Supplementary Materials for

New insights on human essential genes based on integrated analysis and the construction of the HEGIAP web-based platform

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The PDF file includes:

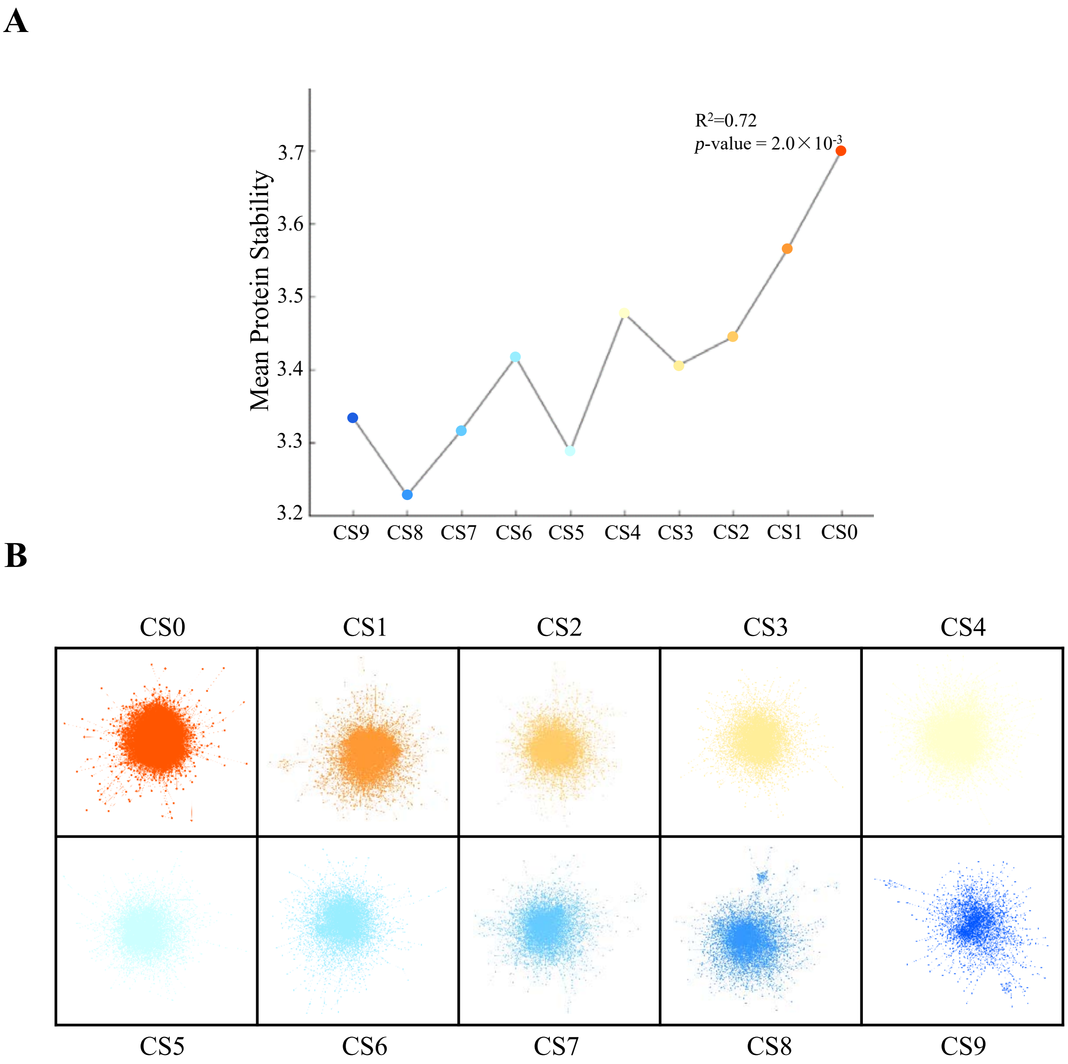
Fig. S15. Relationship between human essential genes and cancer.

Table. S1. Significantly differential expressed genes (DEGs) in cancer-normal tissue pairs.

Table. S2. Candidate drugs.

Table. S3. Data description.

Table. S4. CS threshold of each gene group.



Gene group	Number of nodes	Number of edges	Average node degree
CS0	1871	85728	91.6
CS1	1872	14905	15.9
CS2	1872	8986	9.6
CS3	1876	8798	9.38
CS4	1874	8665	9.25
CS5	1873	8922	9.53
CS6	1873	8893	9.5
CS7	1873	8064	8.61
CS8	1876	8421	8.98
CS9	1103	3060	5.55

Fig S1. Protein characteristics. (A) Stability of proteins encoded by genes in different gene groups. R^2 and *p*-value for linear regression are shown. **(B)** Top: PPI networks of 10 groups of genes. Bottom: topological properties of PPI networks.

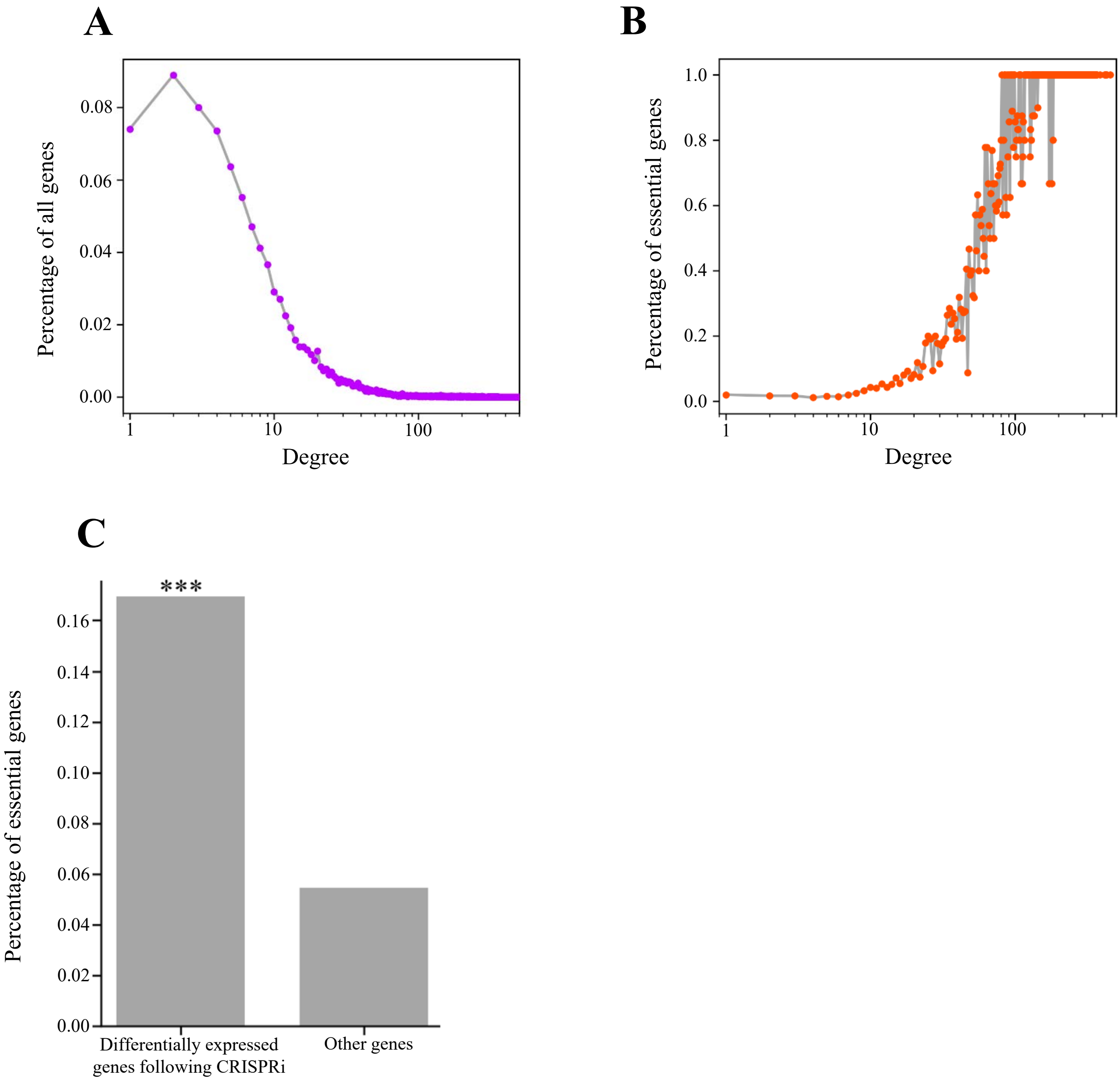


Fig. S2. Regulatory characteristics. Relationship between the degree of connectivity and the number of all genes **(A)** and the number of essential genes **(B)** in PPI network**. (C)** Proportion of essential genes in differentially expressed genes following lncRNA CRISPRi and in other genes. Significance: *** p-value < 0.0001, Fisher's exact test

GO term	CS1	CS2	CS3	CS4	CS5	CS6	CS7	CS8	CS9	CS10
rRNA processing	104.46	0	0	0	0	0	0	0	0	0
translational initiation	76.33	0	0	0	0	0	0	0	0	0
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	66.16	0	0	0	0	0	0	0	0	0
mRNA splicing, via spliceosome	65.48	8.03	0	0	0	0	0	0	0	0
translation	64.60	0	0	0	0	0	0	0	0	0
viral transcription	62.88	0	0	0	0	0	0	0	0	0
SRP-dependent cotranslational protein targeting to membrane	60.56	0	0	0	0	0	0	0	0	0
mitochondrial translational elongation	37.98	0	0	0	0	0	0	0	0	0
DNA replication	36.51	0	0	0	0	0	0	0	0	0
mitochondrial translational termination	35.00	0	0	0	0	0	0	0	0	0
transcription-coupled nucleotide-excision repair	33.96	0	0	0	0	0	0	0	0	0
mitochondrial respiratory chain complex I assembly	0	11.63	0	0	0	0	0	0	0	0
mitochondrial electron transport, NADH to ubiquinone	0	9.19	0	0	0	0	0	0	0	0
transcription, DNA-templated	0	4.75	0	0	0	0	0	0	0	0
DNA repair	0	4.50	0	0	0	0	0	0	0	0
transcription elongation from RNA polymerase II promoter	0	4.49	0	0	0	0	0	0	0	0
snRNA transcription from RNA polymerase II promoter	0	4.25	0	0	0	0	0	0	0	0
transcription initiation from RNA polymerase II promoter	0	4.19	0	0	0	0	0	0	0	0
protein import into peroxisome matrix	0	4.00	0	0	0	0	0	0	0	0
mitotic nuclear division	0	3.95	0	0	0	0	0	0	0	0
cell division	0	3.78	0	0	0	0	0	0	0	0
negative regulation of neuron apoptotic process	0	0	3.74	0	0	0	0	0	0	0
transport	0	0	0	4.49	0	0	0	0	0	0
extracellular matrix disassembly	0	0	0	3.31	0	0	0	0	0	0
positive regulation of GTPase activity	0	0	0	0	5.97	0	0	0	0	0
vascular endothelial growth factor receptor signaling pathway	0	0	0	0	3.57	0	0	0	0	0
intracellular signal transduction	0	0	0	0	3.22	0	0	0	0	0
regulation of GTPase activity	0	0	0	0	3.10	0	0	0	0	0
regulation of cell proliferation	0	0	0	0	3.01	0	0	0	0	0
cell fate commitment	0	0	0	0	0	4.41	0	0	0	0
positive regulation of ERK1 and ERK2 cascade	0	0	0	0	0	3.60	0	0	0	0
cell adhesion	0	0	0	0	0	0	4.39	0	0	0
inflammatory response	0	0	0	0	0	0	4.00	0	0	0
lipid catabolic process	0	0	0	0	0	0	3.62	0	0	0
negative regulation of inflammatory response	0	0	0	0	0	0	3.57	0	0	0
membrane repolarization during ventricular cardiac muscle cell action potential	0	0	0	0	0	0	3.52	0	0	0
potassium ion export	0	0	0	0	0	0	3.20	0	0	0
cell-cell signaling	0	0	0	0	0	0	3.19	0	0	0
homophilic cell adhesion via plasma membrane adhesion molecules	0	0	0	0	0	0	0	0	3.70	0
detection of chemical stimulus involved in sensory perception of bitter taste	0	0	0	0	0	0	0	0	0	3.92

-$\log_{10}$(p-value)

Fig. S3. GO analysis of 10 groups of genes.

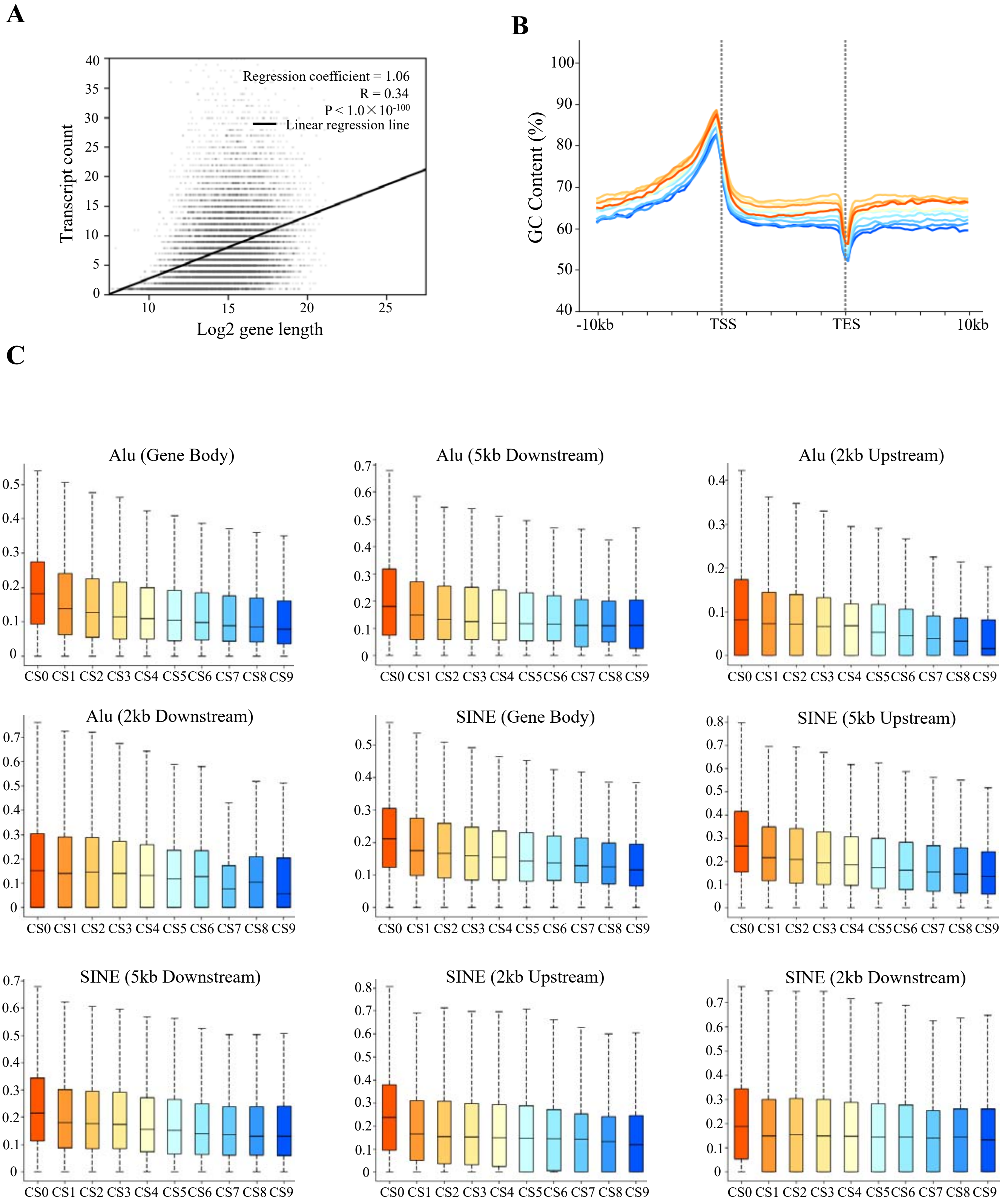

A
Transcript count
Log2 gene length
Regression coefficient = 1.06
R = 0.34
P < 1.0×10-100
Linear regression line
B
GC Content (%)
-10kb
TSS
TES
10kb
C
Alu (Gene Body)
Alu (5kb Downstream)
Alu (2kb Upstream)
Alu (2kb Downstream)
SINE (Gene Body)
SINE (5kb Upstream)
SINE (5kb Downstream)
SINE (2kb Upstream)
SINE (2kb Downstream)
CS0 CS1 CS2 CS3 CS4 CS5 CS6 CS7 CS8 CS9

Fig. S4. Sequences characteristics. (A) Correlation between gene length and transcript count of all protein coding genes in 10 groups. Grey dots: all protein coding genes in 10 groups. Black line: fitted regression line. Regression coefficient, R^2 and *p*-value for linear regression are shown. (**B)** GC content of regions 10-kb up- or downstream of gene body. Red line: human essential genes. Color of gene group changes from red to blue with increasing CS value (decreasing essentiality). (**C)** Repetitive elements of 10 groups of genes.

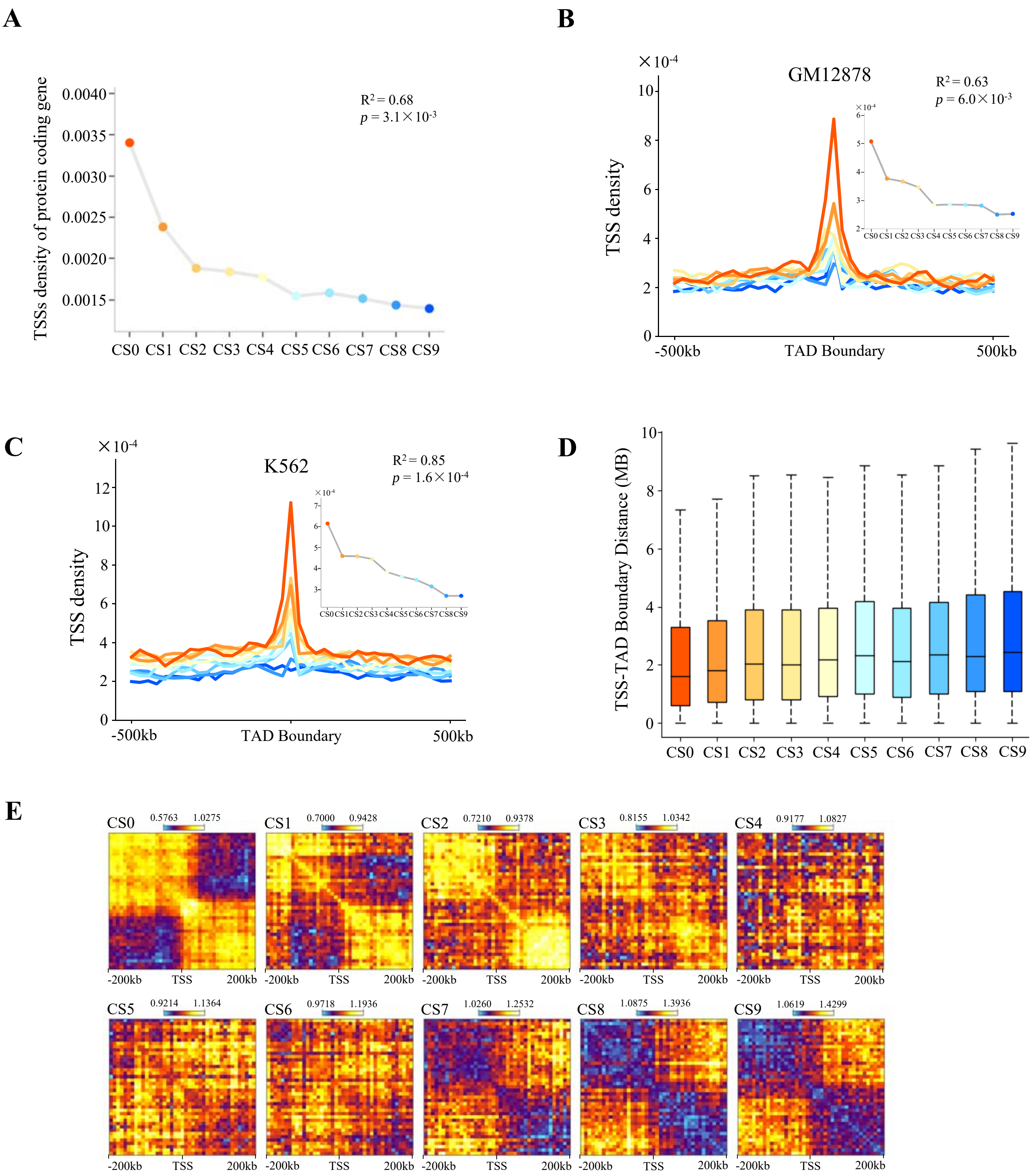
A
TSSs density of protein coding gene
0.0040
0.0035
0.0030
0.0025
0.0020
0.0015
$R^2 = 0.68$
$p = 3.1 \times 10^{-3}$
CS0 CS1 CS2 CS3 CS4 CS5 CS6 CS7 CS8 CS9
B
$\times 10^{-4}$
GM12878
$R^2 = 0.63$
$p = 6.0 \times 10^{-3}$
TSS density
10
8
6
4
2
0
-500kb
TAD Boundary
500kb
C
$\times 10^{-4}$
K562
$R^2 = 0.85$
$p = 1.6 \times 10^{-4}$
TSS density
12
10
8
6
4
2
0
-500kb
TAD Boundary
500kb
D
TSS-TAD Boundary Distance (MB)
10
8
6
4
2
0
CS0 CS1 CS2 CS3 CS4 CS5 CS6 CS7 CS8 CS9
E
CS0 0.5763 1.0275
CS1 0.7000 0.9428
CS2 0.7210 0.9378
CS3 0.8155 1.0342
CS4 0.9177 1.0827
CS5 0.9214 1.1364
CS6 0.9718 1.1936
CS7 1.0260 1.2532
CS8 1.0875 1.3936
CS9 1.0619 1.4299
-200kb TSS 200kb

Fig. S5. Structural characteristics. (A) Level of overlap between 10 types of gene TSSs and all protein-coding gene TSSs. R^2 and *p*-value for linear regression are shown. (**B-C)** Profiles of 10 types of TSSs near TAD boundary of **(B)** GM12878 or **(C)** K562. Inset: mean values of TAD boundary and near-boundary regions (≤100kb). R^2 and *p*-value for linear regression of mean value of 10 gene groups of near-boundary regions(≤100 kb) are shown. (**D)** Average distance between gene and nearest TAD boundary. (**E)** Mean Hi-C contact map near 10 types of TSSs. Value for each bin was normalized by dividing by the mean value of all bins of the same linear genomic distance.

