Supplementary Methods

Antibodies and Reagents

The following antibodies were used in western blot, immunofluorescent, immunoprecipitation, and immunohistochemical analyses: Flag (F3165; Sigma-Aldrich, St Louis, MO), hemagglutinin (11666606001; Roche Diagnostics, Indianapolis, IN), Myc (Sigma-Aldrich), PDL1 (13684; Cell Signaling Technology, Danvers, MA), PDL1 (329702; Bio-Legend, San Diego, CA; ab205921; Abcam, Cambridge, UK), granzyme B (ab4059; Abcam), α -tubulin (B-5-1-2; Sigma-Aldrich), GSK3B (BD Transduction Laboratories, San Diego, CA), TRAF6 (Abcam), β -actin (A2228; Sigma-Aldrich), CD8 (ab22378; Abcam), MET (8198; Cell Signaling Technology), and p-MET (3077; Cell Signaling Technology). Capmatinib was purchased from Selleck Chemicals (Houston, TX) and GSK3B substrate peptide was purchased from Millipore Sigma (Burlington, MA). Active recombinant human MET, puromycin, and staurosporine were obtained from Sigma-Aldrich. Phospho-specific antibodies against phosphorylation of GSK3B at Y56 were generated by EZBiolab (Carmel, IN).

Cell Culture, Plasmids, and Transfection

All cell lines were obtained from the ATCC (Manassas, VA), independently validated using short tandem repeat DNA fingerprinting at The University of Texas MD Anderson Cancer Center, and tested negative for mycoplasma contamination. Cells were maintained in Dulbecco's modified Eagle's medium/F12 medium or RPMI 1640 medium supplemented with 10% fetal bovine serum.

pCR-Flag-TRAF6 was kindly provided by Dr Bryant Darnay. pCGN-GSK3B-WT, pCGN-GSK3B-kinase-dead, pGEX-GSK3B, pRK5-hemagglutinin-tagged ubiquitin WT, Lys48R, and Lys63R were constructed for transient transfection as described previously.¹ A series of WT GSK3B and GSK3B mutants used for various purposes were subsequently constructed using pCMV-Flag, pGEX-6P-1, and pMX-Flagpuro vectors at EcoRI cloning sites. GSK3B Y56F and GSK3B P51A (PE) mutants were generated using pCMV-Flag-GSK3B as a template and QuikChange Site-Directed Mutagenesis Kit (Stratagene, La Jolla, CA). All DNA constructs were validated using enzyme digestion and DNA sequencing; detailed information about the DNA sequence is available upon request. WT TRAF6- and C70A-expressing cell lines were generated by transient transfection with DNA performed with an optimal ratio of DNA to liposomes using Lipofectamine 3000 (Invitrogen, Carlsbad, CA). For stable knockdown of MET expression and induction of MET overexpression, liver cancer cells were transfected with a pGIPZ shRNA vector (control; Thermo Fisher Scientific, Rockford, IL) and pCDH-neo vector (System Biosciences, Palo Alto, CA). The MET shRNA sequences used in knockdown experiments were as follows (5' to 3'): CCATCCA-GAATGTCATTCT (sh1) and GCATTAAAGCAGCGTATC (sh2; targeting the 3'-untranslated region). Using the pCDH-MET-Flag expression vector as a template, MET-Flag kinase mutants were generated by performing site-directed mutagenesis. For generation of stable HCC cells using retroviral infection, recombinant retroviruses were produced by cotransfecting GP293 cells (Clontech, Palo Alto, CA) with a retroviral expression plasmid and VSV-G plasmids using Lipofectamine 3000 (Invitrogen). Culture supernatants containing infectious viruses were harvested 48 hours after transfection, centrifuged to eliminate cell debris, and filtered through 0.22-mm filters. For transduction of retroviral constructs, 70% confluent HCC cells were cultured in virus-containing medium plus hexadimethrine bromide (Polybrene; Chemicon International, Temecula, CA) for 1 day to generate 70% successfully infected cells by visualizing green fluorescent protein expression. Stable clones of different constructs were subsequently selected and maintained in a culture medium with puromycin 2 μ g/ mL. The lentiviral-based shRNA (pGIPZ plasmids) used to knock down expression of human PDL1 was purchased from the shRNA and ORFeome Core at MD Anderson. Using a pGIPZ-shPDL1/Flag-PDL1 dual-expression construct to knock down endogenous PDL1 expression and reconstitute Flag-PDL1 simultaneously, endogenous PDL1-knockdown and WT Flag-PDL1- or 4NQ mutant (N35Q/N192Q/ N200Q/N219Q)-expressing cell lines were established.² Twenty-four hours after transfection, the medium was changed and then collected at 24-hour intervals. The collected medium containing the lentivirus was centrifuged to eliminate cell debris and filtered through $0.45 - \mu m$ filters. Cells were seeded at 50% confluence 12 hours before infection, and the medium was replaced with medium containing the lentivirus. After infection for 24 hours, the medium was replaced with fresh medium, and the infected cells were selected using puromycin 2 µg/mL (InvivoGen, San Diego, CA).

Proliferation Assay

For cell proliferation assays, control HCC cells and cells previously intervened with capmatinib or tivantinib 1 μ mol/L for 48 hours were used. Three thousand cells dispensed in 100- μ L aliquots were seeded in a 96-well plate, and viable cells were measured after 24, 48, and 72 hours according to the manufacturer's protocol. Cells were incubated in 10% Cell Counting Kit-8 (Dojindo Molecular Technologies, Gaithersburg, MD) and diluted in culture medium for an additional 2 hours. The absorbance at a wavelength of 450 nm was used to estimate the viable cells in each well.

