Loss of Tuberous Sclerosis Complex 2 (TSC2) Is Frequent in Hepatocellular Carcinoma and Predicts Response to mTORC1 Inhibitor Everolimus

Hung Huynh¹, Huai-Xiang Hao², Stephen L. Chan³, David Chen⁴, Richard Ong¹, Khee Chee Soo¹, Panisa Pochanard², David Yang², David Ruddy², Manway Liu², Adnan Derti², Marissa N. Balak², Michael R. Palmer², Yan Wang², Benjamin H. Lee², Dalila Sellami¹, Andrew X. Zhu³, Robert Schlegel², and Alan Huang²

Abstract

Hepatocellular carcinoma (HCC) is the third leading cause of cancer deaths worldwide and hyperactivation of mTOR signaling plays a pivotal role in HCC tumorigenesis. Tuberous sclerosis complex (TSC), a heterodimer of TSC1 and TSC2, functions as a negative regulator of mTOR signaling. In the current study, we discovered that TSC2 loss-of-function is common in HCC. TSC2 loss was found in 4 of 8 HCC cell lines and 8 of 28 (28.6%) patient-derived HCC xenografts. TSC2 mutations and deletions are likely to be the underlying cause of TSC2 loss in HCC cell lines, xenografts, and primary tumors for most cases. We further demonstrated that TSC2-null HCC cell lines and xenografts had elevated mTOR signaling and, more importantly, were significantly more sensitive to RAD001/everolimus, an mTORC1 inhibitor. These preclinical findings led to the analysis of TSC2 status in HCC samples collected in the EVOLVE-1 clinical trial of everolimus using an optimized immunohistochemistry assay and identified 15 of 139 (10.8%) samples with low to undetectable levels of TSC2. Although the sample size is too small for formal statistical analysis, TSC2-null/low tumor patients who received everolimus tended to have longer overall survival than those who received placebo. Finally, we performed an epidemiology survey of more than 239 Asian HCC tumors and found the frequency of TSC2 loss to be approximately 20% in Asian HBV+ HCC. Taken together, our data strongly argue that TSC2 loss is a predictive biomarker for the response to everolimus in HCC patients. Mol Cancer Ther; 14(5); 1224–35. ©2015 AACR.

Introduction

Hepatocellular carcinoma (HCC) is the third leading cause of cancer-related deaths, accounting for 250,000 to one million deaths globally each year (1). The annual number of incidence and death of HCC are virtually identical, illustrating the high mortality rate of this aggressive disease. Because of the relative paucity of symptoms in the early stages and the rapid doubling time of the tumor, more than 80% of HCC are diagnosed at advanced stages when surgery is no longer an option (2). Two randomized trials of the multikinase inhibitor sorafenib in HCC patients showed an improvement in median overall survival of close to 3 months, establishing sorafenib as the only targeted therapy and the standard of care in advanced HCC (3, 4). However, the efficacy of sorafenib is transient and modest and there are no established predictive biomarkers for sorafenib. Thus, there is an urgent unmet need for more effective novel therapies to combat this deadly disease.

mTOR is a serine/threonine kinase that plays a critical role in regulating protein translation, cell-cycle progression, and cellular function (5, 6). Two well-characterized substrates of mTOR are S6K1 and 4E-BP1, and mTOR activity is regulated by the PI3K/AKT pathway. These preclinical findings led to the analysis of TSC2 status in HCC samples collected in the EVOLVE-1 clinical trial of everolimus using an optimized immunohistochemistry assay and identified 15 of 139 (10.8%) samples with low to undetectable levels of TSC2. Although the sample size is too small for formal statistical analysis, TSC2-null/low tumor patients who received everolimus tended to have longer overall survival than those who received placebo. Finally, we performed an epidemiology survey of more than 239 Asian HCC tumors and found the frequency of TSC2 loss to be approximately 20% in Asian HBV+ HCC. Taken together, our data strongly argue that TSC2 loss is a predictive biomarker for the response to everolimus in HCC patients.
studies using knockout mice showed that mTOR activation was sufficient to cause HCC in rodent models (14), indicating the pivotal role of mTOR signaling in HCC. The allelic mTORC1 inhibitor RAD001 (everolimus) has been tested in a randomized, placebo-controlled phase III clinical trial in patients with advanced HCC who failed sorafenib (EVOLVE-1; ref. 15). Overall survival (OS), the primary endpoint, showed nonsignificant improvement with everolimus treatment versus placebo. The molecular predictors for a small number of patients who benefited from the everolimus treatment are currently being explored.

The tuberous sclerosis complex (TSC) formed by TSC1 and TSC2 functions as a critical negative regulator of mTOR through the GAP (GTPase-activating protein) activity of TSC2 towards the small GTPase RHEB (16). Therefore, inactivation of either TSC1 or TSC2 gene disrupts the TSC1/TSC2 complex and results in unrestrained kinase activity of mTOR. Everolimus is an approved and effective drug for treating neurologic manifestations of TSC, a hereditary disorder caused by germline mutations in TSC1 or TSC2. Intuitively, TSC lesions in tumors might be potential predictive biomarkers for response to everolimus treatment. However, this link has not been rigorously examined, in part because the frequency of somatic mutations in TSC1/TSC2 in most types of tumors, including HCC, is quite low.

