

## **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](https://doi.org/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**

<b>Antibodies</b>	<b>Yes (indicate where provided: section/paragraph)</b>	<b>n/a</b>
For commercial reagents, provide supplier name, catalogue number and RRID, if available.	Antibodies are not used in this study. This study is based on TCGA database analysis.	<b>n/a</b>
<b>Cell materials</b>	<b>Yes (indicate where provided: section/paragraph)</b>	<b>n/a</b>
<b>Cell lines:</b> Provide species information, strain. Provide accession number in repository <b>OR</b> supplier name, catalog number, clone number, <b>OR</b> RRID	Cell lines are not used in study. This study is based on TCGA database analysis.	<b>n/a</b>
<b>Primary cultures:</b> Provide species, strain, sex of origin, genetic modification status.	Primary cultures are not used in this study. This study is based on TCGA database analysis.	<b>n/a</b>
<b>Experimental animals</b>	<b>Yes (indicate where provided: section/paragraph)</b>	<b>n/a</b>
<b>Laboratory animals:</b> Provide species, strain, sex, age, genetic modification status. Provide accession number in repository <b>OR</b> supplier name, catalog number, clone number, <b>OR</b> RRID	Laboratory animals are not used in this study. This study is based on TCGA database analysis.	<b>n/a</b>
<b>Animal observed in or captured from the field:</b> Provide species, sex and age where possible	Animals are not used in this study. This study is based on TCGA database analysis.	<b>n/a</b>
<b>Model organisms:</b> Provide Accession number in repository (where relevant) <b>OR</b> RRID	Model organisms are not used in this study. This study is based on TCGA database analysis.	<b>n/a</b>
<b>Plants and microbes</b>	<b>Yes (indicate where provided: section/paragraph)</b>	<b>n/a</b>
<b>Plants:</b> provide species and strain, unique accession number if available, and source (including location for collected wild specimens)	Plants are not used in this study. This study is based on TCGA database analysis.	<b>n/a</b>
<b>Microbes:</b> provide species and strain, unique accession number if available, and source	Microbes are not used in this study. This study is based on TCGA database analysis.	<b>n/a</b>
<b>Human research participants</b>	<b>Yes (indicate where provided: section/paragraph)</b>	<b>n/a</b>
Identify authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.	Human participants are not included in this study. This study is based on TCGA database analysis.	<b>n/a</b>
Provide statement confirming informed consent obtained from study participants.	Human participants are not used in this study. This study is based on TCGA database analysis.	<b>n/a</b>
Report on age and sex for all study participants.	Human participants are not used in this study. This study	<b>n/a</b>

**Design**

<b>Study protocol</b>	<b>Yes (indicate where provided: section/paragraph)</b>	<b>n/a</b>
For clinical trials, provide the trial registration number <b>OR</b> cite DOI in manuscript.	Total protocol are described in Section Material and Methods. We also provided a graphical protocol to show the whole procedure of this study (Figure.S1)	
<b>Laboratory protocol</b>	<b>Yes (indicate where provided: section/paragraph)</b>	<b>n/a</b>
Provide DOI or other citation details if detailed step-by-step protocols are available.	This study is based on TCGA database analysis. (bioinformatics).	<b>n/a</b>
<b>Experimental study design (statistics details)</b>	<b>Yes (indicate where provided: section/paragraph)</b>	<b>n/a</b>
State whether and how the following have been done, <b>or</b> if they were not carried out.	Total protocol are described in Section Material and Methods. We also provided a graphical protocol to show the whole procedure of this study.	
Sample size determination	Section Material and Methods, RNA-seq data procession and R packages.	
Randomisation	This study is based on TCGA database analysis.	<b>n/a</b>
Blinding	This study is based on TCGA database analysis.	<b>n/a</b>
Inclusion/exclusion criteria	This study is based on TCGA database analysis.	<b>n/a</b>
<b>Sample definition and in-laboratory replication</b>	<b>Yes (indicate where provided: section/paragraph)</b>	<b>n/a</b>
State number of times the experiment was replicated in laboratory	This study is based on TCGA database analysis. (bioinformatics).	<b>n/a</b>
Define whether data describe technical or biological replicates	This study is based on TCGA database analysis. (bioinformatics).	<b>n/a</b>
<b>Ethics</b>	<b>Yes (indicate where provided: section/paragraph)</b>	<b>n/a</b>
Studies involving human participants: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.	n/a This study is based on TCGA database analysis. (bioinformatics).	<b>n/a</b>
Studies involving experimental animals: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.	n/a This study is based on TCGA database analysis. (bioinformatics).	<b>n/a</b>
Studies involving specimen and field samples: State if relevant permits obtained, provide details of authority approving study; if none were required, explain why.	n/a This study is based on TCGA database analysis. (bioinformatics).	<b>n/a</b>
<b>Dual Use Research of Concern (DURC)</b>	<b>Yes (indicate where provided: section/paragraph)</b>	<b>n/a</b>
If study is subject to dual use research of concern, state the authority granting approval and reference number for the regulatory approval		<b>n/a</b>

**Analysis**

<b>Attrition</b>	<b>Yes (indicate where provided: section/paragraph)</b>	<b>n/a</b>
State if sample or data point from the analysis is excluded, and whether the criteria for exclusion were determined and specified in advance.		n/a
<b>Statistics</b>	<b>Yes (indicate where provided: section/paragraph)</b>	<b>n/a</b>
Describe statistical tests used and justify choice of tests.	Section Material and Methods, Statistical analysis.	
<b>Data Availability</b>	<b>Yes (indicate where provided: section/paragraph)</b>	<b>n/a</b>
State whether newly created datasets are available, including protocols for access or restriction on access.	Section Data Sharing Statement.	
If data are publicly available, provide accession number in repository or DOI or URL.		n/a
If publicly available data are reused, provide accession number in repository or DOI or URL, where possible.		n/a
<b>Code Availability</b>	<b>Yes (indicate where provided: section/paragraph)</b>	<b>n/a</b>
For all newly generated code and software essential for replicating the main findings of the study:		n/a
State whether the code or software is available.	Section Material and Methods, RNA-seq data procession and R packages.	
If code is publicly available, provide accession number in repository, or DOI or URL.	Section Acknowledgement.	

**Reporting**

<b>Adherence to community standards</b>	<b>Yes (indicate where provided: section/paragraph)</b>	<b>n/a</b>
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.	Section Acknowledgement.	
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.	

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