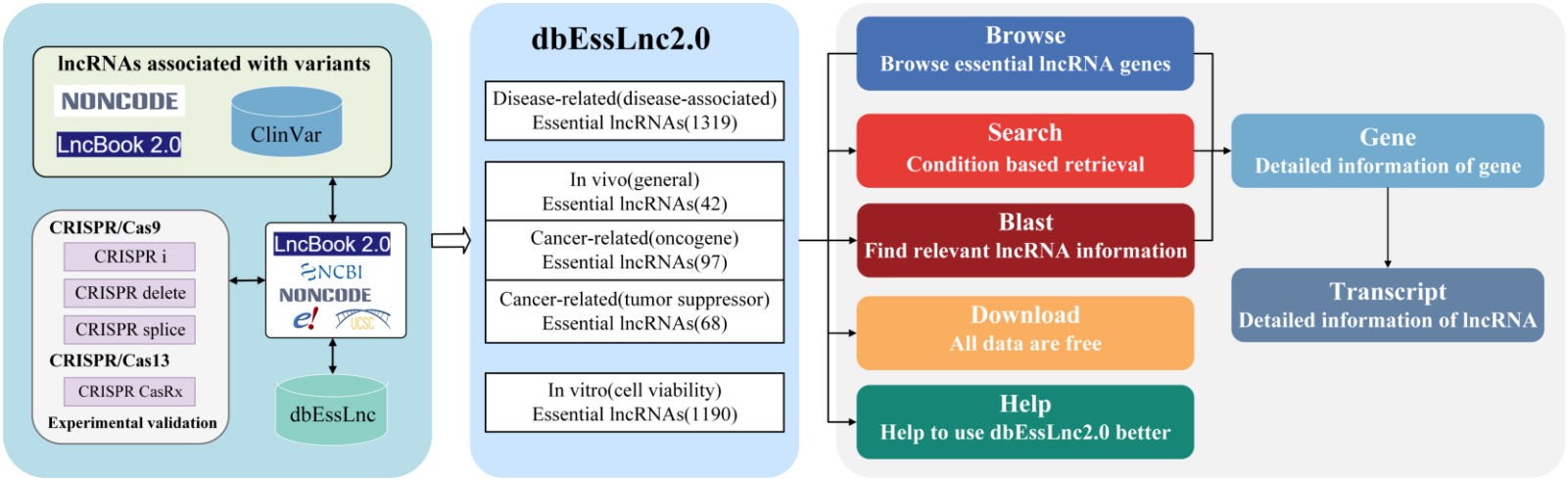
dbEssLnc2.0：exploring disease-associated essential long non-coding RNAs in human cell lines

Yingdong LIU, Xiujun GONG, Wanting SHI, Pufeng DU

Frontiers of Computer Science, DOI: 10.1007/s11704-026-51345-z

Problems & Ideas

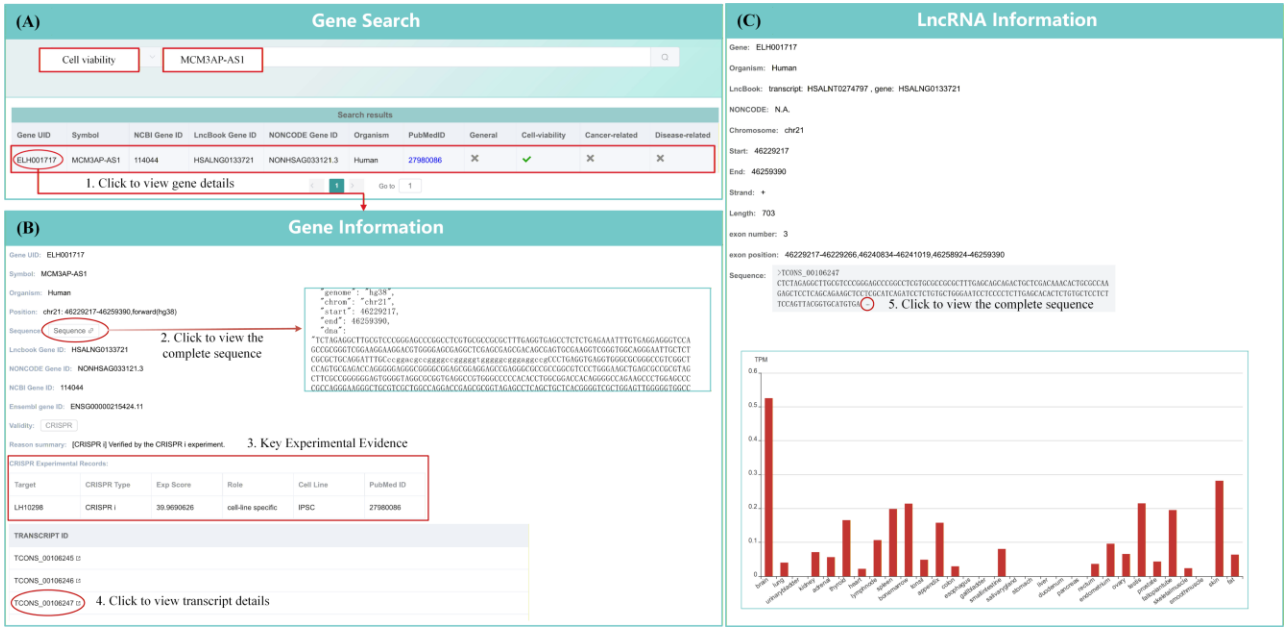
- Problems with existing essential gene repositories:
  - Scarcity of comprehensive repositories for experimentally validated essential lncRNA genes compared to protein-coding genes.
  - Limited data scale and information dimensions in existing lncRNA gene essentiality resources.
- Ideas: Integrate manually 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.



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