In this study, we observed frequent loss of TSC2 in HCC cell lines and demonstrated that TSC2-null cell lines were more sensitive to mTOR inhibition by everolimus. We then confirmed TSC2 loss in patient-derived HCC xenografts and observed remarkable antitumor efficacy of everolimus in TSC2-null xenografts. TSC2 mutations and deletions were identified in many of the TSC2-null HCC cell lines and xenografts, providing a genetic mechanism for TSC2 loss. We also developed a TSC2 immunohistochemical (IHC) assay for identifying TSC2 loss in primary tumor samples. Analysis of TSC2 status in EVOLVE-1 clinical samples suggested that TSC2-null/lower tumor patients who received everolimus tended to have longer OS than those who received placebo. On the basis of our TSC2 IHC profiling of 239 tumors, the frequency of TSC2 loss is estimated to be around 20% in Asian HBV+ HCC. Taken together, our data strongly suggest that TSC2 loss may be used as a predictive biomarker for everolimus efficacy in HCC clinical trials.

Materials and Methods

Antibodies and compounds

Rabbit antibodies against TSC1, TSC2, p-S6K1 (T389), S6K1, p-4E-BP1 (T37/46), p-4E-BP1 (T70), 4E-BP1, p-AKT(S473), AKT, p-CDK2(T14/T15), PTEF and p27 were purchased from Cell Signalling Technology. Tubulin antibody (mouse) was purchased from Sigma. RAD001 (everolimus), BKM120, MK-2206, and MEK162 were synthesized at Novartis. pcDNA3-Flag-TSC2 plasmid was a gift from Dr. Pablo Garcia (Novartis Institutes for Biomedical Research, Emeryville, CA). The TSC2 G305V mutant was generated using the Q5 site-directed mutagenesis kit (New England Biolabs) according to the manufacturer’s instructions. The sequences of mutagenic primers used are: forward, 5’-gccccggtcattccagagcgc-3’; reverse, 5’-gctgtctgggtgaccgccacgc-3’.

Cell culture

Hepatocellular carcinoma cell lines were part of the Novartis Cell line Encyclopedia (CCLE) collection (17) and were authenticated by single-nucleotide polymorphism (SNP) analysis in 2012.

Reverse phase protein array

Reverse phase protein array (RPPA) was performed at the RPPA Core Facility at MD Anderson Cancer Center (Houston, TX) according to standard procedures.

Immunoblotting

Total cell lysates were prepared by lysing cells using RIPA buffer (50 mmol/L Tris-HCl, pH 7.4, 150 mmol/L NaCl, 1% NP-40, 0.5% sodium deoxycholate, 0.1% SDS, 1 mmol/L EDTA) supplemented with protease inhibitors and phosphatase inhibitors, followed by centrifugation at 14,000 rpm for 10 minutes at 4°C. Equal amounts of protein were resolved by SDS-PAGE, transferred to nitrocellulose membranes, and incubated with primary antibodies overnight at 4°C. Secondary antibodies conjugated with either HRP or infrared dyes were used for signal visualization by ECL film method or an LI-COR Odyssey scanner, respectively.

Reverse transcription and TaqMan quantitative RT-PCR

Total RNA was extracted from cells using the RNeasy Plus Mini Kit (Qiagen) and reverse transcribed with TaqMan Reverse Transcription Reagents (Applied Biosystems) according to the manufacturers’ instructions. Transcript levels were assessed using the ABI PRISM 7900HT. Quantitative real-time PCR was performed in 12 μL reactions consisting of 0.6 μL of 20× TaqMan probe and PCR primer mix, 6 μL 2× TaqMan Universal PCR Master Mix, and 5.4 μL diluted cDNA template. The thermocycling conditions utilized were 2 minutes at 50°C, 10 minutes at 95°C, followed by 40 cycles of 15 seconds at 95°C and 1 minute at 60°C. All experiments were performed in quadruplicate. Gene expression analysis was performed using the comparative ΔΔCt method with the housekeeping gene, GUSB, for normalization. All TaqMan primers/probes were purchased from Applied Biosystems (TSC1, Hs01060648_m1; TSC2, Hs01020387_m1; GUSB, Hs99999908_m1; MZB1, Hs00414907_m1).

CellTiter Glo proliferation assay

Cells were seeded in 96-well plates and treated with different doses of everolimus (6 fold serial dilutions starting from 1 μmol/L) for 3 days. A CellTiter Glo assay was performed according to the manufacturers’ protocols. Everolimus dose–response curve and IC50 values were calculated using the XFit add-in in Excel.

Patient-derived HCC xenograft study

This study received ethics board approval at the SingHealth. All mice were maintained according to the Guide for the Care and Use of Laboratory Animals published by the NIH (Bethesda, MD).

The establishment of our collection of HCC patient-derived xenografts has been previously described (18) and the indicated xenograft lines were subcutaneously implanted into male SCID mice (Animal Resources Centre) aged 9 to 10 weeks. For antitumor efficacy experiments, mice bearing the indicated tumors (10 mice per group) were orally administrated with either vehicle (5% dextrose) or varying doses of everolimus (0.25, 0.5, 0.75 or 1.0 mg/kg) daily for indicated days. Treatment started when the tumors reached the size of approximately 170 to 600 mm3.

