

Life Sciences Reporting Summary

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► Experimental design

1. Sample size

Describe how sample size was determined.

Sample sizes were indicated in the legend of each Figure and Supplementary Figure. No statistical methods were used to predetermine sample sizes, but the sample sizes are similar to those generally employed in the field.

2. Data exclusions

Describe any data exclusions.

No animals were excluded from statistical analyses.

3. Replication

Describe whether the experimental findings were reliably reproduced.

Yes, the experimental findings were reliably reproduced. All the data (except animal data) were obtained from at least three times independent biological replicates. The animal works were performed and analyzed from at least 5 mice per group.

4. Randomization

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

For mouse work, the mice were randomly divided into different treatment groups. (Details see manuscript method for mouse study and in vivo tumor model part)

5. Blinding

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

No blinding was used in these studies as the person that performed the experiment also analyzed the data.

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 exact sample size (*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 central tendency (e.g. median, mean) and variation (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.

The analyses were done using Image J (version 1.47), Microsoft EXCEL, Ingenuity Pathway Analysis (IPA), R software (version 3.3.2), GraphPad Prism 7, bwa (version 0.7.12), MuTect (version 1.1.4) and SnpEff software.

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.

There is no restrictions on availability of all materials.

9. Antibodies

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

Anti-ARID1A (A301-040A), anti-BRG1 (A303-877A), and anti-BRM (A301-014A) antibodies were purchased from Bethyl Laboratories. Anti-V5 (R960-25) antibody was purchased from ThermoFisher Scientific. Anti-Flag (14793), anti-PD-L1 (13684 and 64988), and anti-ARID1A (immunofluorescence, 12354) antibodies were purchased from Cell Signaling Technology. Anti-MLH1 (554073) antibody was purchased from BD Biosciences. Anti-MSH2 (ab52266) and anti-MSH6 (ab92471) antibodies were purchased from Abcam. Anti-CD8 (sc-7970) and other antibodies were purchased from Santa Cruz Biotechnology.

For IP: anti-V5, anti-Flag, anti-ARID1A, anti-MSH2 antibodies were used at 1:100 dilution. For IHC: Alexa 488– or Alexa 594–conjugated secondary antibodies (1:500), anti-human ARID1A (1:100, Cell Signaling Technology), anti-human PD-L1 (1:100, Cell Signaling Technology), anti-mouse Pd-L11 (1:100, Cell Signaling Technology), anti-CD8 (1:200, Santa Cruz), anti-Ki67 (1:200, Cell Signaling Technology), and anti-cleaved-Caspase3 (1:50, Cell Signaling Technology) were used. Antibodies are also listed in the Methods section under their respective experimental method. We chose these antibodies by the product data sheets, literature and our pilot studies.

10. Eukaryotic cell lines

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

The colorectal and ovarian cancer cell lines were kindly provided by Dr. Gordon B. Mills' laboratory at The University of Texas MD Anderson Cancer Center. 293T and SW480 cells were maintained in DMEM (high-glucose, Cellgro), and other cell lines were maintained in RPMI1640 medium. The ID8 mouse ovarian surface epithelial cells were kindly provided by Dr. Vahid Afshar-Kharghan's laboratory at MD Anderson. The ID8 cells were maintained in DMEM (high-glucose, Cellgro).

b. Describe the method of cell line authentication used.

Cell lines were validated by short tandem repeat (STR) DNA fingerprinting using the AmpF STR identifier kit according to the manufacturer's instructions (Applied Biosystems, catalogue no. 4322288). The STR profiles were compared to known American Type Culture Collection fingerprints; to the Cell Line Integrated Molecular Authentication database, version 0.1.200808 (Nucleic Acids Research 2009;37:D925-D932); and to the MD Anderson fingerprint database. The STR profiles matched known DNA fingerprints or were unique. The colorectal and ovarian cancer cell lines were kindly provided by Dr. Gordon B. Mills' laboratory at The University of Texas MD Anderson Cancer Center. Cell line authentication was performed in the MD Anderson Characterized Cell Line Core in 2012 and 2013.

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

All cells lines were regularly tested and negative for mycoplasma contamination.

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.

No commonly misidentified cell lines were used.

► 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.

C57BL/6 mice (female, 6–8 weeks old, CRL/NCI) for ID8 model, and BALB/C mice (6–8 weeks old, female, CRL/NCI) for CT26 model

Policy information about [studies involving human research participants](#)

12. Description of human research participants

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

This study did not involve human research participants.