

## Supplementary material for

### **Lnc2Atlas: an atlas of long noncoding RNAs associated with risk of cancers**

Chao Ren<sup>1†</sup>, Gaole An<sup>1†</sup>, Chenghui Zhao<sup>1</sup>, Zhangyi Ouyang<sup>1</sup>, Xiaochen Bo<sup>1\*</sup>, Wenjie Shu<sup>1\*</sup>

<sup>1</sup>Department of Biotechnology, Beijing Institute of Radiation Medicine, Beijing, China

\*To whom correspondence should be addressed. Tel: +86 10 6693 2211; Fax: +86 10 6821 0077; Email: [shuwj@bmi.ac.cn](mailto:shuwj@bmi.ac.cn)

Correspondence may also be addressed to Xiaochen Bo. Email: [boxc@bmi.ac.cn](mailto:boxc@bmi.ac.cn)

†These authors contributed equally to this work as joint First Authors.

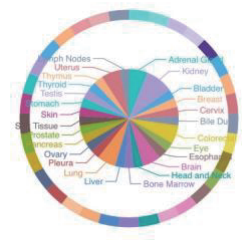
## Supplementary figure legends

**Figure S1.** Mobile device-compatible interfaces of Lnc2Atlas. (A) iPhone-compatible interface. (B) iPad-compatible interface.

**Figure S2.** Simplified diagram of the Lnc2Atlas relational database. The blue blocks represent MySQL tables in Lnc2Atlas. The white blocks represent the columns of a certain table. The primary key is indicated by a yellow block.

**Figure S3.** An example illustrating how Lnc2Atlas helps reveal the potential function of a lncRNA in thyroid cancer. (A) A SNP located in the ENST00000422494.1 transcript significantly impacts the secondary structure; (B) the ENST00000422494.1 transcript is overexpressed in thyroid cancer; and (C) ENST00000422494.1 correlates with the transcript of the thyroid-cancer-related gene MPPED2 (indicated with a red box) in thyroid cancer. (D) GO and pathway analysis of genes that are highly correlated with ENST00000422494.1 involved in the cluster derived from co-expression analysis of thyroid cancer.

(A)



In Lnc2Catlas, we provide interactions between 33 different cancers and 27670 LncRNA transcripts. Three methods were used to explore the relationship between cancers and LncRNAs, via SNPs, proteins and FPKMs separately.

Two ways are provided to explore the relationship. By typing LncRNAs, proteins or SNPs in the search box above or search page, you can view the related LncRNA results and various information. By clicking the browse page, you can view the results categorized by cancer types. All the results are available in the download page. More help information are awaited in help page.

The circle graph left demonstrates cancers and tissues used in this database. By clicking interesting part of the circle, a more detailed results about the cancer will be displayed.

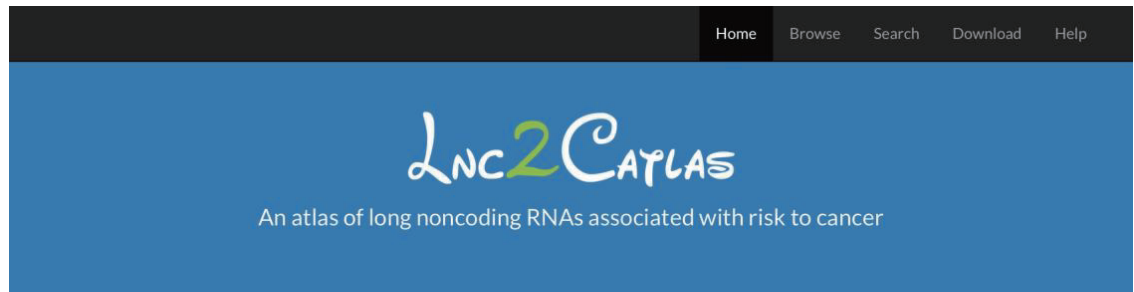
## About

Lnc2Catlas is a database seeking to reveal the relationship between LncRNA and Cancer. Interactions are created between 33 different diseases and 27670 LncRNA transcripts. Using cancer-related SNPs and proteins and tumor FPKM results, a huge network was created and visualized to provide a better understanding into the relationship between LncRNAs and cancers.

