Supplementary Methods

Assessment of similarities between miRNA target predictions

The similarity between two target prediction results A and B was defined as the union of the two datasets divided by the intersection.

$$Similarity = \frac{A \cap B}{A \cup B}$$

The range of similarity values is between 0 and 1, with a higher value indicating a higher degree of similarity between two datasets.

Comparison analysis of miRNA target prediction methods

A comparative analysis was carried out to test whether integrating different algorithms is superior to using a single algorithm by itself. The overlap of miRanda, PITA, TargetScan, RNAhybrid, and their integration with experimentally validated miRNA-lncRNA datasets from starBase v.2.0 (1) and DIANA-LncBase (2) was examined. The significance of the enrichment in overlap between individual methods and the validated dataset was calculated by hypergeometric testing. If N is the total number of all possible miRNA-lncRNA interactions, of which K are included in the validated dataset, and the analytical method of interest has a total of M interactions, of which x overlap with the validated dataset, then the P value corresponding to the significance of enrichment can be calculated as follows:

$$P = 1 - \sum_{t=0}^{x} \frac{\binom{K}{t}\binom{N-K}{M-t}}{\binom{N}{M}}$$

Evaluation of competing activity score score

To test whether the competing activity score is a valuable measurement for the evaluation of the strength of competition in lncACTs, we carried out following analysis:

Comparisons between gold standard triplets and 10-fold random lncACTs PTEN-associated competing triplets (PTENACTs; n = 137) from an extensive ceRNA sub-network that included PTEN, RB1, STAT3, PDGFRA, RUNX1, VEGFA, and their competing miRNAs were identified and experimentally validated in a previous study (3). These were taken as gold standard PTENACTs. For each PTENACT, 10 random competing activity scores were generated by randomly shuffling the expression profiles. PTENACTs competing activity score were significantly higher than random scores across 12 types of cancer (Fig. S4).

Comparisons between gold standard triplets and 10-fold negative triplets Negative examples were randomly derived from 289 negative miRNA-target interactions. The miRNA target pairs were used as negative training examples for mining miRNA-target interactions (4); for each pair, two candidate RNAs (lncRNAs or mRNAs) were identified as lncACTs if they interacted with a common miRNA. In this step, a threshold P value < 0.05 was used for hypergeometric testing. The gold standard and negative lncACTs were merged into a list ranked by competing activity score in descending order for which dynamic thresholds (ranging from minimum to maximum of competing activity scores) were used as cut-off points. Ranking was determined by calculating sensitivity and

specificity (i.e., frequency of gold standards ranked above or below a given cut-off point, respectively). We plotted receiver operating characteristic (ROC) curves using the competing activity scores of the lncACTs to facilitate the comparison between PTENACTs and 10-fold negative lncACTs (Fig S5). In a ROC curve, the sensitivity (true positive rate) is plotted as a function of 1-specificity (false positive rate) for different thresholds. We found high AUC values (from 0.81 to 0.98) for ROC curves across 12 cancers. These results indicated that competing activity scores can give high levels of precision to distinguish positive lncACTs from negative lncACTs.

Supplementary Figure Legends

Figure S1. Evaluation of accuracy of our coding/lncRNA gene quantification pipeline. For OV data (A) and UCEC data (B), we plotted our recalculated RPKM values against the true RPKM values, calculated by Akrami et al. High linear correlation was observed between recalculated RPKM and true RPKM values for both OV (R^2=0.92) and UCEC (R^2=0.95) datasets. The R^2 and F-statistic P-values, calculated by robust linear regression analysis, are shown in each figure. Linear fitting lines are indicated in red. X and Y axes were plotted in the log2 scale.

Figure S2. (A) Venn diagram of the overlap between miRNA-lncRNA interactions predicted using four methods. (B) The similarity between RNAhybrid and PITA results was only 5.13%; the highest similarity was observed between miRanda and TargetScan results at 24.10%. The total number of differentially predicted results is shown on the bottom line. A 5.8-fold difference was observed between the number of results predicted by RNAhybrid (3,502,121) and miRanda (606,081). Similarities between predictions from RNAhybrid and miRanda was 13.07%, while between RNAhybrid and PITA, the IR was only 5.1%. These results indicate a considerable divergence in miRNA-binding sites predicted using the four methods.

Figure S3. Comparison of different miRNA-lncRNA prediction methods overlaping with validated dataset. The integration method hosts the most number of experimentally validated miRNA-lncRNA interactions than other methods. Hypergeometric test indicated that the overlap between integration method and validated dataset has the most significant enrichment P value.

Figure S4. Individual and box plot comparison of competing activity scores between PTENACTs (red points) and random (green points) lncACTs. The scores of PTENACTs were significantly higher than random scores across 12 types of cancers. Significant P values were calculated by the Mann-Whitney U-test

Figure S5. The ROC curves (blue lines) used to distinguish PTENACTs from negative lncACTs, based on the competing activity score. The AUC score is the most frequently used measure for the evaluation of algorithm performance. For example, an AUC score of 1 indicates that every tested gene ranked prior to other genes, whereas a value of 0.5 indicates that the tested genes were randomly ranked throughout the list.

Figure S6. Illustration of lncACT crosstalk network construction. The lncRNAs, miRNAs and coding-genes are colored blue, red and yellow, respectively. Their interactions are indicated by black lines. (A) Illustration of how a single lncACTs is represented. On the left panel, miRNAs can bind to lncRNA and coding gene molecules based on complementary seed sequence. The lncRNAs can compete with coding genes by sharing miRNA binding sites. This kind of competing status between different RNA molecules can be represented as nodes and edges in the network in the right panel. (B) Illustration of how the lncACT network is represented. It was assumed that lncRNAs and mRNAs in one lncACT compete for binding to miRNAs within other lncACTs (left panel). This type of crosstalk can be represented in the network by adding edges of related lncACTs (right panel). The constructed intricate transcriptional regulatory network can aid studies into how intermolecular relationships dictate cellular behavior.

Figure S7. Detailed comparison of disease-associated and other nodes. Based on topological characteristics of the network, disease-associated nodes were found to have a higher degree and betweenness centrality than other nodes.

Figure S8. A genome-wide map of 5,119 functional lncACTs based on Circos-style visualization. Outer circles indicate human chromosomes and genomic locations of lncRNAs (blue), miRNAs (red), and coding genes (yellow) of lncACTs. Lines within the circle denote pairs of miRNA-lncRNA (blue) and miRNA-gene (red) interactions. Detailed maps for each cancer are shown in the bottom panel.

Figure S9. Detailed functional comparison between different methods. (A, B) The GO terms identified by starBaseV2.0 and Linc2GO are listed on the bottom and ranked from left to right, based on the significant P-value. The GO terms identified by our method were mapped to these lists and are indicated as black bars. To investigate functional similarity, we calculated the enrichment score using a slipping window (width=100 terms, step=1 term) along the lists. In each slipping step, the enrichment score was calculated as the number of mapped GO terms/window width. The blue curve of the enrichment score was generated by slipping the window along the list. We found that GO terms identified by our method were enriched on top of the starBaseV2.0 and Linc2GO lists. (C, D) Comparison of enriched KEGG pathways (top ten) with starBaseV2.0 and Linc2GO. Pathways were indicated by red underlines if they were also identified in the top ten pathways of our method. These results indicated that starBaseV2.0 and Linc2GO identified similar functions to our method.

Figure S10. Construction of cancer-specific sub-networks. Each of 10 cancer-specific clusters (left) were converted into a sub-network as follows (right): (a) lncRNA-miRNA-mRNA interactions in the lncACT cluster were identified; (b) lncRNAs, miRNAs, and mRNAs were represented as nodes, and interactions between them were represented as edges; (c) repeated values were merged into single nodes and edges; (d) nodes and edges were use to construct a cancer-specific sub-network. Clusters 4 and 6 were integrated into the same BRCA-specific sub-network.

Figure S11. Detailed information for nine cancer-specific sub-networks. Similar to the global network, sub-networks had a layered organization, with lncRNAs (blue), miRNAs (red), and coding genes (yellow) as nodes.

Figure S12. Degree distribution of nine cancer-specific sub-networks. Similar to the global network, sub-networks presented a scale-free structure.

Figure S13. Kaplan-Meier survival analysis to test whether the HB_module can better distinguish patients than lncRNAs/miRNAs/mRNAs or combinations thereof. Survival curves of classification based on each node of the HB_module (A-N), integration of BRCA2 and miR-20b (O), H19- and BRCA1/2-associated lncACTs (P and Q, respectively), and all lncRNAs, miRNAs, and coding genes in the HB_module (R, S, and T, respectively) were generated. Patients showing no progression or who were still alive at the time of the last follow-up were censored (+). P values were calculated by the log-rank test.

Figure S14. The use of lncACTs to predict the clinical outcomes of cancer patients. The survival analysis revealed that lncACT modules could distinguish patients with different clinical outcomes in (A) BRCA, (B) BLCA, (C) LUSC, (D) LUAD, (E) UCEC and (F) KIRP.

From (A) to (F), the topological graph for each functional module is illustrated in each panel (top). The lncRNAs, miRNAs and coding-genes are colored blue, red and yellow, respectively. The expression heat map is shown on the middle panel. Highly expressed genes are shown in red, low expression genes are shown in green. A corresponding Kaplan-Meier survival plot (bottom) of the two patient subgroups, identified by hierarchical clustering of expression profiles (middle), was generated. Patients that showed no progression or who were still alive at the time of the last follow-up were censored (+). Survival days are shown along the X axis. Overall survival rates are shown along the Y axis.

Figure S15. Kaplan-Meier survival analysis of single nodes in the miR-335-associated network module. The nodes could not distinguish BRCA patients. Patients showing no progression or who were still alive at the time of the last follow-up were censored (+). P values were calculated by the log-rank test.

Figure S16. An overview of the online website framework. (1) A browse module of the database. (2) A flexible gateway to search for relevant lncACTs. (3) Functional annotation tools based on KEGG and GO for lncACTs or lncRNAs. (4) Retrieval of lncACTs based on user-provided expression profiles. (5) A built-in multi-track visualization platform that allows users to browse genome-wide lncACTs. (6) Downloading corresponding datasets. (7) Links to relevant sources of functional data. Downloadable description of the website working principles and user manual are also provided.

Figure S17. Illustration of a potential mechanism to explain the inverse expression patterns of DANCR-miR222-TCEAL1 lncACT.

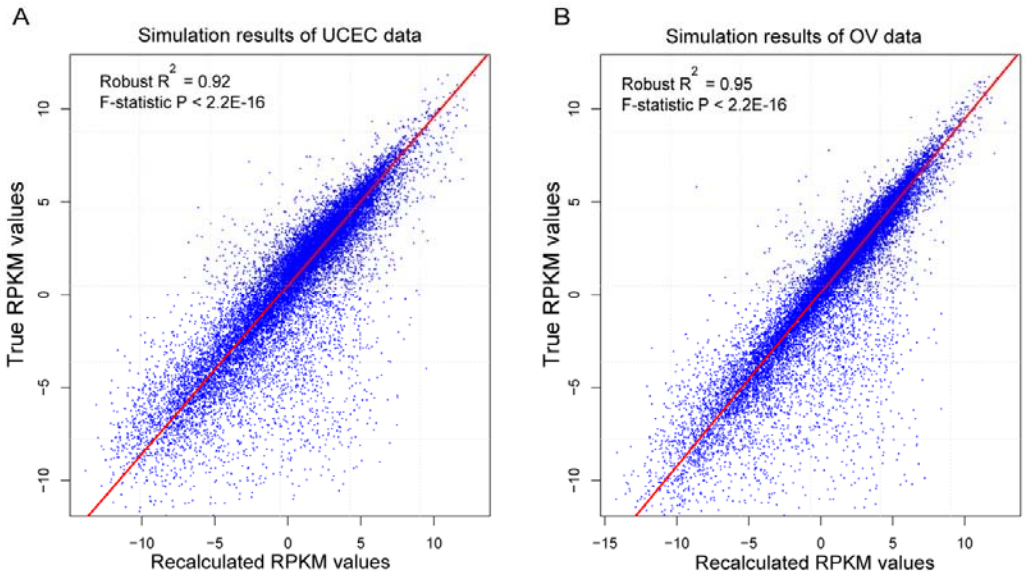
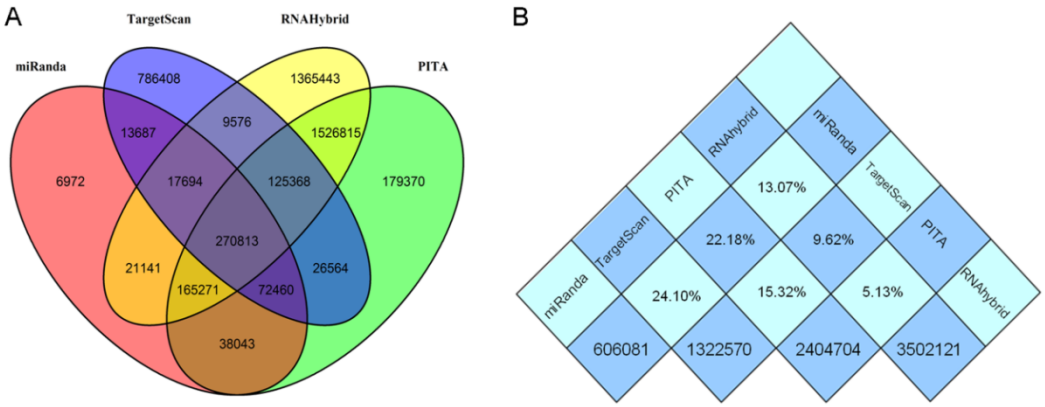

A
Simulation results of UCEC data
Robust R2 = 0.92
F-statistic P < 2.2E-16
True RPKM values
Recalculated RPKM values
B
Simulation results of OV data
Robust R2 = 0.95
F-statistic P < 2.2E-16
True RPKM values
Recalculated RPKM values

Figure S1


A
TargetScan
RNAHybrid
miRanda
PITA
786408
1365443
9576
13687
1526815
6972
17694
125368
179370
270813
21141
26564
165271
72460
38043
B
RNAhybrid
miRanda
PITA
TargetScan
13.07%
TargetScan
PITA
22.18%
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miRanda
RNAhybrid
24.10%
15.32%
5.13%
606081
1322570
2404704
3502121

Figure S2

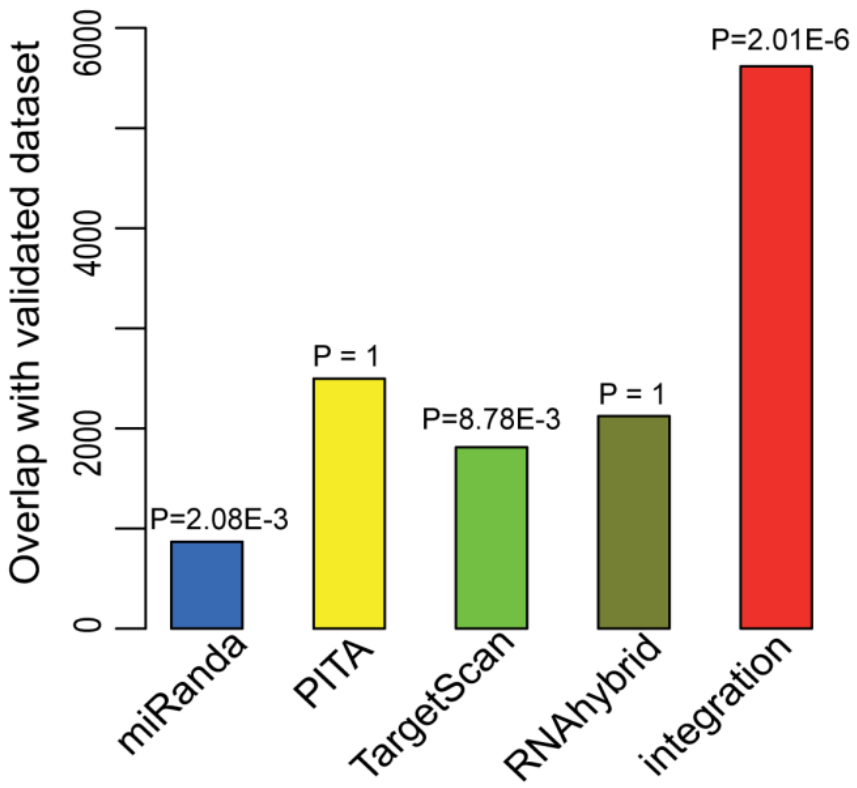
Overlap with validated dataset
0
2000
4000
6000
P=2.08E-3
P = 1
P=8.78E-3
P = 1
P=2.01E-6
miRanda
PITA
TargetScan
RNAhybrid
integration