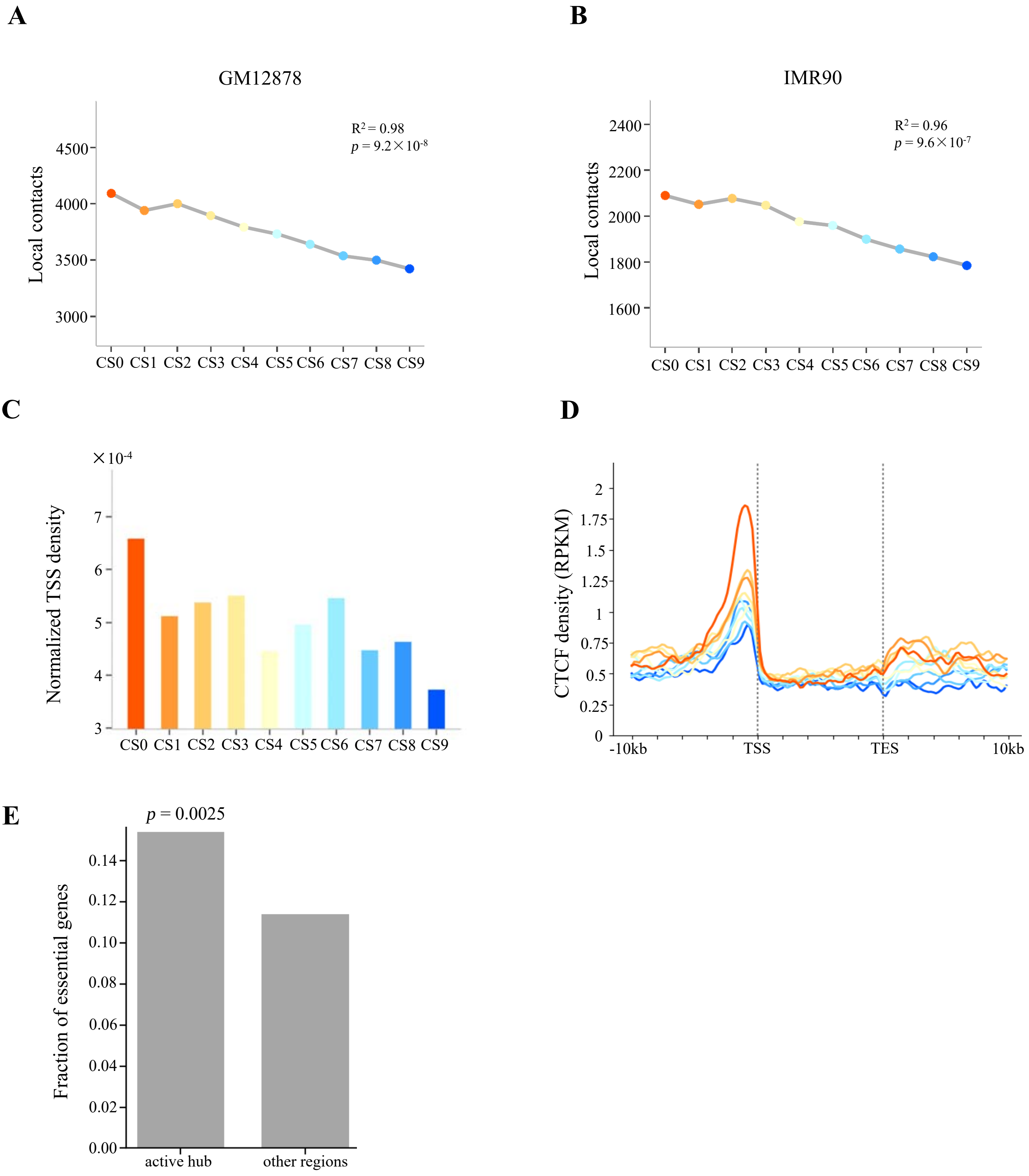


Fig. S6. 3D structure. (A-B) Mean intra-TAD local (<100 kb) Hi-C contacts for bins containing 10 types of TSSs in (**A**) GM12878 and (**B**) IMR90. For each bin containing a TSS, only contacts with bins in the opposite direction to the nearest TAD boundary were counted. R^2 and *p*-value for linear regression are shown. **(C)** Level of overlap between 10 types of gene TSSs and GM12878 chromatin loop anchors. (**D)** ChIP-seq signal of CTCF in region 10-kb up- or downstream of gene body. (**E**) Fraction of essential genes in active inter-chromosome hubs and in other genomic regions. Significance: *p*-value = 0.0025, Fisher's exact test.

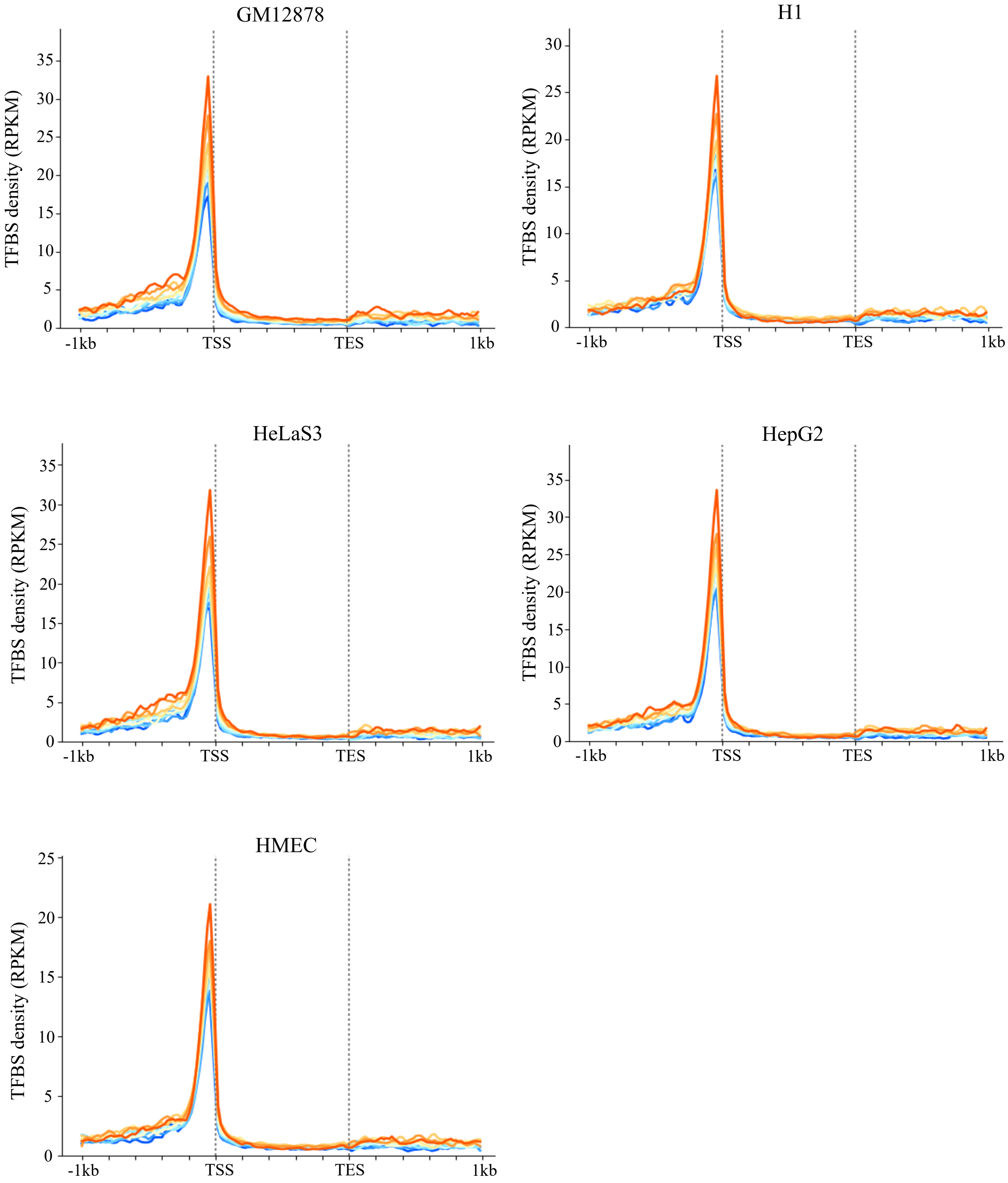


Fig. S7. Distributions of transcription factor binding sites in regions 1-kb up- or downstream of gene body from five human cell lines.

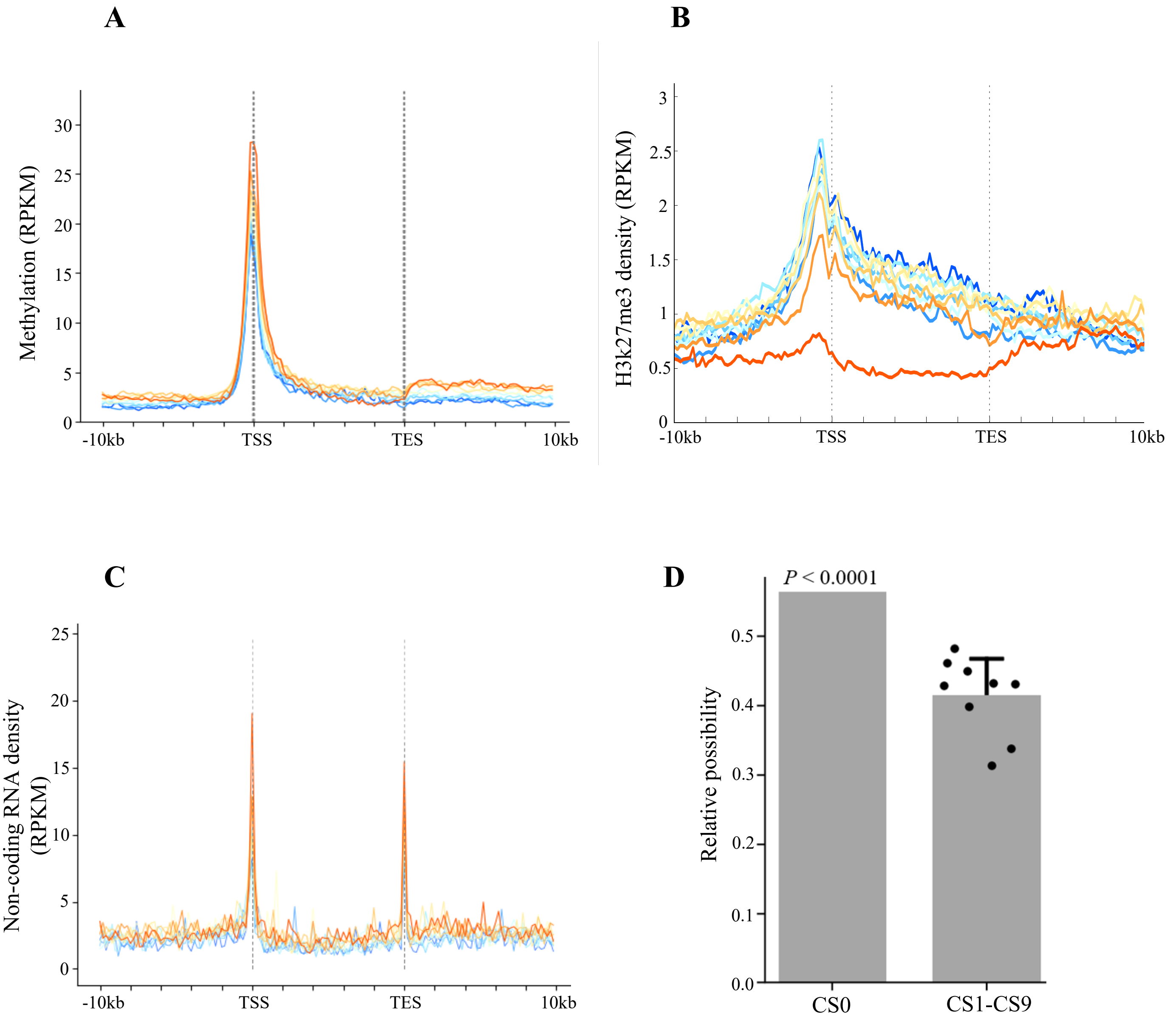


Fig. S8. Epigenetic analyses. Methylation level (MRE) (**A**), H3k27me3 density (**B**), and ncRNA distribution (**C**) in regions 10-kb up- or downstream of gene body. (**D**) Relative possibility of inactive epigenetic hub genes in essential gene group (CS0) and in other gene group (CS1-CS9). Significance: *p*-value < 0.0001, one-sample t-test.

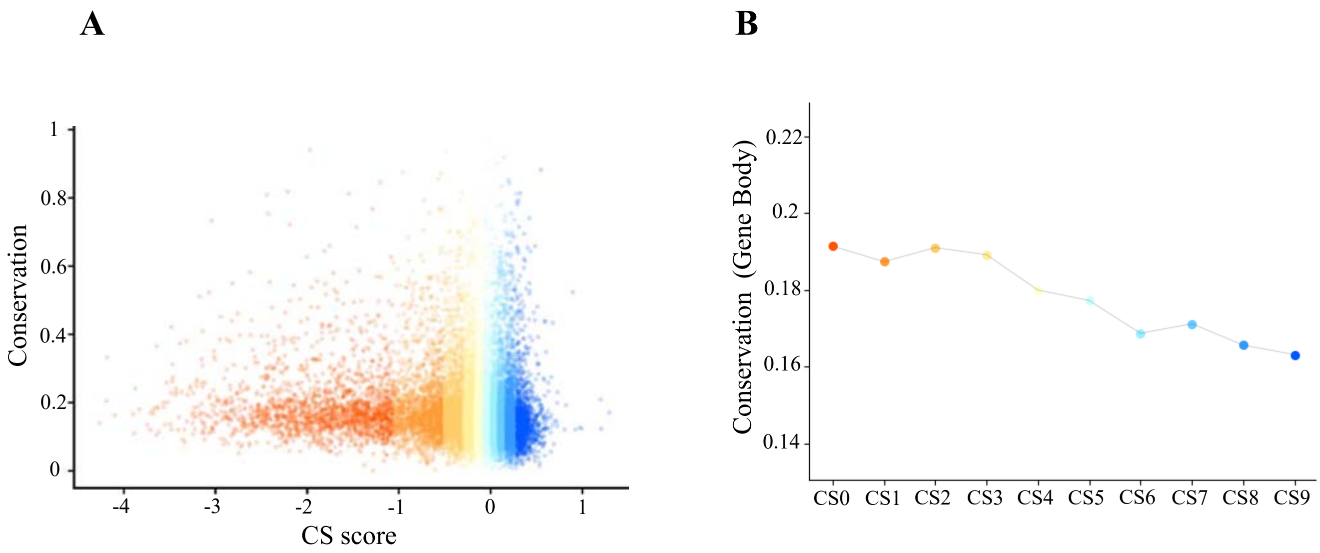


Fig. S9. Essentiality and conservation. (A) Relationship between CS value and conservation. (**B)** Average conservation of gene body regions.

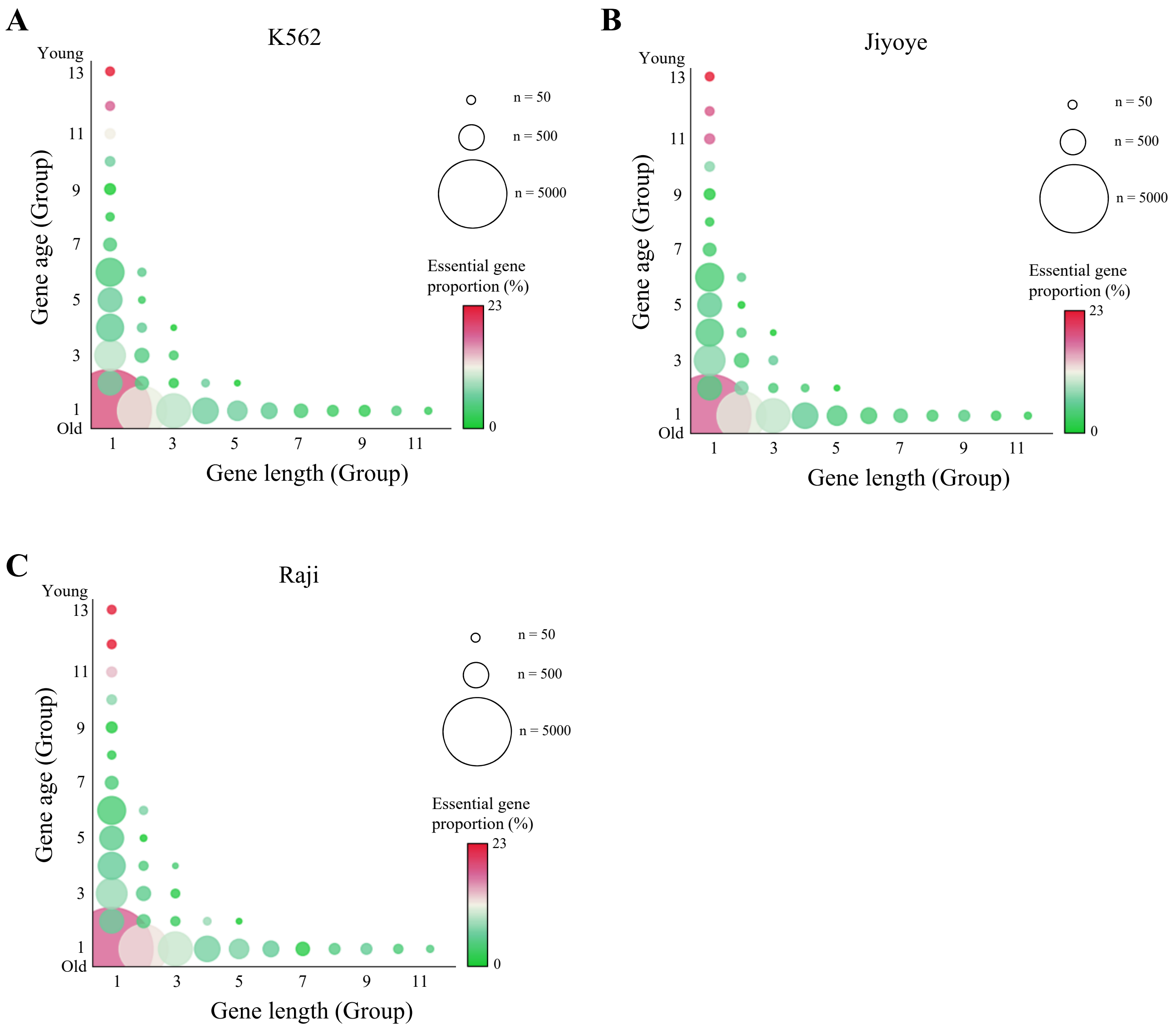


Fig. S10. Essential genes proportion for different cell lines. (A-C), Scatter-plot of gene length and evolutionary age. Size of the circle indicates number of genes; color represents essential gene proportion.

A

GO term	P-value	Benjamini
regulation of Ras GTPase activity	2.3E-04	0.037
regulation of GTPase activity	3.8E-04	0.030
regulation of ARF GTPase activity	4.9E-04	0.026
regulation of ARF protein signal transduction	0.0012	0.049
regulation of Ras protein signal transduction	0.0018	0.057
regulation of small GTPase mediated signal transduction	0.0030	0.079

B

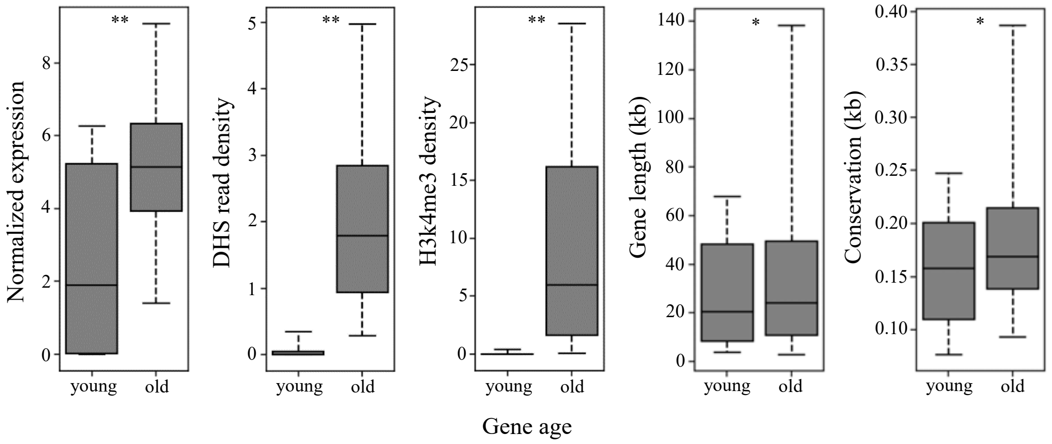


Fig. S11. The difference between young essential genes (gene age group 12-13) and old essential genes. (A) GO analysis of young essential genes. **(B)** Difference of gene length and conservation between young essential genes and old essential genes. Significance: * $p < 0.05$, ** $p < 0.001$.

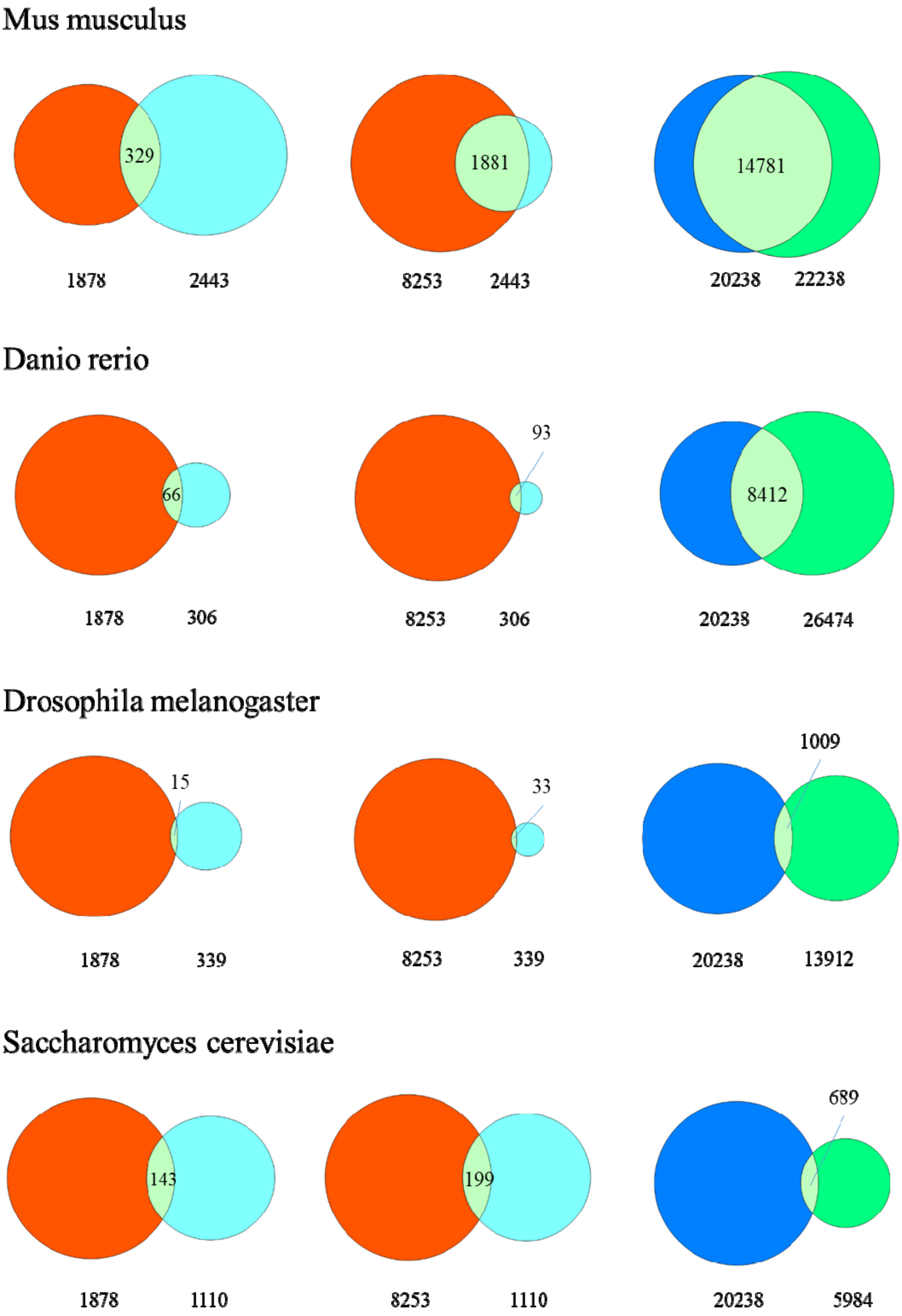


Fig. S12. Comparison of homologous essential genes of different species. Two different sets of human essential genes were used for analysis. The last column of Venn diagram is a comparison of human genes and genes of different species.

