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  Provide a description of all commercial, open source and custom code used to collect the data in this study, specifying the version used OR state that no software was used.

Data analysis  Germ-line and somatic sequencing data were downloaded from https://portal.gdc.cancer.gov and the variants were annotated using Intervar. Allele-specific copy-number profiles were extracted using Sequenza and the whole exome sequencing-based HRD-scores were determined using the scanHRD R package.

For manuscripts utilizing custom algorithms or software that are not 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

The datasets generated during and/or analyzed during the current study are available from the corresponding author upon request.
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/or-reporting-summary-flat.pdf

Life sciences study design

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

| Sample size | For analysis of publicly available clinical and genomic data, all available samples were analyzed. For functional studies, experiments were performed in triplicate. |
|-------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Data exclusions | No data was excluded from analyses. |
| Replication | All functional experiments were performed in triplicate. |
| Randomization | Randomization was not relevant for any of the performed analyses. |
| Blinding | Blinding was not relevant for any of the performed analyses. |

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 | Methods |
|----------------------------------|---------|
| n/a | Involved in the study |
| ◯ | Antibodies |
| ◯ | Eukaryotic cell lines |
| ◯ | Palaeontology and archaeology |
| ◯ | Animals and other organisms |
| ◯ | Human research participants |
| ◯ | Clinical data |
| ◯ | Dual use research of concern |
| n/a | Involved in the study |
| ◯ | ChIP-seq |
| ◯ | Flow cytometry |
| ◯ | MRI-based neuroimaging |

Antibodies

Antibodies used

PALB2, BARD1, gH2AX, Rad51, tubulin

Validation

All antibodies were purchased from commercial vendors and have been previously used and validated in our lab.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)

prostate cancer cell lines (Du145, LNCaP, 22Rv1) were purchased from ATCC. The DR-GFP U2OS reporter line was a gift from Alain D'Andrea lab.

Authentication

All cell lines were validated by STR.

Mycoplasma contamination

All cell lines were confirmed to be mycoplasma free prior to initiation of experiments and were checked every 2 months.

Commonly misidentified lines (See INCLAC register)

N/A
**Clinical data**

Policy information about [clinical studies](#) and [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              | N/A |
| Data collection             | N/A |
| Outcomes                    | N/A |