Supplemental Materials

NLRP12 downregulates the Wnt/ β -catenin pathway via interaction with STK38 to suppress colorectal cancer

Shahanshah Khan, Youn-Tae Kwak, Lan Peng, Shuiqing Hu, Brandi L. Cantarel, Cheryl M. Lewis, Yunpeng Gao, Ram S. Mani, Thirumala-Devi Kanneganti, and Hasan Zaki

Supplemental Methods

Generation of NIrp12-conditional knockout mice. NIrp12^{flox/flox} mice were generated at UT Southwestern Transgenic Core facility by inserting loxP sites flanking 615 bp in exon 4 of NIrp12 using CRISPR/Cas9 system. Two sgRNAs were designed to separately target upstream and downstream of the target sequence. sgRNA was designed, validated, and synthesized by Sigma. The ss oligo donor containing loxP sequences and gRNA target sequence was synthesized by GENEWIZ. gRNA, oligo donors, and CRISPR reagents were mixed and injected into fertilized zygotes of C57BL/6J mice, and blastocysts were transferred into recipient female mice. The transgenic founders were screened by genotyping PCR. Founders with correct insertion of LoxP sites were identified by gene sequencing following PCR using primers targeting both LoxP sites. The founder was crossed with C57BL/6J mice and NIrp12^{flox/flox} mice were maintained in the animal facility at UT Southwestern. The NIrp12^{flox/flox} mice were then bred with Vil-Cre mice (Jackson, #004586) mice to generate intestinal epithelial cell-specific NIrp12 knockout mice (NIrp12^{flox/flox}; Vil-Cre).

Culture and stimulation of mouse embryonic fibroblasts. Mouse embryonic fibroblasts were isolated and cultured, as described previously (1) with minor modifications. Briefly, embryos were

harvested from 13–14 days old pregnant WT and *Nlrp12*^{-/-} mice through cervical dislocation. After removing the embryos head, heart and liver, the remaining embryos were chopped in 0.25% trypsin-EDTA with sterile scissors and resuspended using a pipet. The cell suspension was poured in a Petri dish and incubated at 37°C for 10 min. The cell suspension was mixed well with pipetting several times and incubated for another 10 min at 37°C. Cells were transferred in a 50ml tube containing 20ml DMEM plus 10% FBS and 1% Pen/Strep (MEFs media). After several times of pipetting, the unsuspended tissues were allowed to settle down for 5 min. The supernatant containing single cells was transferred into a T75 flask, which was then incubated at 37°C with 5% CO₂. WT and *Nlrp12*^{-/-} MEFs were seeded in a 12-well plate and stimulated with Wnt3a (100 ng/ml). After washing with chilled-PBS, MEFs were lysed with RIPA and Trizol for protein and RNA, respectively.

Fecal microbiota transplantation. Fecal homogenate from WT and *Nlrp12*^{-/-} mice were orally gavaged into germ-free (GF) mice as described previously (2). Briefly, fresh stool from WT and *Nlrp12*^{-/-} mice were collected and homogenized in 3% thioglycolate broth (20% W/V). Stool homogenates were centrifuged at 1000 rpm, and supernatants were orally gavaged into GF mice every alternate day for a total of 3 doses. Two weeks following the final fecal administration, mice were subjected to AOM-DSS treatment.

Histopathology and immunohistochemistry. Following dissection, colons were washed with prechilled PBS, fixed in 4% paraformaldehyde, embedded in paraffin, and stained with H&E. Histological scoring analysis was performed in a blinded fashion by a pathologist. Tumors were graded as low-grade dysplasia, high-grade dysplasia, and invasive adenocarcinoma. Scoring criteria for tumor histopathology was described previously (3). For immunohistochemistry, 4%-paraformaldehyde-fixed and paraffin-embedded colon tissue sections were deparaffinized and hydrated by sequential dipping into 100%, 95%, 90%, 80% and 70% ethanol. Heat-induced antigen retrieval was performed in 10mM

sodium citrate solution (pH 6.0) for 20 min at 95°C. Tissue sections were blocked with 5% goat serum prepared in PBS plus 0.05% Tween 20 (PBST) for 30 min at room temperature and incubated with anti-β-catenin (8480; Cell Signaling) and anti-Ki67 (ab16667; Abcam) antibodies overnight at 4°C. The tissue sections were then washed three times in PBST and incubated with secondary antibody Cy3-conjugated goat anti-rabbit IgG (Life technologies, A10520) or HRP-conjugate anti-rabbit (Sigma Aldrich, A0545) for 2h in the dark. Following 3 washes, tissue sections were mounted with mounting media with or without DAPI.

Human colon adenocarcinoma tissues. Ten pairs of human colon adenocarcinoma and adjacent normal mucosa snap-frozen tissues were collected from UT Southwestern Medical Center (UTSW) Tissue Management Shared Resource on approval of the Institutional Review Committee Board. These tissue samples were belongings to high-grade adenocarcinoma patients who underwent surgical removal of colorectal cancer at UTSW. The age of these patients ranged between 44 to 80 years (average age 62.8), while tumor size ranged between 3.2 cm to 13.5 cm (average size 6.32 cm). The details of these high-grade adenocarcinoma patients with clinical data are listed in Table S3.

16S rRNA sequencing. Using the Fecal DNA isolation kit (Qiagen, USA), total genomic DNA was extracted from fecal pellets. The quality of DNA was assessed by agarose gel electrophoresis. Bacterial primers 341F 5'-CCTACGGGAGGCAGCAG-3') and 806R (5'-GGACTACHVGGGTWTCTAAT-3') targeting the V3-V4 hyper-variable region of 16S rRNA gene were used for PCR amplification. In library preparation, sample-specific barcode sequences were incorporated to the primers, and then barcoded 16S rRNA gene amplicons were pooled at equimolar concentration prior to sequencing using MiSeq platform (Illumina, Inc., San Diego, California). 16S sequencing was performed by UT Southwestern Microbiome Genomics Core facility. The 16S rRNA gene sequence raw data was analyzed by MOTHUR protocol (4) with the following modifications: (i) sequences were filtered using max length optimizations of 90%, and

(ii) alpha diversity was calculated using Inverse Simpson and Shannon Diversity. The 16S rRNA gene sequence data have been deposited to NCBI BioProject database under Bioproject PRJNA628078.

RNA-seq analysis. RNA sequencing was performed by Novogene (CA). Quality control of RNA-seq data was performed by removing reads containing adapters, low quality (Qscore<= 5) and N > 10% (N represents the base cannot be determined). Sequencing Reads were mapped to hg19 using STAR (5), and gene expression levels for each sample were calculated by RSEM (6) with default setting. Differential Expression Analysis was conducted by EBSeq (7) with FDR=0.05. Heatmap was plotted using normalized expression outputs from RSEM. The raw RNA-seq data have been deposited to NCBI Gene Expression Omnibus (GEO) and is publicly available with the accession number GSE149769.

Cell culture. The human embryonic kidney epithelial cell line HEK293T (ATCC, CRL-3216), and murine colon adenocarcinoma cell line MC38 (shared by Dr. Yang-Xin Fu, UT Southwestern Medical Center) were cultured in Dulbecco's Modified Eagle's medium (DMEM; Sigma, Cat. No. D6429) supplemented with 10% (v/v) FBS (Sigma, Cat. No. F4135) and 1% (v/v) Pen/Strep (Gibco, Cat. No. 15070063) and maintained in a 5% CO₂ incubator at 37°C. Human colorectal carcinoma cells HCT116 (ATCC, CCL-247) and HT-29 (ATCC, HTB-38) were cultured in McCoy's 5A medium (Gibco, Cat. No. 16600082) supplemented with 10% (v/v) FBS (Sigma, Cat. No. D6429) and 1% (v/v) Pen/Strep (Gibco, Cat. No. 15070063) and maintained in a 5% CO₂ incubator at 37°C. Each cell line was confirmed free from mycoplasma contamination by testing with mycoplasma detection kit (InvivoGen, rep-mys-50).

Isolation and 3D culture of intestinal crypts. Mouse intestinal crypts were cultured in vitro to form 3D organoids, as described previously (8). Briefly, small intestines (SI) were collected,

washed vigorously in ice-cold PBS, cut longitudinally and incubated in 1mM DTT for 10 min to remove mucin layer. SI were then cut into small pieces and incubated with 5 mM EDTA in HBSS buffer containing 100 u/ml penicillin/streptomycin and 20 µg/ml gentamicin with gentle shaking. For isolation of SI crypts, the villus fraction was removed after 10 min of incubation. Remaining crypt fractions were incubated with fresh 5 mM EDTA buffer for an additional 15 min at 37°C. Isolated epithelial cells and crypts were passed through 70 µm cell-strainer and washed several times in ice-cold HBSS by centrifugation at 500 rpm. The isolated crypts (2000 crypts/well of 24well) were mixed with matrigel and placed on the center of each 24-well cell culture plate. The plate was incubated for 10 min at 37°C to solidify the matrigel. A total of 500µl basal medium (advanced DMEM/F12 medium, 10mM hepes, 2mM glutamax, 100μg/ml primocin) supplemented with N2 (1X, Invitrogen), B27 (1X, Invitrogen), Noggin (100ng/ml, Peprotech), EGF (50ng/ml, Peprotech), R-spondin (1ug/ml, Peprotech), N-acetyl cysteine (50ng/ml, Sigma), penicillinstreptomycin (100u/ml) and Y-27623 (10mM/ml) were added to each 24-well culture plate. The fresh medium was added to each well every 48h. The number of well-formed organoids per well was counted. The size of the crypts was measured by analyzing the images captured under 40X microscopic field in a Zeiss microscope. For stimulation, organoides were washed and incubated for 4h in a basal medium (without any growth factors and Rspondin). Cells were then stimulated with Wnt3a (100ng/ml).

cDNA constructs and transient transfection. The Flag sequence was cloned in pcDNA4/TO vector at XhoI and ApaI sites. Then, the full-length mouse Nirp12 cDNA was cloned at the KpnI and NotI site into the pcDNA4/TO:Flag vector. Full length of human NLRP12 cDNA was cloned into the flag-tagged pcDNA4/TO vector at the sites of HindIII and EcoRV. Full length of human NLRP3 cDNA was cloned at BamHI and XhoI into the flag-tagged pcDNA4/TO vector. Human NLRP6 was cloned at the site of EcoRI and XhoI into the flag-tagged pcDNA4/TO vector. Full

length of human STK38 cDNA was cloned either at HindIII and PstI or HindIII and BamHI sites into the Flag-tagged or Myc-tagged pcDNA4/TO vector, respectively. As a control, GFP was cloned into the pcDNA4/TO:Flag vector at BamHI and NotI sites. At 50 − 60 % confluency, HEK293T, HT-29 and HCT116 cells were transfected with NLRP12-Flag or GFP-Flag (1 µg/mI) constructs using Lipofectamine 3000 reagent (Invitrogen) according to manufacturer's instructions, and confirmed by observing GFP under fluorescence microscope and Western blot analysis of Nlrp12. After 48h post-transfection, cells were stimulated with Wnt3a (100ng/mI). Cells were lysed with RIPA lysis buffer containing complete protease inhibitor cocktail and phosphatase inhibitor cocktail (Roche) for protein (Western blot) or with TRIzol™ reagent (Invitrogen) for RNA (real-time RT-PCR).

