Electronic Supplementary Material (ESI) for Molecular BioSystems.

Table S1: The number of patient samples in each cancer.

Cancer	Normal	Tumor
BLCA	19	252
BRCA	105	837
HNSC	42	426
LIHC	50	200
LUAD	58	488
LUSC	17	220
KICH	25	66
KIRC	67	448
KIRP	30	198
THCA	52	374

Table S2: The Wilcoxon rank-sum test p-values of expression between Rlncs and NRlncs in normal samples across 10 cancers.

Cancer	P-value
BLCA	6.90E-14
BRCA	5.04E-18
THCA	1.99E-20
HNSC	2.94E-12
KICH	1.11E-16
KIRC	2.19E-20
KIRP	2.83E-11
LIHC	1.55E-1
LUAD	2.72E-9
LUSC	2.85E-12

Table S3: The Wilcoxon rank-sum test p-values of expression between Rlncs and NRlncs in tumor samples across 10 cancers.

Cancer	P-value
BLCA	5.30E-13
BRCA	4.48E-19
THCA	2.46E-19
HNSC	8.13E-13
KICH	6.36E-16
KIRC	1.12E-22
KIRP	7.72E-19
LIHC	1.88E-6
LUAD	3.16E-18
LUSC	1.02E-24

Table S4: The Wilcoxon rank-sum test p-values of expression between differentially expressed Rlncs and NRlncs in tumor samples across 10 cancers.

Cancer	P-value
BLCA	1.53E-5
BRCA	5.60E-8
THCA	1.29E-9
HNSC	1.07E-3
KICH	1.80E-9
KIRC	7.45E-13
KIRP	3.07E-9
LIHC	5.50E-8
LUAD	8.89E-8
LUSC	9.99E-17

Table S5: The Wilcoxon rank-sum test p-values of protein coding potential between differentially expressed Rlncs and NRlncs across 10 cancers.

Cancer	P-value
BLCA	4.44E-3
BRCA	7.46E-5
THCA	1.01E-2
HNSC	1.34E-2
KICH	7.39E-4
KIRC	3.86E-2
KIRP	6.23E-3
LIHC	1.77E-2
LUAD	3.69E-4
LUSC	3.69E-2

Table S6: The Wilcoxon rank-sum test p-values of evolutionary conservation scores between differentially expressed Rlncs and NRlncs across 10 cancers.

Cancer	P-value
BLCA	1.30E-3
BRCA	3.75E-5
THCA	1.79E-4
HNSC	2.27E-4
KICH	1.03E-5
KIRC	1.16E-5
KIRP	2.65E-5
LIHC	3.82E-4
LUAD	2.85E-4
LUSC	3.28E-6

Table S7: The number of neighboring protein-coding genes of the differentially expressed lncRNAs.

Cancer	Rlnc	NRlnc
BLCA	1857	1220
BRCA	1884	1417
THCA	1835	1366
HNSC	1902	1326
KICH	2457	1816
KIRC	2704	2256
KIRP	2120	1612
LIHC	1948	1078
LUAD	2205	1599
LUSC	2468	1715

Table S8: The Wilcoxon rank-sum test p-values of expression between neighbor genes of differentially expressed Rlncs and NRlncs across 10 cancers.

Cancer	P-value
BLCA	1.57E-4
BRCA	9.69E-2
THCA	2.83E-2
HNSC	1.02E-1
KICH	6.31E-1
KIRC	1.41E-1
KIRP	1.56E-2
LIHC	5.91E-1
LUAD	3.09E-2
LUSC	6.81E-3

Table S9: The Wilcoxon rank-sum test p-values of SNPs density between Rlncs and NRlncs across 10 cancers.

Cancer	P-value
BLCA	0.39
BRCA	0.30
THCA	0.32
HNSC	0.50
KICH	0.30
KIRC	0.43
KIRP	0.28
LIHC	0.82
LUAD	0.33
LUSC	0.63

Table S10: The Wilcoxon rank-sum test p-values of SNPs density between differentially expressed Rlncs and NRlncs across 10 cancers.

