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. | This kind of material was not used in our experiment | N/A |

| 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. | This kind of material was not used in our experiment | N/A |
| Primary cultures: Provide species, strain, sex of origin, genetic modification status. | This kind of material was not used in our experiment | N/A |

| 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 | This kind of material was not used in our experiment | N/A |
| Animal observed in or captured from the field: Provide species, sex and age where possible | This kind of material was not used in our experiment | N/A |
| Model organisms: Provide Accession number in repository (where relevant) OR RRID | This kind of material was not used in our experiment | N/A |

| 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) | This kind of material was not used in our experiment | N/A |
| Microbes: provide species and strain, unique accession number if available, and source | Methods/paragraph 1 | Yes |

| 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. | Footnote/paragraph 2 | Yes |
| Provide statement confirming informed consent obtained from study participants. | Methods/paragraph 1 | Yes |
| Report on age and sex for all study participants. | Results/paragraph 3 | Yes |
| **Design** |  |  |
|---|---|---|
| **Study protocol** | Yes (indicate where provided: section/paragraph) | n/a |
| For clinical trials, provide the trial registration number OR cite DOI in manuscript. | Our experiment did not involve clinical trials | N/A |
| **Laboratory protocol** | Yes (indicate where provided: section/paragraph) | n/a |
| Provide DOI or other citation details if detailed step-by-step protocols are available. | The detailed operation shall be carried out according to the instructions of the kit (Methods/paragraph 2) | Yes |
| **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. |  |  |
| Sample size determination | Methods/paragraph 1 | Yes |
| Randomisation | Methods/paragraph 1 | Yes |
| Blinding | Not applicable in this study experiments | N/A |
| Inclusion/exclusion criteria | Methods/paragraph 1 | Yes |
| **Sample definition and in-laboratory replication** | Yes (indicate where provided: section/paragraph) | n/a |
| State number of times the experiment was replicated in laboratory | The essence of high-throughput sequencing is to repeatedly detect the genome of samples | N/A |
| Define whether data describe technical or biological replicates | The essence of high-throughput sequencing is to repeatedly detect the genome of samples | N/A |
| **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. | Footnote/paragraph 2 | Yes |
| Studies involving experimental animals: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval. | Relevant experiments are not involved | N/A |
| Studies involving specimen and field samples: State if relevant permits obtained, provide details of authority approving study; if none were required, explain why. | Relevant experiments are not involved | N/A |
| **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 | Our research does not involve dual-use research | N/A |
### Analysis

| Category            | Yes (indicate where provided: section/paragraph) | n/a   |
|---------------------|--------------------------------------------------|-------|
| **Attrition**       |                                                  | 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. | We exclude irrelevant samples according to the inclusion and exclusion criteria | |
| **Statistics**      |                                                  | n/a   |
| Describe statistical tests used and justify choice of tests. | Methods/paragraph 6 | Yes |
| **Data Availability** |                                                  | n/a   |
| State whether newly created datasets are available, including protocols for access or restriction on access. | Footnote/paragraph 3 | |
| If data are publicly available, provide accession number in repository or DOI or URL. | Methods/paragraph 4 | Yes |
| If publicly available data are reused, provide accession number in repository or DOI or URL, where possible. | Footnote/paragraph 3 (bioproject:CRA005180, access the data from the following links: https://bigd.big.ac.cn/gsa/browse/CRA005180) | N/A |
| **Code Availability** |                                                  | n/a   |
| For all newly generated code and software essential for replicating the main findings of the study: | | |
| State whether the code or software is available. | Our study does not involve generated codes | N/A |
| If code is publicly available, provide accession number in repository, or DOI or URL. | Our study does not involve generated codes | N/A |

### Reporting

| Category                        | Yes (indicate where provided: section/paragraph) | n/a   |
|---------------------------------|--------------------------------------------------|-------|
| **Adherence to community standards** |                                                  | 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. | | |
| State if relevant guidelines (eg., ICMJE, MIBBI, ARRIVE) have been followed, and whether a checklist (eg., CONSORT, PRISMA, ARRIVE) is provided with the manuscript. | ICMJE guidelines were followed, as the journal follows ICMJE recommendations for publication. | Yes |

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