Overexpression and immunoprecipitation of NLRP12 for mass spectrometry analysis. A CMV expression vector encoding Flag-tagged NLRP12 was transfected into HEK293T cells to establish a stable cell line. Affinity-purified Flag-tagged NLRP12 protein and associated proteins were isolated from HEK293T cells stably expressing Flag-tagged NLRP12. The cells were harvested and homogenized in Tris-buffered saline (TBS) (50 mM Tris HCl [pH 7.4], 150 mM NaCl). After centrifugation at 3,000 rpm for 10 min in a CS-6R Beckman centrifuge, the supernatant was applied to an anti-Flag M2 affinity gel column (Sigma) as specified by the manufacturer. Flag-tagged NLRP12 and associated proteins were eluted with TBS containing Flag peptide (Sigma) at 100 µg/ml. The eluted proteins were digested with trypsin and precipitated with TCA, and the peptides were analyzed by matrix-assisted laser description ionization time-of-flight (MALDI-TOF) mass spectra.

Cytosolic and nuclear subcellular fractionation. Nuclear and cytoplasmic protein extracts were separated by NE-PER nuclear and cytoplasmic extraction reagents (Thermo Fisher

Scientific, 78835) according to manufacturer instructions. Briefly, the cell pellet was suspended in ice-cold CER I reagent supplemented with protease inhibitor cocktail and phosphatase inhibitor cocktails (Roche). After incubation on ice for 10 minutes, the CER II reagent was added, and the cells were lysed by vortexing. The homogenate was centrifuged for 5 minutes at 16,000 x g. The supernatant representing the cytosolic fraction was collected, and the pellet containing the cellular nuclei was dissolved in ice-cold NER reagent supplemented with protease and phosphatase inhibitors. The Eppendorf tube containing the nuclear fraction was incubated for 40 min on ice and vortexed for 15 seconds in every 10 minutes. After centrifugation for 10 min at 16,000 x g at 4°C, the supernatant (nuclear fraction) was transferred to a clean pre-chilled tube. The cytoplasmic and nuclear fractions were resolved by SDS-PAGE.

STK38 knockdown in HEK293T cells using siRNA. HEK293T cells at 70% confluency were transfected with MISSION® pLKO.1-puro (shControl, Sigma) or STK38 specific SiRNA (Clone ID: NM_007271.21231s21c1, Sigma) using Lipofectamine 3000 reagent (Invitrogen) according to manufacturer's instructions. 48h post transfection, co-transfected HEK293T cells were selected using media containing 2 μg/ml puromycin (A1113803, Gibco). The STK38 knockdown in HEK293T cells was further confirmed by Western Blot analysis. The selected STK38 knockdown-HEK293T and shControl-HEK293T cells were seeded in a 12-well plate for overnight and stimulated with Wnt3a (100ng/ml). After 1X washing with pre-chilled PBS, cells were lysed with RIPA lysis buffer containing complete protease inhibitor and phosphatase inhibitor cocktails (Roche).

Immunofluorescent staining. HEK293T cells were grown on coverslips and transfected with GFP and NLRP12 plasmids using Lipofectamine 3000 reagent (Invitrogen) according to manufacturer's instructions. 48h post transfection, cells were stimulated with Wnt3a (100ng/ml) for 2h, and fixed in 4% paraformaldehyde for 15 min at RT, washed 3X with PBS for 5 min each

and blocked with PBS containing 5% goat normal serum and 0.3% Triton-X100 for 1h. Cells were then incubated with primary antibodies against β -catenin (8480, Cell Signaling) overnight at 4°C. After 3X washing in PBS, cells were incubated with secondary antibody Cy3-conjugated goat antirabbit IgG (Life technologies, A10520) for 1h at RT. Following three washes in PBS, cells were mounted with mounting media containing DAPI. Images were taken with a fluorescence microscope (Zeiss).

Co-immunoprecipitation. HEK293T and HCT116 cells were transfected with Flag-tagged GFP, NLRP12, or STK38 (1μg/ml) plasmids using Lipofectamine 3000 reagent (Invitrogen) according to manufacturer's instructions. 48h post-transfection, cells were stimulated with Wnt3a (100ng/ml) for various times and lysed in Peirce® IP lysis buffer supplemented with complete protease inhibitor cocktail and phosphatase inhibitor cocktail (Roche), according to manufacturer's instruction (87787, ThermoFisher). Cell lysates were centrifuged to pellet cell debris, and the supernatants were processed for immunoprecipitation using anti-Flag®M2 (F1804, Sigma-Aldrich) or anti-Myc (2376, Cell Signaling) antibodies with Dynabeads® Protein G according to manufacturer's protocol (Novex® by Life Technologies™).

Generation of NIrp12 knockout cells using CRISPR/Cas9. At 50 – 60 % confluency, HEK293T, HCT116 or HT-29 cells were transfected with scrambled sgRNA CRISPR/Cas9 (abm-K010), NLRP12 sgRNA CRISPR/Cas9 (abm-K1434706 and abm-K1434708, accession number: NM_144687) plasmids using Lipofectamine 3000 reagent (invitrogen) according to manufacturer's instructions. MC38 cells were transfected with scrambled sgRNA CRISPR/Cas9 (VB180911-1190rqd) and NIrp12 two-sgRNA CRISPR/Case9 (VB190527-1100acq, accession number: NM_001033431.1) plasmids using Lipofectamine 3000 reagent (invitrogen) according to manufacturer's instructions. After 48h post-transfection, CRISPR/Cas9 plasmids co-transfected HEK293T, HCT116, HT-29, and MC38 cells were selected using media containing 2 μg/ml

puromycin (A1113803, Gibco). The NLRP12 knockout HEK293T, HCT116, HT-29, and MC38 cells were further confirmed by Western blot analysis. The selected NLRP12 knockout HEK293T, HCT116, HT-29, or MC38 and scrambled HEK293T, HCT116, HT-29, or MC38 cells were seeded in 12-well plates for overnight and stimulated with Wnt3a (100ng/ml), as indicated time points. After washing with pre-chilled PBS once, cells were lysed with RIPA lysis buffer containing complete protease inhibitor and phosphatase inhibitor cocktails (Roche).

Real-time cell proliferation by IncuCyte live-cell imaging system. Scrambled MC38 and NIrp12 knockout MC38 cells were seeded in 96-well plate (1.5x10³/well) and incubated at 37°C in a humidified CO₂ incubator. 6h following seeding, the plate was placed into the IncuCyte live-cell imaging system under 10x objective with four fields imaged per well. The real-time cell proliferation was measured at 6h intervals (9). The percentage of cell confluence was automatically calculated by analyzing the images captured by the IncuCyte software (Essen Bioscience, Ann Arbor, MI, USA).

Migration and invasion assay using IncuCyte live-cell imaging system. About 2x10⁴ MC38 (Scramble) and Nlrp12 knockout (Nlrp12-KO) MC38 cells were seeded in 96-well ImageLock microplate (Essen Bioscience) and allowed overnight to form a uniform monolayer. The uniform and reproducible scratches were created using the WoundMaker (Essen Bioscience) in the 96-well ImageLock microplate. The medium is aspirated, and the wells were washed two times with fresh medium to remove any detached cells from the scratched area. Following the final wash, 100 μL of fresh medium was added to each well of the ImageLock plate containing cells and then placed into the IncuCyte live-cell imaging system. The real-time scratch closure images were captured every 2h intervals by IncuCyte software (Essen Bioscience). The percentage of wound density and percentage of wound confluence were automatically calculated and analyzed by the

IncuCyte software. The percent wound density represents the cell density in the scratched area relative to the outside cell density over time. Similarly, percent wound confluence is the cell confluence in the scratched area over time.

Clonogenic assay. Scrambled and Nlrp12 knockout MC38 cells were seeded at a density of 2x10² cells/well of a 6-well plate. At day 9, culture medium was aspirated and cells were washed with PBS. The cells were then fixed and stained with a mixture of 6% glutaraldehyde and 0.5% crystal violet for 30 min at room temperature. The glutaraldehyde crystal violet mixture was washed with tap water and the plate was air-dried.

GSK3β kinase assay. HEK293T and HCT116 cells were stimulated with Wnt3a for 4h and lysed with RIPA buffer containing complete protease and phosphatase inhibitor cocktails (Roche). The lysates of control and stimulated cells were centrifuged at 10000 rpm for 10 min at 4°C. Supernatants were used to measure the GSK3β kinase activity according to the manufacturer's instruction (GSK3β Assay Kit, #79700, BPS Bioscience). Briefly, 10μg protein was mixed with 25μl of master mix (5μl of 5x Kinase assay buffer + 1μl of 500μM ATP + 5μl of 10x GSK3b substrate peptide + 14μl distilled water) in a 96-well plate. 20 μl of GSK3β enzyme (0.6 ng/μl) was added to each well except blank (20μl of 1x Kinase assay buffer). Plate was incubated at 30°C for 45 minutes, after which 50μl of Kinase-Glo® Max reagent (V6071, Promega) was added to each well and cover with aluminum foil. Following 15 minutes incubation at room temperature, luminescence was measured in a microplate luminometer. The kinase activity is inversely related in luminescence (RLU) reading.

Induction of colitis in mice. Colitis was induced by feeding mice ad libitum with 3% DSS (molecular mass, 36–40 kDa; TdB Consultancy) in regular drinking water for 5 days, followed by

normal drinking water until the end of the experiment. Body weight changes, diarrhea and occult bleeding were monitored daily. Diarrhea scoring (0-3) was done as 0 = well-formed pellets, 1 = semiformed stools that did not adhere to the anus, 2 = semiformed stools that adhered to the anus, 3 = liquid stools that adhered to the anus. Bleeding scoring (0-3) was done as 0 = no blood by using hemoccult (Helena Pharmaceuticals), 1 = positive hemoccult, 2 = blood traces in stool visible, 3 = gross rectal bleeding.

Bone marrow-derived macrophages (BMDMs) culture and stimulation. Both femurs and tibias were collected from WT and NIrp12^{-/-} mice. Bone marrow cells from both the femurs and tibias were flushed out and cultured in Iscove's Modified Dulbecco Medium (IMDM) containing 30% L929 conditioned medium, 10% FBS, 1% Pen/Strep and 1% non-essential amino acids as described previously (8). Differentiated macrophages collected at day 6 were cultured with DMEM medium plus 10% FBS and 1% Pen/Strep in 12-well cell culture plates overnight at 37°C in a CO₂ incubator. Cells were then stimulated with Wnt3a (100 ng/mL) or LPS (1 μg/mL). Following the removal of the culture medium and washing with cold PBS, cells were lysed with RIPA buffer and used for Western blot.