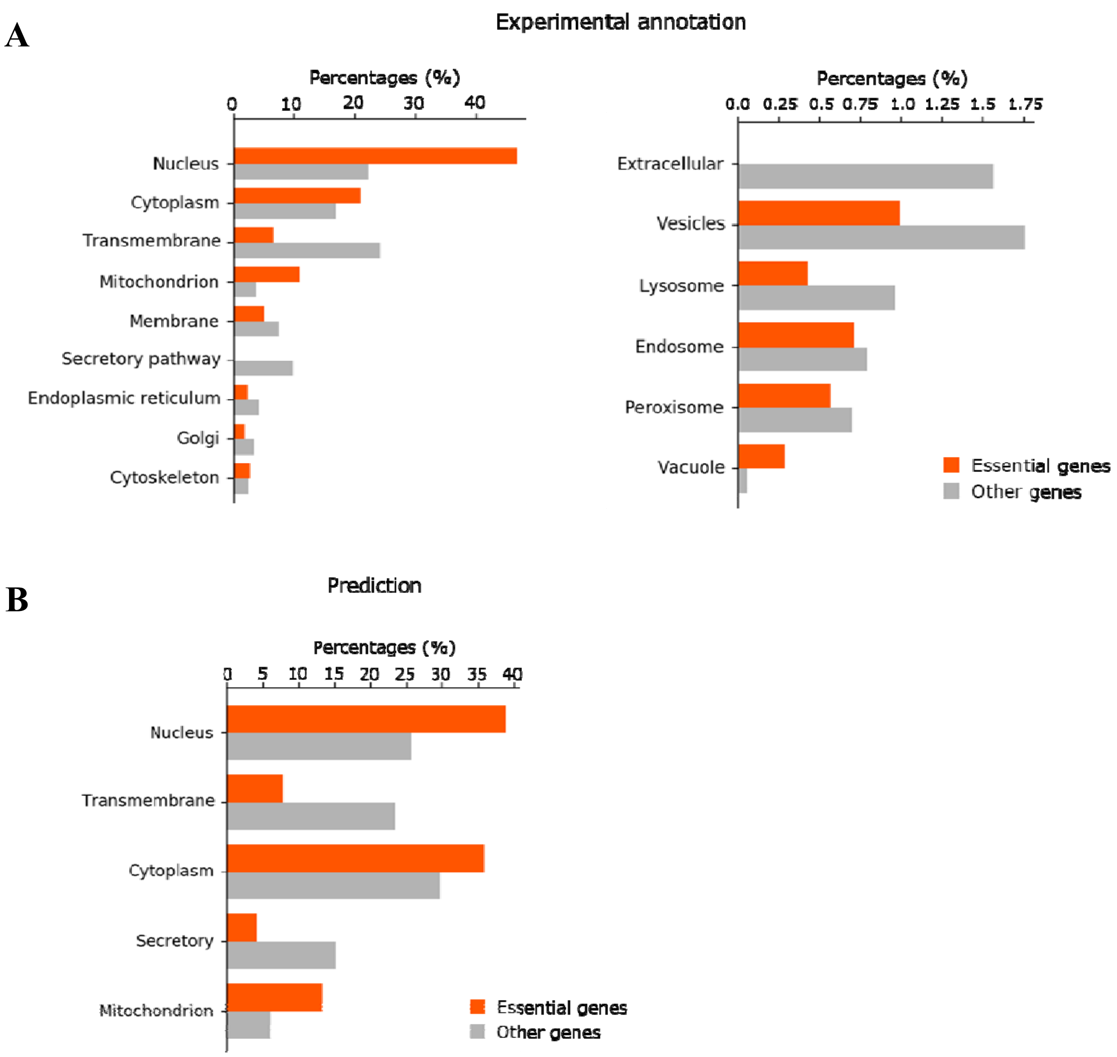


Fig. S13. Protein localization analysis using experimental annotation and predicted data. (A) Percentages of proteins located in different cellular locations for human essential gens (red bars) and human non-essential genes (grey bars) using experimental annotation data. **(B)** Percentages of proteins located in different cellular locations for human essential gens (red bars) and human non-essential genes (grey bars) using predicted data.

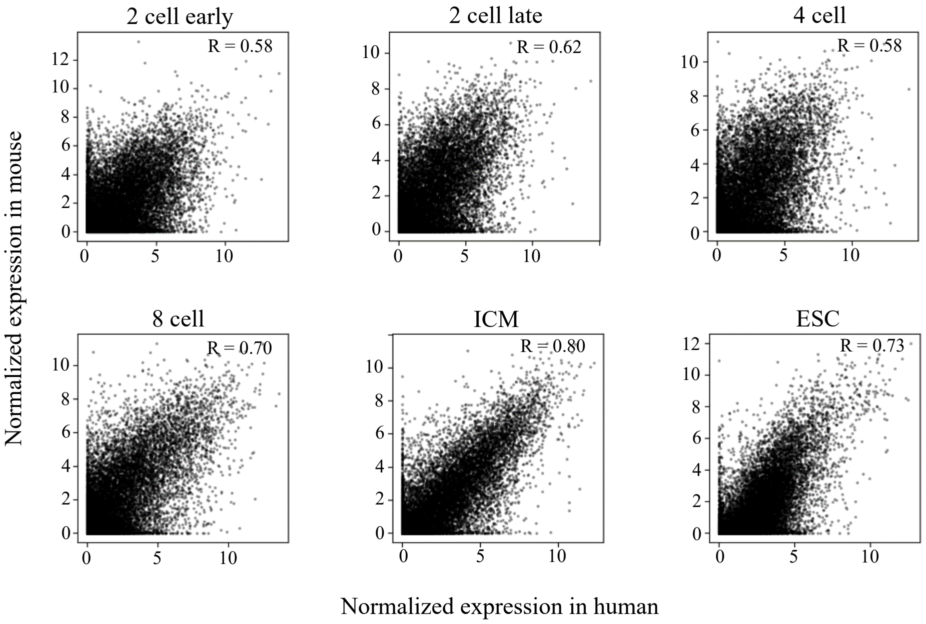


Fig. S14. Gene expression similarity during human and mouse embryonic development . 2D-Scatter plot of normalized gene expression. Correlation coefficients of normalized expression level between shared genes in human and mouse embryos are shown.

A

Ref	Cancer genes					Essential genes
Schroeder et al.	100%	39%	36%	46%	27%	24.56%
Lawrence et al.	43%	100%	33%	47%	29%	20.77%
Kandoth et al.	80%	67%	100%	70%	50%	24.41%
Berger et al.	24%	23%	16%	100%	22%	17.25%
Vogelstein et al.	62%	61%	51%	94%	100%	23.20%

B

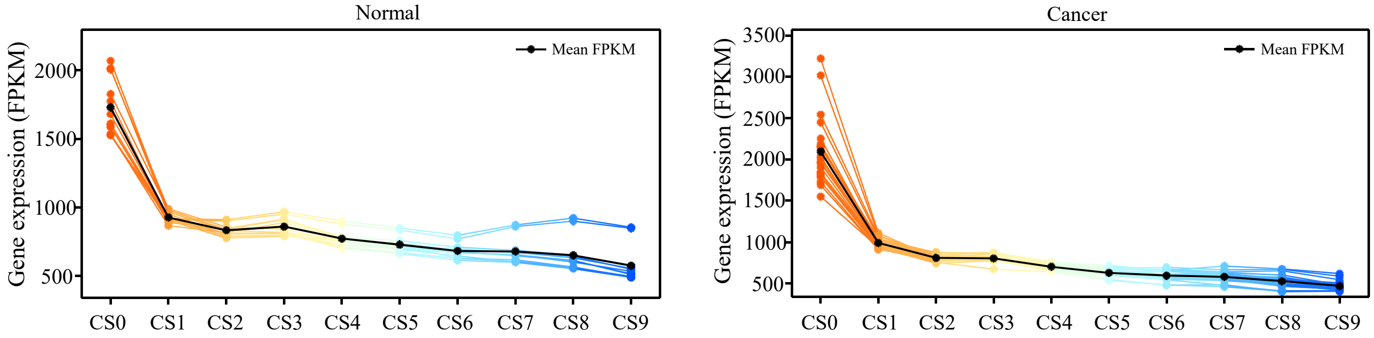


Fig. S15. Relationship between human essential genes and cancer. (A) Comparison of sets of human essential genes and cancer genes from different studies. Each value of the first five columns represents the common part between two studies, and the last column shows the proportion of essential genes in cancer genes for each study. **(B)** Gene expression in normal and tumor tissues from TCGA database, based on gene essentiality. Each colored line represents mean gene expression of all cancer or normal samples in each tumor type.

Supplementary Table 1. Significantly differential expressed genes (DEGs) in cancer-normal tissue pairs.

