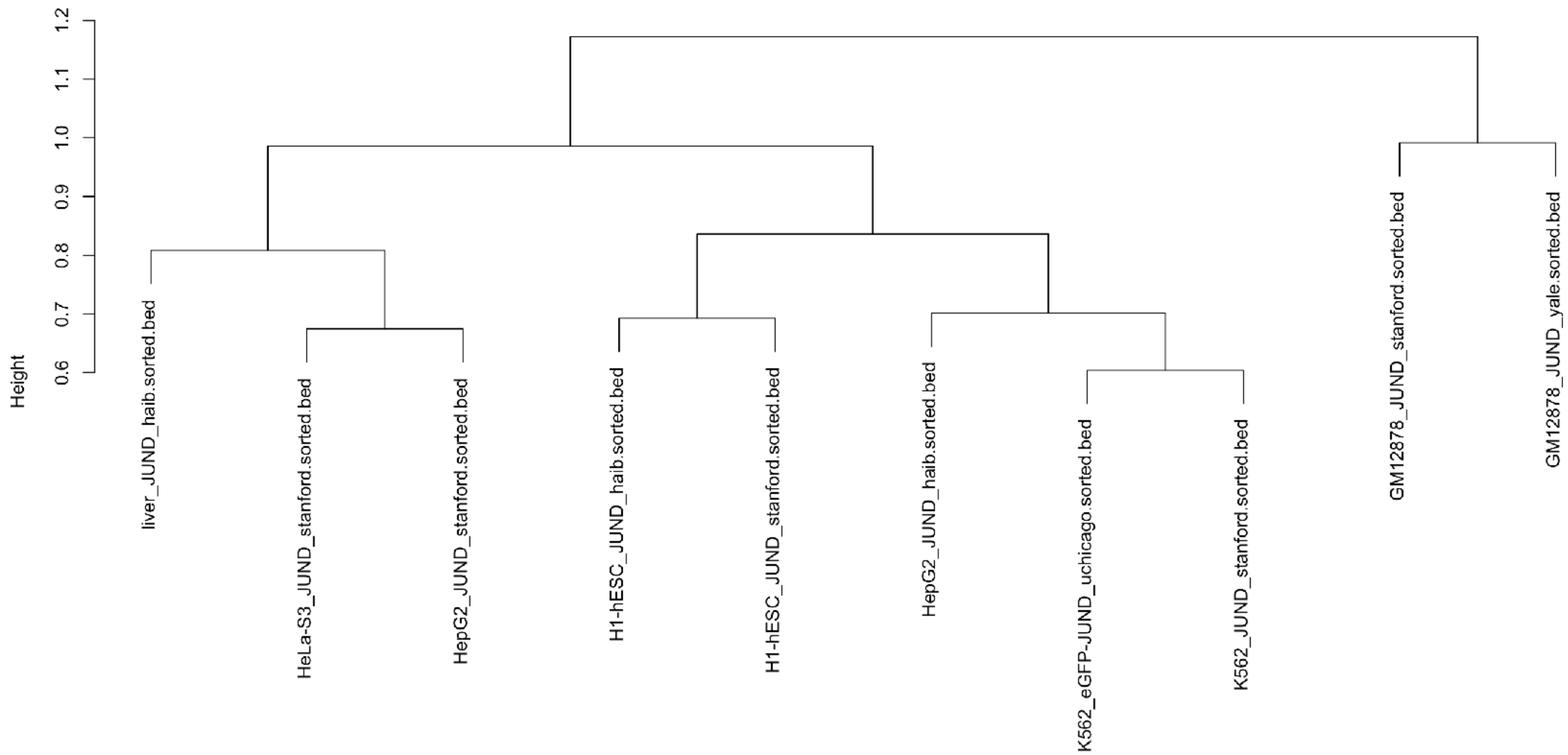


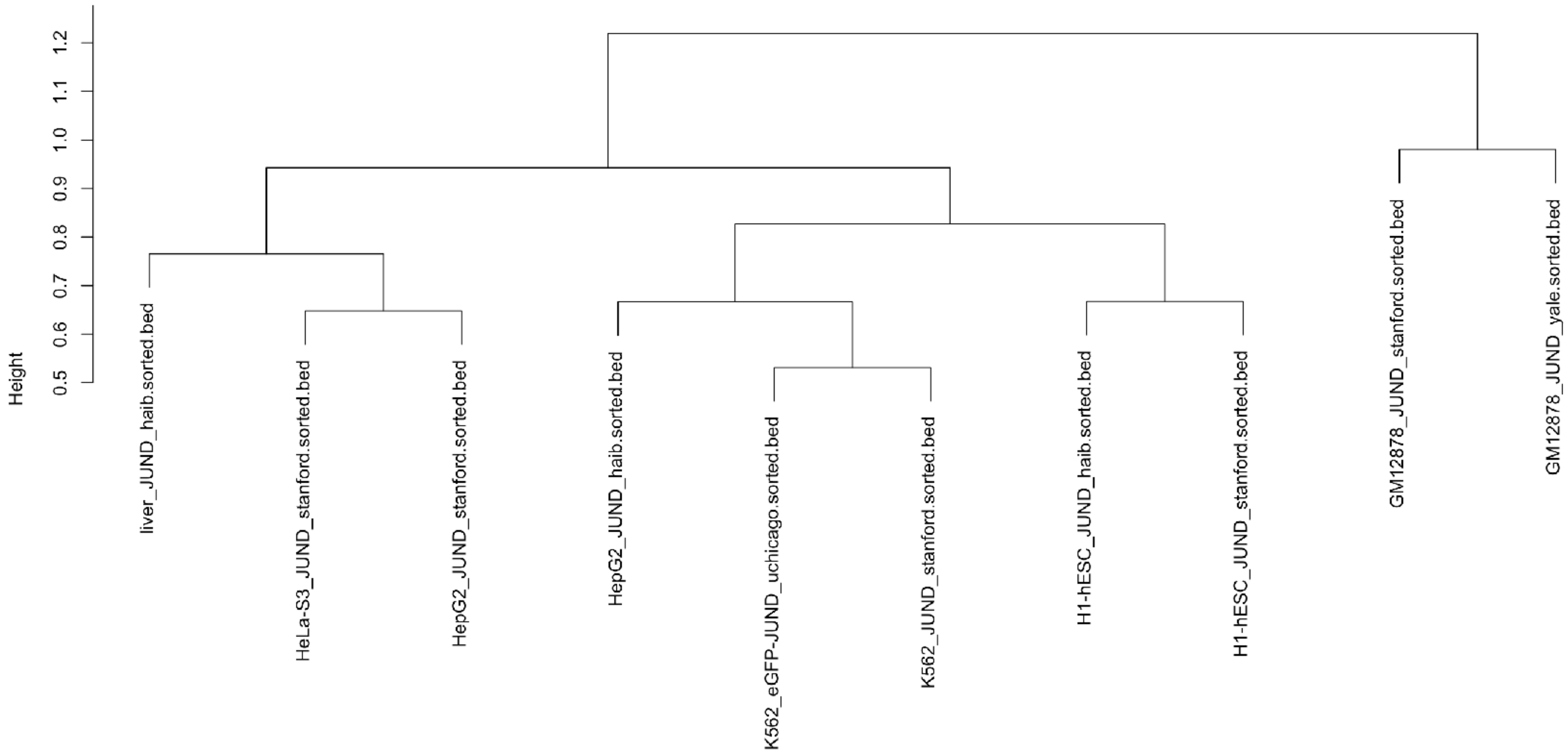
