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Data Article

Supporting data for characterization of non-coding RNAs associated with the Neuronal growth regulator 1 (NEGR1) adhesion protein

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ABSTRACT

Long non-coding RNAs and microRNAs control gene expression to determine central nervous system development and function. Neuronal growth regulator 1 (NEGR1) is a cell adhesion molecule that plays an important role in neurite outgrowth during neuronal development and its precise expression is crucial for correct brain development. The data described here is related to the research article titled "A long non-coding RNA, BC048612 and a microRNA, miR-203 coordinate the gene expression of Neuronal growth regulator 1 (NEGR1) adhesion protein" [1]. This data article contains detailed bioinformatics analysis of genetic signatures at the *Negr1* gene locus retrieved from the UCSC genome browser. This approach could be adopted to identify putative regulatory non-coding RNAs in other tissues and diseases.

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Specifications Table

Subject area	*Biology*
More specific subject area	*Non-coding RNA mediated regulation of gene expression*
Type of data	*Table and figure*
How data was acquired	*In silico analysis: UCSC Genome browser and RegRNA* *qPCR: Applied Biosystems 7500 sequence detection system*
Data format	*Raw and analyzed data*
Experimental factors	*Primary neuronal cultures on Day 6 were transfected with either LNA™ GapmeR against the BC048612 lncRNA or mammalian expression vector containing BC048612.*
Experimental features	*Total cellular RNA was used to quantify expression levels.*
Data source location	*Singapore*
Data accessibility	*Within this article*

Value of the data

- This data provides a comprehensive *in silico* analysis of the genetic signatures and expression pattern of long non-coding RNAs associated with the *Negr1* gene.
- This data is useful in understanding the regulatory relationship between non-coding RNA gene expression and *Negr1* gene expression.
- The methodology provided can be used to postulate regulatory relationships between long non-coding RNAs and proximal genes.
- This approach could be adopted to identify putative regulatory non-coding RNAs in other tissues and diseases which could be evaluated with further functional studies.

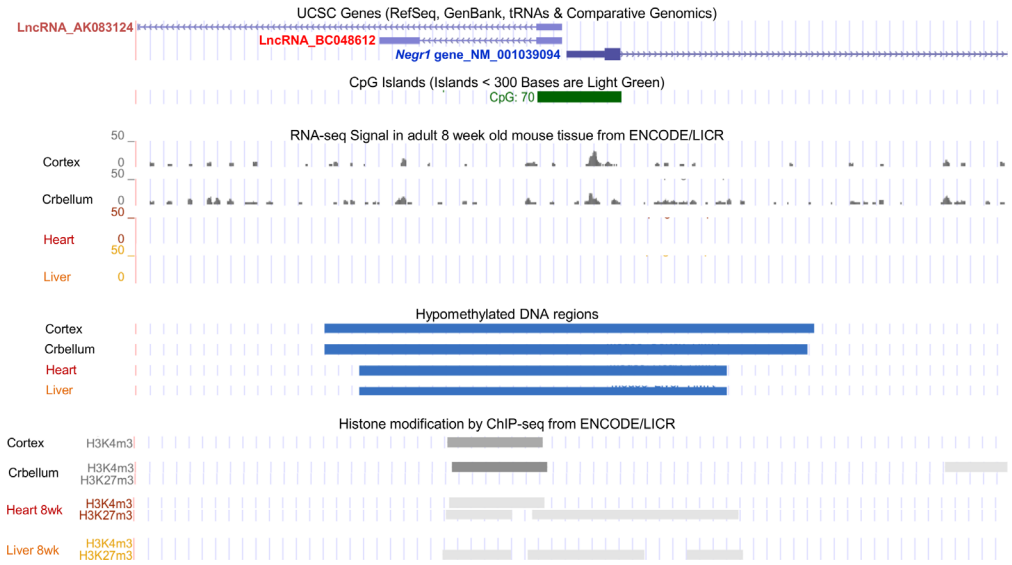

Fig. 1. UCSC Genome Browser showing CpG islands, RNA sequencing data from ENCODE/LICR, DNA hypomethylation status and histone modification ChIP-seq data from ENCODE/LICR for the *Negr1* gene locus. Data in 8 week old mouse cortex, cerebellum, heart and liver was extracted from the UCSC Genome Browser [2–9] on the Mouse July 2007 (NCBI37/mm9) assembly.