TCGA tumor	BLCA		BRCA		CESC		CHOL		COAD		KICH		KIRC		KIRP		LIHC		LUAD		PRAD		UCEC	
gene	log2FC	pvalue	log2FC	pvalue	log2FC	pvalue	log2FC	pvalue	log2FC	pvalue	log2FC	pvalue	log2FC	pvalue	log2FC	pvalue	log2FC	pvalue	log2FC	pvalue	log2FC	pvalue	log2FC	pvalue
AATF	4.1E-01	1.2E-02	4.7E-01	1.3E-09	4.1E-01	1.7E-01	1.2E+00	6.2E-03	6.6E-01	4.5E-07	-4.5E-02	7.9E-01	5.4E-01	2.7E-14	5.2E-01	4.1E-05	5.6E-01	1.2E-09	5.6E-01	5.9E-10	7.0E-01	8.1E-10	-1.7E-01	3.3E-01
ABHD11	1.7E-01	6.1E-01	1.2E+00	9.9E-16	2.6E+00	4.2E-01	1.5E+00	4.6E-03	3.2E-01	5.8E-03	1.0E+00	1.3E-04	-2.2E-01	4.9E-02	1.5E+00	4.1E-05	8.4E-01	2.2E-04	1.3E+00	2.1E-08	7.3E-01	7.5E-05	1.6E+00	2.9E-02
ACLY	1.1E+00	5.1E-07	4.1E-01	1.5E-04	4.7E-02	9.3E-01	1.5E+00	1.4E-03	7.6E-01	4.5E-08	-8.2E-01	1.4E-03	1.6E+00	8.8E-22	4.2E-01	1.7E-03	1.1E+00	7.6E-10	5.7E-01	7.3E-10	5.5E-01	2.5E-07	3.6E-01	2.6E-01
ACTL6A	1.3E+00	2.8E-05	8.6E-01	9.2E-18	2.2E+00	2.7E-01	1.4E+00	2.6E-03	7.9E-01	2.1E-07	-5.3E-01	1.3E-02	-8.7E-02	1.4E-01	1.6E-01	1.9E-01	6.6E-01	1.7E-07	1.1E+00	1.0E-12	2.4E+00	8.7E-10	1.3E+00	3.6E-02
ADRM1	4.3E-01	2.4E-03	6.5E-01	4.1E-09	8.0E-01	1.8E-01	-1.7E-02	9.0E-01	1.0E+00	8.5E-07	2.4E-01	2.3E-02	3.7E-01	2.9E-05	5.2E-01	2.5E-03	2.3E-01	1.3E-02	5.0E-01	5.6E-09	7.8E-01	1.5E-10	6.0E-01	2.2E-02
ADSS	4.7E-01	9.4E-04	9.0E-01	5.5E-22	7.3E-01	1.3E-01	1.4E+00	4.1E-04	1.9E-01	5.5E-03	-4.1E-01	7.4E-05	-5.6E-01	1.4E-08	-2.0E-01	1.7E-01	4.1E-01	3.0E-05	6.7E-01	4.6E-09	8.8E-01	4.7E-09	6.6E-01	6.5E-02
ALDOA	3.4E-01	4.0E-02	9.4E-01	6.3E-07	1.4E+00	1.7E-01	2.4E+00	1.7E-03	-9.4E-02	2.6E-01	1.3E+00	3.3E-06	1.3E+00	3.8E-16	1.4E+00	1.6E-05	1.3E+00	5.7E-04	1.2E+00	5.4E-14	1.2E+00	5.9E-14	8.5E-01	2.0E-01
ANAPC11	5.7E-01	4.7E-04	7.2E-01	3.7E-11	1.8E+00	3.7E-01	-3.1E-01	1.8E-01	2.4E-01	4.3E-02	6.3E-03	9.7E-01	2.5E-02	7.9E-01	5.3E-01	2.3E-03	5.4E-01	3.0E-04	7.3E-01	3.9E-08	6.5E-01	1.1E-05	1.1E+00	6.2E-03
AP2S1	4.2E-01	2.5E-03	7.3E-01	6.4E-18	1.6E+00	1.2E-01	-3.6E-01	4.8E-02	1.9E-02	8.3E-01	3.6E-01	7.3E-05	5.2E-01	6.8E-07	4.0E-01	3.9E-03	4.7E-02	7.0E-01	3.3E-01	4.2E-05	7.0E-01	6.9E-06	1.2E+00	7.9E-04
ATAD5	2.2E+00	2.2E-07	1.0E+00	9.3E-09	3.3E+00	1.9E-01	2.8E+00	2.6E-03	1.4E+00	5.1E-06	1.9E-01	6.4E-01	9.8E-01	2.7E-08	1.4E+00	2.9E-04	1.6E+00	4.4E-06	1.8E+00	5.2E-09	2.8E+00	2.0E-13	1.4E+00	1.1E-02
ATIC	4.7E-01	1.5E-02	8.8E-01	2.6E-23	4.6E-01	6.3E-01	1.3E+00	1.1E-05	8.8E-01	5.4E-09	-4.9E-01	1.6E-02	5.3E-02	4.2E-01	7.9E-01	3.2E-05	6.7E-01	2.5E-08	1.3E+00	2.3E-20	1.1E+00	3.9E-10	1.1E+00	6.8E-03
ATP6V1F	4.7E-01	1.3E-02	6.1E-01	1.1E-13	5.1E-01	4.4E-01	1.1E+00	1.4E-03	9.2E-01	3.0E-07	1.1E+00	9.8E-07	2.3E-02	8.4E-01	6.6E-01	1.3E-04	8.0E-01	9.9E-06	-2.6E-02	7.8E-01	1.2E-01	3.1E-01	5.6E-01	1.8E-03
ATR	7.1E-01	4.0E-03	-3.4E-02	5.4E-01	6.1E-01	4.3E-01	1.4E+00	2.2E-03	8.4E-01	1.3E-06	5.8E-01	1.9E-03	-1.3E-01	1.3E-01	2.3E-01	1.9E-02	5.8E-01	5.3E-06	6.1E-01	9.5E-10	1.1E+00	2.3E-11	3.4E-01	3.3E-01
ATXN2L	8.5E-01	2.0E-04	4.4E-01	2.0E-14	5.1E-01	4.0E-01	1.2E+00	1.3E-05	6.3E-01	8.9E-08	1.1E+00	4.3E-08	5.5E-01	3.1E-16	8.7E-01	5.1E-10	6.0E-01	3.9E-08	5.8E-01	1.5E-10	6.7E-01	7.9E-13	2.8E-01	2.6E-01
AURKA	2.3E+00	2.4E-06	2.9E+00	8.1E-20	4.4E+00	4.7E-02	2.8E+00	6.4E-03	1.5E+00	3.0E-07	2.7E+00	6.3E-06	1.0E+00	3.1E-06	1.9E+00	1.1E-04	2.5E+00	1.0E-08	2.7E+00	2.8E-11	3.3E+00	3.2E-12	3.5E+00	2.6E-03
AURKB	2.1E+00	6.5E-06	2.7E+00	2.0E-15	5.9E+00	3.0E-02	5.3E+00	7.3E-03	9.0E-01	5.8E-05	2.5E+00	9.4E-02	2.4E+00	7.2E-08	3.9E+00	9.4E-04	3.2E+00	5.3E-10	3.4E+00	1.6E-10	4.6E+00	1.0E-14	4.4E+00	1.3E-02
AZI1	1.1E+00	3.5E-06	5.0E-01	4.0E-05	9.2E-01	4.8E-02	2.2E+00	1.4E-03	6.2E-01	9.1E-05	8.8E-01	2.0E-05	3.4E-01	1.7E-04	7.5E-01	8.4E-05	1.8E+00	2.4E-11	7.2E-01	1.5E-06	8.7E-01	1.0E-06	7.6E-01	2.1E-02
BANF1	6.6E-01	2.6E-04	6.5E-01	1.1E-15	3.6E-01	8.5E-02	4.9E-01	1.3E-01	4.0E-01	3.7E-04	6.0E-01	2.4E-04	1.5E-01	6.8E-02	5.1E-01	3.2E-04	5.2E-01	1.3E-06	4.6E-01	2.4E-08	8.1E-01	5.0E-08	3.4E-01	3.0E-01
BIRC5	1.9E+00	1.2E-04	2.9E+00	1.7E-17	5.3E+00	1.1E-01	5.3E+00	1.4E-02	1.2E+00	4.5E-06	2.2E+00	3.8E-02	2.4E+00	6.9E-07	3.7E+00	3.7E-04	4.1E+00	7.4E-09	4.1E+00	1.0E-10	4.9E+00	5.0E-15	5.0E+00	6.1E-03
BOP1	8.3E-01	3.7E-03	1.2E+00	6.0E-10	1.6E+00	2.0E-01	1.8E+00	1.1E-02	1.8E+00	3.5E-06	1.1E+00	4.6E-03	6.8E-01	5.6E-06	6.4E-01	2.3E-02	1.9E+00	6.3E-06	2.0E+00	1.2E-09	2.5E+00	2.7E-08	1.8E+00	1.6E-02
BRCA1	1.5E+00	4.9E-06	1.1E+00	7.8E-14	2.9E+00	4.6E-02	1.2E+00	6.2E-02	1.2E+00	6.0E-06	1.8E-01	6.7E-01	8.8E-01	3.1E-10	1.8E+00	1.7E-05	8.2E-01	4.5E-04	1.6E+00	2.7E-09	2.2E+00	3.3E-13	1.2E+00	1.2E-01
BRCA2	2.0E+00	4.2E-04	1.5E+00	3.6E-14	3.7E+00	1.6E-01	2.1E+00	5.2E-03	1.9E+00	5.4E-09	6.8E-01	2.1E-01	1.8E+00	2.9E-11	1.9E+00	2.7E-04	1.5E+00	9.5E-06	1.0E+00	8.6E-09	1.7E+00	3.2E-07	1.9E+00	4.3E-02
BRIX1	7.4E-01	2.0E-02	5.5E-01	1.5E-10	1.1E+00	1.1E-01	1.1E+00	2.2E-03	1.1E+00	2.8E-10	3.1E-02	8.3E-01	3.1E-01	4.4E-06	2.2E-01	8.9E-02	4.5E-01	2.1E-05	1.2E+00	2.1E-11	1.7E+00	1.3E-11	6.4E-01	9.9E-02
BUB1B	2.2E+00	4.0E-06	2.6E+00	4.4E-20	5.8E+00	1.3E-01	5.4E+00	3.4E-03	1.3E+00	2.6E-06	2.4E+00	5.2E-02	1.3E+00	1.5E-07	2.5E+00	1.4E-04	3.6E+00	6.9E-09	3.9E+00	5.2E-12	4.7E+00	2.3E-14	4.0E+00	6.1E-03
BYSL	2.2E-01	2.2E-01	6.5E-01	5.7E-15	3.9E-01	2.4E-01	1.5E+00	4.9E-05	1.3E+00	8.0E-14	-3.4E-01	7.2E-02	5.9E-01	8.1E-12	5.6E-01	8.3E-04	6.2E-01	6.6E-06	1.2E+00	3.0E-13	1.3E+00	1.3E-09	5.1E-01	3.7E-02
C12orf45	5.2E-01	4.0E-04	2.3E-01	2.1E-03	1.4E+00	3.8E-01	2.5E-01	2.8E-01	7.4E-01	6.9E-07	5.8E-01	1.2E-02	8.4E-01	6.5E-12	1.3E+00	8.2E-05	5.4E-01	4.5E-04	9.0E-01	2.5E-12	8.6E-01	2.0E-06	1.4E+00	5.1E-02
C14orf80	6.0E-01	9.0E-04	1.1E+00	7.6E-18	3.1E+00	2.5E-01	2.6E-01	6.0E-01	4.2E-01	2.3E-02	1.9E-01	4.1E-01	6.0E-01	2.5E-05	9.8E-01	2.9E-05	2.7E-01	5.1E-01	2.6E-01	3.8E-02	8.1E-01	3.6E-06	1.8E+00	8.0E-02
C16orf59	2.1E+00	1.7E-03	2.4E+00	6.5E-22	4.5E+00	1.5E-01	3.9E+00	5.0E-03	1.4E+00	2.7E-09	1.1E+00	1.9E-02	8.2E-01	4.8E-04	2.6E+00	2.2E-07	2.8E+00	5.0E-08	3.5E+00	1.2E-12	4.0E+00	4.1E-13	3.5E+00	3.5E-03
CASC5	1.9E+00	4.6E-05	2.5E+00	6.3E-19	6.2E+00	2.0E-01	6.3E-01	2.4E-01	1.3E+00	2.5E-05	1.3E+00	3.8E-02	-3.0E-01	1.1E-01	-7.9E-01	2.6E-03	1.2E+00	7.2E-04	3.0E+00	3.6E-11	3.8E+00	2.8E-14	3.3E+00	3.3E-02
CCAR1	5.1E-01	2.6E-04	5.3E-01	3.3E-17	8.1E-01	1.1E-01	1.2E+00	6.3E-04	5.3E-01	1.0E-06	-1.6E-01	1.0E-01	-1.1E-01	4.0E-02	-1.4E-02	8.3E-01	5.0E-01	2.6E-07	6.7E-01	2.4E-16	7.4E-01	1.4E-10	6.6E-01	1.3E-02
CCDC86	6.4E-01	8.7E-03	1.9E-01	7.5E-03	-2.2E-01	6.8E-01	1.1E+00	1.1E-02	1.3E+00	3.6E-14	6.2E-01	1.2E-04	5.7E-01	3.2E-12	5.2E-01	2.2E-04	6.2E-01	1.4E-07	9.4E-01	8.3E-14	1.3E+00	2.2E-11	3.8E-01	1.7E-01
CCNA2	1.6E+00	1.0E-04	2.6E+00	1.3E-17	4.3E+00	1.8E-01	4.1E+00	1.1E-02	1.0E+00	7.9E-06	2.7E+00	1.6E-02	1.9E+00	1.3E-08	2.6E+00	3.2E-05	3.9E+00	4.9E-03	3.1E+00	2.0E-11	4.1E+00	1.1E-12	3.0E+00	3.1E-03
CCT2	5.5E-01	1.6E-03	6.5E-01	3.7E-14	4.7E-01	2.7E-01	2.2E+00	1.8E-01	7.5E-01	5.5E-06	-2.3E-01	4.0E-02	-2.6E-02	5.1E-01	3.2E-01	4.4E-04	5.6E-01	1.3E-07	1.3E+00	1.7E-02	9.5E-01	9.3E-10	7.3E-01	3.2E-02
CCT3	7.2E-01	3.6E-06	1.1E+00	7.9E-24	5.3E-01	3.1E-01	1.4E+00	1.2E-03	8.3E-01	4.1E-08	-5.4E-01	5.4E-04	-2.9E-02	5.5E-01	3.1E-01	2.0E-03	1.3E+00	1.8E-06	1.5E+00	1.6E-12	1.4E+00	4.3E-13	9.6E-01	7.9E-03
CCT5	1.3E+00	7.7E-03	8.2E-01	3.3E-17	1.4E+00	1.8E-01	1.2E+00	3.0E-03	6.9E-01	2.3E-08	1.4E-01	3.3E-01	2.1E-01	3.2E-04	5.4E-01	3.0E-04	7.3E-01	3.6E-08	1.3E+00	6.2E-14	1.7E+00	1.9E-13	1.1E+00	4.3E-02
CCT6A	1.1E+00	7.5E-02	8.3E-01	2.5E-04	7.9E-01	2.0E-01	1.2E+00	2.2E-04	1.1E+00	7.1E-10	3.7E-01	3.3E-03	1.1E-01	4.7E-02	6.1E-01	3.0E-06	9.3E-01	1.0E-10	1.6E+00	8.0E-03	1.8E+00	9.8E-04	9.5E-01	8.4E-04
CDC20	2.2E+00	4.9E-06	3.0E+00	1.5E-14	6.0E+00	3.3E-02	6.1E+00	1.5E-02	9.0E-01	3.3E-05	2.2E+00	9.5E-02	1.7E+00	1.8E-05	2.4E+00	3.2E-04	4.2E+00	6.1E-07	4.0E+00	2.5E-11	4.8E+00	2.8E-13	4.7E+00	3.1E-03
CDC45	2.1E+00	5.4E-07	2.8E+00	1.1E-20	6.3E+00	3.1E-02	5.4E+00	5.0E-03	1.4E+00	1.1E-06	2.6E+00	4.9E-02	2.3E+00	7.3E-09	3.8E+00	4.6E-05	3.2E+00	8.0E-09	3.8E+00	2.0E-08	5.0E+00	4.5E-14	4.9E+00	9.4E-03
CDC6	2.0E+00	1.0E-05	2.6E+00	3.7E-11	5.7E+00	1.7E-02	4.4E+00	2.8E-03	1.6E+00	1.5E-08	1.5E+00	1.0E-01	2.1E+00	3.6E-13	3.8E+00	7.7E-05	3.1E+00	6.4E-07	3.6E+00	9.6E-13	4.3E+00	2.6E-14	3.4E+00	1.5E-02
CDC7	1.8E+00	2.0E-04	1.9E+00	3.8E-12	3.1E+00	1.0E-01	2.8E+00	3.6E-03	1.1E+00	7.1E-05	1.7E-01	7.5E-01	5.4E-01	5.6E-05	1.2E+00	3.5E-06	2.2E+00	6.1E-05	1.5E+00	7.8E-08	1.7E+00	1.1E-10	1.9E+00	2.0E-02
CDCA5	1.9E+00	5.3E-04	2.5E+00	2.3E-18	4.9E+00	5.9E-02	4.3E+00	1.8E-03	1.5E+00	7.2E-10	2.0E+00	5.0E-03	1.6E+00	4.7E-09	2.3E+00	3.4E-04	3.3E+00	5.4E-10	3.1E+00	1.3E-09	4.2E+00	1.2E-15	4.0E+00	8.2E-03
CDCA8	2.5E+00	5.2E-05	2.6E+00	1.1E-16	5.0E+00	6.3E-02	4.6E+00	3.0E-03	1.1E+00	2.8E-07	2.1E+00	1.1E-01	1.5E+00	1.2E-07	2.3E+00	3.2E-05	3.2E+00	5.2E-09	3.4E+00	2.5E-09	4.6E+00	1.3E-02	4.0E+00	5.3E-03
CDH24	1.6E+00	3.6E-03	5.6E-01	3.1E-07	3.5E-01	7.1E-01	3.2E+00	3.6E-03	8.2E-01	2.0E-04	-3.6E-01	4.0E-01	8.4E-01	2.7E-08	1.1E+00	1.3E-04	2.4E+00	1.2E-03	1.7E+00	3.6E-06	1.7E+00	8.5E-10	1.1E+00	1.4E-01
CDK1	2.3E+00	2.2E-04	2.9E+00	1.5E-19	4.9E+00	1.3E-01	4.7E+00	3.1E-03	1.5E+00	2.4E-08	7.6E-01	1.9E-01	7.0E-01	2.4E-03	1.4E+00	6.0E-03	3.4E+00	6.6E-07	2.6E+00	1.1E-07	3.4E+00	1.0E-13	3.6E+00	1.8E-03
CDK7	3.8E-01	1.0E-01	5.6E-01	6.8E-17	8.7E-01	2.7E-01	1.4E+00	4.3E-03	6.8E-01	1.6E-06	2.0E-01	3.0E-01	7.0E-01	8.4E-11	5.2E-01	1.9E-05	4.6E-01	1.0E-04	6.7E-01	1.4E-08	4.4E-01	8.4E-04	7.6E-01	1.4E-01
CDT1	2.1E+00	1.2E-04	2.0E+00	2.0E-16	5.1E+00	8.2E-02	4.6E+00	1.7E-03	1.3E+00	1.6E-08	3.5E+00	1.1E-03	2.2E+00	8.8E-10	3.3E+00	2.6E-04	3.2E+00	1.0E-07	2.8E+00	2.1E-11	3.9E+00	1.0E-10	2.9E+00	1.1E-02
CENPA	2.6E+00	2.2E-05	2.9E+00	2.6E-14	5.2E+00	3.1E-02	5.2E+00	7.0E-03	1.5E+00	9.1E-09	2.9E+00	3.4E-02	2.2E+00	5.4E-06	3.5E+00	1.7E-03	3.8E+00	1.2E-08	3.7E+00	1.2E-10	4.8E+00	2.4E-15	5.0E+00	7.4E-03
CENPE	1.9E+00	1.5E-05	2.4E+00	1.9E-16	4.2E+00	1.4E-01	4.8E+00	6.4E-03	1.4E+00	3.5E-06	2.5E+00	2.0E-02	1.8E+00	7.9E-07	2.2E+00	2.3E-04	3.4E+00	3.2E-07	3.1E+00	1.0E-09	3.8E+00	1.1E-13	3.5E+00	8.9E-03
CENPI	2.2E+00	1.5E-07	2.5E+00	5.5E-19	3.3E+00	1.4E-01	4.3E+00	4.4E-03	2.0E+00	1.3E-05	2.6E+00	1.1E-01	1.6E+00	6.1E-07	2.7E+00	3.7E-04	3.1E+00	5.1E-06	3.5E+00	3.4E-09	4.1E+00	6.1E-14	2.9E+00	6.1E-03
CENPK	2.0E+00	1.5E-05	1.9E+00	1.3E-17	4.7E+00	1.3E-01	3.6E+00	2.6E-03	8.7E-01	2.1E-04	1.6E+00	9.9E-02	1.8E+00	2.3E-10	2.5E+00	3.3E-04	2.7E+00	1.3E-07	2.4E+00	2.1E-10	2.7E+00	2.3E-08	2.3E+00	1.7E-02
CENPM	1.1E+00	1.6E-02	2.4E+00	8.3E-22	5.4E+00	2.3E-01	5.3E+00	6.3E-03	5.4E-01	2.8E-02	3.2E+00	6.4E-04	2.1E+00	3.9E-12	2.3E+00	3.1E-05	3.4E+00	4.4E-08	1.8E+00	1.4E-08	3.1E+00	7.8E-11	1.4E+00	1.5E-02
CENPN	7.1E-01	3.3E-02	1.2E+00	4.7E-11	3.0E+00	3.4E-02	1.7E-01	6.9E-01	1.2E+00	7.6E-10	9.8E-01	2.0E-05	3.4E-01	2.5E-03	4.2E-01	1.4E-02	4.4E-01	7.2E-03	1.1E+00	8.6E-10	1.9E+00	2.0E-11	2.3E+00	1.1E-02
CENPW	1.2E+00	5.0E-04	1.2E+00	9.6E-06	3.3E+00	1.3E-01	2.8E+00	3.4E-02	9.1E-01	1.7E-04	8.1E-01	1.7E-01	8.3E-01	1.1E-04	1.4E+00	8.4E-05	2.4E+00	4.8E-06	1.6E+00	6.5E-07	2.9E+00	1.1E-10	4.0E+00	2.7E-01