Published OnlineFirst February 27, 2015; DOI: 10.1158/1535-7163.MCT-14-0768
(dependent on the lines or experimental purpose). Tumor growth was monitored and tumor volume was calculated as described (18, 19). At the end of the study, mice were sacrificed with body and tumor weights recorded. The efficacy of everolimus was determined by T/C ratio, where T and C are the median weight of everolimus-treated and vehicle-treated tumors, respectively. T/C ratios less than 0.42 were considered active according to the widely adopted criteria from the Drug Evaluation Branch of the Division of Cancer Treatment, NCI (Bethesda, MD).

DNA sequencing and copy number analysis
HCC cell lines DNA sequencing and copy number analysis using SNP6.0 array has been previously described (17). Genomic DNA from HCC xenografts and primary tumors were sequenced using the T5 panel targeted sequencing at Foundation Medicine. Multiplex ligation-dependent probe amplification (MLPA) of TSC2 duplications and deletions was performed using TSC2 SALSA MLPA probemix P046-B2 (MRC-Holland) according to the manufacturer’s instructions and analyzed using GeneMarker software from SoftGenetics LLC.

TSC2 IHC assay
HCC cell lines and patient-derived xenografts were collected, fixed with formalin and processed for paraffin embedding. HCC tissue microarrays were purchased from BioChain (catalog # Z7020056 and Z7020057, unrelated HCC TMAs) and FolioBio (catalog# ARY-HH0225). Formalin-fixed, paraffin-embedded (FFPE) tissue sections (4µm thick) were stained on the Ventana Discovery XT automated staining platform. Standard antigen retrieval condition in cell conditioning 1 buffer was used, followed by incubation with rabbit anti-TSC2 antibody (Cell Signaling Technology, catalog # 4308) at a dilution of 1:200 for 32 minutes at 37°C. Signal was then visualized using Omni Map (OMap) anti-Rabbit HRP and DAB.

TSC2 expression was assessed semiquantitatively by a pathologist using a histo-score (H-score) methodology based on staining intensity and percentage of tumor cells expressing TSC2. Intensity was scored as 0 (none), 1 (weak), 2 (moderate), or 3 (strong). H-score was calculated as follows: H-score = [fraction of cells with intensity grade 1 (%) × 1] + [fraction of cells with intensity grade 2 (%) × 2] + [fraction of cells with intensity grade 3 (%) × 3].

Clinical study
The EVOLVE-1 (clinicaltrial.gov # NCT01035329) clinical trial design, patient inclusion, and exclusion criteria have been published (15). Briefly, 546 patients aged ≥18 years with BCLC stage B or C HCC whose disease progressed during or after sorafenib or who were intolerant to sorafenib were randomized 2:1 to everolimus 7.5 mg/day group or placebo group. Study drug was given continuously until disease progression or intolerable toxicity. CT/MRI scans were performed every 6 weeks and primary endpoint was OS.

The study protocol was reviewed and approved by the Independent Ethics Committee and the Institutional Review Board for each center. The study was conducted according to Good Clinical Practices and according to the ethical principles of the Declaration of Helsinki. Archival formalin-fixed, paraffin-embedded (FFPE) tissue sections were collected from patients who provided informed consent for biomarker study.

Statistical analysis
For xenograft growth curves, results are expressed as the means ± SEM from an appropriate number of replicates for each treatment group versus time as indicated in the figure legends. Paired Student t tests were used to calculate the P values. For immunobots, relevant phosphorylation signals were quantified by densitometry and showed in Supplementary Tables. Statistical significance was assessed using two-tailed Student t tests and described in the Table footnotes.

Results
TSC2 loss in hepatocellular carcinoma cell lines confers everolimus sensitivity
As part of a proteomic effort to comprehensively characterize Novartis’ cancer cell line collection known as the Cancer Cell Line Encyclopedia (CCLE; ref. 17), a RPPA platform was utilized to interrogate the expression levels or phosphorylation status of more than 200 cancer-related proteins in a panel of more than 400 cancer cell lines of various lineages. TSC2 protein levels showed a clear outlier pattern in HCC compared with all other lineages and very low expression was observed in five of the nine HCC cell lines (Fig. 1A). The low TSC2 signal in those five HCC cell lines was unlikely to be due to any quality issue of the cell lysate spotted onto the protein chip as the levels of other proteins in these cell lines were normal (Supplementary Fig. S1A). In addition, these TSC2 low HCC cell lines tended to have elevated mTOR signaling, as demonstrated by the trend of elevated phosphorylation of downstream targets S6K1 (T389), 4E-BP1 (T37/46), and S6(S240/S244; ref. 16). This observation is consistent with the role of TSC2 as a negative regulator of mTOR signaling.