Cluster Dendrogram



TSS +/- 200bp

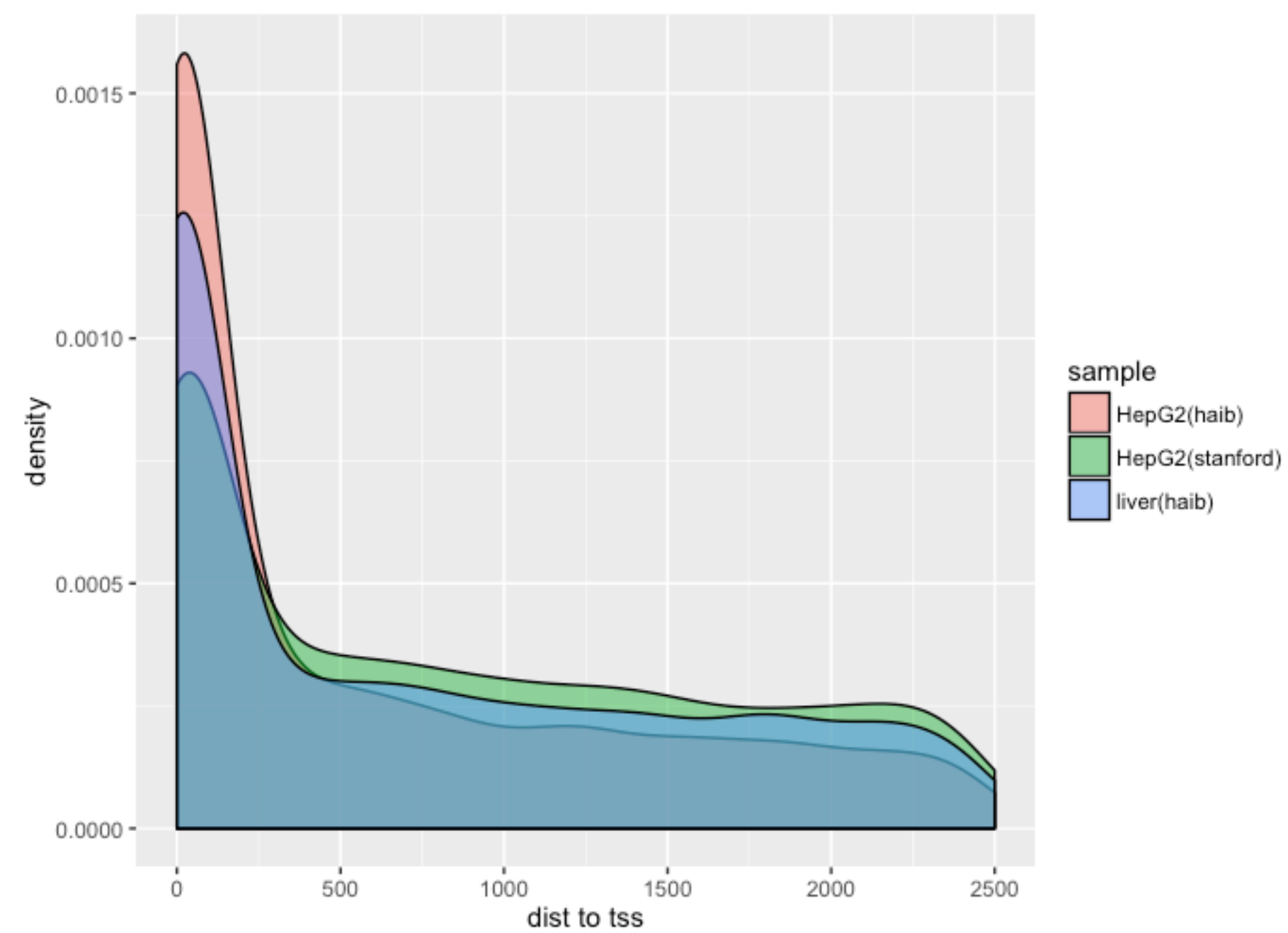
