# #4528 Characterization of microRNA expression profiles in normal human tissues identifies immune response as a potential microRNA target in normal and neoplastic brain



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#### **ABSTRACT**

Measuring the quantity of miRNAs in tissues of different physiological and pathological conditions is an important first step to investigate the functions of miRNAs. Matching samples from normal state provide essential baseline references to analyze the variation of miRNA abundance. We provided expression data of 345 miRNAs in 40 normal human tissues, which identified universally expressed miRNAs, and several groups of miRNAs expressed exclusively or preferentially in certain tissue types. Many miRNAs with coregulated expression patterns are located in the same genomic clusters. Hierarchical clustering of normal tissues by their miRNA expression profiles basically followed the structure, anatomical locations, and physiological functions of the organs, suggesting that functions of a miRNA could be appreciated by linking to the biologies of the tissues in which it is uniquely expressed. Many predicted target genes of miRNAs that had specific reduced expression in brain and peripheral blood mononuclear cells are required for embryonic development of the nervous and hematopoietic systems based on database search. Up to one third of predicted target genes of three brain-specific miRNAs are either directly or indirectly involved in functions of the immune system and cellular response to inflammation.

#### MATERIALS AND METHODS

miRNA targets: 345 human miRNAs.

**Total RNA:** Total RNAs of normal tissues were purchased from Ambion and Stratagene.

RT-PCR: TaqMan® MicroRNA Assays (Applied Biosystems)

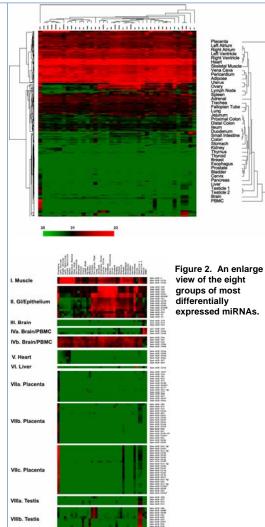
were performed following the instructions (ref. 1).

Data analysis: Agglomerative hierarchical clustering of data was performed using the Cluster and displayed using the TreeView (ref. 2). Prediction of miRNA target genes was based on miRBase (http://microrna.sanger.ac.uk/cgibin/targets/v3/search.pl).

#### **RESULTS**

Figure 1. Unsupervised hierarchical clustering of normal human tissues by variations of miRNA abundance.

Normalized  $C_T$  for each assay was transformed into  $\Delta C_T$  against the average  $C_T$  of all assays examined and clustered without centering the data. A pseudocolor scale outlines the  $C_T$  values represented in the heat map. A detailed view of the clustering patterns of normal tissues is on the right.



# Table 1. Genomic locations of miRNAs in the 8 differentially expressed groups.

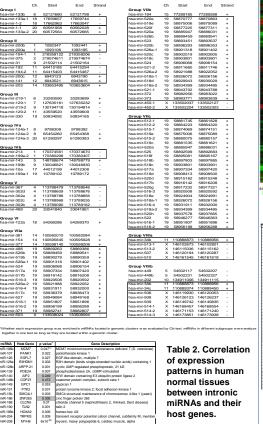


Figure 3. The list of predicted target genes for miR-199a/199b/214 was refined by their expression in 19 normal tissue types extracted from the GNF database.

Blue bars on the right side of the heat map, genes with brain-specific expression; red bars, genes with PBMC-specific expression. The pseudocolor scale represents the gene expression level that has been transformed to the log<sub>2</sub>-based ratio to the average signal of all genes



### REFERENCES

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## **ACKNOWLEDGEMENTS**

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Brain

PBMC

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