We then performed immunobLOTS with eight of the nine HCC cell lines used in the RPPA analysis. TSC2 protein in SNU-886, SNU-878, SNU-398, and Li-7 cells were essentially nondetectable while TSC2-low status for HuH-6 could not be confirmed (Fig. 1B). Those four cell lines were therefore designated as TSC2-null while JHH-7, SNU-761, HuH-7, and HuH-6 were designated as TSC2 wild-type. All eight HCC cell lines had comparable levels of TSC1, the binding partner for TSC2. The phosphorylation of S6K1 (T389) and 4E-BP1 (T37/46) showed a trend of elevation in TSC2-null cell lines compared with the TSC2 wild-type group while the phosphorylation of AKT(S473) tended to be lower, with the exception of HuH-7 (Fig. 1B; Supplementary Table S1). A similar pattern on phosphorylation of S6K1, 4E-BP1, and AKT was observed in the RPPA data (Supplementary Fig. S1A). This is consistent with the previous observation that activation of mTOR and S6K1 caused by TSC2 lesions results in the feedback inhibition of the upstream insulin-like growth factor receptor 1 (IGF1R)/PI3K signaling pathway (20). As the level of S6K1 and 4E-BP1 phosphorylation in HuH-7 is comparable with that of the TSC2-null group, we hypothesized that it is due to activation of the PI3K pathway upstream of TSC1/2. Indeed, treatment of HuH-7 cells with the PI3K inhibitor BKM120 or AKT inhibitor MK-2206, but not the MEK inhibitor MEK162, reduced S6K1 phosphorylation (Supplementary Fig. S1B). No PI3KCA mutation or PTEN loss was found in HuH-7 cells (data not shown), suggesting that activation of mTOR in this cell line may be a result of upstream activation at the level of growth factor receptors such as IGF1R.

To investigate whether TSC2 loss rendered the HCC cell lines sensitive to mTOR inhibition, we studied the antiproliferation...
effect of everolimus on the eight HCC cell lines using a 3 Day CellTiter Glo (CTG) proliferation assay. While the everolimus IC50 values of three of the four TSC2 wild-type cell lines (except HuH-7) were more than 2,000 nmol/L, the IC50 values of the four TSC2-null cell lines ranged from 0.7 nmol/L to 25.1 nmol/L (Fig. 1C; Supplementary Table S2). The maximal growth inhibition by everolimus at 1 µmol/L was approximately 60% for the four TSC2-null cell lines but only about 35% for the three TSC2 wild-type cell lines except HuH-7 (Fig. 1C; Supplementary Table S2). TSC2 wild-type HuH-7 cells were as sensitive as TSC2-null cell lines to everolimus (IC50 = 1 nmol/L and maximal growth inhibition = 66%), possibly due to the activation of mTOR by upstream PI3K signaling (Supplementary Fig. S1B). Consistent with the IC50 values, we observed complete inhibition of S6K1 phosphorylation by 2.5 nmol/L everolimus in all four TSC2-null cell lines (Supplementary Fig. S1C). Taken together, TSC2 expression level is likely to be the main determinant for mTOR activity and everolimus sensitivity in those HCC cell lines. Although we cannot fully rule out other lesions contributing to everolimus sensitivity in the four TSC2-null cell lines, these results strongly suggest that TSC2 loss is a highly penetrant predictive biomarker for everolimus sensitivity in HCC cell lines.
TSC2 loss in patient-derived HCC xenografts predicts everolimus efficacy

We had previously established a large panel of patient-derived HCC xenografts for testing the efficacy of various antitumor agents (21, 22). To determine whether TSC2 loss also occurred in those HCC xenografts, we performed immunoblotting on lysates from 13 randomly selected patient-derived HCC xenograft tumors. As shown in Fig. 2A, four xenografts (HCC05-0411B, HCC19-1010, HCC14-0910, and HCC24-0309) showed no detectable levels of TSC2 and thus were named as TSC2-null xenografts. Consistent with the immunoblot data from cell lines, basal p-S6K1 (T389) was significantly increased in these four TSC2-null tumors (Fig. 2A; Supplementary Table S3). A trend of increased p-4E-BP1 (T70, functionally similar to phosphorylation at T37/T46 shown in HCC cells lines) levels was also observed in three of these four TSC2-null tumors compared with the TSC2 wild-type tumors (Fig. 2A; Supplementary Table S3). Again, p-AKT (S473) levels were relatively high in TSC2 wild-type tumors but significantly reduced in TSC2-null tumors, probably as a result of feedback inhibition of upstream IGF1R signaling by S6K activation. Because p-AKT levels are regulated by PTEN, we then examined the PTEN levels and found two models with PTEN loss (HCC26-1004 and HCC17-0211). Taken together, these data suggest that TSC2 loss may occur in HCC tumors and that mTOR signaling is activated in TSC2-null xenografts.

To determine whether TSC2-null HCC tumors display sensitivity to everolimus, we tested everolimus in the four TSC2-null xenografts along with four TSC2 wild-type xenograft (HCC06-0606, HCC25-0809, HCC13-0109, and HCC13-0212) as determined by TSC2 immunoblot in Fig. 2A. Tumor-bearing mice were treated daily with either vehicle or 1 mg/kg everolimus. Each treatment group involved 8 to 10 independent tumor-bearing mice representing the same xenograft line. It is of note that the dose of everolimus used in this study was approximately 2.5 to 5 times lower than doses used in our previous reports (22) and the toxicity associated with daily 1 mg/kg everolimus treatment was well tolerated. As shown in Fig. 2B, everolimus exhibited potent antitumor activities in all four TSC2-null xenografts and substantial tumor growth inhibition was observed as early as day 5 after dosing. The growth-inhibitory effects were particularly pronounced in TSC2-null xenograft HCC14-0910 and HCC05-0411B (T/C < 0.42, compared with controls) and the T/C ratios from the eight models shown in Fig. 2B were also calculated. Among the 20 xenografts we tested (Fig. 2C), everolimus was considered to be active in 8 (36.4%) xenograft lines, namely HCC05-0411B (T/C = 0.05), HCC01-0207 (T/C = 0.09), HCC14-0910 (T/C = 0.12), HCC19-1010 (T/C = 0.14), HCC25-0705A (T/C = 0.14), HCC24-0309 (T/C = 0.25), HCC24-1005 (T/C = 0.27), and HCC5-1318(3) (T/C = 0.34). Strikingly, all eight everolimus-sensitive models were TSC2-null. TSC2 wild-type models modestly responded to everolimus with T/C ratios ranging from 0.44 to 0.74, indicating the important role of mTOR signaling to HCC tumor growth even in the TSC2 wild-type setting. With 8 of 8 TSC2-null models and 0 of 12 TSC2 wild-type models as everolimus responders, this enrichment is statistically significant at P < 0.01 (Fisher exact test value = 8E-06). Interestingly, the two models with PTEN loss only showed modest responses to everolimus (T/C values ranging from 0.40 for HCC26-1004 and T/C = 0.61 for HCC17-0211), suggesting that PTEN loss may not be as good in predicting everolimus response in HCC models as TSC2 loss. This remarkable enrichment of TSC2-null models in everolimus responders from a relatively large study (20 models with distinct mutation profiles as shown in Supplementary Table S4) strongly argues that TSC2 loss in HCC leads to hyperactivation of the mTOR signaling pathway and robustly predicts everolimus response in xenograft models.