Figure S3

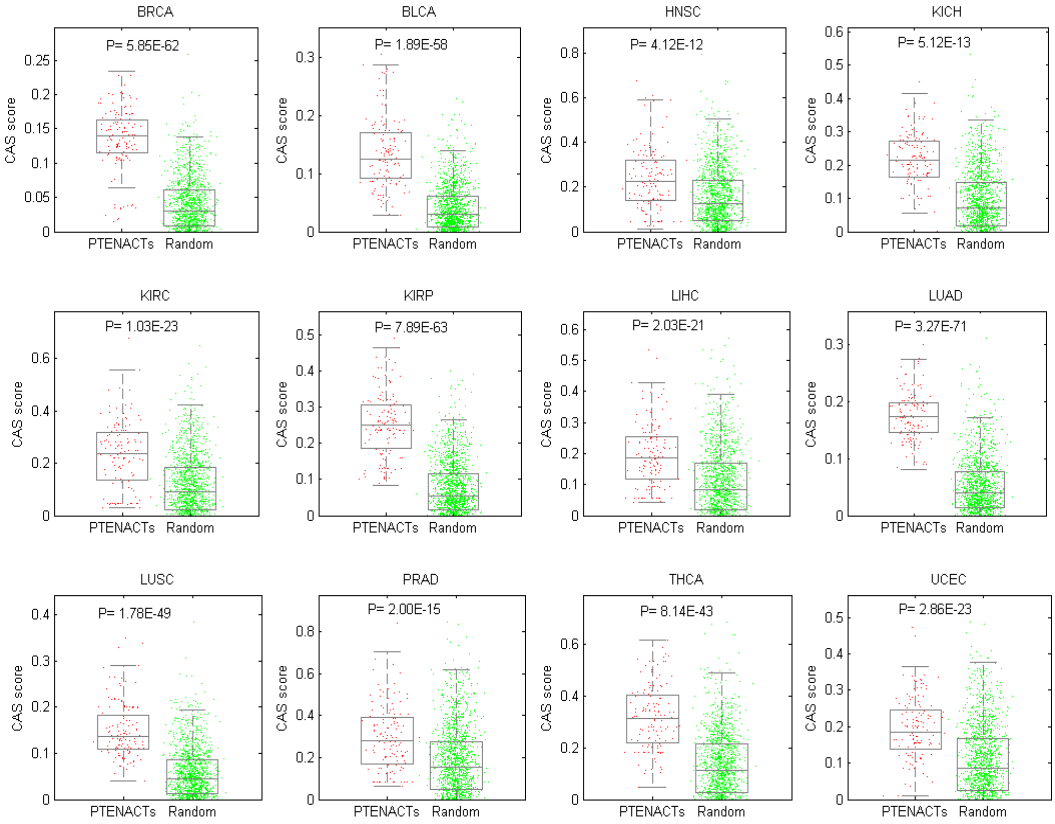
BRCA
P= 5.85E-62
BLCA
P= 1.89E-58
HNSC
P= 4.12E-12
KICH
P= 5.12E-13
KIRC
P= 1.03E-23
KIRP
P= 7.89E-63
LIHC
P= 2.03E-21
LUAD
P= 3.27E-71
LUSC
P= 1.78E-49
PRAD
P= 2.00E-15
THCA
P= 8.14E-43
UCEC
P= 2.86E-23
CAS score
PTENACTs
Random

Figure S4

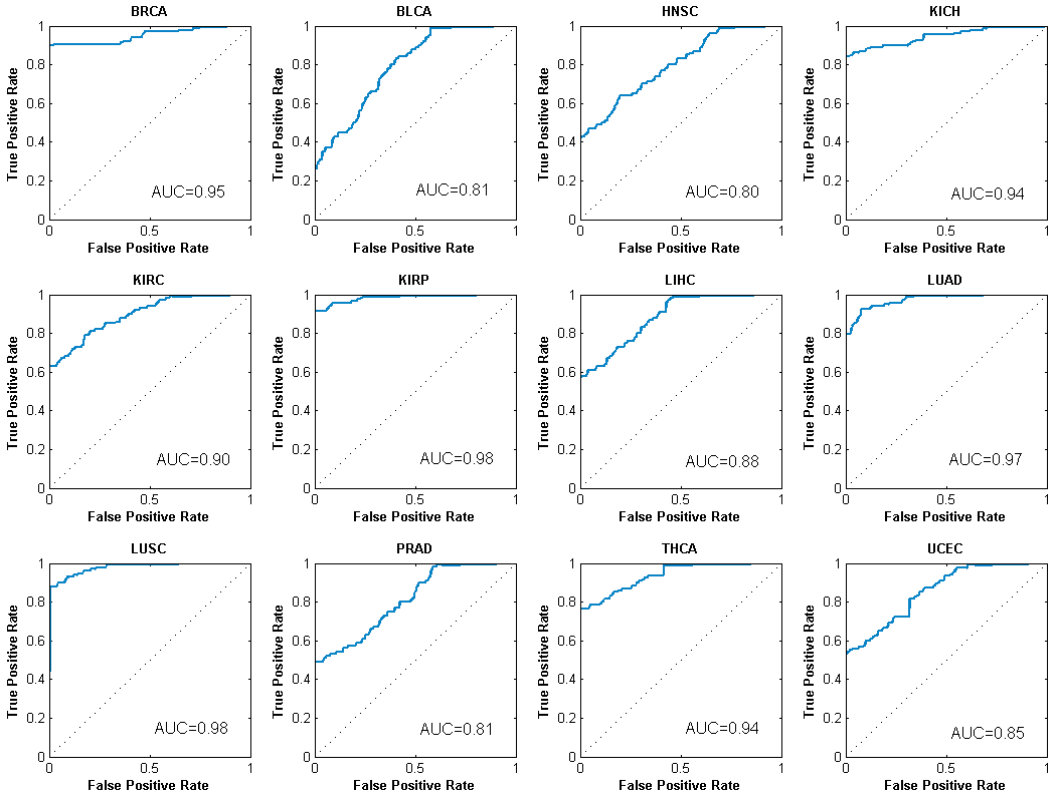
BRCA
AUC=0.95
BLCA
AUC=0.81
HNSC
AUC=0.80
KICH
AUC=0.94
KIRC
AUC=0.90
KIRP
AUC=0.98
LIHC
AUC=0.88
LUAD
AUC=0.97
LUSC
AUC=0.98
PRAD
AUC=0.81
THCA
AUC=0.94
UCEC
AUC=0.85
True Positive Rate
False Positive Rate

Figure S5

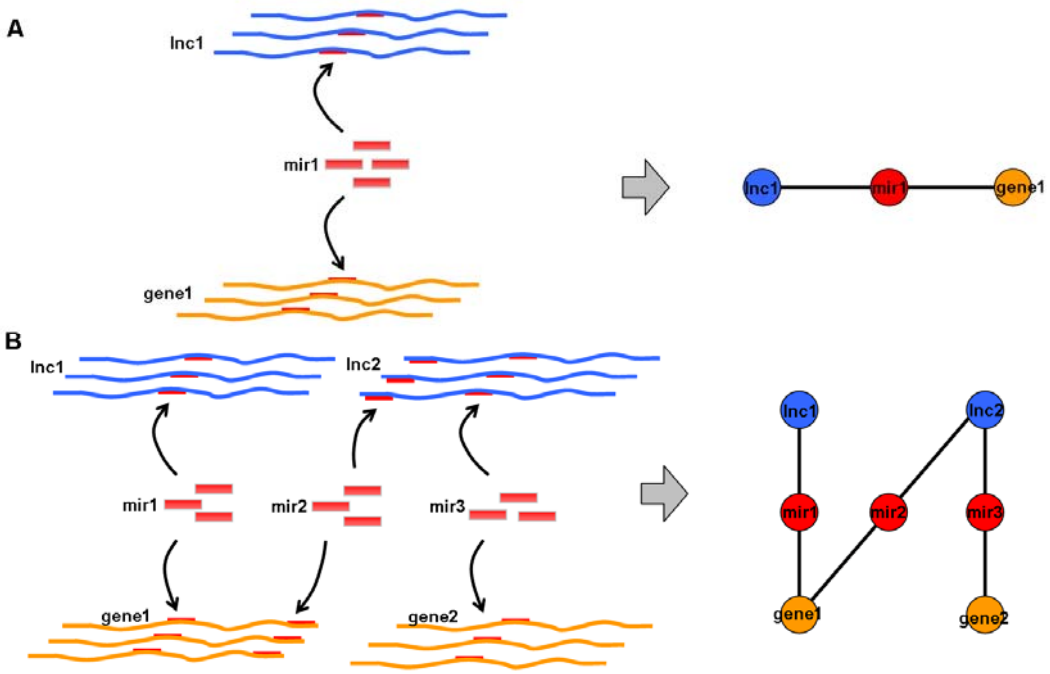
A
lnc1
mir1
gene1
lnc1
mir1
gene1
B
lnc1
lnc2
mir1
mir2
mir3
gene1
gene2
lnc1
lnc2
mir1
mir2
mir3
gene1
gene2

Figure S6

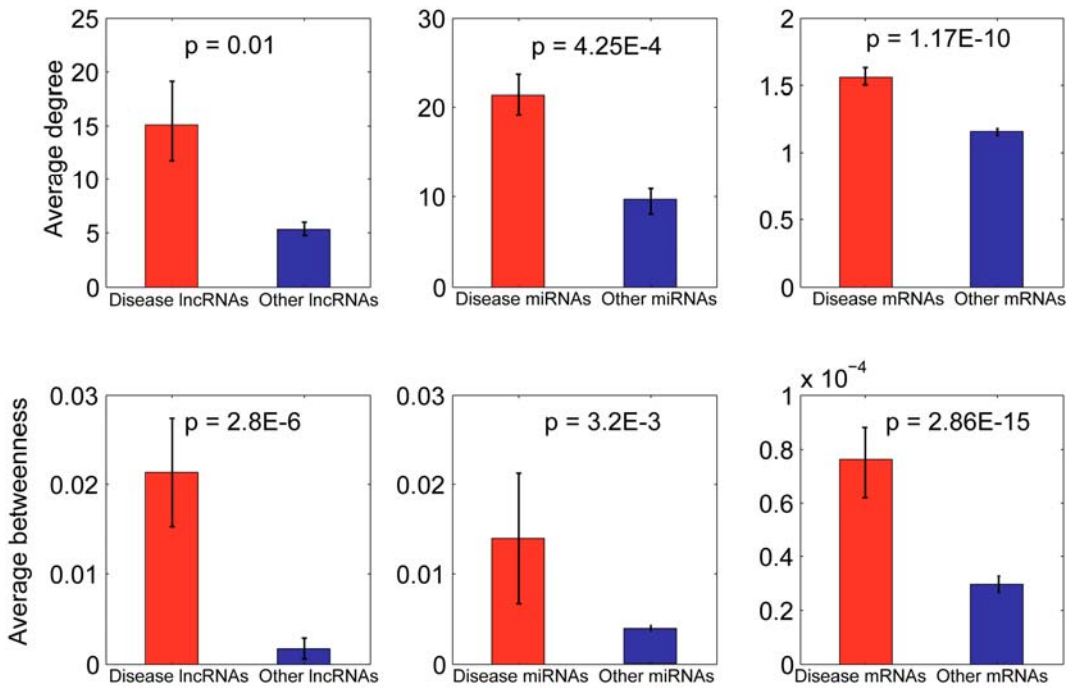
Average degree
p = 0.01
Disease lncRNAs
Other lncRNAs
p = 4.25E-4
Disease miRNAs
Other miRNAs
p = 1.17E-10
Disease mRNAs
Other mRNAs
Average betweenness
p = 2.8E-6
Disease lncRNAs
Other lncRNAs
p = 3.2E-3
Disease miRNAs
Other miRNAs
x 10^-4
p = 2.86E-15
Disease mRNAs
Other mRNAs

Figure S7

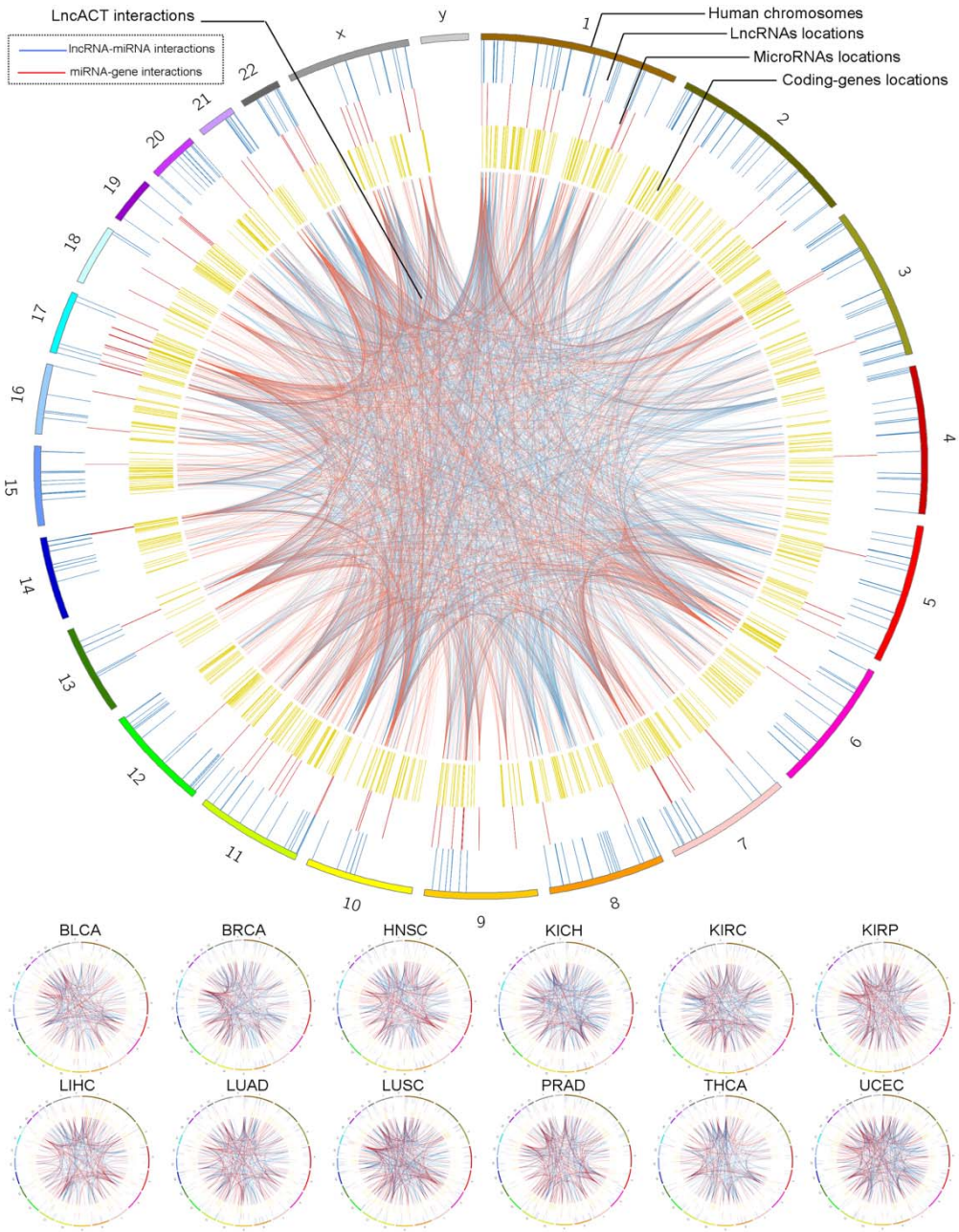
LncACT interactions
lncRNA-miRNA interactions
miRNA-gene interactions
Human chromosomes
LncRNAs locations
MicroRNAs locations
Coding-genes locations
BLCA
BRCA
HNSC
KICH
KIRC
KIRP
LIHC
LUAD
LUSC
PRAD
THCA
UCEC

Figure S8

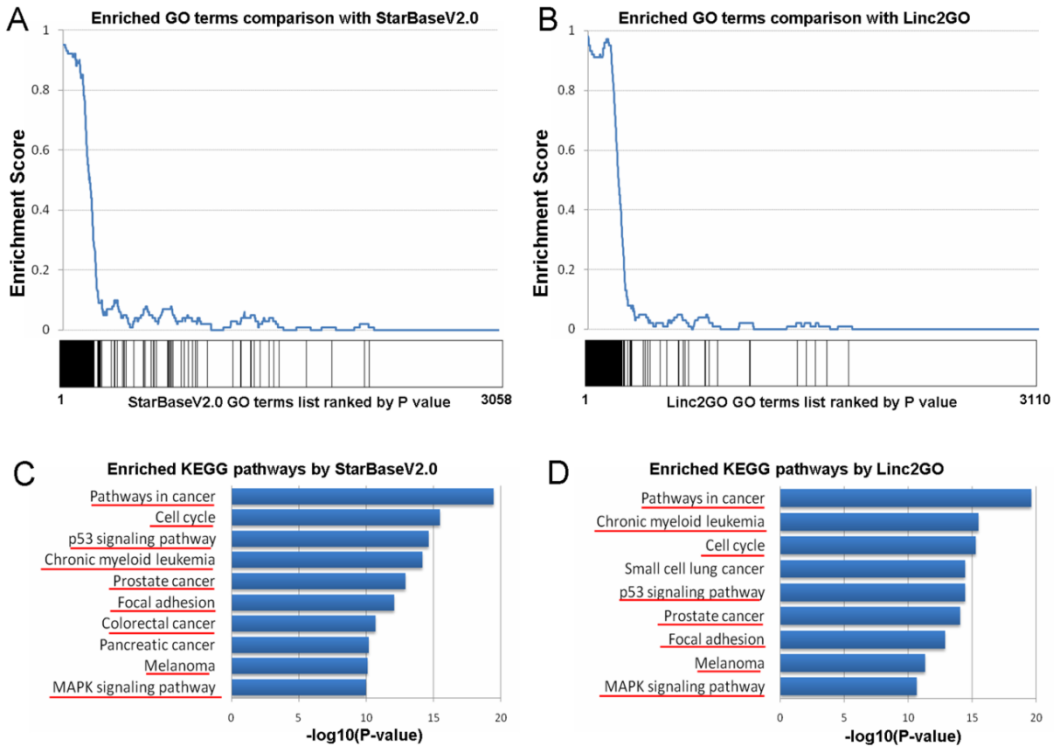
A
Enriched GO terms comparison with StarBaseV2.0
Enrichment Score
1
0.8
0.6
0.4
0.2
0
1
StarBaseV2.0 GO terms list ranked by P value
3058
B
Enriched GO terms comparison with Linc2GO
Enrichment Score
1
0.8
0.6
0.4
0.2
0
1
Linc2GO GO terms list ranked by P value
3110
C
Enriched KEGG pathways by StarBaseV2.0
Pathways in cancer
Cell cycle
p53 signaling pathway
Chronic myeloid leukemia
Prostate cancer
Focal adhesion
Colorectal cancer
Pancreatic cancer
Melanoma
MAPK signaling pathway
0
5
10
15
20
-log10(P-value)
D
Enriched KEGG pathways by Linc2GO
Pathways in cancer
Chronic myeloid leukemia
Cell cycle
Small cell lung cancer
p53 signaling pathway
Prostate cancer
Focal adhesion
Melanoma
MAPK signaling pathway
0
5
10
15
20
-log10(P-value)

