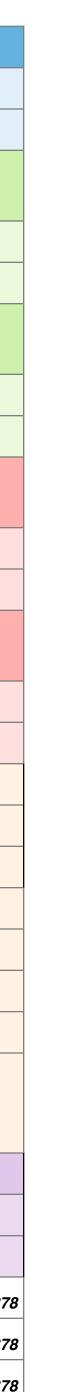
			JL	JND Gained Targ	et (n=0548)				
Expression (TPM)	UP			NC			DN		
n	1291			4597			660		
%		19.7%			70.2%			10.1%	
DHS (TSS Cov) active	UP	NC	DN	UP	NC	DN	UP	NC	DN
n	274	919	98	365	3840	392	48	478	134
%	21.2%	71.2%	7.6%	7.9%	83.5%	8.5%	7.3%	72.4%	20.3%
H3K4me3 (TSS Cov) active promoter	UP	NC	DN	UP	NC	DN	UP	NC	DN
n	242	1025	24	233	4234	130	31	543	86
%	18.7%	79.4%	1.9%	5.1%	92.1%	2.8%	4.7%	82.3%	13.0%
H3K27me3 (TSS Cov) inactive promoter	UP	NC	DN	UP	NC	DN	UP	NC	DN
n	7	1240	44	55	4498	44	23	635	2
%	0.5%	96.0%	3.4%	1.2%	97.8%	1.0%	3.5%	96.2%	0.3%
Methylation (Sig Avg) repressive	UP	NC	DN	UP	NC	DN	UP	NC	DN
n	149	1058	84	235	3920	442	36	551	73
%	11.5%	82.0%	6.5%	5.1%	85.3%	9.6%	5.5%	83.5%	11.1%
	count > 1	has mut	no mut	count > 1	has mut	no mut	count > 1	has mut	no mut
Mutation ext.gene count	65	304	987	189	964	3633	36	179	481
	5.0%	23.5%	76.5%	4.1%	21.0%	79.0%	5.5%	27.1%	72.9%
Mutation		17			66			22	
ext.gene pval < 0.05		1.3%			1.4%			3.3%	
Mutation		2			2			2	
ext.gene pval.adj < 0.05		0.2%			0.0%			0.3%	
Mutation observed[sum(count)]/ expected[sum(mu)]	86.2%		72.6%			91.3%			
Enhancer-based Linkage	>10 gain	NC	>10 loss	>10 gain	NC	>10 loss	>10 gain	NC	>10 loss
n	310	NA	82	574	NA	495	28	NA	134
%	24%	NA	6%	12%	NA	11%	4%	NA	20%
								UP: ΤΡΜκ5	62 >= 2 х ТРМ GM12878
							NC: 1/2 x	^Т ТРМ _{GM12878} < ТРМ _Р	к562 < 2 х ТРМ GM12878
								DN: TPM _{K562}	<= 1/2 x TPM _{GM12878}

JUND Gained Target (n=6548)

DN: $IPM_{K562} \ll 1/2 \times IPM_{GM12878}$



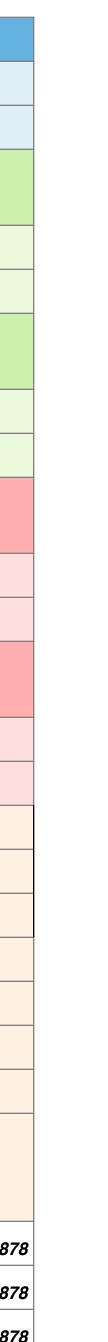
JUND Common Target (n=31)

			_		· 9 · · (·· · · /				
Expression (TPM)		UP		NC			DN		
n	1			15			15		
%		3.2%			48.4%	48.4% 48.4%			
DHS (TSS Cov) active	UP	NC	DN	UP	NC	DN	UP	NC	DN
n	0	1	0	1	11	3	0	12	3
%	0.0%	100.0%	0.0%	6.7%	73.3%	20.0%	0.0%	80.0%	20.0%
H3K4me3 (TSS Cov) active promoter	UP	NC	DN	UP	NC	DN	UP	NC	DN
n	0	1	0	0	13	2	0	11	4
%	0.0%	100.0%	0.0%	0.0%	86.7%	13.3%	0.0%	73.3%	26.7%
H3K27me3 (TSS Cov) inactive promoter	UP	NC	DN	UP	NC	DN	UP	NC	DN
n	0	1	0	0	15	0	0	14	1
%	0.0%	100.0%	0.0%	0.0%	100.0%	0.0%	0.0%	93.3%	6.7%
Methylation (Sig Avg) repressive	UP	NC	DN	UP	NC	DN	UP	NC	DN
n	0	1	0	1	14	0	0	14	1
%	0.0%	100.0%	0.0%	6.7%	93.3%	0.0%	0.0%	93.3%	6.7%
	count > 1	has mut	no mut	count > 1	has mut	no mut	count > 1	has mut	no mut
Mutation ext.gene count	0	0	1	1	4	11	1	4	11
oxtigene count	0.0%	0.0%	100.0%	6.7%	6.7% 26.7% 73.3% 6.7%	26.7%	73.3%		
Mutation		0		1			1		
ext.gene pval < 0.05		0.0%			6.7%		6.7%		
Mutation	Mutation			0			0		
ext.gene pval.adj < 0.05	0.0%			0.0%			0.0%		
Mutation observed[sum(count)]/ expected[sum(mu)]	0.0%		85.0%			143.8%			

UP: TPM_{K562} >= 2 x TPM_{GM12878}

NC: 1/2 x ТРМ_{GM12878} < ТРМ_{K562} < 2 x ТРМ_{GM12878}

DN: ТРМ_{К562} <= 1/2 х ТРМ_{GM12878}



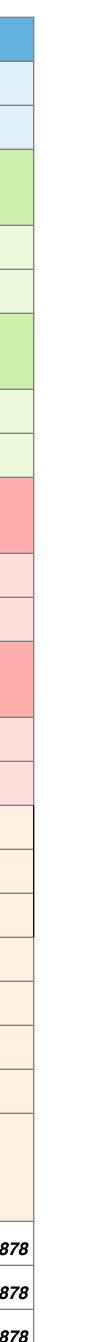
Overall Gene Target (n=15,189)

