

Figure S1: **Cell line specificity analysis of the network nodes.** a) Distribution of expression of protein coding genes for tissue-specific and ubiquitously expressed gene determined from 24 ENCODE cell lines. b) Distribution of expression of lncRNAs for tissue-specific and ubiquitously expressed lncRNAs determined from 24 ENCODE cell lines. 'No expression' refers to lncRNA with no detectable expression in any of the ENCODE cell lines (whole cell RNA-seq) but with detectable expression in the RNA-seq libraries of the chromatin RNA fraction in K562, reflecting expression of nascent transcripts. c) Distribution of gene-lncRNAs Mutual Information values (MI) for tissue-specific and ubiquitously expressed lncRNAs computed from 24 ENCODE cell lines. d) Degree distribution for tissue-specific and ubiquitously expressed lncRNAs.

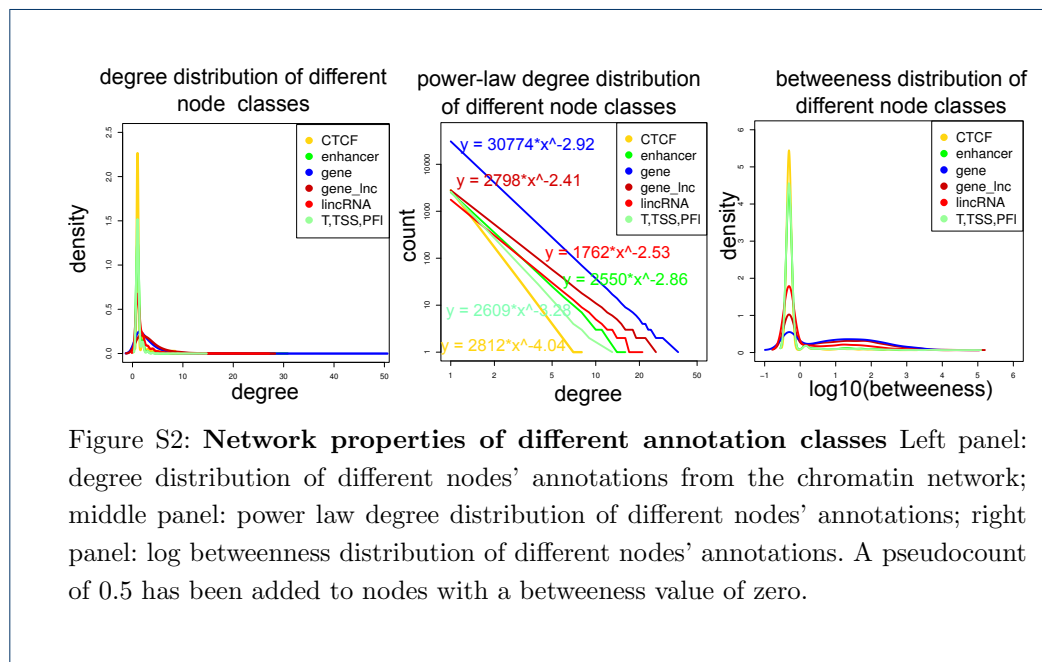
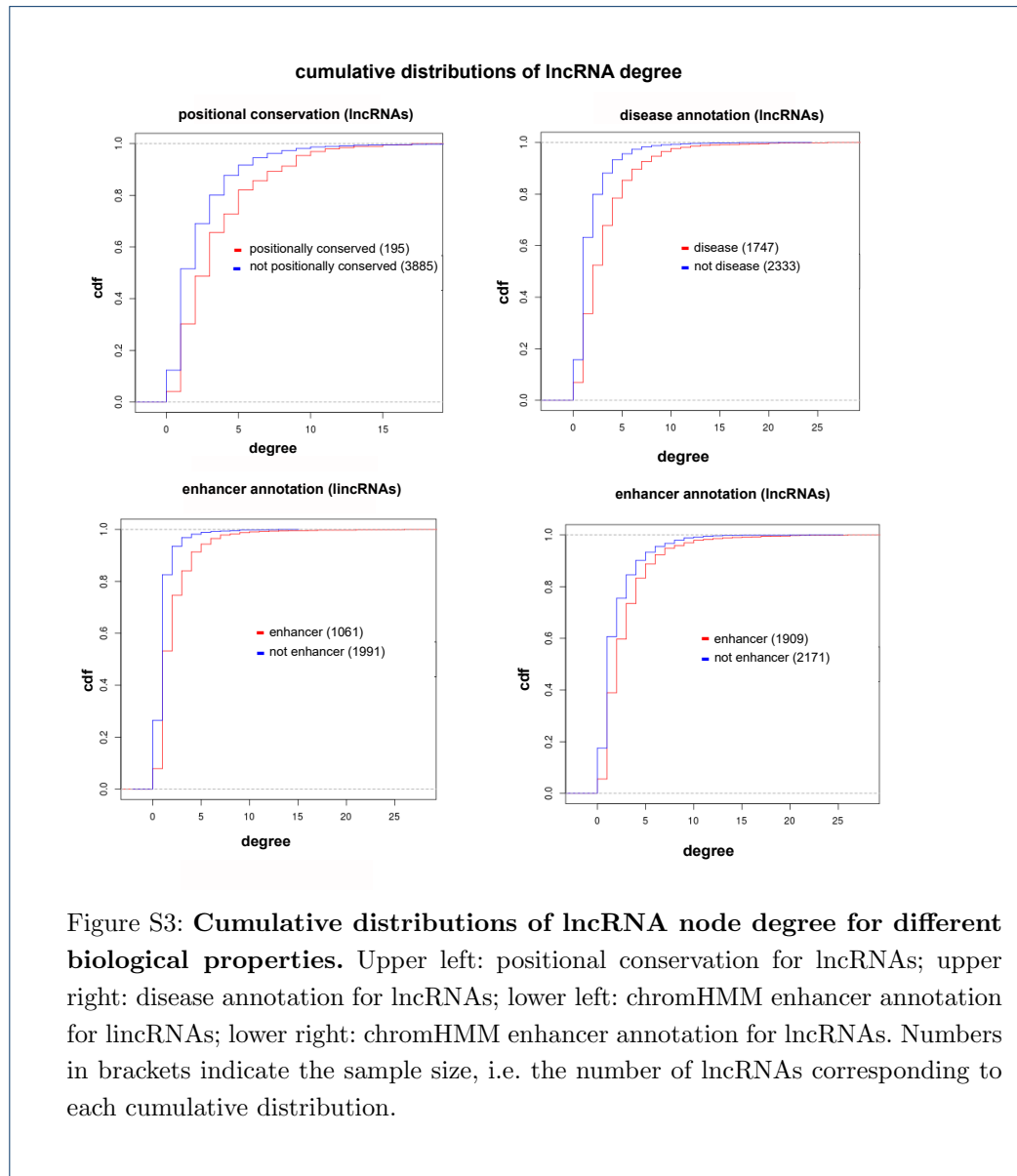