Isolation of small intestine and colon epithelial cells. Both small intestines (SI) and colons were collected from mice, opened longitudinally with fine scissors and washed several times with ice-cold PBS. Tissues were then processed for epithelial cell isolation as described previously (8). Briefly, colons were incubated with PBS supplemented with 1mM DTT on ice for 10 min. Both the colon and small intestine were cut into 5 mm pieces and incubated with RPMI supplemented with 5 mM EDTA, 100 U/ml penicillin, and 100 U/ml streptomycin for 30 min at 37°C on a shaker (250 rpm). The supernatant containing separated crypts was collected into a separate tube and further incubated with RPMI supplemented with 3 mg/mL Dispase (Roche) for 10 min at 37°C on a shaker (250 rpm). The cell suspension was filtered through a 70μm cell strainer and centrifuged

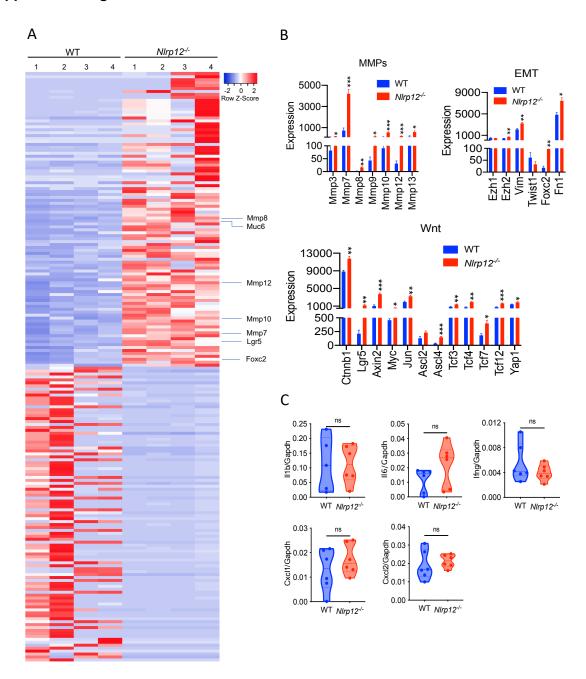
at 1200 rpm. After resuspension of the pellet, immune cells were depleted by negative selection using CD45 MicroBeads (Miltenyi Biotech 130-052-301) following the manufacturer's instructions. Finally, enriched epithelial cells were collected and used for the experiments. To confirm the purity of the epithelial cells, isolated epithelial cells were incubated with CD16/CD32 (eBioscience 14-0161-82) for 15 min at 4°C and then stained with APC-conjugated rat anti-mouse Ep-CAM (Clone G8.8, Biolegend) for 40 min at 4°C. The purity of the epithelial cells was analyzed by LSR-II and FlowJo software (BD Biosciences, San Jose, CA, USA).

Immune and epithelial cell isolation from mouse colorectal tumors. Colorectal tumor tissues were collected from WT and NIrp12^{-/-} mice at 10-12 weeks post AOM/DSS treatment. Tissues were washed with ice-cold PBS and then processed for immune and epithelial cell isolation. Briefly, tissues were mined with a fine scissor and incubated with lysis buffer (RPMI supplemented with 10% FBS, 0.5 mg/mL collagenase type IV and 10 μg/ mL DNase) for 1h at 37 °C with shaking at 250 rpm. After passing through 18G needle, digested tissues were centrifuged for 4 min at 4°C. Pellets were resuspended in RBC lysis buffer (Sigma R7767-100ML) for 1 min at room temperature and filtered through 70-micron strainer. Cell suspensions were centrifuged and the pellets were resuspended in RPMI medium. Epithelial cells were positively selected by staining with CD326 (EpCAM) MicroBeads and magnetic sorting of Microbeads following the manufacturer's instructions (Miltenyi Biotec 130-105-958). For immune cell isolation, single cells were mixed with an equal volume of ficoll-paque and centrifuged at 1500 RPM for 20 min at room temperature. The middle layer containing immune cells were collected and washed with RPMI supplemented with 2% FBS. Enriched lymphocyte suspension used for the magnetic sorting of immune cells using CD45 MicroBeads following the manufacturer's instructions (Miltenyi Biotec 130-052-301). The purity of the epithelial cells and infiltrated immune cells was analyzed by LSR-II and FlowJo software (BD Biosciences, San Jose, CA, USA).

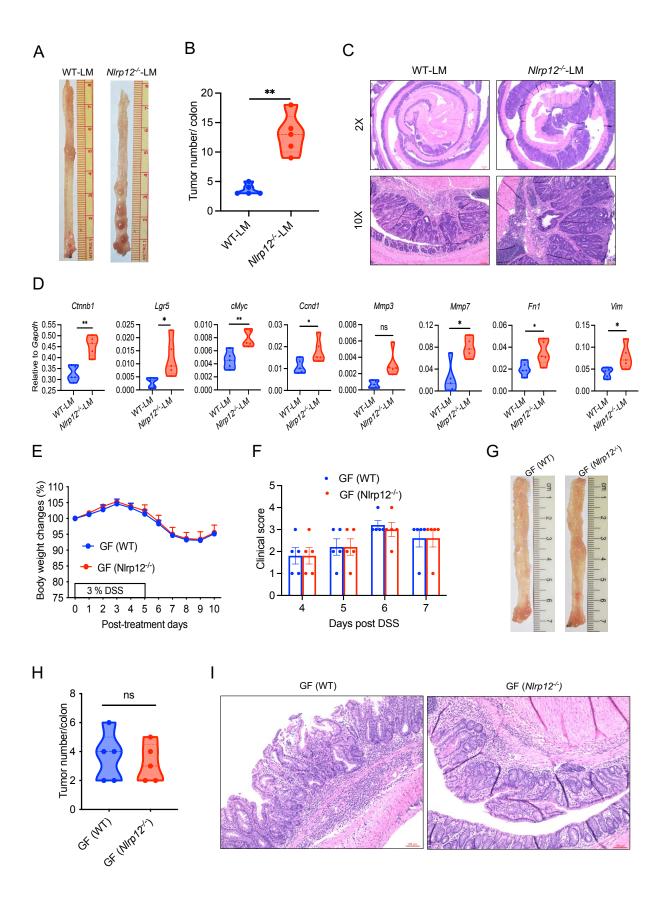
Supplemental References

- 1. Durkin ME, Qian X, Popescu NC, and Lowy DR. Isolation of Mouse Embryo Fibroblasts. *Bio Protoc.* 2013;3(18).
- 2. Khan S, Waliullah S, Godfrey V, Khan MAW, Ramachandran RA, Cantarel BL, et al. Dietary simple sugars alter microbial ecology in the gut and promote colitis in mice. *Sci Transl Med.* 2020;12(567).
- 3. Udden SMN, Peng L, Gan JL, Shelton JM, Malter JS, Hooper LV, et al. NOD2 Suppresses Colorectal Tumorigenesis via Downregulation of the TLR Pathways. *Cell Rep.* 2017;19(13):2756-70.
- 4. Kozich JJ, Westcott SL, Baxter NT, Highlander SK, and Schloss PD. Development of a dual-index sequencing strategy and curation pipeline for analyzing amplicon sequence data on the MiSeq Illumina sequencing platform. *Appl Environ Microbiol.* 2013;79(17):5112-20.
- 5. Dobin A, Davis CA, Schlesinger F, Drenkow J, Zaleski C, Jha S, et al. STAR: ultrafast universal RNA-seq aligner. *Bioinformatics*. 2013;29(1):15-21.
- 6. Li B, and Dewey CN. RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome. *BMC Bioinformatics*. 2011;12:323.
- 7. Leng N, Dawson JA, Thomson JA, Ruotti V, Rissman AI, Smits BM, et al. EBSeq: an empirical Bayes hierarchical model for inference in RNA-seq experiments. *Bioinformatics*. 2013;29(8):1035-43.
- 8. Hu S, Peng L, Kwak YT, Tekippe EM, Pasare C, Malter JS, et al. The DNA Sensor AIM2 Maintains Intestinal Homeostasis via Regulation of Epithelial Antimicrobial Host Defense. *Cell Rep.* 2015;13(9):1922-36.
- 9. Udden SN, Kwak YT, Godfrey V, Khan MAW, Khan S, Loof N, et al. NLRP12 suppresses hepatocellular carcinoma via downregulation of cJun N-terminal kinase activation in the hepatocyte. *Elife*. 2019;8.

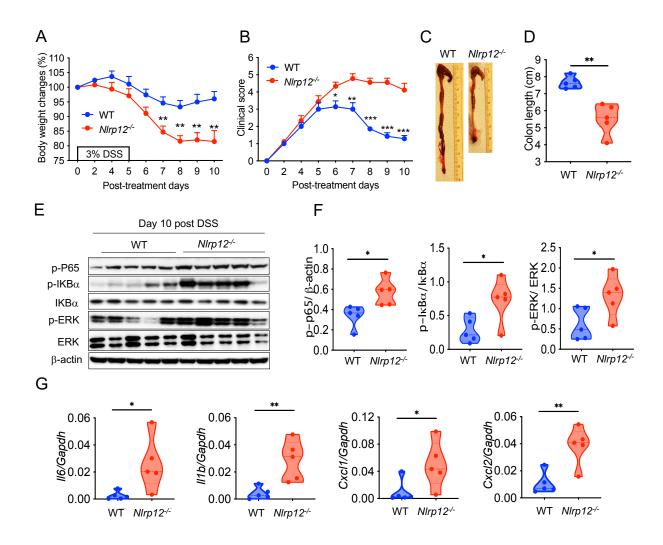
Supplemental Figures



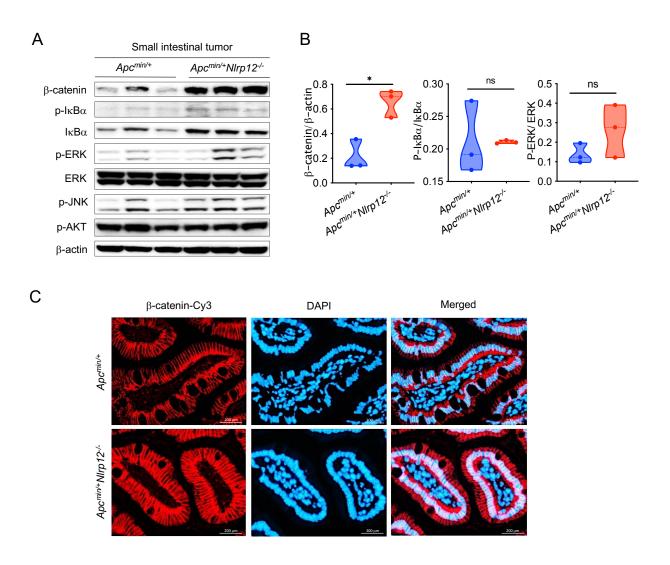
Supplemental Figure 1. NLRP12 suppresses genes involved in proliferation, EMT, and invasion. WT and $NIrp12^{-/-}$ mice were treated with AOM plus 3 cycles of 2.5% DSS. Colorectal tumors were collected at 12 weeks post AOM injection. (A) RNA isolated from WT and $NIrp12^{-/-}$ tumors were analyzed by RNA-seq. Heatmap shows the normalized expression of the top 100 differentially up-and down-regulated genes in WT and $NIrp12^{-/-}$ tumors. (B) Statistical analyses of the expression levels of indicated genes measured by RNA-seq. (C) The expression of indicated genes was measured by real-time RT-PCR. Data represent mean \pm SEM; *p < 0.05, **p < 0.01, ***p < 0.001, determined by unpaired Student's t test.



