

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 [Authors & Referees](#) 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

- | | | |
|-------------------------------------|-------------------------------------|--|
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | The statistical test(s) used AND whether they are one- or two-sided
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | A description of all covariates tested |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | 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) |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
<i>Give P values as exact values whenever suitable.</i> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | 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

No software was used to collect data.

Data analysis

Prism software (GraphPad) was used to generate graphs and perform statistical analyses.
MultiGauge software (Fuji) was used for western blot analyses.
LSM Image Browser (Zeiss) software was used for immunofluorescence confocal microscopy analysis.

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/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

The data that support the findings of this study are available from the corresponding author upon 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.

- 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](https://www.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	Experiments were performed at least three independent times. Sample size in mice experiments were estimated based on previous published experiments. At least three or more mice were used in each experiment to obtain statistical analysis. Exact numbers of animals used in individual experiments are indicated in the figure legends. In this study, the statistic analysis was obtained using student t test and the values represents means plus minus standard deviation or standard error of the mean.
Data exclusions	No data were excluded.
Replication	All experiments were reliably reproduced and results are presented as mean +/- SD or SEM as indicated in the figure legends. The results presented have been successfully replicated in at least three independent experiments, with sufficient independent samples.
Randomization	All mice were age and sex-matched (male mice) and then randomized into the different groups.
Blinding	The investigators were not blinded to group allocation during experiments. Conclusions were made based on quantitative parameters and statistical significance of the data, and thus on experimental observations, independent of blinding.

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
<input type="checkbox"/>	<input checked="" type="checkbox"/> Antibodies
<input type="checkbox"/>	<input checked="" type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology
<input type="checkbox"/>	<input checked="" type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Human research participants
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data

Methods

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

Antibodies

Antibodies used	anti-Ras (Millipore, 05-516), anti-HRas (Santa Cruz Biotechnology, sc-520), anti-KRas (Santa Cruz Biotechnology, sc-30), anti-NRas (Santa Cruz Biotechnology, sc-31), anti-p-ERK (Cell Signaling Technology, #9101S), anti-ERK (Santa Cruz Biotechnology, sc-514302), anti-PCNA (Santa Cruz Biotechnology, sc-56), anti-N-cadherin (BD Bioscience, #610920), anti-aSMA (Abcam, ab7817), anti-Myc (Cell Signaling Technology, #2276S), anti-FLAG (Sigma-Aldrich, F7425), anti-HA (Santa Cruz Biotechnology, sc-7392), anti-V5 (MBL International, M167-3), anti-GFP (Santa Cruz Biotechnology, sc-8334), anti-GST (Santa Cruz Biotechnology, sc-374171), anti-Ki67 (Abcam, ab15580), anti-aSMA (Abcam, ab7817), and anti-b-actin (Santa Cruz Biotechnology, sc-47778). WDR76 polyclonal antibody was generated from immunization of rabbits with partially purified WDR76 proteins (GST-WDR76 1-300; Abfrontier, Korea)
Validation	All these antibodies were validated by manufacturers and largely described in the literature. WDR76 antibody was validated using WDR76 KO mice.

Eukaryotic cell lines

Policy information about [cell lines](#)

Cell line source(s)	All cells (SK-Hep1, Huh7, HepG2, PLC/PRF/5, and Hep3B, Lovo, T24T, HEK 293, and HEK293T) were obtained from the American Type Culture Collection. WDR76+/+ or WDR76-/- MEF cells were prepared from E13.5 mouse embryos.
Authentication	SK-Hep1 cells were authenticated by Cosmogenetech (Daejeon, Korea)

Mycoplasma contamination

Commonly misidentified lines
(See [ICLAC](#) register)

Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

Laboratory animals

Wild animals

Field-collected samples

Ethics oversight

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