Flow Cytometric Analysis

To measure cell surface PDL1 expression, single HCC cells were resuspended in phosphate buffered saline (PBS) and stained with primary antibodies according to standard protocols for flow cytometry. The cells were washed twice and then stained with secondary antibodies conjugated with allophycocyanin (Life Technologies, Carlsbad, CA). Isotype immunoglobulin G or a secondary antibody alone was used as a negative control. Stained cell samples were evaluated using a BD FACSCanto II cytometer (BD Biosciences, San

Jose, CA), and flow cytometric data were analyzed using the FlowJo software program (Ashland, OR).

T-Cell-Mediated Tumor Cell Killing Assay

To analyze T-cell-killing ability in vitro, nuclear restricted red fluorescent protein-expressing tumor cells were cocultured with activated primary human T cells or peripheral blood mononuclear cells (STEMCELL Technologies, Vancouver, BC, Canada) in the presence of a caspase 3/7 substrate (Essen BioScience, Ann Arbor, MI) in 96-well plates. T cells were activated with a CD3 antibody (100 ng/mL) and interleukin-2 (10 ng/mL). After 4 days of coculture of tumor cells and T cells in 12-well plates, wells were washed with PBS twice to remove the T cells, and the surviving tumor cells were fixed and stained with a crystal violet solution. The dried plates were scanned and quantified.

Quantitative Real-Time Polymerase Chain Reaction

HCC cells were washed twice with PBS and immediately lysed in QIAzol lysis reagent. Total RNA was extracted from HCC cells using an RNeasy Plus Mini Kit (QIAGEN, Venlo, Netherlands) according to the manufacturer's instructions and then subjected to complementary DNA synthesis by reverse transcription using a SuperScript III kit (Invitrogen). Quantitative real-time polymerase chain reaction analysis of β -actin and PDL1 was performed using iQ SYBR Green Supermix (Bio-Rad, Hercules, CA) in triplicate with a real-time polymerase chain reaction machine (iQ5; Bio-Rad) and the following primers: human PDL1, 5'-TCACTTGGTAATTCTGGGAGC-3' and (forward) 5'-CTTTGAGTTTGTATCTTGGATGCC-3' (reverse); β -actin, 5'-GCAAAGACCTGTACGCCAACA-3' (forward) and 5'-TGCATCCTGTCGGCAATG-3' (reverse). All data analyses were performed using the comparative threshold cycle method. Results were normalized according to internal control β -actin mRNA expression.

Western Blot Analysis and Immunoprecipitation

Western blot analysis of target proteins was performed as previously described.^{3,4} Image acquisition and band intensity quantitation for western blotting was performed using an Odyssey infrared imaging system (LI-COR Biosciences, Lincoln, NE). For immunoprecipitation, liver cancer cells were lysed in buffer (Tris-HCl 50 mmol/ L. pH 8.0. NaCl 150 mmol/L. EDTA 5 mmol/L. 0.5% Nonidet P-40) and centrifuged at 16,000 \times g for 30 minutes to remove debris. Cleared lysates were subjected to immunoprecipitation with antibodies. Two micrograms of antibodies were added to lysates with 30 μ L of protein A/ G agarose beads. Samples of tagged lysates were incubated on a rotating wheel overnight at 4°C. Beads were collected by centrifugation at 1,000 rpm for 2 minutes at 4°C and washed 5 times with ice-cold PBS buffer. Immunocomplex samples were boiled directly in $2 \times$ sodium dodecyl sulfate (SDS)-polyacrylamide gel electrophoresis sample buffer (Tris-HCl 50 mmol/K, pH 6.8, 2% SDS, 10% glycerol, 1% β -mercaptoethanol, EDTA 12.5 mmol/L, 0.02% bromophenol blue) followed by SDS-polyacrylamide gel electrophoresis and western blot analysis.

In Vitro and In Vivo Ubiquitination Assay

For an in vitro ubiquitination assay, purified GSK3B protein was incubated with in vitro translated TRAF6 or TRAF6 C70A in the presence of a ubiquitin ligation buffer containing Tris-HCl 100 mmol/L (pH 7.4), MgCl₂ 5 mmol/L, NaF 2 mmol/L, okadaic acid 10 nmol/L, ATP 2 mmol/L, dithiothreitol 0.6 mmol/L, E1 60 ng, E2 300 ng, and histidine (His)-tagged ubiquitin 12 mg (Sigma-Aldrich). Reaction mixtures of these materials were incubated at 37°C for 60 minutes, and the reaction was terminated by boiling for 5 minutes with an SDS sample buffer containing dithiothreitol 0.1 mol/L. These reaction products were resolved by SDSpolyacrylamide gel electrophoresis and blotted with a Histagged ubiquitin antibody. For in vivo ubiquitination assays, HCC cells were transfected with hemagglutinintagged ubiquitin, Flag-tagged WT GSK3B, or GSK3B PE and TRAF6 or TRAF6 C70A. GSK3B in HCC cells was immuno-precipitated and then blotted with antibody against ubiquitin or hemagglutinin.