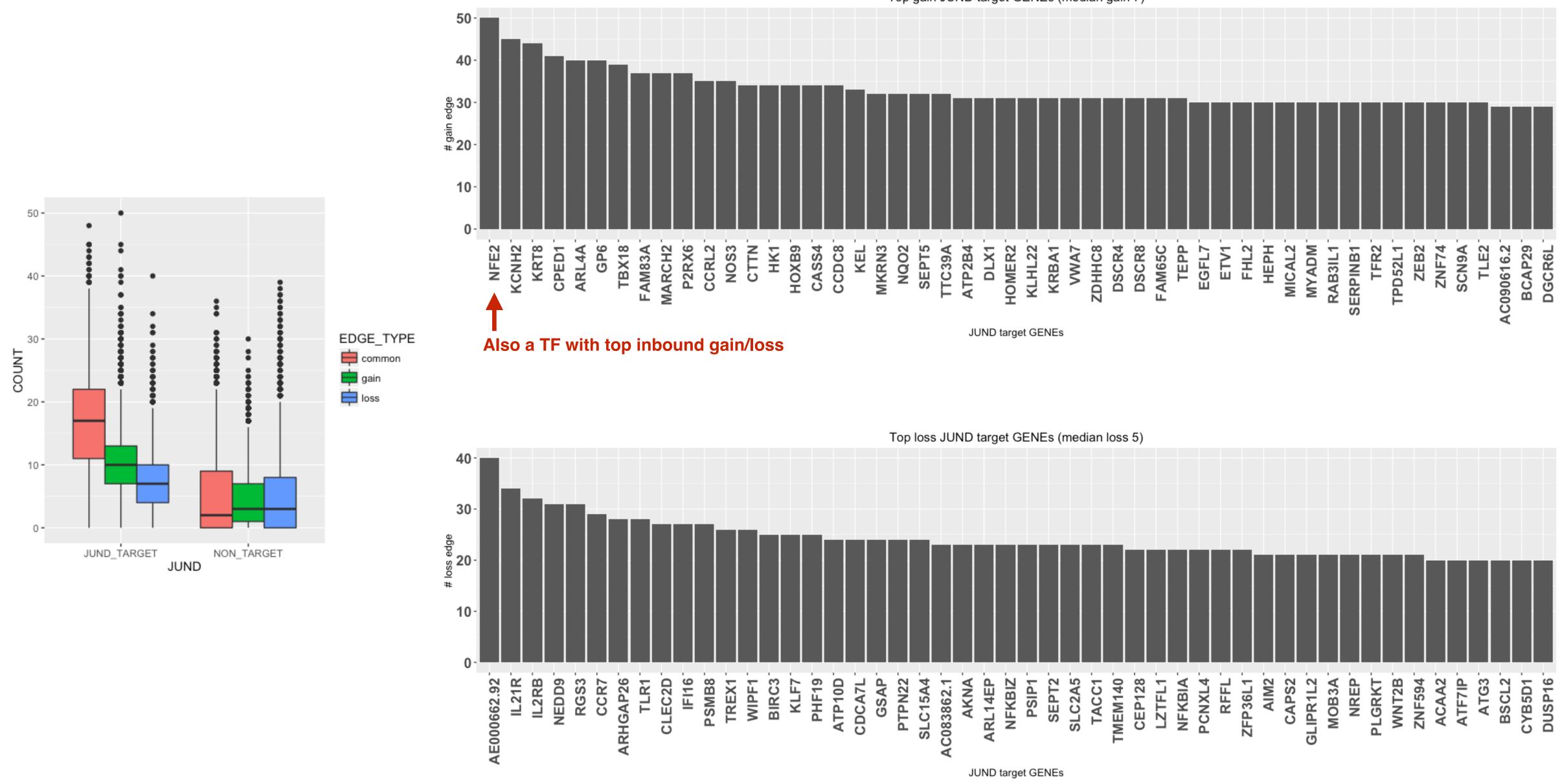
			•	verall Gene Targe	(11-10,100)					
Expression (TPM)		UP		NC				DN		
n	2442			10294			2453			
%		16.1%	16.1% 67.8%	67.8%			16.1%	16.1%		
DHS (TSS Cov) active	UP	NC	DN	UP	NC	DN	UP	NC	DN	
n	622	1622	198	1280	7723	1291	108	1430	915	
%	25.5%	66.4%	8.1%	12.4%	75.0%	12.5%	4.4%	58.3%	37.3%	
H3K4me3 (TSS Cov) 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%	
	count > 1	has mut	no mut	count > 1	has mut	no mut	count > 1	has mut	no mut	
Mutation ext.gene count	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		29			138		57			
<i>ext.gene pval < 0.05</i>		1.2%			1.3%		2.3%			
Mutation	3			3			6			
ext.gene pval.adj < 0.05	0.1%			0.0%			0.2%			
Mutation observed[sum(count)]/ expected[sum(mu)]	79.2%		75.7%			82.5%				

