

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

Antibodies	Yes (indicate where provided: section/paragraph)	n/a
For commercial reagents, provide supplier name, catalogue number and RRID, if available.	As reported in material and methods/Nuclei isolation and multiparameter flow-sorting, we used the following Antibodies: pCK, clone MNF116, Dako, Code-Nr. M0821. TTF-1 (SP141), Ventana cat number 790-4756	
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		No cell lines were used in this study.
Primary cultures: Provide species, strain, sex of origin, genetic modification status.		No primary cultures were generated in this study.
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		We did not use animals in the present study.
Animal observed in or captured from the field: Provide species, sex and age where possible		We did not use animals in the present study.
Model organisms: Provide Accession number in repository (where relevant) OR RRID		We did not use animals in the present study.
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)		We did not use plants in the present study.
Microbes: provide species and strain, unique accession number if available, and source		We did not use microbes in the present study.
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.	The approval reference number obtained by the Ethics Committee of Both Basels (EKBB) and Ethics Committee Northwest and Central Switzerland (EKNZ) is EKBB/EKNZ 31/12, as described in "Materials and methods section/Patient Cohort"	

Provide statement confirming informed consent obtained from study participants.		No written informed consent needed according the ethical approval (retrospective study)
Report on age and sex for all study participants.	Data about patients' characteristics are reported as aggregate in Table 1: "Clinical characteristics of the cohort"	

Design

Study protocol	Yes (indicate where provided:	n/a
For clinical trials, provide the trial registration number OR cite DOI in manuscript.		This is not a clinical trial
Laboratory protocol	Yes (indicate where provided:	n/a
Provide DOI or other citation details if detailed step-by-step protocols are available.		We only collected clinical data and processed FF and FFPE biological specimens as described in Material and Methods section.
Experimental study design (statistics details)	Yes (indicate where provided:	n/a
State whether and how the following have been done, or if they were not carried out.		
Sample size determination		As we are dealing with rare metastatic cancer, we included all cases.
Randomisation		This study is not an interventional randomized trial.
Blinding		This study is not an interventional randomized trial requiring blinding
Inclusion/exclusion criteria	As reported in material and methods/Patient Cohort, only patients histologically confirmed LUSC with regional or distant metastases with enough tissue samples to perform nuclei flow-sorting and whole exome sequencing were included in this study. Moreover for this study were included only patients with almost all clinical and pathological data available	
Sample definition and in-laboratory replication	Yes (indicate where provided:	n/a
State number of times the experiment was replicated in laboratory		Whole exome sequencing was not replicated. The mean coverage of tumor samples was > 50x. We performed for each patient the sequencing of the primary tumor and the metastasis

<p>Define whether data describe technical or biological replicates</p>		<p>Whole exome sequencing was not replicated. The mean coverage of tumor samples was > 50x. We performed for each patient the sequencing of the primary tumor and the metastasis</p>
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Ethics	Yes (indicate where provided:	n/a
<p>Studies involving human participants: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.</p>	<p>The approval reference number obtained by the Ethics Committee of Both Basels (EKBB) and Ethics Committee Northwest and Central Switzerland (EKNZ) is EKBB/EKNZ 31/12, as described in "Materials and methods section/Patient Cohort"</p>	
<p>Studies involving experimental animals: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.</p>		<p>We did not use animals in the present study.</p>
<p>Studies involving specimen and field samples: State if relevant permits obtained, provide details of authority approving study; if none were required, explain why.</p>		<p>We did not use field samples in this study.</p>

Dual Use Research of Concern (DURC)	Yes (indicate where provided:	n/a
<p>If study is subject to dual use research of concern, state the authority granting approval and reference number for the regulatory approval</p>		<p>Data are collected anonymously only for the conduction of this study.</p>

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.	As reported in material and methods/Patient Cohort, only patients histologically confirmed LUSC with regional or distant metastases with enough tissue samples to perform nuclei flow-sorting and whole exome sequencing were included in this study. Moreover for this study were included only patients with almost all clinical and pathological data available	

Statistics	Yes (indicate where provided: section/paragraph)	n/a
Describe statistical tests used and justify choice of tests.	As reported in results/ Mutational landscape of primary-metastatic pairs of LUSC section, we performed a Wilcoxon test to check whether the primary tumors have more non-synonymous mutations than the metastases.	

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.		We created an internal dataset with restriction on access (username and password requested) for a limited number of people.
If data are publicly available, provide accession number in repository or DOI or URL.		Data are not publicly available.
If publicly available data are reused, provide accession number in repository or DOI or URL, where possible.		We did not reuse publicly available data.

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.		We did not generate new code or software.
If code is publicly available, provide accession number in repository, or DOI or URL.		We did not generate new code or software.

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.		No relevant guidelines have been followed. Only MDAR checklist has been provided with the manuscript.
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.	

Article information: <http://dx.doi.org/tlcr-21-48>.