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 IncRNA 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.

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**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.
1. Data

The data in this article describes the initial in silico analysis carried out on the Negr1 gene locus for genetic signatures and expression patterns of long non-coding RNAs in proximity to the Negr1 gene [1] (Figs. 1 and 2, Table 1). The proposed interaction between the BC048612 IncRNA and microRNA-203 were validated using qPCR (Fig. 3).

2. Experimental design, materials and methods

2.1. Bioinformatics analysis of Negr1 gene promoter

The Negr1 gene promoter region was analyzed using the UCSC Genome Browser [2,3]. Two IncRNAs, AK083124 and BC048612, were expressed from the Negr1 gene promoter (Fig. 1). Presence of CpG islands [2,3], expression profiles of the IncRNAs and Negr1 mRNA in four different mouse tissues (8 week old cerebellum, cortex, heart and liver) [4–7], DNA hypomethylation status [8,9] as well as histone modification profiles by ChIP-seq from ENCODE/LICR were retrieved from the UCSC genome browser (Fig. 1). The findings from these analyses are summarized in Table 1.

Further interrogation of the BC048612 IncRNA and Negr1 gene transcription start sites as well as putative regulatory transcription factors was carried out (Fig. 2). RegRNA [10] was employed to predict transcription factor binding sites proximal to the transcription start sites (Fig. 2).

2.2. Determination of effect of IncRNA expression on miR-203 levels

To determine if there is any interaction between the BC048612 IncRNA and miR-203, the BC048612 sequence was analyzed for putative binding sites for miR-203. RegRNA analysis did not

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**Table 1**

| Negr1 mRNA expression | LncRNAs expression | DNA hypomethylation | H3K4m3 | H3K27m3 |
|-----------------------|--------------------|---------------------|--------|---------|
| Cortex                | +                  | ++                  | +      | +/C0    |
| Cerebellum            | +                  | ++                  | +      | +       |
| Heart                 | –                  | +                   | +      | +       |
| Liver                 | –                  | –                   | +      | –       |

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**Fig. 2.** Mouse Negr1 gene locus. UCSC genome browser showing Negr1 gene and IncRNAs (AK083124 and BC048612) transcribed from the mouse Negr1 bidirectional promoter based on the July 2009 mouse assembly. Refseq number for each transcript is indicated. CpG islands overlapping with the promoter are also indicated. Transcription start site of each transcript on the promoter sequence is denoted by letters in bold in specific colours with corresponding arrows denoting transcription direction. Putative Sp1 binding sites (red arrows) as determined by RegRNA [10] are mapped on the Negr1 promoter.
predict any miR-203 binding sites on the BC048612 lncRNA [10]. Further verification of the effect of BC048612 lncRNA expression on miR-203 levels was carried out by quantifying miR-203 expression in both lncRNA knockdown (Fig. 3A) and over-expression of lncRNA (Fig. 3B) in primary neuronal cultures. Primary neuronal cultures on Day 6 were transfected with LNA™ GapmeR against the BC048612 lncRNA or mammalian expression vector (pcDNA4/TO/myc His A) containing BC048612 (pc_BC048612 LncRNA). The cells were harvested 48 h after transfection and total cellular RNA was extracted for quantification of miR-203 expression levels.

Competing interests

The authors declare that they have no competing interests.

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Appendix A. Supplementary material

Supplementary data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.dib.2016.02.053.

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