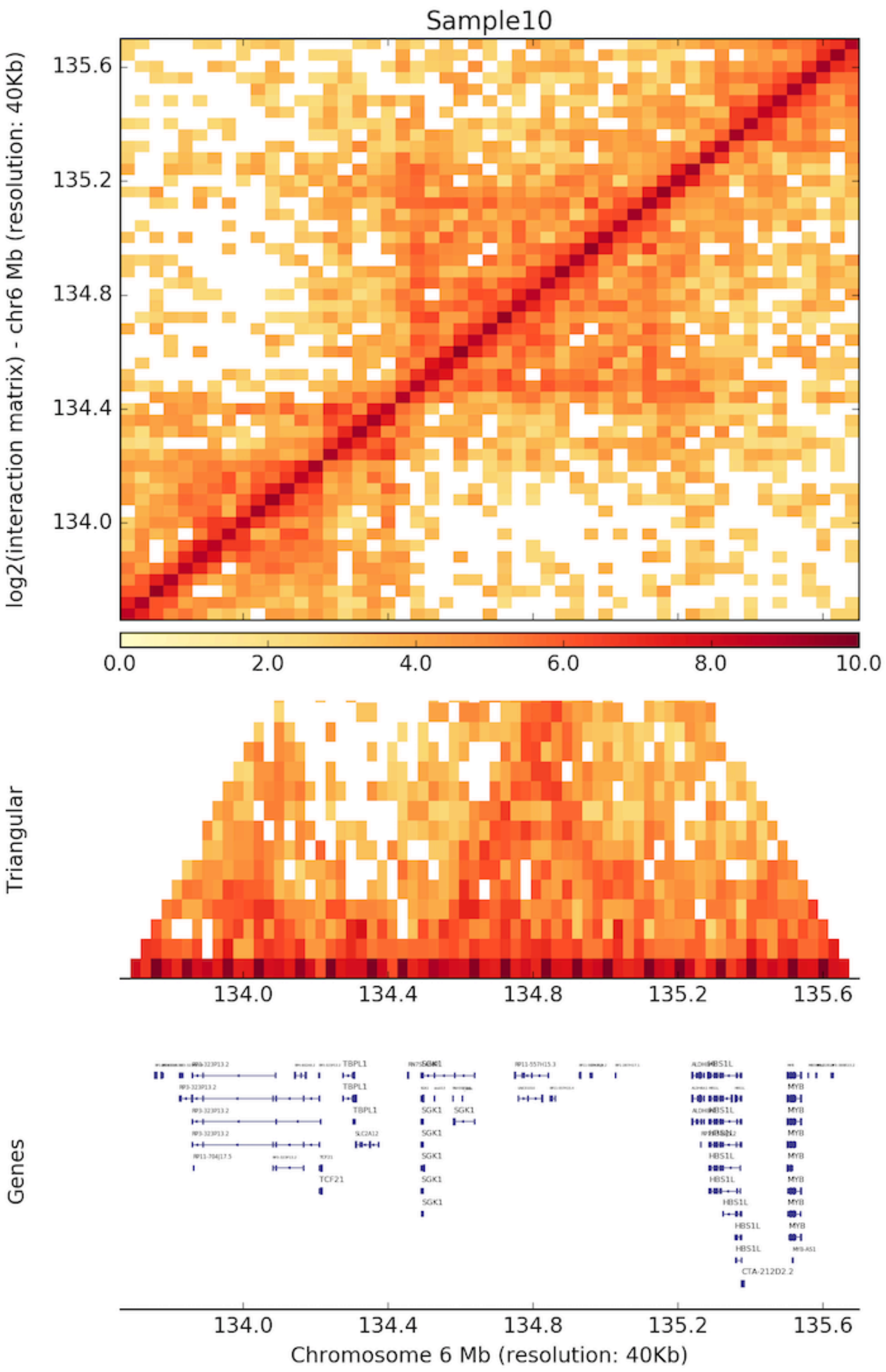