Tumor-Infiltrating Lymphocyte Profiling and Tumor-Cell Analysis Using Time-of-Flight Mass Cytometry or Flow Cytometry

Excised hepatocellular tumors were digested to single cells using a gentleMACS Dissociator with a mouse Tumor Dissociation Kit (Miltenyi Biotec, Auburn, CA). Tumorinfiltrating lymphocytes and tumor cells were enriched on a Ficoll gradient (Sigma-Aldrich). For time-of-flight mass cytometric analysis, tumor-infiltrating lymphocytes and tumor cells were incubated with a mixture of metal-labeled antibodies (Supplementary Table 1) for 30 minutes at room temperature, washed twice, and incubated with Cell-ID Intercalator-¹⁰³Rh (Fluidigm, San Francisco, CA) overnight at 4°C. A sample of labeled tumor-infiltrating lymphocytes or tumor cells was analyzed using a time-offlight mass cytometry 2 instrument (Fluidigm) at the Flow Cytometry and Cellular Imaging Facility at MD Anderson. For flow cytometry, cells were stained with CD3 and peridinin-chlorophyll protein, CD8 and allophycocyanin or cyanine 7, and granzyme B-Pacific Blue antibodies (Bio-Legend). Stained samples were analyzed using the BD FACSCanto II cytometer.

Identification of Phosphorylation Sites in HCC Cells Using Mass Spectrometry

Hep3B cells overexpressing Flag-tagged GSK3B and MET were subjected to immunoprecipitation. After protein gel electrophoresis, the gel was stained with Coomassie blue. The band corresponding to GSK3B phosphorylation by MET was excised from the gel and subjected to tryptic digestion. The band containing GSK3B was subsequently isolated

Gastroenterology Vol. 156, No. 6

using immobilized metal affinity chromatography, and enriched phospho-peptides were analyzed using microliquid chromatography and tandem mass spectrometry. The peptide sequences were searched against the National Center for Biotechnology Information protein sequence database using the Mascot search engine.

In Vitro Kinase Assay and Phosphorylation Analysis

Expression of glutathione S-transferase and glutathione S-transferase–GSK3B–kinase-dead fusion proteins was induced in *Escherichia coli* BL-21 cells, and these proteins were purified using glutathione-agarose beads (17-0756-01; Amersham, Little Chalfont, UK) using a standard procedure. Purified proteins were incubated with active human recombinant MET (Sigma-Aldrich) in the presence of ATP 50 μ mol/L in a kinase buffer for 30 minutes at 30°C. Reaction products were subjected to SDS-polyacrylamide gel electrophoresis and then blotted with an antibody against a target protein.

For complex immune analysis, GSK3B was immunoprecipitated from whole cell lysates by incubating total cell protein 75 μ g for 2 hours with a rabbit GSK3B antibody 2 μ g in the presence of protein A/G agarose beads and washed as previously described.⁵ The immuno-precipitates were incubated for 45 minutes at 30°C in $4 \times$ kinase assay buffer, $[\gamma^{-32}P]$ ATP 10 μ Ci, and synthetic peptide substrate of GSK3B 150 µmol/L, spotted onto P81 phospho-cellulose, and washed in 0.75% H₃PO₄. The activity was determined by scintillation counting. Purified GSK3B (0.2 μ g; Upstate Biotechnology, Waltham, MA) was used as a positive kinase control, and a negative GSK3B substrate peptide (Calbiochem, San Diego, CA) was used to detect background phosphorylation (eg, GSK3B autophosphorylation). The resulting GSK3B activity data were obtained after the background phosphorylation was subtracted.

Yeast Two-Hybrid Assay

pGBT9, pGBT-GSK3B, and pGBT-GSK3B PE paired with pACT-TRAF6 were co-transformed into yeast Y190 cells using a Matchmaker Two-Hybrid System 2 (Clontech) according to the manufacturer's instructions. Yeast cells containing corresponding vectors were grown in tryptophan and leucine selection media for 24 hours at 30°C. For a yeast survival assay, yeast transformants at an optical density of 1.6 were resuspended in PBS. Ten-fold serially diluted yeast cells were spotted onto synthetic complete medium plates lacking tryptophan, leucine, and His with or without 3amino-1,2,4-triazole 20 mmol/L (Sigma-Aldrich). The plates were incubated at 30°C until colonies were observed.

Clinical Tumor Samples and Follow-up

Tumor samples were collected from 268 patients with HCC who underwent surgical resection from August 2001 to November 2007 at the Fudan Liver Cancer Institute (Shanghai, People's Republic of China) for use in tissue microarrays. Patients were monitored after surgery until March 15, 2009 at the Liver Surgery Department at the Zhongshan Hospital of the Fudan University (Shanghai, People's Republic of China). The Research Ethics Committee of the Zhongshan Hospital approved the use of tumor samples. Postsurgical follow-up was conducted as previously described.⁶ Overall survival was defined as the interval from tumor resection to death or last follow-up examination, and disease-free survival was defined as the interval from the date of resection to the date of tumor recurrence.

Immunohistochemistry

Tissue microarrays containing HCC patient samples were constructed as previously described.⁷ Mouse liver tumor samples were obtained from tumor xenografts. Immunohistochemical staining of the samples was performed as previously described.⁴ Briefly, each tissue sample was stained with specific antibodies as indicated and a biotin-conjugated secondary antibody and then incubated with an avidin-biotin-peroxidase complex. Visualization of the target protein was performed using 3-amino-9ethylcarbazole chromogen. The samples were scored using an H-score method combining the values of immunoreaction intensity and percentage of tumor-cell staining. The final immunohistochemical score was calculated by multiplying the percentage of target protein positive cells by the intensity score. The staining intensity was ranked in 4 groups according to histologic score: high (+++), medium (++), low (+), and negative (-).

