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.	Methods Immunohistochemistry (IHC): Ventana BenchMark ultra-automated system, SMO mAb, distributed by Origene, TA318627, clone 3E5 diluter 1:500.	

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 our Ethical Committee is INT 91/13, as described in "METHODS/Selection of patients and sample collection."	
Provide statement confirming informed consent obtained from study participants.	In "METHODS/Selection of patients and sample collection" we explained the retrospective nature of the study. The patients were not in treatment or in active follow-up; therefore, according to Italian law (Gazzetta Ufficiale n. 72, 26/03/2012; n. 303, 29/12/2016), the informed consent was not required.	
Report on age and sex for all study participants.	Data about patients' characteristics are reported as aggregate in Table 1: "Patients main characteristics overall and for NS and LS."	

Design

Study protocol	**Yes (indicate where provided: section/paragraph)**	**n/a**
For clinical trials, provide the trial registration number **OR** cite DOI in manuscript.		Due to the retrospective and observational nature of the study, we have not registered it on Clinicaltrial.gov

Laboratory protocol	**Yes (indicate where provided: section/paragraph)**	**n/a**
Provide DOI or other citation details if detailed step-by-step protocols are available.		We only collected clinical data and processed FFPE biological specimens as described in Methods.

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.		
Sample size determination		As we are dealing with rare cancer, we included all cases, then, to avoid selection bias we applied corrections through statistical techniques.
Randomisation		This study is not an interventional randomized trial.

Blinding		This study is not an interventional randomized trial requiring blinding.
Inclusion/exclusion criteria	In METHODS/Selection of patients and sample collection: The recruitment period was 2002-2014 and three Italian institutions contributed. We considered only patients with enough tissue samples to perform molecular tests and with almost all clinical and pathological data available.	

Sample definition and in-laboratory replication	**Yes (indicate where provided: section/paragraph)**	**n/a**
State number of times the experiment was replicated in laboratory	Next generation Sequencing was not replicated; both strands were sequenced. The median coverage was >500x. For SMO, confirmation by Sanger will be performed as described in RESULTS/Gene variations in the 21 MPM associated genes.	
Define whether data describe technical or biological replicates	We have validated the results obtained by NGS with another technique as described in RESULTS/Gene variations in the 21 MPM associated genes.	

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.	The study was approved by INT Independent Ethics Committee, code INT 91/13 as reported in METHODS/Selection of patients and sample collection.	
Studies involving experimental animals: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.		We did not use animals in the present study.
Studies involving specimen and field samples: State if relevant permits obtained, provide details of authority approving study; if none were required, explain why.		We did not use field samples in this study.

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		Data are collected anonymously only for the conduction of this study.

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 METHODS/Selection of patients and sample collection, only patients with enough tissue samples to perform molecular tests and with almost all clinical and pathological data available were included in this study.	

Statistics	Yes (indicate where provided: section/paragraph)	n/a
Describe statistical tests used and justify choice of tests.	In METHODS/Statistical analysis: association between gene mutations and clinical features were assessed by the non-parametric Fisher's exact test. T test was used for the association of gene mutations with age. OS was analyzed with the Kaplan Meier method. To assess the association between mutated genes and OS, SMO mutations and OS, we applied the univariate Cox proportional hazard model. Rubin's rule was used to pool the 100 estimates from the models defined in order to remove the bias of having a sample with a high proportion of long survivors. To compare median survival across SMO expression groups we used Laplace regression models for percentiles.	

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 persons.
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.

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