Data in Brief 9 (2016) 382–387

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib

Data Article

Data of methylome and transcriptome derived from human dilated cardiomyopathy

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ARTICLE INFO

Article history:
Received 12 July 2016
Received in revised form
29 August 2016
Accepted 6 September 2016
Available online 14 September 2016

Keywords:
Methylome
Transcriptome
DMP
DEG
DCM

ABSTRACT

Alterations in DNA methylation and gene expression have been implicated in the development of human dilated cardiomyopathy (DCM). Differentially methylated probes (DMPs) and differentially expressed genes (DEGs) were identified between the left ventricle (LV, a pathological locus for DCM) and the right ventricle (RV, a proxy for normal hearts). The data in this DiB are for supporting our report entitled "Methylome analysis reveals alterations in DNA methylation in the regulatory regions of left ventricle development genes in human dilated cardiomyopathy" (Bong-Seok Jo, In-Uk Koh, Jae-Bum Bae, Ho-Yeong Yu, Eun-Seok Jeon, Hae-Young Lee, Jae-Joong Kim, Murim Choi, Sun Shim Choi, 2016) [1].

DOI of original article: http://dx.doi.org/10.1016/j.ygeno.2016.07.001
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http://dx.doi.org/10.1016/j.dib.2016.09.006

Specifications Table

Subject area	*Biology*
More specific subject area	*Epigenomics, Transcriptomics, Bioinformatics*
Type of data	*Tables and figures*
How data was acquired	*Infinium 450 K HumanMethylation Bead chip and Human HT-12 v4 Expression BeadChip*
Data format	*Analyzed*
Experimental factors	*DMPs identified using RnBeads software. Statistical tests using R. And, a batch-scale comparison done by home-built Python script*
Experimental features	*Comparison of methylome and transcriptome between left ventricle (case) and right ventricle (control) in DCM patients*
Data source location	*National Institute of Health in Korea (KNIH)*
Data accessibility	*The data are within this article and deposited in GEO under accession number (GEO:* GSE81339*)* http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?token=erezeeaojpyvbqn&acc=GSE81339

Value of the data

- Provide a new insight on DNA methylation alteration in understanding the DCM etiology.
- Investigate the role of DNA methylation occurring in different genic regions associated with the regulation of gene expression.
- Provide new insights on the interaction network constructed by genes of DMP–DEG pairs.

1. Data

DCM samples where methylome and transcriptome data were produced used in the present DiB were listed in Table S1. The present data contain as followings: cleaning and normalization procedures (Figs. S1 and S2), global DNA methylation pattern (Figs. S3 and S4), multidimensional scaling (MDS) (Fig. S5), list of DMPs (Figs. S6 and S7; Table S2), identification of important variable probes (IVPs) (Figs. S8 and S9), DMP distribution in genic regions (Fig. S10), 984 DMP–DEG pairs (Fig. 1; Table S3), methylation alteration in DNase I hypersensitive site (DHS) and enhancer (Fig. 2), functional networks of the 984 DMP–DEG pairs (Fig. 3), gene ontology (Fig. S11), 45 cardiac ventricle development-related genes (Table 1), protein–protein interactions for the 45 genes (Fig. S12), and the relationship between methylation and expression of genes (i.e., TBX5 and HAND1) (Fig. S13).

2. Experimental design, materials and methods

2.1. Ethics statement

The data were prepared in accordance with principles (the Helsinki Declaration). It was approved by the Institutional Review Board (IRB) of The Samsung Medical Center (South Korea) (No. 2012-02-065). All participants have provided written informed consent and obtained the IRB approval for the consent procedure.