

Life Sciences Reporting Summary

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For further information on the points included in this form, see [Reporting Life Sciences Research](#). For further information on Nature Research policies, including our [data availability policy](#), see [Authors & Referees](#) and the [Editorial Policy Checklist](#).

► Experimental design

1. Sample size

Describe how sample size was determined.

Sample sizes were chosen based on previous literature in nanomedicine and tumor biology, and our own expertise.

2. Data exclusions

Describe any data exclusions.

No data was excluded.

3. Replication

Describe whether the experimental findings were reliably reproduced.

Myc/b-catenin liver cancer model was repeated 3 times. HCT116 colon cancer xenografts experiments were done 3 times.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

For HCT116 xenografts, we used stratified randomization: 7 days after tumor inoculation the tumor volume was measured and mice were randomized to different cages so that the average tumor volume will be similar in all groups. In the liver cancer model we used simple randomization - meaning the assignment of inoculated mice to a treatment was random.

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

The survival experiment of liver cancer bearing mice was blinded as the person taking the data did not know which groups were treated or not (done by animal core facility). For tumor volume experiments we didn't use blinding because it's a quantitative objective measurement.

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a Confirmed

- | | | |
|--------------------------|-------------------------------------|--|
| ☐ | ☒ | The <u>exact sample size</u> (n) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.) |
| ☐ | ☒ | A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| ☐ | ☒ | A statement indicating how many times each experiment was replicated |
| ☐ | ☒ | The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section) |
| ☐ | ☒ | A description of any assumptions or corrections, such as an adjustment for multiple comparisons |
| ☐ | ☒ | The test results (e.g. P values) given as exact values whenever possible and with confidence intervals noted |
| ☐ | ☒ | A clear description of statistics including <u>central tendency</u> (e.g. median, mean) and <u>variation</u> (e.g. standard deviation, interquartile range) |
| ☐ | ☒ | Clearly defined error bars |

See the web collection on [statistics for biologists](#) for further resources and guidance.

► Software

Policy information about [availability of computer code](#)

7. Software

Describe the software used to analyze the data in this study.

GraphPad Prism was used to analyze experimental data. All Python scripts used in the QSNAP analysis, performance analysis of chemical descriptors, and predicted INP formation results of DrugBank small molecule drugs based on the decision tree can be found in the following two repositories, hosted on the collaborative open source software development platform GitHub:

1. nano-drugbank (<http://www.github.com/choderalab/nanodrugbank>).
2. IR783-QSNAP (<https://github.com/choderalab/IR783-QSNAP>, DOI: 10.5281/zenodo.1117393)

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* [guidance for providing algorithms and software for publication](#) provides further information on this topic.

► Materials and reagents

Policy information about [availability of materials](#)

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.

All materials are generally commercially available without restrictions.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

CAV1, R&D Systems, MAB5736, pMAPK antibodies (Cell Signaling, cat# 4370, 1ug/ml), biotinylated goat anti-rabbit IgG (Vector labs, cat#PK6101) at 1:200 dilution. Ki67 (Vector, cat# VP-K451, 0.4ug/ml) , biotinylated goat anti-rabbit IgG (Vector labs, cat#PK6101) at 1:200 dilution. CD31 antibodies (Dianova, cat# DIA-310, 1ug/ml) , biotinylated rabbit anti-rat IgG (Vector labs, cat#PK-4004) at 1:200 dilution.

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

All cell lines were purchased from ATCC except for SK136 which was a primary cell line derived from liver tumors from Scott Lowe's Laboratory, Memorial Sloan Kettering Cancer Center.

b. Describe the method of cell line authentication used.

Cell lines were used as purchased directly from ATCC. The MCF-7 cell line is on the ICLAC Register of Misidentified Cell Lines (the contaminating cell line is OVCAR-8), and therefore we used these cells only up to ten passages after receiving the frozen vial directly from ATCC. Our CAV1 immunohistochemistry data for MCF-7 is in agreement with the Broad Institute Cancer Cell Line Encyclopedia mRNA data, but not with OVCAR-8.

c. Report whether the cell lines were tested for mycoplasma contamination.

All cells were tested negative for mycoplasma contamination at the time of experiments.

d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by [ICLAC](#), provide a scientific rationale for their use.

The MCF-7 cell line was used due its known CAV1 expression and our extensive previously collected and published data on the permeability/density of 3D tumor spheroids made with this line (Jena, et. al., Carbon, 2016).

► Animals and human research participants

Policy information about [studies involving animals](#); when reporting animal research, follow the [ARRIVE guidelines](#)

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.

FVB and athymic nude, nu/nu were purchased from Jackson Laboratories.

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.

Provide all relevant information on human research participants, such as age, gender, genotypic information, past and current diagnosis and treatment categories, etc. OR state that the study did not involve human research participants.