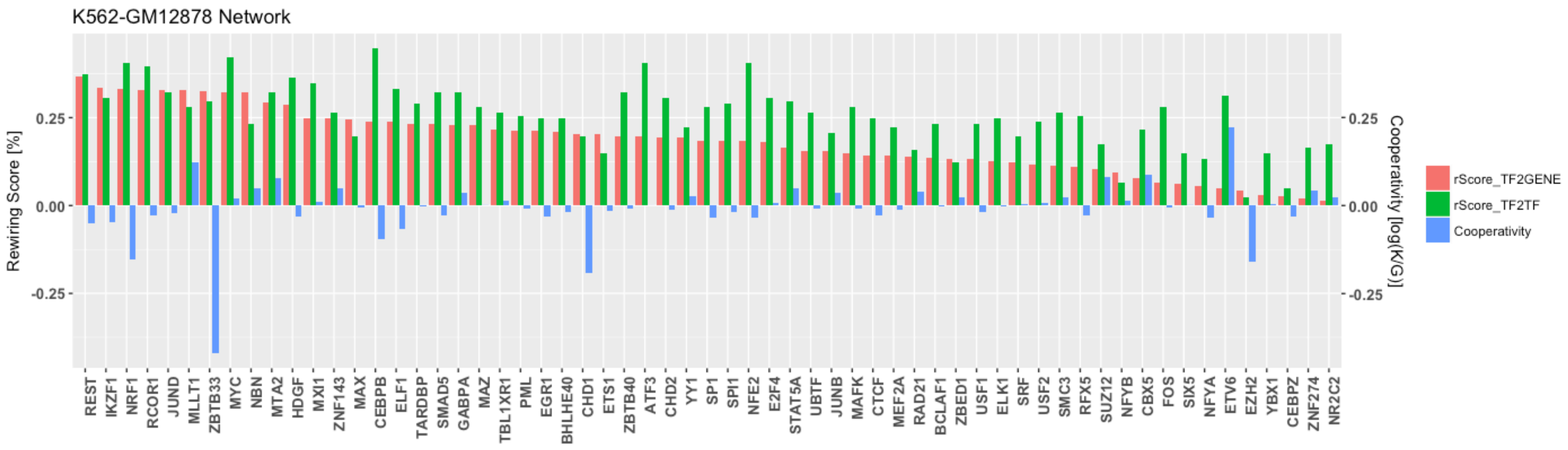