Figure S9

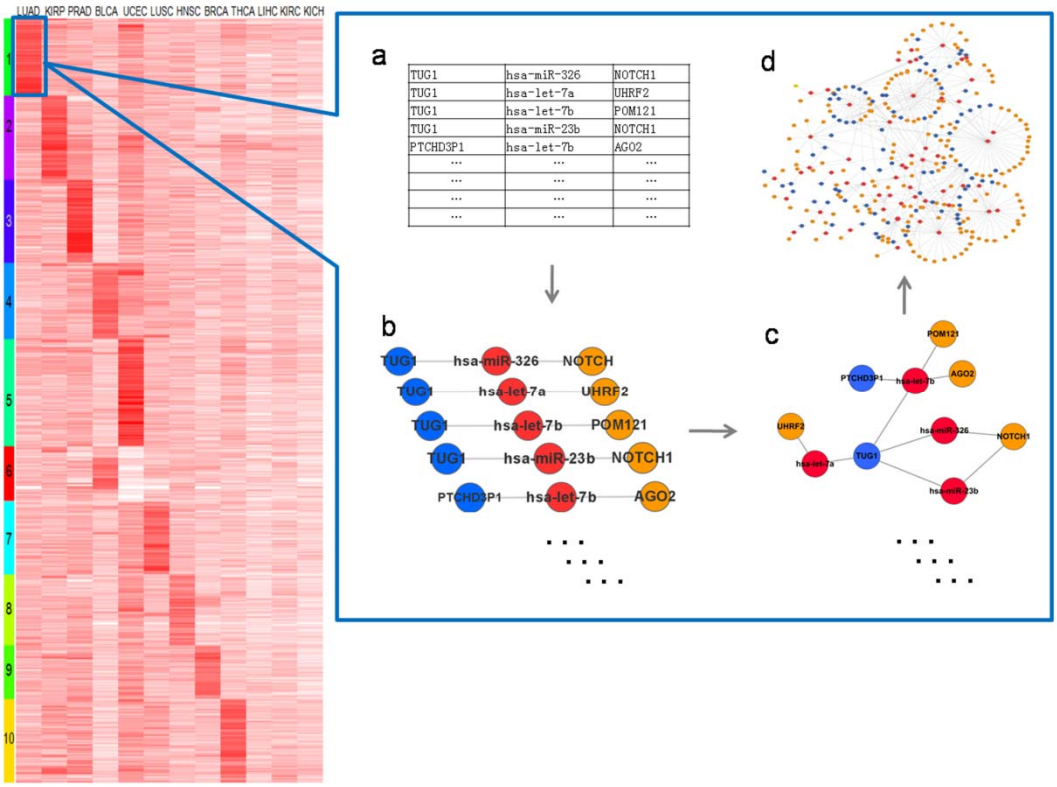
LUAD KIRP PRAD BLCA UCEC LUSC HNSC BRCA THCA LIHC KIRC KICH
1
2
3
4
5
6
7
8
9
10
a
TUG1 hsa-miR-326 NOTCH1
TUG1 hsa-let-7a UHRF2
TUG1 hsa-let-7b POM121
TUG1 hsa-miR-23b NOTCH1
PTCHD3P1 hsa-let-7b AGO2
b
TUG1 hsa-miR-326 NOTCH
TUG1 hsa-let-7a UHRF2
TUG1 hsa-let-7b POM121
TUG1 hsa-miR-23b NOTCH1
PTCHD3P1 hsa-let-7b AGO2
c
POM121
PTCHD3P1
hsa-let-7b
AGO2
UHRF2
hsa-miR-326
NOTCH1
hsa-let-7a
TUG1
hsa-miR-23b
d

Figure S10

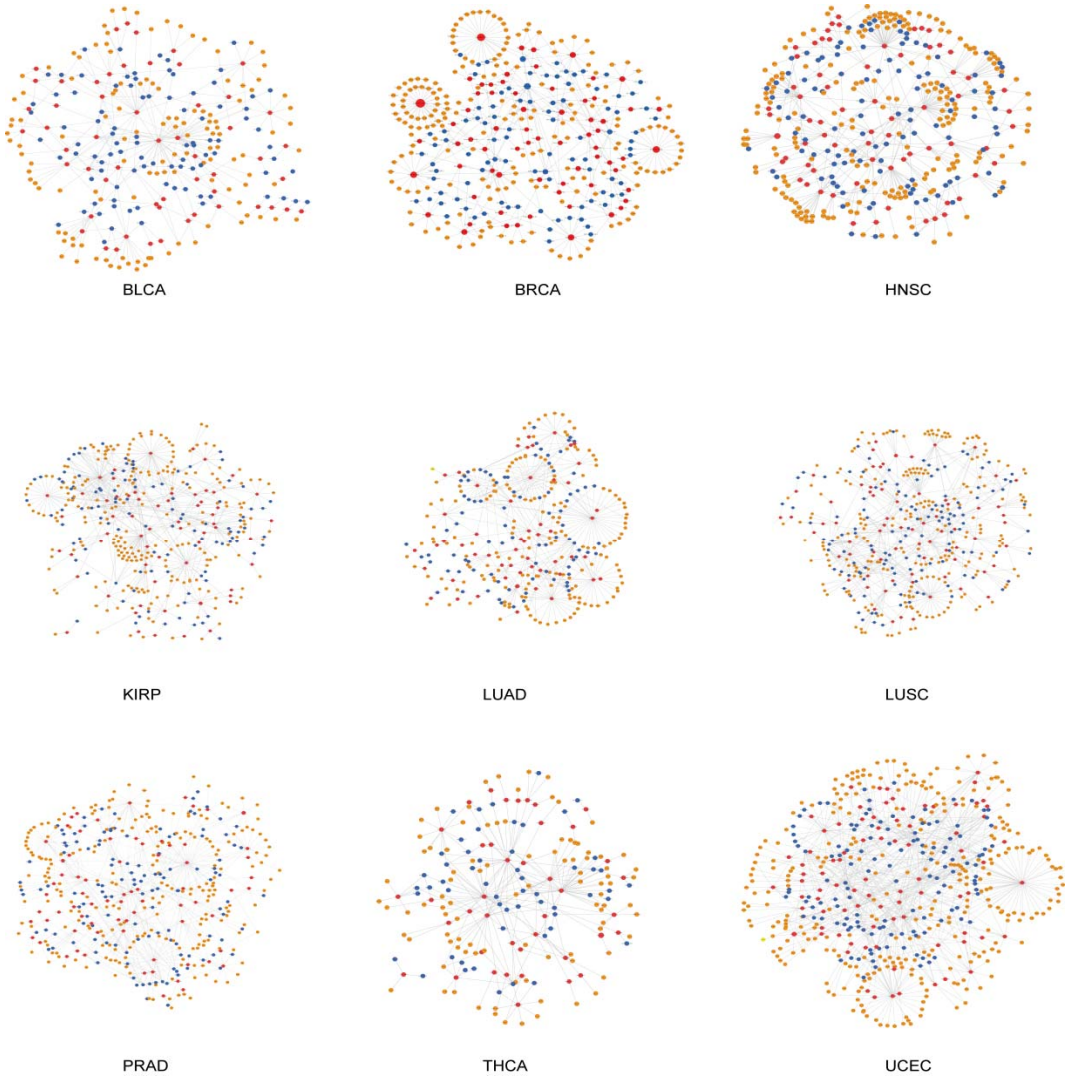

Figure S11

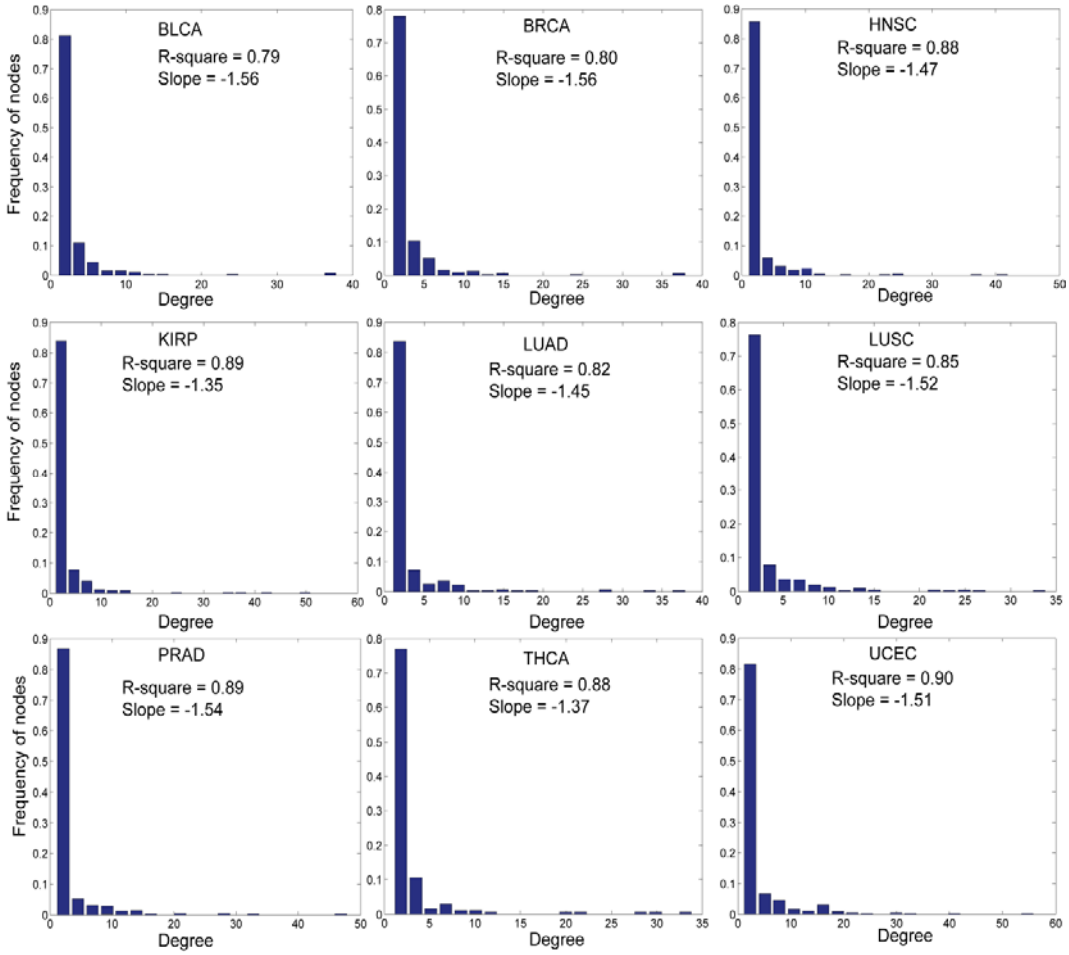
BLCA
R-square = 0.79
Slope = -1.56
BRCA
R-square = 0.80
Slope = -1.56
HNSC
R-square = 0.88
Slope = -1.47
KIRP
R-square = 0.89
Slope = -1.35
LUAD
R-square = 0.82
Slope = -1.45
LUSC
R-square = 0.85
Slope = -1.52
PRAD
R-square = 0.89
Slope = -1.54
THCA
R-square = 0.88
Slope = -1.37
UCEC
R-square = 0.90
Slope = -1.51
Frequency of nodes
Degree

Figure S12

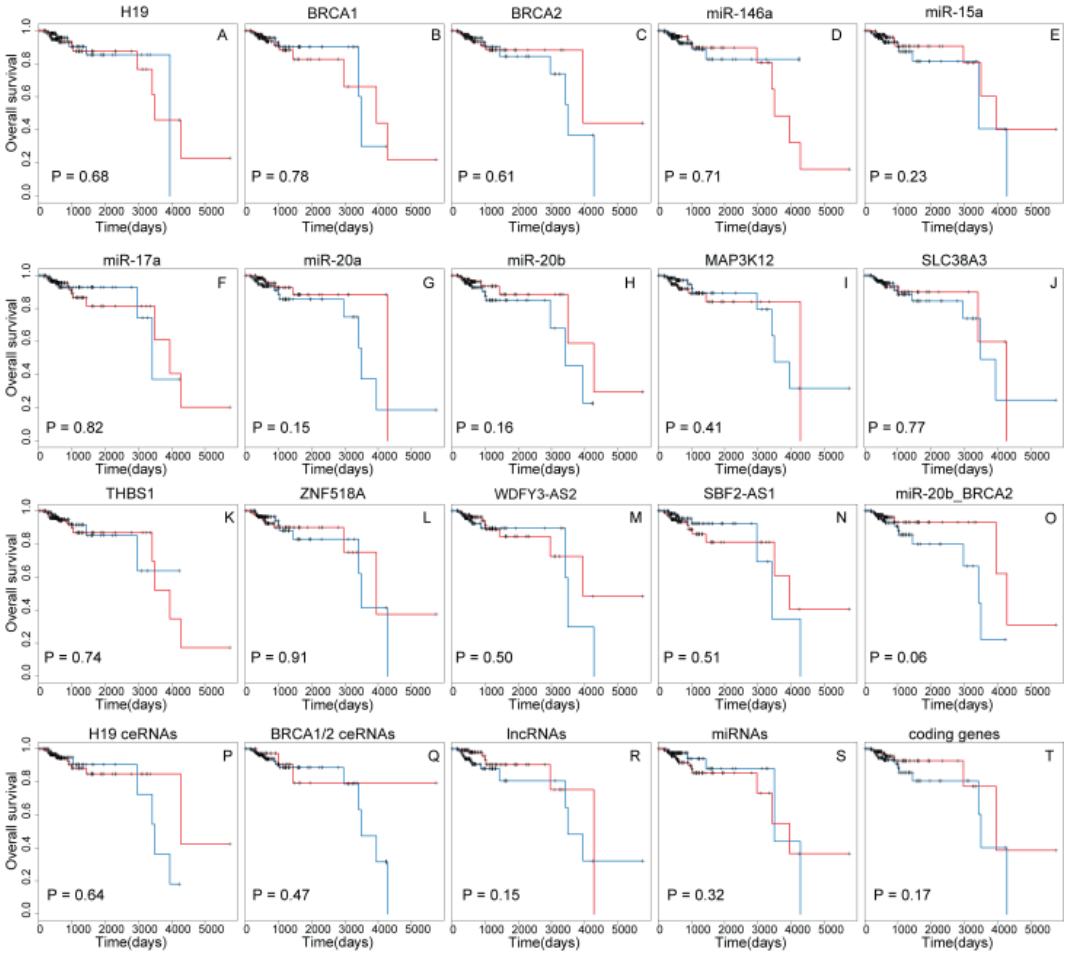
H19
A
P = 0.68
BRCA1
B
P = 0.78
BRCA2
C
P = 0.61
miR-146a
D
P = 0.71
miR-15a
E
P = 0.23
miR-17a
F
P = 0.82
miR-20a
G
P = 0.15
miR-20b
H
P = 0.16
MAP3K12
I
P = 0.41
SLC38A3
J
P = 0.77
THBS1
K
P = 0.74
ZNF518A
L
P = 0.91
WDFY3-AS2
M
P = 0.50
SBF2-AS1
N
P = 0.51
miR-20b_BRCA2
O
P = 0.06
H19 ceRNAs
P
P = 0.64
BRCA1/2 ceRNAs
Q
P = 0.47
lncRNAs
R
P = 0.15
miRNAs
S
P = 0.32
coding genes
T
P = 0.17
Overall survival
Time(days)

