

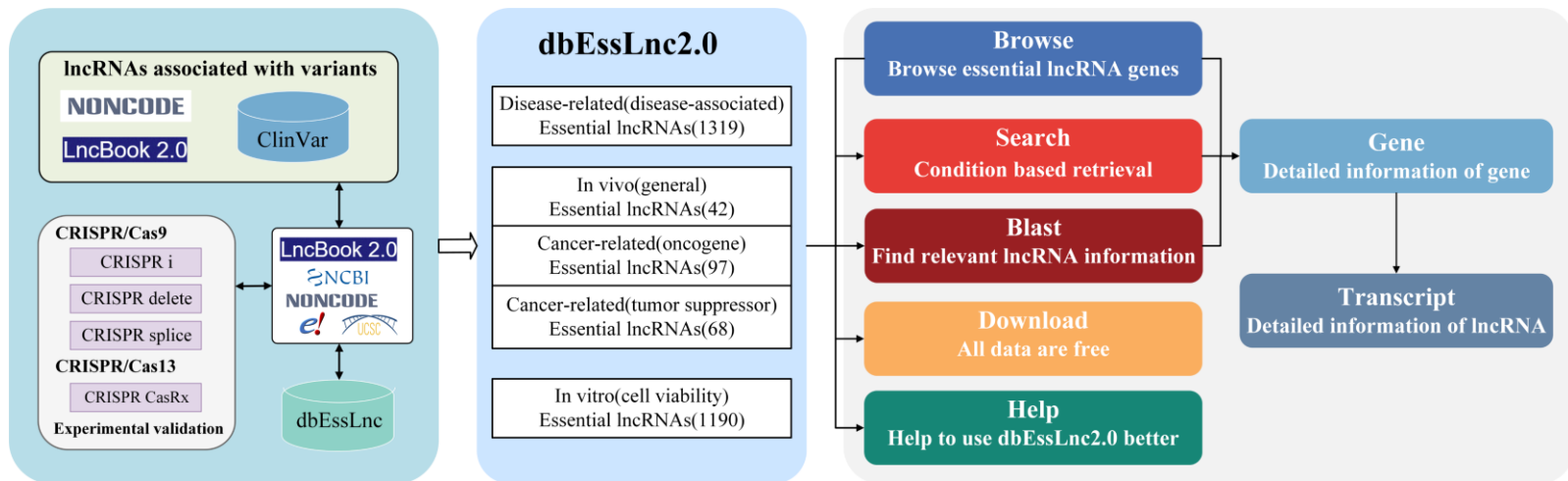
dbEssLnc2.0: exploring disease-associated essential long non-coding RNAs in human cell lines

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Problems & Ideas

- Problems with existing essential gene repositories:
 - Scarcity of comprehensive repositories for experimentally validated essential lncRNA genes compared to protein-coding genes.
 - Limited data scale and information dimensions in existing lncRNA gene essentiality resources.
- Ideas: Integrate manually curated CRISPR screening data for lncRNA genes with the results of lethal phenotype analysis related to lncRNA genes.



Essential lncRNA genes is derived from CRISPR screening experiments or by mapping disease-associated variants in the ClinVar database. Records in dbEssLnc2.0 are categorized into 5 major groups. The number of records in each group is marked after the group name. The web interface provides five main functions : Browse, Search, Blast, Download, and Help.

Main Contributions

- Contributions:
 - Significant repository expansion to 2,509 human essential lncRNA records, a 20-fold increase over the previous version;
 - Integration of 1,190 CRISPR-validated records and 1,319 putative essential lncRNAs associated with lethal variants;
 - Developed a user-centric web portal with an intuitive interface to facilitate data exploration.

The image displays a workflow in the dbEssLnc2.0 web portal, divided into three panels: (A) Gene Search, (B) Gene Information, and (C) LncRNA Information.

(A) Gene Search: A search bar contains "Cell viability" and "MCM3AP-AS1". Below, a table of search results is shown. The first row is highlighted with a red box and labeled "1. Click to view gene details".

Gene UID	Symbol	NCBI Gene ID	LincBook Gene ID	NONCODE Gene ID	Organism	PubMedID	General	Cell-viability	Cancer-related	Disease-related
ELH001717	MCM3AP-AS1	114044	HSALNG0133721	NONHSAG03121.3	Human	27980086	X	✓	X	X

(B) Gene Information: Shows details for Gene UID: ELH001717, Symbol: MCM3AP-AS1, Organism: Human, Position: chr21:46229217-46259390, forward(hg38). A red box highlights the "Sequence" field, labeled "2. Click to view the complete sequence".

(C) LncRNA Information: Shows details for Gene: ELH001717, Organism: Human, LincBook: transcript: HSALNT0274797, gene: HSALNG0133721, NONCODE: N.A., Chromosome: chr21, Start: 46229217, End: 46259390, Strand: +, Length: 703, exon number: 3, exon position: 46229217-46229266, 46240834-46241019, 46258924-46259390. A red box highlights the "Sequence" field, labeled "3. Click to view the complete sequence".

Key Experimental Evidence: A table shows CRISPR experimental records. A red box highlights the first row, labeled "3. Key Experimental Evidence".

Target	CRISPR Type	Exp Score	Role	Cell Line	Published ID
LH10298	CRISPR I	39.9690626	cell-line specific	IPSC	27980086

Transcript ID: A list of transcript IDs is shown. A red box highlights "TC0NS_00106247", labeled "4. Click to view transcript details".

LncRNA Information: A bar chart shows the TMI (Transcript Maturity Index) for various transcripts. A red box highlights the bar for "TC0NS_00106247", labeled "5. Click to view the complete sequence".

Use-case example demonstrating a typical workflow in dbEssLnc2.0.