CEP55	1.7E+00	5.0E-04	2.7E+00	1.1E-15	5.4E+00	1.6E-02	5.9E+00	1.9E-02	1.6E+00	3.7E-08	3.1E+00	2.1E-01	2.4E+00	2.5E-08	3.5E+00	4.1E-04	2.8E+00	8.9E-08	3.5E+00	3.6E-11	4.2E+00	2.1E-15	4.0E+00	6.6E-04
CHAF1A	1.1E+00	1.3E-05	8.8E-01	4.8E-10	3.1E+00	1.4E-02	2.1E+00	7.8E-04	7.8E-01	1.1E-05	1.4E+00	5.3E-05	8.2E-01	5.8E-14	8.5E-01	5.8E-04	1.4E+00	2.3E-08	1.1E+00	1.7E-08	2.2E+00	8.3E-12	2.0E+00	2.5E-02
CHAF1B	2.0E+00	3.0E-05	1.2E+00	4.0E-13	2.1E+00	3.9E-02	3.4E+00	9.2E-05	1.1E+00	5.9E-07	1.2E+00	1.4E-02	-7.5E-02	6.2E-01	4.4E-01	1.2E-01	2.7E+00	1.5E-05	2.2E+00	3.4E-12	2.7E+00	3.3E-12	1.4E+00	2.9E-02
CHEK1	1.5E+00	3.1E-05	1.4E+00	1.0E-14	2.7E+00	1.9E-02	2.3E+00	1.0E-02	1.1E+00	5.6E-09	6.6E-01	4.4E-03	5.9E-01	2.4E-09	8.5E-01	6.8E-04	1.5E+00	1.7E-07	2.4E+00	6.0E-11	3.0E+00	4.4E-14	1.7E+00	9.8E-03
CHTF18	1.5E+00	9.7E-05	1.2E+00	2.3E-14	2.6E+00	8.2E-02	2.4E+00	2.8E-03	1.5E+00	3.1E-07	7.2E-01	4.8E-03	8.4E-01	1.1E-06	1.3E+00	4.4E-06	1.6E+00	8.7E-06	1.4E+00	3.7E-11	2.2E+00	6.5E-10	1.4E+00	5.0E-02
CKAP5	7.7E-01	1.6E-03	7.3E-01	1.2E-17	6.5E-01	4.0E-01	9.5E-01	8.5E-03	7.7E-01	6.0E-07	9.8E-01	1.2E-08	5.0E-02	2.9E-01	4.2E-01	2.8E-03	8.1E-01	1.5E-09	9.8E-01	1.4E-08	1.4E+00	1.7E-07	5.0E-01	1.3E-02
CLNS1A	7.6E-01	6.2E-03	7.2E-01	1.4E-05	1.2E-01	7.7E-01	-8.2E-02	7.1E-01	6.3E-01	9.4E-07	3.9E-01	1.9E-04	2.7E-01	1.2E-07	2.7E-01	3.8E-03	-7.1E-03	9.2E-01	7.8E-01	8.4E-11	1.1E+00	7.7E-13	9.4E-01	1.9E-01
CLSPN	2.3E+00	1.5E-05	2.7E+00	3.9E-20	6.3E+00	1.8E-01	4.7E+00	9.5E-03	1.1E+00	2.6E-04	2.4E+00	1.0E-01	1.8E+00	1.6E-08	2.7E+00	2.9E-05	2.9E+00	3.0E-04	3.5E+00	2.6E-09	3.5E+00	1.9E-11	3.4E+00	5.9E-02
CPSF1	6.7E-01	8.6E-05	4.9E-01	3.0E-06	7.1E-01	5.1E-02	7.5E-01	1.3E-02	7.3E-01	3.7E-04	5.5E-01	2.0E-03	2.5E-01	9.7E-04	5.2E-01	3.2E-06	8.0E-01	1.3E-10	6.4E-01	7.3E-09	7.8E-01	2.3E-06	6.6E-01	1.9E-01
CPSF3	9.0E-01	4.7E-07	5.4E-01	4.0E-14	1.3E+00	7.4E-02	5.4E-01	9.8E-03	6.9E-01	8.9E-09	-2.2E-01	1.9E-01	9.0E-02	4.8E-02	3.1E-01	2.4E-03	5.6E-01	5.4E-09	8.6E-01	1.3E-17	1.2E+00	1.2E-10	1.3E+00	2.5E-03
CSE1L	8.2E-01	5.2E-06	9.1E-01	1.9E-08	1.2E+00	1.3E-01	9.4E-01	9.0E-04	1.5E+00	7.5E-09	-6.5E-02	6.9E-01	-2.0E-01	1.3E-04	-1.3E-01	3.1E-01	6.3E-01	1.0E-08	8.3E-01	5.2E-09	1.5E+00	2.8E-14	1.0E+00	6.9E-03
DDX49	7.6E-01	3.2E-04	5.5E-01	7.2E-12	1.0E+00	8.8E-02	4.7E-01	7.3E-02	4.2E-01	5.6E-05	2.2E-01	4.0E-02	6.4E-01	6.5E-10	2.5E-01	9.9E-04	9.2E-01	2.3E-06	4.0E-01	1.9E-04	1.0E+00	2.1E-08	1.0E+00	2.6E-02
DDX52	6.2E-01	1.5E-04	2.8E-01	2.2E-05	7.9E-01	1.6E-01	1.1E+00	1.1E-04	4.0E-01	3.0E-04	-5.6E-01	2.6E-04	-4.0E-01	3.2E-06	3.9E-01	3.7E-03	2.1E-01	5.2E-03	7.5E-01	1.4E-14	7.9E-01	1.6E-07	7.4E-01	1.2E-02
DHX37	7.7E-01	3.8E-06	3.8E-01	5.6E-09	6.1E-01	1.8E-01	1.3E+00	3.5E-04	8.3E-01	5.1E-08	5.6E-01	1.2E-04	5.7E-01	1.3E-13	9.6E-01	2.0E-09	7.6E-01	1.8E-10	7.5E-01	2.1E-10	8.5E-01	7.6E-10	5.1E-01	1.4E-01
DKC1	1.0E+00	5.7E-05	5.6E-01	2.6E-10	1.5E+00	3.0E-01	1.3E+00	6.0E-03	1.6E+00	1.8E-08	1.6E-01	1.7E-01	4.1E-02	4.3E-01	3.2E-01	1.4E-02	6.2E-01	6.4E-09	1.2E+00	5.8E-16	1.8E+00	3.9E-09	7.1E-01	4.7E-02
DNAJC9	6.1E-01	1.8E-02	8.1E-01	3.1E-13	1.4E+00	6.7E-02	1.5E+00	3.8E-06	5.4E-01	1.7E-05	1.1E+00	4.9E-05	2.1E-01	2.5E-04	4.5E-01	2.2E-04	6.5E-01	6.0E-08	9.6E-01	1.5E-11	1.4E+00	4.0E-13	1.1E+00	1.4E-02
DNMT1	1.3E+00	2.9E-05	9.8E-01	1.1E-11	1.9E+00	1.3E-01	1.6E+00	2.2E-04	9.5E-01	1.6E-06	3.7E-01	7.5E-02	3.8E-01	6.8E-06	6.9E-01	3.7E-04	1.2E+00	6.9E-06	9.5E-01	1.8E-08	1.3E+00	5.0E-10	1.0E+00	2.0E-02
DOLPP1	8.9E-01	9.2E-04	6.5E-01	1.6E-19	1.4E+00	1.0E-01	-9.5E-01	2.8E-03	-7.6E-01	1.8E-07	4.7E-01	1.0E-03	-3.8E-01	8.3E-08	2.7E-01	2.1E-02	-1.1E-01	3.0E-01	8.4E-01	7.2E-12	9.4E-01	7.8E-09	8.6E-01	6.4E-02
DONSON	1.7E+00	1.6E-04	1.3E+00	1.6E-19	2.0E+00	6.1E-02	2.5E-01	3.3E-01	8.8E-01	1.1E-07	-1.1E-01	6.5E-01	7.6E-01	6.0E-07	1.3E+00	5.0E-06	8.8E-01	3.3E-07	1.7E+00	6.4E-13	1.9E+00	2.2E-10	1.0E+00	5.9E-02
DSCC1	1.7E+00	1.6E-02	1.3E+00	4.0E-13	1.9E+00	8.0E-02	2.8E+00	6.1E-03	1.9E+00	2.4E-08	6.7E-01	2.9E-01	1.1E+00	4.3E-11	1.2E+00	7.6E-04	2.1E+00	4.1E-10	2.1E+00	8.5E-08	2.6E+00	6.5E-14	2.4E+00	1.7E-02
DSN1	1.0E+00	2.3E-06	1.0E+00	2.0E-19	2.7E+00	1.9E-02	1.5E+00	4.5E-04	1.2E+00	1.1E-07	5.8E-01	5.9E-03	6.3E-01	6.1E-13	7.2E-01	3.7E-04	1.3E+00	9.4E-08	1.0E+00	4.1E-10	1.4E+00	2.8E-10	1.7E+00	3.7E-02
DTL	1.9E+00	1.3E-04	2.9E+00	7.7E-24	4.7E+00	6.4E-02	4.9E+00	7.2E-04	1.3E+00	5.0E-07	2.2E+00	4.4E-02	2.2E+00	4.4E-14	3.8E+00	3.8E-04	3.4E+00	5.4E-07	2.1E+00	2.7E-10	2.8E+00	9.0E-13	2.9E+00	6.5E-03
DTYMK	8.8E-01	3.0E-04	8.4E-01	3.8E-21	1.8E+00	3.1E-01	1.7E+00	6.2E-03	8.6E-01	2.0E-06	-4.1E-01	4.6E-02	3.3E-01	1.0E-03	9.0E-01	1.6E-05	1.1E+00	3.8E-11	1.2E+00	1.4E-11	1.4E+00	1.2E-12	1.4E+00	5.3E-03
EBNA1BP2	6.9E-01	2.7E-04	6.4E-01	1.0E-16	7.3E-01	8.2E-02	8.0E-01	1.2E-02	6.9E-01	5.2E-06	-6.6E-01	4.4E-05	-9.1E-02	5.3E-02	-4.1E-02	6.1E-01	8.1E-01	9.8E-07	7.0E-01	1.8E-11	7.7E-01	4.9E-09	5.5E-01	6.4E-02
ECT2	2.0E+00	1.1E-04	1.8E+00	2.0E-21	4.0E+00	9.5E-02	4.8E+00	5.8E-03	1.8E+00	1.0E-08	8.1E-01	4.2E-02	2.5E-01	1.6E-01	9.2E-01	9.3E-05	2.6E+00	2.1E-08	2.3E+00	5.4E-14	3.3E+00	2.8E-11	3.1E+00	2.0E-02
EHMT2	8.8E-01	2.1E-02	4.3E-01	2.5E-10	-2.6E-01	2.9E-01	1.9E+00	7.3E-06	7.5E-01	9.4E-08	-4.9E-01	1.9E-02	1.6E-01	4.1E-03	3.3E-01	2.6E-03	1.2E+00	1.2E-10	6.3E-01	9.5E-09	7.5E-01	4.7E-07	6.4E-01	9.3E-02
EIF3C	7.3E-01	4.0E-02	6.7E-01	4.1E-03	1.7E+00	2.4E-01	1.3E+00	5.7E-02	7.3E-01	2.6E-03	4.4E-01	7.0E-02	5.5E-02	6.7E-01	3.6E-01	2.9E-01	1.2E+00	2.9E-06	1.2E+00	1.5E-07	1.4E+00	1.3E-06	4.1E-01	1.6E-01
ENO1	1.1E+00	4.8E-05	3.1E-01	5.0E-03	2.1E+00	2.0E-01	5.3E-01	3.0E-01	7.5E-01	2.5E-05	-1.2E+00	1.1E-05	7.2E-01	2.3E-10	4.5E-01	1.7E-02	4.6E-01	1.2E-03	1.3E+00	3.8E-17	1.3E+00	6.7E-09	1.8E+00	1.6E-01
ESPL1	6.4E-01	3.4E-01	2.6E+00	3.5E-21	5.8E+00	1.2E-01	1.9E+00	1.7E-02	1.3E+00	4.3E-07	4.8E-01	5.3E-01	5.8E-02	7.5E-01	-2.3E-01	4.2E-01	1.2E+00	2.1E-04	3.5E+00	4.0E-09	4.1E+00	3.6E-16	3.9E+00	9.2E-04
EXOSC4	5.5E-01	5.2E-03	9.5E-01	1.3E-13	1.4E+00	3.8E-01	3.6E-01	1.1E-01	9.7E-01	5.4E-05	-2.4E-02	8.7E-01	-1.7E-02	8.5E-01	-7.3E-02	6.2E-01	1.1E+00	1.7E-03	9.9E-01	1.5E-08	1.2E+00	1.3E-09	1.2E+00	1.8E-03
EXOSC5	7.2E-01	8.2E-04	5.1E-01	4.9E-07	1.5E+00	1.8E-02	7.5E-01	6.0E-03	1.2E+00	3.3E-08	3.6E-01	1.1E-01	1.4E+00	1.3E-12	9.0E-01	9.1E-05	6.8E-01	1.0E-05	1.1E+00	5.0E-09	1.6E+00	1.5E-09	5.5E-01	5.0E-02
EZH2	1.7E+00	3.9E-04	2.1E+00	3.2E-20	4.1E+00	3.1E-02	3.5E+00	1.3E-03	1.3E+00	5.5E-09	1.6E+00	7.1E-02	1.7E+00	7.5E-15	2.2E+00	8.9E-07	2.5E+00	1.6E-11	2.7E+00	1.8E-10	3.1E+00	3.2E-11	2.9E+00	1.1E-03
FAM50A	4.2E-01	4.5E-03	4.9E-01	1.2E-08	1.7E+00	2.6E-01	1.0E+00	4.7E-03	4.6E-01	2.0E-06	9.9E-01	3.0E-07	4.5E-01	1.2E-07	8.0E-01	9.9E-06	1.1E+00	1.7E-05	4.0E-01	6.9E-06	2.4E-01	1.6E-01	1.0E+00	5.3E-02
FAM72A	2.5E+00	3.4E-06	2.8E+00	7.6E-14	2.8E+00	2.5E-01	3.8E+00	7.3E-02	1.6E+00	1.4E-06	8.5E-01	2.4E-01	9.4E-01	2.3E-04	1.7E+00	3.3E-04	2.9E+00	1.6E-05	2.4E+00	6.7E-09	3.3E+00	9.0E-11	2.2E+00	2.9E-02
FAM72B	2.7E+00	1.1E-05	2.3E+00	1.4E-13	3.6E+00	9.0E-02	3.6E+00	6.1E-02	1.4E+00	3.6E-06	1.3E+00	1.2E-01	1.2E+00	4.6E-06	1.8E+00	1.2E-04	2.6E+00	6.9E-06	2.5E+00	2.4E-08	3.3E+00	1.1E-12	3.0E+00	3.1E-03
FAM72D	2.8E+00	1.3E-04	2.5E+00	1.5E-09	4.3E+00	1.2E-01	3.7E+00	8.8E-02	1.6E+00	1.5E-09	1.3E+00	1.2E-01	1.4E+00	1.6E-07	1.9E+00	6.8E-05	3.1E+00	9.7E-06	2.7E+00	1.2E-06	3.4E+00	6.0E-11	2.7E+00	1.5E-03
FANCG	1.3E+00	9.2E-06	5.8E-01	2.3E-09	1.3E+00	1.2E-01	2.0E+00	1.5E-04	8.5E-01	5.4E-04	-6.5E-02	7.3E-01	5.2E-01	4.4E-08	5.7E-01	2.6E-04	1.4E+00	2.8E-09	1.2E+00	2.9E-12	1.9E+00	4.2E-09	7.0E-01	1.0E-01
FANCI	1.7E+00	1.3E-07	1.8E+00	3.6E-20	3.9E+00	3.4E-02	3.7E+00	1.4E-03	1.3E+00	1.5E-07	1.5E+00	3.7E-02	1.4E+00	1.9E-14	1.8E+00	1.3E-07	2.4E+00	1.1E-09	2.2E+00	2.7E-11	3.1E+00	5.6E-14	2.2E+00	1.0E-02
FBL	7.8E-01	6.4E-02	-1.1E-01	4.2E-01	4.7E-01	2.8E-01	1.2E+00	2.5E-03	8.1E-01	1.5E-05	-4.0E-02	7.7E-01	8.0E-01	2.4E-09	3.5E-01	5.1E-03	6.3E-01	1.8E-03	6.7E-01	1.9E-07	1.8E+00	3.0E-04	8.9E-02	6.8E-01
FCGR1B	7.5E-01	6.9E-02	1.3E+00	2.9E-12	1.8E+00	3.2E-01	1.6E+00	1.5E-01	5.9E-01	2.1E-01	1.2E+00	1.5E-03	3.1E+00	5.2E-10	2.9E+00	6.1E-03	-2.0E-01	5.3E-01	-8.2E-01	7.0E-07	-1.4E+00	6.6E-10	6.1E-01	3.1E-01
FDXR	8.2E-01	1.3E-02	9.9E-01	4.6E-10	2.2E+00	7.7E-02	-4.6E-01	1.1E-01	6.1E-01	4.5E-02	-6.1E-02	7.7E-01	1.4E+00	2.5E-20	1.8E+00	1.2E-08	2.9E-01	4.6E-02	2.5E-01	5.8E-02	7.9E-01	1.4E-05	-9.5E-01	3.2E-01
FEN1	1.5E+00	3.4E-04	1.3E+00	1.4E-22	3.6E+00	6.7E-02	1.7E+00	1.4E-03	8.6E-01	1.6E-05	9.2E-01	2.0E-03	5.8E-01	3.7E-11	6.2E-01	1.4E-03	1.5E+00	7.3E-11	1.7E+00	4.7E-14	2.4E+00	4.9E-12	2.4E+00	2.5E-02
FKBPL	9.8E-01	7.2E-03	7.4E-01	3.8E-14	1.5E+00	2.0E-01	1.3E+00	1.9E-03	1.3E-01	2.1E-01	-7.1E-01	1.6E-04	4.6E-01	3.0E-08	2.9E-01	2.7E-02	8.2E-01	5.2E-06	7.3E-01	8.7E-11	8.7E-01	1.1E-07	1.0E+00	2.3E-03
GALE	6.1E-01	4.3E-02	1.5E+00	2.3E-18	1.9E+00	1.6E-01	-1.4E+00	9.6E-05	-7.3E-02	6.4E-01	1.5E-01	5.4E-01	4.6E-01	4.0E-04	1.1E+00	3.6E-05	-2.8E-02	8.0E-01	8.7E-01	3.9E-07	-1.9E-01	2.8E-01	1.6E+00	5.7E-02
GAPDH	6.7E-01	2.9E-03	8.4E-01	1.2E-06	1.9E+00	1.4E-01	7.7E-01	1.4E-02	4.5E-01	1.2E-03	9.7E-01	1.4E-05	1.6E+00	2.1E-13	1.3E+00	6.7E-08	5.8E-01	7.6E-05	1.7E+00	5.9E-13	2.5E+00	5.7E-12	2.0E+00	6.7E-02
GARS	8.1E-01	2.4E-04	8.3E-01	9.3E-16	6.2E-01	9.7E-02	1.1E+00	5.5E-03	1.2E+00	1.2E-11	1.3E+00	5.1E-06	1.9E-01	2.8E-02	8.3E-01	1.0E-06	8.9E-01	2.9E-08	1.2E+00	3.4E-09	1.2E+00	6.7E-08	1.2E+00	4.0E-03
GINS1	2.2E+00	1.8E-07	2.3E+00	3.1E-21	4.5E+00	4.0E-02	3.5E+00	1.4E-03	1.9E+00	4.5E-05	1.5E-01	7.8E-01	3.2E-01	5.8E-03	1.3E+00	4.3E-04	2.6E+00	1.1E-07	3.1E+00	4.0E-10	4.1E+00	1.3E-12	3.0E+00	7.8E-03
GINS2	1.6E+00	1.2E-03	1.9E+00	3.1E-18	3.4E+00	4.0E-02	2.0E+00	1.6E-02	1.0E+00	4.8E-06	1.9E+00	1.2E-07	2.0E+00	1.4E-09	2.8E+00	2.6E-05	1.6E+00	9.8E-06	2.8E+00	1.3E-13	3.6E+00	1.4E-11	2.4E+00	8.4E-03
GINS3	9.6E-01	7.5E-03	5.5E-01	8.2E-08	1.7E+00	3.3E-02	1.9E+00	3.4E-04	9.7E-01	5.3E-06	6.3E-02	7.6E-01	6.0E-01	3.1E-08	1.1E+00	1.0E-06	1.4E+00	3.7E-07	1.1E+00	6.8E-08	2.1E+00	4.4E-10	1.2E+00	3.5E-02
GINS4	1.8E+00	1.6E-02	1.6E+00	1.8E-12	3.5E+00	3.7E-02	2.2E+00	5.2E-03	1.3E+00	3.5E-06	1.2E+00	1.6E-03	5.3E-01	7.3E-05	1.5E+00	7.1E-06	1.7E+00	2.7E-06	2.9E+00	3.2E-05	3.4E+00	1.3E-10	3.0E+00	6.1E-03
GMPS	8.3E-01	1.7E-03	8.2E-01	2.1E-16	1.7E+00	2.4E-01	9.4E-01	2.3E-05	9.2E-01	3.1E-09	1.3E+00	1.5E-04	2.0E-01	2.9E-03	2.9E-01	1.6E-02	8.1E-01	2.7E-09	9.6E-01	3.9E-10	2.2E+00	9.9E-11	8.8E-01	5.7E-02
GNB1L	4.3E-01	1.2E-02	6.0E-01	6.5E-05	8.6E-01	7.8E-02	1.7E+00	1.1E-03	1.4E+00	1.4E-07	1.1E+00	1.2E-04	4.6E-01	1.5E-05	4.3E-01	9.4E-03	1.2E+00	6.0E-06	4.5E-01	1.8E-03	1.4E+00	2.8E-07	8.9E-01	2.0E-01
GSDMC	-2.0E-01	8.5E-01	1.9E+00	1.4E-02	8.7E+00	1.8E-01	3.3E+00	1.1E-01	1.8E+00	1.0E-04	6.2E+00	2.0E-05	2.8E-01	6.6E-01	2.0E+00	7.0E-02	2.6E+00	6.5E-04	2.5E+00	2.0E-05	4.0E+00	9.7E-08	2.5E+00	1.3E-01
GSS	5.8E-01	4.6E-03	4.8E-01	7.1E-09	1.7E+00	3.4E-02	-7.9E-02	5.9E-01	3.7E-01	1.5E-02	1.8E-01	2.3E-01	5.1E-02	5.8E-01	1.0E+00	1.1E-05	2.2E-01	6.0E-04	7.9E-01	2.1E-11	1.2E+00	7.6E-09	7.6E-01	2.8E-02