Figure S13

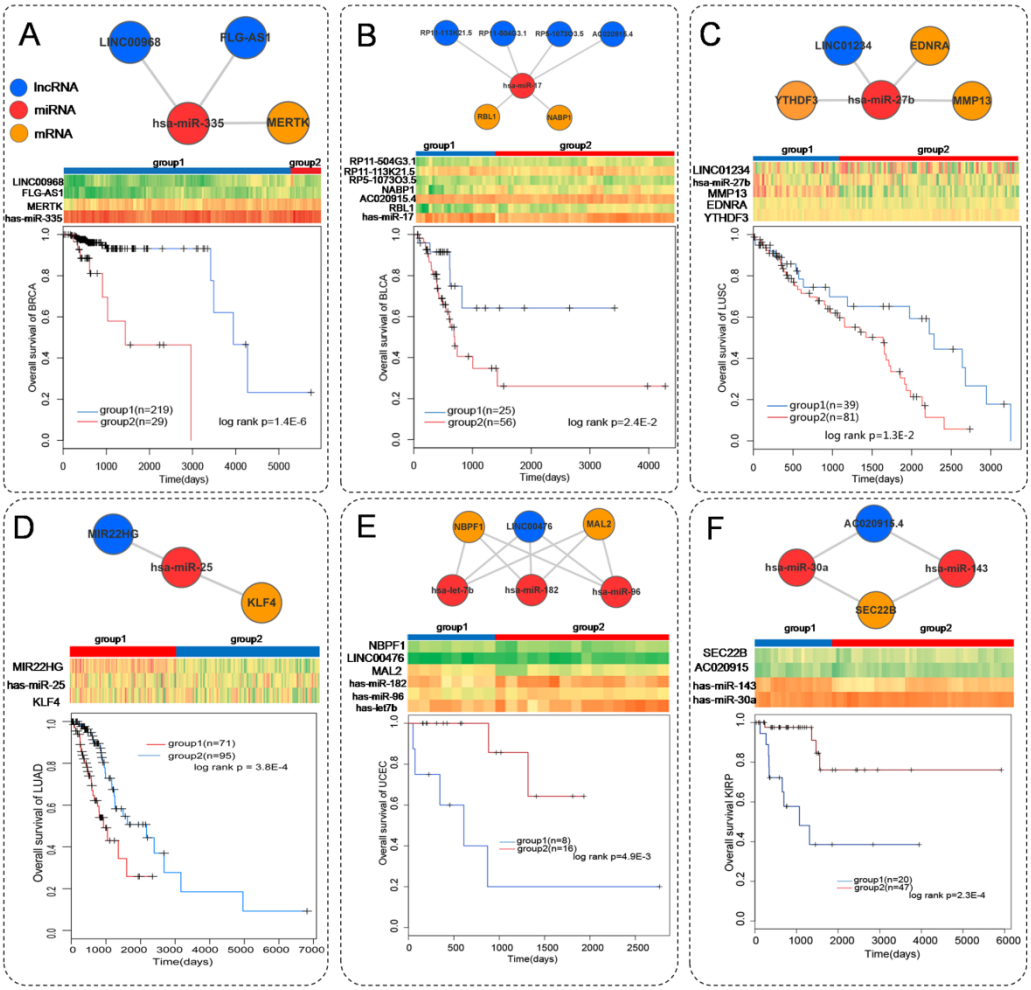
A
LINC00968
FLG-AS1
lncRNA
miRNA
mRNA
hsa-miR-335
MERTK
group1
group2
LINC00968
FLG-AS1
MERTK
has-miR-335
Overall survival of BRCA
group1(n=219)
group2(n=29)
log rank p=1.4E-6
Time(days)
B
group1
group2
RP11-504G3.1
RP11-113K21.5
RP5-1073O3.5
NABP1
AC020915.4
RBL1
has-miR-17
Overall survival of BLCA
group1(n=25)
group2(n=56)
log rank p=2.4E-2
Time(days)
C
LINC01234
EDNRA
YTHDF3
hsa-miR-27b
MMP13
group1
group2
LINC01234
hsa-miR-27b
MMP13
EDNRA
YTHDF3
Overall survival of LUSC
group1(n=39)
group2(n=81)
log rank p=1.3E-2
Time(days)
D
MIR22HG
hsa-miR-25
KLF4
group1
group2
MIR22HG
has-miR-25
KLF4
Overall survival of LUAD
group1(n=71)
group2(n=95)
log rank p = 3.8E-4
Time(days)
E
NBPF1
LINC00476
MAL2
hsa-let-7b
hsa-miR-182
hsa-miR-96
group1
group2
NBPF1
LINC00476
MAL2
has-miR-182
has-miR-96
has-let7b
Overall survival of UCEC
group1(n=8)
group2(n=16)
log rank p=4.9E-3
Time(days)
F
AC020915.4
hsa-miR-30a
hsa-miR-143
SEC22B
group1
group2
SEC22B
AC020915
has-miR-143
has-miR-30a
Overall survival of KIRP
group1(n=20)
group2(n=47)
log rank p=2.3E-4
Time(days)

Figure S14

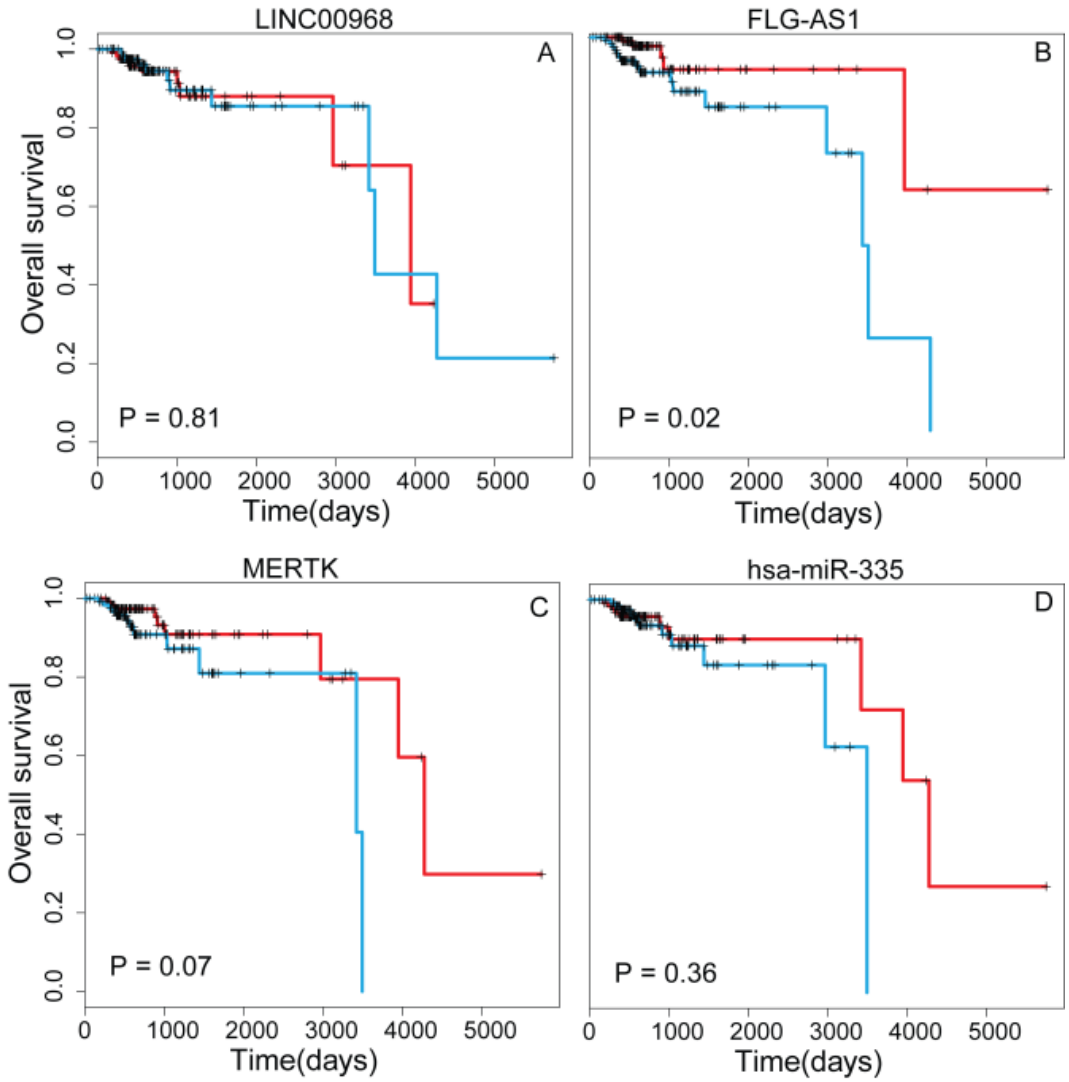
LINC00968
A
Overall survival
P = 0.81
Time(days)
FLG-AS1
B
P = 0.02
Time(days)
MERTK
C
Overall survival
P = 0.07
Time(days)
hsa-miR-335
D
P = 0.36
Time(days)

Figure S15

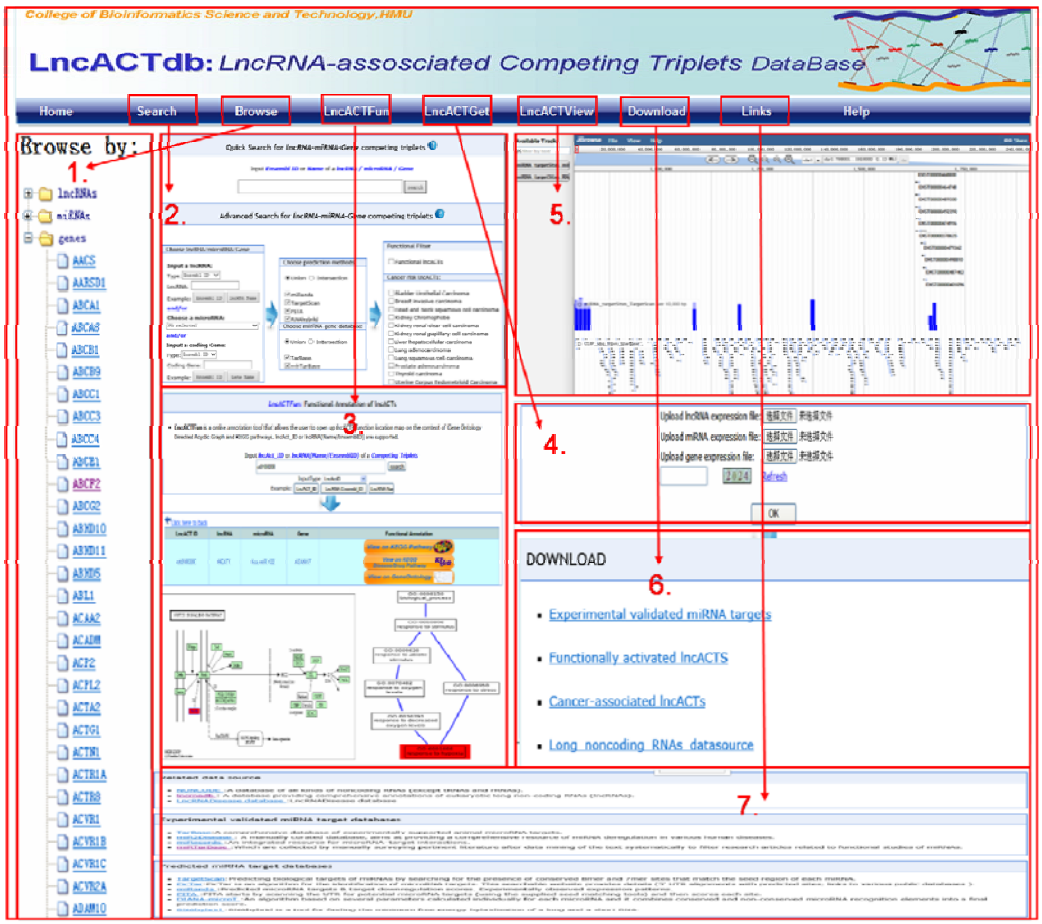
College of Bioinformatics Science and Technology,HMU
LncACTdb: LncRNA-assosciated Competing Triplets DataBase
Home
Search
Browse
LncACTFun
LncACTGet
LncACTView
Download
Links
Help
Browse by:
1.
2.
3.
4.
5.
6.
7.
DOWNLOAD
Experimental validated miRNA targets
Functionally activated lncACTS
Cancer-associated lncACTs
Long noncoding RNAs datasource

Figure S16

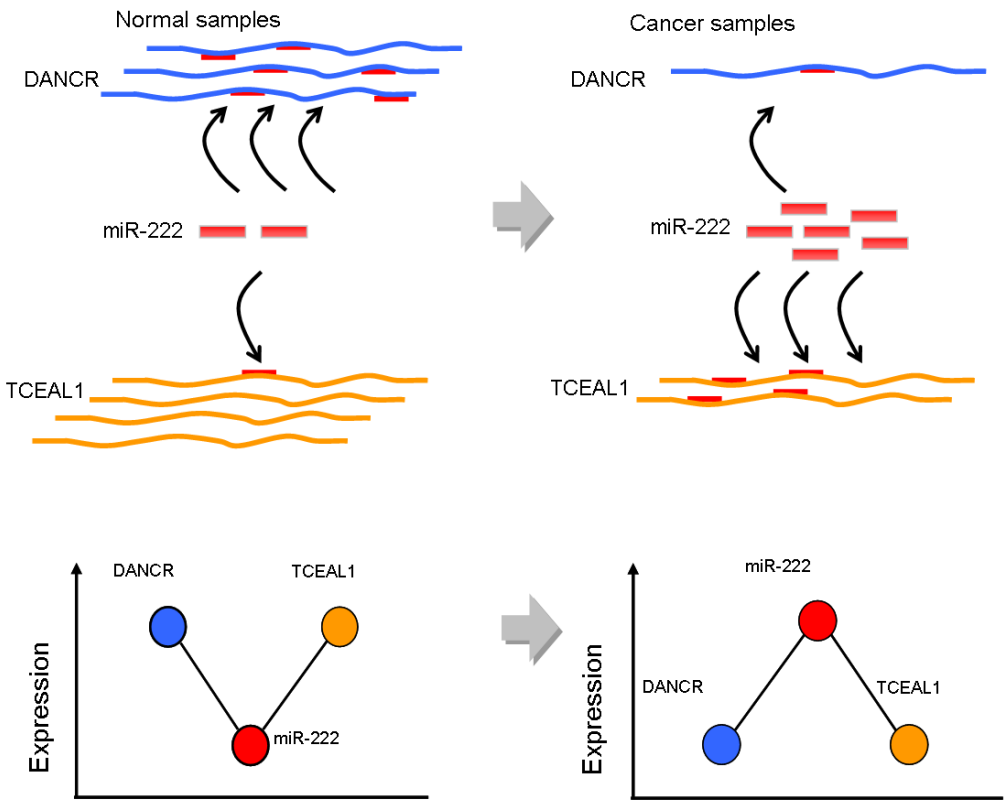
Normal samples
DANCR
miR-222
TCEAL1
Cancer samples
DANCR
miR-222
TCEAL1
Expression
DANCR
TCEAL1
miR-222
Expression
miR-222
DANCR
TCEAL1

Figure S17

Supplementary Table S1. RNA sequencing data for 12 types of cancer from TCGA

Abbreviations	Cancer names	No.of samples
BLCA	Bladder Urothelial Carcinoma	81
BRCA	Breast invasive carcinoma	248
HNSC	Head and Neck squamous cell carcinoma	158
KICH	Kidney Chromophobe	50
KIRC	Kidney renal clear cell carcinoma	30
KIRP	Kidney renal papillary cell carcinoma	67
LIHC	Liver hepatocellular carcinoma	71
LUAD	Lung adenocarcinoma	166
LUSC	Lung squamous cell carcinoma	120
PRAD	Prostate adenocarcinoma	59
THCA	Thyroid carcinoma	229
UCEC	Uterine Corpus Endometrioid Carcinoma	24

Supplementary Table S2. List of lncRNAs used in this work which identified from TCGA RNA-seq data.

