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 article is a purely bioinformatics article that does not involve any clinical trials.

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 article is a purely bioinformatics article that does not involve any clinical trials.
Primary cultures: Provide species, strain, sex of origin, genetic modification status.		This article is a purely bioinformatics article that does not involve any clinical trials.

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 article is a purely bioinformatics article that does not involve any clinical trials.
Animal observed in or captured from the field: Provide species, sex and age where possible		This article is a purely bioinformatics article that does not involve any clinical trials.
Model organisms: Provide Accession number in repository (where relevant) **OR** RRID		This article is a purely bioinformatics article that does not involve any clinical trials.

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 article is a purely bioinformatics article that does not involve any clinical trials.
Microbes: provide species and strain, unique accession number if available, and source		This article is a purely bioinformatics article that does not involve any clinical trials.

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.		This article uses sequencing data from public databases for analysis, including TCGA and GTEx. These data were downloaded from the UCSC Xena website (https://xenabrowser.net/).

Provide statement confirming informed consent obtained from study participants.		This article uses sequencing data from public databases for analysis, including TCGA and GTEx. These data were downloaded from the UCSC Xena website (https://xenabrowser.net/).
Report on age and sex for all study participants.	**Page 8, Line 164** 3. Results 3.1 Clinical characteristics, Paragraph 1. For details see Annex - Table I	

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Study protocol	**Yes (indicate where provided: section/paragraph)**	**n/a**
For clinical trials, provide the trial registration number **OR** cite DOI in manuscript.		This article is a purely bioinformatics article that does not involve any clinical trials.

Laboratory protocol	**Yes (indicate where provided: section/paragraph)**	**n/a**
Provide DOI or other citation details if detailed step-by-step protocols are available.		This article is a purely bioinformatics article that does not involve any clinical

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.		This article is a purely bioinformatics article that does not involve any clinical trials.
Sample size determination		This article is a purely bioinformatics article that does not involve any clinical trials.
Randomisation		This article is a purely bioinformatics article that does not involve any clinical trials.
Blinding		This article is a purely bioinformatics article that does not involve any clinical trials.
Inclusion/exclusion criteria		This article is a purely bioinformatics article that does not involve any clinical trials.

Sample definition and in-laboratory replication	**Yes (indicate where provided: section/paragraph)**	**n/a**
State number of times the experiment was replicated in laboratory		This article is a purely bioinformatics article that does not involve any clinical trials.
Define whether data describe technical or biological replicates		This article is a purely bioinformatics article that does not involve any clinical trials.

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.		This article is a purely bioinformatics article that does not involve any clinical trials.
Studies involving experimental animals: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.		This article is a purely bioinformatics article that does not involve any clinical trials.
Studies involving specimen and field samples: State if relevant permits obtained, provide details of authority approving study; if none were required, explain why.		This article uses sequencing data from public databases for analysis, including TCGA and GTEx. These data were downloaded from the UCSC Xena website (https://xenabrowser.net/).

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		This article is a purely bioinformatics article that does not involve any clinical trials.

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.	**Page 5, Line 91-101** 2. Methods 2.1 Data from the UCSC Xena website Paragraph 1.	

Statistics	**Yes (indicate where provided: section/paragraph)**	**n/a**
Describe statistical tests used and justify choice of tests.	**Page 5-8, Line 148-158** 2. Methods 2.6 Statistical analysis Paragraph 1.	

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.	**Page 5, Line 91-101** 2. Methods 2.1 Data from the UCSC Xena website Paragraph 1.	
If data are publicly available, provide accession number in repository or DOI or URL.	**Page 5, Line 93** 2. Methods 2.1 Data from the UCSC Xena website Paragraph 1 (UCSC, https://xenabrowser.net/); **Page 5, Line 106** 2. Methods 2.2 Screening immune-related differential genes Paragraph 1 (ImmPort, https://immport.niaid.nih.gov).	

If publicly available data are reused, provide accession number in repository or DOI or URL, where possible.	**Page 5, Line 93** 2. Methods 2.1 Data from the UCSC Xena website Paragraph 1 (UCSC, https://xenabrowser.net/); **Page 5, Line 106** 2. Methods 2.2 Screening immune-related differential genes Paragraph 1 (ImmPort, https://immport.niaid.nih.gov).	

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:	**Page 9-10, Line 182-215** 3. Results 3.3 Construction and evaluation of prognostic signature based on IRDEGs	
State whether the code or software is available.	**Page 5-8, Line 102-158** 2. Methods 2.2 Screening immune-related differential genes-2.6 Statistical analysis.	
If code is publicly available, provide accession number in repository, or DOI or URL.	**Page 5-8, Line 102-158** 2.Methods 2.2 Screening immune-related differential genes-2.6 Statistical analysis. (GSEA, https://www.gsea-msigdb.org/gsea/downloads.jsp) (STRING, https://string-db.org) (R version 3.5.3, https://www.r-project.org)	

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.	**Page 4, Line 85-87** 1.Introduction Paragraph 3; **Page 17, Line 357-358** Footnote	
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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