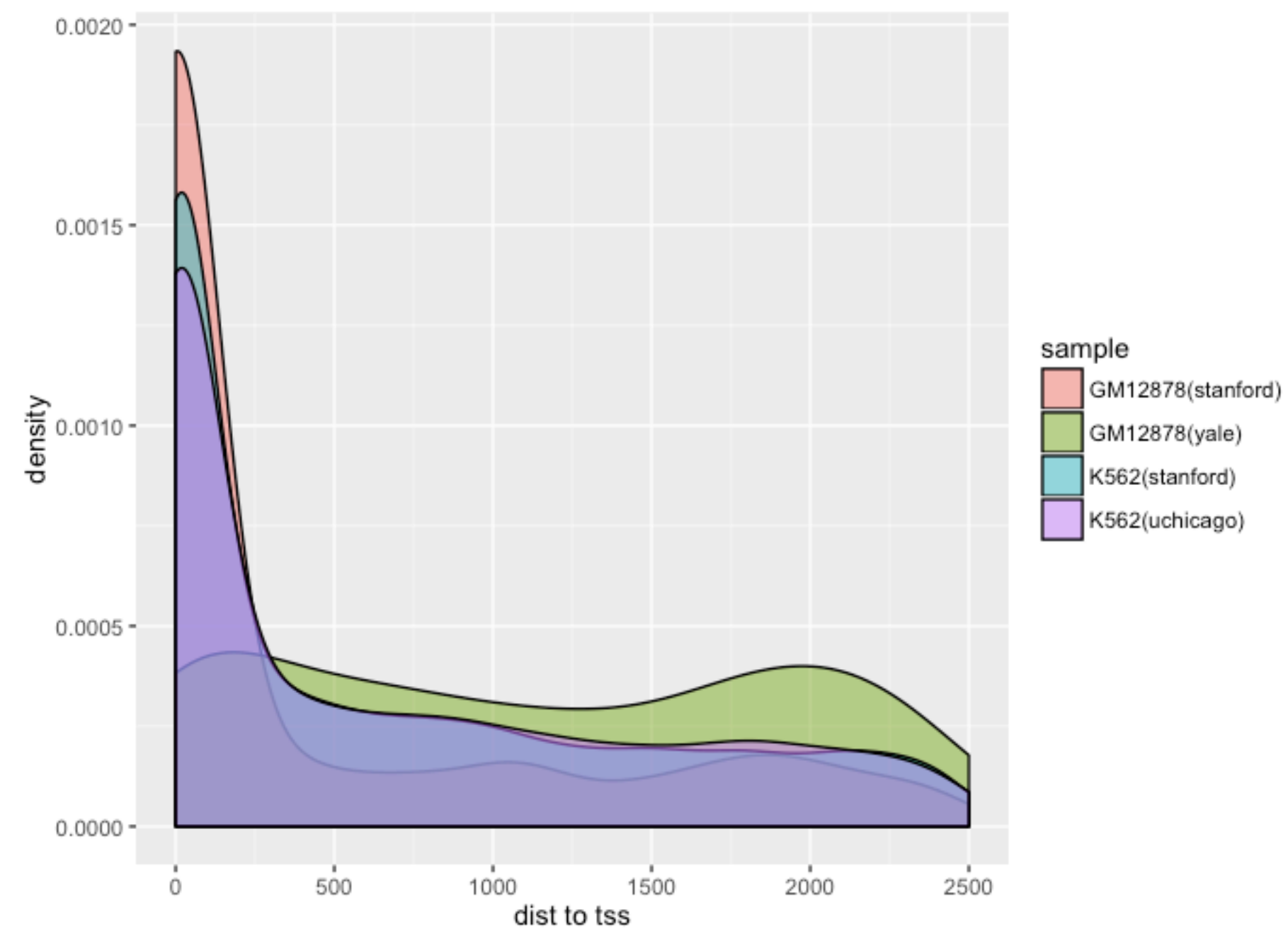