Ensembl ID	lncRNA Name	Ensembl ID	lncRNA Name
ENSG00000093100	XXbac-B461K10.4	ENSG00000237125	HAND2-AS1
ENSG00000100181	TPTEP1	ENSG00000237149	ZNF503-AS2
ENSG00000122043	LINC00544	ENSG00000237152	DLEU7-AS1
ENSG00000124915	DKFZP434K028	ENSG00000237159	CNTFR-AS1
ENSG00000125514	LINC00029	ENSG00000237166	AC007163.3
ENSG00000125804	FAM182A	ENSG00000237187	NR2F1-AS1
ENSG00000126005	MMP24-AS1	ENSG00000237188	RP11-337C18.8
ENSG00000129816	TTTY1B	ENSG00000237212	RP11-569G13.2
ENSG00000129845	TTTY1	ENSG00000237233	RP11-809M12.1
ENSG00000130600	H19	ENSG00000237248	LINC00987
ENSG00000131007	TTTY9B	ENSG00000237250	RP11-193H5.1
ENSG00000131538	TTTY6	ENSG00000237267	RP11-181F12.1
ENSG00000131548	TTTY6B	ENSG00000237292	RP11-540K16.1
ENSG00000132204	LINC00470	ENSG00000237298	TTN-AS1
ENSG00000132832	LINC01260	ENSG00000237339	RP11-98L5.2
ENSG00000136315	RP11-84C10.2	ENSG00000237361	TUSC8
ENSG00000137808	RP11-809H16.2	ENSG00000237380	HOXD-AS2
ENSG00000142396	ERVK3-1	ENSG00000237399	PITRM1-AS1
ENSG00000145063	FLJ33534	ENSG00000237401	LINC01304
ENSG00000146666	LINC00525	ENSG00000237413	MGC27382
ENSG00000147753	TTTY7	ENSG00000237438	CECR7
ENSG00000147761	TTTY7B	ENSG00000237461	RP11-554F20.1
ENSG00000149656	LINC00266-1	ENSG00000237463	RP11-280O1.2
ENSG00000151303	AGAP11	ENSG00000237479	AC007557.2
ENSG00000152931	PART1	ENSG00000237484	AP000476.1
ENSG00000153363	LINC00467	ENSG00000237489	LINC00959
ENSG00000157306	THTPA	ENSG00000237499	RP11-356I2.4
ENSG00000163364	LINC01116	ENSG00000237505	PKN2-AS1
ENSG00000163597	SNHG16	ENSG00000237513	RP11-325F22.2
ENSG00000164621	SMAD5-AS1	ENSG00000237517	DGCR5
ENSG00000166770	ZNF667-AS1	ENSG00000237523	LINC00857
ENSG00000167117	LINC00483	ENSG00000237548	TTLL11-IT1
ENSG00000167355	OR51B5	ENSG00000237563	TTTY21B
ENSG00000167459	LINC00905	ENSG00000237594	AP000251.3
ENSG00000167912	RP11-25K19.1	ENSG00000237596	RP13-143G15.4
ENSG00000168367	LINC00917	ENSG00000237613	FAM138A
ENSG00000170161	GLIDR	ENSG00000237637	FRY-AS1
ENSG00000170846	AC093323.3	ENSG00000237647	ERICH1-AS1
ENSG00000170919	TPT1-AS1	ENSG00000237654	AP003025.2
ENSG00000171671	SHANK2-AS3	ENSG00000237667	LINC01115
ENSG00000171889	MIR31HG	ENSG00000237675	TEX36-AS1

ENSG00000172250	SERHL	ENSG00000237686	RP5-1120P11.1
ENSG00000172965	MIR4435-1HG	ENSG00000237737	DCTN1-AS1
ENSG00000173867	RP11-97O12.7	ENSG00000237742	RP11-624M8.1
ENSG00000174171	RP11-23P13.6	ENSG00000237750	AC007740.1
ENSG00000174365	SNHG11	ENSG00000237753	FLJ42351
ENSG00000174403	C20orf166-AS1	ENSG00000237803	LINC00211
ENSG00000174680	GRIK1-AS1	ENSG00000237807	RP11-400K9.4
ENSG00000175061	LRRC75A-AS1	ENSG00000237836	PHKA2-AS1
ENSG00000175147	TMEM51-AS1	ENSG00000237862	RP1-63G5.7
ENSG00000175611	LINC00476	ENSG00000237870	AC073130.1
ENSG00000175699	LINC00521	ENSG00000237914	RP11-77C3.3
ENSG00000175701	LINC00116	ENSG00000237927	RP3-393E18.2
ENSG00000175772	LINC01106	ENSG00000237928	NFIA-AS2
ENSG00000175773	RP11-121M22.1	ENSG00000237940	AC093642.3
ENSG00000175873	AC004840.9	ENSG00000237941	KCNQ1DN
ENSG00000175967	FLJ34503	ENSG00000237945	LINC00649
ENSG00000176320	RP11-404O13.5	ENSG00000237954	RP11-14O19.2
ENSG00000176515	RP5-856G1.2	ENSG00000237975	FLG-AS1
ENSG00000176728	TTTY14	ENSG00000237978	RP11-385J1.2
ENSG00000176754	LINC00303	ENSG00000237986	CELF2-AS2
ENSG00000176840	MIR7-3HG	ENSG00000238005	RP11-443B7.1
ENSG00000177112	MRVI1-AS1	ENSG00000238035	AC138035.2
ENSG00000177133	LINC00982	ENSG00000238039	AF011889.2
ENSG00000177337	DLGAP1-AS1	ENSG00000238045	AC009133.12
ENSG00000177338	LINC00469	ENSG00000238062	SPATA3-AS1
ENSG00000177340	FLJ13224	ENSG00000238078	LINC01352
ENSG00000177369	FLJ40194	ENSG00000238099	RP11-12A2.3
ENSG00000177406	RP11-218M22.1	ENSG00000238113	LINC01410
ENSG00000177410	ZFAS1	ENSG00000238120	CTA-941F9.9
ENSG00000177596	RP11-512C24.3	ENSG00000238121	LINC00426
ENSG00000177640	CASC2	ENSG00000238122	RP11-483I13.2
ENSG00000177738	CTD-2201E18.3	ENSG00000238133	MLK7-AS1
ENSG00000177822	MGC45800	ENSG00000238164	RP3-395M20.8
ENSG00000178193	RP4-682C21.5	ENSG00000238184	CD81-AS1
ENSG00000178248	AP000345.1	ENSG00000238197	PAXBP1-AS1
ENSG00000178457	LINC00314	ENSG00000238198	RP11-31F15.2
ENSG00000178803	ADORA2A-AS1	ENSG00000238217	AC093590.1
ENSG00000178947	LINC00086	ENSG00000238266	LINC00707
ENSG00000178977	LINC00324	ENSG00000238268	RP11-229P13.19
ENSG00000179082	C9orf106	ENSG00000238755	RP11-23D24.2
ENSG00000179136	LINC00670	ENSG00000239219	RP11-379K17.4
ENSG00000179141	MTUS2-AS1	ENSG00000239225	TTTY23
ENSG00000179406	LINC00174	ENSG00000239265	CLRN1-AS1
ENSG00000179447	RP5-1027G4.3	ENSG00000239440	RP11-260O18.1

ENSG00000179676	LINC00305	ENSG00000239482	RP11-90K6.1
ENSG00000179743	FLJ37453	ENSG00000239513	LINC01210
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ENSG00000179935	LINC00652	ENSG00000239533	GOLGA2P2Y
ENSG00000180139	ACTA2-AS1	ENSG00000239589	LINC00879
ENSG00000180279	MGC45922	ENSG00000239653	PSMD6-AS2
ENSG00000180422	LINC00304	ENSG00000239791	AC002310.7
ENSG00000180712	RP11-290F5.2	ENSG00000239877	IGSF11-AS1
ENSG00000180769	WDFY3-AS2	ENSG00000239911	PRKAG2-AS1
ENSG00000180846	CSNK1G2-AS1	ENSG00000239920	AC015691.13
ENSG00000180910	TTTY11	ENSG00000239921	RP11-59J16.1
ENSG00000181171	FER1L6-AS1	ENSG00000239922	RP11-71N10.1
ENSG00000181211	HECW1-IT1	ENSG00000240040	AC096579.13
ENSG00000181798	LINC00471	ENSG00000240045	RP11-451G4.2
ENSG00000181995	LINC00301	ENSG00000240050	RP1-93H18.1
ENSG00000182021	RP11-381O7.3	ENSG00000240207	RP11-379F4.4
ENSG00000182057	OGFRP1	ENSG00000240291	RP11-499P20.2
ENSG00000182109	PPIEL	ENSG00000240405	LINC01212
ENSG00000182165	TP53TG1	ENSG00000240423	LINC00636
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ENSG00000182376	RP5-1142A6.8	ENSG00000240707	LINC01168
ENSG00000182586	LINC00334	ENSG00000240710	RP11-430C7.4
ENSG00000182824	AC008132.15	ENSG00000240770	C21orf91-OT1
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ENSG00000183385	TTTY8	ENSG00000240875	LINC00886
ENSG00000183535	COL18A1-AS1	ENSG00000240889	NDUFB2-AS1
ENSG00000183674	LINC00518	ENSG00000240973	RP11-458K10.2
ENSG00000184115	RP13-1039J1.2	ENSG00000240990	HOXA11-AS
ENSG00000184856	LINC00308	ENSG00000240996	FLJ37201
ENSG00000184906	AC129778.2	ENSG00000241158	ADAMTS9-AS1
ENSG00000184991	TTTY13	ENSG00000241163	LINC00877
ENSG00000185065	AC000068.5	ENSG00000241168	RP11-10O22.1
ENSG00000185168	LINC00482	ENSG00000241219	RP11-572M11.1
ENSG00000185186	LINC00313	ENSG00000241224	FLJ22763
ENSG00000185433	LINC00158	ENSG00000241280	RP11-221J22.2
ENSG00000185700	TTTY8B	ENSG00000241313	WWTR1-AS1
ENSG00000185847	LINC01405	ENSG00000241316	SUCLG2-AS1
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ENSG00000186019	AC084219.4	ENSG00000241336	RP11-451G4.1
ENSG00000186056	MATN1-AS1	ENSG00000241345	RP4-630C24.3
ENSG00000186148	AC013271.3	ENSG00000241369	LINC01192
ENSG00000186369	LINC00643	ENSG00000241469	LINC00635
ENSG00000186594	MIR22HG	ENSG00000241472	PTPRG-AS1

ENSG00000186615	KTN1-AS1	ENSG00000241490	RP11-553L6.2
ENSG00000187012	LINC00207	ENSG00000241560	ZBTB20-AS1
ENSG00000187185	CTD-2600O9.1	ENSG00000241684	ADAMTS9-AS2
ENSG00000187621	TCL6	ENSG00000241769	LINC00893
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ENSG00000188185	LINC00265	ENSG00000241990	RP6-109B7.3
ENSG00000188206	HNRNPU-AS1	ENSG00000242048	RP13-452N2.1
ENSG00000188525	AC010969.1	ENSG00000242049	DNAJB8-AS1
ENSG00000188660	LINC00319	ENSG00000242086	LINC00969
ENSG00000188693	CYP51A1-AS1	ENSG00000242094	FOXP1-IT1
ENSG00000188825	LINC00910	ENSG00000242125	SNHG3
ENSG00000189149	CRYM-AS1	ENSG00000242258	LINC00996
ENSG00000189223	PAX8-AS1	ENSG00000242282	AC108488.4
ENSG00000189229	AC069277.2	ENSG00000242288	RP11-464F9.1
ENSG00000189238	LINC00943	ENSG00000242349	NPPA-AS1
ENSG00000189419	SPATA41	ENSG00000242375	RP11-498P14.3
ENSG00000196167	COLCA1	ENSG00000242385	LINC00901
ENSG00000196273	LINC00523	ENSG00000242428	C3orf67-AS1
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ENSG00000196668	LINC00173	ENSG00000242622	RP11-18H7.1
ENSG00000196696	PDXDC2P	ENSG00000242641	LINC00971
ENSG00000196756	SNHG17	ENSG00000242686	RP11-1191J2.2
ENSG00000196810	CTBP1-AS2	ENSG00000242687	AC004893.11
ENSG00000196893	AC090286.4	ENSG00000242753	RP11-716O23.2
ENSG00000196951	SCOC-AS1	ENSG00000242759	LINC00882
ENSG00000196979	RP11-88G17.6	ENSG00000242808	SOX2-OT
ENSG00000197085	NPSR1-AS1	ENSG00000243008	RP11-556N21.1
ENSG00000197176	RP11-76E12.1	ENSG00000243069	ARHGEF26-AS1
ENSG00000197210	KB-1592A4.15	ENSG00000243083	LINC00870
ENSG00000197251	LINC00336	ENSG00000243150	RP11-538P18.2
ENSG00000197291	RAMP2-AS1	ENSG00000243179	AC110769.3
ENSG00000197332	ZNF833P	ENSG00000243197	TUSC7
ENSG00000197503	LINC00477	ENSG00000243276	RP11-384F7.1
ENSG00000197558	SSPO	ENSG00000243319	FGF14-IT1
ENSG00000197813	CTC-301O7.4	ENSG00000243349	RP11-445N18.7
ENSG00000197989	SNHG12	ENSG00000243593	RP11-500K19.1
ENSG00000198106	SNX29P2	ENSG00000243629	LINC00880
ENSG00000198547	C20orf203	ENSG00000243637	AC019221.4
ENSG00000198788	MUC2	ENSG00000243701	LINC00883
ENSG00000203279	RP11-498P14.5	ENSG00000243715	CACNA2D3-AS1
ENSG00000203280	CTA-221G9.11	ENSG00000243766	HOTTIP
ENSG00000203288	RP11-98D18.9	ENSG00000243797	CTB-111H14.1

ENSG00000203321	RP11-197P3.4	ENSG00000243818	RP11-372E1.4
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ENSG00000203499	FAM83H-AS1	ENSG00000244040	IL12A-AS1
ENSG00000203527	Z99756.1	ENSG00000244041	LINC01011
ENSG00000203585	RP11-542B15.1	ENSG00000244151	RP11-148K1.12
ENSG00000203650	LINC01285	ENSG00000244203	FOXP1-AS1
ENSG00000203688	RP11-351J23.1	ENSG00000244215	RP11-88I21.2
ENSG00000203709	C1orf132	ENSG00000244227	LINC01330
ENSG00000203721	LINC00862	ENSG00000244231	CSPG4P2Y
ENSG00000203729	LINC00272	ENSG00000244300	RP11-475N22.4
ENSG00000203739	RP11-296O14.3	ENSG00000244342	LINC00698
ENSG00000203801	LINC00222	ENSG00000244471	RP11-78J21.4
ENSG00000203808	BVES-AS1	ENSG00000244479	OR2A1-AS1
ENSG00000203865	ATP1A1-AS1	ENSG00000244578	LINC01391
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ENSG00000203897	SPATA42	ENSG00000244926	ALKBH3-AS1
ENSG00000203930	LINC00632	ENSG00000244953	RP11-613D13.8
ENSG00000203987	RP11-188C12.3	ENSG00000244968	LIFR-AS1
ENSG00000203999	LINC01270	ENSG00000245025	RP11-875O11.1
ENSG00000204025	TRPC5OS	ENSG00000245060	LINC00847
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ENSG00000204054	LINC00963	ENSG00000245080	RP11-320N21.1
ENSG00000204055	RP11-247A12.2	ENSG00000245105	A2M-AS1
ENSG00000204148	LINC00474	ENSG00000245112	SMARCA5-AS1
ENSG00000204241	RP11-713P17.3	ENSG00000245146	LINC01024
ENSG00000204272	LINC01420	ENSG00000245156	RP11-867G23.3
ENSG00000204282	TNRC6C-AS1	ENSG00000245164	LINC00861
ENSG00000204380	AC005042.4	ENSG00000245213	RP11-10K16.1
ENSG00000204460	AC079586.1	ENSG00000245248	USP2-AS1
ENSG00000204528	PSORS1C3	ENSG00000245275	SAP30L-AS1
ENSG00000204581	AC096670.3	ENSG00000245281	CTD-2547L16.1
ENSG00000204588	LINC01123	ENSG00000245293	RP11-286E11.1
ENSG00000204603	LINC01257	ENSG00000245311	ARNTL2-AS1
ENSG00000204623	ZNRD1-AS1	ENSG00000245384	AC004053.1
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ENSG00000204666	FLJ26850	ENSG00000245479	RP11-387D10.3
ENSG00000204684	RP5-1004I9.1	ENSG00000245498	RP11-677M14.7
ENSG00000204685	STARD7-AS1	ENSG00000245522	RP11-540A21.2
ENSG00000204706	MAMDC2-AS1	ENSG00000245526	LINC00461
ENSG00000204758	CTC-308K20.1	ENSG00000245534	RP11-219B17.1
ENSG00000204792	LINC01291	ENSG00000245552	RP11-712B9.2
ENSG00000204832	ST8SIA6-AS1	ENSG00000245571	AP001258.4
ENSG00000204850	CTB-158D10.3	ENSG00000245573	BDNF-AS
ENSG00000204860	FAM201A	ENSG00000245598	DACT3-AS1

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ENSG00000204934	ATP6V0E2-AS1	ENSG00000245648	RP11-277P12.20
ENSG00000204949	FAM83A-AS1	ENSG00000245685	AF146191.4
ENSG00000205037	RP11-863P13.4	ENSG00000245694	CRNDE
ENSG00000205054	LINC01121	ENSG00000245729	RP11-480D4.1
ENSG00000205231	TTLL10-AS1	ENSG00000245750	RP11-279F6.1
ENSG00000205266	AL353997.3	ENSG00000245812	RP11-175K6.1
ENSG00000205396	LINC00661	ENSG00000245832	RP11-179A16.1
ENSG00000205424	AL592528.1	ENSG00000245870	LINC00682
ENSG00000205488	CALML3-AS1	ENSG00000245904	RP11-796E2.4
ENSG00000205500	AC013472.3	ENSG00000245910	SNHG6
ENSG00000205559	CHKB-AS1	ENSG00000245937	LINC01184
ENSG00000205562	RP11-497E19.1	ENSG00000245954	RP11-18H21.1
ENSG00000205632	LINC01310	ENSG00000246022	ALDH1L1-AS2
ENSG00000205634	LINC00898	ENSG00000246067	RAB30-AS1
ENSG00000205663	RP11-706O15.5	ENSG00000246084	CTD-2506J14.1
ENSG00000205786	AC002511.1	ENSG00000246089	RP11-115C21.2
ENSG00000205791	LOH12CR2	ENSG00000246090	RP11-696N14.1
ENSG00000205837	LINC00487	ENSG00000246100	LINC00900
ENSG00000205861	C1QTNF9B-AS1	ENSG00000246130	RP11-875O11.2
ENSG00000205865	FAM99B	ENSG00000246211	RP11-632K5.3
ENSG00000205866	FAM99A	ENSG00000246225	RP11-17A1.3
ENSG00000205885	C1RL-AS1	ENSG00000246228	CASC8
ENSG00000205913	SRRM2-AS1	ENSG00000246250	RP11-613D13.5
ENSG00000205930	C21orf49	ENSG00000246263	KB-431C1.4
ENSG00000206028	CTA-373H7.7	ENSG00000246273	SBF2-AS1
ENSG00000206113	RP11-503N18.1	ENSG00000246316	RP11-492A10.1
ENSG00000206140	TMEM191C	ENSG00000246334	PRR7-AS1
ENSG00000206195	AP000525.9	ENSG00000246339	EXTL3-AS1
ENSG00000206417	H1FX-AS1	ENSG00000246350	RP5-1186N24.3
ENSG00000206567	AC022007.5	ENSG00000246363	RP11-13A1.1
ENSG00000207955	MIR219A2	ENSG00000246375	RP11-10L7.1
ENSG00000212163	SNORD91A	ENSG00000246379	RP11-461O7.1
ENSG00000212694	LINC01089	ENSG00000246422	CTD-2024I7.13
ENSG00000212766	LINC00277	ENSG00000246430	LINC00968
ENSG00000212855	TTTY2	ENSG00000246451	RP11-894P9.1
ENSG00000212856	TTTY2B	ENSG00000246465	RP11-57A19.2
ENSG00000212978	AC016747.3	ENSG00000246477	AF131216.6
ENSG00000213057	C1orf220	ENSG00000246523	RP11-736K20.6
ENSG00000213373	LINC00671	ENSG00000246582	RP11-1149O23.3
ENSG00000213468	FIRRE	ENSG00000246627	CACNA1C-AS1
ENSG00000213742	ZNF337-AS1	ENSG00000246695	RASSF8-AS1
ENSG00000213904	LIPE-AS1	ENSG00000246731	MGC16275
ENSG00000213963	AC074286.1	ENSG00000246763	RGMB-AS1

