RNA sequencing data from patients with heart disease and controls

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Creator/Principal investigator(s)

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Description

RNA sequencing analysis of atrial cardiac tissue from patients undergoing coronary artery bypass grafting (CABG) or aortic valve replacement (AVR) was performed and compared with atrial cardiac tissue from organ donors and purchased human atrial cardiac RNA.

RNA sequencing analysis was performed at the Genomics Core Facility at University of Gothenburg, Sweden. All samples (ten controls, ten CABG patients and ten AVR patients) were quality checked by the RNA integrity number (RIN) using Tapestation 2200 RNA screenTape (Agilent Technologies, Santa Clara, CA) and RNA concentration was measured by NanoDrop (Thermo Fisher, Waltham, MA). RIN values ranged between 6.6 and 9.0 for all samples. TruSeq Total Stranded RNA kit with RiboZero (Gold) Sample Preparation Guide (15,031,048 Rev. E) was used for RNA sample preparation (Illumina, San Diego, CA).
A total of 10 µl (~1 µg) RNA from each sample was used for library preparation. Directly after depletion, a cleanup step was performed using 110 ul of the RNAClean XP beads (Beckman Coulter, USA) for each sample. The fragmentation step was performed for 8 min. 12 PCR cycles were run for all samples.
Libraries were quantified and normalized with Qubit DNA HS Assay kit (Life Technologies, Carlsbad, CA) and fragment size determined by Tapestation 2200 (Agilent Technologies, Santa Clara, CA). The libraries were pooled together by using the Illumina protocol for pooling and sequenced with NovaSeq 6000 S1 (Illumina, San Diego, CA) for the read length of 2 × 100 bp.

Data contains personal data

Yes

Sensitive personal data

Yes

Type of personal data

Pseudonymized human data (RNA)

Code key exists

Yes

Language

English

Swedish

Unit of analysis

Individual/Patient

Population

Patients undergoing coronary artery bypass grafting (CABG) or aortic valve replacement (AVR) (experimental group) and organ donors and purchased human RNA (control group).

Study design

Experimental study

Preclinical study

Sampling procedure

Non-probability: Availability

Data format / data structure

Numeric

Geographic spread

Geographic location: Sweden

Responsible department/unit

Department of Laboratory Medicine, Institute of Biomedicine

Ethics Review

Gothenburg - Ref. 560-12 and 436-15

Research area

Biochemistry and molecular biology (Standard för svensk indelning av forskningsämnen 2011)

Genetics (Standard för svensk indelning av forskningsämnen 2011)

Bioinformatics and systems biology (Standard för svensk indelning av forskningsämnen 2011)

Basic medicine (Standard för svensk indelning av forskningsämnen 2011)

Medical genetics (Standard för svensk indelning av forskningsämnen 2011)

Cell and molecular biology (Standard för svensk indelning av forskningsämnen 2011)

Cardiac and cardiovascular systems (Standard för svensk indelning av forskningsämnen 2011)

Keywords

Heart diseases, Aortic valve, Coronary artery bypass, Cadherins, Heart valve prosthesis implantation, Rna, long noncoding, Cadherin related proteins

Publications

Joakim Sandstedt, Kristina Vukusic, Elham Rekabdar, Göran Dellgren, Anders Jeppsson, Lillemor Mattsson Hultén, Victoria Rotter Sopasakis. Markedly reduced myocardial expression of γ-protocadherins and long non-coding RNAs in patients with heart disease. International Journal of Cardiology, vol 344 (2021), page 149–159.
DOI: https://doi.org/10.1016/j.ijcard.2021.09.046

If you have published anything based on these data, please notify us with a reference to your publication(s). If you are responsible for the catalogue entry, you can update the metadata/data description in DORIS.

Accessibility level

Access to data through SND
Access to data is restricted

Use of data

Things to consider when using data shared through SND

Versions

Version 1. 2023-04-17

Contacts for questions about the data

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DataCite

DDI 2.5

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DCAT-AP-SE 2.0

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Citation (CLS)

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