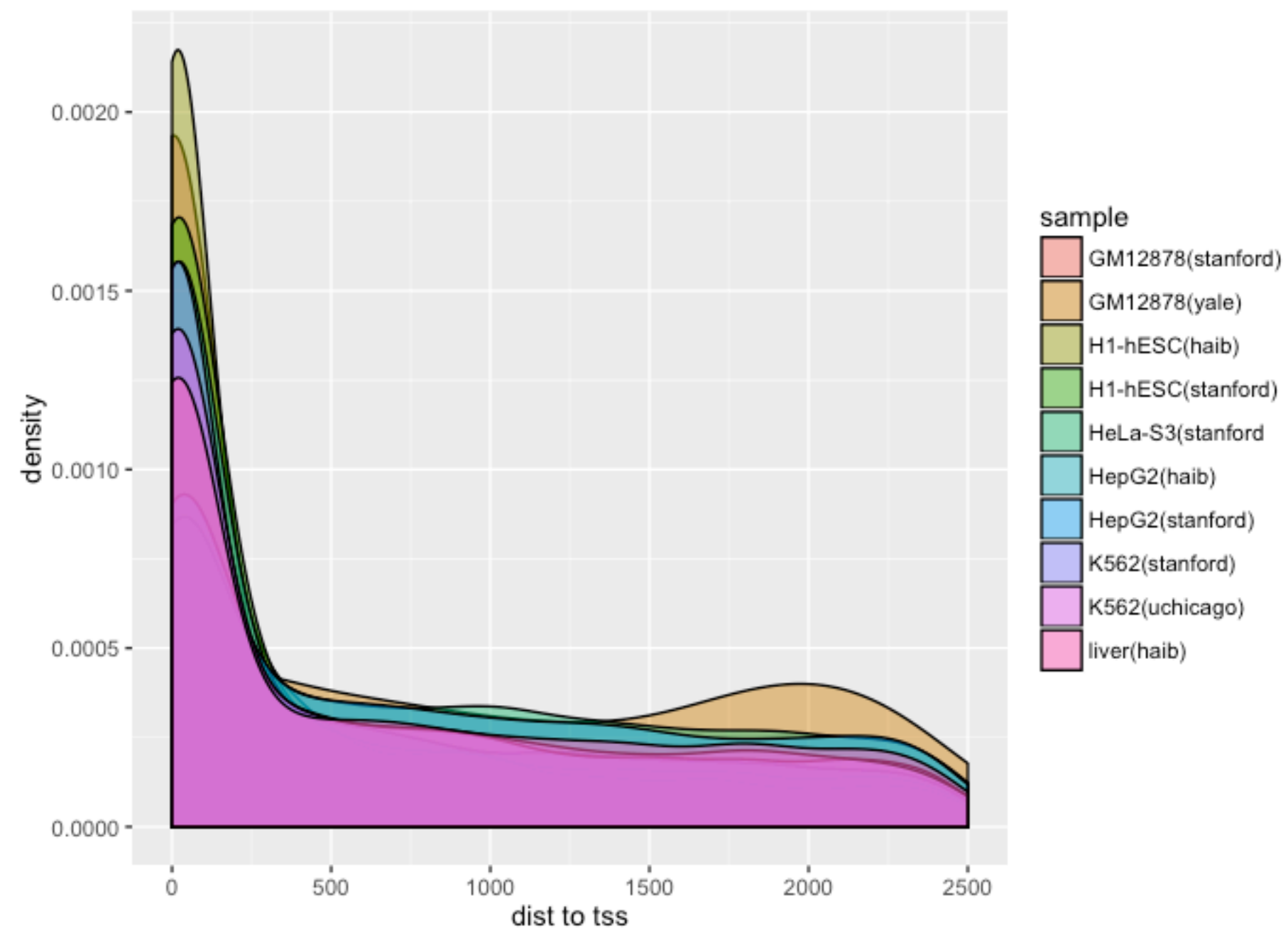
dist(tab, method = "binary")
hclust (*, "ward.D")