UP: TPM_{K562} >= 2 x TPM_{GM12878}

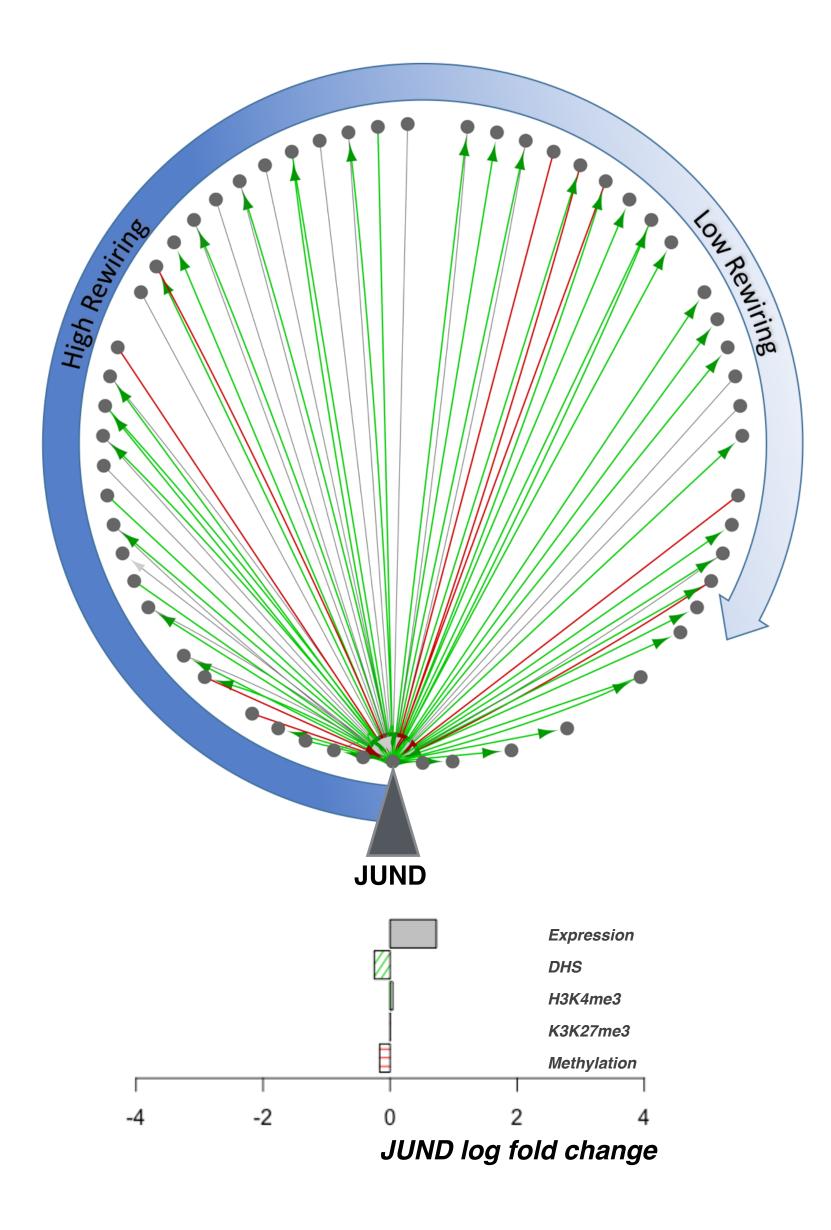
NC: 1/2 x ТРМ_{GM12878} < ТРМ_{K562} < 2 x ТРМ_{GM12878}