Cancer	P-value
BLCA	0.50
BRCA	0.49
THCA	0.31
HNSC	0.38
KICH	0.26
KIRC	0.20
KIRP	0.67
LIHC	0.36
LUAD	0.14
LUSC	0.33

Table S15: The Wilcoxon rank-sum test p-values of ORF length between differentially expressed Rlncs and NRlncs across 10 cancers.

Cancer	P-value
BLCA	4.92E-6
BRCA	4.74-E10
THCA	1.81E-4
HNSC	3.38E-3
KICH	1.26E-5
KIRC	1.48E-5
KIRP	1.83E-6
LIHC	7.04E-4
LUAD	2.48E-11
LUSC	5.18E-7

Table S16: The Wilcoxon rank-sum test p-values of sequence length between differentially expressed Rlncs and NRlncs across 10 cancers.

Cancer	P-value
BLCA	7.06E-12
BRCA	2.81E-20
THCA	1.28E-17
HNSC	6.67E-14
KICH	1.84E-21
KIRC	6.50E-18
KIRP	1.10E-15
LIHC	2.79E-21
LUAD	1.37E-25
LUSC	6.44E-13

Figure S1

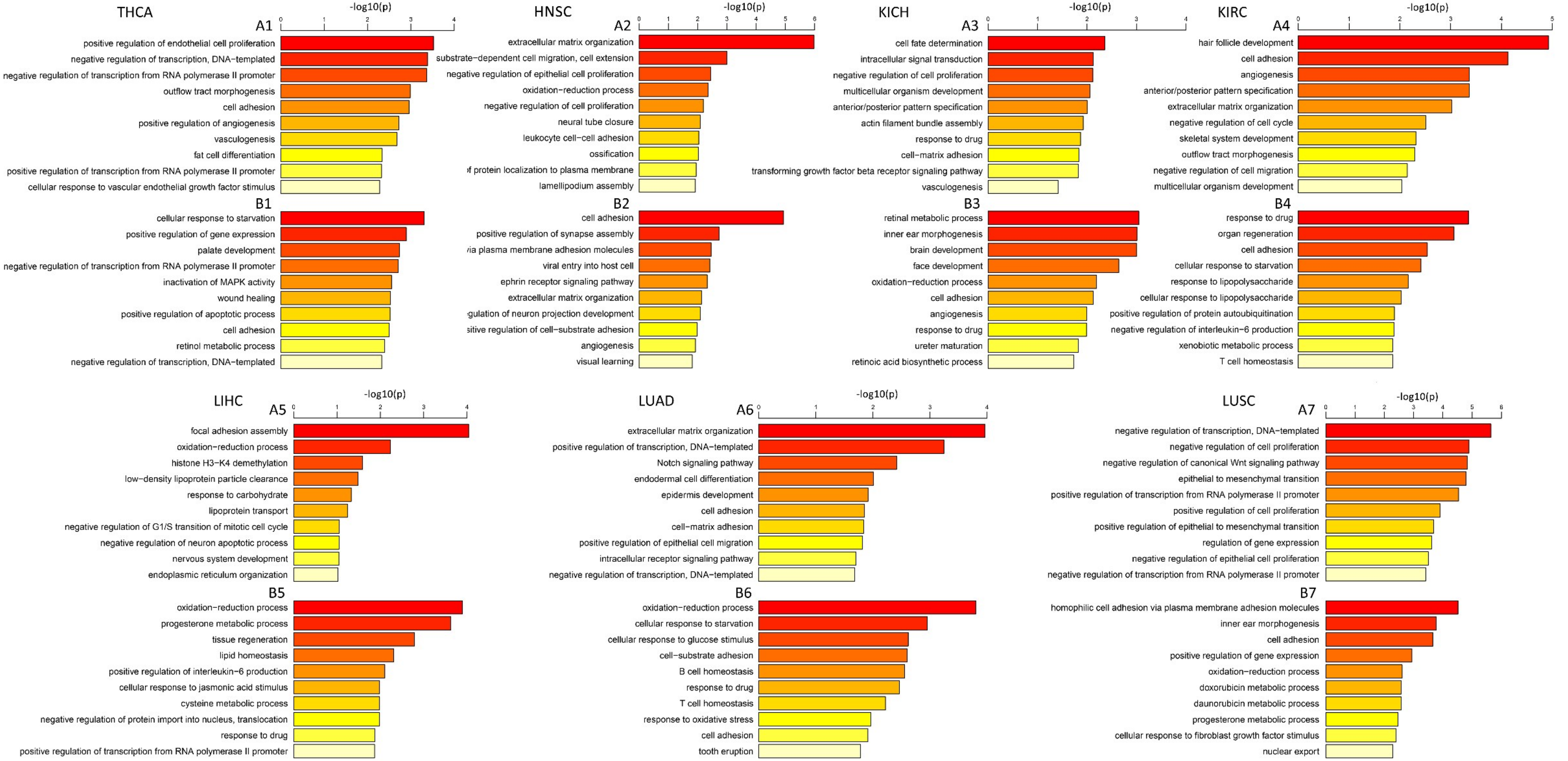

THCA
A1
-log10(p)
0
1
2
3
4
positive regulation of endothelial cell proliferation
negative regulation of transcription, DNA−templated
negative regulation of transcription from RNA polymerase II promoter
outflow tract morphogenesis
cell adhesion
positive regulation of angiogenesis
vasculogenesis
fat cell differentiation
positive regulation of transcription from RNA polymerase II promoter
cellular response to vascular endothelial growth factor stimulus
B1
cellular response to starvation
positive regulation of gene expression
palate development
negative regulation of transcription from RNA polymerase II promoter
inactivation of MAPK activity
wound healing
positive regulation of apoptotic process
cell adhesion
retinol metabolic process
negative regulation of transcription, DNA−templated
HNSC
A2
-log10(p)
0
1
2
3
4
5
6
extracellular matrix organization
substrate−dependent cell migration, cell extension
negative regulation of epithelial cell proliferation
oxidation−reduction process
negative regulation of cell proliferation
neural tube closure
leukocyte cell−cell adhesion
ossification
f protein localization to plasma membrane
lamellipodium assembly
B2
cell adhesion
positive regulation of synapse assembly
ia plasma membrane adhesion molecules
viral entry into host cell
ephrin receptor signaling pathway
extracellular matrix organization
gulation of neuron projection development
sitive regulation of cell−substrate adhesion
angiogenesis
visual learning
KICH
A3
-log10(p)
0
1
2
3
4
cell fate determination
intracellular signal transduction
negative regulation of cell proliferation
multicellular organism development
anterior/posterior pattern specification
actin filament bundle assembly
response to drug
cell−matrix adhesion
transforming growth factor beta receptor signaling pathway
vasculogenesis
B3
retinal metabolic process
inner ear morphogenesis
brain development
face development
oxidation−reduction process
cell adhesion
angiogenesis
response to drug
ureter maturation
retinoic acid biosynthetic process
KIRC
A4
-log10(p)
0
1
2
3
4
5