Immunofluorescence

For immunocytochemistry, HCC cells were fixed in 4% paraformaldehyde at room temperature for 15 minutes, made permeable in 5% Triton X-100 for 5 minutes, and then stained with primary antibodies. Secondary antibodies used were anti-mouse Alexa Fluor 488 or 594 dye conjugate and anti-rabbit Alexa Fluor 488 or 594 dye conjugate (Life Technologies). Nuclei were stained with 4,6-diamidino-2-phenylindole (blue; Life Technologies). After mounting, the cells were visualized using a multiphoton confocal laser-scanning microscope (LSM700; Carl Zeiss, Oberkochen, Germany).

Mouse liver tumor samples were frozen in an optimal cutting temperature block immediately after extraction. Cryostat sections of samples that were 5 μ m thick were attached to saline-coated slides. The cryostat sections were fixed with 4% paraformaldehyde for 15 minutes at room temperature and blocked with a blocking solution (5% bovine serum albumin, 2% donkey serum, and PBS 0.1 mol/L) at room temperature for 30minutes. Sample sections were stained with primary antibodies overnight at 4°C followed by secondary antibodies at room temperature for 1hour. The LSM700 microscope was used for image analysis.

Animal Studies

All procedures using C3H, nonobese diabetic and severe combined immunodeficiency gamma (NOD.Cg-Prkdc^{scid}Il2rg^{tm1Wjl}/SzJ), and C57BL/6 mice (male, 6 weeks old; The Jackson Laboratory, Bar Harbor, ME, USA) were conducted under guidelines approved by the MD Anderson Institutional Animal Care and Use Committee. Tumorigenicity assays were performed using mouse subcutaneous and orthotopic liver cancer models. For the subcutaneous tumor model, HCA-1 and Hep1-6 liver cancer cells (5 \times 10⁶) were subcutaneously injected into the right inguinal fold regions of C3H and C57BL/6 mice. For the orthotopic tumor model, subcutaneous Hep1-6 tumors were cut into cubes (1 mm³) under aseptic conditions. Then, single cubes were inoculated into the liver parenchyma of C57BL/6 mice anesthetized using xylazine. Mice were randomly assigned to groups according to mean tumor volume. For antibody-based drug intervention, PD1 antibody 100 μ g (RMP1-14; Bio X Cell, West Lebanon, NH) or rat immunoglobulin G (control; Bio X Cell) were injected intraperitoneally every 3 days 1 week after tumor-cell inoculation. For drug-based drug intervention, mice were given daily oral doses of capmatinib 10 mg/kg reconstituted in 0.5% methylcellulose and 5% dimethylacetamide⁸ or tivantinib 100 mg/kg⁹ formulated in tocopherol polyethylene glycol 1000 succinate (BioXtra, water-soluble vitamin E conjugate). Subcutaneous tumors were measured using a caliper, and orthotopic tumors were evaluated using high-frequency ultrasound (Vevo 2100 imaging system; FUJIFILM VisualSonics Inc, Toronto, ON, Canada) twice a week (Supplementary Figure 4A). Tumor volumes were calculated using the formula (length \times width²)/2. At the experimental end point, mice were killed using CO₂ exposure followed by cervical dislocation, and tumors were excised for subsequent histologic analysis or processed immediately for mass cytometric and flow cytometric analyses.

Statistical Analysis

The relation of the expression of different proteins in liver tumors was determined by Pearson correlation analysis. Statistical analysis was performed using SPSS (IBM Corporation, Armonk, NY). The level of significance was set at .05.

References

- 1. Lee DF, Kuo HP, Liu M, et al. KEAP1 E3 ligase-mediated downregulation of NF-kappaB signaling by targeting IKKbeta. Mol Cell 2009;36:131–140.
- Li CW, Lim SO, Xia W, et al. Glycosylation and stabilization of programmed death ligand-1 suppresses T-cell activity. Nat Commun 2016;7:12632.
- Lim SO, Gu JM, Kim MS, et al. Epigenetic changes induced by reactive oxygen species in hepatocellular carcinoma: methylation of the E-cadherin promoter. Gastroenterology 2008;135:2128–2140 e1-8.
- Lee DF, Kuo HP, Chen CT, et al. IKK beta suppression of TSC1 links inflammation and tumor angiogenesis via the mTOR pathway. Cell 2007;130:440–455.
- Singer CA, Vang S, Gerthoffer WT. Coupling of M(2) muscarinic receptors to Src activation in cultured canine colonic smooth muscle cells. Am J Physiol Gastrointest Liver Physiol 2002;282:G61–G68.
- Sun HC, Zhang W, Qin LX, et al. Positive serum hepatitis B e antigen is associated with higher risk of early recurrence and poorer survival in patients after curative resection of hepatitis B-related hepatocellular carcinoma. J Hepatol 2007;47:684–690.
- Zhou SL, Dai Z, Zhou ZJ, et al. Overexpression of CXCL5 mediates neutrophil infiltration and indicates poor prognosis for hepatocellular carcinoma. Hepatology 2012; 56:2242–2254.
- Liu X, Wang Q, Yang G, et al. A novel kinase inhibitor, INCB28060, blocks MET-dependent signaling, neoplastic activities, and cross-talk with EGFR and HER-3. Clin Cancer Res 2011;17:7127–7138.
- Rimassa L, Assenat E, Peck-Radosavljevic M, et al. Second-line tivantinib (ARQ 197) vs placebo in patients (Pts) with MET-high hepatocellular carcinoma (HCC): results of the METIV-HCC phase III trial. J Clin Oncol 2017;35:4000.