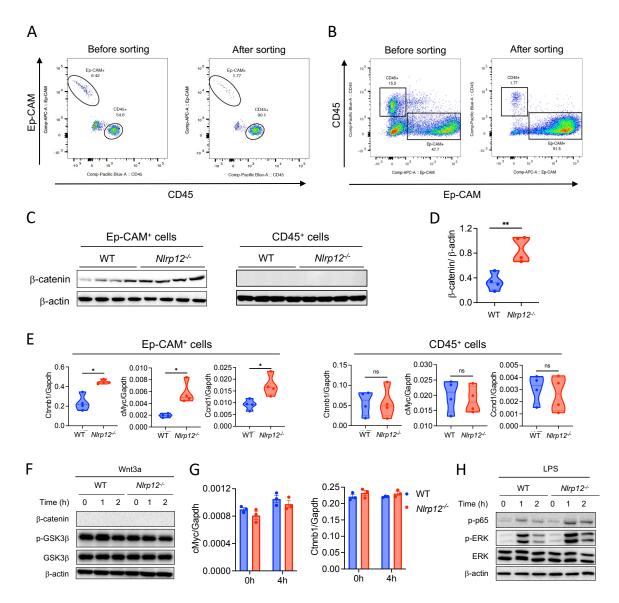
Supplemental Figure 2. Gut microbiota of *NIrp12*^{-/-} mice are not tumorigenic. (A-D) Littermate WT and *NIrp12*^{-/-} mice were treated with AOM/DSS regimen. (A-B) 12-week post AOM injection, mice were sacrificed and tumor burden in the colon was counted. (C) Tumor-bearing colon sections were stained with H&E and representative images are shown (scale bar= $100\mu m$). (D) RNA isolated from tumor tissues were analyzed for the indicated genes. Data represent mean \pm SEM (n=5/group); *p <0.01, **p < 0.001 by unpaired Student's t test. (E-I) Fecal homogenates from WT and *NIrp12*^{-/-} mice were orally gavaged into germ-free (GF) mice. After two weeks of fecal transplantation, fecal recipient mice were treated with AOM plus 3 cycles of DSS (2.5% for 5 days). (E-F) Body weight changes and clinical scores for diarrhea and rectal bleeding were measured during 1^{st} cycle of DSS. (G-H) 10 weeks post AOM, mice were sacrificed, and tumor burden was counted. (I) Histopathological changes in the colons were examined following H&E staining. Data represent mean \pm SEM (n=5/group), ns=no significant, determined by unpaired Student's t test. All experiments were repeated two times, and data from a representative experiment are presented.



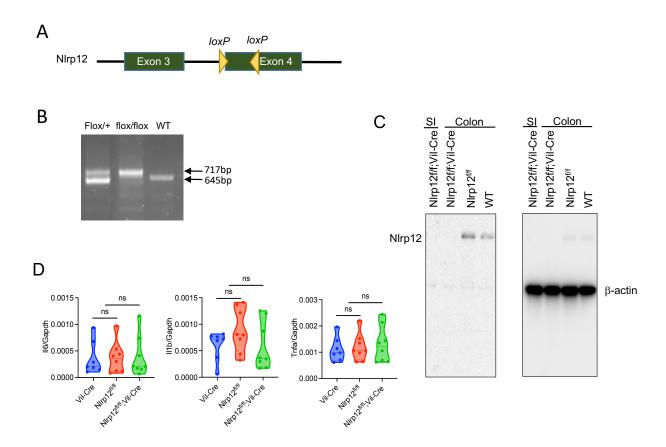
Supplemental Figure 3. NLRP12 dampens NF-κB and ERK activation in the colon during acute colitis. (A-F) WT and $NIrp12^{-/-}$ mice were injected with AOM. Five days post AOM injection, mice were fed with 3% DSS for 5 days. Body weight changes (A), clinical scorings for diarrhea, and rectal bleeding (B) were monitored daily. (C-D) Mice were sacrificed at day 10 and colon lengths were measured. (E) Colon tissue lysates were analyzed for p-P65, p-IκBα, IκBα, p-ERK , ERK and β-actin. (F) Densitometric analysis of band intensities shown in E. (G) RNA isolated from WT and $NIrp12^{-/-}$ colons were used to measure the expression of II6, II1b, CxcI1, and CxcI2 by real-time RT-PCR. Data represent mean ± SEM; *p < 0.05, **p < 0.01, determined by unpaired Student's t test. Experiments were repeated three times, and data of a representative experiment are presented.



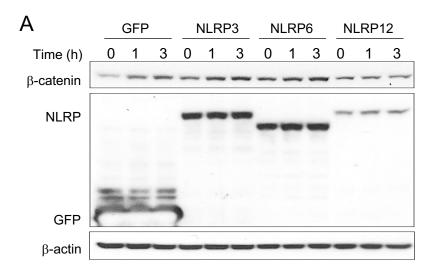
Supplemental Figure 4. NIrp12 deficiency promotes β-catenin activation in $Apc^{min/+}$ mice. $Apc^{min/+}$ and $Apc^{min/+}$ mice were sacrificed 5 months after birth. Tumors from the small intestine were processed for Western blotting and analyzed for β-catenin, p-lκBα, lκBα, p-ERK, ERK, p-JNK, p-AKT, and β-actin. (B) Densitometric analyses of p-lκBα, p-ERK and β-catenin reactive bands. Data represent mean \pm SD; *p < 0.05, **p < 0.01, determined by unpaired Student's t test. (C) Small intestinal tissues were stained for β-catenin (red). The nucleus was stained with DAPI (blue). Experiments were repeated three times, and data from a representative experiment are presented.



Supplemental Figure 5. NIrp12 downregulates β-catenin activation in epithelial cells of colorectal tumors. (A-E) Immune cells (CD45+ve cells) and epithelial cells (Ep-CAM+ve cells) were isolated from WT and $NIrp12^{-/-}$ colorectal tumor tissues using magnetic beads. (A-B) The purity of isolated immune cells and epithelial cells were measured by flow cytometry. (C) Ep-CAM⁺ and CD45⁺ cells were measured for β-catenin by Western blotting. (D) Densitometric analysis of β-catenin reactive bands (Ep-CAM⁺ cells). (E) RNA was isolated from Ep-CAM⁺ and CD45⁺ cells and the expression of Ctnnb1, cMyc, and Ccnd1 was measured by real-time RT-PCR. Data represents mean ± SEM; *p < 0.05, **p < 0.01, determined by unpaired Student's t test. Experiments were repeated two times, and data of a representative experiment are presented. (F-G) WT and $NIrp12^{-/-}$ BMDMs were stimulated with Wnt3a (100 ng/mL). (F) The cell lysates were used for measurement of β-catenin, p-GSK3β, GSK3β and β-actin. (G) The expression of Ctnnb1 and cMyc was measured by real-time RT-PCR. (H) BMDMs were stimulated with LPS (1 μg/mL) and the activation of p-P65, p-ERK, ERK and β-actin was measured by Western blotting. Experiments were repeated two times, and data from a representative experiment are presented.

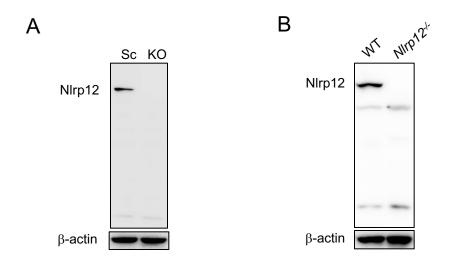


Supplemental Figure 6. Intestinal epithelial cell-specific NIrp12-KO mice are susceptible to colorectal tumorigenesis. (A) Design of loxP site flanking DNA sequences in exon 4 of *NIrp12 gene*. (B) Genotyping PCR of founder (F0) NIrp12^{flox/flox} mice; 717bp band indicates loxP site and 645bp band indicates no loxP site insertion (WT). (C) Epithelial cells were isolated from the small intestine (SI) and colon of respective mice. Western blotting was performed in epithelial cell lysates to measure the expression of NIrp12. β-actin was used as a loading control. (D) Colorectal tumors were induced in *NIrp12^{flox/flox}*, *Vil-Cre* and *NIrp12^{flox/flox}*; *Vil-Cre* mice with AOM/DSS treatment. The expression of indicated genes were analyzed by real-time RT-PCR. Data represent mean ± SEM. Statistical analysis was performed by one-way ANOVA. Experiments were repeated at least two times, and data from a representative experiment are presented.

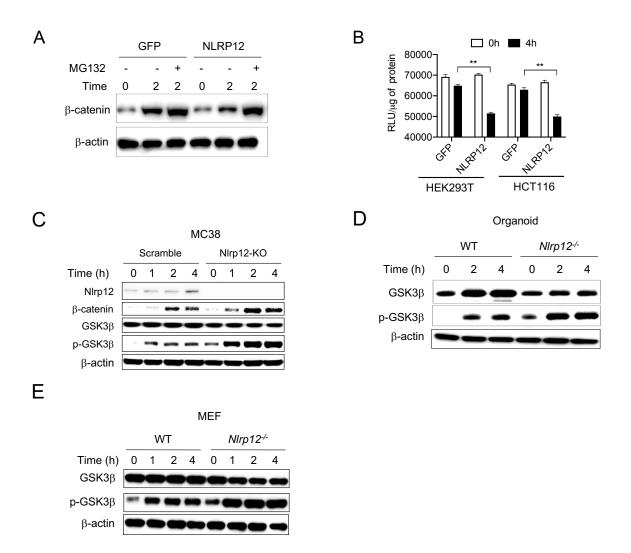




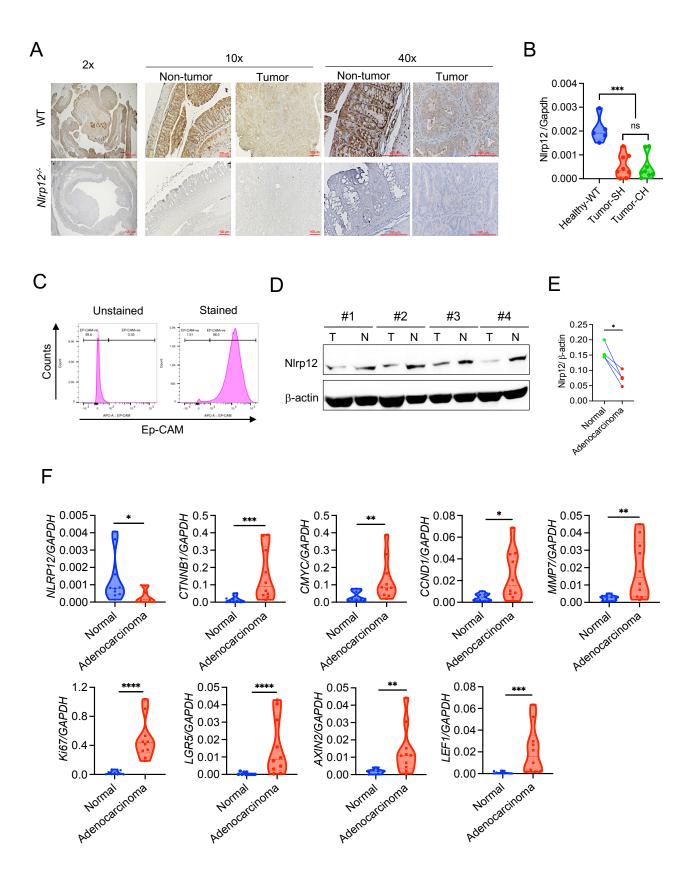
Supplemental Figure 7. NLRP12 suppresses β-catenin activation independent of NF- κ B. (A) NLRP3, NLRP6, or NLRP12 were overexpressed in HEK293T cells with transfection of respective flag-tagged plasmids. GFP-plasmid was transfected as a control. Cells were then stimulated with Wnt3a for indicated times and cell lysates were analyzed for β -catenin by Western blotting. The expression of GFP and NLRs was detected by anti-flag antibody. (B) GFP or NLRP12 expressing HEK293T cells were stimulated with Wnt3a in the presence or absence of Sc514, an inhibitor of NF- κ B. β -catenin levels were measured by western blotting. Experiments were repeated three times, and data of a representative experiment are presented.