(A)
High
Low
Fraction
1.0
0.6
0.2
p = 0.007
0
50
150
250
OS (days)
(B)
Target
None
Fraction
1.0
0.6
0.2
p = 3.10e-25
−1
0
1
shRNA logFC
1.0
0.6
0.2
p = 6.96e-14
0.0
0.5
1.0
1.5
Decay rate (hour^−1)
(C)
Normalized RLU
5
4
3
2
1
0
WT
Mutant
s2
s4
s5
s6
s7
s8
s9
s10
(D)
Hi-C (±1Mb)
EYA4
MGC34034
TBPL1
HMGA1P7
SGK1
LOC154092
ALDH8A1
MYB
AHI1
Signal Enrichment
80
60
40
20
0
DNase
H3K4me1
H3K27ac
H3K4me3
134695000
134697500
134700000
134702500
134705000
SNV
MA0741.1
bits
2
1
0
ref(+): GACGCGCCCCC
alt(-): GACGCGCTCCC
D-score: 30.424
ZNF217
RCOR1
RAD21
MAZ
GATA3
DPF2
CTBP1

Figure 5

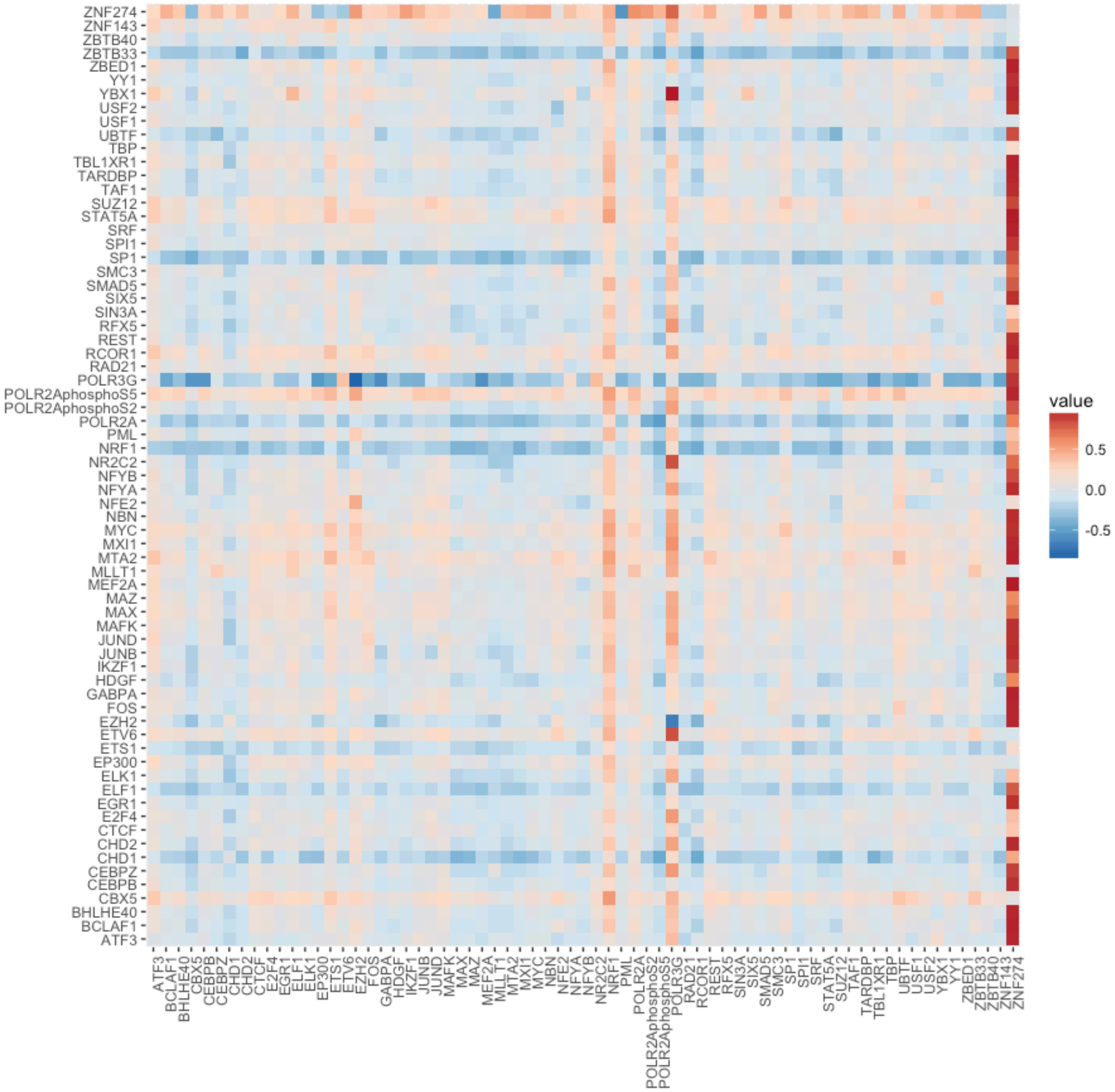

Sample10
log2(interaction matrix) - chr6 Mb (resolution: 40Kb)
138.0
136.0
134.0
132.0
0.0
2.0
4.0
6.0
8.0
10.0
Triangular
132.0
134.0
136.0
138.0
Genes
132.0
134.0
136.0
138.0
Chromosome 6 Mb (resolution: 40Kb)


Sample10
log2(interaction matrix) - chr6 Mb (resolution: 40Kb)
135.6
135.2
134.8
134.4
134.0
0.0
2.0
4.0
6.0
8.0
10.0
Triangular
134.0
134.4
134.8
135.2
135.6
Genes
TBPL1
TCF21
SLC2A12
SGK1
HBS1L
MYB
CTA-212D2.2
134.0
134.4
134.8
135.2
135.6
Chromosome 6 Mb (resolution: 40Kb)