Supplementary Figure 2. MET binds to and phosphorylates GSK3B at Tyr56 to down-regulate its ubiquitination. (*A*) Hep3B cells coexpressing MET and an empty vector, Flag-GSK3B, Flag- IKK α , Flag-IKK β , Flag-IKK γ , or Flag-ERK were immunoprecipitated with a Flag antibody. The total amount of immuno-precipitates was determined by western blotting with a phospho-tyrosine antibody (4G10) to detect phosphorylation. (*B* and *C*) Mass spectrometric analyses identifying GSK3B Y56 phosphorylation (*B*) in vivo and (*C*) in vitro. (*D*) Immunofluorescent staining of the PDL1, CD8, and granzyme B protein expression patterns in HCA-1 cells after drug intervention. ERK, extracellular signal-regulated kinase; E.V., empty vector; IKK, I κ B kinase; Tyr56, Y56.

Supplementary Figure 1. MET inhibition drives PDL1 expression that correlates with poor prognosis for HCC. (*A*) Control HCA-1 cells or cells treated with capmatinib or tivantinib for 48 hours at a concentration of 1 μ mol/L were subjected to a Cell Counting Kit-8 assay, and viable cells were measured after 24, 48, and 72 hours. (*B*) Immunoblot analysis of whole cell lysates derived from HCA-1 and Hep3B cell lines treated with or without the MET inhibitor capmatinib or tivantinib at the indicated concentrations for 48 hours. (*C* and *D*) Prognostic value of PDL1 expression according to Kaplan-Meier analysis of overall (*C*) and disease-free (*D*) survival in patients with HCC. (*E*) Representative HCC samples exhibiting expression and PDL1 (*yellow*) at low (*top*) and high (*bottom*) levels. Scale bars, 100 μ m. (*F*) (*Left*) immunoblot of MET protein expression and PDL1 expression and PDL1 expression induced by a vector control and MET knockdown in HA22T and HA59T cells. (*Middle*) Immunoblot of MET protein expression and PDL1 expression and PDL1 expression for levels. (*Right*) PDL1 quantification of western blot results from left and middle panels. Intensity of PDL1 protein was quantified using a densitometer. (*G*) (*Left*) Western blot analysis of PDL1 protein and p-MET in HCC cell lines. (*Right*) Intensity of PDL1 protein and p-MET was quantified using a densitometer. (*H*) Immunoblot of MET protein and PDL1 expression in vector control, WT MET-expressing Hep3B, and MET kinase-dead Hep3B cells. (*I*) Results of quantitative real-time polymerase chain reaction analysis of PDL1 mRNA expression in MET-knockdown Hep3B and SK-HEP-1 cells are shown. CCK8, Cell Counting Kit-8; CTRL, control; KD, kinase-dead; OE, overexpression.



Supplementary Figure 3. MET up-regulates GSK3B activity in HCC cells by suppression of TRAF6-mediated GSK3B K63 ubiquitination. (*A*) Interaction between GSK3B and TRAF6 based on a yeast 2-hybrid assay. Yeast cells containing corresponding vectors were grown in tryptophan and leucine selection media for 24 hours at 30°C. Ten-fold serially diluted yeast cells were spotted onto synthetic complete medium plates lacking tryptophan, leucine, and histidine with or without 3-amino-1,2,4-triazole. (*B*) Hep3B cells were transfected with hemagglutinin-tagged GSK3B together with a plasmid expressing His₆, His-tagged fused ubiquitin, or Nedd8 with or without TRAF6. A covalently conjugated His-tagged ubiquitin of GSK3B in the cells was pulled down using Ni²⁺ agarose beads under denaturing conditions and analyzed using western blotting with the indicated antibodies. (*C*) Mass spectrometric analyses identifying 2 ubiquitination sites in GSK3B (K86 and K197) in Hep3B cells. (*D*) Hep3B cells were transfected with the indicated plasmids and subjected to immunoprecipitation using a Flag antibody. Ubiquitination of transfected cells was analyzed by Western blotting. (*E*) Hep3B cells were transfected with the indicated plasmids and subjected to immunoprecipitation using a Flag antibody. Ubiquitination of transfected cells was analyzed by western blotting. (*F*) Immunoprecipitation of Hep3B cells transfected with the indicated plasmids. GST, glutathione S-transferase; PAGE, polyacrylamide gel electrophoresis; Ubi, ubiquitination.



Supplementary	Table	1. Antibodies	Used for	^r Time-of-	Flight
		Mass Cyto	metry An	alysis (Pro	ovided
		bv Fluidian	ר)		

, ,		
Clone	Label	
RB6-8C5	141Pr	
N418	142Nd	
30-F11	147Sm	
M1/70	148Nd	
6D5	149Sm	
145-2C11	152Sm	
53-6.7	168Er	
H57-597	169Tm	
PK136	170Er	
RM4-5	172Yb	
RA3-6B2	176Yb	
29F.1A12	159Tb	
10F.9G2	154Sm	
93H1	149Sm	
M9C6	152Sm	
M89-61	159Tb	
B56	168Er	
G8.8	166Er	
D13.14.4.E	167Er	
p-Tyr-100	144Nd	
N7-548	172Yb	
196624	147Sm	
	Clone RB6-8C5 N418 30-F11 M1/70 6D5 145-2C11 53-6.7 H57-597 PK136 RM4-5 RA3-6B2 29F.1A12 10F.9G2 93H1 M9C6 M89-61 B56 G8.8 D13.14.4.E p-Tyr-100 N7-548 196624	