Cluster Dendrogram

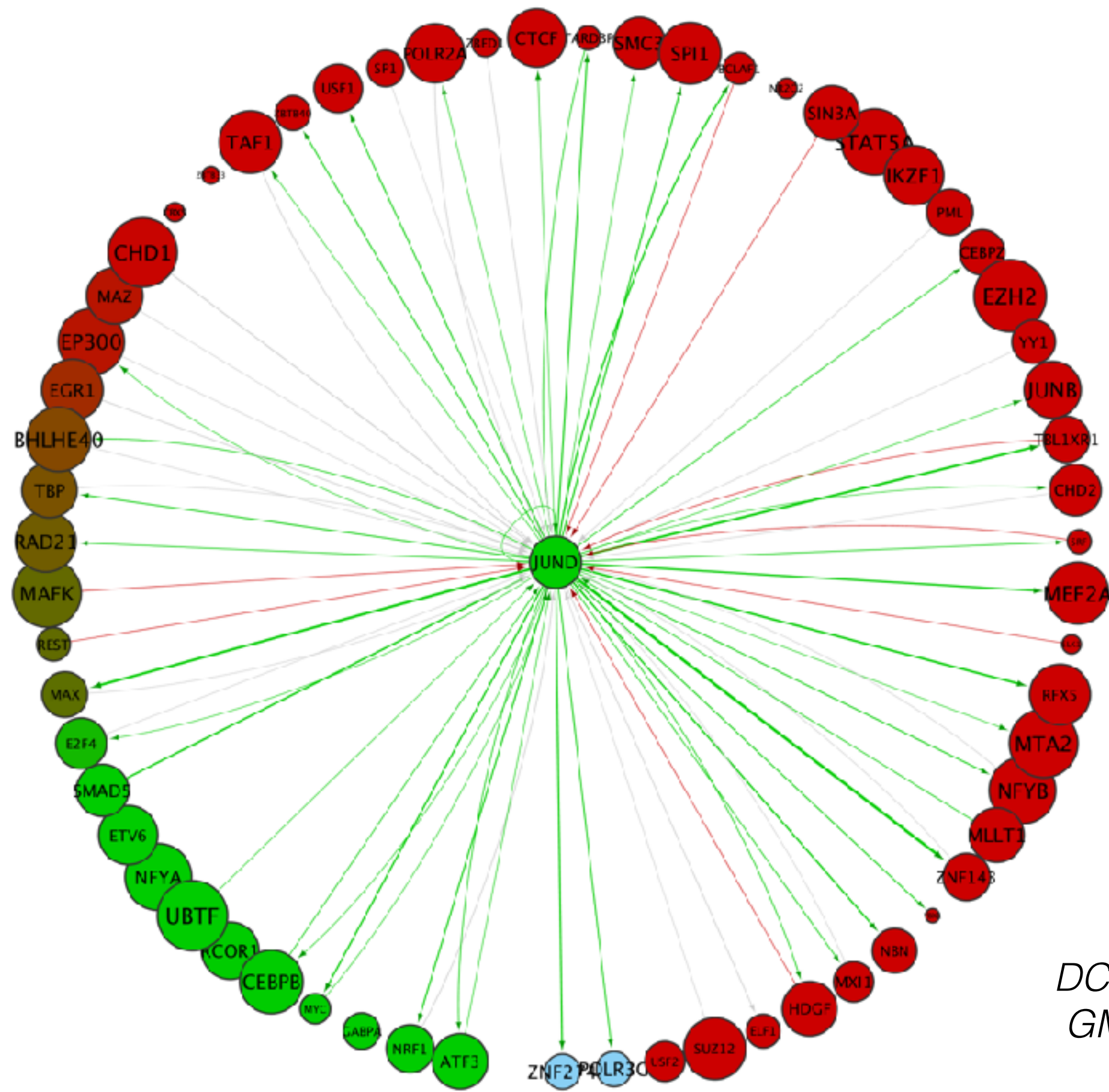


TSS +/- 1kb

dist(tab, method = "binary")
hclust (*, "ward.D")