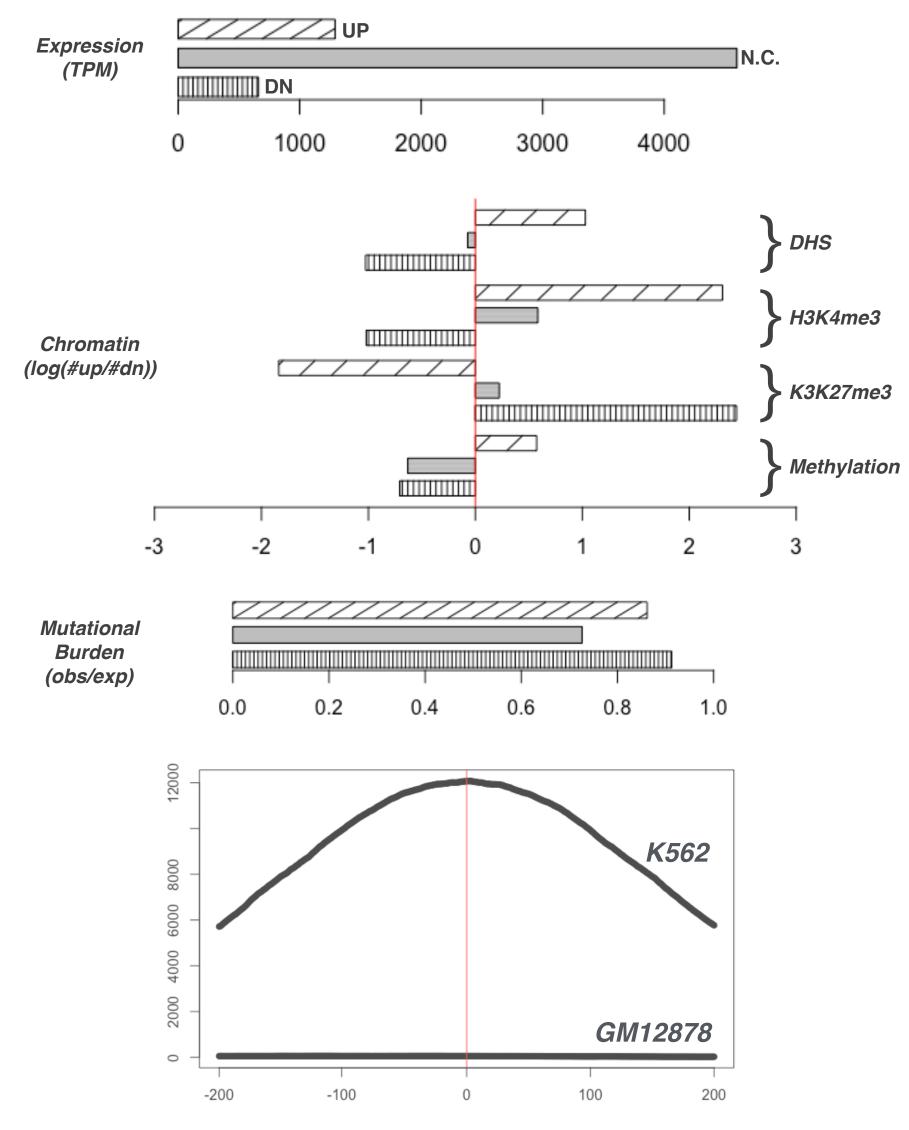
DN: ТРМ_{К562} <= 1/2 х ТРМ_{GM12878}





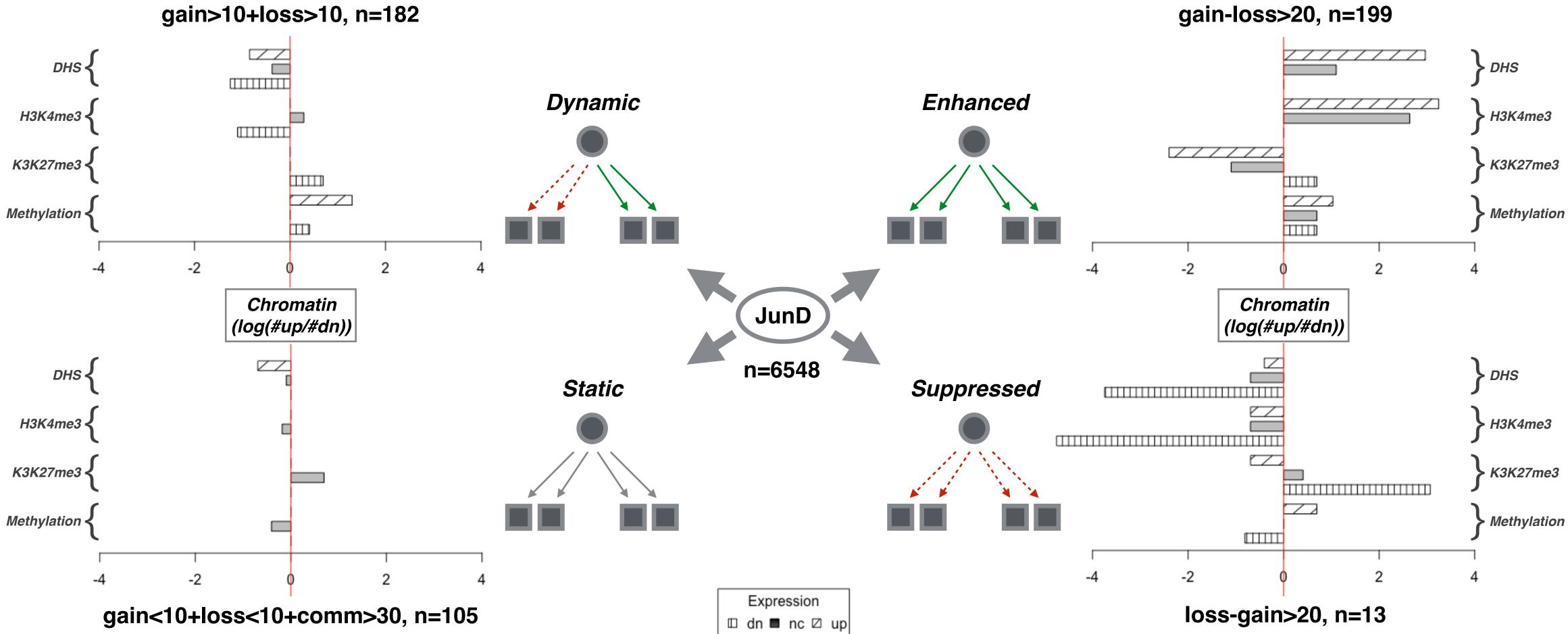
Top gain JUND target GENEs (median gain 7)

