Reporting Summary

Nature Research 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 Research 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

Data was aggregated from the original studies included in the review. All results used are listed in the data tables in the manuscript and supplementary materials.

Data analysis

Forest plots of sensitivity and specificity (clinical validity pooled results) in Figure 3c. A bivariate meta-analysis was performed to obtain a pooled summary estimate for sensitivity and specificity indicated in the forest plots (1: for all studies that reported results that could be included in this pooled analysis and 2: for studies with ≥5 responders/non-responders). The analysis was performed in R (Version 3.6.1) using the “mada” package.

Forest plot of reported AUROC per study, treatment and index test in Suppl. Fig 1: the forest plot was created in R (Version 3.6.1) using the “mada” package.

Meta-analysis and forest plots of reported organoid establishment rates per study in Suppl. Fig 2: A random effects meta-analysis of the reported organoid establishment rates per study was performed using a generalized linear mixed model. The analysis was performed in R (Version 3.6.1) using the “binom”, “tidyverse”, “metafor” and “meta” packages.

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 Research 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 list of figures that have associated raw data
- A description of any restrictions on data availability

Data and materials availability: All aggregated data used in the analysis is reported in the manuscript and/or supplementary materials. The aggregated datasets analyzed during the current study are available from the corresponding author on reasonable request.

Code availability: All analysis was performed in R (Version 3.6.1) using publicly available packages. The packages used for analysis are indicated in the legend of each corresponding figure. The used code scripts are available from the corresponding author on reasonable 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.

- [x] 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 | Not applicable, since the analysis is a review of available data in published studies fulfilling the search criteria. |
|-------------|-------------------------------------------------------------------------------------------------------------|
| Data exclusions | For the pooled analysis, all data was included in the analysis if the appropriatedata type was reported in each study or could be extracted from the supplementary materials reported by the study. E.g., organoid establishment rate for pooling of organoid establishment rates, or reported sensitivity and/or specificity for the correlation between organoid drug response results and clinical outcome or pooling of clinical validity results. |
| Replication | Not applicable. |
| Randomization | Not applicable. |
| 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 | Methods |
|---------------------------------|---------|
| n/a                             | n/a     |
| [x] Involved in the study       | [x] Involved in the study |
| [ ] Antibodies                  | [ ] ChiP-seq |
| [x] Eukaryotic cell lines       | [ ] Flow cytometry |
| [x] Palaeontology and archaeology | [x] MRI-based neuroimaging |
| [x] Animals and other organisms |         |
| [x] Human research participants |         |
| [x] Clinical data               |         |
| [x] Dual use research of concern|         |