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 study was mainly based on bioinformatics, and the main experiments were RNA extraction and qPCR.	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 study was mainly based on bioinformatics, and the main experiments were RNA extraction from tissue specimens and qPCR.	n/a
Primary cultures: Provide species, strain, sex of origin, genetic modification status.	This study was mainly based on bioinformatics, and the main experiments were RNA extraction from tissue specimens and qPCR.	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 study was mainly based on bioinformatics, and the main experiments were RNA extraction from tissue specimens and qPCR.	n/a
Animal observed in or captured from the field: Provide species, sex and age where possible	This study was mainly based on bioinformatics, and the main experiments were RNA extraction from tissue specimens and qPCR.	n/a
Model organisms: Provide Accession number in repository (where relevant) **OR** RRID	This study was mainly based on bioinformatics, and the main experiments were RNA extraction from tissue specimens and qPCR.	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 study was mainly based on bioinformatics, and the main experiments were RNA extraction from tumor specimens and qPCR.	n/a
Microbes: provide species and strain, unique accession number if available, and source	This study was mainly based on bioinformatics, and the main experiments were RNA extraction from tumor specimens and qPCR.	n/a

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.	Page 11，section “Tissue samples” /paragraph 1	
Provide statement confirming informed consent obtained from study participants.	Page 11，section “Tissue samples” /paragraph 1	
Report on age and sex for all study participants.	Page 11，section “Tissue samples” /paragraph 1	

Design

Study protocol	Yes (indicate where provided: section/paragraph)	n/a
For clinical trials, provide the trial registration number **OR** cite DOI in manuscript.	This study was not a clinical trial.	**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.	RNA extraction and qPCR were routine experiments.	**n/a**

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.	Page 11, section “Tissue samples” /paragraph 1	
Sample size determination	We randomly elected 50 pairs of PTC, and the sample size was relatively larger than those reported in the previous literatures. Thus, we suppose that the sample size was adequate to support the conclusion.	**n/a**
Randomisation	Page 11，section “Tissue samples” /paragraph 1	
Blinding	The tissues were selected randomly and all the PTCs and normal tissues were paired.	**n/a**
Inclusion/exclusion criteria	Page 11，section “Tissue samples” /paragraph 1	

Sample definition and in-laboratory replication	Yes (indicate where provided: section/paragraph)	n/a
State number of times the experiment was replicated in laboratory	Page 13, section” Statistical analysis” / paragraph 1	
Define whether data describe technical or biological replicates	Page 13, section” Statistical analysis” / paragraph 1	

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.	Page 11，section “Tissue samples” /paragraph 1	
Studies involving experimental animals: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.	The study was just involved in tissue samples.	**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.	Page 11，section “Tissue samples” /paragraph 1	**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	The study was not subject to dual use research of concern,	**n/a**

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.	No sample or data was excluded.	n/a

Statistics	Yes (indicate where provided: section/paragraph)	n/a
Describe statistical tests used and justify choice of tests.	Page 13, section Statistical Analysis / paragraph 1	n/a

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 22, section "Data Sharing Statement"/ paragraph 1	
If data are publicly available, provide accession number in repository or DOI or URL.	Page 7, section "Microarray data"/ paragraph 1 Page 9, section "GO and KEGG pathway enrichment analyses of DEGs" / paragraph 1	
If publicly available data are reused, provide accession number in repository or DOI or URL, where possible.	Page 7, section "We completed…"/ paragraph 1 Page 9, section "GO and KEGG pathway enrichment analyses of DEGs" / paragraph 1	

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:	This study did not involve in newly generated code and software .	n/a
State whether the code or software is available.	This study did not involve in newly generated code	n/a
If code is publicly available, provide accession number in repository, or DOI or URL.	Page 9, section "Microarray data"/ paragraph 1 Page 9, section "GO and KEGG pathway enrichment analyses of DEGs" / paragraph 1	

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 7, section Introduction/ paragraph 4	
State if relevant guidelines (eg., ICMJE, MIBBI, ARRIVE) have been followed, and whether a checklist (eg., CONSORT, PRISMA, ARRIVE) is provided with the manuscript.	Page 21 section Reporting checklist/ paragraph 1 ICMJE guidelines were followed, as the journal follows ICMJE recommendations for publication.	

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