H2AFX	1.0E+00	1.3E-05	1.5E+00	1.5E-18	2.1E+00	2.0E-01	2.2E+00	6.0E-02	6.9E-01	1.9E-05	6.6E-01	8.6E-03	5.7E-01	7.0E-05	1.0E+00	8.2E-03	1.3E+00	1.1E-09	1.2E+00	5.2E-10	1.7E+00	1.9E-10	2.0E+00	4.4E-03
HAUS5	9.5E-01	6.9E-03	2.7E-01	1.2E-02	1.2E+00	1.8E-01	1.1E+00	1.2E-03	1.1E+00	2.6E-09	2.8E-01	8.1E-02	3.7E-01	1.6E-05	4.7E-01	4.1E-04	8.6E-01	9.4E-11	6.9E-01	6.1E-06	1.3E+00	4.7E-06	1.0E-01	6.9E-01
HAUS8	9.3E-01	2.7E-05	7.2E-01	3.7E-10	2.3E+00	1.2E-01	1.2E+00	9.3E-02	1.7E-01	8.8E-02	-1.9E-01	2.2E-01	4.8E-01	1.3E-06	6.5E-01	6.8E-04	2.7E-01	3.6E-02	5.1E-01	3.5E-08	1.2E+00	2.5E-10	1.8E+00	2.2E-02
HEATR1	7.7E-01	1.9E-04	4.3E-01	9.5E-08	2.3E-01	6.5E-01	1.8E+00	7.3E-04	1.0E+00	6.2E-09	-1.9E-02	9.4E-01	2.9E-01	7.2E-06	6.5E-01	3.2E-04	1.0E+00	1.8E-07	1.1E+00	1.3E-17	1.4E+00	1.4E-14	4.0E-01	1.6E-01
HIST1H2BF	2.5E+00	8.5E-02	2.2E+00	1.3E-07	1.6E+00	2.8E-01	3.0E+00	1.5E-02	6.8E-01	6.6E-02	-1.3E-02	9.5E-01	1.1E+00	3.1E-02	7.1E-01	8.7E-02	1.3E+00	1.5E-03	1.3E+00	8.6E-07	1.5E+00	3.2E-06	7.4E-01	3.8E-01
HIST1H2BN	1.2E+00	2.0E-04	1.3E+00	1.0E-08	8.3E-02	9.2E-01	8.3E-01	2.9E-01	7.9E-01	7.3E-03	3.0E-02	9.1E-01	1.2E+00	8.8E-16	1.0E+00	7.7E-04	1.1E+00	8.6E-06	1.4E+00	1.6E-08	1.2E+00	5.9E-04	1.3E+00	3.5E-01
HIST2H2AA3	1.7E+00	1.2E-03	2.7E+00	8.6E-12	3.5E-01	6.0E-01	1.4E+00	3.7E-02	3.9E-01	1.3E-01	-7.7E-01	2.2E-02	1.1E+00	2.1E-05	1.3E+00	1.1E-01	2.1E+00	1.2E-02	1.7E+00	3.1E-09	1.4E+00	6.1E-05	8.9E-01	3.0E-01
HIST2H3C	2.0E+00	3.3E-04	2.2E+00	1.4E-07	2.1E+00	6.6E-02	2.2E+00	4.6E-02	6.7E-01	1.3E-02	9.7E-02	7.5E-01	-5.4E-02	6.3E-01	3.3E-01	2.0E-01	2.2E+00	5.2E-05	1.3E+00	1.2E-04	1.5E+00	4.5E-08	1.1E+00	2.2E-01
HIST2H4A	1.4E+00	1.6E-03	2.2E+00	2.0E-07	4.9E-01	6.3E-01	2.5E+00	7.0E-02	-3.9E-03	9.9E-01	-1.7E+00	1.6E-03	-5.7E-02	7.4E-01	7.8E-02	8.3E-01	2.2E+00	7.2E-07	1.4E+00	2.1E-07	1.5E+00	2.1E-05	2.8E-01	7.5E-01
HJURP	2.6E+00	2.1E-05	2.9E+00	1.0E-18	5.4E+00	2.1E-02	5.6E+00	1.0E-02	1.6E+00	6.3E-10	2.3E+00	8.8E-02	2.3E+00	1.6E-06	3.9E+00	2.3E-03	3.8E+00	2.0E-07	4.0E+00	3.8E-09	4.6E+00	3.2E-15	4.6E+00	1.7E-03
HMBS	8.4E-01	2.8E-05	4.8E-01	1.8E-08	1.3E+00	3.2E-01	2.7E-02	9.2E-01	3.3E-01	1.9E-02	5.9E-01	3.1E-04	-6.5E-02	4.1E-01	6.5E-01	5.8E-04	5.3E-01	1.2E-07	1.1E+00	1.6E-08	1.2E+00	4.9E-07	1.2E+00	1.1E-02
HMGB3	2.2E+00	6.4E-04	2.2E+00	4.5E-18	2.5E+00	7.8E-03	-5.4E-02	8.6E-01	1.0E+00	1.4E-04	1.5E+00	1.6E-07	-6.1E-01	1.5E-05	1.4E+00	1.8E-05	5.5E-01	1.7E-02	3.2E+00	6.7E-10	2.3E+00	2.0E-09	2.7E+00	1.6E-03
HSPD1	7.6E-01	8.9E-04	6.0E-01	2.7E-10	4.9E-02	8.6E-01	-5.4E-01	4.4E-03	1.2E+00	2.0E-09	3.9E-01	5.7E-03	-6.1E-02	5.1E-01	3.7E-01	1.7E-02	2.3E-01	9.1E-02	1.3E+00	8.7E-15	1.7E+00	3.9E-09	6.8E-01	9.0E-02
HSPE1	8.6E-01	1.1E-04	9.7E-01	5.1E-17	1.2E+00	3.8E-01	-5.4E-01	1.6E-03	8.1E-01	1.9E-04	2.8E-01	5.8E-02	-2.8E-02	8.0E-01	5.2E-01	1.2E-03	2.6E-01	5.8E-02	1.1E+00	1.4E-14	1.5E+00	8.3E-10	1.4E+00	7.6E-05
IER5L	1.6E+00	2.3E-04	1.1E+00	1.2E-16	5.5E-01	7.3E-01	5.9E-01	4.0E-01	1.7E+00	1.4E-04	-1.9E+00	5.3E-07	6.9E-03	9.6E-01	9.8E-01	2.9E-02	-3.1E-01	4.8E-01	1.6E+00	8.1E-09	1.2E+00	4.0E-06	9.2E-01	4.3E-02
ILF2	8.3E-01	9.9E-05	8.3E-01	1.1E-16	6.8E-01	4.1E-02	1.8E+00	4.8E-04	5.3E-01	7.8E-06	-9.3E-01	1.1E-07	-2.0E-01	1.9E-04	2.0E-02	8.5E-01	1.1E+00	4.9E-10	1.2E+00	1.1E-11	1.2E+00	9.8E-11	1.1E+00	1.1E-02
INCENP	1.4E+00	3.7E-04	8.4E-01	2.9E-14	2.1E+00	2.0E-01	2.0E+00	2.0E-03	8.1E-01	1.6E-06	7.3E-01	1.5E-02	2.3E-01	1.5E-03	2.7E-01	4.8E-02	1.5E+00	8.6E-09	1.4E+00	6.7E-11	1.9E+00	1.5E-12	2.1E+00	3.1E-02
INTS8	7.1E-01	2.0E-05	8.0E-01	1.8E-16	6.4E-01	5.3E-01	1.2E+00	1.3E-05	7.6E-01	2.7E-07	6.6E-01	3.7E-03	7.1E-01	5.6E-16	5.7E-01	1.2E-05	9.5E-01	1.2E-07	1.0E+00	4.9E-14	1.2E+00	2.1E-13	1.0E+00	4.1E-02
KAT2A	1.1E+00	8.5E-06	4.9E-02	5.6E-01	3.2E-01	3.0E-01	1.6E+00	1.1E-03	1.4E+00	1.4E-12	-6.0E-01	3.8E-03	3.7E-01	9.9E-05	7.8E-01	3.6E-03	1.1E+00	1.7E-11	1.2E+00	1.8E-15	1.4E+00	4.2E-12	2.0E-01	7.5E-01
KIF11	1.8E+00	1.7E-05	2.4E+00	2.1E-21	5.0E+00	8.9E-02	3.6E+00	2.2E-03	1.1E+00	1.2E-05	6.1E-01	3.5E-01	1.1E+00	2.0E-07	1.4E+00	2.1E-03	2.3E+00	1.3E-07	3.2E+00	5.8E-11	3.9E+00	1.2E-14	3.2E+00	4.2E-04
KIF18A	2.2E+00	1.6E-05	2.4E+00	7.2E-22	5.2E+00	9.3E-02	5.0E+00	1.8E-03	1.5E+00	3.2E-09	1.7E+00	1.2E-01	1.8E+00	5.0E-12	2.2E+00	1.8E-03	3.6E+00	7.9E-07	1.6E+00	8.3E-10	2.5E+00	1.7E-13	3.5E+00	3.8E-03
KIF20A	2.1E+00	4.2E-06	3.1E+00	7.0E-22	5.7E+00	1.1E-01	5.0E+00	3.4E-03	1.6E+00	6.4E-08	2.7E+00	5.4E-02	2.7E+00	1.5E-06	3.9E+00	3.9E-04	4.0E+00	1.6E-08	3.6E+00	5.7E-14	4.0E+00	4.4E-12	4.0E+00	3.1E-03
KIF23	2.2E+00	6.3E-04	2.4E+00	5.1E-19	3.3E+00	7.2E-02	5.2E+00	3.0E-03	1.4E+00	4.6E-08	8.0E-01	3.3E-01	5.9E-01	7.7E-03	7.7E-01	2.2E-02	3.7E+00	2.9E-07	3.0E+00	1.4E-11	3.9E+00	6.7E-17	2.7E+00	9.7E-03
KIFC2	1.3E+00	1.1E-03	1.5E+00	2.5E-12	1.1E+00	2.0E-02	1.9E+00	2.9E-04	9.3E-01	3.3E-04	1.3E+00	2.4E-04	3.3E-01	8.9E-03	8.8E-01	3.0E-03	1.7E+00	9.2E-07	1.1E+00	7.9E-06	1.4E+00	2.9E-05	2.2E+00	1.1E-01
LIG1	1.2E+00	4.9E-09	8.2E-01	1.6E-14	2.4E+00	1.3E-01	1.3E+00	7.0E-04	8.4E-01	8.9E-06	-9.6E-02	6.6E-01	9.6E-01	2.0E-14	8.8E-01	6.7E-08	1.0E+00	6.6E-08	7.9E-01	1.3E-09	1.7E+00	1.4E-06	7.3E-01	4.9E-02
LIN9	1.3E+00	1.6E-04	9.9E-01	2.1E-14	2.0E+00	2.0E-01	2.6E+00	1.4E-04	7.1E-01	7.7E-05	-1.9E-01	3.7E-01	1.7E-01	3.8E-02	3.0E-01	5.1E-02	1.7E+00	5.1E-07	7.6E-01	1.4E-06	1.3E+00	8.3E-09	1.1E+00	1.2E-02
LSM2	8.3E-01	1.1E-03	4.0E-01	2.5E-10	8.3E-01	3.3E-01	1.4E+00	4.8E-03	4.7E-01	6.1E-03	-9.3E-01	1.8E-04	2.0E-01	2.5E-03	2.5E-01	7.1E-02	7.5E-01	3.0E-05	7.4E-01	5.9E-08	8.4E-01	1.6E-06	9.6E-01	1.3E-02
LSM4	7.8E-01	8.4E-06	1.1E+00	4.9E-24	1.7E+00	1.8E-01	8.8E-01	9.3E-02	4.9E-01	1.6E-05	4.8E-01	3.5E-03	-4.0E-01	1.7E-07	2.2E-01	4.6E-02	9.3E-01	7.9E-07	5.5E-01	3.3E-05	1.1E+00	1.2E-07	1.3E+00	1.5E-02
LSM7	6.8E-01	1.7E-04	5.6E-01	4.4E-08	1.5E+00	3.5E-01	9.0E-01	1.7E-02	6.8E-01	2.4E-06	2.4E-01	9.4E-02	5.1E-01	1.3E-04	4.8E-01	1.4E-03	5.0E-01	1.7E-03	5.0E-01	4.9E-04	8.9E-01	1.1E-06	6.7E-01	2.2E-02
MAD2L2	1.2E+00	4.2E-03	6.4E-01	1.0E-10	3.0E-01	4.8E-01	-2.2E-01	5.1E-01	8.6E-01	2.2E-06	1.2E+00	9.2E-05	8.9E-03	9.0E-01	1.3E-01	3.9E-01	3.0E-01	6.4E-02	9.9E-01	9.5E-10	1.1E+00	1.5E-07	1.5E+00	2.9E-02
MARS	6.9E-01	7.3E-04	6.2E-01	6.2E-20	9.9E-01	8.1E-02	8.2E-01	7.2E-04	7.4E-01	1.4E-07	9.0E-01	3.7E-05	-1.8E-01	3.6E-03	4.4E-01	6.2E-05	8.0E-01	1.9E-09	8.6E-01	3.5E-10	8.3E-01	1.0E-10	1.0E+00	8.4E-03
MASTL	9.4E-01	2.2E-03	6.9E-01	3.0E-12	1.8E+00	1.3E-01	1.2E+00	2.1E-04	8.6E-01	1.5E-07	-3.8E-01	1.6E-02	2.9E-01	4.2E-05	3.1E-01	3.9E-03	6.4E-01	2.8E-06	7.7E-01	9.9E-06	1.5E+00	8.6E-08	1.3E+00	7.1E-03
MCM2	2.1E+00	8.8E-05	1.5E+00	1.6E-17	3.2E+00	3.4E-02	3.0E+00	5.8E-04	1.2E+00	2.5E-07	1.2E+00	4.7E-02	6.2E-01	2.6E-06	1.3E+00	1.0E-05	2.4E+00	1.1E-07	2.2E+00	1.8E-08	3.5E+00	5.3E-13	1.8E+00	1.2E-02
MCM3	6.7E-01	8.7E-04	6.8E-01	2.6E-13	1.4E+00	4.8E-02	2.5E+00	3.2E-07	9.7E-01	8.1E-09	-7.1E-01	2.1E-03	-1.4E-01	7.2E-02	5.5E-01	6.3E-03	1.4E+00	3.2E-09	8.6E-01	5.4E-09	1.4E+00	2.1E-09	8.1E-01	2.4E-02
MCM4	1.6E+00	1.7E-05	1.7E+00	4.2E-16	4.0E+00	1.5E-01	2.0E+00	8.0E-04	1.1E+00	8.4E-06	4.7E-01	1.2E-01	-3.0E-01	1.8E-04	5.5E-01	4.5E-02	1.5E+00	9.3E-07	2.4E+00	1.8E-11	3.2E+00	1.6E-14	2.2E+00	4.5E-02
MCM5	8.7E-01	6.4E-03	4.5E-01	6.8E-06	2.3E+00	2.6E-02	1.6E+00	5.5E-03	5.7E-01	8.7E-04	1.1E-01	6.6E-01	1.1E+00	3.9E-18	8.2E-01	1.8E-05	1.4E+00	2.3E-07	8.8E-01	7.4E-05	1.8E+00	3.9E-09	3.6E-01	2.7E-01
MCM6	1.1E+00	3.7E-04	9.3E-01	1.7E-17	1.5E+00	9.2E-03	2.2E+00	5.5E-05	8.9E-01	2.2E-06	-1.2E-01	5.4E-01	4.4E-01	1.4E-08	7.7E-01	5.1E-03	1.8E+00	8.8E-08	1.6E+00	1.9E-12	2.0E+00	5.8E-10	1.1E+00	2.7E-02
MCM7	1.1E+00	2.1E-03	4.8E-01	7.5E-06	1.9E+00	1.1E-01	1.8E+00	4.2E-04	1.2E+00	2.2E-08	4.1E-01	1.9E-01	9.7E-01	4.1E-15	1.0E+00	3.1E-06	1.2E+00	9.8E-11	1.3E+00	4.7E-09	2.1E+00	5.8E-13	9.1E-01	1.7E-02
MOCS3	5.1E-01	1.6E-02	6.9E-01	4.1E-09	2.6E-01	6.4E-01	4.6E-01	2.7E-02	1.1E+00	8.2E-05	4.8E-01	6.3E-04	3.3E-01	2.9E-09	7.6E-01	9.6E-07	1.6E-01	6.8E-02	5.2E-01	4.5E-08	8.2E-01	5.0E-08	2.3E-01	4.1E-01
MRPL12	6.9E-01	3.9E-06	7.5E-01	2.5E-09	1.6E+00	2.7E-01	-7.0E-01	1.7E-03	-6.0E-02	6.7E-01	6.1E-01	1.5E-03	-1.2E-01	1.6E-01	6.4E-01	4.9E-03	2.5E-01	7.5E-02	1.2E+00	4.0E-13	1.4E+00	2.6E-09	1.5E+00	2.4E-02
MRPL17	6.4E-01	2.1E-04	7.7E-01	5.3E-23	1.4E+00	1.2E-01	8.7E-01	5.8E-04	8.1E-01	2.1E-06	2.5E-02	8.4E-01	5.2E-01	8.8E-08	5.1E-01	7.3E-04	3.5E-01	1.8E-05	7.9E-01	2.1E-11	6.0E-01	1.7E-05	7.8E-01	6.6E-02
MRPL9	5.2E-01	5.9E-05	5.7E-01	1.1E-12	5.4E-01	1.8E-01	1.3E+00	2.5E-03	5.5E-01	7.2E-07	-4.2E-01	2.6E-04	1.8E-01	6.0E-04	1.8E-01	2.6E-02	7.7E-01	1.1E-05	9.8E-01	6.3E-09	8.7E-01	6.3E-11	7.2E-01	1.4E-03
MRPS12	6.4E-01	1.4E-03	9.7E-01	7.3E-09	1.7E+00	1.4E-01	5.5E-01	8.2E-03	5.1E-01	1.3E-03	7.0E-01	1.3E-05	-3.6E-02	7.2E-01	1.9E-01	1.6E-01	8.9E-01	5.8E-05	9.8E-01	1.5E-08	1.6E+00	5.0E-05	8.8E-01	1.2E-03
MRPS23	7.4E-01	8.0E-05	9.7E-01	8.5E-16	7.8E-01	4.9E-03	1.0E+00	1.3E-05	8.0E-01	2.3E-04	-5.0E-01	6.0E-03	3.6E-02	6.0E-01	6.6E-01	7.6E-04	7.8E-01	1.3E-08	8.7E-01	2.4E-09	6.3E-01	4.3E-05	6.5E-01	4.8E-02
MRPS34	3.6E-01	9.4E-03	1.1E+00	4.1E-25	1.3E+00	2.7E-01	3.3E-01	1.9E-01	4.4E-01	1.4E-04	6.6E-01	8.3E-04	4.2E-01	2.2E-05	6.1E-01	5.1E-03	3.3E-01	1.1E-02	7.4E-01	7.7E-11	8.7E-01	4.8E-08	5.1E-01	2.8E-01
MTHFD1L	1.7E+00	4.8E-05	6.6E-01	2.7E-03	1.7E+00	1.5E-01	3.1E+00	1.0E-02	2.3E+00	7.8E-12	9.5E-01	4.4E-03	6.5E-01	1.4E-06	1.3E+00	5.0E-05	1.6E+00	4.5E-08	1.0E+00	1.4E-13	1.0E+00	1.1E-09	1.2E+00	4.3E-03
MTHFD2	9.2E-01	9.2E-03	1.4E+00	3.9E-16	8.9E-01	2.2E-02	2.5E+00	4.5E-02	1.3E+00	6.8E-07	1.7E+00	2.8E-03	1.0E+00	2.4E-07	1.4E+00	1.3E-02	3.3E-01	1.9E-01	1.7E+00	4.3E-13	1.8E+00	4.5E-08	1.5E+00	7.8E-02
MYB	1.8E+00	7.0E-03	9.0E-01	1.8E-09	2.5E+00	1.1E-01	4.8E+00	2.1E-01	2.4E-01	2.4E-01	5.9E-01	3.9E-01	3.9E-01	6.2E-01	1.6E+00	1.1E-02	6.2E-01	8.8E-02	3.0E-01	5.5E-01	2.4E+00	5.0E-02	2.0E-01	8.5E-01
MYBBP1A	7.7E-01	2.1E-03	-1.4E-01	5.8E-02	6.4E-02	9.4E-01	1.2E+00	6.7E-03	8.3E-01	5.2E-07	6.3E-01	7.2E-04	4.4E-01	3.2E-09	8.3E-01	9.3E-06	4.0E-01	1.8E-03	7.7E-01	1.5E-08	9.8E-01	1.1E-11	-3.1E-03	9.9E-01
MYBL2	2.0E+00	1.0E-06	2.4E+00	3.8E-10	6.6E+00	9.2E-02	5.8E+00	4.9E-03	2.1E+00	3.8E-06	2.9E+00	6.4E-02	2.6E+00	6.8E-06	4.6E+00	1.3E-03	4.2E+00	1.2E-07	4.1E+00	1.1E-08	5.0E+00	2.0E-13	5.7E+00	4.7E-03
NAA10	4.4E-01	2.2E-03	4.1E-01	8.7E-09	1.8E+00	1.4E-01	5.7E-01	8.1E-03	9.5E-01	2.1E-06	2.4E-01	1.4E-01	2.0E-01	1.7E-02	3.4E-01	1.7E-02	8.5E-01	4.1E-06	7.0E-01	3.1E-12	8.4E-01	6.4E-04	9.5E-01	3.1E-02
NAT10	6.7E-01	7.4E-06	6.3E-01	2.4E-07	1.4E-01	6.2E-01	8.4E-01	4.4E-03	1.0E+00	1.3E-11	7.0E-01	1.3E-05	3.9E-01	5.4E-13	3.8E-01	9.1E-06	4.5E-01	7.8E-10	6.9E-01	1.3E-13	9.8E-01	1.8E-12	5.2E-01	2.1E-01
NCAPD2	1.4E+00	1.6E-05	7.2E-01	2.0E-10	1.8E+00	8.1E-02	2.7E+00	2.1E-03	7.7E-01	9.4E-06	6.5E-01	1.8E-02	3.6E-01	1.1E-04	8.3E-01	3.5E-06	1.3E+00	1.9E-07	1.0E+00	7.6E-10	2.3E+00	4.4E-12	1.7E+00	9.6E-02
NCAPG	1.7E+00	1.4E-05	2.7E+00	1.5E-19	5.5E+00	3.1E-02	5.0E+00	1.0E-02	1.1E+00	3.0E-05	3.1E+00	1.4E-02	2.2E+00	2.1E-09	3.3E+00	2.4E-04	3.7E+00	2.5E-08	3.4E+00	2.6E-11	3.9E+00	4.5E-15	3.8E+00	6.5E-04
NCAPH	2.3E+00	4.6E-06	2.5E+00	2.1E-19	5.5E+00	8.3E-02	4.9E+00	1.6E-04	1.2E+00	1.6E-06	2.1E+00	5.0E-02	2.0E+00	2.2E-09	3.1E+00	6.0E-04	3.4E+00	5.5E-08	3.4E+00	1.0E-11	4.4E+00	1.9E-16	4.3E+00	3.5E-03
NCLN	6.1E-01	5.2E-06	4.6E-01	1.2E-10	8.3E-01	2.0E-01	3.2E-01	1.2E-01	4.0E-01	8.5E-05	1.1E+00	1.4E-07	6.2E-01	1.7E-12	5.7E-01	2.6E-04	3.2E-01	1.0E-03	1.3E-01	6.2E-02	4.6E-01	2.7E-05	7.6E-01	8.1E-05
NDC80	1.7E+00	1.3E-06	3.1E+00	1.0E-16	2.9E+00	2.5E-01	4.8E+00	5.6E-03	7.9E-01	1.5E-03	2.2E+00	8.5E-02	2.0E+00	3.4E-12	2.3E+00	8.7E-04	3.6E+00	1.9E-08	3.5E+00	4.9E-10	4.1E+00	2.9E-14	2.6E+00	2.8E-02
NDOR1	4.6E-01	5.0E-02	7.5E-01	2.3E-16	1.7E+00	1.5E-01	1.4E+00	1.0E-03	-8.3E-02	3.4E-01	5.6E-01	7.3E-04	-6.0E-01	1.1E-12	2.6E-01	2.6E-02	8.3E-01	2.0E-08	3.7E-01	5.7E-05	4.6E-01	2.1E-06	6.4E-01	3.4E-03
NLE1	5.9E-01	5.3E-03	-3.8E-01	9.3E-06	1.4E-01	6.2E-01	1.6E+00	3.5E-04	1.3E+00	3.0E-09	-2.3E-02	9.4E-01	6.4E-01	8.4E-13	7.4E-01	8.9E-05	6.6E-01	4.2E-05	9.4E-01	2.9E-11	1.1E+00	8.5E-10	-3.7E-01	1.9E-01
NOP16	3.0E-01	1.6E-01	6.4E-01	2.4E-09	7.9E-01	9.5E-02	4.7E-01	2.3E-02	9.5E-01	1.2E-07	6.9E-01	4.9E-04	1.1E+00	6.4E-13	7.9E-01	8.1E-03	3.2E-01	3.5E-02	9.7E-01	4.5E-09	8.9E-01	7.1E-05	9.1E-01	7.1E-02
NOP2	8.1E-01	2.0E-03	7.1E-01	6.2E-12	9.9E-01	3.6E-02	1.2E+00	2.0E-03	1.3E+00	4.8E-13	5.4E-01	5.7E-03	6.7E-01	4.5E-10	1.1E+00	5.3E-09	5.3E-01	2.3E-06	9.6E-01	2.2E-11	1.6E+00	2.7E-08	1.4E+00	6.0E-02
NOP56	5.5E-01	4.8E-04	5.3E-01	2.0E-12	4.0E-01	3.9E-01	1.6E+00	2.2E-05	1.4E+00	1.8E-07	7.8E-02	7.3E-01	5.2E-01	1.2E-12	7.1E-01	1.3E-04	8.2E-01	1.7E-07	7.5E-01	4.6E-08	1.4E+00	2.3E-08	4.2E-01	6.9E-02
NR2C2AP	1.0E+00	1.5E-05	8.0E-01	9.4E-08	1.7E+00	1.2E-01	1.9E+00	1.4E-03	1.0E+00	3.0E-10	6.3E-01	1.5E-04	9.3E-01	2.7E-09	1.0E+00	6.4E-07	1.4E+00	2.2E-07	8.3E-01	1.5E-10	1.2E+00	4.2E-08	5.9E-01	5.4E-02
NUF2	2.6E+00	2.7E-04	3.4E+00	9.0E-17	5.8E+00	1.4E-01	5.8E+00	8.7E-03	1.7E+00	2.5E-08	1.6E+00	1.4E-01	1.9E+00	2.6E-07	2.9E+00	1.7E-04	4.5E+00	1.3E-05	4.1E+00	3.0E-10	4.7E+00	6.5E-13	4.7E+00	1.1E-03
NUP155	1.3E+00	1.1E-02	7.0E-01	1.5E-12	1.8E+00	1.7E-01	1.0E+00	3.9E-03	9.2E-01	5.3E-11	7.2E-01	5.6E-03	2.8E-01	5.2E-05	2.9E-01	7.1E-02	9.6E-01	9.6E-09	1.6E+00	1.1E-09	2.2E+00	3.8E-12	9.5E-01	8.5E-02
NUP205	8.4E-01	2.3E-04	4.8E-01	2.5E-08	7.6E-01	3.4E-01	1.4E+00	3.3E-04	9.2E-01	6.4E-07	7.8E-01	6.6E-06	2.0E-01	3.0E-03	4.4E-01	9.7E-05	7.7E-01	2.2E-08	8.5E-01	2.1E-09	1.3E+00	2.1E-14	4.2E-01	1.7E-01
NUP62	5.1E-01	1.1E-04	5.7E-01	5.8E-20	8.1E-01	2.6E-01	1.6E+00	1.4E-04	4.6E-01	1.4E-06	1.5E-01	1.2E-01	7.3E-01	1.8E-19	6.3E-01	5.3E-08	6.4E-01	1.7E-05	6.6E-01	3.3E-12	1.0E+00	1.0E-09	1.9E-01	3.3E-01
NUP85	9.4E-01	2.2E-06	4.6E-01	2.5E-09	1.1E+00	5.5E-04	7.2E-01	7.2E-04	6.6E-01	7.0E-08	-6.2E-01	5.0E-05	5.0E-01	6.4E-16	8.0E-01	8.7E-08	4.7E-01	1.4E-05	8.4E-01	4.0E-11	9.4E-01	1.1E-11	6.7E-01	1.4E-02
OIP5	2.0E+00	1.1E-05	2.4E+00	6.7E-22	5.5E+00	5.8E-02	3.3E+00	1.3E-02	8.9E-01	2.3E-04	1.6E+00	1.0E-01	1.7E+00	9.3E-14	1.9E+00	2.0E-04	2.8E+00	1.3E-05	2.7E+00	1.6E-08	3.7E+00	1.0E-11	3.5E+00	1.4E-02
PABPC1	9.9E-01	4.5E-02	5.7E-01	6.1E-04	6.0E-01	3.2E-01	9.0E-01	2.7E-04	1.0E+00	1.9E-07	8.4E-01	1.0E-01	6.8E-01	4.2E-11	5.9E-01	1.1E-03	8.5E-01	2.3E-05	1.0E+00	5.6E-10	1.3E+00	4.7E-12	7.9E-01	2.1E-02
PAICS	9.4E-01	1.5E-06	9.6E-01	7.9E-18	9.4E-01	2.8E-01	-4.3E-01	3.8E-02	1.2E+00	1.5E-09	4.5E-01	3.3E-03	1.5E-01	8.6E-03	3.7E-02	8.4E-01	-2.3E-02	8.0E-01	1.8E+00	3.0E-19	2.3E+00	6.1E-11	8.0E-01	1.1E-01
PALB2	1.1E+00	2.1E-04	5.0E-01	3.8E-11	1.2E+00	3.0E-01	1.2E+00	8.8E-06	1.1E+00	2.8E-11	2.6E-01	4.5E-02	1.8E-01	1.0E-03	6.3E-01	3.2E-06	5.4E-01	3.5E-05	8.7E-01	5.7E-15	1.2E+00	2.8E-14	1.5E-01	6.6E-01
PCNA	1.2E+00	3.1E-05	1.3E+00	7.7E-24	3.0E+00	9.1E-02	1.3E+00	7.7E-03	9.8E-01	7.3E-05	2.1E-01	4.2E-01	2.5E-01	2.8E-03	6.1E-01	4.2E-03	9.7E-01	5.7E-08	1.2E+00	3.6E-08	1.9E+00	5.2E-10	1.5E+00	8.9E-03
PDRG1	8.8E-01	5.5E-05	9.6E-01	4.4E-15	7.5E-01	6.9E-02	1.1E+00	2.1E-03	1.2E+00	1.8E-06	8.9E-01	3.9E-07	1.1E-01	3.1E-02	2.9E-01	4.5E-02	7.0E-01	1.1E-09	4.9E-01	6.2E-07	8.8E-01	6.3E-07	8.2E-01	5.6E-02
PFDN2	9.4E-01	5.1E-04	8.6E-01	1.3E-09	7.4E-01	3.9E-01	5.7E-01	1.6E-02	7.8E-01	8.2E-08	-2.5E-01	7.5E-02	1.3E-01	1.4E-01	3.7E-01	1.4E-02	5.6E-01	5.6E-05	1.0E+00	9.2E-05	1.0E+00	4.6E-10	1.1E+00	1.3E-02
PFDN6	8.5E-01	9.2E-03	8.6E-01	1.0E-15	1.1E+00	2.5E-01	1.9E-01	2.7E-01	4.7E-01	3.2E-04	-1.2E-01	3.0E-01	2.4E-01	5.1E-03	5.7E-01	4.2E-03	7.2E-01	7.8E-06	9.3E-01	1.2E-11	7.8E-01	1.5E-06	1.2E+00	2.8E-02
PGK1	7.0E-01	3.7E-03	9.5E-01	7.4E-13	1.5E+00	1.6E-01	8.2E-01	2.0E-02	9.3E-01	2.4E-04	2.8E-01	6.8E-02	1.1E+00	1.5E-15	2.8E-01	3.4E-02	5.6E-01	3.3E-04	1.0E+00	9.6E-10	1.0E+00	9.0E-09	1.5E+00	9.1E-02
PGM3	8.0E-01	2.1E-03	4.7E-01	2.3E-08	6.2E-01	3.4E-02	-5.8E-01	2.6E-02	5.3E-01	6.0E-04	-3.8E-01	2.2E-02	7.4E-01	1.4E-14	5.6E-01	1.9E-03	-4.7E-01	1.7E-04	9.5E-01	4.0E-10	6.9E-01	1.4E-07	1.1E+00	1.7E-02
PKMYT1	1.2E+00	1.4E-03	3.4E+00	4.9E-24	5.7E+00	3.4E-02	4.8E+00	2.8E-03	1.6E+00	9.6E-10	2.7E+00	9.8E-03	2.5E+00	1.0E-09	4.2E+00	2.1E-04	3.3E+00	2.3E-08	3.2E+00	4.3E-11	4.4E+00	5.6E-12	4.4E+00	6.9E-03
PLK1	2.2E+00	9.9E-05	2.8E+00	2.5E-18	4.7E+00	2.2E-02	5.5E+00	3.5E-02	1.4E+00	1.5E-08	2.8E+00	5.0E-02	2.0E+00	3.8E-06	3.0E+00	9.0E-05	3.6E+00	1.9E-08	3.6E+00	4.0E-11	4.4E+00	1.2E-14	3.7E+00	1.1E-02
PLK4	1.6E+00	1.3E-05	1.7E+00	2.0E-17	4.0E+00	1.8E-01	3.5E+00	4.3E-03	1.0E+00	6.0E-06	1.1E+00	1.2E-02	9.2E-01	4.4E-08	1.2E+00	2.6E-05	2.4E+00	2.2E-04	2.3E+00	8.8E-09	2.8E+00	1.7E-15	2.2E+00	2.2E-03
PMM2	5.6E-01	2.9E-02	9.5E-01	2.6E-23	6.8E-01	4.6E-01	5.6E-01	1.6E-02	3.5E-01	2.1E-03	1.0E+00	1.4E-04	1.2E+00	3.7E-15	1.3E+00	1.1E-07	-4.1E-02	5.8E-01	1.0E+00	3.4E-14	7.4E-01	1.3E-09	7.0E-01	6.1E-02
PNKP	7.1E-01	2.4E-03	5.0E-01	1.7E-09	1.4E+00	2.1E-01	7.5E-01	4.3E-02	2.9E-01	4.5E-03	5.5E-01	9.7E-06	5.6E-02	5.0E-01	4.4E-01	5.9E-04	4.6E-01	5.1E-04	2.8E-01	1.4E-04	7.2E-01	9.1E-06	4.3E-01	1.0E-01
POLA2	1.1E+00	1.2E-04	8.1E-01	1.8E-17	2.1E+00	1.7E-01	1.4E+00	2.0E-02	7.9E-01	4.9E-06	4.3E-01	2.2E-02	2.8E-01	1.9E-04	3.5E-01	1.1E-02	1.3E+00	1.8E-11	8.6E-01	7.7E-07	1.3E+00	7.3E-11	9.0E-01	2.7E-02
POLD2	8.0E-01	9.5E-04	5.4E-01	9.4E-11	1.4E+00	8.7E-02	-4.0E-01	5.5E-03	1.2E+00	3.8E-10	5.6E-02	8.3E-01	5.2E-01	1.2E-07	9.3E-01	7.7E-08	6.8E-02	5.3E-01	8.3E-01	4.1E-10	1.3E+00	5.4E-09	4.1E-01	1.8E-02
POLE	9.6E-01	5.8E-06	5.5E-01	2.5E-11	1.9E+00	2.0E-02	1.6E-01	2.9E-01	4.3E-01	9.1E-03	4.3E-01	2.4E-02	4.3E-01	6.4E-06	9.7E-01	9.7E-06	1.2E-01	2.9E-01	8.8E-01	3.0E-06	1.5E+00	8.0E-09	9.1E-01	4.4E-03
POLE2	1.9E+00	1.3E-04	1.7E+00	1.9E-21	3.9E+00	1.5E-02	1.1E+00	3.5E-02	1.2E+00	4.2E-05	1.6E+00	1.7E-02	1.2E+00	3.6E-08	2.5E+00	3.5E-04	1.9E+00	6.0E-05	2.8E+00	5.8E-10	3.1E+00	4.2E-12	2.4E+00	1.0E-02
POLR2H	1.0E+00	2.5E-05	8.2E-01	1.6E-17	1.4E+00	3.5E-01	8.9E-01	6.1E-03	3.6E-01	2.0E-03	-3.4E-01	1.1E-02	3.6E-01	5.8E-05	2.5E-02	8.6E-01	3.9E-01	3.5E-04	1.0E+00	3.9E-13	1.8E+00	3.6E-09	1.7E+00	1.1E-01
POLR3K	4.4E-01	4.9E-02	1.4E+00	1.2E-22	1.2E+00	8.2E-02	8.9E-01	2.3E-02	8.2E-01	1.6E-07	8.6E-01	2.0E-07	-4.0E-02	5.3E-01	4.6E-01	7.1E-03	5.9E-01	2.0E-06	6.7E-01	1.0E-08	7.7E-01	1.6E-04	6.1E-01	1.9E-01
POP1	6.9E-01	4.8E-02	1.0E+00	6.5E-10	9.4E-01	1.7E-01	1.6E+00	5.6E-04	1.4E+00	1.1E-07	-6.7E-03	9.7E-01	4.2E-01	6.2E-06	7.7E-02	3.9E-01	8.8E-01	9.8E-07	1.0E+00	4.4E-08	1.5E+00	3.0E-10	8.0E-01	5.3E-04
POP7	7.3E-01	1.4E-05	7.3E-01	5.2E-20	8.2E-01	4.0E-01	3.0E-01	2.3E-01	6.6E-01	2.8E-06	6.8E-01	5.6E-06	5.9E-01	5.3E-08	6.2E-01	2.4E-05	1.2E-01	2.9E-01	8.1E-01	1.1E-11	1.2E+00	2.7E-08	7.5E-01	8.0E-03
PPAN	4.2E-01	5.7E-03	4.7E-01	2.5E-04	5.7E-01	9.4E-02	7.4E-01	2.9E-03	9.9E-01	4.3E-10	7.1E-01	5.2E-06	6.3E-01	2.1E-09	5.6E-01	1.6E-04	3.8E-01	1.3E-02	5.0E-01	1.1E-04	9.4E-01	5.3E-08	3.3E-01	3.3E-01
PPAT	1.0E+00	1.5E-04	8.9E-01	3.4E-12	1.4E+00	2.7E-01	8.5E-01	8.4E-03	1.6E+00	2.7E-10	-5.9E-02	7.7E-01	2.4E-01	4.5E-03	3.6E-01	6.5E-02	6.5E-01	3.2E-05	2.0E+00	7.6E-15	2.3E+00	1.6E-12	8.3E-01	4.7E-02
PRC1	1.6E+00	2.8E-04	2.2E+00	4.1E-18	3.7E+00	2.1E-01	4.9E+00	4.8E-03	1.2E+00	8.0E-07	1.7E+00	5.2E-02	1.3E+00	3.0E-13	1.6E+00	3.9E-04	3.3E+00	4.7E-09	2.8E+00	1.5E-10	3.7E+00	1.5E-14	3.0E+00	9.4E-03
PRIM1	1.6E+00	1.0E-04	7.6E-01	2.0E-12	2.5E+00	1.6E-02	7.5E-01	5.1E-02	9.0E-01	1.9E-07	-1.4E-01	7.6E-01	7.5E-01	1.5E-11	8.2E-01	4.4E-03	1.5E+00	1.6E-07	1.1E+00	6.2E-07	1.5E+00	2.5E-09	5.1E-01	2.7E-01
PSMB2	8.0E-01	2.3E-06	4.9E-01	3.9E-13	1.3E+00	4.4E-02	1.7E-01	4.5E-01	4.6E-01	9.0E-05	-2.8E-01	8.6E-03	3.5E-01	8.8E-08	3.9E-01	2.8E-04	1.4E-01	1.1E-01	7.0E-01	1.1E-12	7.4E-01	2.6E-08	6.8E-01	1.3E-02
PSMB3	9.4E-01	3.6E-03	8.4E-01	1.2E-10	1.8E+00	2.6E-01	3.8E-02	8.8E-01	2.6E-01	3.9E-02	-4.8E-01	3.2E-04	1.9E-01	3.1E-02	6.7E-01	1.4E-04	2.9E-01	2.4E-02	7.1E-01	3.7E-11	7.6E-01	7.8E-07	1.0E+00	1.3E-01
PSMD14	8.8E-01	2.4E-04	8.3E-01	2.3E-21	9.5E-01	1.8E-02	6.4E-01	1.0E-02	6.9E-01	8.5E-05	-1.2E-01	4.5E-01	1.4E-01	4.9E-02	5.2E-01	3.6E-05	7.1E-01	4.4E-06	8.5E-01	5.6E-13	1.1E+00	9.2E-11	1.4E+00	3.6E-03
PSMG3	1.2E+00	1.2E-06	8.0E-01	7.8E-16	1.9E+00	2.6E-01	1.4E+00	7.2E-03	6.9E-01	6.4E-06	4.2E-01	2.5E-02	3.5E-01	3.1E-03	7.1E-01	1.3E-03	8.9E-01	7.4E-09	1.4E+00	2.4E-10	1.5E+00	1.3E-07	7.9E-01	4.7E-03
RACGAP1	1.2E+00	8.2E-05	1.9E+00	4.6E-21	3.7E+00	6.6E-02	3.6E+00	1.6E-03	1.1E+00	6.2E-08	1.7E+00	3.6E-03	8.4E-01	4.1E-08	1.3E+00	7.5E-06	2.5E+00	6.2E-10	1.7E+00	3.0E-08	2.5E+00	1.8E-16	2.6E+00	6.3E-03
RAD51	1.8E+00	7.8E-07	2.1E+00	8.6E-18	4.5E+00	6.5E-02	4.1E+00	3.7E-03	6.1E-01	2.7E-03	1.3E+00	3.6E-02	1.6E+00	1.4E-13	2.3E+00	2.4E-05	2.4E+00	3.5E-07	2.4E+00	7.8E-12	3.7E+00	5.1E-15	3.1E+00	1.1E-02
RAD9A	8.8E-01	5.8E-05	3.8E-01	1.9E-04	1.7E+00	1.8E-02	1.2E+00	1.8E-02	2.7E-01	1.7E-02	5.3E-01	3.1E-02	4.9E-01	1.4E-09	8.7E-01	6.1E-05	7.0E-01	4.5E-09	4.3E-01	5.5E-06	7.3E-01	1.0E-08	6.9E-01	1.9E-01
RAE1	9.0E-01	2.7E-06	9.1E-01	6.9E-11	7.1E-01	2.7E-01	1.2E+00	1.5E-04	1.4E+00	3.3E-07	3.2E-01	2.0E-03	-1.7E-02	6.5E-01	3.3E-01	1.5E-02	4.9E-01	5.3E-09	8.0E-01	5.1E-10	1.4E+00	2.9E-13	7.6E-01	6.2E-02
RAN	6.1E-01	8.7E-06	7.6E-01	3.5E-21	1.1E+00	9.2E-02	1.4E+00	6.7E-05	8.5E-01	8.5E-06	1.2E-01	3.6E-01	2.8E-01	6.9E-05	6.0E-01	7.4E-07	7.0E-01	2.9E-08	7.9E-01	1.4E-09	1.1E+00	1.8E-09	8.6E-01	8.9E-02
RANGAP1	4.2E-01	4.3E-03	6.6E-01	5.9E-12	2.2E+00	5.5E-02	1.7E+00	1.0E-03	9.2E-01	3.8E-09	1.6E-01	3.0E-01	-3.8E-01	3.1E-07	-6.8E-03	9.5E-01	5.4E-01	2.2E-04	6.8E-01	4.7E-07	1.5E+00	6.7E-14	9.6E-01	3.6E-03
RCC1	1.6E+00	6.1E-07	1.3E+00	3.1E-20	2.7E+00	5.1E-02	9.8E-01	1.8E-02	1.1E+00	1.6E-06	2.5E-01	5.3E-01	1.0E+00	5.8E-07	1.6E+00	2.0E-06	5.4E-01	8.0E-05	2.1E+00	2.1E-20	2.2E+00	1.7E-15	1.7E+00	7.1E-03
RFC2	1.0E+00	1.9E-05	9.3E-01	2.5E-16	1.4E+00	1.7E-01	6.3E-01	8.0E-03	7.1E-01	5.1E-06	4.1E-01	8.2E-02	1.2E+00	1.2E-19	1.1E+00	1.5E-09	5.2E-01	7.0E-05	9.4E-01	2.0E-10	1.2E+00	1.2E-12	8.2E-01	1.0E-02