Table S1: Network properties of different genomic regions

annotation	min_d	q1_d	median_d	mean_d	q3_d	max_d	min_b	q1_b	median_b	mean_b	q3_b	max_b
CTCF	1	1	1	1.09	1	8	0	0	0	3.34	0	1410
enhancer	1	1	1	1.18	1	30	0	0	0	31.5	0	61845
gene	1	1	2	2.78	4	49	0	0	3	211.67	51	62024.27
gene_lnc	1	2	3	3.51	4	26	0	0	12	236.41	85.375	27307.88
lincRNA	1	1	1	1.87	2	26	0	0	0	134.99	4.895	45314.76
T,TSS,PFI	1	1	1	1.14	1	14	0	0	0	30.52	0	84898.53
unknown	1	1	1	1	1	1	0	0	0	0	0	0

For each genomic annotation we report minimum degree, 25% lower quantile of the degree distribution, median degree, mean degree, 75% upper quantile of the degree distribution and maximum degree. The same quantities are reported for different annotations regarding the betweenness distribution.



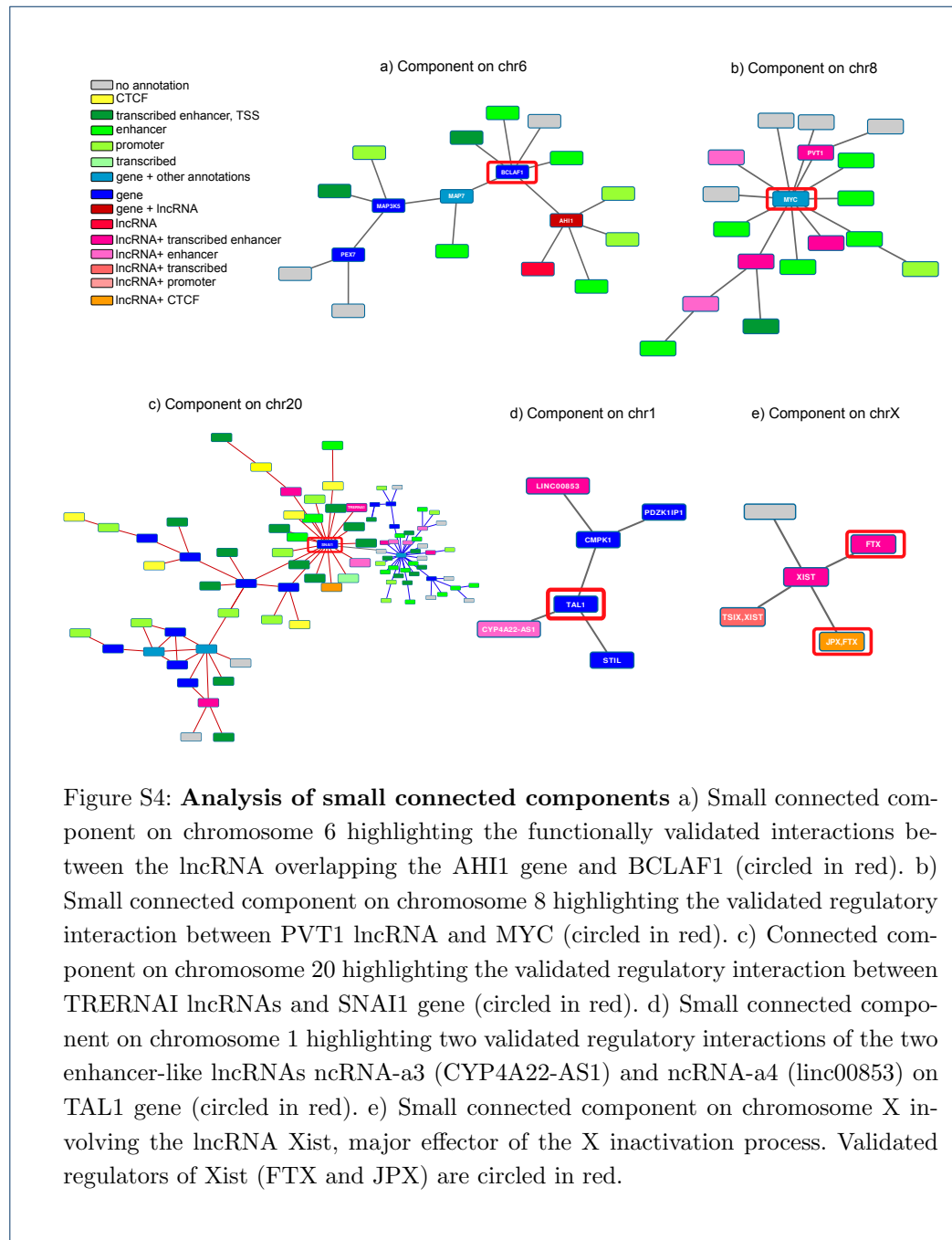


Table S2: Network properties of lincRNAs in the biggest connected component of chromosome 1

lincRNA	degree	to_gene degree	betweenness	expression
RP11-442N24..B.1,RNU11	26	12	28958.62	5.465
RP4-798A10.7	21	6	32092.38	16.0232
RP11-495P10.3	12	0	5456	1.0816
SNHG12	9	7	2514.22	229.3524
RP11-458D21.1	9	6	22924.47	52.9613
ADAMTSL4-AS1	6	3	2249	50.9546
FLJ37453	5	3	4126.5	7.1451
RP1-212P9.3	4	1	397.41	0.5435
RP11-337C18.8,RP11-337C18.10	3	1	250.67	0.044
CH17-373J23.1	3	0	6056.3	35.8141
SEC22B	2	1	0	26.7178
RP5-888M10.2	2	2	0	1.2264
RP5-1092A3.5	2	1	0	2.3792
RP4-798A10.2	2	1	501	14.2565
RP1-37C10.3	2	2	0	0.1157
RP11-474O21.5	2	2	0	111.6587
RP11-337C18.10	2	0	249.33	0.0371