Supplementary Figure 4. In vivo therapeutic study and toxicity detection. (A) Sonogram of orthotopic tumor growth. Highfrequency ultrasound was used to noninvasively monitor the growth of intrahepatic HCC. Tumor size was marked by circling the maximum diameter of the largest tumor area in the ultrasound plane. (B) Schematic of drug intervention protocol for tivantinib and the PD1 antibody in C57/BL6 mice. (C) Growth of orthotopic Hep1-6 tumors in tivantinib- and/or PD1 antibodytreated C57/BL6 mice. Tumors were measured at the indicated time points. (D) Survival of mice bearing Hep1-6 tumors after drug intervention with tivantinib and/or PD1 antibody. Significance was determined using log-rank test. (E) Immunohistochemical stains of PDL1, CD8, and granzyme B protein expression patterns in Hep1-6 cells. Scale bar, 50 µm. (F) Histogram showing mean immunohistochemistry score \pm standard error of the mean in each group. *P < .05; **P < .01. (G) Growth of orthotopic MET KO Hep1-6 tumors in tivantinib- and/or PD1 antibody-treated C57/BL6 mice. Tumors were measured at the indicated time points. (H) Immunofluorescent staining of p-GSK3B (Y56) and PDL1 expression patterns in HCA-1 cells after drug intervention with capmatinib. (/) Curves showing body weight changes of mice during drug intervention. (J) Quantitative analysis of indicated biochemistry indices for liver and kidney function after the experiments. All error bars represent mean ± standard deviation. (*K*) Flow cytometric quantification of MET⁺ neutrophils in tumors of mice treated as indicated (n = 6; mean \pm standard error of the mean). ***P* < .01. (*L*) Immunofluorescent staining of MPO and MET expression patterns in HCA-1 tumors of mice treated as indicated (M) (Left) Western blot analysis of PDL1 protein and p-MET in lung cancer cell lines. (Right) Quantification of intensity of PDL1 protein and p-MET by a densitometer. ALT, alanine aminotransferase; BUN, serum urea nitrogen; DAPI, 4',6-diamidino-2-phenylindole; IHC, immunohistochemistry; KO, knockout; MPO, myeloperoxidase; NS, not significant.

Supplemental Table 2. Components of	of GSK3B Comp	plex Identified by	/ Mass Spectrometry	y and Their	Confidence Scores
-------------------------------------	---------------	--------------------	---------------------	-------------	-------------------

Entry name	Coverage, %	Description	Score
G3P_HUMAN	82	Glyceraldehyde-3-phosphate dehydrogenase	3285
ANXA2_HUMAN	76	Annexin A2	2330
LDHB_HUMAN	58	L-lactate denydrogenase B chain	1509
	45	60S acidic ribosomal protein P0	703
PP1R HUMAN	4J 59	Serine- and threonine-protein phosphatase PP1-beta catalytic subunit	674
I BC59 HUMAN	56	Leucine-rich repeat-containing protein 59	549
MDHM HUMAN	53	Malate dehydrogenase, mitochondrial	516
MDHC HUMAN	37	Malate dehydrogenase, cytoplasmic	495
NACA HUMAN	36	Nascent polypeptide-associated complex subunit alpha	488
EF1D_HUMAN	30	Elongation factor 1-delta	481
PDLI1_HUMAN	51	PDZ and LIM domain protein 1	480
RL6_HUMAN	41	60S ribosomal protein L6	411
CNN2_HUMAN	32	Calponin-2	388
EF1A1_HUMAN	34	Elongation factor 1-alpha 1	369
ALDR_HUMAN	60	Aldose reductase	316
ROA2_HUMAN	28	Heterogeneous nuclear ribonucleoproteins A2/B1	314
PP2AA_HUMAN	39	Serine- and threonine-protein phosphatase 2A catalytic subunit alpha isoform	311
PDXK_HUMAN	33	Pyridoxal kinase	247
ENOA_HUMAN		Alpha-enolase	232
GALE_HUMAN	20	UDP-glucose 4-epimerase	223
RPR1B_HUMAN	40	Regulation of nuclear pre-mRNA domain-containing protein 1B	217
ALBU_HUMAN	11	Serum albumin	213
APEX1_HUMAN	42	DNA-(apurinic or apyrimidinic site) lyase	186
AIMP1_HUMAN	33	Aminoacyl tRNA synthetase complex-interacting multifunctional protein 1	183
SSRA_HUMAN	11	Translocon-associated protein subunit alpha	1/5
	0	Perovisione multifunctional enzyme type 2	103
	34	Libiquitin this esterase OTLIP1	147
	20	Dolymerase delta-interacting protain 2	112
HMOX2 $HIMAN$	20	Heme ovugenase 2	116
NDUA9 HUMAN	28	NADH dehydrogenase [ubiquinone] 1 alpha sub-complex subunit 9 mitochondrial	112
KPYM HUMAN	74	Pyruvate kinase isozymes M1/M2	3356
TCPB HUMAN	56	T-complex protein 1 subunit beta	1898
PDIA1 HUMAN	64	Protein disulfide-isomerase	1621
G6PI_HUMAN	66	Glucose-6-phosphate isomerase	1614
TCPD_HUMAN	56	T-complex protein 1 subunit delta	1422
TCPQ_HUMAN	65	T-complex protein 1 subunit theta	1409
TCPH_HUMAN	49	T-complex protein 1 subunit eta	1276
G6PD_HUMAN	63	Glucose-6-phosphate 1-dehydrogenase	998
CH60_HUMAN	39	60-kDa heat shock protein, mitochondrial	966
TCPA_HUMAN	57	T-complex protein 1 subunit alpha	939
IMDH2_HUMAN	46	Inosine-5'-monophosphate dehydrogenase 2	869
AL1A3_HUMAN	46	Aldehyde dehydrogenase family 1 member A3	854
PTBP1_HUMAN	42	Poly-pyrimidine tract-binding protein 1	756
PDIA3_HUMAN	45	Protein disulfide-isomerase A3	686
FKBP4_HUMAN	61	FK506-binding protein 4	625
	50	Adenyiyi cyclase-associated protein 1	500
	20	D 3 phosphoglycorate debudrogopace	550
CPNE3 HUMAN	25 //1	Conine-3	544
NP1I 1 HUMAN	32	Nucleosome assembly protein 1-like 1	500
RCC2 HUMAN	40	Protein RCC2	491
TRXR1 HUMAN	29	Thioredoxin reductase 1. cvtoplasmic	478
TBA1B_HUMAN	40	Tubulin alpha-1B chain	381
SYYC_HUMAN	39	Tyrosyl-tRNA synthetase, cytoplasmic	350
PRS4_HUMAN	31	26S protease regulatory subunit 4	345
UGDH_HUMAN	29	UDP-glucose 6-dehydrogenase	312
NONO_HUMAN	30	Non-POU domain-containing octamer-binding protein O	290
HNRPK_HUMAN	15	Heterogeneous nuclear ribonucleoprotein K	277
COPD_HUMAN	29	Coatomer subunit delta	259

