

## **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:</b>	<b>n/a</b>
For commercial reagents, provide supplier name, catalogue number and RRID, if available.		No antibody was used in this experiment.
<b>Cell materials</b>	<b>Yes (indicate where provided:</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	We used the human PTC cell lines BCPAP and Nthy Ori3-1 from American Type Culture Collection (ATCC, Manassas, VA, USA). (Page 8, Line 156-157)	
<b>Primary cultures:</b> Provide species, strain, sex of origin, genetic modification status.		n/a
<b>Experimental animals</b>	<b>Yes (indicate where provided:</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		No animals were used in this experiment.
<b>Animal observed in or captured from the field:</b> Provide species, sex and age where possible		No animals were used in this experiment.
<b>Model organisms:</b> Provide Accession number in repository (where relevant) <b>OR</b> RRID		No model organisms were used in this
<b>Plants and microbes</b>	<b>Yes (indicate where provided:</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)		No plants were used in this experiment.
<b>Microbes:</b> provide species and strain, unique accession number if available, and source		No microbes were used in this
<b>Human research participants</b>	<b>Yes (indicate where provided:</b>	<b>n/a</b>
Identify authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.		All the data about human research participants came from the public
Provide statement confirming informed consent obtained from study participants.		All the data about human research participants came from the public database TCGA.
Report on age and sex for all study participants.	Among the 502 samples, the mean age was 47.35years (range from 15 to 89 years). Male were 135, and female were 367. (Page10, Line 195-196.)	

**Design**

<b>Study protocol</b>	<b>Yes (indicate where provided:</b>	<b>n/a</b>
For clinical trials, provide the trial registration number <b>OR</b> cite DOI in manuscript.		All the data that we used came from the public database TCGA: a bioinformatics analysis.
<b>Laboratory protocol</b>	<b>Yes (indicate where provided:</b>	<b>n/a</b>
Provide DOI or other citation details if detailed step-by-step protocols are available.		no
<b>Experimental study design (statistics details)</b>	<b>Yes (indicate where provided:</b>	<b>n/a</b>
State whether and how the following have been done, <b>or</b> if they were not carried out.		
Sample size determination	We downloaded the RNA sequencing (RNA-Seq) expression data of 560 samples, and the corresponding clinical information of 502 cases from The Cancer Genome Atlas (TCGA) database, and microarray data of 49 PTC samples and 45 adjacent normal thyroid samples (GSE33630) from the NCBI Gene Expression Omnibus (GEO) database( <a href="http://www.ncbi.nlm.nih.gov/geo/">http://www.ncbi.nlm.nih.gov/geo/</a> ). (Page 5, Line 93-95; Page 6, Line 104-107.)	
Randomisation	116 samples of PTC were randomly selected from the dataset of 502 PTC samples by using the random number method to be 2:1 matched with normal tissues. (Page 5, Line 97-98.)	
Blinding		this research is not applicable.
Inclusion/exclusion criteria	We used all the data t from the public database TCGA.	
<b>Sample definition and in-laboratory</b>	<b>Yes (indicate where provided:</b>	<b>n/a</b>
State number of times the experiment was replicated in laboratory	Three times.	
Define whether data describe technical or biological replicates		this research is not applicable.
<b>Ethics</b>	<b>Yes (indicate where provided:</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.		this research is not applicable.
Studies involving experimental animals: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.		this research is not applicable.
Studies involving specimen and field samples: State if relevant permits obtained, provide details of authority approving study; if none were required, explain why.		this research is not applicable.
<b>Dual Use Research of Concern (DURC)</b>	<b>Yes (indicate where provided:</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		this research is not applicable.
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**Analysis**

<b>Attrition</b>	<b>Yes (indicate where provided:</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.		no
<b>Statistics</b>	<b>Yes (indicate where provided:</b>	<b>n/a</b>
Describe statistical tests used and justify choice of tests.	We used Wilcox test to verify the gene difference in silicon; used Student's t-test to verify the gene difference in vitro; and used Kruskal test to test gene difference among T, N, M and AJCC stages.	
<b>Data Availability</b>	<b>Yes (indicate where provided:</b>	<b>n/a</b>
State whether newly created datasets are available, including protocols for access or restriction on access.	for access	
If data are publicly available, provide accession number in repository or DOI or URL.	<a href="https://portal.gdc.cancer.gov/projects/TCGA-THCA">https://portal.gdc.cancer.gov/projects/TCGA-THCA</a>	
If publicly available data are reused, provide accession number in repository or DOI or URL, where possible.	<a href="https://portal.gdc.cancer.gov/projects/TCGA-THCA">https://portal.gdc.cancer.gov/projects/TCGA-THCA</a>	
<b>Code Availability</b>	<b>Yes (indicate where provided:</b>	<b>n/a</b>
For all newly generated code and software essential for replicating the main findings of the study:	We use R software to analyze the data.	
State whether the code or software is available.	R version 3.61	
If code is publicly available, provide accession number in repository, or DOI or URL.	<a href="https://cran.r-project.org/">https://cran.r-project.org/</a>	

**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.		No
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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