Tumor growth inhibition by everolimus was through inhibition of mTOR signaling

As shown in Fig. 2B, the growth-inhibitory effects were particularly pronounced in TSC2-null xenograft HCC14-0910 and HCC05-0411B at the dose of 1 mg/kg everolimus. To determine the degree and dose-dependent effect of everolimus, we tested its antitumor activity at the doses of 0.25, 0.5, 0.75, and 1 mg/kg in those two models. As shown in Fig. 3A, tumor stasis was achieved at 0.75 mg/kg everolimus and there was a dose-dependent growth inhibition by the four doses of everolimus in HCC14-0910. Similar results were observed in model HCC05-0411B (data not shown).

We then performed pharmacodynamic analysis by immunoblot at the end of the efficacy study. As shown in Fig. 3B, everolimus caused a dose-dependent decrease in p-S6K1 (T389) and p-4E-BP1 (T70), indicating successful mTOR inhibition in TSC2-null xenograft HCC14-0910. Similar to previous studies (22), everolimus treatment led to a dose-dependent elevation of p-AKT (S473), probably as a result of relieving the feedback inhibition of IGF1R by S6K1 activation. Everolimus treatment also significantly reduced the phosphorylation of CDK2 (T14/T15) and induced p27 accumulation, both of which are well-established markers of cell-cycle arrest. Our data are in agreement with previous studies showing that inhibition of mTOR leads to G1-S cell cycle arrest through increased levels of p27 (23). In addition, as in our previous study (22), the antiangiogenic effect of everolimus, measured by microvessel density, was also observed in HCC14-0910 and other TSC2-null HCC xenografts (data not shown).

TSC2 loss in HCC is caused predominantly by TSC2 deletions and mutations

To understand the molecular mechanism responsible for TSC2 loss in TSC2-null HCC cell lines, we examined the TSC2 mRNA levels by TaqMan RT-PCR assay. TSC2 mRNA levels in all four TSC2-null cell lines were less than 5% of that of JHH-7 cells, which
Figure 2.
TSC2 loss in patient-derived HCC xenografts predicts everolimus efficacy. A, levels of TSC2, p-S6K1(T389), p-4E-BP1(T70) and p-AKT(S473) in patient-derived HCC xenografts. Indicated HCC tumors were subcutaneously implanted in SCID mice. Tumors were collected when they reached 800–1,000 mm³ and processed for immunoblotting. Note that HCC05-0411B, HCC19-1010, HCC14-0910, and HCC24-0309 xenografts had undetectable levels of TSC2 protein and increased phosphorylation of mTOR substrate S6K1. B, effects of 1 mg/kg everolimus on growth rates of HCC xenografts. SCID mice bearing the indicated tumors were treated with vehicle or 1 mg/kg everolimus. Each treatment arm involved 8 to 10 independent tumor-bearing mice representing the same xenograft line. Mean tumor volume is shown and error bars represent SEM. The experiments were repeated at least twice with similar results. P values were calculated by paired Student t tests for the vehicle group versus the everolimus treatment group. *P<0.01 and P values of the last measurement are shown. Note that tumor stasis or regression was only observed in TSC2-null xenografts. C, bar graph showing endpoint HCC tumor weight T/C (treated vs. control) at 1 mg/kg everolimus dosing. SCID mice bearing indicated tumors were treated with vehicle or 1 mg/kg everolimus daily for 14–18 days. Each treatment arm involved 8 to 10 independent tumor-bearing mice representing the same xenograft line. Efficacy of everolimus was evaluated by comparing the final mean weight of tumors in the treated arms (T) to those in the control arm (C, T/C ratio). Note that the 8 best responders to everolimus were TSC2-null xenografts and this enrichment was statistically significant at P<0.01 (Fisher exact test value = 8E–06). *P<0.01, models with PTEN loss as determined by immunoblot in A.
result does not completely rule out the possibility of TSC2 (Supplementary Fig. S2B). Although suggestive, this negative
ylation abnormalities have been shown to be a common lesion and oral squamous cell carcinoma (24, 25), and DNA meth-
treatment of the DNA methylase inhibitor decitabine and/or TSC2 to observe a robust re-expression of
in HCC cell lines, including Li-7 (26). However, we were unable to observe a robust re-expression of TSC2 transcripts with treatment of the DNA methylase inhibitor decitabine and/or HDAC inhibitor trichostatin (TSA) while another known meth-