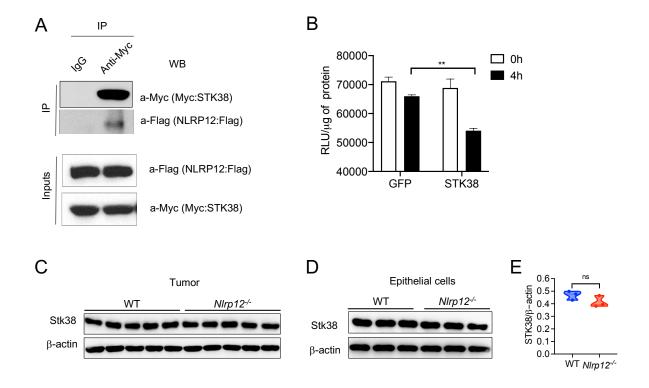
Supplemental Figure 8. Generation of NIrp12 KO MC38 cells. (A) NIrp12 was knocked out in MC38 cells with CRISPR/cas9. Deletion of NIrp12 in MC38 cells was confirmed by Western blot analysis of NIrp12. (B) The specificity of NIrp12 antibody was confirmed by Western blot analysis of colon tissue lysates collected from WT and NIrp12^{-/-} mice.



Supplemental Figure 9. NLRP12 inhibits GSK3β phosphorylation and promotes the degradation of β-catenin. (A) GFP or NLRP12 expressing HEK293T cells were stimulated with Wnt3a in the presence or absence of MG132. Cell lysates were analyzed for β-catenin by Western blotting. (B) GFP or NLRP12 expressing HEK293T and HCT116 cells were stimulated with Wnt3a. GSK3β kinase activity in Wnt3a-stimulated HEK293T and HCT116 cell lysates was measured. Kinase activity is inversely related to RLU (relative luminescence unit). (C) Nlrp12 knockout (KO) MC38 cells were generated with CRISPR/Cas9. Scramble or Nlrp12-KO MC38 cells were stimulated with Wnt3a. At indicated times, cells were lysed with RIPA buffer, and the lysates were used to measure Nlrp12, β-catenin, GSK3β, p-GSK3β, and β-actin by Western blotting. (D) Crypts from the small intestine of WT and $Nlrp12^{-/-}$ mice were cultured for organoid development. Organoids were stimulated with Wnt3a for 2h and 4h. Cell lysates were measured for GSK3β, p-GSK3β and β-actin by Western blotting. (E) WT and $Nlrp12^{-/-}$ MEFs were stimulated with Wnt3a (100 ng/ml). At indicated times, MEFs were lysed with RIPA buffer, and lysates were used to measure GSK3β, p-GSK3β, and β-actin by Western blotting. Experiments were repeated two times, and data from a representative experiment are presented.



Supplemental Figure 10. The expression of NLRP12 is downregulated in tumor tissues. (A) Tumor-bearing colons of WT and $Nlrp12^{-/-}$ mice were immunostained for Nlrp12. (B) WT mice were separately housed or co-housed with $Nlrp12^{-/-}$ mice. Colorectal tumors were induced with AOM/DSS treatment. The expression of NLRP12 in the tumor and healthy colons were measured by real-time PCR. Data represent mean \pm SEM (n=5-7/group); ***p < 0.001. (C-E) Epithelial cells were isolated from colorectal tumors and adjacent non-tumor tissues from WT mice (n=4) using Ep-CAM MicroBeads. (C) The purity of epithelial cells was measured by flow cytometric analysis of Ep-CAM⁺ cells. (D) Immunoreactive bands of Nlrp12 were measured in isolated epithelial cells by Western blot. (E) Densitometric analysis of Western blot shown in D. (F) Colorectal adenoma and adjacent non-tumor tissue biopsy samples were collected from stage 3 or 4 human colorectal cancer patients. The expression of NLRP12 and Wnt target genes was measured by real-time RT-PCR. Data represent mean \pm SEM (n=10/group); **p < 0.01, ***p < 0.001, ****p < 0.0001, analyzed by unpaired Student's t test. Experiments were repeated two times, and data of a representative experiment are presented.



Supplemental Figure 11. NLRP12 regulates the kinase activity of STK38, but not the expression of STK38. (A) Flag-tagged NLRP12 and Myc-tagged STK38 were overexpressed in HEK293T cells. STK38 was pulled down with anti-Myc antibody and immunoblotted with anti-Flag antibody. Inputs were used to measure the expression of NLRP12 and STK38 by western blotting with anti-Flag and anti-Myc antibodies, respectively. (B) STK38-Flag or GFP-Flag were overexpressed in HEK293T cells. Cells were stimulated with Wnt3a for 4 h. Unstimulated and stimulated cell lysates were measured for GSK3β kinase activity, which is inversely related to RLU value. (C-E) Colorectal tumors were induced in WT and Nlrp12^{-/-} mice following the AOM/DSS treatment. (C) Immunoreactive bands of Stk38 and β-actin were measured by Western blotting in WT and Nlrp12^{-/-} tumor lysates. (D) Epithelial cells were isolated from WT and Nlrp12^{-/-} tumors using anti-Ep-CAM MicroBeads. The expression of Stk38 in the tumor epithelium cells were measured by Western blot analysis. (E) Densitometric analysis of Stk38 immunoreactive bands shown in D. Data represent mean ± SD. Experiments were repeated two times, and data of a representative experiment are presented.

Supplemental Tables

Supplemental Table 1. Raw data of RNA-seq analysis showing top 100 up and downregulated genes in *Nlrp12^{-/-}* tumors as shown in Supplementary Figure 1A.

Gene	Name	WT-1	WT-2	WT3	WT-4	KO-1	KO-2	KO-3	KO-4
ENSMUSG00000102 364.1	lghv8-5	0	0	0	0	4.19262 067	1.10028 098	33.4867 861	36.6285 412
ENSMUSG00000048 830.3	2310057N15 Rik	0	0	0	0	0	0	0	71.1438 973
ENSMUSG00000046 008.7	Pnlip	0	0	0	1.03283 582	0	0	698.438 681	510.686 392
ENSMUSG00000029 882.5	2210010C04 Rik	0	0	0	2.06567 164	0	0	381.749 361	230.337 173
ENSMUSG00000057 163.3	Prss2	0	2.41056 737	0.95281 607	0	1.04815 517	1.10028 098	570.232 129	409.957 903
ENSMUSG00000023 140.4	Reg2	0	0	0	1.03283 582	0	0	100.460 358	108.476 834
ENSMUSG00000066 108.7	Muc5b	0	1.20528 369	0	0	53.4559 135	121.030 907	0	2.81758 009
ENSMUSG00000011 463.5	Cpb1	5.17319424 2	1.20528 369	4.76408 033	0	0	0	363.570 82	308.525 02
ENSMUSG00000059 654.7	Reg1	0	4.82113 475	0	0	2.09631 033	0	93.7630 011	97.2065 132
ENSMUSG00000094 818.1	Defa32	0	18.0792 553	8.57534 459	32.0179 104	430.791 774	231.059 005	28.7029 595	1446.82 738
ENSMUSG00000074 443.1	Defa22	0	24.1056 737	20.0091 374	50.6089 551	663.482 221	461.017 729	60.2762 15	2123.04 66
ENSMUSG00000095 066.1	Defa20	0	18.0792 553	15.2450 57	47.5104 477	539.799 911	338.886 54	48.7950 312	1683.50 411
ENSMUSG00000074 444.4	Defa30	0	18.0792 553	31.4429 302	80.5611 939	705.408 427	565.544 421	102.373 889	2561.18 03
ENSMUSG00000085 620.2	G630018N1 4Rik	0	0	0.95281 607	0	2.09631 033	4.40112 39	2.87029 595	19.7230 606
ENSMUSG00000074 447.2	Defa21	0	20.4898 227	24.7732 177	42.3462 686	424.502 843	293.775 02	36.3570 82	1776.48 425

ENSMUSG00000066 755.2	Tnfsf18	1.03463884 8	0	0	0	11.5297 068	3.30084 293	4.78382 658	8.45274 028
ENSMUSG00000098 078.1	Gm26992	0.97256051	0	0	0	0	5.03928 687	19.1831 446	2.15544 877
ENSMUSG00000096 295.2	Defa2	1.03463884	27.7215 248	49.5464 354	54.7402 984	708.552 893	461.017 729	69.8438 681	2149.10 922
ENSMUSG00000055 030.1	Sprr2e	1.03463884	0	0	0	0	0	0	26.0626 159
ENSMUSG00000076 550.3	lgkv4-63	0	1.20528 369	5.71689 639	1.03283 582	9.43339 65	9.90252 878	63.1465 109	107.772 439
ENSMUSG00000068 078.4	2310034C09 Rik	0	6.02641 843	2.85844 82	1.03283 582	1.04815 517	0	0	213.431 692
ENSMUSG00000074 439.4	Defa5	0	9.64226 95	7.62252 852	6.19701 491	142.549 103	95.7244 448	1.91353 063	238.789 913
ENSMUSG00000050 092.3	Sprr2b	5.17319424 2	4.82113 475	0.95281 607	5.16417 91	9.43339 65	1.10028 098	9.56765 317	307.116 23
ENSMUSG00000042 157.2	Sprr2i	4.13855539 3	0	0	0	1.04815 517	0	0	81.7098 227
ENSMUSG00000020 177.12	9530003J23 Rik	0	0	0	1.03283 582	5.24077 583	6.60168 585	7.65412 253	1.40879 005
ENSMUSG00000063 206.4	Defa34	0	1.20528 369	0.95281 607	3.09850 746	20.9631 033	19.8050 576	0	54.9428 118
ENSMUSG00000064 213.5	Defa24	2.06927769 7	121.733 652	176.270 972	357.361 193	2897.10 088	1801.15 996	340.608 453	6403.65 515
ENSMUSG00000069 722.4	Krtap3-3	5.17319424 2	1.20528 369	0	0	3.14446 55	1.10028 098	0	104.250 463
ENSMUSG00000018 727.19	Cpsf4I	0	0	1.90563 213	0	11.5297 068	3.30084 293	12.4379 491	4.22637 014
ENSMUSG00000069 721.2	Krtap3-2	1.03463884 8	0	0	1.03283 582	1.04815 517	0	0	30.2889 86
ENSMUSG00000055 826.5	Tescl	1.03463884 8	0	0	1.03283 582	9.43339 65	6.60168 585	2.87029 595	11.9747 154
ENSMUSG00000052 861.13	Dnah6	1.03463884 8	0	0.95281 607	0	9.43339 65	9.90252 878	1.91353 063	8.45274 028
ENSMUSG00000074 440.3	Defa3	0	3.61585 106	1.90563 213	3.09850 746	28.3001 895	29.7075 863	2.87029 595	64.8043 421
ENSMUSG00000095 328.1	Defa-ps6	0	2.41056 737	0	0	4.19262 067	6.60168 585	0	23.9494 308