Supplemental Table 2. Continued

Entry name	Coverage, %	Description	Score
PACN2_HUMAN	15	Protein kinase C and casein kinase substrate in neurons protein 2	222
PAK2_HUMAN	20	Serine-threonine-protein kinase PAK 2	203
HSP71_HUMAN	66	Heat shock 70-kDa protein 1	2989
HSP7C_HUMAN	58	Heat shock cognate 71-kDa protein	2639
GRP75_HUMAN	50	Stress-70 protein, mitochondrial	1913
LKHA4_HUMAN	49	Leukotriene A-4 hydrolase	1002
LMNB1 HUMAN	50	Lamin-B1	691
SYRC HUMAN	31	Arginvl-tRNA synthetase, cytoplasmic	441
DDX5 HUMAN	29	Probable ATP-dependent RNA helicase DDX5	354
SYFB HUMAN	25	Phenvlalanvl-tRNA synthetase beta chain	327
ABCE1 HUMAN	30	ATP-binding cassette sub-family E member 1	304
CMC2 HUMAN	20	Calcium-binding mitochondrial carrier protein aralar2	265
FUBP1 HUMAN	23	Far upstream element-binding protein 1	260
TRI25 HUMAN	26	Tripartite motif-containing protein 25	239
RFA1 HUMAN	38	Replication protein A 70-kDa DNA-binding subunit	220
IF2B3 HUMAN	24	Insulin-like growth factor 2 mRNA-binding protein 3	209
TBA1A HUMAN	25	Tubulin alpha-1A chain	174
AMPB HUMAN	11	Aminopeptidase B	141
GRP78 HUMAN	59	78-kDa alucose-regulated protein	2917
MOES HUMAN	58	Moesin	1846
PABP1 HUMAN	44	Polvadenvlate-binding protein 1	1367
I MNA HUMAN	57	Lamin-A/C	1322
HSP7C HUMAN	37	Heat shock cognate 71-kDa protein	1320
CAN2 HUMAN	55	Calpain-2 catalytic subunit	1246
GLIAA HUMAN	62	GMP synthese (qlutamine-hydrolyzing)	982
SBC8 HUMAN	33	Src substrate cortactin	957
PDIA4 HUMAN	44	Protein disulfide-isomerase A4	824
TRAP1 HUMAN	28	Heat shock protein 75-kDa, mitochondrial	765
DDX3X HUMAN	31	ATP-dependent RNA helicase DDX3X	716
FCHA HUMAN	42	Trifunctional enzyme subunit aloba, mitochondrial	653
K6PI HUMAN	31	6-phosphofructokinase liver type	642
CAN1 HUMAN	38	Calpain-1 catalytic subunit	559
TTI 12 HUMAN	34	Tubulin-tyrosine ligase-like protein 12	558
ACSL3 HUMAN	25	Long-chain-fatty-acid_CoA ligase 3	530
SYG HUMAN	33	Glycyl-tRNA synthetase	466
SEPT9 HUMAN	32	Septin-9	445
KEYM HUMAN	34	Pyrijvate kinase isozymes M1/M2	442
	36	Lamina-associated polypentide 2 isoform alpha	386
	12	Serum albumin	363
HNRPM HIMAN	27	Heterogeneous nuclear ribonucleoprotein M	202
PVRG1 HUMAN	27	CTP synthase 1	232
	21	Glycerol-3-nhosnhate dehydrogenase, mitochondrial	200
	12	Vacualar protein sorting-associated protein 35	205
GEPT1 HUMAN	14	Glucosamine-fructose-6-phosphate aminotransferase (isomerizing) 1	220
	19	Cytoplasmic dynain 1 intermediate chain 2	220
SBD72 HIMAN	20	Signal recognition particle 72-kDa protein	217
	18	Dipentidul-pentidase 3	200
GLU2B HUMAN	23	Chucosidase 2 subunit beta	203
	12	Acul amino acid relaccing onzymo	107
	17	NADH ubiquipana avidaraduatasa 75 kDa subunit, mitashandrial	17/
	62	Hast shock protein 00 bote	2024
	03 71	Alpha actinin 1	3652
	50	Flongetion factor 2	202
	29	Endralosmin	2020
	59 59	Liuupiasiilii Transitional ondonlasmia ratioulum ATPasa	1461
	00	mananunai enuopiaaniio reliculum ATFase Importin cubunit bata 1	1401
	39 20	Importin suburiti beta-i Noutral alpha alugosidaso AR	993 075
	30	Incurar alpha-ylucosluase AD	٥/5 حتم
	29	Chargen phenohendene liver form	1/6
	33	Ciycogen phosphorylase, liver form	644 FF4
	29	Furomycin-sensitive antinopeptidase	551
SFPQ_HUMAN	21	Splicing lactor, proline- and glutamine-rich	530