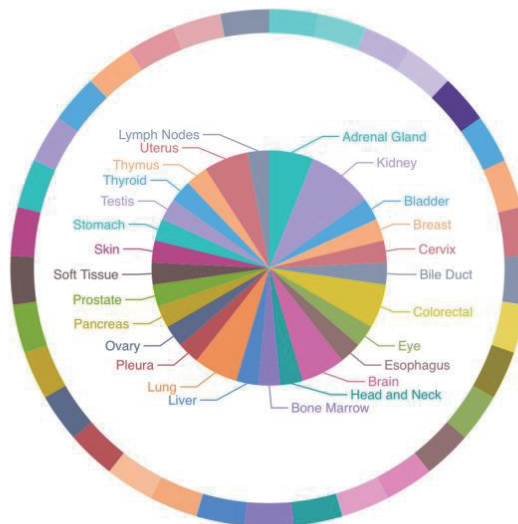
## Contact

Chao Ren : requiem116@gmail.com

(B)



LncRNA ID or SNP ID or Disease



In Lnc2Catlas, we provide interactions between 33 different cancers and 27670 LncRNA transcripts. Three methods were used to explore the relationship between cancers and LncRNAs, via SNPs, proteins and FPKMs separately.

Two ways are provided to explore the relationship. By typing LncRNAs, proteins or SNPs in the search box above or search page, you can view the related LncRNA results and various information. By clicking the browse page, you can view the results categorized by cancer types. All the results are available in the download page. More help information are awaited in help page.

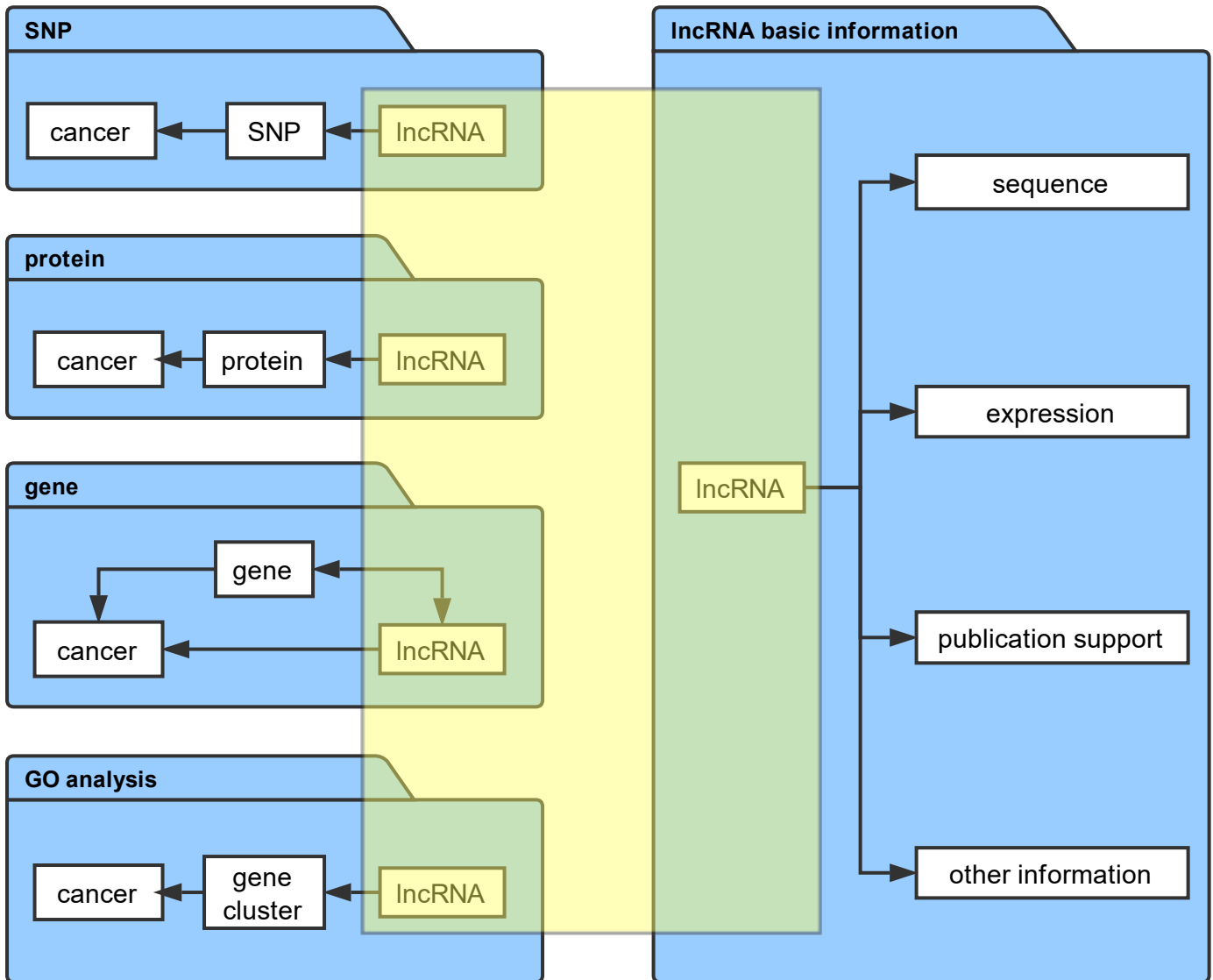
The circle graph left demonstrates cancers and tissues used in this database. By clicking interesting part of the circle, a more detailed results about the cancer will be displayed.

