

Mouse mRNA&IncRNA Epitranscriptomic microarray 数据库

参考文献

1. Kozomara A., miRBase: annotating high confidence microRNAs using deep sequencing data. *Nucleic Acid Res*, 2014. 42(Database issue): p. D68-73.
2. Harrow J., et al., GENCODE: the reference human genome annotation for the ENCODE project, 2012. 22(9): p. 1760-74.
3. Pruitt, K.D., T. Tatusova, and D.R. Maglott, NCBI Reference Sequence (RefSeq): a curated nonredundant sequence database of genomes, transcripts and proteins. *Nucleic Acids Res*, 2005. 33(Database issue): p. D501-4.
4. Amaral, P.P., et al., lncRNAdb: a reference database for long noncoding RNAs. *Nucleic Acids Res*, 2011. 39(Database issue): p. D146-51.
5. Dinger, M.E., et al., NRED: a database of long noncoding RNA expression. *Nucleic Acids Res*, 2009. 37(Database issue): p. D122-6.
6. Pang, K.C., et al., RNAdb 2.0--an expanded database of mammalian non-coding RNAs. *Nucleic Acids Res*, 2007. 35(Database issue): p. D178-82.
7. Pang, K.C., et al., RNAdb--a comprehensive mammalian noncoding RNA database. *Nucleic Acids Res*, 2005. 33(Database issue): p. D125-30.
8. Guttman, M., et al., Chromatin signature reveals over a thousand highly conserved large noncoding RNAs in mammals. *Nature*, 2009. 458(7235): p. 223-7.
9. Khalil, A.M., et al., Many mouse large intergenic noncoding RNAs associate with chromatinmodifying complexes and affect gene expression. *Proc Natl Acad Sci U S A*, 2009. 106(28): p. 11667- 72.
10. Alexander, D.R., et al., Integration of Genome-wide Approaches Identifies lncRNAs of Adult Neural Stem Cells and Their Progeny In Vivo. *Cell Stem Cell*, 2013. 12(5):p616-28.
11. Sigova, A.A., et al., Divergent transcription of long noncoding RNA/mRNA gene pairs in embryonic stem cells. *Proc Natl Acad Sci U S A*, 2013. 110(8): p. 2876-81.
12. Bejerano, G., et al., Ultraconserved elements in the mouse genome. *Science*, 2004. 304(5675): p. 1321-5.
13. Willingham, A.T., et al., A strategy for probing the function of noncoding RNAs finds a repressor of NFAT. *Science*, 2005. 309(5740): p. 1570-3.
14. Hsu, F., et al., The UCSC Known Genes. *Bioinformatics*, 2006. 22(9): p. 1036-46.
15. Benson, D.A., et al., GenBank: update. *Nucleic Acids Res*, 2004. 32(Database issue): p. D23-6.
16. Kim M., et al., Differential Expression profiling of long noncoding RNA and mRNA during osteoblast differentiation in mouse. *Int J Genomics*, 2018. 2018: p. 7691794.
17. Butchart L.C., et al., Expression patterns of regulatory RNAs, including lncRNAs and tRNAs, during postnatal growth of normal and dystrophic (mdx) mouse muscles, and their response to taurine treatment. 99: p. 52-63.
18. Pal D., et al., Long Noncoding RNAs in pluripotency of stemcells and cell fate specification. *Adv Exp Med Biol*, 2017. 1008: p. 223-252.
19. Tan J.Y., et al., Extensive microRNA-mediated crosstalk between lncRNAs and mRNAs in mouse embryonic stem cells. *Genome Res*, 2015. 25(5): p. 655-66.
20. White R.R., et al., Comprehensive transcriptional landscape of aging mouse liver. *BMC genomics*, 2015. 16: p. 899.

21. Mercer, T.R., et al., Specific expression of long noncoding RNAs in the mouse brain. *Proc Natl Acad Sci U S A*, 2008. 105(2): p. 716-21.
22. Carninci, P., et al., The transcriptional landscape of the mammalian genome. *Science*, 2005. 309(5740): p. 1559-63.