Supplemental Table 2. Continued

Entry name	Coverage, %	Description	Score
PSMD2_HUMAN	33	26S proteasome non-ATPase regulatory subunit 2	463
SSRP1_HUMAN	24	FACT complex subunit SSRP1	395
MCM3_HUMAN	24	DNA replication licensing factor MCM3	394
4F2_HUMAN	22	4F2 cell-surface antigen heavy chain	307
MCM6_HUMAN	14	DNA replication licensing factor MCM6	307
GELS_HUMAN	22	Gelsolin	305
AP2B1_HUMAN	11	AP-2 complex subunit beta-1	304
PDC6I_HUMAN	12	Programmed cell death 6-interacting protein	295
COPB2_HUMAN	16	Coatomer subunit beta'	292
COPG_HUMAN	14	Coatomer subunit gamma	292
CTND1_HUMAN	16	Catenin delta-1	280
HGFR_HUMAN	8	Hepatocyte growth factor receptor (HGFR)	276
SYMC_HUMAN	10	Methionyl-tRNA synthetase, cytoplasmic	252
NIBL1_HUMAN	16	Niban-like protein 1	226
RIR1_HUMAN	24	Ribonucleoside-diphosphate reductase large subunit	216
CSDE1_HUMAN	16	Cold shock domain-containing protein E1	210
NSUN2_HUMAN	12	tRNA (cytosine-5-)-methyltransferase NSUN2	205
CAPR1_HUMAN	10	Caprin-1	202
SYQ_HUMAN	11	Glutaminyl-tRNA synthetase	155
CTNB1_HUMAN	15	Catenin beta-1	151
MOGS_HUMAN	6	Mannosyl-oligosaccharide glucosidase	143
C1TC_HUMAN	63	C-1-tetrahydrofolate synthase, cytoplasmic	2726
VINC HUMAN	56	Vinculin	2557
UBA1 HUMAN	39	Ubiguitin-like modifier-activating enzyme 1	1901
NUCL HUMAN	41	Nucleolin	1807
XPO2 HUMAN	39	Exportin-2	1335
MYO1B HUMAN	37	Mvosin-Ib	1298
CTNA1 HUMAN	49	Catenin alpha-1	1236
IPO5 HUMAN	35	Importin-5	1211
ACLY HUMAN	31	ATP-citrate synthase	944
HS105 HUMAN	39	Heat shock protein 105 kDa	928
PARP1 HUMAN	34	Polv(ADP-ribose) polvmerase 1	883
FF2 HUMAN	39	Flongation factor 2	781
PUR2 HUMAN	32	Trifunctional purine biosynthetic protein adenosine-3	753
ACTN1 HUMAN	38	Alpha-actinin-1	734
SND1 HUMAN	39	Staphylococcal nuclease domain-containing protein 1	726
HNRPU HUMAN	20	Heterogeneous nuclear ribonucleoprotein U	724
XPO1 HUMAN	29	Exportin-1	712
FIF3B HUMAN	33	Eukarvotic translation initiation factor 3 subunit B	638
IPO7 HUMAN	27	Importin-7	604
PSA HUMAN	28	Puromycin-sensitive aminopeptidase	576
TIF1B HUMAN	25	Transcription intermediary factor 1-beta	542
ENPL HUMAN	25	Endoplasmin	524
SYAC HUMAN	24	Alanyl-tBNA synthetase, cytoplasmic	464
KINH HUMAN	22	Kinesin-1 heavy chain	423
HS90B HUMAN	20	Heat shock protein 90-beta	419
PSMD1 HUMAN	18	26S proteasome non-ATPase regulatory subunit 1	380
NALP2 HUMAN	17	NACHT L BB and PYD domains containing protein 2	353
ITB1 HUMAN	19	Integrin beta-1	300
ICAL HUMAN	31	Calpastatin	289
4F2 HUMAN	14	4F2 cell-surface antigen heavy chain	279
HXK1 HUMAN	23	Hexokinase-1	269
FIF3C HUMAN	18	Fukarvotic translation initiation factor 3 subunit C	200
CAPR1 HIIMAN	12	Caprin-1	240
AP1B1 HIIMAN	15	AP-1 complex subunit beta-1	243
	20	116-kDa 115 small nuclear ribonucleoprotein component	240
SYIM HI MAN	11	Isoleucyl-tRNA synthetase mitochondrial	230
	24	Maior vault protein	214
	10	Endonlasmic reticulum aminopentidase 1	190
	68	Myosin-9	10//6
FAS HIMAN	50	Fatty acid synthese	12440
	52	ratty aola synthasis	4202

Supplemental Table 2. Continued

Entry name	Coverage, %	Description	Score
IQGA1 HUMAN	44	Ras GTPase-activating-like protein IQGAP1	2164
HGFR_HUMAN	38	Hepatocyte growth factor receptor (HGFR)	1479
MYOF_HUMAN	30	Myoferlin	1298
IF4G1_HUMAN	22	Eukaryotic translation initiation factor 4 gamma 1	943
FLNA_HUMAN	19	Filamin-A	900
PYR1_HUMAN	14	CAD protein	803
CLH1_HUMAN	10	Clathrin heavy chain 1	198
ALBU HUMAN	10	Serum albumin	198
ZO1_HUMAN	6	Tight junction protein ZO-1	177
UBIQ_HUMAN	56	Ubiquitin	170