RFC3	1.2E+00	8.5E-04	7.2E-01	3.3E-10	1.5E+00	1.3E-01	1.0E+00	8.2E-02	1.8E+00	4.6E-09	-7.3E-01	4.4E-03	-1.0E-01	1.8E-01	2.2E-01	2.1E-01	1.2E+00	2.7E-06	9.3E-01	1.2E-08	1.5E+00	1.8E-08	1.1E+00	2.8E-02
RFC4	1.5E+00	3.8E-04	9.8E-01	1.4E-10	2.0E+00	1.1E-01	2.0E+00	9.7E-05	1.0E+00	3.5E-08	3.2E-01	2.5E-01	9.0E-01	5.1E-12	1.0E+00	1.2E-06	1.6E+00	2.2E-10	1.8E+00	1.7E-09	3.4E+00	5.9E-11	1.5E+00	8.6E-02
RFC5	1.3E+00	9.4E-07	6.3E-01	9.2E-12	2.1E+00	1.8E-01	6.7E-01	1.0E-02	7.6E-01	7.6E-05	-4.6E-01	2.3E-03	2.1E-01	7.2E-04	6.4E-01	4.9E-04	4.7E-01	8.2E-04	1.1E+00	2.1E-07	1.8E+00	5.6E-12	3.0E-01	3.3E-01
RFWD3	1.3E+00	2.0E-05	5.4E-01	4.3E-10	1.4E+00	2.6E-01	1.8E+00	5.6E-05	1.1E+00	2.7E-10	-6.9E-01	5.1E-07	-3.9E-01	2.6E-10	3.3E-01	2.0E-02	5.3E-01	4.3E-06	1.1E+00	1.2E-14	1.5E+00	7.6E-10	8.3E-01	5.0E-02
RNASEH2A	1.3E+00	5.6E-07	1.6E+00	3.4E-20	3.5E+00	1.0E-01	2.0E+00	1.6E-02	1.2E+00	3.9E-10	5.7E-01	1.5E-01	9.0E-01	1.5E-09	1.2E+00	8.6E-06	1.7E+00	4.3E-08	1.4E+00	8.7E-08	2.1E+00	4.8E-14	1.8E+00	7.9E-03
RPL8	1.0E-01	5.3E-01	1.6E-01	7.3E-02	3.1E-03	9.9E-01	1.1E+00	1.2E-02	7.3E-01	9.9E-04	9.5E-01	7.4E-04	6.5E-01	3.3E-07	5.6E-01	2.5E-04	9.0E-01	2.6E-03	6.0E-01	1.6E-05	6.8E-01	7.9E-05	-4.5E-02	9.1E-01
RPN2	7.5E-01	7.2E-05	8.5E-01	1.8E-18	8.3E-01	2.4E-01	4.7E-01	3.0E-02	1.0E+00	3.4E-06	2.9E-01	2.7E-04	3.6E-01	6.0E-07	3.1E-01	1.5E-02	5.9E-01	1.0E-08	7.3E-01	3.3E-14	8.3E-01	1.1E-08	1.4E+00	5.3E-02
RPP21	7.4E-01	6.1E-03	5.5E-01	1.9E-09	1.1E+00	2.0E-01	1.1E+00	4.6E-03	2.6E-01	4.7E-02	-2.9E-01	2.6E-02	5.2E-01	2.7E-06	4.3E-01	9.6E-03	5.8E-01	3.8E-04	7.4E-01	6.3E-11	8.9E-01	7.6E-08	6.8E-01	1.4E-01
RPP40	9.1E-01	6.9E-04	6.5E-01	3.9E-09	1.2E+00	2.3E-01	-7.3E-02	7.7E-01	1.1E+00	7.6E-06	-4.7E-01	2.3E-01	2.3E-01	7.2E-03	5.7E-01	4.9E-04	7.4E-01	1.1E-04	1.7E+00	8.1E-15	1.9E+00	7.8E-10	1.1E+00	1.1E-03
RPS19	3.6E-01	7.3E-02	-6.9E-02	5.4E-01	1.1E+00	4.2E-01	1.2E+00	3.7E-03	6.1E-01	1.8E-04	6.4E-01	4.9E-03	1.4E+00	6.5E-13	1.5E+00	4.1E-05	4.5E-01	3.7E-02	4.9E-01	3.2E-04	7.8E-01	1.3E-05	3.0E-01	2.8E-01
RPS2	-7.4E-02	6.6E-01	2.2E-01	1.2E-02	3.5E-01	5.4E-01	1.3E+00	6.1E-03	7.3E-01	1.3E-07	1.4E+00	1.9E-05	1.4E+00	1.6E-12	1.4E+00	1.9E-06	4.9E-01	3.3E-03	6.5E-01	2.2E-09	8.0E-01	3.2E-09	3.0E-01	3.3E-01
RRM2	1.5E+00	4.7E-04	3.4E+00	7.0E-13	6.3E+00	1.3E-01	4.0E+00	2.9E-03	1.3E+00	7.2E-06	1.8E+00	2.0E-01	2.2E+00	1.2E-08	3.6E+00	1.1E-03	3.0E+00	9.0E-10	3.4E+00	2.0E-10	4.1E+00	8.6E-14	4.2E+00	9.6E-03
RRP1	6.8E-01	5.5E-03	4.4E-01	2.4E-06	1.3E+00	1.4E-01	3.0E-01	8.3E-02	9.5E-01	3.2E-10	1.6E-01	2.0E-01	6.2E-01	5.5E-10	3.4E-01	1.4E-02	4.9E-01	5.3E-05	7.1E-01	9.6E-11	9.9E-01	6.5E-11	7.6E-01	9.1E-03
RRS1	1.2E-01	5.0E-01	8.1E-01	1.7E-11	-3.4E-01	4.4E-01	1.2E+00	5.0E-05	1.2E+00	2.1E-08	9.3E-01	1.1E-04	2.9E-01	4.2E-03	6.6E-01	6.1E-04	9.2E-01	1.5E-05	9.3E-01	2.0E-06	8.3E-01	6.1E-06	2.8E-01	1.5E-01
RTEL1	6.7E-01	2.3E-03	2.3E-01	5.7E-03	1.0E+00	4.8E-01	1.0E+00	5.5E-04	1.0E+00	4.4E-03	3.0E-01	8.4E-02	9.9E-01	9.1E-17	6.4E-01	1.3E-04	9.1E-01	4.1E-10	7.2E-01	3.2E-08	4.8E-01	9.4E-04	2.7E-01	3.1E-01
RUNX1	4.7E-01	7.2E-02	2.5E-01	3.1E-03	2.4E+00	8.8E-02	1.6E+00	2.4E-03	1.3E+00	1.0E-07	8.2E-01	1.2E-02	1.7E+00	9.1E-11	1.5E+00	8.3E-03	1.8E-01	3.6E-01	5.8E-01	2.9E-08	2.9E-01	1.6E-02	1.2E+00	3.1E-01
RUVBL1	1.3E+00	9.6E-04	8.3E-01	6.9E-18	4.9E-01	1.3E-01	1.4E+00	1.8E-03	1.2E+00	1.3E-09	-9.4E-02	4.8E-01	-2.5E-01	6.7E-05	2.8E-01	1.9E-02	6.3E-01	4.4E-08	8.5E-01	2.5E-07	1.6E+00	1.5E-12	3.5E-01	3.9E-01
RUVBL2	7.0E-01	8.9E-04	7.3E-01	4.2E-13	1.1E+00	1.6E-01	4.5E-01	2.0E-02	6.5E-01	6.4E-07	2.1E-01	5.5E-02	4.7E-01	8.1E-06	6.1E-01	1.4E-05	5.7E-01	3.4E-06	3.7E-01	5.3E-04	9.5E-01	2.1E-07	7.6E-02	8.4E-01
SCD	2.4E+00	5.7E-03	-1.3E+00	1.6E-03	3.1E+00	3.4E-01	-3.8E+00	2.2E-02	1.7E+00	7.4E-06	4.0E+00	1.9E-05	3.1E+00	4.2E-16	2.1E+00	1.1E-05	3.6E-01	2.2E-01	-8.4E-01	3.4E-09	-9.3E-03	9.6E-01	1.9E+00	1.1E-01
SEC61A1	9.0E-01	9.3E-04	5.7E-01	9.5E-18	2.7E-01	6.9E-01	4.2E-01	8.0E-03	4.2E-01	3.4E-04	8.3E-01	1.1E-07	3.8E-01	4.3E-07	5.4E-01	1.6E-04	5.2E-01	3.6E-05	7.6E-01	3.9E-14	7.0E-01	3.8E-09	7.7E-01	1.2E-02
SF3A2	6.0E-01	1.8E-04	8.5E-02	2.3E-01	3.1E-02	9.2E-01	1.3E+00	1.1E-03	6.0E-01	1.3E-07	7.2E-01	4.7E-04	7.7E-01	3.3E-10	6.0E-01	4.4E-04	8.8E-01	2.4E-06	1.0E-01	2.5E-01	6.3E-01	1.7E-06	-1.6E-01	4.9E-01
SHFM1	9.2E-01	2.5E-03	6.1E-01	4.3E-11	9.1E-01	5.1E-01	-9.8E-02	6.8E-01	6.8E-01	3.5E-05	1.4E+00	2.8E-10	9.0E-01	7.2E-08	9.5E-01	4.0E-05	3.8E-01	1.0E-02	9.3E-01	3.2E-14	1.6E+00	3.6E-08	9.8E-01	8.1E-03
SHMT2	1.2E+00	8.8E-07	8.1E-01	2.4E-13	1.9E+00	6.1E-02	-1.6E+00	5.3E-06	1.3E+00	7.0E-09	1.3E+00	1.4E-03	2.1E+00	5.7E-21	1.0E+00	3.7E-05	-4.8E-01	8.8E-07	1.4E+00	8.4E-13	1.8E+00	3.7E-13	1.5E+00	8.1E-02
SKA1	1.9E+00	2.9E-05	3.0E+00	7.5E-17	5.6E+00	8.7E-02	5.1E+00	1.8E-02	1.0E+00	2.4E-04	2.6E+00	4.7E-02	1.9E+00	3.6E-08	2.6E+00	3.5E-04	4.1E+00	1.8E-07	3.3E+00	7.7E-09	4.4E+00	8.9E-17	3.9E+00	9.8E-03
SKA3	1.9E+00	2.2E-05	2.6E+00	8.3E-23	5.9E+00	5.2E-02	4.7E+00	7.2E-03	1.9E+00	9.0E-11	1.9E+00	5.8E-02	2.1E+00	4.5E-10	2.5E+00	2.6E-04	3.4E+00	7.1E-08	3.3E+00	1.3E-12	4.1E+00	7.4E-15	4.0E+00	1.7E-04
SLC38A5	7.6E-01	1.8E-01	1.9E+00	9.5E-11	2.6E+00	9.8E-02	3.6E+00	1.2E-01	1.9E+00	1.0E-05	-3.4E+00	1.9E-08	2.2E+00	9.9E-02	5.9E-01	3.6E-01	1.1E+00	1.8E-01	-2.2E-01	1.7E-01	6.1E-01	1.1E-01	-3.5E-01	6.5E-01
SLC4A5	5.8E-01	2.5E-02	8.6E-01	1.0E-15	6.3E-01	3.4E-01	2.3E+00	9.4E-03	9.6E-01	1.1E-04	4.2E+00	1.4E-05	7.4E-01	1.0E-07	7.4E-01	6.3E-02	4.9E-01	7.5E-02	-1.0E-01	5.7E-01	2.8E-01	9.0E-02	8.4E-01	3.8E-02
SMARCA4	7.9E-01	8.1E-05	8.8E-01	4.5E-12	9.9E-01	6.0E-02	2.0E+00	5.7E-05	7.1E-01	5.4E-07	3.2E-01	1.8E-03	-3.9E-01	7.6E-10	9.9E-02	2.1E-01	1.0E+00	8.2E-10	4.5E-01	6.4E-05	7.2E-01	5.6E-06	1.1E+00	1.0E-02
SMC2	1.2E+00	5.7E-04	5.9E-01	6.8E-10	2.3E+00	2.2E-01	1.5E+00	7.5E-03	7.7E-01	1.2E-04	2.2E-01	3.5E-01	-1.2E-01	1.1E-01	-2.1E-01	1.7E-01	1.1E+00	2.5E-08	7.9E-01	3.6E-05	1.8E+00	2.4E-11	1.3E+00	1.5E-01
SMC4	1.2E+00	2.8E-04	1.5E+00	8.3E-21	3.5E+00	2.1E-01	2.0E+00	7.5E-03	7.8E-01	1.3E-06	1.1E+00	1.4E-02	7.5E-01	1.1E-08	5.8E-01	1.7E-02	1.3E+00	9.7E-08	6.2E-01	2.4E-04	1.7E+00	1.6E-12	2.0E+00	2.8E-03
SMG7	8.7E-01	1.5E-05	7.5E-01	8.5E-25	4.5E-01	1.5E-01	1.3E+00	1.1E-03	4.3E-01	1.1E-03	4.2E-01	3.5E-02	1.1E-01	1.0E-02	2.2E-01	9.6E-02	7.4E-01	3.5E-08	5.8E-01	1.3E-11	7.8E-01	3.7E-12	6.0E-01	2.2E-02
SNRPB	9.7E-01	3.3E-05	8.6E-01	4.7E-20	1.3E+00	1.9E-02	1.6E+00	7.8E-04	1.0E+00	1.4E-05	8.4E-01	3.2E-06	5.7E-01	5.3E-08	1.0E+00	2.5E-06	1.0E+00	1.2E-09	6.8E-01	1.6E-06	1.3E+00	7.1E-11	1.0E+00	5.1E-03
SNRPD1	8.1E-01	4.8E-06	7.3E-01	3.1E-18	1.1E+00	7.5E-02	1.5E+00	1.7E-04	4.8E-01	1.1E-02	1.5E-01	2.9E-01	3.3E-01	2.5E-07	2.4E-01	2.9E-02	6.5E-01	5.0E-08	8.5E-01	1.2E-09	1.4E+00	3.9E-08	1.1E+00	6.1E-03
SNRPD2	3.8E-01	1.2E-02	3.4E-01	7.4E-06	7.8E-01	4.7E-01	1.1E+00	9.1E-03	6.1E-01	3.4E-04	2.4E-01	8.7E-02	5.2E-01	1.3E-06	5.6E-01	1.8E-04	7.3E-01	1.1E-04	6.1E-01	9.3E-07	9.4E-01	2.1E-08	4.0E-01	8.8E-02
SNRPE	6.8E-01	1.7E-05	9.7E-01	6.4E-19	1.2E+00	4.5E-01	1.6E+00	6.5E-04	6.6E-01	1.2E-05	-1.7E-01	1.6E-01	4.4E-01	5.9E-07	3.0E-01	3.8E-02	1.1E+00	1.9E-07	1.1E+00	2.4E-13	1.3E+00	1.2E-10	7.4E-01	5.6E-03
SNRPF	9.9E-01	6.9E-05	6.9E-01	7.1E-16	1.3E+00	1.1E-01	4.3E-01	2.3E-01	7.4E-01	6.3E-06	4.2E-01	1.5E-04	5.0E-01	1.9E-06	7.2E-01	5.1E-06	1.8E-01	5.3E-02	6.5E-01	6.5E-07	1.1E+00	1.4E-08	1.2E+00	1.1E-02
SOX12	9.5E-01	7.2E-02	1.5E+00	6.9E-18	-4.3E-01	6.8E-01	1.9E+00	3.9E-04	1.3E+00	3.1E-03	8.7E-01	2.9E-04	4.2E-01	1.1E-04	6.2E-01	2.4E-03	1.4E+00	1.9E-05	1.2E+00	4.9E-08	1.9E+00	2.7E-07	1.4E+00	2.5E-02
SPAG5	2.2E+00	2.0E-06	2.7E+00	1.4E-19	3.9E+00	9.1E-03	1.1E+00	2.7E-02	8.9E-01	3.0E-05	-1.3E+00	3.7E-02	-4.5E-01	5.8E-02	-1.9E+00	3.2E-05	1.1E+00	1.0E-04	3.4E+00	1.7E-09	3.8E+00	3.3E-12	3.7E+00	3.1E-02
SPATS2	7.1E-01	2.5E-04	7.8E-01	7.4E-20	7.3E-01	2.0E-01	2.9E+00	1.1E-04	5.2E-01	7.2E-08	4.4E-01	7.6E-03	2.8E-01	1.0E-05	4.5E-01	2.6E-04	1.6E+00	1.6E-11	1.2E+00	1.1E-12	1.3E+00	1.1E-15	1.5E+00	8.7E-02
SPC24	1.4E+00	9.6E-03	2.8E+00	1.3E-15	4.0E+00	7.7E-02	3.5E+00	6.2E-03	9.2E-01	1.1E-05	2.0E+00	8.2E-02	1.7E+00	8.3E-10	2.6E+00	8.4E-05	3.4E+00	2.9E-07	3.0E+00	3.0E-10	3.6E+00	1.1E-11	3.4E+00	3.3E-02
SPC25	1.9E+00	1.5E-04	2.9E+00	2.1E-26	4.8E+00	1.2E-03	4.6E+00	2.3E-03	1.2E+00	2.9E-08	1.4E+00	8.1E-02	1.9E+00	7.0E-10	2.8E+00	1.2E-03	3.4E+00	1.1E-08	3.0E+00	1.2E-11	4.0E+00	3.7E-14	4.2E+00	5.7E-03
SRD5A3	7.7E-01	1.4E-02	1.1E+00	2.2E-12	1.4E+00	5.1E-01	3.5E-01	8.1E-02	7.2E-01	2.4E-02	-5.8E-01	1.2E-04	8.3E-01	4.2E-17	3.6E-01	1.9E-03	6.0E-01	4.4E-04	1.8E+00	3.8E-09	9.2E-01	1.0E-04	1.6E+00	2.3E-02
SRM	6.7E-01	1.3E-04	1.7E-01	5.7E-02	-1.7E-01	3.2E-01	6.4E-01	1.8E-01	1.0E+00	5.4E-09	2.4E-01	2.8E-01	8.0E-01	9.7E-09	1.0E+00	4.9E-07	7.6E-01	3.2E-06	1.1E+00	1.3E-12	9.0E-01	5.7E-08	2.9E-01	1.7E-01
SRPRB	6.7E-01	1.5E-02	7.4E-01	6.5E-18	6.9E-01	3.5E-01	-2.1E-01	6.3E-02	7.5E-01	3.2E-03	1.2E-01	3.7E-01	-1.2E-02	8.6E-01	4.3E-01	3.4E-05	4.3E-01	1.0E-04	1.0E+00	1.3E-14	1.3E+00	6.3E-06	8.1E-01	3.6E-02
SSBP1	4.6E-01	7.8E-03	5.2E-01	1.5E-11	4.8E-01	5.6E-01	2.4E-01	1.7E-01	7.7E-01	2.1E-06	6.2E-01	3.8E-06	5.4E-01	2.0E-09	6.1E-01	3.5E-04	3.3E-01	2.4E-05	7.3E-01	2.1E-13	7.9E-01	2.4E-10	7.4E-01	8.2E-03
TACC3	1.3E+00	2.4E-04	2.0E+00	7.3E-22	3.5E+00	1.6E-01	3.1E+00	6.6E-03	7.2E-01	3.0E-04	9.6E-01	1.4E-02	1.4E+00	2.3E-12	1.5E+00	8.3E-06	2.1E+00	1.1E-10	1.7E+00	1.9E-11	2.1E+00	3.8E-12	3.4E+00	1.8E-02
TBC1D3G	6.9E-01	4.1E-01	1.1E+00	1.7E-01	3.6E+00	4.2E-01	3.1E+00	4.6E-02	8.8E-01	2.0E-01	-4.9E-01	4.4E-01	1.7E+00	1.7E-03	3.0E+00	1.4E-02	4.4E-02	9.4E-01	3.9E-01	3.7E-01	-6.3E-02	8.8E-01	2.4E+00	2.3E-01
TBC1D3H	3.3E-01	3.6E-01	4.4E-01	6.3E-02	3.9E-01	5.7E-01	2.1E+00	4.4E-02	5.8E-01	1.2E-01	3.5E-01	4.1E-01	9.3E-01	3.0E-03	1.5E+00	2.1E-02	-4.2E-02	8.4E-01	5.2E-01	2.3E-03	1.9E-01	4.4E-01	-3.9E-01	7.1E-01
TELO2	2.4E-01	2.2E-02	5.7E-01	2.3E-09	4.3E-01	1.3E-01	9.3E-01	7.1E-04	8.7E-01	1.8E-09	6.5E-01	9.0E-05	3.3E-01	1.2E-05	6.4E-01	2.6E-06	6.2E-01	4.4E-07	6.6E-01	3.3E-09	6.3E-01	1.6E-07	2.0E-01	2.8E-01
TFAP4	1.3E+00	3.4E-06	3.4E-01	5.0E-04	1.7E-01	8.9E-01	1.9E+00	1.1E-05	1.6E+00	1.3E-11	5.2E-01	1.8E-02	4.3E-01	1.7E-04	8.0E-01	4.9E-04	6.7E-01	6.5E-07	1.1E+00	1.4E-13	1.9E+00	1.2E-08	-7.7E-02	7.8E-01
TFRC	2.0E+00	1.6E-02	1.1E+00	1.2E-08	2.1E+00	1.8E-01	1.6E+00	9.4E-03	6.9E-01	1.0E-03	1.4E+00	2.4E-02	1.1E-01	4.1E-01	-4.9E-01	1.6E-02	1.1E+00	4.8E-07	-1.0E+00	8.6E-09	1.5E+00	1.5E-04	1.3E+00	2.3E-02
THOC3	7.9E-01	1.5E-02	8.1E-01	3.9E-19	2.2E+00	8.4E-02	6.5E-01	1.4E-02	7.7E-01	4.3E-06	-5.7E-02	7.1E-01	3.0E-01	1.7E-04	3.3E-01	1.9E-02	2.4E-01	5.3E-03	9.8E-01	1.2E-15	2.1E+00	9.0E-08	1.2E+00	2.3E-02
TIMELESS	1.7E+00	1.4E-05	1.5E+00	5.7E-22	3.1E+00	6.5E-02	8.7E-01	1.6E-02	1.0E+00	2.0E-07	2.5E-01	3.0E-01	-1.2E-01	1.7E-01	9.0E-01	5.6E-05	7.2E-01	3.8E-06	1.8E+00	1.9E-10	2.4E+00	7.7E-15	2.5E+00	2.7E-03
TIMM10	3.8E-01	2.8E-02	5.8E-01	4.4E-05	1.6E+00	4.2E-01	-5.8E-01	1.6E-02	3.9E-01	5.0E-03	9.2E-01	2.3E-05	3.3E-01	2.5E-05	4.4E-02	7.1E-01	4.1E-01	6.6E-03	6.5E-01	1.3E-10	7.1E-01	1.3E-06	9.2E-01	6.6E-03
TKT	5.7E-01	1.0E-02	-4.3E-01	2.2E-03	1.2E+00	1.8E-01	1.0E+00	1.6E-01	8.8E-01	8.9E-11	9.7E-01	3.2E-06	1.3E-01	1.5E-01	1.8E+00	1.4E-06	1.6E+00	8.5E-05	6.2E-01	1.8E-04	1.7E-01	2.0E-01	1.1E+00	2.8E-02
TOMM40	7.1E-01	5.5E-04	8.7E-01	4.4E-15	1.4E+00	1.2E-02	6.0E-01	2.2E-02	5.6E-01	2.8E-05	1.2E+00	1.1E-08	3.4E-01	5.5E-05	5.5E-01	2.7E-04	7.8E-01	2.4E-10	1.0E+00	7.2E-05	1.3E+00	6.4E-12	1.1E+00	4.7E-04
TOP2A	2.2E+00	7.6E-06	3.4E+00	1.9E-08	5.8E+00	6.5E-02	5.6E+00	7.5E-03	1.5E+00	1.2E-09	2.9E+00	8.3E-02	2.1E+00	5.0E-08	4.3E+00	6.8E-04	4.0E+00	3.9E-07	4.2E+00	8.6E-11	4.8E+00	1.7E-13	3.6E+00	1.1E-02
TOPBP1	1.3E+00	4.3E-03	4.9E-01	7.7E-09	1.7E+00	1.7E-01	1.3E+00	1.0E-03	7.6E-01	4.8E-08	8.3E-01	3.3E-03	5.8E-01	9.0E-11	7.0E-01	1.1E-06	9.5E-01	4.2E-09	8.9E-01	3.5E-08	1.9E+00	3.0E-08	6.0E-01	1.2E-03
TPI1	7.7E-01	1.2E-04	7.8E-01	1.2E-11	1.8E+00	1.9E-01	2.5E-01	2.8E-01	1.6E-01	1.2E-01	4.4E-01	1.6E-03	1.2E+00	1.0E-18	6.5E-01	8.2E-07	1.6E-01	1.1E-01	1.1E+00	6.6E-14	1.7E+00	1.6E-09	2.0E+00	8.3E-02
TPX2	2.3E+00	5.6E-06	3.0E+00	1.1E-19	5.8E+00	4.8E-02	3.2E+00	9.2E-03	2.0E+00	4.0E-08	3.4E+00	5.8E-02	2.3E+00	3.4E-08	3.8E+00	6.9E-04	2.1E+00	5.9E-08	4.0E+00	3.1E-10	4.8E+00	7.7E-16	4.5E+00	4.6E-03
TRAF2	6.7E-01	1.5E-03	8.5E-01	7.7E-18	1.7E+00	7.3E-02	1.6E+00	7.0E-03	5.6E-01	8.0E-09	8.5E-01	3.3E-06	9.5E-01	4.9E-15	8.7E-01	1.1E-07	8.8E-01	1.6E-12	7.4E-01	5.2E-09	7.5E-01	1.2E-04	2.9E-01	1.2E-01
TRAIP	1.7E+00	1.2E-05	1.1E+00	1.5E-12	2.2E+00	1.6E-01	2.9E+00	1.1E-03	1.0E+00	1.4E-08	1.0E+00	1.9E-02	4.6E-01	1.8E-03	1.5E+00	2.4E-08	3.0E+00	5.8E-10	2.0E+00	3.5E-11	2.4E+00	3.2E-14	2.2E+00	9.7E-03
TSEN54	8.1E-01	8.9E-06	9.1E-01	3.6E-15	1.3E+00	1.6E-01	1.5E+00	1.0E-03	5.0E-01	1.8E-05	-4.6E-02	7.2E-01	-2.2E-01	7.1E-04	4.5E-01	7.4E-04	9.8E-01	1.3E-09	5.8E-01	2.1E-10	6.1E-01	3.3E-06	6.3E-01	8.5E-04
TTF2	1.6E+00	7.2E-05	6.0E-01	2.4E-07	1.9E+00	2.1E-01	2.4E+00	4.7E-05	9.4E-01	1.7E-07	3.7E-01	5.1E-03	6.7E-02	2.6E-01	7.3E-01	5.3E-06	1.3E+00	5.3E-06	9.9E-01	7.6E-10	1.7E+00	2.4E-12	1.4E+00	8.6E-03
TUBA1B	3.6E-01	1.5E-01	7.2E-01	1.8E-17	8.5E-01	8.1E-02	1.4E+00	1.5E-02	2.6E-01	6.6E-02	1.1E+00	8.7E-05	1.4E+00	7.1E-15	1.5E+00	7.2E-10	9.6E-01	9.4E-11	3.1E-01	3.4E-03	5.5E-01	2.8E-08	1.1E+00	3.2E-02
TUBB	1.2E+00	2.2E-02	6.9E-01	3.7E-18	4.4E-01	2.4E-01	9.9E-01	3.3E-03	4.3E-01	2.7E-03	6.2E-02	8.8E-01	9.3E-01	9.7E-16	9.6E-01	2.9E-06	5.4E-01	5.0E-05	9.0E-01	1.2E-09	1.3E+00	3.6E-11	7.3E-01	1.6E-02
TUBB8	1.4E+00	6.7E-03	1.1E+00	1.9E-11	2.0E+00	1.8E-01	2.4E+00	1.7E-02	3.1E-01	1.2E-02	2.3E-01	2.9E-01	-8.9E-01	4.8E-07	-2.4E-01	2.3E-01	5.9E-01	2.7E-02	6.6E-01	6.3E-04	9.8E-01	1.5E-03	1.8E+00	3.2E-02
TUBG1	9.4E-01	3.8E-05	9.4E-01	4.8E-18	1.6E+00	1.3E-01	8.9E-01	3.9E-02	5.7E-01	9.7E-06	-1.2E-01	4.0E-01	-1.1E-01	2.2E-01	5.2E-01	9.8E-04	9.8E-01	2.0E-11	1.1E+00	6.6E-13	1.4E+00	4.3E-12	1.1E+00	2.8E-02
TXN	8.0E-01	2.5E-01	8.3E-01	9.0E-15	1.8E+00	1.9E-01	-7.1E-02	8.5E-01	2.1E-02	8.5E-01	-2.0E-01	2.8E-01	1.1E-01	3.9E-01	7.1E-01	2.0E-02	6.8E-01	3.6E-03	9.0E-01	2.5E-04	1.4E+00	2.1E-05	7.6E-01	2.0E-01
TYMS	1.3E+00	4.0E-03	2.0E+00	5.1E-13	4.3E+00	1.5E-01	2.0E+00	5.9E-03	4.4E-01	1.7E-01	8.2E-01	2.6E-01	2.3E+00	2.3E-21	2.0E+00	2.3E-08	1.8E+00	9.2E-07	2.3E+00	1.6E-10	2.8E+00	1.9E-10	2.5E+00	8.4E-03
UBE2I	1.2E-01	2.3E-01	5.5E-01	5.0E-18	3.0E-01	9.8E-02	1.3E+00	6.4E-04	8.4E-01	8.5E-11	9.0E-01	3.1E-06	6.7E-01	1.4E-14	1.0E+00	5.2E-10	4.3E-01	3.9E-05	6.3E-01	3.1E-17	6.9E-01	3.4E-09	9.7E-02	2.6E-01
UBE2S	1.2E+00	3.0E-03	2.2E+00	8.0E-15	2.7E+00	1.1E-01	2.3E+00	2.0E-02	1.4E+00	1.3E-08	1.1E+00	5.6E-04	5.6E-01	1.4E-03	8.2E-01	1.2E-03	1.8E+00	1.5E-11	1.9E+00	1.6E-06	2.8E+00	3.4E-10	2.4E+00	2.1E-02
UTP20	6.4E-01	1.2E-03	9.2E-02	2.0E-01	-1.9E-01	7.2E-01	1.8E+00	3.2E-04	8.3E-01	1.5E-06	1.9E+00	5.2E-05	3.8E-01	1.3E-05	8.8E-01	3.2E-05	6.3E-01	7.6E-08	6.4E-01	1.2E-07	6.5E-01	1.3E-08	-2.0E-01	5.1E-01
VARS	9.8E-01	3.0E-04	4.8E-01	1.0E-09	4.6E-01	3.2E-01	9.5E-01	9.0E-08	8.8E-01	4.0E-09	1.8E-02	9.4E-01	2.8E-01	2.3E-05	7.1E-01	1.1E-05	9.3E-01	8.8E-09	1.3E+00	3.1E-14	9.8E-01	2.0E-08	7.8E-01	3.9E-04
WDR12	7.9E-01	3.1E-06	5.0E-01	2.3E-10	6.5E-01	1.7E-01	1.2E+00	1.2E-04	1.0E+00	7.1E-08	-4.1E-01	2.0E-02	-7.0E-02	2.3E-01	4.0E-01	4.7E-03	6.1E-01	2.5E-10	1.3E+00	1.9E-16	1.9E+00	1.5E-05	1.6E+00	6.9E-03
WDR4	1.0E+00	8.8E-04	4.4E-01	1.5E-06	8.5E-01	6.4E-02	1.1E+00	2.4E-04	1.2E+00	1.1E-07	-8.2E-02	6.5E-01	1.8E-01	1.1E-02	4.6E-01	2.2E-02	1.1E+00	1.3E-07	9.6E-01	2.5E-11	1.3E+00	2.4E-08	4.6E-01	1.0E-01
XPO5	7.7E-01	1.3E-05	7.6E-01	7.3E-11	8.8E-01	1.5E-01	1.4E+00	1.1E-04	1.2E+00	7.6E-10	-3.2E-01	1.4E-01	-2.9E-02	5.6E-01	9.0E-01	2.6E-05	1.0E+00	3.2E-10	1.1E+00	1.8E-13	1.5E+00	4.1E-14	1.2E+00	1.1E-02
XRCC2	2.4E+00	5.7E-07	1.6E+00	2.0E-16	3.2E+00	9.1E-03	3.6E+00	6.5E-03	2.0E+00	1.7E-09	1.5E+00	1.0E-02	1.2E+00	2.4E-07	2.1E+00	5.0E-04	2.6E+00	6.2E-07	3.1E+00	3.0E-10	3.9E+00	8.2E-15	2.6E+00	2.5E-03
XRCC3	1.3E+00	2.8E-06	3.7E-01	3.6E-05	2.3E+00	8.3E-02	1.5E+00	1.1E-02	8.9E-01	2.3E-06	1.0E+00	1.5E-03	4.5E-01	6.9E-06	1.0E+00	2.1E-05	1.6E+00	1.3E-06	8.3E-01	4.1E-07	1.6E+00	3.0E-10	8.9E-01	8.6E-02
YARS	6.8E-01	1.4E-03	6.3E-01	1.5E-14	1.6E+00	1.2E-01	-1.8E-02	9.5E-01	8.3E-01	3.3E-08	9.7E-01	4.2E-06	4.4E-01	2.6E-09	4.8E-01	2.1E-04	1.8E-01	1.6E-01	5.9E-01	8.5E-12	5.8E-01	3.9E-07	1.1E+00	1.4E-02
YKT6	7.0E-01	6.2E-04	5.8E-01	1.5E-15	2.7E-01	5.2E-01	1.6E+00	1.5E-04	2.2E-01	1.8E-02	1.0E+00	5.2E-08	5.4E-02	3.9E-01	5.9E-01	2.2E-08	8.4E-01	1.2E-08	8.5E-01	1.3E-10	1.0E+00	1.0E-07	1.0E+00	2.7E-02
ZC3H3	4.9E-01	7.4E-05	8.3E-01	8.7E-15	5.0E-01	4.8E-01	8.2E-01	3.3E-03	4.4E-01	2.0E-04	7.9E-01	1.5E-04	4.8E-01	8.6E-06	5.1E-01	3.7E-04	1.1E+00	7.4E-12	5.3E-01	9.8E-06	6.9E-01	8.9E-09	8.0E-01	1.1E-01
ZWINT	1.9E+00	1.3E-04	2.4E+00	1.4E-23	4.6E+00	2.9E-02	3.6E+00	5.9E-03	7.3E-01	4.3E-04	-1.9E-01	5.2E-01	5.7E-01	9.8E-07	9.0E-01	4.3E-04	2.3E+00	4.4E-08	2.7E+00	2.0E-12	3.2E+00	7.5E-12	3.8E+00	1.8E-04