ENSMUSG00000031 896.7	Ctrl	5.17319424	4.82113 475	6.66971 246	5.16417 91	7.33708	0	171.260 992	129.608 684
ENSMUSG00000050	Krtap13	1.03463884	3.61585	1.90563	7.22985	617 0	3.30084	1.91353	173.985
224.3	Kitapis	8	106	213	073	0	293	063	571
ENSMUSG00000056	Krtap13-1	4.13855539	6.02641	0	0	1.04815	1.10028	0	128.904
350.7	Tap 10-1	3	843			517	098		289
ENSMUSG00000108	Gm43890	0	0	1.90563	0	9.43339	3.30084	9.56765	2.11318
053.1	011110000			213		65	293	317	507
ENSMUSG00000102	2310046K23	4.13855539	0	0	5.16417	0	0	0	116.225
308.1	Rik	3			91				179
ENSMUSG00000079	Mptx2	0	10.8475	1.90563	1.03283	78.6116	59.4151	1.91353	28.8801
180.4			532	213	582	375	727	063	959
ENSMUSG00000068	Slc4a5	0	0	0	2.06567	11.5297	4.40112	5.74059	3.52197
323.12					164	068	39	19	512
ENSMUSG00000040	Chil3	0	3.61585	3.81126	7.22985	35.6372	25.3064	66.9735	41.5593
809.10			106	426	073	757	624	722	064
ENSMUSG00000076	lgkv6-13	1.03463884	1.20528	3.81126	26.8537	6.28893	5.50140	224.839	142.287
594.2		8	369	426	313	1	488	849	795
ENSMUSG00000081	Gm11668	0	0	0.95281	2.06567	13.6260	8.80224	3.82706	8.45274
392.1				607	164	172	78	127	028
ENSMUSG00000112	Gm48868	0	1.20528	0.95281	0	10.4815	2.20056	7.65412	4.22637
677.1	01.0.40		369	607	4 40404	517	195	253	014
ENSMUSG00000030	Slc6a13	0	1.20528	2.85844	4.13134	27.2520	15.4039	22.0056	26.7670
108.14	14:1a.F1a	4.0040004	369	82	328	343 18.8667	337	023	109 15.4966
ENSMUSG00000087 149.8	Itih5I-ps	1.03463884 8	2.41056 737	3.81126 426	2.06567 164	93	28.6073 054	40.1841 433	905
ENSMUSG00000085	A730046J19	0	15.6686	12.3866	9.29552	80.7079	69.3177	224.839	13.3835
139.1	Rik	U	879	088	237	479	09.3177	849	054
ENSMUSG00000056	Jakmip3	1.03463884	2.41056	3.81126	3.09850	18.8667	26.4067	41.1409	21.1318
856.12	Jakinipo	8	737	426	746	93	434	086	507
ENSMUSG00000005	Mmp8	1.03463884	2.41056	0	3.09850	14.6741	9.90252	22.0056	19.0186
800.3		8	737		746	723	878	023	656
ENSMUSG00000048	Muc6	6.20783309	32.5426	45.7351	52.6746	319.687	297.075	434.371	289.506
191.15			595	711	268	326	863	454	354
ENSMUSG00000079	Gzmc	0	0	1.90563	1.03283	5.24077	8.80224	2.87029	11.9747
186.3				213	582	583	78	595	154
ENSMUSG00000096	lghv1-5	1.03463884	6.02641	0	3.09850	35.6372	35.2089	18.1785	8.45274
499.2		8	843		746	757	912	41	028

ENSMUSG00000036 500.4	Akp3	0	0	2.85844 82	1.03283 582	13.6260 172	11.0028 098	2.87029 595	9.15713 53
ENSMUSG00000081	Gm15922	0	0	0	4.13134	5.24077	9.90252	15.3082	7.74834
665.2	Omroozz				328	583	878	451	525
ENSMUSG00000025	Dach2	3.10391654	6.02641	2.85844	2.06567	38.7817	45.1115	9.56765	31.6977
592.17	2 6.6	5	843	82	164	412	2	317	76
ENSMUSG00000069	Lyz1	284.525683	2027.28	1858.94	2929.12	18172.9	11183.2	7481.90	22442.0
515.6		3	716	414	238	143	558	478	254
ENSMUSG00000095	lgkv1-122	0	6.02641	4.76408	5.16417	8.38524	6.60168	32.5300	84.5274
497.2			843	033	91	134	585	208	028
ENSMUSG00000093	Gm20695	2.00719936	0	0	2.68537	7.89260	16.6802	11.5003	2.64148
575.1		6			313	841	596	191	134
ENSMUSG00000105	Gm42427	0	0	4.76408	13.4268	46.1188	51.7132	2.87029	44.3768
263.1				033	656	273	058	595	864
ENSMUSG00000002	Shh	3.10391654	6.02641	34.3013	22.7223	224.305	158.440	68.8871	68.3263
633.4		5	843	784	88	206	46	028	172
ENSMUSG00000112	Gm10741	0	4.82113	8.57534	6.19701	36.6854	52.8134	35.4003	25.3582
431.1		<u> </u>	475	459	491	308	868	167	208
ENSMUSG00000025	Gm7628	5.17319424	0	6.66971	2.06567	19.9149	39.6101	27.7461	18.3142
644.10	1.1.00	2	0.44050	246	164	482	151	942	706
ENSMUSG00000094	lghv2-3	1.03463884	2.41056	4.76408	9.29552	7.33708	0	48.7950	75.3702
164.2	A d = == 4 = 4 C	8	737	033	237	617	22.4050	312	675
ENSMUSG00000049 538.14	Adamts16	2.06927769	1.20528 369	4.76408 033	3.09850	26.2038 792	23.1059 005	5.74059	26.7670 109
ENSMUSG00000057	Ces1c	8.27711078	12.0528	4.76408	746 7.22985	88.0450	75.9193	19 11.4811	59.8735
400.14	Cesic	7	369	033	073	34	873	838	77
ENSMUSG00000053	Adh6a	6.20783309	2.41056	0.95281	5.16417	36.6854	26.4067	6.69735	35.9241
054.13			737	607	91	308	434	722	462
ENSMUSG00000110	Gm45496	0	2.41056	8.57534	2.06567	25.1557	15.4039	41.1409	9.86153
187.1			737	459	164	24	337	086	032
ENSMUSG00000115	Gm49132	3.10391654	0	0	2.06567	6.28893	16.5042	7.65412	5.63516
207.1		5			164	1	146	253	018
ENSMUSG00000038	Aox4	10.3463884	8.43698	20.0091	20.6567	110.056	64.9165	134.903	96.5021
242.12		8	581	374	164	293	775	91	182
ENSMUSG00000033	Fgg	0	0	0	6.19701	12.5778	6.60168	13.3947	8.45274
860.13		1			491	62	585	144	028
ENSMUSG00000049	Mmp12	3.10391654	50.6219	35.2541	36.1492	171.897	174.944	227.710	241.607
723.14		5	149	944	537	447	675	145	493

ENSMUSG00000025	Habp2	15.5195827	95.2174	57.1689	73.3313	428.695	498.427	276.505	361.354
075.14		3	113	639	432	463	282	177	647
ENSMUSG00000025	Pnliprp2	33.1084431	120.528	412.569	426.561	2153.95	1740.64	1029.47	1458.09
091.3		5	369	356	193	887	45	948	77
ENSMUSG00000113	Gm47982	0	0	0	5.16417	8.38524	4.40112	13.3947	7.04395
288.1					91	134	39	144	023
ENSMUSG00000074	Gm14548	1.03463884	9.64226	1.90563	1.03283	16.7704	34.1087	19.1353	16.9054
417.9		8	95	213	582	827	102	063	806
ENSMUSG00000106	Gm43352	3.10391654	14.4634	26.6788	27.8865	124.730	115.529	140.644	73.9614
086.1		5	042	498	671	465	502	502	774
ENSMUSG00000025	Padi4	12.4156661	63.8800	101.951	96.0537	379.432	448.914	453.506	438.133
330.6		8	354	319	312	17	638	76	704
ENSMUSG00000039	Gabbr2	1.03463884	1.20528	0.95281	2.06567	11.5297	6.60168	11.4811	3.52197
809.10		8	369	607	164	068	585	838	512
ENSMUSG00000020	Wif1	85.8750244	996.769	1051.90	992.555	5073.07	4711.40	6795.90	2714.03
218.11		1	609	894	222	101	314	405	402
ENSMUSG00000110	Gm9172	0	0	3.81126	5.16417	18.8667	19.8050	8.61088	7.74834
666.1				426	91	93	576	785	525
ENSMUSG00000054	Adam12	13.4503050	44.5954	42.8767	58.8716	269.375	344.387	133.947	214.136
555.11		3	964	229	417	878	945	144	087
ENSMUSG00000033	Strc	47.5933870	10.8475	2.85844	17.5582	177.138	143.036	58.3626	95.7977
498.14		2	532	82	089	223	527	843	231
ENSMUSG00000047	Mmp10	23.7966935	235.030	28.5844	75.3970	693.878	491.825	428.630	564.220
562.3		1	319	82	148	721	596	862	413
ENSMUSG00000022	Robo1	78.6325524	179.587	243.920	131.170	785.068	908.832	1349.99	712.143
883.11		7	269	913	149	22	085	586	368
ENSMUSG00000010	Prox1	80.7018301	626.747	1080.49	864.483	3805.85	4210.77	4467.13	3112.72
175.13		7	517	342	581	141	529	726	161
ENSMUSG00000110	Cbx3-ps8	2.06927769	16.8739	12.3866	22.7223	81.7561	53.9137	86.1088	95.0933
887.1		7	716	088	88	03	678	785	281
ENSMUSG00000113	4921525009	0	16.8739	5.71689	17.5582	70.2263	59.4151	66.9735	38.7417
211.1	Rik		716	639	089	962	727	722	263
ENSMUSG00000018	Mmp7	55.8704978	934.094	695.555	1194.99	4938.90	3246.92	3806.96	4817.35
623.9		1	857	728	104	715	916	92	756
ENSMUSG00000098	lgkv19-93	7.24247193	7.23170	20.9619	34.0835	53.4559	83.6213	108.114	146.514
814.2		8	212	534	82	135	541	481	165
ENSMUSG00000071	Apcdd1	190.373548	433.902	397.324	348.065	1832.17	1697.73	3020.50	1146.75
847.12		1	127	299	671	523	354	811	51