had the highest level of TSC2 mRNA (Supplementary Fig. S2A). The TSC2 mRNA levels in the other three TSC2 wild-type lines (SNU-761, HuH-7, and HuH-6) were approximately 50%, 57%, and 26% of that in JHH-7 cells, respectively. The mRNA levels of TSC1 were comparable in all cell lines. The extremely low levels of TSC2 mRNA in TSC2-null cell lines prompted us to examine the status of TSC2 gene in these cell lines. As shown in Table 1, SNU-886 and SNU-878 cells harbored TSC2 nonsense mutations (R1032X and S1514X, respectively) and TSC2 wild-type alleles were lost as indicated by the near 100% mutant allele frequency. SNU-398 cells contain a focal deletion in TSC2 from exon 9 to exon 36. No mutation or deletion in TSC2 was detected in Li-7 cells, raising the possibility that the absence of TSC2 mRNA in this cell line may be due to epigenetic silencing of TSC2. The TSC2 promoter has been found to be methylated in several cancer types, including breast cancer and oral squamous cell carcinoma (24, 25), and DNA methylation abnormalities have been shown to be a common lesion in HCC cell lines, including Li-7 (26). However, we were unable to observe a robust re-expression of TSC2 transcripts with treatment of the DNA methylase inhibitor decitabine and/or HDAC inhibitor trichostatin (TSA) while another known methylated gene MZB1 was successfully induced by those treatments (Supplementary Fig. S2B). Although suggestive, this negative result does not completely rule out the possibility of TSC2 epigenetic silencing in Li-7 cells. To determine whether TSC2 mutations and deletions are similarly responsible for TSC2 loss in HCC xenografts as in HCC cell lines, we analyzed the exons of both TSC1 and TSC2 (together with 294 other cancer-related genes) using next-generation sequencing. As shown in Table 1, among the eight TSC2-null HCC models we previously identified, TSC2 deletions were found in model HCC19-1010 and model HCC24-1005. In addition, a TSC2 splicing mutation c.1444-2A>T was found in model HCC14-0910 at 100% allele frequency and model HCC24-0309 contained a G305V missense mutation at 99% allele frequency. The impacted glycine residue resides within the TSC1 binding domain of TSC2 (amino acid 1–418) and is highly conserved from mouse to man. To test the functional consequence of the G305V mutation, we expressed the TSC2 G305V mutant by transient transfection of HEK293T cells and evaluated its relative expression at both the mRNA level and the protein level. As shown in Supplementary Fig. S2C, the mRNA level of G305V mutant was only about 30% that of wild-type TSC2 mRNA when equal amount of plasmids were transfected, suggesting that the missense mutation may cause reduced mRNA expression. Importantly, there was no detectable G305V-mutant TSC2 protein by immunoblot regardless of its mRNA levels (Supplementary Fig. S2D), suggesting that the G305V mutant protein is unstable. For the four TSC2-null xenografts in which no TSC2 genetic lesions were identified by sequencing, we performed TSC2 multiplex ligation-dependent probe amplification (MLPA). This PCR-based assay measures the copy number of each exon of the TSC2 gene and its neighboring regions and provides a better resolution of TSC2 copy number than the broad sequencing method. Indeed, loss of two upstream regions that possibly contain the TSC2 promoter and duplication of exon 16–23 were identified in HCC5-1318(3) and HCC05-0411B, respectively (Table 1). Exon duplication of TSC2 has been found in TSC patients and the duplicated exons may disrupt the reading frame of TSC2. All together, we have identified genetic mechanisms for TSC2 loss in 6 of the 8 TSC2-null models shown in Fig. 2C. It is known that a xenograft tumor may undergo genetic drift when compared with the original tumor and that certain genetic lesions may be enriched for during the model establishment and passaging process. To validate that TSC2 genetic lesions exist in primary HCC tumors, we sequenced DNA samples from 13 randomly selected Hong Kong HCC biopsies using the same T5
Frequent TSC2 Loss in HCC and Everolimus Response

Table 1. TSC2 deletions and mutations identified in TSC2-null HCC cell lines, xenografts, and primary tumors