hair follicle development
cell adhesion
angiogenesis
anterior/posterior pattern specification
extracellular matrix organization
negative regulation of cell cycle
skeletal system development
outflow tract morphogenesis
negative regulation of cell migration
multicellular organism development
B4
response to drug
organ regeneration
cell adhesion
cellular response to starvation
response to lipopolysaccharide
cellular response to lipopolysaccharide
positive regulation of protein autoubiquitination
negative regulation of interleukin−6 production
xenobiotic metabolic process
T cell homeostasis
LIHC
A5
-log10(p)
0
1
2
3
4
focal adhesion assembly
oxidation−reduction process
histone H3−K4 demethylation
low−density lipoprotein particle clearance
response to carbohydrate
lipoprotein transport
negative regulation of G1/S transition of mitotic cell cycle
negative regulation of neuron apoptotic process
nervous system development
endoplasmic reticulum organization
B5
oxidation−reduction process
progesterone metabolic process
tissue regeneration
lipid homeostasis
positive regulation of interleukin−6 production
cellular response to jasmonic acid stimulus
cysteine metabolic process
negative regulation of protein import into nucleus, translocation
response to drug
positive regulation of transcription from RNA polymerase II promoter
LUAD
A6
-log10(p)
0
1
2
3
4
extracellular matrix organization
positive regulation of transcription, DNA−templated
Notch signaling pathway
endodermal cell differentiation
epidermis development
cell adhesion
cell−matrix adhesion
positive regulation of epithelial cell migration
intracellular receptor signaling pathway
negative regulation of transcription, DNA−templated
B6
oxidation−reduction process
cellular response to starvation
cellular response to glucose stimulus
cell−substrate adhesion
B cell homeostasis
response to drug
T cell homeostasis
response to oxidative stress
cell adhesion
tooth eruption
LUSC
A7
-log10(p)
0
1
2
3
4
5
6
negative regulation of transcription, DNA−templated
negative regulation of cell proliferation
negative regulation of canonical Wnt signaling pathway
epithelial to mesenchymal transition
positive regulation of transcription from RNA polymerase II promoter
positive regulation of cell proliferation
positive regulation of epithelial to mesenchymal transition
regulation of gene expression
negative regulation of epithelial cell proliferation
negative regulation of transcription from RNA polymerase II promoter
B7
homophilic cell adhesion via plasma membrane adhesion molecules
inner ear morphogenesis
cell adhesion
positive regulation of gene expression
oxidation−reduction process
doxorubicin metabolic process
daunorubicin metabolic process
progesterone metabolic process
cellular response to fibroblast growth factor stimulus
nuclear export