ENSMUSG00000020	Lgr5	21.7274158	232.619	315.382	275.767	1392.99	1530.49	1027.56	745.249
140.15	D 11 40	2	752	118	164	822	084	595	934
ENSMUSG00000051	Pcdh19	21.7274158	32.5426	24.7732	20.6567	161.415	181.546	130.120	76.0746
323.16		2	595	177	164	896	361	083	625
ENSMUSG00000070	Lilra5	0	1.20528	5.71689	9.29552	15.7223	22.0056	24.8758	26.7670
873.5	0 11	0.40004054	369	639	237	275	195	982	109
ENSMUSG00000005	Spo11	3.10391654	1.20528 369	15.2450	8.26268	64.9856	20.9053	18.1785	47.8988
883.15	A : :-O	5		57	655	203	385	41	616
ENSMUSG00000021 986.8	Amer2	0	18.0792 553	43.8295 39	50.6089 551	176.090 068	169.443 27	144.471 563	119.042 759
ENSMUSG00000042	Pnliprp1	26.9006100	180.792	478.313	501.958	1357.36	1543.69	1184.47	2289.28
179.5		6	553	665	208	094	421	546	382
ENSMUSG00000046	Foxc2	3.10391654	9.64226	34.3013	25.8208	122.634	94.6241	110.984	61.2823
714.7		5	95	784	955	155	639	777	67
ENSMUSG00000085	Cep112it	3.10391654	6.02641	24.7732	21.6895	84.9005	29.7075	97.5900	83.1186
811.1		5	843	177	522	685	863	623	127
ENSMUSG00000018	Ccl4	3.10391654	4.82113	0	0	4.19262	8.80224	10.5244	18.3142
930.3		5	475			067	78	185	706
ENSMUSG00000079	Alpi	6.20783309	36.1585	129.582	127.038	3.14446	2.20056	0.95676	4.93076
440.2			106	985	806	55	195	532	516
ENSMUSG00000029	Nmu	22.7620546	9.64226	49.5464	32.0179	3.14446	1.10028	0	0
236.4		6	95	354	104	55	098		
ENSMUSG00000045	Lrtm1	41.3855539	98.8332	6.66971	4.13134	2.09631	0	0	3.52197
776.3		3	623	246	328	033			512
ENSMUSG00000023	Fabp2	136.572328	248.288	807.035	1169.17	9.43339	9.90252	23.9191	45.0812
057.5			44	207	015	65	878	329	815
ENSMUSG00000096	Lhx8	23.7966935	24.1056	0	0	1.04815	0	0	0.70439
225.7		1	737			517			502
ENSMUSG00000030	Aqp8	1951.32886	485.729	1001.40	831.432	16.7704	12.1030	68.8871	61.2823
762.11		8	326	968	834	827	907	028	67
ENSMUSG00000030	Ckm	5728.79530	11013.8	225.817	192.107	93.2858	168.342	30.6164	346.562
399.2		3	823	407	462	099	989	901	351
ENSMUSG00000020	Tmigd1	15.5195827	97.6279	532.624	727.116	2.09631	11.0028	22.0056	15.4966
839.16		3	786	181	417	033	098	023	905
ENSMUSG00000025	Phkg1	77.5979136	145.839	0.95281	0	3.14446	2.20056	0	2.81758
537.12		3	326	607		55	195		009
ENSMUSG00000085	Gm12055	16.5542215	1.20528	3.81126	8.26268	1.04815	0	0	0
979.1		7	369	426	655	517			

ENSMUSG00000070 385.12	Ampd1	163.472938	262.751 844	0	0	2.09631 033	0	0	13.3835 054
ENSMUSG00000044	Klhl31	175.888604	286.857	2.85844	0	2.09631	7.70196	0	7.04395
938.8	Tallio	2	517	82		033	683		023
ENSMUSG00000111	Gm47108	10.3463884	16.8739	2.85844	0	1.04815	0	0	0
000.1		8	716	82		517			
ENSMUSG00000050	Apol10a	57.9397755	640.005	1569.28	1367.47	9.43339	8.80224	98.5468	14.0879
982.13		1	638	806	462	65	78	276	005
ENSMUSG00000071	3425401B19	129.329856	210.924	11.4337	3.09850	1.04815	2.20056	0.95676	8.45274
540.4	Rik		645	928	746	517	195	532	028
ENSMUSG00000019	Trdn	196.581381	355.558	4.76408	4.13134	5.24077	1.10028	0.95676	12.6791
787.9		2	688	033	328	583	098	532	104
ENSMUSG00000021	Ckmt2	194.512103	286.857	18.1035	12.3940	9.43339	4.40112	0	4.22637
622.3		5	517	052	298	65	39		014
ENSMUSG00000019	Mrln	24.8313323	14.4634	0	2.06567	0	0	0	1.40879
933.7		6	042		164				005
ENSMUSG00000020	Pgam2	623.887225	1295.67	7.62252	3.09850	13.6260	12.1030	3.82706	37.3329
475.3		6	996	852	746	172	907	127	362
ENSMUSG00000073	H2-BI	2.06927769	0	14.2922	12.3940	0	0	0.95676	0
406.10		7		41	298			532	
ENSMUSG00000002	Rpl3l	180.027159	282.036	2.85844	2.06567	1.04815	2.20056	0	12.6791
500.15	07	6	383	82	164	517	195		104
ENSMUSG00000079	C7	121.052745	54.2377	0	1.03283	1.04815	0	0	4.93076
105.4	0000450540	3	659	00 5070	582	517	4.40000		516
ENSMUSG00000004 360.9	9330159F19 Rik	33.1084431 5	48.2113 475	29.5372 98	17.5582 089	1.04815 517	1.10028 098	0	2.11318 507
ENSMUSG00000047	Cmya5	909.447547	1691.01	13.3394	8.26268	14.6741	18.7047	4.78382	49.3076
419.5	Ciliyas	7	301	249	655	723	766	658	516
ENSMUSG00000005	Tmod4	122.087384	220.566	0	1.03283	2.09631	4.40112	0	4.93076
628.12	1111004	122.007304	915	0	582	033	39	0	516
ENSMUSG00000027	Sypl2	177.957881	241.056	5.71689	9.29552	2.09631	5.50140	1.91353	4.93076
887.11	Jypi2	9	737	639	237	033	488	063	516
ENSMUSG00000087	Nctc1	42.4201927	67.4958	0	0	0	2.20056	0	1.40879
090.7		8	865		_	-	195	_	005
ENSMUSG00000095	D630033O1	7.24247193	1.20528	3.81126	10.3283	0	0	0	0.70439
385.3	1Rik	8	369	426	582				502
ENSMUSG00000086	Gm13010	9.31174963	9.64226	0.95281	3.09850	0	0	0	0.70439
845.1		5	95	607	746				502

ENSMUSG00000053	Kcnip1	12.4156661	6.02641	46.6879	26.8537	0	2.20056	0	0.70439
519.15		8	843	872	313	10 ==0 1	195	0.05050	502
ENSMUSG00000031	Myom2	569.051366	1084.75	18.1035	12.3940	16.7704	11.0028	0.95676	24.6538
461.4		6	532	052	298	827	098	532	258
ENSMUSG00000061	Btnl7-ps	1.03463884	3.61585	29.5372	22.7223	1.04815	0	0	0.70439
728.5		8	106	98	88	517			502
ENSMUSG00000030	Ryr1	1299.50639	2316.55	9.52816	9.29552	13.6260	23.1059	22.9623	53.5340
592.18		4	525	065	237	172	005	676	217
ENSMUSG00000031	Tnni2	3369.81872	6988.23	19.0563	17.5582	42.9743	50.6129	17.2217	212.727
097.15		9	482	213	089	618	249	757	297
ENSMUSG00000023	Gabrr2	10.3463884	32.5426	0.95281	3.09850	0	0	0	1.40879
267.10		8	595	607	746				005
ENSMUSG00000027	Car3	3970.9439	8587.64	10.4809	36.1492	11.5297	60.5154	13.3947	300.072
559.5			627	767	537	068	536	144	28
ENSMUSG00000031	Acta1	10879.2274	20061.9	56.2161	78.4955	63.9374	113.328	47.8382	721.300
972.5		9	47	479	223	652	94	658	504
ENSMUSG00000062	Hsd3b3	262.798267	102.449	744.149	940.913	12.5778	9.90252	19.1353	20.4274
410.14		5	113	347	431	62	878	063	557
ENSMUSG00000020	Jsrp1	132.433772	237.440	0	0	3.14446	0	0.95676	7.04395
216.13		6	886			55		532	023
ENSMUSG00000063	Hsd3b2	70.3554416	21.6951	213.430	196.238	3.14446	2.20056	4.78382	4.93076
730.13		9	064	799	806	55	195	658	516
ENSMUSG00000032	Tbx18	24.8313323	71.1117	0	0	0	0	0	2.81758
419.8		6	375						009
ENSMUSG00000039	Cdh26	12.4156661	2.41056	0.95281	9.29552	0	0	0	0.70439
155.15		8	737	607	237				502
ENSMUSG00000022	Hoxc10	44.4894704	89.1909	1.90563	1.03283	1.04815	0	0	2.81758
484.7		8	928	213	582	517			009
ENSMUSG00000030	Mylpf	2308.27927	3598.97	1.90563	5.16417	19.9149	15.4039	11.4811	121.860
672.12		1	709	213	91	482	337	838	339
ENSMUSG00000100	Gm28230	1.68646132	4.56802	50.4230	55.9177	1.04815	0	0	2.09909
642.1		3	517	262	312	517			717
ENSMUSG00000017	Tnnc2	4637.25131	8103.12	0	2.06567	25.1557	46.2118	0.95676	283.871
300.9		8	223		164	24	01	532	194
ENSMUSG00000055	Myh8	12178.7338	25611.0	0	0	125.778	228.858	1.91353	695.942
775.16		8	731			62	443	063	283
ENSMUSG00000051	Ttn	2436.57448	4660.83	38.1126	43.3791	47.1669	33.0084	11.4811	106.363
747.14		8	202	426	044	825	293	838	648

ENSMUSG00000087	Gm11586	0	1.20528	12.3866	13.4268	0	0	0	0.70439
339.1	_	4 4 40 40 400	369	088	656				502
ENSMUSG00000015	Rxrg	14.4849438	28.9268	5.71689	4.13134	0	0	0	1.40879
843.10		8	085	639	328	101015	0.000=0		005
ENSMUSG00000020	Cacng1	180.027159	253.109	0	0	1.04815	2.20056	0	8.45274
722.5		6	574	4.00=00		517	195	0.05050	028
ENSMUSG00000027	Acoxl	14.4849438	101.243	1.90563	0	1.04815	1.10028	0.95676	0
380.10		8	83	213		517	098	532	
ENSMUSG00000021	ccdc198	0	4.82113	40.9710	25.8208	1.04815	0	0	0.70439
850.14		400 000 40=	475	908	955	517			502
ENSMUSG00000062	Trim54	182.096437	359.174	2.85844	3.09850	3.14446	5.50140	0	4.93076
077.14		3	539	82	746	55	488		516
ENSMUSG00000027	Tbx15	126.225939	161.508	0.95281	0	1.04815	1.10028	0	4.93076
868.11		5	014	607	407.000	517	098	4.04050	516
ENSMUSG00000054	Ugt2b5	0	3.61585	109.573	127.038	0	1.10028	1.91353	2.81758
630.7		45.540.500	106	848	806		098	063	009
ENSMUSG00000001	Hoxc11	15.5195827	40.9796	0	3.09850	0	0	0	1.40879
656.3		3	454	0.05004	746	5.04077	4 40440	4.04050	005
ENSMUSG00000024	Myot	378.677818	566.483	0.95281	2.06567	5.24077	4.40112	1.91353	10.5659
471.12	D 14	5	333	607	164	583	39	063	253
ENSMUSG00000063	Dupd1	19.6581381	13.2581	0	0	0	0	0	0.70439
821.6	0 47045	2	206	45.0450	45 4005			•	502
ENSMUSG00000110	Gm47345	1.03463884	1.20528	15.2450	15.4925	0	0	0	0.70439
815.1	\(' \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	8	369	57	373	40.0000	0.00004	•	502
ENSMUSG00000027	Xirp2	521.457979	1075.11	7.62252	6.19701	13.6260	3.30084	0	16.9054
022.13	T10	6	305	852	491	172	293	0.05070	806
ENSMUSG00000061	Tnnt3	5229.06474	11664.7	2.85844	1.03283	26.2038	62.7160	0.95676	258.512
723.18	D400044D0	F 47040404	355	82	582	792	156	532	973
ENSMUSG00000068	D430041D0	5.17319424	32.5426	0	0	0	0	0	0.70439
373.15	5Rik	2	595	4.70400	0	0	0		502
ENSMUSG00000030	Art1	82.7711078	94.0121	4.76408	0	0	0	0	3.52197
996.8	A4=0=4	7	276	033	0.00507	25 6270	00 0477	0.05070	512
ENSMUSG00000030	Atp2a1	4767.61581	9208.36	0	2.06567	35.6372	69.3177	0.95676	162.010
730.12	NA: da la a Q	3	737	10 1070	164	757	014	532	855
ENSMUSG00000038	Mybpc2	986.010822	2879.42	16.1978	9.29552	11.5297	22.0056	1.91353	37.3329
670.11	C==0000	5	273	731	237	068	195	063	362
ENSMUSG00000073	Gm8909	1.03463884	6.02641	66.6971	37.1820	1.04815	0	0.95676	0
402.11	1	8	843	246	895	517	İ	532	