<table>
<thead>
<tr>
<th>Sample name</th>
<th>Sample type</th>
<th>TSC2 mutation</th>
<th>Allele frequency</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>SNU-886</td>
<td>Cell line</td>
<td>p.R1012X</td>
<td>97%</td>
<td></td>
</tr>
<tr>
<td>SNU-878</td>
<td>Cell line</td>
<td>p.S1514X</td>
<td>100%</td>
<td></td>
</tr>
<tr>
<td>SNU-398</td>
<td>Cell line</td>
<td>Deletion</td>
<td>—</td>
<td></td>
</tr>
<tr>
<td>HCC14-0910</td>
<td>Xenograft</td>
<td>Splicing</td>
<td>100%</td>
<td>c.1444-2A&gt;G, psplice</td>
</tr>
<tr>
<td>HCC19-1010</td>
<td>Xenograft</td>
<td>Deletion</td>
<td>—</td>
<td></td>
</tr>
<tr>
<td>HCC24-0309</td>
<td>Xenograft</td>
<td>p.G305V</td>
<td>99%</td>
<td>Within TSC2 binding domain</td>
</tr>
<tr>
<td>HCC24-1005</td>
<td>Xenograft</td>
<td>Deletion</td>
<td>—</td>
<td>28 exons deleted</td>
</tr>
<tr>
<td>HCC5-1318(3)</td>
<td>Xenograft</td>
<td>p.S211Y</td>
<td>19</td>
<td>2 upstream exon deleted (MLPA)</td>
</tr>
<tr>
<td>HCC05-0411B</td>
<td>Xenograft</td>
<td>Deletion</td>
<td>—</td>
<td>Exon 16-23 duplication (MLPA)</td>
</tr>
<tr>
<td>B253</td>
<td>Tumor</td>
<td>Splicing</td>
<td>54%</td>
<td>c.1443-15del, p.splice</td>
</tr>
<tr>
<td>B266</td>
<td>Tumor</td>
<td>Deletion</td>
<td>—</td>
<td>Exons 41 of 41 deleted</td>
</tr>
<tr>
<td>B277</td>
<td>Tumor</td>
<td>p.A1141T</td>
<td>92%</td>
<td>Reported in TSC patients</td>
</tr>
</tbody>
</table>

NOTE: TSC2 mutations and deletions in HCC cell lines from South Korea were identified by targeted sequencing of about 2,000 genes and SNP6.0 array copy number analysis, respectively. TSC2 mutations and deletions in most Singapore HCC xenografts and in all Hong Kong primary HCC tumors were identified by targeted DNA sequencing at Foundation Medicine, Inc. TSC2 deletions in HCC5-1318(3) and HCC05-0411B were identified by Multiplex Ligation-dependent Probe Amplification (MLPA; noted in the table). Mutant vs. wild-type allele frequencies are provided for TSC2 mutations.

Panel at Foundation Medicine. As shown in Table 1, a TSC2 splicing mutation and a TSC2 deletion were identified in sample B253 and B266, respectively. Sample B277 contained a point mutation at 92% allele frequency resulting in an A1141T amino acid change. This mutation was also found in Taiwanese TSC patients (27) and therefore it likely inactivates TSC2. In addition, the majority of disease-associated mutations of TSC2 result in a substantial decrease in the TSC2 protein level (28, 29). In summary, TSC2 mutations and deletions exist in primary HCC tumors.

TSC2 immunohistochemistry assay identified TSC2 loss in primary HCC tumors

As not all TSC2-null cell lines and xenografts had mutations or deletions in the TSC2 gene, it raised the possibility that nongenetic mechanisms such as epigenetic silencing may be responsible for TSC2 loss in HCC. It might also be challenging to predict the functional consequence of TSC2 missense mutations as in the case of the G305V mutation we identified. Furthermore, for tumor suppressor genes like TSC2, loss of heterozygosity or extremely high mutant allele frequency is needed to predict loss-of-function at the protein level. To overcome these limitations of the sequencing approach, we developed a TSC2 IHC assay to identify TSC2 loss in HCC tumors. We first validated the IHC assay using TSC2 wild-type and TSC2-null HCC cell lines. As shown in Supplementary Fig. S3A, intense staining was observed in TSC2 wild-type HuH-6 cells and little signal was detected in TSC2-null SNU-398 cells, suggesting that the assay is robust and specific. We further validated the IHC assay using patient-derived HCC xenografts, which are more heterogeneous than the cell lines. Again, there was strong staining in TSC2 wild-type xenograft HCC06-0606 but very faint staining in TSC2-null xenograft HCC24-1005 (Supplementary Fig. S3B).

We then used the TSC2 IHC assay to address whether TSC2 loss in our xenograft models occurred in primary tumors or was acquired during propagation in the mice. As shown in Supplementary Fig. S3C, TSC2 was not detected in the four primary HCC tumors from which the TSC2-null xenografts HCC05-0411B, HCC19-1010, HCC14-0910, and HCC24-0309 were derived. The TSC2 staining in primary HCC sections was from adjacent normal liver tissues and served as positive controls. These data strongly argue that the TSC2 loss observed in our HCC xenografts was a faithful representation of the primary tumors from which they were derived and that our IHC assay could robustly identify TSC2 loss in HCC clinical samples.

HCC patients with TSC2-null/low tumors benefited from everolimus treatment

EVOLVE-1 was a double-blind, randomized, placebo controlled (2:1 everolimus vs. placebo), multicenter phase III study to evaluate the efficacy and safety of everolimus in adult patients with advanced HCC who had progressed on or after sorafenib treatment, or were intolerant of sorafenib treatment. The trial did not meet its primary endpoint of improving OS by everolimus over placebo. The median OS for the everolimus group and placebo group were 7.56 months and 7.33 months, respectively (HR: 1.05; 95% CI: 0.86-1.27; P = 0.675; ref. 15). To test whether patients with no or low TSC2 expression in their tumors had an OS benefit from everolimus treatment, we quantified TSC2 expression in tumor samples from the EVOLVE-1 patients using our IHC assay and an H-score scoring system as described in the Materials and Methods. Evaluable TSC2 IHC results were obtained for 139 EVOLVE-1 patients for whose archival formalin-fixed paraffin-embedded tumor samples were available. We defined 15 tumors with H-scores ranging from 0 to 120 (Table 2) as TSC2-null/low. The 120 H-score cutoff was partially guided by the H-scores of TSC2-null patient-derived HCC xenografts (ranging from 0 to 135, data not shown). These included 8 samples (5.8%) with minimal TSC2 expression (H-score = 0-60) and 7 samples (5.0%) with low TSC2 expression (H-score = 61–120). The seven TSC2-low samples had only some or universal weak staining (1+). Two tumors with H-score of 90 and 120, respectively, but had substantial (40%) 2+ or even some 3+ intensity staining were annotated as TSC2 wild-type.