ENSG00000213971	RP11-15H20.6	ENSG00000246790	RP11-730K11.1
ENSG00000213981	AC007277.3	ENSG00000246792	RP11-68L18.1
ENSG00000214039	RP11-474D1.3	ENSG00000246876	RP11-519M16.1
ENSG00000214043	RP5-944M2.3	ENSG00000246877	DNM1P35
ENSG00000214049	UCA1	ENSG00000246889	AP000487.5
ENSG00000214145	LINC00887	ENSG00000246898	LINC00920
ENSG00000214184	AC012487.2	ENSG00000246982	RP1-179N16.6
ENSG00000214347	CTB-180A7.8	ENSG00000246985	SOCS2-AS1
ENSG00000214353	VAC14-AS1	ENSG00000247049	CTC-338M12.7
ENSG00000214381	LINC00488	ENSG00000247081	BAALC-AS1
ENSG00000214407	RP11-221J22.1	ENSG00000247095	MIR210HG
ENSG00000214432	AC068831.10	ENSG00000247131	RP11-588G21.2
ENSG00000214548	MEG3	ENSG00000247134	RP11-11N9.4
ENSG00000214691	AC104654.1	ENSG00000247151	CSTF3-AS1
ENSG00000214719	AC005562.1	ENSG00000247157	LINC01252
ENSG00000214725	CDIPT-AS1	ENSG00000247193	RP11-431M7.3
ENSG00000214783	POLR2J4	ENSG00000247199	RP11-373N22.3
ENSG00000214837	LINC01347	ENSG00000247228	RP11-296I10.3
ENSG00000214870	AC004540.5	ENSG00000247240	UBL7-AS1
ENSG00000214894	LINC00243	ENSG00000247271	ZBED5-AS1
ENSG00000214922	HLA-F-AS1	ENSG00000247287	RP11-902B17.1
ENSG00000214970	CTC-297N7.7	ENSG00000247317	RP11-273G15.2
ENSG00000215022	RP1-257A7.4	ENSG00000247324	RP11-510M2.2
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ENSG00000231993	EP300-AS1	ENSG00000261582	RP4-614O4.11

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ENSG00000232170	LINC00708	ENSG00000261760	RP11-1223D19.1
ENSG00000232224	LINC00202-1	ENSG00000261771	DYX1C1-CCPG1
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ENSG00000232445	RP11-132A1.4	ENSG00000261879	RP11-333E1.1
ENSG00000232504	AC105053.4	ENSG00000261924	CTD-2561B21.5
ENSG00000232520	AC012507.3	ENSG00000261971	RP11-473M20.7
ENSG00000232527	RP11-14N7.2	ENSG00000262001	DLGAP1-AS2
ENSG00000232593	KANTR	ENSG00000262152	LINC00514
ENSG00000232600	AC084125.4	ENSG00000262188	RP11-353N14.4
ENSG00000232648	RP11-367N14.2	ENSG00000262468	RP11-95P2.1
ENSG00000232656	IDI2-AS1	ENSG00000262880	RP11-104H15.7
ENSG00000232677	LINC00665	ENSG00000263069	CTD-2047H16.4
ENSG00000232684	ATP11A-AS1	ENSG00000263072	ZNF213-AS1
ENSG00000232685	LINC00442	ENSG00000263212	LA16c-306E5.3
ENSG00000232712	RP4-777D9.2	ENSG00000263214	ZNF205-AS1
ENSG00000232721	RP11-403I13.5	ENSG00000263327	TAPT1-AS1
ENSG00000232729	AC083884.8	ENSG00000263715	RP11-105N13.4
ENSG00000232756	RP5-1185I7.1	ENSG00000263724	DLGAP1-AS3
ENSG00000232759	AC002480.3	ENSG00000263753	LINC00667
ENSG00000232803	RP11-93B14.5	ENSG00000263798	RP11-6N17.9
ENSG00000232808	TTTY20	ENSG00000263812	LINC00908
ENSG00000232821	AC003986.6	ENSG00000263874	LINC00672
ENSG00000232825	RP5-896L10.1	ENSG00000263917	RP11-53I6.2
ENSG00000232827	LINC01189	ENSG00000264066	MIR451A
ENSG00000232860	SMG7-AS1	ENSG00000264112	RP11-159D12.2
ENSG00000232907	RP5-977B1.7	ENSG00000264151	RP11-739N10.1
ENSG00000232909	RP3-510O8.4	ENSG00000264243	RP11-6N17.1
ENSG00000232913	RP11-429H9.4	ENSG00000264269	RP11-15F12.1
ENSG00000232931	LINC00342	ENSG00000264515	CTC-525D6.1
ENSG00000232956	SNHG15	ENSG00000264630	RP11-4F22.2
ENSG00000232973	CYP1B1-AS1	ENSG00000264660	RP11-381P6.1

ENSG00000232977	LINC00327	ENSG00000264772	SNORA67
ENSG00000232995	RGS5	ENSG00000264859	RP11-75N4.2
ENSG00000233006	AC034220.3	ENSG00000265091	RP11-835E18.5
ENSG00000233008	RP11-475O6.1	ENSG00000265096	C1QTNF1-AS1
ENSG00000233013	FAM157B	ENSG00000265125	RP11-31I22.3
ENSG00000233016	SNHG7	ENSG00000265142	MIR133A1HG
ENSG00000233038	AC011899.9	ENSG00000265148	BZRAP1-AS1
ENSG00000233058	LINC00884	ENSG00000265206	MIR142
ENSG00000233093	LINC00892	ENSG00000265257	RP11-21J18.1
ENSG00000233098	RP11-344E13.3	ENSG00000265369	PCAT18
ENSG00000233101	HOXB-AS3	ENSG00000265408	RP11-361L15.4
ENSG00000233123	LINC01007	ENSG00000265479	DTX2P1-UPK3BP1-PMS2P11
ENSG00000233183	RP3-468B3.2	ENSG00000265485	RP11-449D8.1
ENSG00000233184	RP11-421L21.3	ENSG00000265544	AA06
ENSG00000233208	LINC00642	ENSG00000265688	MAFG-AS1
ENSG00000233215	AP000472.2	ENSG00000265692	RP13-516M14.4
ENSG00000233221	AC133785.1	ENSG00000265702	RP11-156L14.1
ENSG00000233237	LINC00472	ENSG00000265766	CXADRP3
ENSG00000233251	AC007743.1	ENSG00000265787	CYP4F35P
ENSG00000233261	LINC00264	ENSG00000265794	RP11-227G15.3
ENSG00000233288	RP11-760D2.5	ENSG00000265845	RP11-20B24.5
ENSG00000233296	AC092159.2	ENSG00000265933	LINC00668
ENSG00000233304	LINC01346	ENSG00000265992	ESRG
ENSG00000233316	DSCR10	ENSG00000266079	SNORA59B
ENSG00000233332	RP4-799P18.2	ENSG00000266088	RP5-1028K7.2
ENSG00000233351	RP1-69D17.3	ENSG00000266106	RP11-647F2.2
ENSG00000233354	LINC00028	ENSG00000266149	RP11-789C17.3
ENSG00000233360	Z83844.1	ENSG00000266413	RP11-88L24.4
ENSG00000233392	AC104809.4	ENSG00000266560	RP11-1007I13.4
ENSG00000233395	LINC00841	ENSG00000266677	RP11-258F1.1
ENSG00000233399	RP11-111I12.1	ENSG00000266821	RP11-6N17.2
ENSG00000233410	LINC01222	ENSG00000266835	RP11-838N2.4
ENSG00000233429	HOTAIRM1	ENSG00000266904	LINC00663
ENSG00000233452	STXBP5-AS1	ENSG00000266921	RP11-15A1.7
ENSG00000233485	RP3-467K16.2	ENSG00000266923	RP11-693J15.4
ENSG00000233491	AC010091.1	ENSG00000266929	RP11-400F19.8
ENSG00000233515	AL022344.4	ENSG00000266952	RP11-909B2.1
ENSG00000233521	RP5-1172A22.1	ENSG00000266988	RP11-749H17.1
ENSG00000233522	FAM224A	ENSG00000267002	RP11-242D8.1
ENSG00000233527	AC092295.7	ENSG00000267009	RP11-120M18.2
ENSG00000233532	LINC00460	ENSG00000267013	CTD-2171N6.1
ENSG00000233542	RP11-547D24.1	ENSG00000267014	CTD-2081K17.2
ENSG00000233559	AC016831.7	ENSG00000267039	RP11-58G13.1

ENSG00000233570	LINC00690	ENSG00000267040	RP11-35G9.3
ENSG00000233593	RP4-665J23.1	ENSG00000267047	RP11-589P10.7
ENSG00000233630	FAM138F	ENSG00000267048	RP11-566K11.7
ENSG00000233639	LINC01158	ENSG00000267058	RP11-15A1.3
ENSG00000233642	GPR158-AS1	ENSG00000267080	ASB16-AS1
ENSG00000233651	RP11-111F5.8	ENSG00000267097	RP11-309E23.2
ENSG00000233656	RP11-716O23.1	ENSG00000267104	TBC1D3P1-DHX40P1
ENSG00000233694	AC007365.1	ENSG00000267107	PCAT19
ENSG00000233699	TTTY18	ENSG00000267121	CTD-2020K17.1
ENSG00000233718	MYCNOS	ENSG00000267122	AC004490.1
ENSG00000233723	LINC01122	ENSG00000267128	RNF157-AS1
ENSG00000233725	LINC00284	ENSG00000267134	RP11-146N18.1
ENSG00000233791	LINC01136	ENSG00000267147	CTC-548K16.1
ENSG00000233800	RP11-295G24.4	ENSG00000267149	CTC-550B14.6
ENSG00000233828	CTC-242N15.1	ENSG00000267169	CTB-55O6.12
ENSG00000233854	POU6F2-AS2	ENSG00000267174	CTC-510F12.4
ENSG00000233864	TTTY15	ENSG00000267188	CTC-512J12.4
ENSG00000233878	AC073133.1	ENSG00000267239	RP11-794M8.1
ENSG00000233896	RP4-684O24.5	ENSG00000267243	AC005307.3
ENSG00000233926	RP11-154D17.1	ENSG00000267244	CTB-31O20.4
ENSG00000233930	KRTAP5-AS1	ENSG00000267254	ZNF790-AS1
ENSG00000233937	CTC-338M12.4	ENSG00000267272	LINC01140
ENSG00000233968	RP11-354E11.2	ENSG00000267278	MAP3K14-AS1
ENSG00000233973	LINC01360	ENSG00000267288	RP13-890H12.2
ENSG00000233997	AP000475.2	ENSG00000267302	RP11-178C3.2
ENSG00000234026	RP11-310E22.4	ENSG00000267313	KC6
ENSG00000234028	AC062029.1	ENSG00000267325	RP11-397A16.2
ENSG00000234062	RP11-308D16.4	ENSG00000267337	CTC-782O7.1
ENSG00000234111	RP11-364P22.1	ENSG00000267339	LINC00906
ENSG00000234129	RP11-120D5.1	ENSG00000267374	LINC00669
ENSG00000234155	RP11-30P6.6	ENSG00000267413	RP11-636O21.1
ENSG00000234171	RNASEH1-AS1	ENSG00000267439	AC002398.11
ENSG00000234177	LINC01114	ENSG00000267454	ZNF582-AS1
ENSG00000234186	C16orf82	ENSG00000267465	AC011525.4
ENSG00000234199	LINC01191	ENSG00000267470	ZNF571-AS1
ENSG00000234229	RP11-308N19.4	ENSG00000267506	RP11-13K12.1
ENSG00000234264	DEPDC1-AS1	ENSG00000267532	MIR497HG
ENSG00000234277	CTD-2090I13.1	ENSG00000267535	LINC00868
ENSG00000234323	RP11-308N19.1	ENSG00000267559	RP11-383M4.6
ENSG00000234336	JAZF1-AS1	ENSG00000267575	CTC-459F4.3
ENSG00000234350	AC007405.4	ENSG00000267581	CTC-559E9.4
ENSG00000234352	MIR490	ENSG00000267586	LINC00907
ENSG00000234377	RNF219-AS1	ENSG00000267603	LINC01028

ENSG00000234380	AP000330.8	ENSG00000267606	AC006116.21
ENSG00000234384	LINC01049	ENSG00000267629	AC138430.4
ENSG00000234423	LINC01250	ENSG00000267640	CTD-2554C21.2
ENSG00000234437	RP1-206D15.3	ENSG00000267665	RP11-13K12.2
ENSG00000234449	RP11-706O15.3	ENSG00000267690	LDLRAD4-AS1
ENSG00000234456	MAGI2-AS3	ENSG00000267696	CTB-151G24.1
ENSG00000234492	RPL34-AS1	ENSG00000267698	AC002116.7
ENSG00000234497	ERICH3-AS1	ENSG00000267709	AC024592.9
ENSG00000234509	AP000253.1	ENSG00000267712	RP11-456O19.4
ENSG00000234572	AC007880.1	ENSG00000267750	AC003102.3
ENSG00000234608	MAPKAPK5-AS1	ENSG00000267761	CTD-2130O13.1
ENSG00000234636	MED14OS	ENSG00000267767	CTC-523E23.4
ENSG00000234661	CHL1-AS1	ENSG00000267779	CTC-360P9.3
ENSG00000234663	AC104820.2	ENSG00000267787	RP11-35G9.5
ENSG00000234665	RP11-262H14.3	ENSG00000267827	CTC-471J1.8
ENSG00000234684	SDCBP2-AS1	ENSG00000267858	AC016629.8
ENSG00000234688	RP1-293L6.1	ENSG00000267943	CTD-2620I22.3
ENSG00000234690	AC073283.4	ENSG00000268006	PTOV1-AS1
ENSG00000234696	GPR50-AS1	ENSG00000268038	AC011516.2
ENSG00000234736	FAM170B-AS1	ENSG00000268049	CTD-2619J13.9
ENSG00000234741	GAS5	ENSG00000268061	NAPA-AS1
ENSG00000234754	C1orf140	ENSG00000268119	CTD-2561J22.5
ENSG00000234771	RP11-395P17.3	ENSG00000268218	AC137932.4
ENSG00000234773	CTD-2666L21.1	ENSG00000268230	CTD-2619J13.8
ENSG00000234787	LINC00458	ENSG00000268240	RP11-678G14.4
ENSG00000234807	LINC01135	ENSG00000268262	CTC-246B18.8
ENSG00000234810	RP11-466L17.1	ENSG00000268362	CTD-2017D11.1
ENSG00000234817	RP3-400B16.1	ENSG00000268364	SMC5-AS1
ENSG00000234828	RP11-526A4.1	ENSG00000268388	FENDRR
ENSG00000234840	LINC01239	ENSG00000268460	DKFZp434J0226
ENSG00000234855	RP11-453E2.2	ENSG00000268516	CTD-3138B18.5
ENSG00000234859	AC003958.2	ENSG00000268530	CTC-273B12.5
ENSG00000234880	LINC00163	ENSG00000268573	RP11-158H5.7
ENSG00000234883	MIR155HG	ENSG00000268575	RP1-283E3.8
ENSG00000234899	SOX9-AS1	ENSG00000268621	AC006262.5
ENSG00000234902	AC007879.2	ENSG00000268649	MIR296
ENSG00000234912	SNHG20	ENSG00000268654	MIMT1
ENSG00000234945	GTF3C2-AS1	ENSG00000268658	LINC00664
ENSG00000234962	LINC00700	ENSG00000268751	SCGB1B2P
ENSG00000234986	XX-C2158C12.1	ENSG00000268818	CITF22-62D4.1
ENSG00000234996	RP11-480I12.7	ENSG00000268894	PLCE1-AS1
ENSG00000235016	RP11-493K19.3	ENSG00000268895	A1BG-AS1
ENSG00000235023	AP001626.2	ENSG00000269086	CTC-523E23.5
ENSG00000235026	DPP10-AS1	ENSG00000269107	RP11-15H20.7