For each intergenic lincRNA we report its name (*lincRNA*), its degree centrality inside the connected component (*degree*), its degree centrality computed only from gene connections (*to-gene degree*), its betweenness (*betweenness*) and its expression value (RPKM) in the K562 cell line (*expression*).

Table S3: Network properties of lincRNAs in the biggest connected component of chromosome 17

lincRNA	degree	to_gene degree	betweenness	expression
LINC00910	17	8	45314.76	37.0585
SNHG16,RP11-666A8.8	9	5	8527.74	73.5648
LINC00854	8	3	1776.27	70.9481
RP13-516M14.1,RP13-516M14.4	6	2	1834.12	62.6496
RP11-1055B8.9	6	4	513.68	9.3433
RP11-400F19.8	5	5	7618.89	3.1249
RP13-766D20.4	4	3	1130.2	1.2599
LINC00482	4	2	348	15.868
CTD-2020K17.1	4	4	423.66	8.9101
RP11-285E9.6	3	2	1040	0.0321
RP11-1055B8.3	3	1	695	0.5555
RP11-1055B8.10,RP11-1055B8.4	3	1	695	3.095
CTD-3014M21.1	3	0	35.83	6.4664
RP11-666A8.8	2	0	0	2.8546
RP11-392O1.4	2	1	10.47	0.0438
RP11-358B23.1	2	1	173.5	0.9049
RP11-1055B8.3,RP11-1055B8.10,RP11-1055B8.4	2	1	348	0.5555
MAP3K14-AS1	2	1	348	12.5812
CTD-2561B21.11	2	1	348	8.7781

For each lincRNA we report its name (*lincRNA*), its degree centrality inside the connected component (*degree*), its degree centrality computed only from gene connections (*to-gene degree*), its betweenness (*betweenness*) and its expression value (RPKM) in the K562 cell line (*expression*).

Table S4: Network properties of lincRNAs in the biggest connected component of chromosome 11

lincRNA	degree	to_gene degree	betweenness	rpkm
MALAT1	8	6	4023.77	10426.3926
NEAT1	6	4	361.67	1685.197
MIR194-2HG	2	2	0	3.3122

For each lincRNA we report its name (*lincRNA*), its degree centrality inside the connected component (*degree*), its degree centrality computed only from gene connections (*to-gene degree*), its betweenness (*betweenness*) and its expression value (RPKM) in the K562 cell line (*expression*).

Table S5: Fuzzy clustering or inter-modular nodes

lincRNA	chr	type	expr	degree
RP11-661A12.5	chr8	linc_TSS	11.36	2
RP11-838N2.5	chr18	linc_enhancer	0.65	6
AC073842.19	chr7	linc_transcr_enhancer	1.06	13
RP11-400F19.8	chr17	linc_transcr_enhancer	3.13	5
RP13-516M14.1	chr17	linc_transcr_enhancer	62.65	6
RP11-388C12.5	chr17	linc_TSS	9.55	1
RP4-798A10.2	chr1	linc_transcribed	14.26	1
CH17-373J23.1	chr1	linc_promoter	35.81	3
RP11-403I13.5	chr1	linc_enhancer	0.27	1
CTD-2555K7.2	chr14	linc_transcr_enhancer	1.1	2
RP11-298I3.4	chr14	linc_CTCF	0.74	3
RP11-57206.1	chr3	linc_transcribed	35.16	2
U91328.21	chr6	linc_TSS	0.15	2

For each lincRNA we report its name (*lincRNA*), the chromosomal location (*chr*), its genomic annotation (*type*), its expression value (RPKM) in the K562 cell line (*expr*) and degree centrality (*degree*)