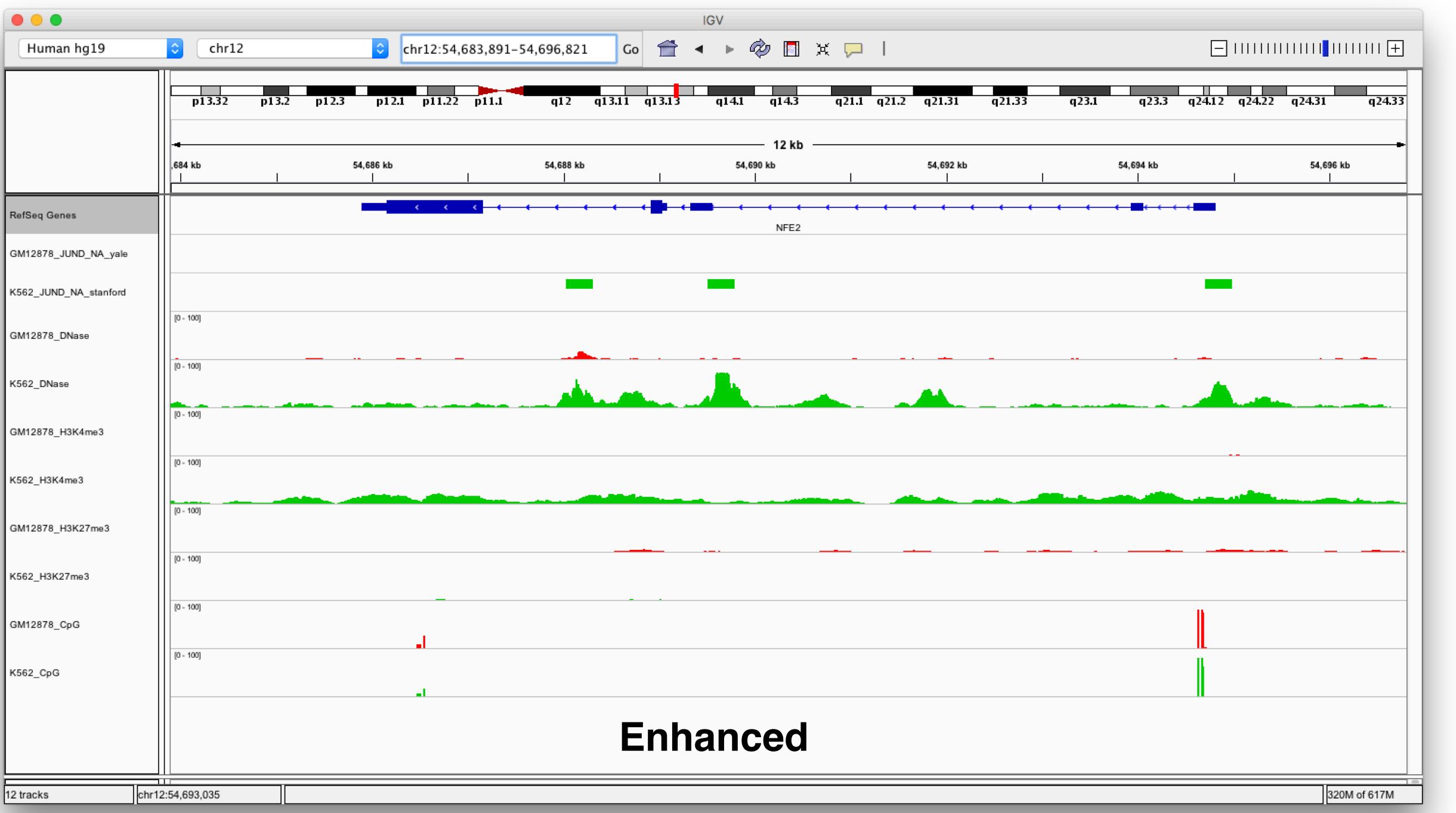


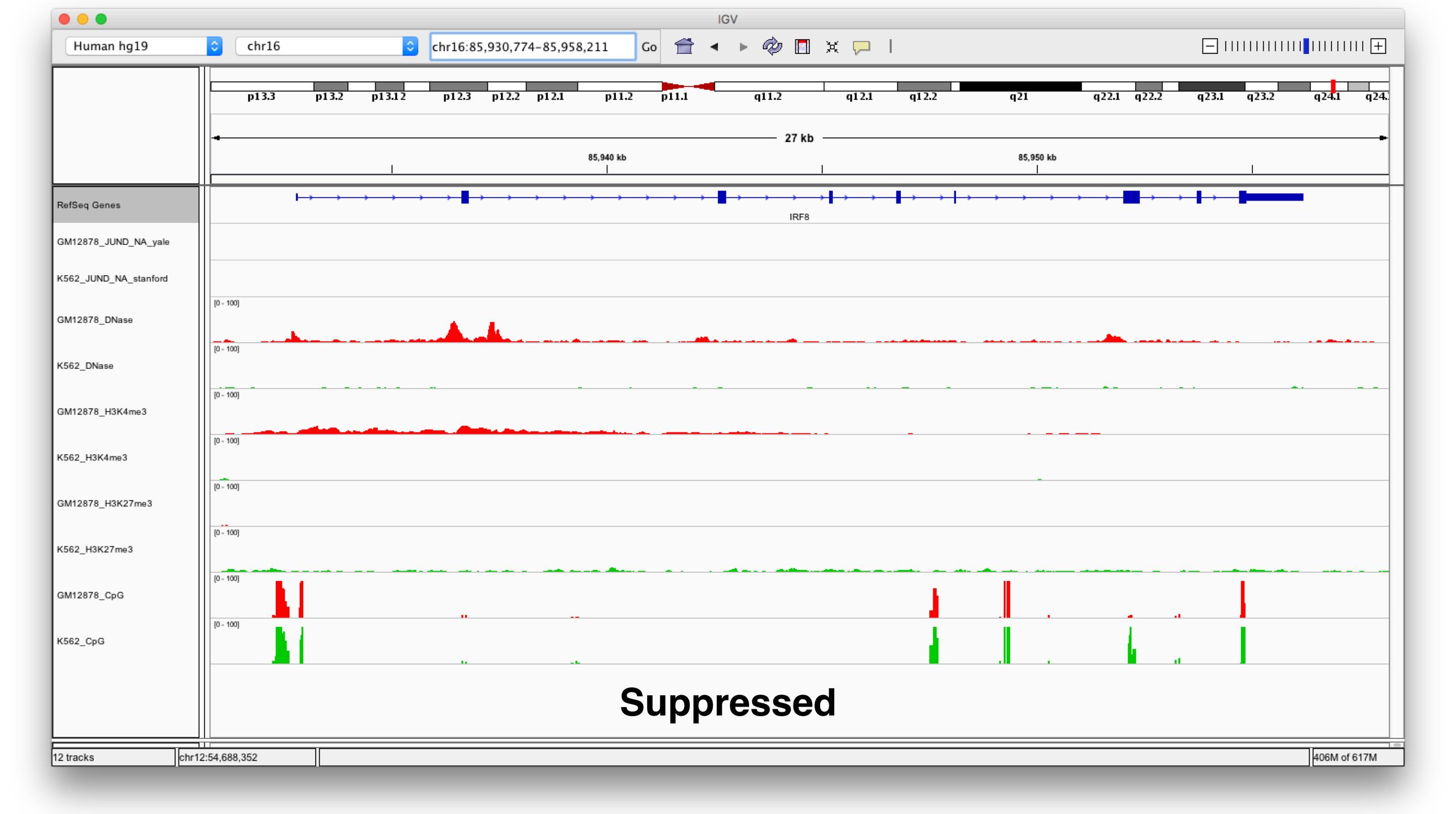


JUND Gained Targets