ENSG00000235033	RP11-61I13.3	ENSG00000269110	CTC-513N18.7
ENSG00000235049	LINC00940	ENSG00000269235	HCCAT3
ENSG00000235054	RP5-1166F10.1	ENSG00000269243	CTD-2231E14.8
ENSG00000235106	LINC00094	ENSG00000269289	CTB-92J24.3
ENSG00000235118	AC010731.4	ENSG00000269293	ZSCAN16-AS1
ENSG00000235123	DSCAM-AS1	ENSG00000269386	RAB11B-AS1
ENSG00000235139	AC003984.1	ENSG00000269416	LINC01224
ENSG00000235142	RP1-60O19.1	ENSG00000269535	CTD-2525I3.6
ENSG00000235172	LINC01366	ENSG00000269604	AC005523.2
ENSG00000235244	RP11-761E20.1	ENSG00000269609	RPARP-AS1
ENSG00000235257	ITGA9-AS1	ENSG00000269640	CTD-2521M24.9
ENSG00000235295	FLJ41941	ENSG00000269696	AC007228.11
ENSG00000235304	LINC01281	ENSG00000269749	AC005614.5
ENSG00000235381	RP11-477D19.2	ENSG00000269793	AC006115.3
ENSG00000235387	LINC00961	ENSG00000269834	CTD-3018O17.3
ENSG00000235408	SNORA71B	ENSG00000269893	SNHG8
ENSG00000235412	TTTY4B	ENSG00000269959	SPACA6P-AS
ENSG00000235437	LINC01278	ENSG00000269994	RP11-276H19.2
ENSG00000235453	TOPORS-AS1	ENSG00000270002	RP11-93H12.4
ENSG00000235475	LINC01372	ENSG00000270066	SCARNA2
ENSG00000235480	RP11-363D14.1	ENSG00000270246	SNORD109A
ENSG00000235481	UBE2R2-AS1	ENSG00000270279	RP4-806M20.5
ENSG00000235513	RP4-756G23.5	ENSG00000270362	HMGN3-AS1
ENSG00000235527	HIPK1-AS1	ENSG00000270547	LINC01235
ENSG00000235532	LINC00402	ENSG00000270574	RP11-171I2.2
ENSG00000235535	RP11-532N4.2	ENSG00000270580	RP11-1186N24.5
ENSG00000235560	AC002310.12	ENSG00000270641	TSIX
ENSG00000235563	RP11-334A14.8	ENSG00000270726	AJ271736.10
ENSG00000235584	AC008268.1	ENSG00000271086	NAMA
ENSG00000235590	GNAS-AS1	ENSG00000271147	RP4-769N13.6
ENSG00000235597	LINC01102	ENSG00000271270	TMCC1-AS1
ENSG00000235609	AF127936.7	ENSG00000271430	RP3-368A4.5
ENSG00000235621	LINC00494	ENSG00000271593	RP11-335E6.4
ENSG00000235641	LINC00484	ENSG00000271758	RP11-35J10.5
ENSG00000235652	RP11-545I5.3	ENSG00000271762	RP11-213H15.4
ENSG00000235665	LINC00298	ENSG00000271816	BMS1P4
ENSG00000235699	CXorf51B	ENSG00000271826	PLS3-AS1
ENSG00000235703	LINC00894	ENSG00000271853	RP1-178F15.5
ENSG00000235706	DICER1-AS1	ENSG00000271880	RP11-96C23.5
ENSG00000235726	AC010148.1	ENSG00000271894	RP11-482H16.1
ENSG00000235733	RP3-522P13.3	ENSG00000272005	RP11-91J19.4
ENSG00000235740	RP11-436I24.1	ENSG00000272009	RP1-313I6.12
ENSG00000235770	LINC00607	ENSG00000272030	RP1-178F15.4
ENSG00000235831	BHLHE40-AS1	ENSG00000272053	RP11-367G6.3

ENSG00000235862	RP11-338C15.5	ENSG00000272084	RP5-1126H10.2
ENSG00000235884	LINC00941	ENSG00000272097	RP11-421M1.8
ENSG00000235885	AC023115.2	ENSG00000272140	RP11-574K11.29
ENSG00000235897	TM4SF19-AS1	ENSG00000272142	RP11-428J1.5
ENSG00000235903	CPB2-AS1	ENSG00000272154	AC005754.7
ENSG00000235914	MACROD2-AS1	ENSG00000272168	CASC15
ENSG00000235947	EGOT	ENSG00000272180	RP11-481J13.1
ENSG00000235954	TTC28-AS1	ENSG00000272259	RP11-305P22.9
ENSG00000235958	UBOX5-AS1	ENSG00000272298	RP11-386M24.8
ENSG00000235989	MORC2-AS1	ENSG00000272328	RP4-594A5.1
ENSG00000235994	RP3-470B24.5	ENSG00000272329	RP11-65L19.4
ENSG00000235997	AC109642.1	ENSG00000272446	RP1-225E12.3
ENSG00000236013	RP3-332B22.1	ENSG00000272485	RP11-284J1.1
ENSG00000236017	ASMTL-AS1	ENSG00000272508	RP11-96C23.14
ENSG00000236065	RP1-117O3.2	ENSG00000272549	RP11-351J23.2
ENSG00000236088	COX10-AS1	ENSG00000272568	CTB-113D17.1
ENSG00000236107	AC010127.3	ENSG00000272610	MAGI1-IT1
ENSG00000236133	LINC01069	ENSG00000272620	AFAP1-AS1
ENSG00000236144	AD000090.2	ENSG00000272657	AP000320.7
ENSG00000236200	KDM4A-AS1	ENSG00000272679	RP11-216L13.18
ENSG00000236268	LINC01361	ENSG00000272736	RP11-799N11.1
ENSG00000236301	MRGPRG-AS1	ENSG00000272780	RP11-822E23.8
ENSG00000236306	LINC01241	ENSG00000272801	RP1-170O19.23
ENSG00000236333	TRHDE-AS1	ENSG00000272815	RP11-219A15.4
ENSG00000236340	AC000099.1	ENSG00000272884	RP11-104H15.10
ENSG00000236366	RP11-440G9.1	ENSG00000272888	AC013394.2
ENSG00000236383	LINC00854	ENSG00000272902	RP11-299H21.1
ENSG00000236384	LINC00479	ENSG00000272917	RP11-705C15.5
ENSG00000236404	VLDLR-AS1	ENSG00000272944	CTD-2308L22.1
ENSG00000236423	LINC01134	ENSG00000272949	RP11-514P8.8
ENSG00000236432	AC097662.2	ENSG00000272975	MYHAS
ENSG00000236438	FAM157A	ENSG00000273000	KB-1572G7.2
ENSG00000236445	LINC00608	ENSG00000273018	CTD-2303H24.2
ENSG00000236449	AC018890.6	ENSG00000273065	RP11-58E21.5
ENSG00000236466	RP11-795J1.1	ENSG00000273066	RP11-216L13.19
ENSG00000236467	RP11-443A13.5	ENSG00000273112	RP11-25K21.6
ENSG00000236532	AL035610.2	ENSG00000273125	RP11-115H18.1
ENSG00000236548	STL	ENSG00000273184	RP11-212P7.3
ENSG00000236653	AC005235.1	ENSG00000273189	CTD-3148I10.15
ENSG00000236656	RP11-144L1.4	ENSG00000273299	CTB-13L3.1
ENSG00000236671	PRKG1-AS1	ENSG00000273311	DGCR11
ENSG00000236678	LINC00347	ENSG00000273313	RBAKDN
ENSG00000236700	LINC01010	ENSG00000273328	RP11-141M3.6
ENSG00000236719	OVAAL	ENSG00000273345	CTD-2410N18.4

ENSG00000236740	RP11-411K7.1	ENSG00000273409	RP11-480C22.1
ENSG00000236751	LINC01186	ENSG00000273432	RP5-1165K10.2
ENSG00000236753	MKLN1-AS	ENSG00000273471	RP13-1039J1.4
ENSG00000236780	AC078941.1	ENSG00000198788	MUC2
ENSG00000236790	LINC00299	ENSG00000206082	LINC01002
ENSG00000236810	TCEB3-AS1	ENSG00000218839	FAM138C
ENSG00000236830	CBR3-AS1	ENSG00000225489	RP11-390F4.3
ENSG00000236850	BMS1P20	ENSG00000225706	PTPRD-AS1
ENSG00000236854	AL121656.5	ENSG00000227917	RP11-143M1.3
ENSG00000236859	NIFK-AS1	ENSG00000230724	LINC01001
ENSG00000236908	RP5-1063M23.2	ENSG00000233296	AC092159.2
ENSG00000236914	RP11-1008C21.2	ENSG00000233630	FAM138F
ENSG00000236963	LINC01141	ENSG00000236404	VLDLR-AS1
ENSG00000236990	RP11-433J20.1	ENSG00000237613	FAM138A
ENSG00000237021	RP3-486I3.7	ENSG00000240859	AC093627.10
ENSG00000237037	NDUFA6-AS1	ENSG00000247095	MIR210HG
ENSG00000237048	TTTY12	ENSG00000251661	RP11-326C3.11
ENSG00000237069	TTTY23B	ENSG00000254815	RP11-496I9.1
ENSG00000237070	AC005550.3	ENSG00000263724	DLGAP1-AS3
ENSG00000237094	RP4-669L17.10	ENSG00000272485	RP11-284J1.1

Supplementary Table S3. List of GO terms enriched in 10 clusters (Top 10 terms for each cluster are listed).

Cluster	GO Term	Definition	P-value	FDR
cluster1	GO:0042981	regulation of apoptosis	6.10E-09	1.20E-05
cluster1	GO:43067	regulation of programmed cell death	8.00E-09	7.90E-06
cluster1	GO:0010941	regulation of cell death	8.80E-09	5.80E-06
cluster1	GO:0012501	programmed cell death	1.30E-08	6.60E-06
cluster1	GO:0008219	cell death	1.40E-08	5.60E-06
cluster1	GO:0016265	death	1.70E-08	5.50E-06
cluster1	GO:0006915	apoptosis	3.50E-08	9.90E-06
cluster1	GO:0051329	interphase of mitotic cell cycle	9.50E-08	2.40E-05
cluster1	GO:0051325	interphase	1.30E-07	2.90E-05
cluster1	GO:0051329	positive regulation of molecular function	2.50E-07	4.90E-05
cluster2	GO:0007049	cell cycle	2.10E-11	4.50E-08
cluster2	GO:0042127	regulation of cell proliferation	1.20E-10	1.30E-07
cluster2	GO:0042981	regulation of apoptosis	3.00E-09	2.10E-06
cluster2	GO:0043067	regulation of programmed cell death	3.90E-09	2.10E-06
cluster2	GO:0010941	regulation of cell death	4.30E-09	1.90E-06
cluster2	GO:0010033	response to organic substance	7.00E-09	2.50E-06
cluster2	GO:0009719	response to endogenous stimulus	1.20E-08	3.80E-06
cluster2	GO:0010604	positive regulation of macromolecule metabolic process	1.70E-08	4.60E-06
cluster2	GO:0043066	negative regulation of apoptosis	1.90E-08	4.60E-06
cluster2	GO:0043069	negative regulation of programmed cell death	2.50E-08	5.30E-06
cluster3	GO:0010604	positive regulation of macromolecule metabolic process	3.50E-11	3.60E-08
cluster3	GO:0051329	interphase of mitotic cell cycle	2.10E-10	1.50E-07
cluster3	GO:0043067	regulation of programmed cell death	3.00E-10	1.60E-07
cluster3	GO:0010941	regulation of cell death	3.40E-10	1.40E-07
cluster3	GO:0042981	regulation of apoptosis	8.00E-10	2.80E-07
cluster3	GO:0031328	positive regulation of cellular biosynthetic process	5.40E-09	1.60E-06
cluster3	GO:0009891	positive regulation of biosynthetic process	7.80E-09	2.00E-06
cluster3	GO:0043069	negative regulation of programmed cell death	1.20E-08	2.70E-06
cluster3	GO:0051726	regulation of cell cycle	1.20E-08	2.40E-06
cluster3	GO:0060548	negative regulation of cell death	1.20E-08	2.30E-06
cluster4	GO:0042981	regulation of apoptosis	1.10E-05	1.70E-02
cluster4	GO:0043067	regulation of programmed cell death	1.30E-05	1.00E-02
cluster4	GO:0010941	regulation of cell death	1.40E-05	7.10E-03
cluster4	GO:0051329	interphase of mitotic cell cycle	3.40E-05	1.20E-02
cluster4	GO:0051325	interphase	4.10E-05	1.20E-02
cluster4	GO:0007049	cell cycle	5.60E-05	1.40E-02
cluster4	GO:0043065	positive regulation of apoptosis	6.30E-05	1.30E-02
cluster4	GO:0043068	positive regulation of programmed cell death	6.90E-05	1.30E-02

cluster4	GO:0010942	positive regulation of cell death	7.20E-05	1.20E-02
cluster4	GO:0043488	regulation of mRNA stability	1.30E-04	1.80E-02
cluster5	GO:0042127	regulation of cell proliferation	7.90E-14	1.60E-10
cluster5	GO:0051325	interphase	1.40E-11	1.40E-08
cluster5	GO:0012501	programmed cell death	1.50E-11	1.00E-08
cluster5	GO:0007049	cell cycle	6.00E-11	3.10E-08
cluster5	GO:0043067	regulation of programmed cell death	6.30E-11	2.60E-08
cluster5	GO:0010941	regulation of cell death	7.10E-11	2.40E-08
cluster5	GO:0000082	G1/S transition of mitotic cell cycle	7.50E-11	2.20E-08
cluster5	GO:0010604	positive regulation of macromolecule metabolic process	9.10E-11	2.30E-08
cluster5	GO:0051329	interphase of mitotic cell cycle	1.10E-10	2.40E-08
cluster5	GO:0051726	regulation of cell cycle	1.60E-10	3.30E-08
cluster6	GO:0045944	positive regulation of transcription from RNA polymerase II promoter	3.80E-07	6.10E-04
cluster6	GO:0006974	response to DNA damage stimulus	4.10E-07	3.30E-04
cluster6	GO:0045893	positive regulation of transcription, DNA-dependent	6.40E-07	3.40E-04
cluster6	GO:0051254	positive regulation of RNA metabolic process	7.30E-07	2.90E-04
cluster6	GO:0010629	negative regulation of gene expression	1.50E-06	4.70E-04
cluster6	GO:0045934	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1.90E-06	4.90E-04
cluster6	GO:0007049	cell cycle	1.90E-06	4.30E-04
cluster6	GO:0010033	response to organic substance	1.90E-06	3.70E-04
cluster6	GO:0006357	regulation of transcription from RNA polymerase II promoter	2.20E-06	3.80E-04
cluster6	GO:0051172	negative regulation of nitrogen compound metabolic process	2.30E-06	3.60E-04
cluster7	GO:0045597	positive regulation of cell differentiation	6.70E-15	1.40E-11
cluster7	GO:0042127	regulation of cell proliferation	1.70E-14	1.80E-11
cluster7	GO:0051094	positive regulation of developmental process	7.60E-14	5.30E-11
cluster7	GO:0009890	negative regulation of biosynthetic process	1.00E-12	5.30E-10
cluster7	GO:0031327	negative regulation of cellular biosynthetic process	2.80E-12	1.20E-09
cluster7	GO:0043067	regulation of programmed cell death	4.40E-12	1.50E-09
cluster7	GO:0010941	regulation of cell death	4.90E-12	1.50E-09
cluster7	GO:0045934	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	5.90E-12	1.50E-09
cluster7	GO:0010558	negative regulation of macromolecule biosynthetic process	6.90E-12	1.60E-09
cluster7	GO:0051172	negative regulation of nitrogen compound metabolic process	8.40E-12	1.80E-09
cluster8	GO:0042981	regulation of apoptosis	1.10E-17	2.50E-14
cluster8	GO:0043067	regulation of programmed cell death	1.60E-17	1.90E-14

cluster8	GO:0010941	regulation of cell death	1.90E-17	1.40E-14
cluster8	GO:0042127	regulation of cell proliferation	9.30E-16	5.00E-13
cluster8	GO:0010604	positive regulation of macromolecule metabolic process	4.20E-15	1.90E-12
cluster8	GO:0043066	negative regulation of apoptosis	3.10E-14	1.20E-11
cluster8	GO:0043069	negative regulation of programmed cell death	4.40E-14	1.40E-11
cluster8	GO:0060548	negative regulation of cell death	4.70E-14	1.30E-11
cluster8	GO:0051726	regulation of cell cycle	1.90E-12	4.90E-10
cluster8	GO:0045597	positive regulation of cell differentiation	2.00E-12	4.70E-10
cluster9	GO:0042127	regulation of cell proliferation	3.20E-15	6.50E-12
cluster9	GO:0008285	negative regulation of cell proliferation	6.10E-11	6.10E-08
cluster9	GO:0019220	regulation of phosphate metabolic process	3.80E-09	2.60E-06
cluster9	GO:0051174	regulation of phosphorus metabolic process	3.80E-09	2.60E-06
cluster9	GO:0051338	regulation of transferase activity	3.90E-09	2.00E-06
cluster9	GO:0043067	regulation of programmed cell death	8.40E-09	3.40E-06
cluster9	GO:0042325	regulation of phosphorylation	8.70E-09	2.90E-06
cluster9	GO:0010941	regulation of cell death	9.10E-09	2.60E-06
cluster9	GO:0048545	response to steroid hormone stimulus	1.10E-08	2.70E-06
cluster9	GO:0043549	regulation of kinase activity	1.10E-08	2.40E-06
cluster10	GO:0010604	positive regulation of macromolecule metabolic process	3.60E-11	5.90E-08
cluster10	GO:0051254	positive regulation of RNA metabolic process	5.40E-10	4.40E-07
cluster10	GO:0010628	positive regulation of gene expression	6.30E-10	3.40E-07
cluster10	GO:0043067	regulation of programmed cell death	1.20E-09	4.70E-07
cluster10	GO:0010941	regulation of cell death	1.30E-09	4.10E-07
cluster10	GO:0042325	regulation of phosphorylation	1.80E-09	5.00E-07
cluster10	GO:0007049	cell cycle	2.00E-09	4.70E-07
cluster10	GO:0006357	regulation of transcription from RNA polymerase II promoter	2.40E-09	4.80E-07
cluster10	GO:0045935	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	2.60E-09	4.80E-07
cluster10	GO:0045893	positive regulation of transcription, DNA-dependent	2.80E-09	4.60E-07

Supplementary Table S4. List of KEGG pathways enriched in 10 clusters (Top 10 pathways for each cluster are listed).