GG's new cooperativity
logR of K/G
+ve means it's more cooperative in K, vice versa

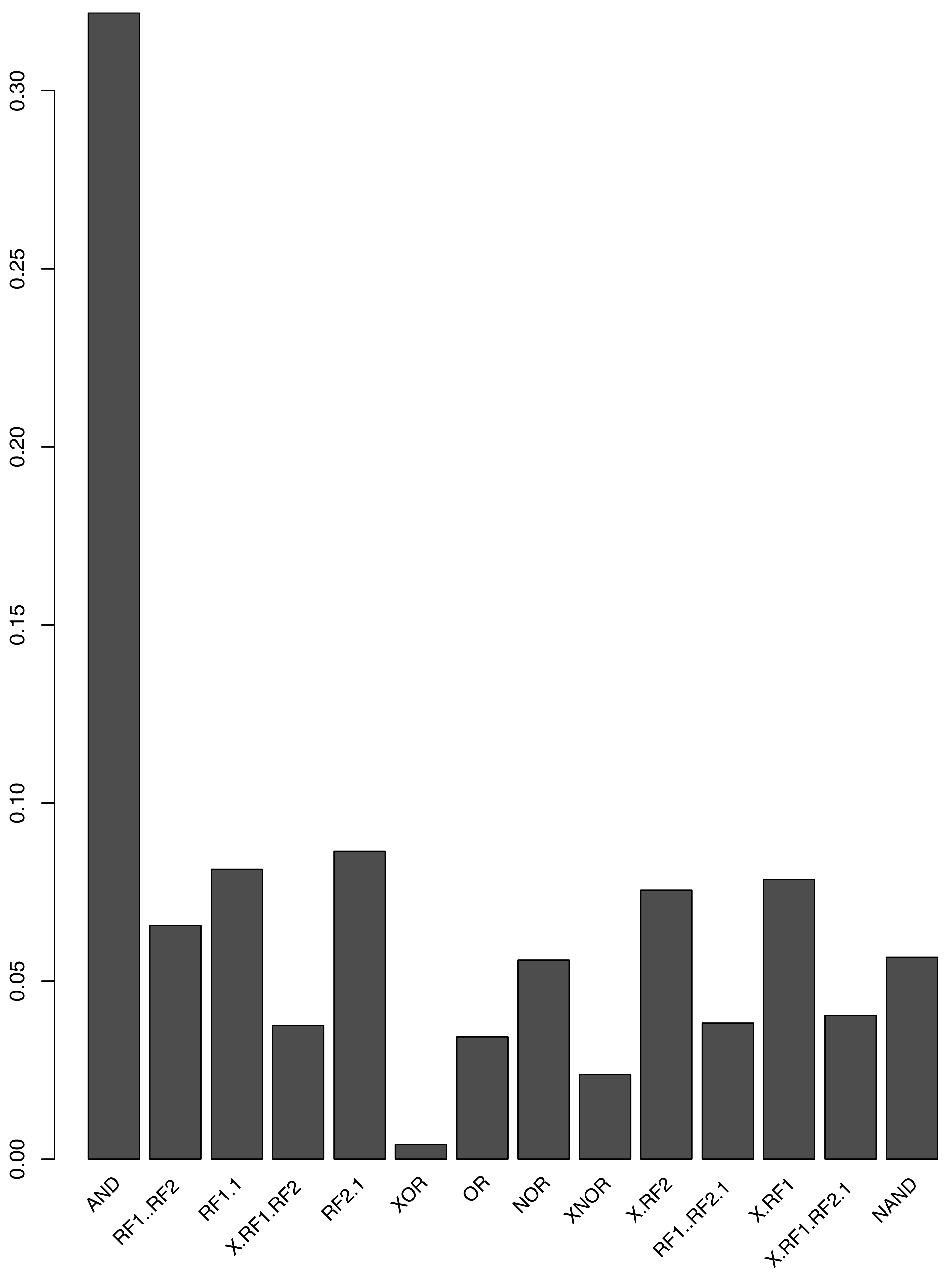


ZBTB33 becomes less cooperative in K
it "could" mean that its targets are unique in K
ETV6 becomes more cooperative in K
this "could" mean they become more ubiquitous

