# Materials Design Analysis Reporting (MDAR) Checklist for Authors

The MDAR framework establishes a minimum set of requirements in transparent reporting applicable to studies in the life sciences (see Statement of Task: doi:10.31222/osf.io/9sm4x.). The MDAR checklist is a tool for authors, editors and others seeking to adopt the MDAR framework for transparent reporting in manuscripts and other outputs. Please refer to the MDAR Elaboration Document for additional context for the MDAR framework.

## Materials

| Antibodies | Yes (indicate where provided: section/paragraph) | n/a |
|---|---|---|
| For commercial reagents, provide supplier name, catalogue number and RRID, if available. | | x |

| Cell materials | Yes (indicate where provided: section/paragraph) | n/a |
|---|---|---|
| **Cell lines:** Provide species information, strain. Provide accession number in repository **OR** supplier name, catalog number, clone number, **OR** RRID | | x |
| **Primary cultures:** Provide species, strain, sex of origin, genetic modification status. | | x |

| Experimental animals | Yes (indicate where provided: section/paragraph) | n/a |
|---|---|---|
| **Laboratory animals:** Provide species, strain, sex, age, genetic modification status. Provide accession number in repository **OR** supplier name, catalog number, clone number, **OR** RRID | | x |
| **Animal observed in or captured from the field:** Provide species, sex and age where possible | | x |
| **Model organisms:** Provide Accession number in repository (where relevant) **OR** RRID | | x |

| Plants and microbes | Yes (indicate where provided: section/paragraph) | n/a |
|---|---|---|
| **Plants:** provide species and strain, unique accession number if available, and source (including location for collected wild specimens) | | x |
| **Microbes:** provide species and strain, unique accession number if available, and source | | x |

| Human research participants | Yes (indicate where provided: section/paragraph) | n/a |
|---|---|---|
| Identify authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval. | The study was approved by local institutions (2019-091). (Provided at: Method section page 6 paragraph 1 and Footnotes page 19, last paragraph). | |
| Provide statement confirming informed consent obtained from study participants. | Informed consent was taken from all the patients. According to the German data protection and gene diagnostic law we reported the pathogenic variants in Secondary findings (ACMG list v2.0 of 59 genes) back. Variants of unknown significance, whose involvement in disease at the current time was unclear, were not reported.<br>(Provided at: Method section page 6, paragraph 1) | |
| Report on age and sex for all study participants. | | x |

## Design

| Study protocol | Yes (indicate where provided: section/paragraph) | n/a |
|---|---|---|
| For clinical trials, provide the trial registration number **OR** cite DOI in manuscript. | | x |

| Laboratory protocol | Yes (indicate where provided: section/paragraph) | n/a |
|---|---|---|
| Provide DOI or other citation details if detailed step-by-step protocols are available. | | x |

| Experimental study design (statistics details) | Yes (indicate where provided: section/paragraph) | n/a |
|---|---|---|
| State whether and how the following have been done**, or** if they were not carried out. | 6605 NGS data (individuals unrelated to cardiovascular disease) were analysed for variants in selected actionable genes of the American College of Medical Genetics and Genomics (ACMG ) secondary findings (SF) v2.0 list (ACMG list v2.0 of 59 actionable genes). (provided at: method section, page 6, paragraph 1 "Patient cohort"). | x |
| Sample size determination | | x |
| Randomisation | | x |
| Blinding | | x |
| Inclusion/exclusion criteria | | x |

| Sample definition and in-laboratory replication | Yes (indicate where provided: section/paragraph) | n/a |
|---|---|---|
| State number of times the experiment was replicated in laboratory | | x |
| Define whether data describe technical or biological replicates | | x |

| Ethics | Yes (indicate where provided: section/paragraph) | n/a |
|---|---|---|
| Studies involving human participants: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval. | The study was approved by local institutions (2019-091). Informed consent was taken from all the patients. (provided at: Method section page 6, paragraph 1 and Footnotes page 19, last paragraph) | |
| Studies involving experimental animals: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval. | | x |
| Studies involving specimen and field samples: State if relevant permits obtained, provide details of authority approving study; if none were required, explain why. | | x |

| Dual Use Research of Concern (DURC) | Yes (indicate where provided: section/paragraph) | n/a |
|---|---|---|
| If study is subject to dual use research of concern, state the authority granting approval and reference number for the regulatory approval | | x |

## Analysis

| Attrition | Yes (indicate where provided: section/paragraph) | n/a |
|---|---|---|
| State if sample or data point from the analysis is excluded, and whether the criteria for exclusion were determined and specified in advance. | | x |

| Statistics | Yes (indicate where provided: section/paragraph) | n/a |
|---|---|---|
| Describe statistical tests used and justify choice of tests. | | x |

| Data Availability | Yes (indicate where provided: section/paragraph) | n/a |
|---|---|---|
| State whether newly created datasets are available, including protocols for access or restriction on access. | The variants in actionable ARVC genes are available at https://databases.lovd.nl/shared/variants/DSC2, https://databases.lovd.nl/shared/variants/DSG2, https://databases.lovd.nl/shared/variants/DSP, https://databases.lovd.nl/shared/variants/PKP2, https://databases.lovd.nl/shared/variants/TMEM43 (provided at: Data availability statement, page 9, paragraph 1) | |
| If data are publicly available, provide accession number in repository or DOI or URL. | LOVD allows retrieval of submitted data based on the DOI or PubMed ID assigned to the paper. We submitted our findings to LOVD and mentioned this in the method section (Data available statement)<br>DSP_000766; DSP_000767; DSP_000769; DSP_000770<br>DSC2_000243; DSC2_000244; DSC2_000245; DSC2_000246<br>DSG2_000369; DSG2_000370; DSG2_000371; DSG2_000190; DSG2_000163 | |
| If publicly available data are reused, provide accession number in repository or DOI or URL, where possible. | | x |

| Code Availability | Yes (indicate where provided: section/paragraph) | n/a |
|---|---|---|
| For all newly generated code and software essential for replicating the main findings of the study: | Next-generation sequencing (NGS) analysis of a custom capture kit (Agilent SureSelectXT) was carried out on an Illumina NextSeq 500 system (Illumina, San Diego, CA) as 150 bp paired-end sequencing runs using v2.0 SBS chemistry. Sequencing reads were aligned to the human reference genome (GRCh37/hg19) using BWA (v0.7. 13-r1126) with standard parameters. SNV, CNV and INDEL calling on the genes was conducted using the varvis software platform (varvis™, Limbus Technologies) with subsequent coverage and quality dependent filter steps. (Provided at: Method section page 7 last paragraph “High throughput sequencing and bioinformatics pipeline”). | |
| State whether the code or software is available. | | x |
| If code is publicly available, provide accession number in repository, or DOI or URL. | | x |

## Reporting

| Adherence to community standards | Yes (indicate where provided: section/paragraph) | n/a |
|---|---|---|
| MDAR framework recommends adoption of discipline-specific guidelines, established and endorsed through community initiatives. Journals have their own policy about requiring specific guidelines and recommendations to complement MDAR. | According to the German data protection and gene diagnostic law we reported the pathogenic variants in Secondary findings (ACMG list v2.0 of 59 genes) back. Variants of unknown significance, whose involvement in disease at the current time was unclear, were not reported. | |
| State if relevant guidelines (eg., ICMJE, MIBBI, ARRIVE) have been followed, and whether a checklist | The identified variants were classified according to the American College of Medical Genetics and Genomics (ACMG) guidelines with the 5-tier classification system. | |

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|---|---|---|
| (eg., CONSORT, PRISMA, ARRIVE) is provided with the manuscript. | | |

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