Figure S2

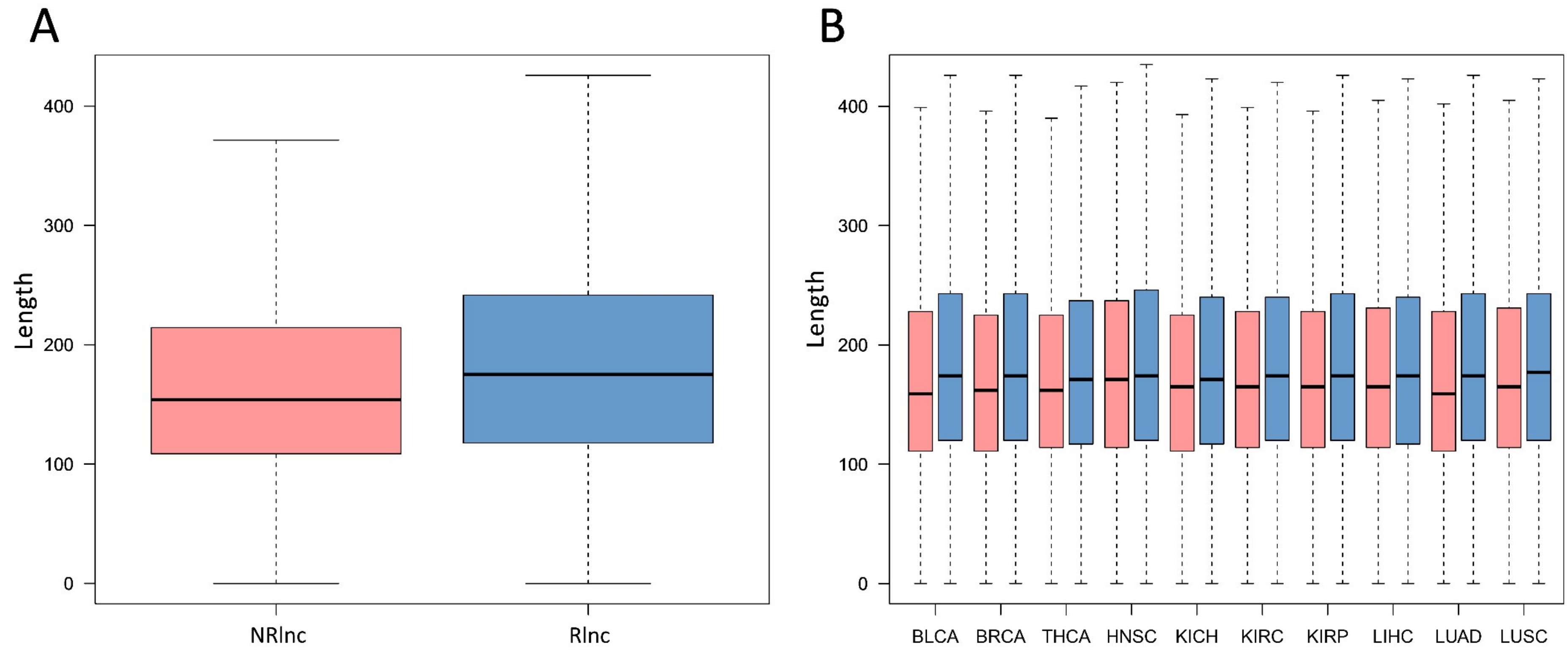