Supplementary Table 2. Candidate drugs.

1	(3AR,6R,6AS)-6-((S)-((S)-CYCLOHEX-2-ENYL)(HYDROXY)METHYL)-6A-METHYL-4-OXO-HEXAHYDRO-2H-FURO[3,2-C]PYRROLE-6-CARBALDEHYDE
2	L-ASPARTIC ACID
3	2'-MONOPHOSPHOADENOSINE 5'-DIPHOSPHORIBOSE
4	URIDINE-DIPHOSPHATE-N-ACETYLGLUCOSAMINE
5	DB04395
6	BORTEZOMIB
7	CARFILZOMIB
8	ANISOMYCIN
9	PUROMYCIN
10	L-TYROSINE
11	TYROSINAL
12	N6-ISOPENTENYL-ADENOSINE-5'-MONOPHOSPHATE
13	DB08617
14	L-GLUTAMINE
15	L-VALINE
16	PHOSPHONOTHREONINE
17	COENZYME A
18	EPOTHILONE B
19	CYT997
20	2-MERCAPTO-N-[1,2,3,10-TETRAMETHOXY-9-OXO-5,6,7,9-TETRAHYDRO-BENZO[A]HEPTALEN-7-YL]ACETAMIDE
21	VINCRISTINE
22	VINBLASTINE
23	COLCHICINE
24	VINORELBINE
25	GLUTATHIONE
26	GLYCINE
27	L-CYSTEINE
28	GAMMA-GLUTAMYLCYSTEINE
29	ADENOSINE-5'-[BETA, GAMMA-METHYLENE]TRIPHOSPHATE
30	3-PHOSPHOGLYCERIC ACID
31	DACARBAZINE
32	TETRAHYDROFOLIC ACID
33	PEMETREXED
34	5--MONOPHOSPHATE-9-BETA-D-RIBOFURANOSYL XANTHINE
35	BETA-DADF, MSA, MULTISUBSTRATE ADDUCT INHIBITOR
36	L-GLUTAMIC ACID
37	PHOSPHOGLYCOLOHYDROXAMIC ACID
38	[2(FORMYL-HYDROXY-AMINO)-ETHYL]-PHOSPHONIC ACID
39	PYRIDOXAL PHOSPHATE
40	CLADRIBINE
41	DB03280

42	3'-AZIDO-3'-DEOXYTHYMIDINE-5'-MONOPHOSPHATE
43	P1-(5'-ADENOSYL)P5-(5'-(3'AZIDO-3'-DEOXYTHYMIDYL))PENTAPHOSPHATE
44	DECITABINE
45	PROCAINAMIDE
46	1,6-FRUCTOSE DIPHOSPHATE (LINEAR FORM)
47	CAPECITABINE
48	FLOXURIDINE
49	LEUCOVORIN
50	RALTITREXED
51	6-ETHYL-5-PHENYLPYRIMIDINE-2,4-DIAMINE
52	N-(3,5-DIMETHOXYPHENYL)IMIDODICARBONIMIDIC DIAMIDE
53	10-PROPARGYL-5,8-DIDEAZAFOLIC ACID
54	S,S-(2-HYDROXYETHYL)THIOCYSTEINE
55	GEMCITABINE
56	TRIMETHOPRIM
57	TRIFLURIDINE
58	(5S)-5-(3-AMINOPROPYL)-3-(2,5-DIFLUOROPHENYL)-N-ETHYL-5-PHENYL-4,5-DIHYDRO-1H-PYRAZOLE-1-CARBOXAMIDE
59	(2S)-4-(2,5-DIFLUOROPHENYL)-N,N-DIMETHYL-2-PHENYL-2,5-DIHYDRO-1H-PYRROLE-1-CARBOXAMIDE
60	(2S)-4-(2,5-DIFLUOROPHENYL)-N-METHYL-2-PHENYL-N-PIPERIDIN-4-YL-2,5-DIHYDRO-1H-PYRROLE-1-CARBOXAMIDE
61	(5R)-N,N-DIETHYL-5-METHYL-2-[(THIOPHEN-2-YLCARBONYL)AMINO]-4,5,6,7-TETRAHYDRO-1-BENZOTHIOPHENE-3-CARBOXAMIDE
62	MONASTROL
63	3-[(5S)-1-ACETYL-3-(2-CHLOROPHENYL)-4,5-DIHYDRO-1H-PYRAZOL-5-YL]PHENOL
64	ADENOSINE-5-DIPHOSPHORIBOSE
65	4-(2-AMINOETHYL)BENZENESULFONYL FLUORIDE
66	BLEOMYCIN
67	AT9283
68	HESPERIDIN
69	4-(4-METHYLPIPERAZIN-1-YL)-N-[5-(2-THIENYLACETYL)-1,5-DIHYDROPYRROLO[3,4-C]PYRAZOL-3-YL]BENZAMIDE
70	N-[3-(1H-BENZIMIDAZOL-2-YL)-1H-PYRAZOL-4-YL]BENZAMIDE
71	2-[(5,6-DIPHENYLFURO[2,3-D]PYRIMIDIN-4-YL)AMINO]ETHANOL
72	18-CHLORO-11,12,13,14-TETRAHYDRO-1H,10H-8,4-(AZENO)-9,15,1,3,6-BENZODIOXATRIAZACYCLOHEPTADECIN-2-ONE
73	1-(5-CHLORO-2,4-DIMETHOXYPHENYL)-3-(5-CYANOPYRAZIN-2-YL)UREA
74	(2R)-1-[(5,6-DIPHENYL-7H-PYRROLO[2,3-D]PYRIMIDIN-4-YL)AMINO]PROPAN-2-OL
75	2-[5,6-BIS-(4-METHOXY-PHENYL)-FURO[2,3-D]PYRIMIDIN-4-YLAMINO]-ETHANOL
76	DB07243
77	REL-(9R,12S)-9,10,11,12-TETRAHYDRO-9,12-EPOXY-1H-DIINDOLO[1,2,3-FG:3',2',1'-KL]PYRROLO[3,4-I][1,6]BENZODIAZOCINE-1,3(2H)-DIONE
78	1-[(2S)-4-(5-PHENYL-1H-PYRAZOLO[3,4-B]PYRIDIN-4-YL)MORPHOLIN-2-

	YL]METHANAMINE
79	N-(4-OXO-5,6,7,8-TETRAHYDRO-4H-[1,3]THIAZOLO[5,4-C]AZEPIN-2-YL)ACETAMIDE
80	2-(METHYLSULFANYL)-5-(THIOPHEN-2-YLMETHYL)-1H-IMIDAZOL-4-OL
81	1-[(2S)-4-(5-BROMO-1H-PYRAZOLO[3,4-B]PYRIDIN-4-YL)MORPHOLIN-2-YL]METHANAMINE
82	1-(5-CHLORO-2-METHOXYPHENYL)-3-{6-[2-(DIMETHYLAMINO)-1-METHYLETHOXY]PYRAZIN-2-YL}UREA
83	(5-{3-[5-(PIPERIDIN-1-YLMETHYL)-1H-INDOL-2-YL]-1H-INDAZOL-6-YL}-2H-1,2,3-TRIAZOL-4-YL)METHANOL
84	2-(CYCLOHEXYLAMINO)BENZOIC ACID
85	(2S)-1-AMINO-3-[(5-NITROQUINOLIN-8-YL)AMINO]PROPAN-2-OL
86	2,2'-{[9-(HYDROXYIMINO)-9H-FLUORENE-2,7-DIYL]BIS(OXY)}DIACETIC ACID
87	N-{5-[4-(4-METHYLPIPERAZIN-1-YL)PHENYL]-1H-PYRROLO[2,3-B]PYRIDIN-3-YL}NICOTINAMIDE
88	SU9516
89	ALSTERPAULLONE
90	HYMENIALDISINE
91	AT7519
92	OLOMOUCINE
93	INDIRUBIN-3'-MONOXIME
94	DOXORUBICIN
95	TENIPOSIDE
96	VALRUBICIN
97	IDARUBICIN
98	EPIRUBICIN
99	MITOXANTRONE
100	DAUNORUBICIN
101	AMONAFIDE
102	ELSAMITRUCIN
103	BANOXANTRONE
104	GENISTEIN
105	FINAFLOXACIN
106	LUCANTHONE
107	FLEROXACIN
108	SPARFLOXACIN
109	OFLOXACIN
110	LEVOFLOXACIN
111	NORFLOXACIN
112	LOMEFLOXACIN
113	TROVAFLOXACIN
114	CIPROFLOXACIN
115	PEFLOXACIN
116	ENOXACIN
117	DEXRAZOXANE

118	AMSACRINE
119	MOTEXAFIN GADOLINIUM
120	IMEXON
121	GALLIUM NITRATE
122	4-[(7-OXO-7H-THIAZOLO[5,4-E]INDOL-8-YLMETHYL)-AMINO]-N-PYRIDIN-2-YL-BENZENESULFONAMIDE
123	2-ANILINO-6-CYCLOHEXYLMETHOXYPURINE
124	(2S)-N-[(3Z)-5-CYCLOPROPYL-3H-PYRAZOL-3-YLIDENE]-2-[4-(2-OXOIMIDAZOLIDIN-1-YL)PHENYL]PROPANAMIDE
125	6-CYCLOHEXYLMETHOXY-2-(3'-CHLOROANILINO) PURINE
126	5-[5,6-BIS(METHYLOXY)-1H-BENZIMIDAZOL-1-YL]-3-{[1-(2-CHLOROPHENYL)ETHYL]OXY}-2-THIOPHENECARBOXAMIDE
127	N-[4-(2,4-DIMETHYL-THIAZOL-5-YL)-PYRIMIDIN-2-YL]-N',N'-DIMETHYL-BENZENE-1,4-DIAMINE
128	1-(3,5-DICHLOROPHENYL)-5-METHYL-1H-1,2,4-TRIAZOLE-3-CARBOXYLIC ACID
129	HYDROXY(OXO)(3-{[(2Z)-4-[3-(1H-1,2,4-TRIAZOL-1-YLMETHYL)PHENYL]PYRIMIDIN-2(5H)-YLIDENE]AMINO}PHENYL)AMMONIUM
130	4-METHYL-5-{(2E)-2-[(4-MORPHOLIN-4-YLPHENYL)IMINO]-2,5-DIHYDROPYRIMIDIN-4-YL}-1,3-THIAZOL-2-AMINE
131	4-(6-CYCLOHEXYLMETHOXY-9H-PURIN-2-YLAMINO)--BENZAMIDE
132	3-(6-CYCLOHEXYLMETHOXY-9H-PURIN-2-YLAMINO)-BENZENESULFONAMIDE
133	3-({2-[(4-{[6-(CYCLOHEXYLMETHOXY)-9H-PURIN-2-YL]AMINO}PHENYL)SULFONYL]ETHYL}AMINO)PROPAN-1-OL
134	4-{[4-AMINO-6-(CYCLOHEXYLMETHOXY)-5-NITROSOPYRIMIDIN-2-YL]AMINO}BENZAMIDE
135	DB06963

Supplementary Table 3. Data description.

Data description for each evaluation and figure, software or package generating the figures, and other related details

Figures		Datasets	Softwares	Packages	Commands
Fig 1		Three essential gene sets generated by different experimental methods (Science.350(6264):1096-101; Cell. 163(6):1515-26; Science. 350(6264):1092-6)	python	-	-
Fig2	A	Expression of genes in ten groups. Expression of each gene was calculated as the mean RPKM level of 2,916 individuals from the GTEx program (Consortium 2013, http://commonfund.nih.gov/GTEx/).	python	python matplotlib package (visualization)	matplotlib.pyplot.violinplot()
	B	Protein-protein associations were obtained from STRING database (Nucleic acids research, 2014, 43(D1): D447-D452.) (version: 10.5).	python; Centiscape (Connectivity degree calculation; http://apps.cytoscape.org/apps/centiscape)	python matplotlib package (visualization)	matplotlib.pyplot.bar()
	C	Gene length was calculated based on Genecode v19 annotation (https://www.gencodegenes.org/)	python	python scipy package (statistical tests); python matplotlib package (visualization)	scipy.stats.pearsonr(); matplotlib.pyplot.plot()
	D	Gene length and transcription count was calculated based on Genecode v19 annotation (https://www.gencodegenes.org/)	python	python scipy package (statistical tests);python matplotlib package (visualization)	scipy.stats.pearsonr(); matplotlib.pyplot.scatter();matplotlib.pyplot.plot();
	E	Genomic coordinates of gene TSSs were calculated based on Genecode v19 annotation (https://www.gencodegenes.org/)	python	python matplotlib package (visualization)	matplotlib.pyplot.imshow()

	F	Genomic coordinates of gene TSSs were calculated based on Genecode v19 annotation (https://www.gencodegenes.org/)	python	python scipy package (statistical tests);python matplotlib package (visualization)	scipy.stats.pearsonr(); matplotlib.pyplot.plot()
	G, H, I	Dnase-seq, Chip-seq data of H1-hESC cell line is downloaded from ENCODE (http://hgdownload.soe.ucsc.edu/goldenPath/hg19/encodeDCC/wgEncodeUwDnase/; http://hgdownload.soe.ucsc.edu/goldenPath/hg19/encodeDCC/wgEncodeBroadHistone/)	python	python matplotlib package (visualization)	matplotlib.pyplot.plot()
Fig3	A	Gene age are defined by the evolutionarily most distant species group where homologs can be found. Data used: (Proceedings of the National Academy of Sciences, 2009, 106(18): 7273-7280)	python	python scipy package (statistical tests);python matplotlib package (visualization)	scipy.stats.pearsonr(); matplotlib.pyplot.plot();
	B	Gene age data (Proceedings of the National Academy of Sciences, 2009, 106(18): 7273-7280); Gene length was calculated based on Genecode v19 annotation (https://www.gencodegenes.org/)	python	python matplotlib package (visualization)	matplotlib.pyplot.scatter()
	C	Gene age data (Proceedings of the National Academy of Sciences, 2009, 106(18): 7273-7280)	python	python scipy package (statistical tests);python matplotlib package (visualization)	scipy.stats.fisher_exact(); matplotlib.pyplot.bar()
	D	Gene age data (Proceedings of the National Academy of Sciences, 2009, 106(18): 7273-7280)	python	python scipy package (statistical tests);python matplotlib package (visualization)	scipy.stats.ttest_ind(); matplotlib.pyplot.boxplot()

	E	Essential genes of various species from DEG database (http://essentialgene.org/); Protein-protein associations were obtained from STRING database (Nucleic acids research, 2014, 43(D1): D447-D452.) (version: 10.5).	Cytoscape (PPI network visualization; https://cytoscape.org/download.html)	-	-
Fig4	A	Gene Expression Om-nibus (GEO) (Accession No. GSE66582)	python	python matplotlib package (visualization)	matplotlib.pyplot.plot()
	B	Gene Expression Om-nibus (GEO) (Accession No. GSE66390)	python	python matplotlib package (visualization)	matplotlib.pyplot.plot()
	C	Gene Expression Om-nibus (GEO) (Accession No. GSE71434)	python	python matplotlib package (visualization)	matplotlib.pyplot.plot()
	D	Gene Expression Om-nibus (GEO) (Accession No. GSE71434) and H3K4me3 for H7es and derived cells were from ENCODE project	python	python matplotlib package (visualization)	matplotlib.pyplot.plot()
	E	Gene Expression Om-nibus (GEO) (Accession No. GSE76505)	python	python matplotlib package (visualization)	matplotlib.pyplot.plot()
	F	Gene Expression Om-nibus (GEO) (Accession No. GSE66582 and GSE76505)	python	python matplotlib package (visualization)	matplotlib.pyplot.plot()
Fig5	A	Cancer gene lists are from: (Nature, 2013, 502(7471): 333)(Nature, 2014, 505(7484): 495.)(Bioinformatics, 2014, 30(17): i549-i555)(science, 2013, 339(6127): 1546-1558)(Nature medicine, 2017, 23(6): 703)	python	python scipy package (statistical tests);python matplotlib package (visualization)	scipy.stats.fisher_exact(); matplotlib.pyplot.bar()
	B	Gene expression datasets were downloaded from TCGA project (https://portal.gdc.cancer.gov/)	python	python matplotlib package (visualization)	matplotlib.pyplot.plot()

Supplementary Table 4. CS threshold of each gene group.

Gene_group	Low_threshold	High_threshold
CS0	-4.261	-1.056
CS1	-1.056	-0.508
CS2	-0.507	-0.293
CS3	-0.293	-0.167
CS4	-0.167	-0.07
CS5	-0.07	0.01
CS6	0.01	0.087
CS7	0.087	0.172
CS8	0.172	0.287
CS9	0.287	1.295