Data in Brief 17 (2018) 662–666

Contents lists available at ScienceDirect

Data in Brief

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

Data Article

Methylation profile of induced pluripotent stem cells generated by integration and integration-free approaches

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ARTICLE INFO

Article history:
Received 31 October 2017
Received in revised form
16 January 2018
Accepted 22 January 2018
Available online 31 January 2018

Keywords:
Induced pluripotent stem cells
Illumina 450K Methylation BeadChip
DNA methylation
Sendai virus reprogramming
Lentiviral reprogramming

ABSTRACT

The genetic reprogramming technology allows generation of induced pluripotent stem cells (iPSCs) from somatic cells (Takahashi and Yamanaka, 2006) [1]. iPSCs have the ability to self-renew, and to differentiate into any type of somatic cells, and are considered as a promising tool for drug development, disease modeling, and regenerative medicine. The reprogramming factors (oct4, sox2, klf4, c-myc) can be delivered to the cell nucleus either by vectors integrating into the genome (lentiviruses, retroviruses) or by non-integrative methods (e.g., plasmids, Sendai virus, synthetic mRNAs and recombinant proteins). To evaluate the contribution of the reprogramming process isogenic system should be utilized (Shutova et al., 2016) [2]. Isogenic iPSC lines, obtained in different ways can serve the ideal system to investigate DNA methylation changes. The data presented in this article report methylation profiles for iPSC lines derived from fibroblasts of a healthy donor and PARK8-associated Parkinson's disease patient via integrating (lentiviral transfection) and non-integrating (Sendai virus infection) reprogramming using an Illumina 450K

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https://doi.org/10.1016/j.dib.2018.01.061

Methylation BeadChip platform. The data on DNA methylation of neurons differentiated from iPSC lines are also provided here.

Specifications Table

Subject area	Cell biology
More specific subject area	Isogenic induced pluripotent stem cells derived from fibroblasts
Type of data	idat-files, tables with beta-values
How data was acquired	Genome methylation data was obtained using the Illumina Human Methylation BeadChip 450K platform
Data format	Raw data, analyzed data
Experimental factors	Total DNA was extracted from fibroblasts derived iPSC lines and neurons differentiated from healthy donor and Parkinson's disease patients
Experimental features	DNA methylation of iPSCs generated by integrating (lentiviral) and isogenic iPSCs generated by non-integrating (Sendai virus) methods was analyzed using Illumina 450K Methylation BeadChip and RnBeads package. DNA methylation of iPSCs derived neurons was also analyzed.
Data source location	Vavilov Institute of General Genetics of the Russian Academy of Sciences or Moscow Russia
Data accessibility	Microarray data has been deposited into the NCBI GEO database (Accession number GSE105093), https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE105093

Value of the data

- For the first time, data on DNA methylation of isogenic iPSCs obtained by integrating and non-integrating methods are reported.
- There is little data on genome-wide studies of isogenic iPSC lines. DNA methylation data of isogenic iPSCs lines, obtained by lentiviruses and Sendai virus, allow comparison of the results obtained by different reprogramming methods, including data on rare diseased iPSCs, and to combine them into large data sets.
- Epigenome-wide analysis of iPSCs often require comparison of the lines, not only with different genetic backgrounds, but also obtained in various ways. Our data will allow understanding, whether the way of reprogramming makes significant changes in the DNA methylation landscape.

1. Data

The data presented here originates from four iPSC lines of a healthy donor generated via integrating (IPSRG2L, IPSRG6L) and isogenic cell lines generated by non-integrating (IPSRG4S, IPSRG10S) methods at different passages [1,2]. Two iPSC lines from the same Parkinson's disease (PD) patient with the PARK8 gene mutation were obtained by integrating (IPSPDL2.15L) and non-integrating (IPSPDL2.9S) methods and used at passage 15. Three neuronal populations enriched with tyrosine hydroxylase-positive (TH-positive) neurons differentiated from the iPSCs obtained via integrating method from a healthy donor (IPSRG2L) and two PD patients with the PARK8 gene mutation (IPSPDL1.6L and IPSPDL2.15L) were chosen for DNA methylation analysis. Cell lines are summarized in Table 1.