nature portfolio

Corresponding author(s): Isabelle Ray-Coquard

Last updated by author(s): May 13, 2025

Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our Editorial Policies and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☒	☐ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒ The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☒	☐ A description of all covariates tested
☐	☒ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒ For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☒	☐ Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	Clinical Data Management System: Clinsight v8.2.110, Euraxi Pharma. Web interface: CSonline v8.2.110 (https://ecrf.euraxipharma.fr/CSOnline/. Backend database: Oracle 11g. Medical coding: MedDRA v21.1 and WhoDrug Format C March 2017
Data analysis	Analyses were performed using SAS version 9.4 (SAS Institute Inc., Cary, NC, USA), R version 4.1.1, and GraphPad Prism 9.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

Source data for all published figures and tables are provided with this paper. The raw and processed HTG data and metadata generated in this study have been deposited in the GEO database under accession code GSE303300 (https://www.ncbi.nlm.nih.gov/geo/). Currently, no mechanism is in place to allow sharing of individual deidentified patient data. Requests to access the de-identified data for further scientific use can be sent to ARCAGY-GINECO (Sébastien Armanet,

sarmanet@arcagy.org) and will be considered on a case-by-case basis in a timely manner beginning 3 months and ending 5 years after publication of this article, taking into consideration that some translational research is still ongoing. The request must contain a proposal with scientific and methodologically justified objectives. A data transfer agreement will be established to provide a formal framework regarding the use of the data.

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	All patients enrolled in this study in cervical cancer were female.
Reporting on race, ethnicity, or other socially relevant groupings	Information on race was not collected as this is not allowed in France, where all patients were enrolled.
Population characteristics	Characteristics of the study population are provided in Table 1.
Recruitment	Patients were recruited by the investigators according to the inclusion/exclusion criteria of the study protocol (no recruitment by internet, no recruitment by advertisement). There was no compensation for participation. The trial enrolled patients in a rare disease setting. Nevertheless, it was fully recruited within approximately 1 year, making us confident that investigators systematically recruited all potential patients.
Ethics oversight	Comite de Protection des Personnes Est I

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	It was planned to enroll 40 patients. Assuming a standard deviation of 14 units, this would provide a 95% CI with a precision of 5 units around the mean estimation of the CD8+/FOXP3+ relative change of lymphocytes between pre- and post-treatment biopsies.
Data exclusions	No data were excluded; analyses were performed according to intent-to-treat principles.
Replication	No measures were taken to verify the reproducibility of the experimental findings.
Randomization	Not applicable in this single-arm study.
Blinding	Not applicable.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☐	☒ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions.

Clinical trial registration	NCT04256213
Study protocol	The protocol is provided as a supplementary appendix.
Data collection	All patients were enrolled in France from sites with gynecologic oncology expertise between June 28, 2020, and August 4, 2021. The data extraction date was February 11, 2023.
Outcomes	The primary objective was to evaluate changes in the CD8+/FOXP3+ T-cell ratio in biopsies collected before versus after nivolumab and ipilimumab combination treatment before chemoradiation. The CD8+/FOXP3+ ratio was assessed by evaluating the composition of the immune infiltrate using seven-color spatial mIF. Key secondary objectives included assessment of dynamic changes in the immune microenvironment (including CD8+, FOXP3+ Tregs, CD4+ T cells, and CD20 B cells) before and after chemoradiation using mIF tissue imaging and HTG sequencing, clinical activity (including objective response rate according to RECIST version 1.1 (by MRI and PET-CT if required) before and after chemoradiation (and at treatment completion as an exploratory objective), potential correlations between biologic changes in the tumor microenvironment and clinical activity, and tolerability.

Plants

Seed stocks	*Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.*
Novel plant genotypes	*Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*
Authentication	*Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*