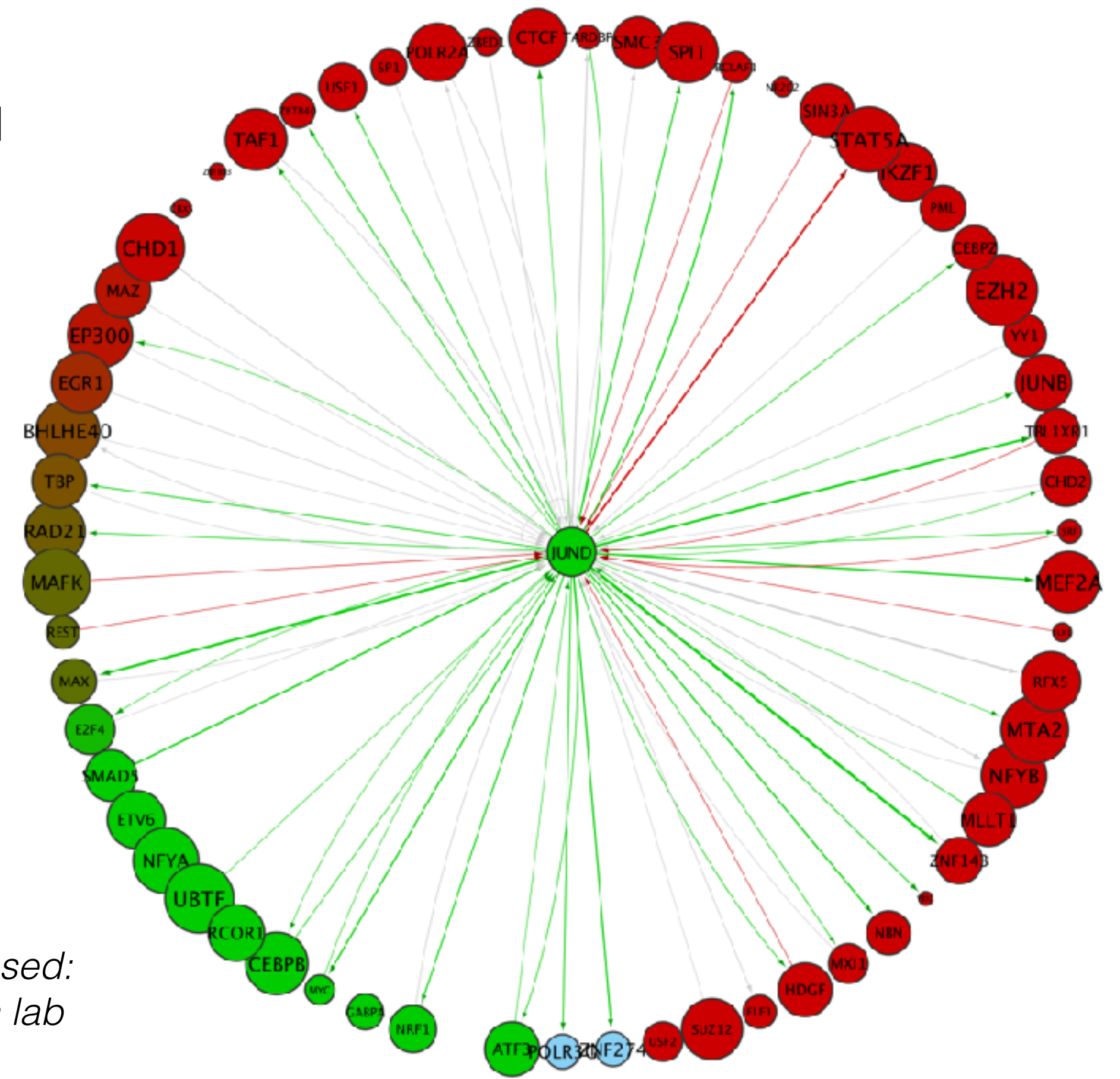
Yale vs. Stanford



GM12878_JUND_yale_ENC SR000EYV

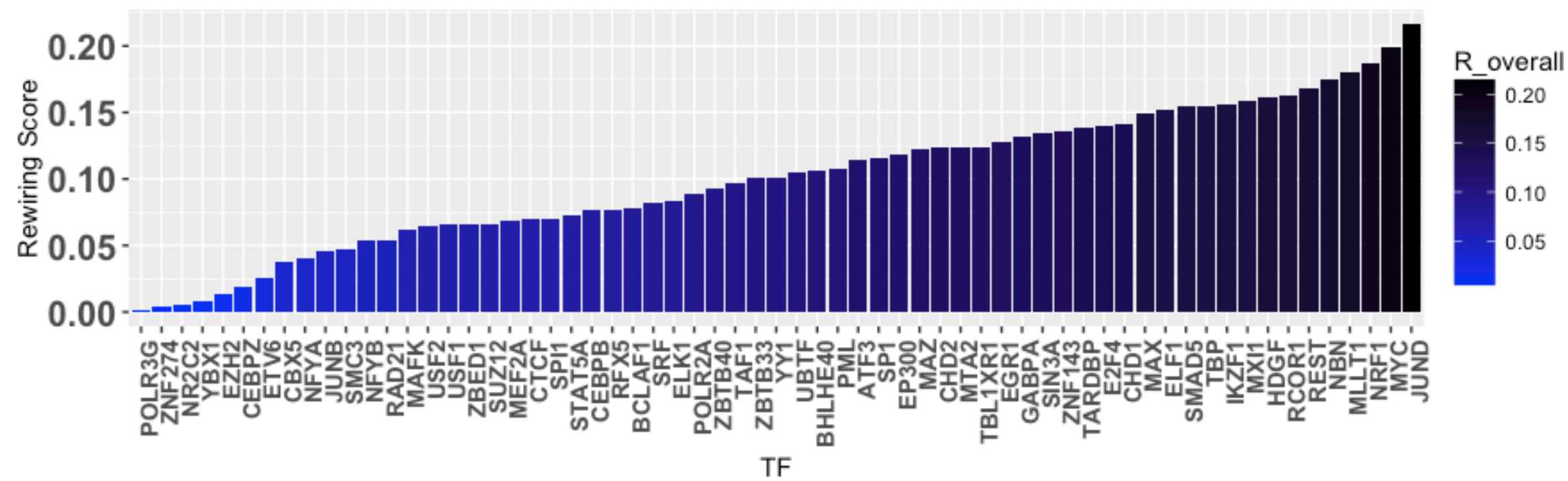
*DCC has uniformly processed:
GM12878 from Weissman lab
K562 from Snyder lab*