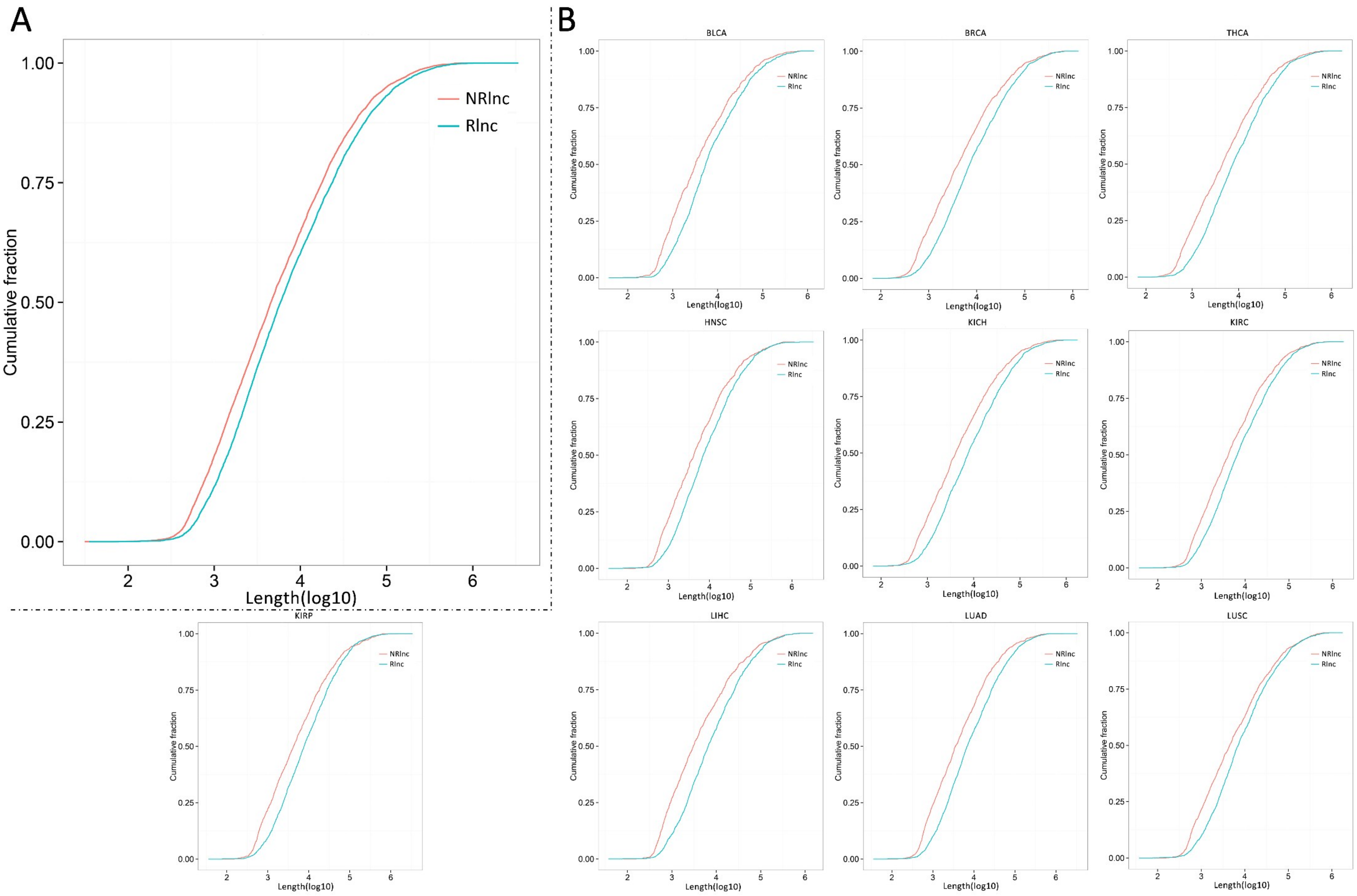