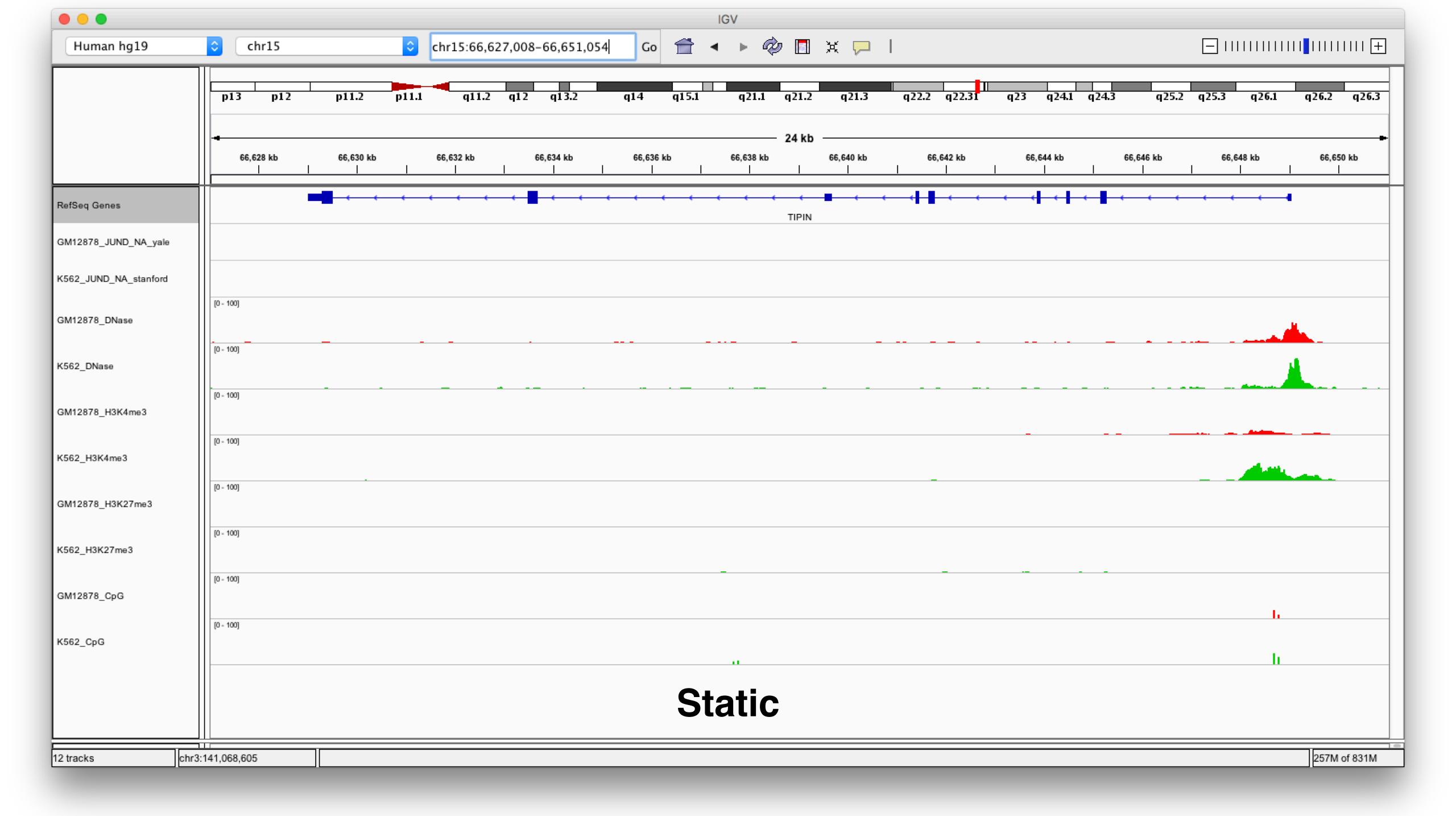
Chromatin change around TSS (mock-up, shown is binding profile)