but not GM12878 from Snyder lab

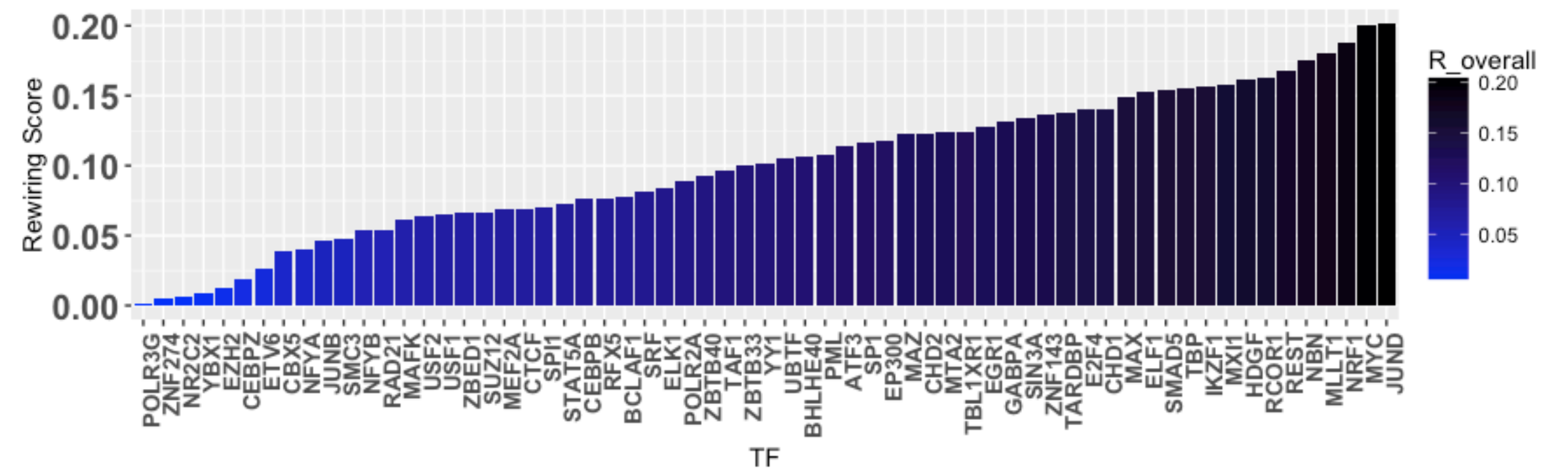


GM12878_JUND_stanford_ENC SR000DYS

TF-GENE network

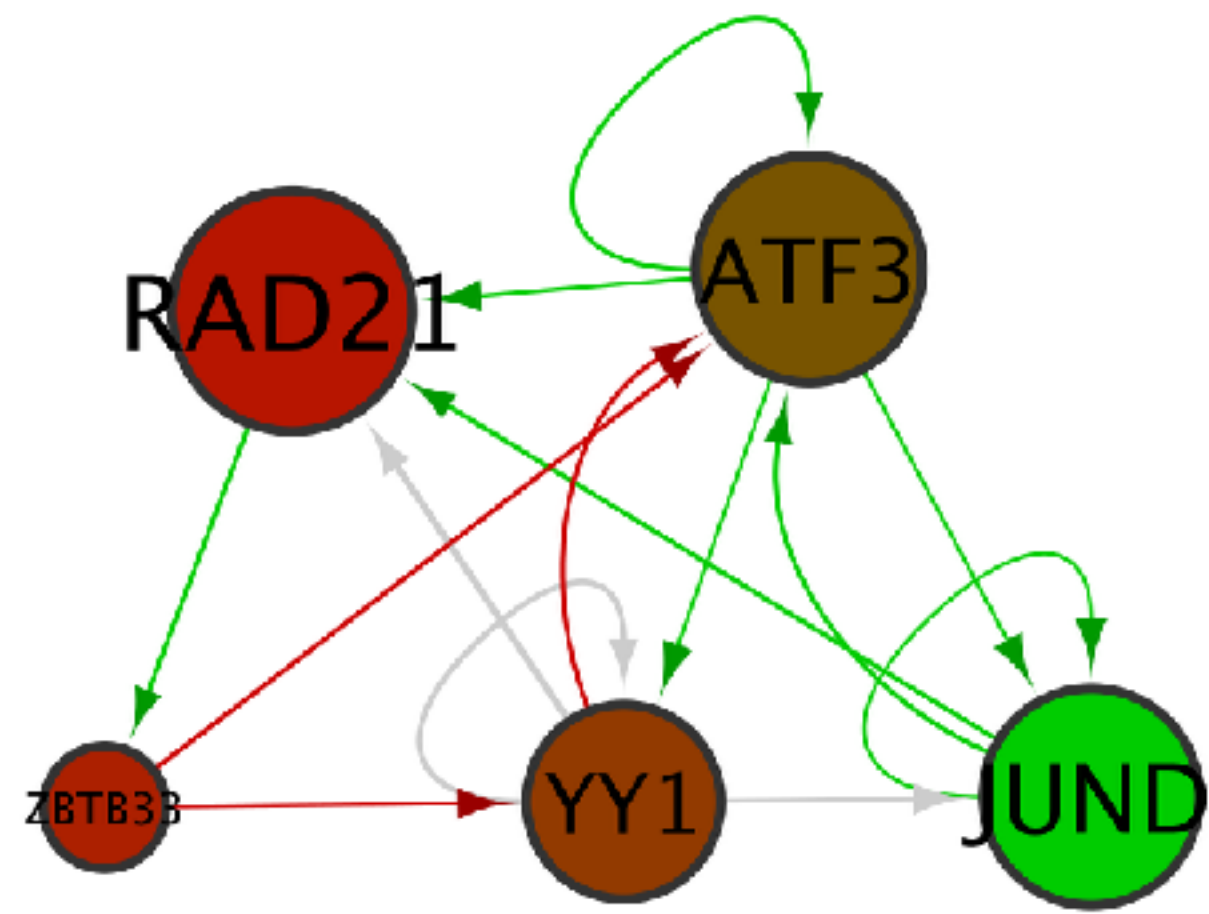


TF-GENE network

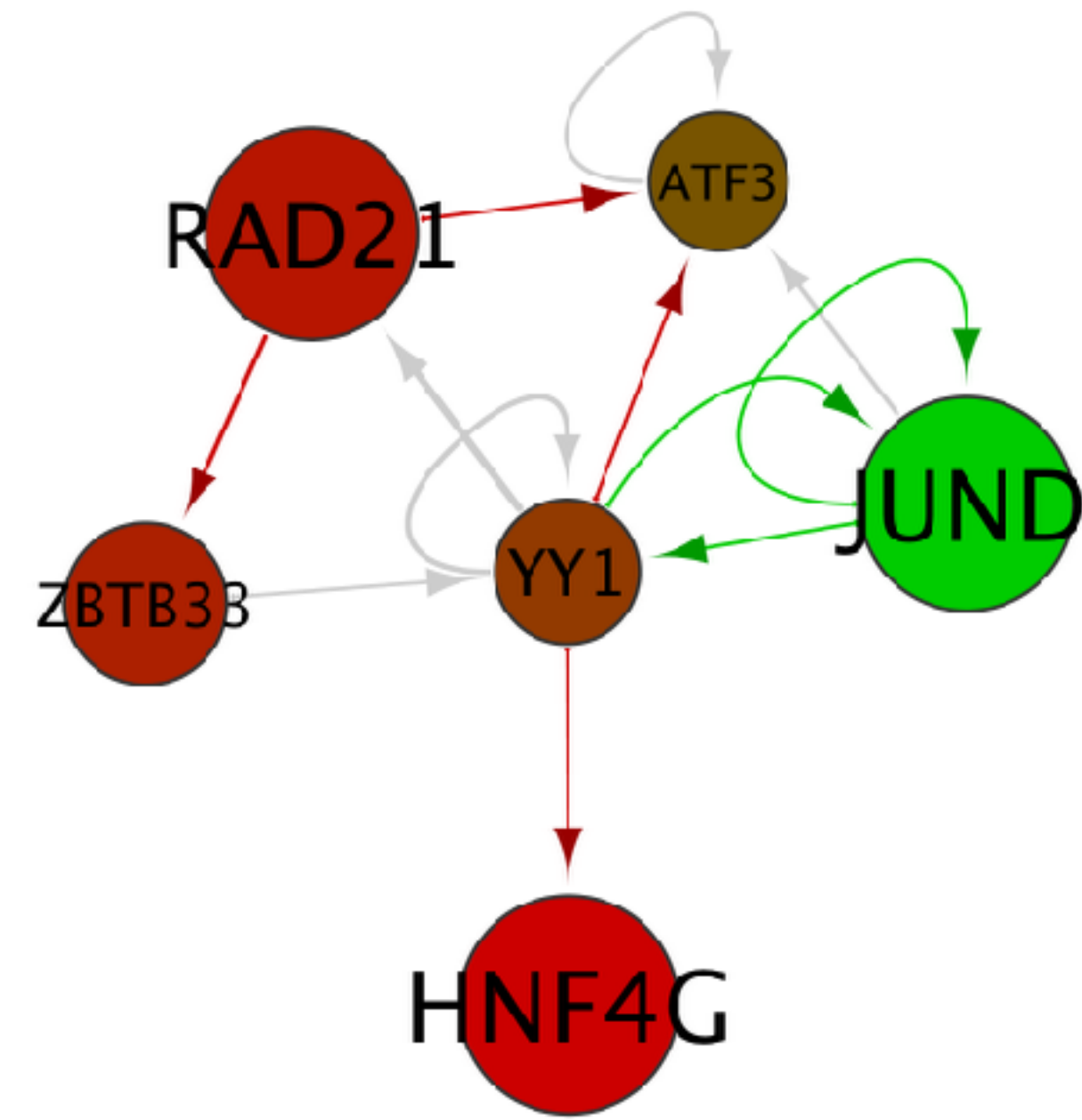


JUND Gained Target (n=6548)

Expression (TPM)	UP			NC			DN		
<i>n</i>	1291			4597			660		
%	19.7%			70.2%			10.1%		
DHS (TSS Cov) active	UP	NC	DN	UP	NC	DN	UP	NC	DN
<i>n</i>	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
<i>n</i>	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
<i>n</i>	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
<i>n</i>	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%