A
B
Length
0
100
200
300
400
NRlnc
Rlnc
BLCA
BRCA
THCA
HNSC
KICH
KIRC
KIRP
LIHC
LUAD
LUSC

Figure S3


A
Cumulative fraction
1.00
0.75
0.50
0.25
0.00
2
3
4
5
6
Length(log10)
NRlnc
Rlnc
B
BLCA
BRCA
THCA
HNSC
KICH
KIRC
KIRP
LIHC
LUAD
LUSC

Additional files

Additional file 1: Fig. S1~S3. Fig. S1: The function annotation of Rlncs and NRlncs. A1-A7 represent the top 10 functions of Rlncs in THCA, HNSC, KICH, KIRC, LIHC, LUAD and LUSC, respectively. B1-B7 represent the top 10 functions of NRlncs in THCA, HNSC, KICH, KIRC, LIHC, LUAD, LUSC, respectively; Fig. S2: The ORF length of lncRNAs. Blue represents Rlncs, red represents NRlncs. (A) The ORF length of Rlncs and NRlncs; (B) The ORF length of the differentially expressed lncRNAs in each cancer; Fig. S3: The length of lncRNAs sequences. Blue represents Rlncs, red represents NRlncs. (A) The sequence length of all lncRNAs. (B) The sequence length of lncRNAs that differentially expressed in each cancer. **Table S1~S10, S15, S16.** Table S1: The number of patient samples in each cancer; Table S2: The Wilcoxon rank-sum test p-values of expression between Rlncs and NRlncs in normal samples across 10 cancers; Table S3: The Wilcoxon rank-sum test p-values of expression between Rlncs and NRlncs in tumor samples across 10 cancers; Table S4: The Wilcoxon rank-sum test p-values of expression between differentially expressed Rlncs and NRlncs in tumor samples across 10 cancers; Table S5: The Wilcoxon rank-sum test p-values of protein coding potential between differentially expressed Rlncs and NRlncs across 10 cancers; Table S6: The Wilcoxon rank-sum test p-values of evolutionary conservation scores between differentially expressed Rlncs and NRlncs across 10 cancers; Table S7:
The number of neighboring protein-coding genes of the differentially expressed lncRNAs; Table S8: The Wilcoxon rank-sum test p-values of expression between neighbor genes of differentially expressed Rlncs and NRlncs across 10 cancers; Table S9: The Wilcoxon rank-sum test p-values of SNPs density between Rlncs and NRlncs across 10 cancers; Table S10: The Wilcoxon rank-sum test p-values of SNPs density between differentially expressed Rlncs and NRlncs across 10 cancers; Table S15: The Wilcoxon rank-sum test p-values of ORF length between differentially expressed Rlncs and NRlncs across 10 cancers; Table S16: The Wilcoxon rank-sum test p-values of sequence length between differentially expressed Rlncs and NRlncs across 10 cancers. (.docx)

Additional file 2: Table S11. The KEGG pathway enrichment of Rlncs in THCA, HNSC, KICH, KIRP, LIHC, LUAD, LUSC. (.xlsx); **Table S12.** The KEGG pathway enrichment of NRlncs in THCA, HNSC, KICH, KIRP, LIHC, LUAD, LUSC. (.xlsx); **Table S13.** Prognosis-related Rlncs across 10 cancer types. (.xlsx); **Table S14.** Prognosis-related NRlncs across 10 cancer types. (.xlsx)