## About

Lnc2Catlas is a database seeking to reveal the relationship between LncRNA and Cancer. Interactions are created between 33 different diseases and 27670 LncRNA transcripts. Using cancer-related SNPs and proteins and tumor FPKM results, a huge network was created and visualized to provide a better understanding into the relationship between LncRNAs and cancers.

## Contact

Chao Ren : requiem116@gmail.com



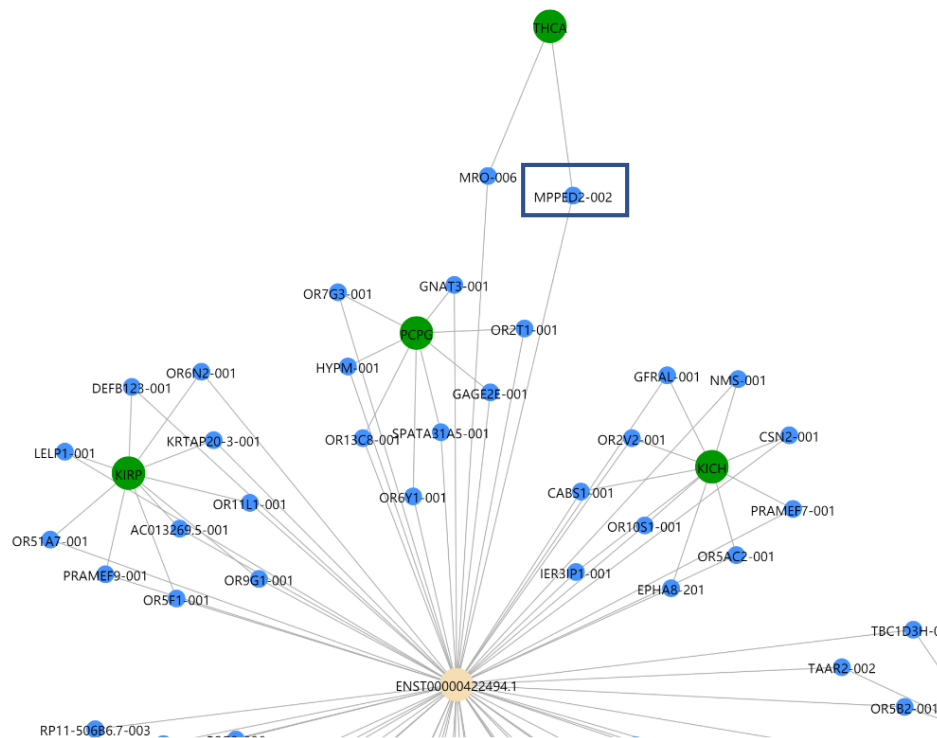
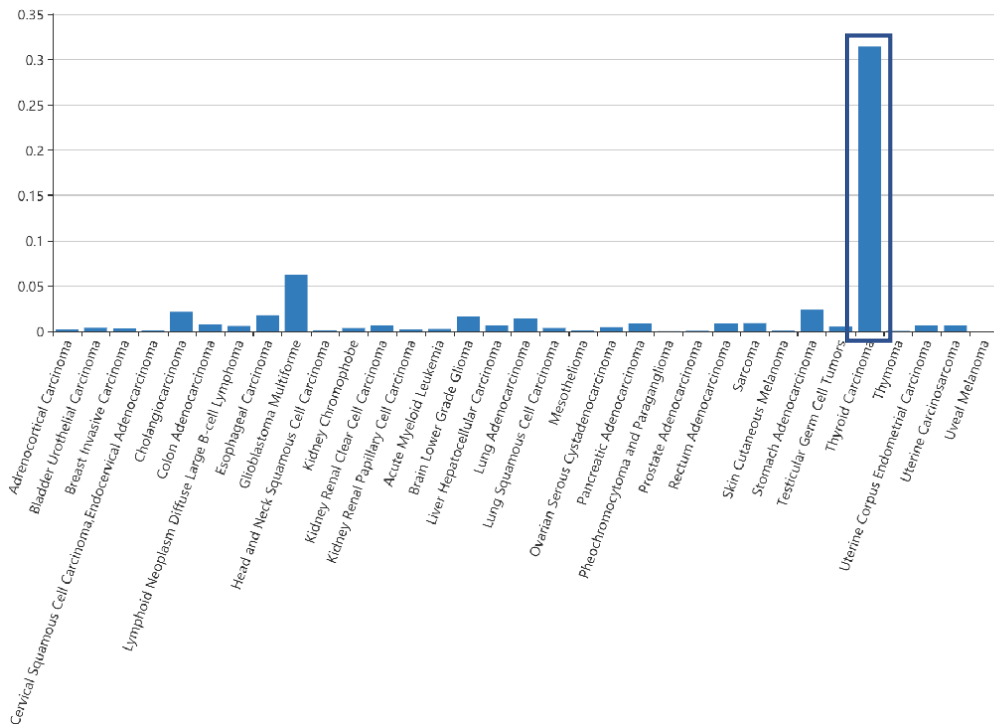
**(A)**

Only results with p-value < 0.2 are shown in the table, which indicate significant changes on lncRNAs

SNP ID	Source	Score	Disease	Option
rs946797230	dbSNP	0.0308	-	<a href="#">View</a>
rs953691404	dbSNP	0.0415	-	<a href="#">View</a>
rs995734	dbSNP	0.0465	-	<a href="#">View</a>
rs1045143938	dbSNP	0.0465	-	<a href="#">View</a>
rs995026293	dbSNP	0.051	-	<a href="#">View</a>
rs976162497	dbSNP	0.0744	-	<a href="#">View</a>
rs944378489	dbSNP	0.08	-	<a href="#">View</a>
rs1056683120	dbSNP	0.1244	-	<a href="#">View</a>

**(C)**

Weighted scores between lncRNAs and genes are provided in downloadable file, reflecting the expression similarity of lncRNA and gene.

**(B)****(D)**

Thyroid Carcinoma [Download](#)

source	term name	term ID	term genes	query genes	common genes	corrected p-value	matched gene list
KEGG	Thyroid hormone signaling pathway	KEGG:04919	118	78	8	0.00289	<a href="#">Detail</a>
KEGG	Insulin resistance	KEGG:04931	109	78	7	0.0128	<a href="#">Detail</a>
KEGG	Circadian entrainment	KEGG:04713	96	78	6	0.0443	<a href="#">Detail</a>