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.	RIPA lysis buffer (Beyotime Biotechnological Co., Ltd, catalog No. P0013B); β-catenin, rabbit monoclonal antibody, 1:1,000, SCT, catalog No.8480S; GAPDH, rat monoclonal antibody, 1:1,000, Santa Cruz; catalog No.sc-47724; the secondary antibody (anti-rabbit, 1:10,000; anti-rat, 1:5,000; Jackson); CCK solution (Beyotime Biotechnological Co., Ltd, catalog No.C0040); 0.25% trypsin (Gibco, catalog No.25200-072); 0.25% trypsin (Gibco, catalog No.25200-072); RPMI 1640 culture medium (Gibco BRL, catalog No. C11875500BT); 10% fetal bovine serum (Gibco BRL, catalog No. 10099141); 1% penicillin/streptomycin (Gibco BRL, catalog No. 15140-122); Plasmid Extraction Kit (Tiangen, catalog No. DP116); Lipfectamine 2000 (Invirtrogn, catalog No.11668019); Trizol (TaKaRa, catalog No.9109); 5× primeScript RT Master MIX (TaKaRa, catalog No. RR036A)	

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	LUAD NCI-H1299 cells and NCI-H1975 cells (Cell Bank, Chinese Academy of Sciences, Shanghai)	
Primary cultures: Provide species, strain, sex of origin, genetic modification status.	LUAD NCI-H1299 cells and NCI-H1975 cells (Cell Bank, Chinese Academy of Sciences, Shanghai)	

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	The study was not invoved in experimental animals.	
Animal observed in or captured from the field: Provide species, sex and age where possible	The study was not invoved in experimental animals.	
Model organisms: Provide Accession number in repository (where relevant) **OR** RRID	The study was not invoved in experimental animals.	

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)	The study was not invoved in plants.	
Microbes: provide species and strain, unique accession number if available, and source	The study was not invoved in microbes.	

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.	No human participants.	
Provide statement confirming informed consent obtained from study participants.	No human participants.	
Report on age and sex for all study participants.	No human participants.	

Design

Study protocol	Yes (indicate where provided: section/paragraph)	n/
For clinical trials, provide the trial registration number **OR** cite DOI in manuscript.	The study was a molecular and foundational research.	

Laboratory protocol	Yes (indicate where provided: section/paragraph)	n/
Provide DOI or other citation details if detailed step-by-step protocols are available.	The protocol was a common experimental method in our laboratory.	

Experimental study design (statistics details)	Yes (indicate where provided: section/paragraph)	n/
State whether and how the following have been done**, or** if they were not carried out.		
Sample size determination	For transcriptome sequencing analysis, there were divided into NC group (n = 3) and mutation group (n=3) in H1299 cells; To elucidate the celluar function, there were divided into normal control (NC) group, wide type (WT) group and mutation group in H1299 cells and H1975 cells, respectively.	
Randomisation	Experiments are grouped and operated strictly in accordance with experimental purposes and standards.	
Blinding	Experiments are grouped and operated strictly in	
Inclusion/exclusion criteria	There is nothing to declare.	

Sample definition and in-laboratory replication	Yes (indicate where provided: section/paragraph)	n/
State number of times the experiment was replicated in laboratory	The experiments were repeated three times.	
Define whether data describe technical or biological replicates	Biological replicates	

Ethics	Yes (indicate where provided: section/paragraph)	n/
Studies involving human participants: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.	The study was a molecular and foundamental research.	
Studies involving experimental animals: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.	The study was not invoved in experimental animals.	
Studies involving specimen and field samples: State if relevant permits obtained, provide details of authority approving study; if none were required, explain why.	The study was not invoved specimen.	

Dual Use Research of Concern (DURC)	Yes (indicate where provided: section/paragraph)	n/
If study is subject to dual use research of concern, state the authority granting approval and reference number for the regulatory approval	No, it isn't subject to dual use research of concern.	

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.	After sequnencing and analytically screening, the clean reads and subsequnt differentially expressed genes were preserved in Table 1,.	

Statistics	Yes (indicate where provided: section/paragraph)	n/a
Describe statistical tests used and justify choice of tests.	One-way ANOVA and Newman-Keuls test were used. When using ANOV It is more likely to reveal significant means of differences beteewn more than two samples via Newman-Keuls test.	

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 raw data involved in the paper is not publicly available, because further research will cover it.	
If data are publicly available, provide accession number in repository or DOI or URL.	No, the reason is given as above.	
If publicly available data are reused, provide accession number in repository or DOI or URL, where possible.	No, the date is original.	

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:		
State whether the code or software is available.	Available	
If code is publicly available, provide accession number in repository, or DOI or URL.	The software we used is free public resource.	

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.		
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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