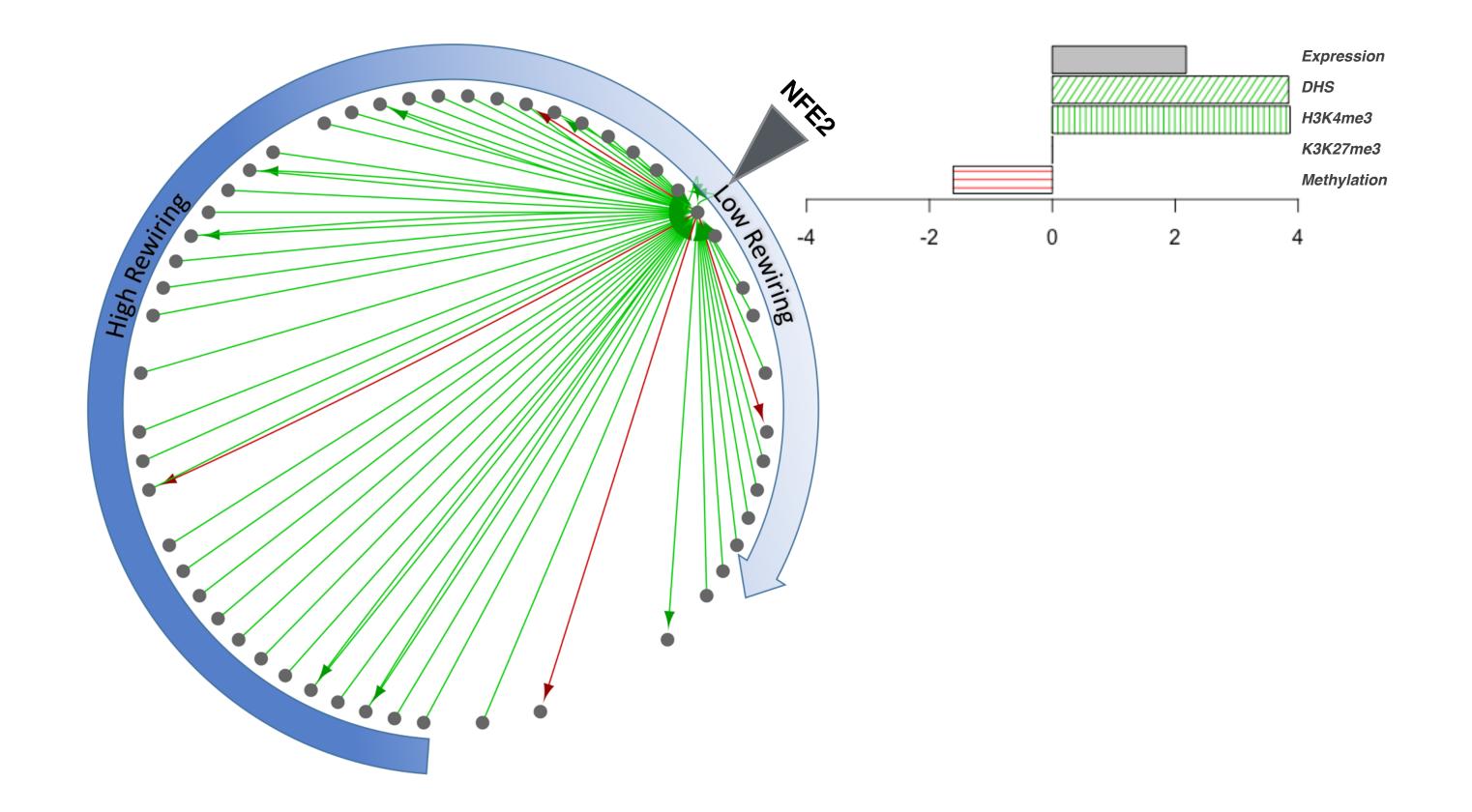




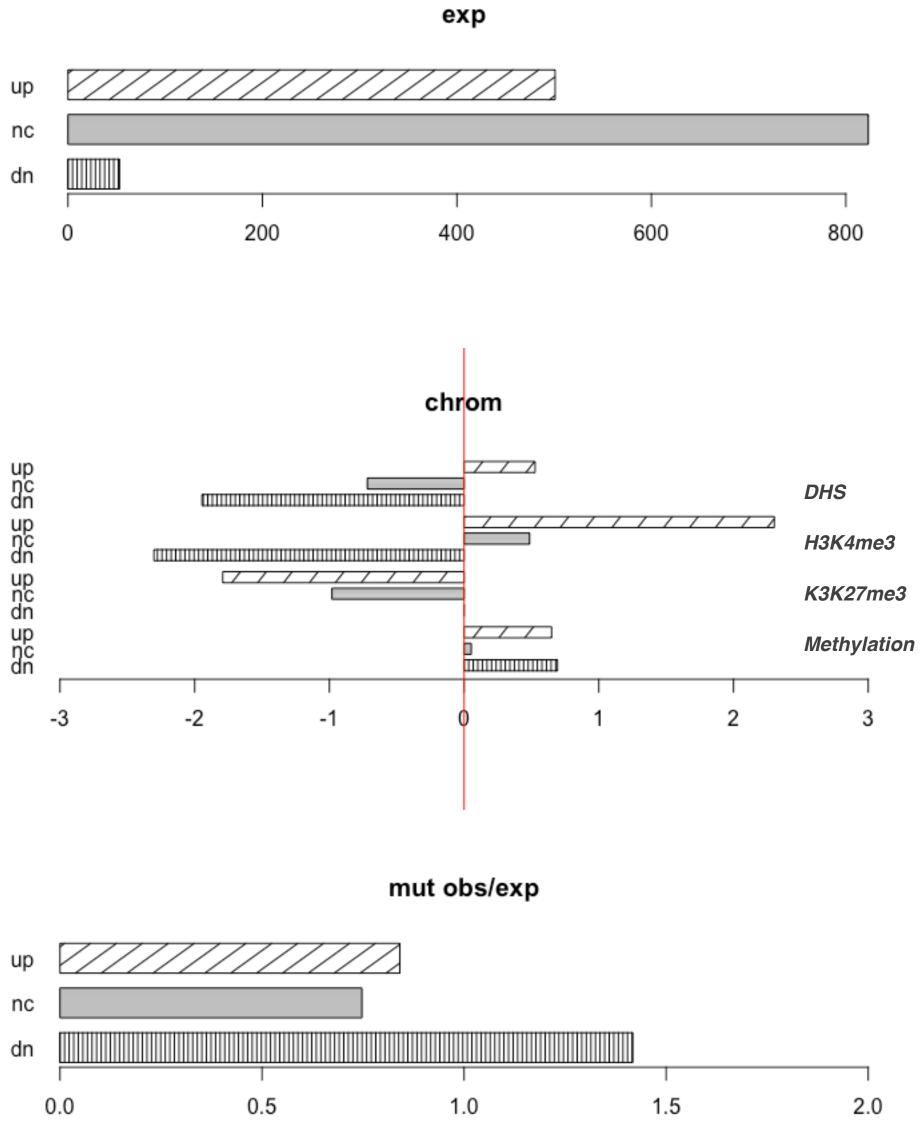




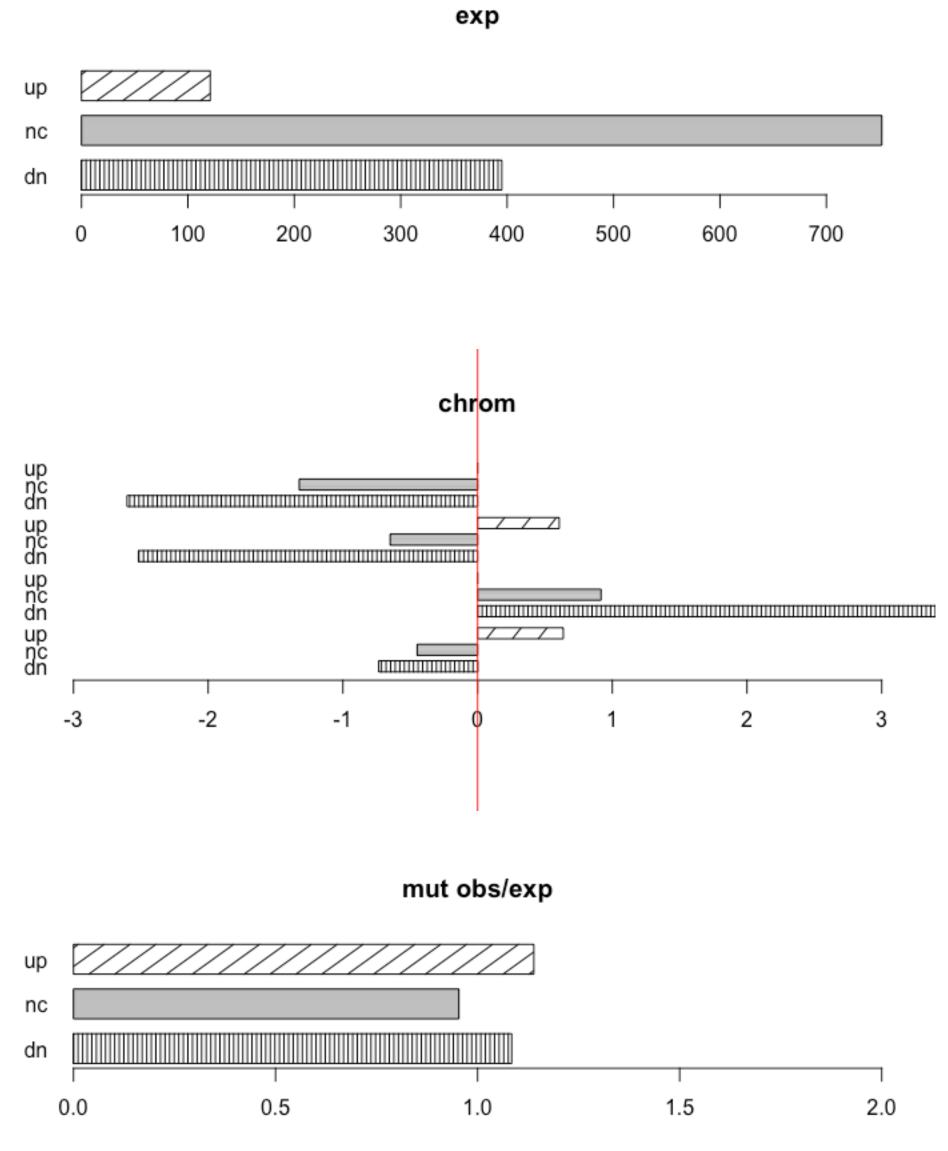




