Corresponding Author Name: Ivan Costa Filho

Manuscript Number: NMETH-AS24264B-Z

Reporting Checklist for Research Articles at *Nature Methods*

This checklist is used to ensure good reporting standards and to improve the reproducibility of published results. For more information, please read Reporting Life Sciences Research.

▶ Figure legends

Each figure legend should contain, for each panel where they are relevant:

- the **exact sample size (n)** for each experimental group/condition, given as a number, **not a range**;
- a **description of the sample collection** allowing the reader to understand whether the samples represent **technical or biological replicates** (including how many animals, litters, cultures, etc.);
- a **statement of how many times the experiment shown was replicated in the laboratory** (for image data state whether it is a representative image and of how many images and/or experiments it is representative of);
- **definitions of statistical methods and measures**:
  - ○ very common tests, such as t-test, simple χ2 tests, Wilcoxon and Mann-Whitney tests, can be unambiguously identified by name only, but more complex techniques should be described in the methods section;
  - ○ are tests one-sided or two-sided?
  - ○ are there adjustments for multiple comparisons?
  - ○ **statistical test results**, e.g., **P values**;
  - ○ definition of '**center values**' as **median or mean**;
  - ○ definition of **error bars as s.d. or s.e.m.**

Any descriptions too long for the figure legend should be included in the methods section. We recommend reading *Nature Methods*' Points of Significance column if you would like an overview of basic statistics for researchers.

Important: In addition to the required information above, please ensure that the answers to the following questions are reported in the manuscript itself. We encourage you to include a specific subsection in the methods section for statistics, reagents and animal models. Below, provide the page number(s) or figure legend(s) where the information can be located.

▶ Statistics and general methods

Reported on page(s) or figure legend(s):

1. How was the sample size chosen to ensure adequate power to detect a pre-specified effect size?

   For animal studies, include a statement about sample size estimate even if no statistical methods were used.

   N.A.

2. Describe inclusion/exclusion criteria if samples or animals were excluded from the analysis. Were the criteria pre-established?

   N.A.

3. If a method of randomization was used to determine how samples/animals were allocated to experimental groups and processed, describe it.

   For animal studies, include a statement about randomization even if no randomization was used.

   N.A.

4. If the investigator was blinded to the group allocation during the experiment and/or when assessing the outcome, state the extent of blinding.

   For animal studies, include a statement about blinding even if no blinding was done.

   N.A.

5. For every figure, are statistical tests justified as appropriate?

   Do the data meet the assumptions of the tests (e.g., normal distribution)?

   Is there an estimate of variation within each group of data? Is the variance similar between the groups that are being statistically compared?

   Yes. Only non-parametrical tests were employed, so no normality test is necessary. See Statistical Methods on online methods for detailed description.

Reported on page(s) or figure legend(s):

6. To show that antibodies were profiled for use in the system under study (assay and species), provide a citation, catalog number and/or clone number, supplementary information or reference to an antibody validation profile (e.g., Antibodypedia, 1DegreeBio).

N.A.

7. Cell line identity:
   a. Are any cell lines used in this paper listed in the database of commonly misidentified cell lines maintained by ICLAC and NCBI Biosample?

N.A.

   b. If yes, include in the Methods section a scientific justification of their use -indicate here on which page (or section and paragraph) the justification can be found.

N.A.

   c. For each cell line, include in the Methods section a statement that specifies:
   - the source of the cell lines

N.A.

   - have the cell lines been authenticated? If so, by which method?

N.A.

   - have the cell lines been tested for mycoplasma contamination? In this checklist, indicate on which page (or section and paragraph) the information can be found.

N.A>

8. Identify all custom software or scripts that were required to implement the methodology being described and where in the procedures each was used. Include a statement indicating how the software is being made available or that it is not available.

We provide source code of all relevant sofware (see Online Methods - Software Availability) and location of all third party software were indicated in the Online Methods.

▶ Animal models and tissues

Reported on page(s) or figure legend(s):

9. Report species, strain, sex and age of animals.

N.A.

10. For experiments involving live vertebrates or tissues from same, include a statement of compliance with ethical regulations and identify the committee(s) approving the experiments.

N.A.

11. We recommend consulting the ARRIVE guidelines (PLoS Biol. 8(6), e1000412, 2010) to ensure that other relevant aspects of animal studies are adequately reported.

N.A.

▶ Human subjects

Reported on page(s) or figure legend(s):

12. Identify the committee(s) approving the study protocol.

N.A.

13. Include a statement confirming that informed consent was obtained from all subjects.

N.A.

14. For publication of patient photos, include a statement confirming that consent to publish was obtained.

N.A.

15. Report the clinical trial registration number (at ClinicalTrials.gov or equivalent).

N.A.

16. For phase II and III randomized controlled trials, please refer to the CONSORT statement and submit the CONSORT checklist with your submission.

17. For tumor marker prognostic studies, we recommend that you follow the REMARK reporting guidelines.

18. Provide accession codes for deposited data.
    Data deposition in a public repository is mandatory for:

    a. Protein, DNA and RNA sequences
    b. Macromolecular structures
    c. Crystallographic data for small molecules
    d. Microarray data

    Deposition is strongly recommended for many other datasets
    for which structured public repositories exist; more details
    on our data policy are available here. We encourage the
    provision of other source data in supplementary information
    or in unstructured repositories such as Figshare and Dryad.

    Accession code of all evaluated data are described in the
    supplementary tables 1 and 2.

19. Is computer source code provided with the paper or deposited
    in a public repository? If so, indicate how it can be obtained.

    Source code are listed in our web page www.costalab.org/hint-
    bc. Moreover, code for HINT is deposited at www.github.org