

Table 1 Classification of lncRNA databases

Database name	Characteristics	Website
Noncode	Established by Institute of Computing, Chinese Academy of Sciences, it is by far the most complete database of non-coding RNA (Liu, 2004). When using this database, there is a place that needs to be paid special attention. Since this database uses a set of lncRNA naming system specified by itself, if the general naming system is used to search in this database, the desired lncRNA cannot be found. Here is a way to find the lncRNA we want in this database. Blast function is provided in this database. If the user has the nucleic acid sequence of lncRNA, the corresponding number of lncRNA in this database can be found according to blast results, so as to further find the annotation information that the user wants.	http://www.noncode.org
lncRNADisease	The database collects more than 160 disease-related lncRNA and provides annotations of disease-related lncRNA reported in literature (Chen et al., 2012). It is worth mentioning that this database provides the function of browsing lncRNA annotation information on the website, which makes it much easier for us to annotate lncRNA.	http://cmbi.bjmu.edu.cn/lncrnadisease
CHIPBase	This database is significantly rich in content, so you can find a lot of lncRNA comments here. This database also provides the loci that bind lncRNA and expression map to transcription factors identified by RNA-seq (Yang et al., 2013).	http://deepbase.sysu.edu.cn/chipbase/
lncRNAdb	The database collects eukaryotes lncRNA information that has been reported in the literature. Each entry in the database contains reference information about RNA, the expression of lncRNA, subcellular localization and conservative, functional evidence and other relevant information. We can use the lncRNAdb database to continuously proofread the literature related to lncRNA and other genomic elements (Amaral et al., 2011).	http://www.lncrnadb.org/