Cluster	Pathway	Definition	P-value	FDR
cluster1	path:05215	Prostate cancer	3.10E-10	3.40E-08
cluster1	path:05220	Chronic myeloid leukemia	3.90E-08	2.10E-06
cluster1	path:05200	Pathways in cancer	5.20E-08	1.90E-06
cluster1	path:05214	Glioma	5.80E-08	1.60E-06
cluster1	path:05218	Melanoma	2.10E-07	4.60E-06
cluster1	path:04110	Cell cycle	2.80E-07	5.10E-06
cluster1	path:05210	Colorectal cancer	1.20E-06	1.90E-05
cluster1	path:05223	Non-small cell lung cancer	1.50E-06	2.10E-05
cluster1	path:05211	Renal cell carcinoma	1.70E-06	2.10E-05
cluster1	path:05222	Small cell lung cancer	9.10E-06	1.00E-04
cluster2	path:05200	Pathways in cancer	1.80E-12	2.20E-10
cluster2	path:05218	Melanoma	5.50E-11	3.30E-09
cluster2	path:05220	Chronic myeloid leukemia	1.30E-10	5.10E-09
cluster2	path:05214	Glioma	1.60E-09	4.80E-08
cluster2	path:05219	Bladder cancer	2.00E-09	4.90E-08
cluster2	path:05212	Pancreatic cancer	8.90E-09	1.80E-07
cluster2	path:05215	Prostate cancer	1.50E-08	2.60E-07
cluster2	path:05223	Non-small cell lung cancer	3.50E-08	5.40E-07
cluster2	path:04115	p53 signaling pathway	4.50E-08	6.00E-07
cluster2	path:05222	Small cell lung cancer	6.20E-08	7.50E-07
cluster3	path:05200	Pathways in cancer	5.60E-11	7.00E-09
cluster3	path:05215	Prostate cancer	9.60E-07	4.00E-05
cluster3	path:04110	Cell cycle	1.20E-06	3.60E-05
cluster3	path:04115	p53 signaling pathway	3.60E-06	9.00E-05
cluster3	path:05220	Chronic myeloid leukemia	9.00E-06	1.90E-04
cluster3	path:05214	Glioma	1.10E-04	1.90E-03
cluster3	path:05218	Melanoma	2.50E-04	3.40E-03
cluster3	path:04510	Focal adhesion	8.80E-04	9.10E-03
cluster3	path:04360	Axon guidance	9.00E-04	8.60E-03
cluster3	path:04010	MAPK signaling pathway	1.50E-03	1.20E-02
cluster4	path:05200	Pathways in cancer	8.40E-07	7.40E-05
cluster4	path:05215	Prostate cancer	2.20E-06	9.50E-05
cluster4	path:05218	Melanoma	3.70E-06	1.10E-04
cluster4	path:04110	Cell cycle	4.90E-06	1.10E-04
cluster4	path:05214	Glioma	1.70E-05	3.00E-04
cluster4	path:05212	Pancreatic cancer	4.10E-05	6.10E-04
cluster4	path:04520	Adherens junction	6.40E-05	8.10E-04
cluster4	path:05223	Non-small cell lung cancer	7.10E-05	7.80E-04
cluster4	path:05219	Bladder cancer	2.10E-04	2.10E-03
cluster4	path:05220	Chronic myeloid leukemia	4.50E-04	3.90E-03
cluster5	path:05200	Pathways in cancer	2.40E-17	2.80E-15

cluster5	path:05220	Chronic myeloid leukemia	1.40E-13	8.50E-12
cluster5	path:05218	Melanoma	7.40E-13	3.00E-11
cluster5	path:04110	Cell cycle	2.00E-12	6.10E-11
cluster5	path:05215	Prostate cancer	3.30E-12	8.00E-11
cluster5	path:05219	Bladder cancer	1.20E-11	2.40E-10
cluster5	path:05214	Glioma	2.00E-11	3.40E-10
cluster5	path:05223	Non-small cell lung cancer	4.10E-10	6.10E-09
cluster5	path:05222	Small cell lung cancer	1.50E-09	2.10E-08
cluster5	path:05212	Pancreatic cancer	1.70E-09	2.10E-08
cluster6	path:05210	Colorectal cancer	2.90E-09	2.70E-07
cluster6	path:04110	Cell cycle	3.10E-08	1.50E-06
cluster6	path:05220	Chronic myeloid leukemia	1.30E-07	4.20E-06
cluster6	path:05200	Pathways in cancer	2.30E-07	5.60E-06
cluster6	path:04115	p53 signaling pathway	6.20E-07	1.20E-05
cluster6	path:05223	Non-small cell lung cancer	1.10E-06	1.80E-05
cluster6	path:05212	Pancreatic cancer	1.00E-05	1.40E-04
cluster6	path:05214	Glioma	3.90E-05	4.70E-04
cluster6	path:05215	Prostate cancer	5.00E-05	5.40E-04
cluster6	path:05218	Melanoma	8.50E-05	8.10E-04
cluster7	path:05200	Pathways in cancer	3.90E-12	4.10E-10
cluster7	path:04110	Cell cycle	3.00E-11	1.60E-09
cluster7	path:05212	Pancreatic cancer	1.20E-09	4.10E-08
cluster7	path:05215	Prostate cancer	1.70E-09	4.60E-08
cluster7	path:05220	Chronic myeloid leukemia	2.00E-09	4.20E-08
cluster7	path:05219	Bladder cancer	1.40E-06	2.50E-05
cluster7	path:05222	Small cell lung cancer	5.90E-06	8.90E-05
cluster7	path:05210	Colorectal cancer	5.90E-06	8.90E-05
cluster7	path:04115	p53 signaling pathway	7.40E-06	9.70E-05
cluster7	path:04350	TGF-beta signaling pathway	8.20E-06	9.60E-05
cluster8	path:05200	Pathways in cancer	5.50E-18	5.90E-16
cluster8	path:05215	Prostate cancer	8.40E-12	4.50E-10
cluster8	path:05222	Small cell lung cancer	3.80E-11	1.40E-09
cluster8	path:05220	Chronic myeloid leukemia	7.80E-11	2.10E-09
cluster8	path:04115	p53 signaling pathway	2.30E-10	4.90E-09
cluster8	path:05210	Colorectal cancer	4.20E-10	7.60E-09
cluster8	path:05218	Melanoma	4.90E-09	7.50E-08
cluster8	path:04510	Focal adhesion	2.00E-08	2.60E-07
cluster8	path:05212	Pancreatic cancer	6.00E-08	7.10E-07
cluster8	path:04110	Cell cycle	1.20E-07	1.30E-06
cluster9	path:05200	Pathways in cancer	6.60E-13	7.40E-11
cluster9	path:04110	Cell cycle	9.10E-08	5.10E-06
cluster9	path:05215	Prostate cancer	1.60E-07	6.20E-06
cluster9	path:05212	Pancreatic cancer	2.00E-07	5.70E-06
cluster9	path:05219	Bladder cancer	3.00E-07	6.60E-06

cluster9	path:04115	p53 signaling pathway	1.30E-06	2.50E-05
cluster9	path:05220	Chronic myeloid leukemia	3.10E-06	4.90E-05
cluster9	path:05222	Small cell lung cancer	8.00E-06	1.10E-04
cluster9	path:05218	Melanoma	1.50E-04	1.80E-03
cluster9	path:05223	Non-small cell lung cancer	2.30E-04	2.60E-03
cluster10	path:05200	Pathways in cancer	4.20E-17	3.70E-15
cluster10	path:05212	Pancreatic cancer	2.30E-11	1.00E-09
cluster10	path:05215	Prostate cancer	2.50E-11	7.40E-10
cluster10	path:05220	Chronic myeloid leukemia	9.00E-09	2.00E-07
cluster10	path:04110	Cell cycle	2.60E-08	4.60E-07
cluster10	path:05222	Small cell lung cancer	3.10E-08	4.50E-07
cluster10	path:05214	Glioma	3.40E-06	4.30E-05
cluster10	path:05210	Colorectal cancer	3.40E-06	3.80E-05
cluster10	path:05211	Renal cell carcinoma	7.70E-06	7.50E-05
cluster10	path:05218	Melanoma	8.60E-06	7.50E-05

Supplementary Table S5. Univariate Cox analysis of lncRNAs/miRNAs/mRNAs in the lncACT network module of *BRCA*

Variable	HR (95% CI)	Coefficient	P-value
H19	1.17 (0.82–1.67)	0.16	3.74E−01
hsa-miR-20a	0.93 (0.60–1.44)	−0.08	7.36E−01
hsa-miR-20b	0.67 (0.49–0.90)	−0.40	**8.00E−03**
THBS1	1.03 (0.65–1.62)	0.03	9.05E−01
MAP3K12	0.85 (0.56–1.31)	−0.16	4.66E−01
ZNF518A	0.50 (0.25–1.02)	−0.69	5.66E−02
SLC38A3	0.92 (0.73–1.15)	−0.09	4.65E−01
hsa-miR-15a	0.59 (0.30–1.14)	−0.53	1.18E−01
hsa-miR-146a	0.98 (0.69–1.40)	−0.02	9.19E−01
BRCA1	1.11 (0.72–1.71)	0.10	6.46E−01
BRCA2	0.65 (0.43–0.99)	−0.43	**4.43E−02**
SBF2-AS1	0.60 (0.26–1.39)	−0.51	2.35E−01
has-miR-17	0.93 (0.67–1.31)	−0.07	6.92E−01
WDFY3-AS2	1.20 (0.79–1.81)	0.18	3.88E−01
HB_module	2.45 (1.60–3.76)	0.90	**3.73E−05**

Singificant P value ($P < 0.05$) was represented as bold.

The network module of all variables in the table was tested in the last line.

Supplementary Table S6. Univariate Cox analysis of lncRNAs/miRNAs/mRNAs in the miR-335-associated lncACT network module of BRCA

Variable	HR (95% CI)	Coefficient	P value
has-miR-335	1.27 (0.93–1.75)	0.24	1.36E−01
MERTK	1.46 (0.95–2.23)	0.38	8.09E−02
FLG-AS1	1.29 (0.97–1.71)	0.25	7.85E−02
LINC00968	1.22 (0.95–1.57)	0.20	1.25E−01
Network module	1.95 (1.17–3.25)	0.67	**1.04E−02**

Singificant P value ($P < 0.05$) was represented as bold.

The network module of all variables in the table was tested in the last line.

Supplementary Table S7. List of KEGG pathways enriched among miR-335 targets (P<0.05).

Pathway	Pathway name	P-Value
path:04060	Cytokine-cytokine receptor interaction	5.49E-05
path:04020	Calcium signaling pathway	1.41E-04
path:04062	Chemokine signaling pathway	2.20E-04
path:04010	MAPK signaling pathway	2.45E-04
path:04640	Hematopoietic cell lineage	3.10E-04
path:04710	Circadian rhythm - mammal	4.78E-04
path:04512	ECM-receptor interaction	5.28E-04
path:04610	Complement and coagulation cascades	7.50E-04
path:05200	Pathways in cancer	1.50E-03
path:04970	Salivary secretion	1.85E-03
path:04920	Adipocytokine signaling pathway	2.76E-03
path:04972	Pancreatic secretion	3.64E-03
path:03320	PPAR signaling pathway	3.83E-03
path:05144	Malaria	4.03E-03
path:04360	Axon guidance	5.44E-03
path:05412	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	6.96E-03
path:04670	Leukocyte transendothelial migration	7.52E-03
path:05150	Staphylococcus aureus infection	9.48E-03
path:04350	TGF-beta signaling pathway	1.29E-02
path:05219	Bladder cancer	1.46E-02
path:05146	Amoebiasis	1.51E-02
path:05140	Leishmaniasis	1.80E-02
path:04514	Cell adhesion molecules (CAMs)	2.35E-02
path:04510	Focal adhesion	2.41E-02
path:04310	Wnt signaling pathway	2.55E-02
path:04720	Long-term potentiation	3.02E-02
path:00120	Primary bile acid biosynthesis	3.14E-02
path:05214	Glioma	3.59E-02
path:04630	Jak-STAT signaling pathway	3.67E-02
path:05020	Prion diseases	3.87E-02
path:04910	Insulin signaling pathway	4.36E-02
path:04744	Phototransduction	4.56E-02

Table S8. List of GO terms enriched among miR-335 targets (P<1.0E-3).

GO Term	Name	P-Value
GO:0006695	cholesterol biosynthetic process	5.03E-06
GO:0007267	cell-cell signaling	2.64E-05
GO:0045669	positive regulation of osteoblast differentiation	5.21E-05
GO:0007160	cell-matrix adhesion	6.50E-05
GO:0030335	positive regulation of cell migration	8.32E-05
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	1.14E-04
GO:0045907	positive regulation of vasoconstriction	2.90E-04
GO:0008285	negative regulation of cell proliferation	2.98E-04
GO:0009887	organ morphogenesis	3.70E-04
GO:0001503	ossification	4.78E-04
GO:0007586	digestion	4.83E-04
GO:0060346	bone trabecula formation	5.97E-04
GO:0051894	positive regulation of focal adhesion assembly	5.97E-04
GO:0090263	positive regulation of canonical Wnt receptor signaling pathway	8.26E-04
GO:0007411	axon guidance	8.76E-04
GO:0042423	catecholamine biosynthetic process	8.85E-04
GO:0001502	cartilage condensation	8.85E-04
GO:0016525	negative regulation of angiogenesis	8.91E-04
GO:0030182	neuron differentiation	9.16E-04
GO:0051046	regulation of secretion	9.31E-04

Supplementary Table S9. Univariate Cox analysis of lncRNAs/miRNAs/mRNAs and their combinations in the lncACT network across different diseases.

Disease	Variable	HR (95% CI)	Coefficient	P-value
	hsa-miR-17	1.21 (0.85–1.72)	0.19	2.88E−01
	RBL1	1.49 (1.00–2.20)	0.40	**4.90E−02**
	AC020915.4	0.89 (0.43–1.86)	−0.11	7.61E−01
BLCA	NABP1	1.09 (0.85–1.41)	0.09	4.86E−01
	RP5-1073O3.5	1.52 (0.85–2.72)	0.42	1.58E−01
	RP11-113K21.5	0.82 (0.52–1.31)	−0.20	4.10E−01
	RP11-504G3.1	1.79 (0.96–3.33)	0.58	6.66E−02
	Network module	1.71 (1.11–2.62)	0.53	**1.42E−02**
	hsa-miR-27b	0.78 (0.48–1.25)	−0.25	3.01E−01
	MMP13	0.95 (0.89–1.02)	−0.05	1.52E−01
LUSC	EDNRA	1.02 (0.84–1.25)	0.02	8.34E−01
	YTHDF3	1.30 (0.91–1.85)	0.26	1.43E−01
	LINC01234	0.98 (0.90–1.05)	−0.02	5.24E−01
	Network module	4.55 (1.59–12.95)	1.51	**4.61E−03**
	hsa-miR-25	1.23 (0.88–1.73)	0.21	2.21E−01
LUAD	KLF4	1.18 (0.99–1.40)	0.16	6.54E−02
	MIR22HG	0.84 (0.63–1.12)	−0.18	2.28E−01
	Network module	2.95 (1.37–6.34)	1.08	**5.65E−03**
	hsa-let-7b	0.66 (0.38–1.14)	−0.42	1.34E−01
	hsa-miR-96	0.43 (0.17–1.04)	−0.85	6.20E−02
	hsa-miR-182	0.58 (0.30–1.11)	−0.55	1.02E−01
UCEC	MAL2	1.79 (0.91–3.49)	0.58	8.99E−02
	LINC00476	0.54 (0.24–1.25)	−0.61	1.51E−01
	NBPF1	3.88 (1.00–15.03)	1.36	5.00E−02
	Network module	1.52 (1.12–2.07)	0.42	**7.38E−03**
	hsa-miR-30a	0.18 (0.06–0.56)	−1.72	**2.93E−03**
	hsa-miR-143	2.39 (1.34–4.26)	0.87	**3.13E−03**
KIRP	AC020915.4	0.39 (0.13–1.14)	−0.94	8.54E−02
	SEC22B	0.92 (0.30–2.75)	−0.09	8.74E−01
	Network module	2.20 (1.46–3.31)	0.79	**1.73E−04**

Singificant P value ($P < 0.05$) was represented as bold.

The network module was tested in the last line of each cancer, respectively.

Table S10. Known lncACTs involving protein-coding genes and lncRNA in our framwork.

LncRNAs	**Coding-genes**	**References**
PVT1	CDH1	(5)
PVT1	TP53	(5)
PVT1	RUNX1	(5)
H19	HMGA2	(6) (7)
H19	MYCN	(8)
LINC00152	THBS1	(8)
HOTAIR	HER2	(9)

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