nature portfolio

Corresponding author(s): David Juncker

Last updated by author(s): Nov 25, 2024

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	Nikon NIS-Elements Advanced Research Software
Data analysis	Microsoft Excel, COMSOL Multiphysics 5.5, ImageJ 1.48v

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

All raw and processed data are available upon request

Human research participants

Policy information about studies involving human research participants and Sex and Gender in Research.

Reporting on sex and gender	Biological sex is tracked and recorded in this study. All 17 EOC patients are female. We attempted to have equal sex distribution of CRCLM patients. Eight and five out of a total of 13 CRCLM patients are male and female, respectively. We did not perform data analysis using sex as a parameter in this small cohort. Patient sample collections were conducted with informed consent at both the CHUM and MUHC sites.
Population characteristics	EOC: patients were recruited upon diagnosis of EOC. Disease stage, histopathology, chemotherapy and surgery status are provided and included in the analyses (Table 1 in the manuscript). Treatment status at the time of of blood sample collection was recorded but not included in the analyses, except for the time-course study on OC1. Age and other parameters were not tracked. CRCLM: patients were recruited upon diagnosis of CRCLM and biological sex tracked. Histopathological growth pattern of the tumor was identified after surgery. Treatment status (surgery and chemotherapy status) at the time of blood sample collection was recorded but not included in the analyses.
Recruitment	Participants were recruited after diagnosis of the diseases studied in this work.
Ethics oversight	Comité d'éthique de la recherche du CHUM; McGill Research Ethics Office; MUHC Institutional Review Board

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	No sample size calculation was performed. EOC: early and advanced stages of EOC were included. 10/17 EOC patients presented the serous cystadenocarcinoma subtype; while 7/17 presented at least four other subtypes. CRCLM: Individual of both sexes were included. All sample were collected before surgery, with varying chemotherapy status including chemo-naive patients.
Data exclusions	No data were excluded when microfiltration of the blood sample was successful.
Replication	At least three replicates were performed for CTC isolation of spiked blood for characterization of the analytical method; three replicates were performed with blood samples of mouse models. Patient samples: CTC isolation was done once on the collected blood samples. Cell number in cCTCs and area covered by the cCTCs were measured on all the captured cCTCs.
Randomization	Randomization is not relevant in this method development and validation study, and was not performed.
Blinding	The nature of all samples were known to the investigators. Blinding during data collection was not required in this work. Potential bias may occur during image analysis where scCTC and small cCTCs (i.e. cluster of 1-2 cells) were identified manually.

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

Methods

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

Antibodies

Antibodies used: Anti-human CD45-PE (cluster of differentiation 45, Cat. #FAB1430P), anti-CK 18-AF 488 (cytokeratin 18, labeled with Alexa Fluor 488, Cat. #IC7619G) and anti-E-Cad (E-cadherin, Cat. #MAB18382, from mouse) were obtained from R&D systems. Anti-Vim (Vimentin, Cat. #SAB4503081, from rabbit), anti-ZO-1 (Zonula occludens-1, Cat. #AB2272, from rabbit), anti-ZEB-1 (Zinc finger E-box-binding homeobox 1, Cat. #SAB3500514, from rabbit), and anti-Snail (Drosophila embryonic protein, Cat. #SAB2108482, from rabbit) were purchased from Sigma-Aldrich. Anti-EpCAM-PE (anti-epithelial cell adhesion molecule labeled with phycoerythrin, Cat. #12-9326-42), anti-c-MET-FITC (hepatocyte growth factor receptor, labeled with fluorescein isothiocyanate, Cat. #11-8858-42), and detection antibodies goat anti-mouse-Alexa Fluor 647 (Cat. #A21240) and goat anti-rabbit-Cy3 (Cyanine 3, Cat. #A10520) were obtained from Fisher Scientific.

Validation: Validation data are available through the manufacturers

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s): The ovarian cancer OV-90 cell line was developed in the laboratory of Drs. Provencher and Mes-Masson and has been well characterized (see reference 48). OVCAR-3 cells were obtained from ATCC (ATCC number HTB-161).

Authentication: No additional authentication of the cell line was performed.

Mycoplasma contamination: Mycoplasma contamination in cell culture facilities were routinely checked by commercial tests such as the MycoProbe Mycoplasma Detection Kit (CUL001B, R&D Systems)

Commonly misidentified lines (See ICLAC register): n/a

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals: Female (8–12 weeks old) athymic nude mice (Crl:NU (NCr)-Foxn1nu; Charles River)

Wild animals: n/a

Reporting on sex: Mouse model was made by orthotopic ovarian injections of ovarian cancer cells and thus only female mice were used.

Field-collected samples: n/a

Ethics oversight: Animal Resource Centre of McGill University

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

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: n/a

Study protocol: EOC sample collection: McGill IRB study #A05-M27-16B; CRCLM sample collection: MUHC IRB protocol SDR-11-066

Data collection: EOC: tumor stage was determined by a gynecologic oncologist at time of surgery, CA125 levels were measured during patient visit at the clinic; histopathology and tumor grade were determined by a gynecological pathologist. Blood samples used for CTC capture were kept at 4°C and processed within 1-14 hours of collection.

	CRCLM: Clinical data were collected for each patient through the locally established hospital database and medical records. Blood samples were collected fresh the day of the experiment in EDTA tubes and processed within 6 hrs.
Outcomes	n/a