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Reporting Summary

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Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
☐	☒	An indication of 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 statistics 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
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	No software was used for data collection.
Data analysis	The human IPI databases version 3.6 (determination of peptide sequences) and SEQUEST ver.28 (fragmentation patterning) are used for analysis of mass spectrometry result. All statistical analyses and plots were generated using GraphPad Prism 7. Correlation analysis was conducted in R. Heatmap was generated with the GraphPad Prism 7. Images were analyzed using AxioVision and Zen software.

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 upon request. 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

Microarray data that support the findings of this study have been deposited in the Gene Expression Omnibus (GEO) under accession code GDS2947. Mass

spectrometry data used in this study is available from Supplementary Table 2. The CRAD expression data in CRC cells were derived from the cBioportal using the TCGA Research Network: http://cancergenome.nih.gov/ and Genetech datesets. The data-set derived from this resource that supports the findings of this study is available in Oncomine (https://www.oncomine.org/resource). CRAD expression data were also derived from cBioportal (http://www.cbioportal.org/) and COSMIC database (Catalogue of Somatic Mutations in Cancer) (https://cancer.sanger.ac.uk/cosmic). Source data for Figs. 1-8 and Supplementary Figs. 1-8 have been provided as Supplementary Table 4. All other data supporting the findings of this study are available from the corresponding author on reasonable request.

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf

Life sciences study design

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

Sample size	For animal studies, sample size was estimated by power calculation, as following; Using StatsToDo software (http://www.statstodo.com/SSiz2Means_Pgm.php; alpha level P=0.05; power 80%; expected background standard deviation=0.5; difference between two means to be detected=0.5).
Data exclusions	No samples or animals were excluded. Also, the criteria were not pre-established in experiments.
Replication	All experiments were performed using at least three biological replicas unless specified. All experiments were successfully replicated.
Randomization	Tumor-bearing and genetic engineered animals in tumorigenesis studies were examined in certain aged groups (3-12 months of age) for determine the tumor suppressive effect.
Blinding	Yes. Blinding was used for all analyses.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☒	☐ Unique biological materials
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology
☐	☒ Animals and other organisms
☒	☐ Human research participants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	See Supplementary Table 5
Validation	All antibodies used were validated by the respective commercial source for the application used in this manuscript.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	All cell lines were purchased from American Type Culture Collection (ATCC). KM12, HCT15, HT29, HCT116, COLO205, SW620, HCC2998, and 293T cells were maintained in Dulbecco's modified Eagle's medium (DMEM; Corning; 10-013-CV) containing 10% fetal bovine serum (FBS; Hyclone; SH3.007.003). FHC cell was maintained in DMEM: F-12 (Invitrogen; 11330-032) containing 10% FBS, cholera toxin (10ng/ml; Sigma; C-8052), insulin (5µg/ml; Sigma; I-1882), transferrin (5µg/ml; Fisher; 354204), and hydrocortisone (100ng/ml; Sigma; H-0008). CCD-841CoN, LS-174T, and RKO cells were maintained in Eagle's Minimum Essential Medium (EMEM; ATCC; 30-2003) containing 10% FBS. DLD-1 and NCI-H508 cells were maintained

	RPMI1640 (Corning; 10-049-CMR) containing 10% FBS. Mycoplasma contamination was examined using MycoAlert mycoplasma detection kit (Lonza; LT07-218).
Authentication	None of the cell lines were authenticated.
Mycoplasma contamination	All cell lines tested were negative for mycoplasma contamination
Commonly misidentified lines (See ICLAC register)	No commonly misidentified lines were used.

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	C57BL/B6 mice (wildtype, APCmin, and CRAD KO), both gender, 3-12months of age, determination of tumorigenesis BALB/c nude mice, male, 4 months of age, xenograft
Wild animals	The study did not involve wild animals.
Field-collected samples	The study did not involve field-collected samples.