Mutation ext.gene count	count > 1	has mut	no mut	count > 1	has mut	no mut	count > 1	has mut	no mut
	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 ext.gene pval < 0.05	17			66			22		
	1.3%			1.4%			3.3%		
Mutation ext.gene pval.adj < 0.05	2			2			2		
	0.2%			0.0%			0.3%		
	BACH2 BCL6			SF3B1 ST6GAL1			BTG2 TP53		
UP: $TPM_{K562} \geq 2 \times TPM_{GM12878}$									
NC: $1/2 \times TPM_{GM12878} < TPM_{K562} < 2 \times TPM_{GM12878}$									
DN: $TPM_{K562} \leq 1/2 \times TPM_{GM12878}$									

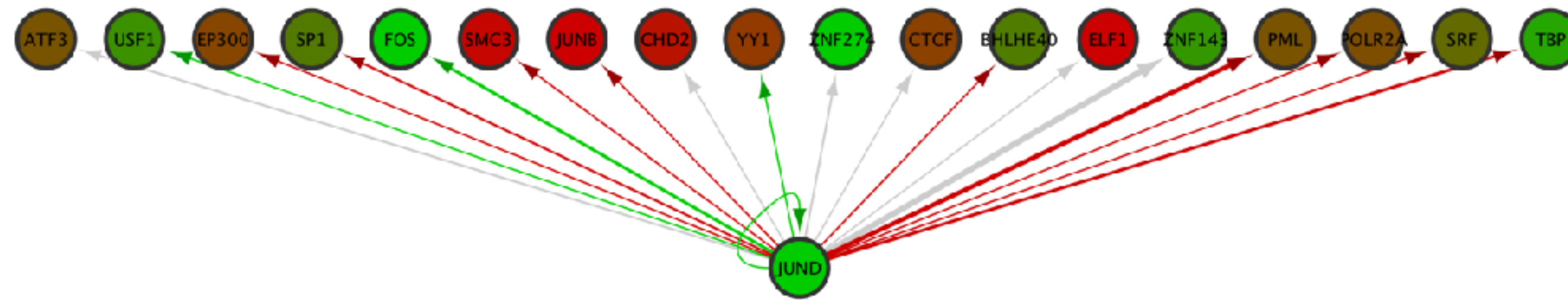


<GM12878 vs K562>



<liver vs HepG2>

<liver vs HepG2>



<GM12878 vs K562>