ENSMUSG00000016 327.9	Atp1b4	12.4156661 8	28.9268 085	0	0	0	0	0	0.70439 502
ENSMUSG00000067 231.4	Cyp2c65	68.2861639 9	31.3373 759	1057.62 583	1003.91 642	8.38524 134	2.20056 195	11.4811 838	16.2010 855
ENSMUSG00000111 283.1	E230034D0 1Rik	1.03463884	0	31.4429 302	29.9522 388	1.04815 517	0	0	0
ENSMUSG00000073 403.11	Gm10499	6.20783309	4.82113 475	15.2450 57	16.5253 731	0	0	0	0.70439 502
ENSMUSG00000026 100.6	Mstn	41.3855539	87.9857 091	0	0	0	0	0	2.11318 507
ENSMUSG00000013 653.2	1810065E05 Rik	468.691398 3	509.835	7680.65 03	8491.97 61	24.1075 688	29.7075 863	157.866 277	66.2131 322
ENSMUSG00000068 697.7	Myoz1	594.917337 8	1046.18 624	0	0	1.04815 517	11.0028 098	0	14.0879 005
ENSMUSG00000042 540.12	Acot5	13.4503050	31.3373 759	0	3.09850 746	0	0	0	0.70439 502
ENSMUSG00000044 951.15	Mylk4	287.629599 8	460.418 368	1.90563 213	0	2.09631 033	1.10028 098	0	7.74834 525
ENSMUSG00000054 128.16	H2-T3	0	14.4634 042	242.015 281	265.438 806	0	0	3.82706 127	3.52197 512
ENSMUSG00000079 278.1	Tmem233	77.5979136 3	95.2174 113	0	0	0	0	0.95676 532	1.40879 005
ENSMUSG00000061 816.15	Myl1	2169.63766 5	3949.71 464	2.85844 82	1.03283 582	5.24077 583	11.0028 098	0	68.3263 172
ENSMUSG00000030 433.15	Sbk2	256.590434 4	296.499 787	0.95281 607	1.03283 582	2.09631 033	2.20056 195	1.91353 063	1.40879 005
ENSMUSG00000040 705.2	A930016O2 2Rik	18.6234992 7	32.5426 595	0	4.13134 328	0	0	0	0.70439 502
ENSMUSG00000057 003.12	Myh4	105.533162 5	115.707 234	0	0	1.04815 517	1.10028 098	0	0.70439 502
ENSMUSG00000116 378.1	Gcat	15.4161188 4	55.5635 78	29.3181 503	0	0	1.25432 031	0	0
ENSMUSG00000040 113.14	Mettl11b	37.2469985 4	42.1849 29	0	0	0	0	0	0.70439 502
ENSMUSG00000049 173.7	Myoz3	48.6280258 7	51.8271 985	0	0	0	0	0	0.70439 502
ENSMUSG00000006 457.3	Actn3	828.745717 5	2517.83 762	0	7.22985 073	1.04815 517	15.4039 337	2.87029 595	1.40879 005

ENSMUSG00000025	Cyp2c55	1333.64947	127.760	5110.90	3700.65	5.24077	5.50140	11.4811	32.4021
002.5		6	071	537	074	583	488	838	711
ENSMUSG00000035	Myf6	65.1822474	87.9857	0	0	0	0	0	0.70439
923.4	-	5	091						502
ENSMUSG00000026	Slc30a10	270.040739	1.20528	639.339	375.952	1.04815	2.20056	0	2.81758
614.6		4	369	58	238	517	195		009
ENSMUSG00000005	Pvalb	344.534736	532.735	0	0	1.04815	0	0	2.81758
716.16		5	39			517			009
ENSMUSG00000033	Dhrs7c	63.1129697	107.270	0.95281	1.03283	0	0	0	0.70439
044.12		5	248	607	582				502
ENSMUSG00000056	Myh1	10611.2560	20987.6	0	0	5.24077	13.2033	1.91353	65.5087
328.14		3	048			583	717	063	371
ENSMUSG00000102	Zbed6	8.95997242	0	0	50.6502	0	0	0	0
049.1		7			686				
ENSMUSG00000094	lgkv3-3	0	0	0	73.3313	0	0	0	0
478.1					432				
ENSMUSG00000096	lgkv1-132	0	10.8475	40.0182	23.7552	0	0	0	0
580.1			532	747	238				
ENSMUSG00000028	2310002L09	35.1777208	51.8271	0.95281	0	0	0	0	0
396.5	Rik	4	985	607					
ENSMUSG00000109	Exosc6	113.023947	0	0	0	0	0	0	0
941.1		8							
ENSMUSG00000097	Gm2061	50.6973035	2.41056	103.856	52.6746	0	0	0	0
615.1		7	737	951	268				
ENSMUSG00000090	Gm15446	79.6671913	0	60.0274	82.6268	0	0	0	0
015.8		2		121	655				
ENSMUSG00000085	Myhas	104.498523	232.619	0	0	0	0	0	0
348.1		7	752						

Supplemental Table 2. List of primers for measurement of mouse (m) and human (h) mRNA by real-time qPCR.

Gene Name	Forward	Reverse
mll1b	GCCTCGTGCTGTCGGACCCATA	TGCAGGGTGGGTGTGCCGTCTT
mII6	CAA GAA AGA CAA AGC CAG AGT C	GAA ATT GGG GTA GGA AGG AC
mTNFa	TCCCAGGTTCTCTTCAAGGGA	GGTGAGGAGCACGTAGTCGG
mIFNg	GAAAGACAATCAGGCCATCA	TTGCTGTTGCTGAAGAAGGT
mCxcl1	TGAGCTGCGCTGTCAGTGCCT	AGAAGCCAGCGTTCACCAGA
mCxcl2	CAA GAA CAT CCA GAG CTT GAG TGT	GCC CTT GAG AGT GGC TAT GAC TT
mKi67	AGAAGTCCAGGTCTACAG	TCGTTGCTATTGCTAAGG
mCdh2	CAATGACGTCCACCCTGTTCT	CAATGACGTCCACCCTGTTCT
mFn1	CCCAGACTTATGGTGGCAATT	ATATTCCGACTCGAGTCTGA
mVim	CCGTTCAAGGTCAAGACGTGCCA	AGGAGGCCGAAAGCACCCTGC
mEzh2	CAGGCTGGGGCATCTTTATC	ACGAATTTTGTTGCCCTTTC
mZeb2	CAGATCAGCACCAAATGCTAAC	ACACTCCGTGCACTTGAACTT
mFoxc2	GCAACCCAACAGCAAACTTTC	GACGGCGTAGCTCGATAGG
тМтр3	ACCAACCTATTCCTGGTTGCTGCT	ATGGAAACGGGACAAGTCTGTGGA
тМтр7	ACCAACCTATTCCTGGTTGCTGCT	ATGGAAACGGGACAAGTCTGTGGA
тМтр8	AATCCTTGCCCATGCCTTTCAACC	CCAAATTCATGAGCAGCCACGAGA
mMmp10	GACCCCAGACAAATGTGATCCT	TTCAGGCTCGGGATTCCA
mMmp12	TAGAAGCAACTGGGCAACTGGACA	ACCGCTTCATCCATCTTGACCTCT
mMmp13	TTCTGGTCTTCTGGCACACGCTTT	CCAAGCTCATGGGCAGCAACAATA
mCtnnb1	AAG GGC AAG GTT CGA ATC AA	AGC CGA GAT GGC CCA GAA T
mLgr5	CGGGACCTTGAAGATTTCCT	GATTCGGATCAGCCAGCTAC
тМус	CCTTTGGGCGTTGGAAACC	TCCTCGTCGCAGATGAAATAGG
mAxin2	GCAGCTCAGCAAAAAGGGAAAT	TACATGGGGAGCACTGTCTCGT
mCcnd1	TGCCATCCATGCGGAAA	AGCGGGAAGAACTCCTCTTC
mYap1	TACATAAACCATAAGAACAAGACCACA	GCTTCACTGGAGCACTCTGA
mNlrp12	CCT CTT TGA GCC AGA CGA AG	GCC CAG TCC AAC ATC ACT TT
mGapdh	TGG CAA AGT GGA GAT TGT TGC C	AAG ATG GTG ATG GGC TTC CCG

hNLRP12	AAATGCACTGGAGGATTTGG	CAGGCTCTGGTTCACACTGA
hCTNNB1	CAGAAGCTATTGAAGCTGAGG	TTCCATCATGGGGTCCATAC
hAXIN2	ACTGCCCACACGATAAGGAG	CTGGCTATGTCTTTGGACCA
hLEF1	CTTTATCCAGGCTGGTCTGC	TCGTTTTCCACCATGTTTCA
hMYC	TGAGGAGACACCGCCCAC	CAACATCGATTTCTTCCTCATCTTC
hCCND1	AAGCTCAAGTGGAACCT	AGGAAGTTGTTGGGGC
hMMP7	TGAGCTACAGTGGGAACAGG	TCATCGAAGTGAGCATCTCC
hKI67	GAGGTGTGCAGAAAATCCAAA	CTGTCCCTATGACTTCTGGTTGT
hLGR5	CTTCCAACCTCAGCGTCTTC	TTTCCCGCAAGACGTAACTC
hGAPDH	TCTGGTAAAGTGGATATTGTTG	GATGGTGATGGGATTTCC

Supplemental Table 3. Patients information of colorectal high-grade adenocarcinoma specimens.

Case	Gender	Age	Path Dx	Path comments	Tumor Size (cm)	Tumor Grade	IOR Treatment	Anatomy Site
1	Male	68	Poorly differentiated signet ring cell adenocarcinoma with mucinous features	Histologic Grade: High-grade, poorly differentiated	4.7	High	No	Colon, NOS
2	Male	80	Adenocarcinoma		13.5	4	No	Sigmoid colon
3	Male	69	Adenocarcinoma	Histologic Grade: High-grade	7.5	4	No	Rectum, NOS
4	Female	66	Adenocarcinoma	Histologic Grade: poorly differentiated	4.5	High	Yes	Colon, NOS
5	Female	67	Poorly differentiated adenocarcinoma with neuroendocrine features		2	High	No	Rectum, NOS
6	Female	44	Mucinous adenocarcinoma-Signet- ring cell carcinoma		9	3	No	Colon, NOS
7	Female	71	Adenocarcinoma	Histologic Grade: poorly differentiated with signet-ring cell features	3.2	High	No	Colon, NOS
8	Female	58	Adenocarcinoma with focal medullary features (40%)		10.8	3	No	Colon, NOS
9	Female	54	Adenocarcinoma	Invasive adenocarcinoma, poorly-differentiated with focal mucinous features, arising from tubular adenoma with high-grade dysplasia	4.2	3	No	Colon, NOS
10	Male	51	Adenocarcinoma		3.8	3	No	Colon, NOS