

An integrated expression atlas of miRNAs and their promoters in human and mouse

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Abstract

© 2017 Nature America, Inc., part of Springer Nature. MicroRNAs (miRNAs) are short non-coding RNAs with key roles in cellular regulation. As part of the fifth edition of the Functional Annotation of Mammalian Genome (FANTOM5) project, we created an integrated expression atlas of miRNAs and their promoters by deep-sequencing 492 short RNA (sRNA) libraries, with matching Cap Analysis Gene Expression (CAGE) data, from 396 human and 47 mouse RNA samples. Promoters were identified for 1,357 human and 804 mouse miRNAs and showed strong sequence conservation between species. We also found that primary and mature miRNA expression levels were correlated, allowing us to use the primary miRNA measurements as a proxy for mature miRNA levels in a total of 1,829 human and 1,029 mouse CAGE libraries. We thus provide a broad atlas of miRNA expression and promoters in primary mammalian cells, establishing a foundation for detailed analysis of miRNA expression patterns and transcriptional control regions.

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