Enhancer edge gain > 10

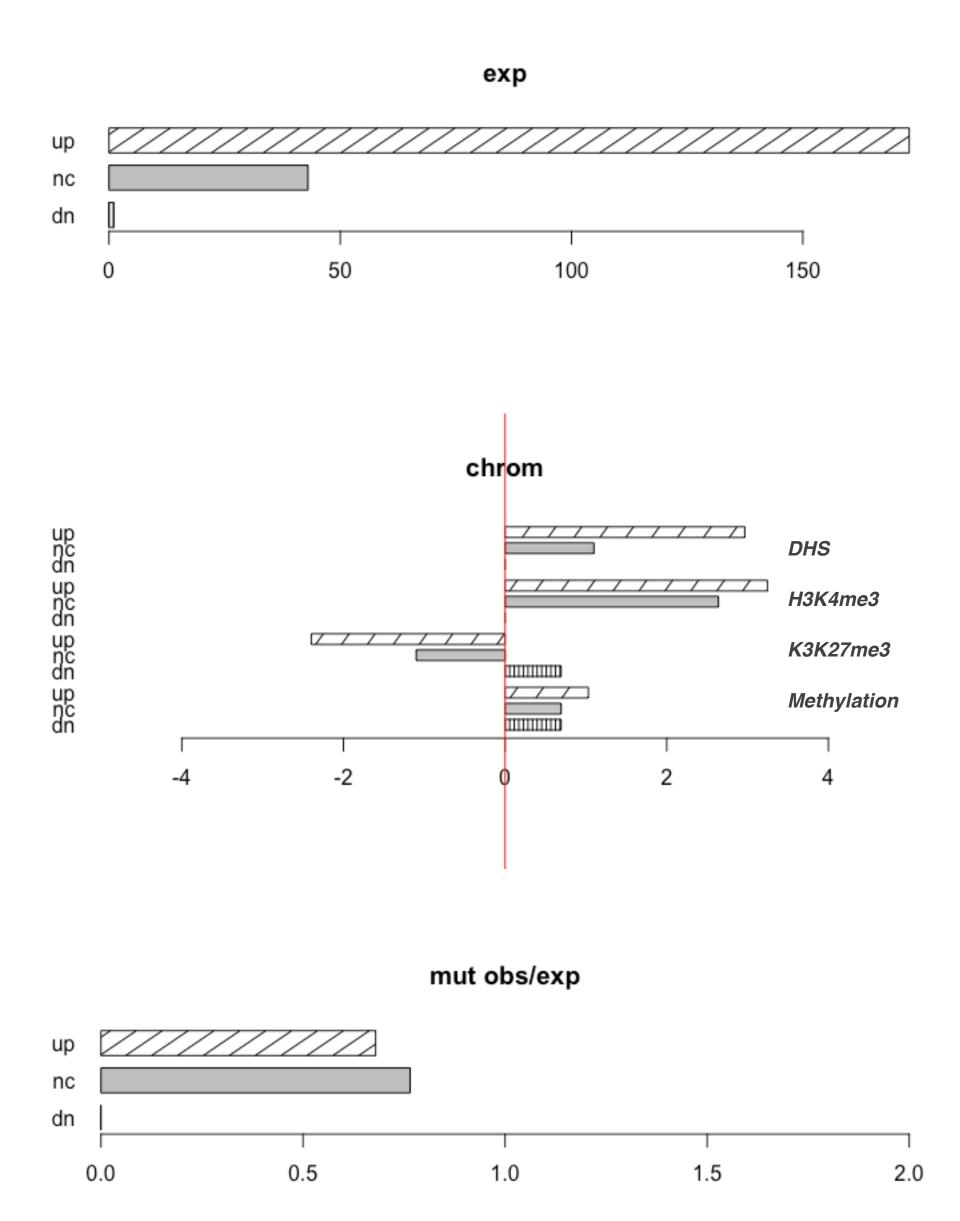


Enhancer edge loss > 10





Inbound edge gain > 20



Inbound edge loss > 20