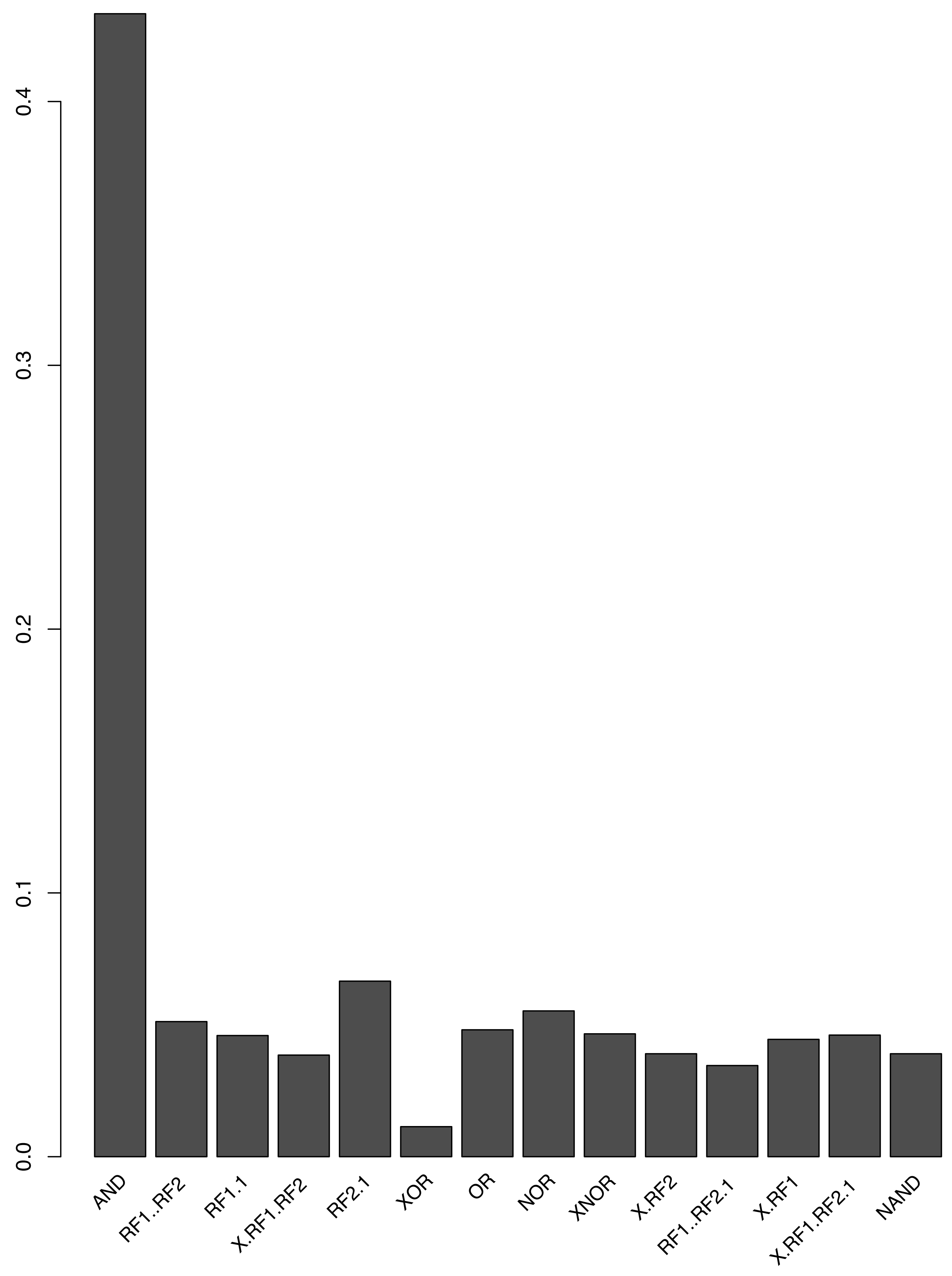


K-G Co-binding

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



GM12878



K562