The treatment assignment, overall survival (OS), and demographic features of the 15 patients with TSC2-null/low tumors are listed in Table 2. The patients treated with everolimus (n = 10) had longer OS than those treated with placebo (n = 5). Six of the 10 TSC2-null/low patients treated with everolimus (patient 10–15) had OS ranging from 9.53 to more than 32.72 months, compared with the 7.56 months median OS of the overall everolimus group.

To test whether patients with very short OS (patient 6 and patient 7) were on treatment for only 2 weeks and discontinued from the study due to either complications of the underlying cirrhosis or intolerable adverse events. Another patient with a short survival of 4.63 months (patient 8) only received treatment for 6 weeks and discontinued due to disease progression. In contrast, 4 of the 5 TSC2-null/low patients treated with placebo had OS ranging from 1.25 to 5.59 months, much shorter than the 7.33 months median OS of the overall placebo group. These findings may suggest an...
TSC2 loss is more common in Asian HBV+ HCC than in Caucasian HCC

The frequency of TSC2 loss in EVOLVE-1 samples (5.8%–10.8%, Fig. 4A) is much lower than that in Singapore HCC patient-derived xenografts (28.6%, 28 models) and in Hong Kong primary HCC (23.1%, 13 tumors). This is likely due to the heterogeneity of the ethnic makeup of the EVOLVE-1 patients (55% Caucasian, 35% Asian, and 10% others). While the overall profile of the 139 patients with TSC2 IHC results reflected this ethnic diversity, the percentage of Asian in the 15 TSC2-null/low tumor patients increased to 53% (Supplementary Fig. S4A). This raised the possibility that the prevalence of TSC2 loss may vary by ethnicity. To investigate this, we segmented the TSC2 H-scores into three groups: 0–60 (likely to be TSC2-null), 61–120 (TSC2-low), and 121–300 (TSC2 wild-type), and compared the H-score distribution of each race in the 139 EVOLVE-1 samples. As shown in Fig. 4A, the percentage of TSC2-null/low in the 48 Asian HCC samples is 18.7%, about 3 times that of the 78 Caucasian HCC tumors (6.4%). There were only 13 tumors in the group of other ethnicity, which was too few for a meaningful frequency estimate. The racial composition in each of the three TSC2 H-score segments is shown in Supplementary Fig. S4B and the ratio of Asian to Caucasian increased significantly from the high to the low H-score segments. Taken together, these epidemiology data suggest that TSC2 loss in HCC is more common in Asian than in Caucasian population.

To obtain a more accurate frequency of TSC2 loss in the Asian HCC population, we analyzed additional 322 Asian HCC tumors of which greater than 90% were HBV+ in the tumor microarray (TMA) format. The H-score range distribution in 239 evaluable cases is shown in Fig. 4B. There were 20.0% samples with an H-score below 60 and 19.7% samples had an H-score from 61 to 120, indicating minimal to low TSC2 expression. Therefore, we estimated TSC2 loss to be at least 20% in Asian HBV+ HCC. Consistent with the HBV association, seven of the eight EVOLVE-1 TSC2-null/low Asian HCC tumors were HBV+ (Table 2).

### Discussion

One major factor limiting the effective treatment of HCC is the high degree of tumor heterogeneity. The same treatment can produce remarkably different responses ranging from complete response to disease progression in patients with indistinguishable tumors at the histopathologic level (31). Understanding the molecular factors that may predict patient benefits derived from novel targeted therapies will be crucial for the successful development of HCC treatments. Despite the high frequency of mTOR activation in HCC, the EVOLVE-1 phase III trial showed essentially no OS benefit by everolimus in unselected HCC patients (15). The fact that mTOR inhibition was not sufficient to suppress tumor growth in many HCC patients suggests that mTOR dependence cannot solely be predicted by general mTOR activation. Rather, specific lesions in mTOR pathway components such as PTEN or TSC1/TSC2 are more likely to be useful in identifying HCC patients who will most likely benefit from mTORC1 inhibitors. In the current study, we demonstrated the remarkable prediction of antigrowth effect of everolimus by TSC2 loss in both HCC cell lines and patient-derived xenografts. More importantly, the analysis of a subset of EVOLVE-1 patients suggests that those with TSC2-null/low tumors indeed benefited from everolimus treatment. These clinical data extended our preclinical correlations to human and support the utility of TSC2 loss as a HCC patient selection biomarker for mTORC1 inhibitors, as illustrated in Supplementary Fig. S5.

The molecular mechanisms responsible for TSC2 loss in HCC are likely diverse. The TSC2 deletions and mutations we identified in HCC cell lines, xenografts and primary tumors provided genetic explanations for the majority of TSC2 loss we observed. However, TSC2-null HCC cell line Li-7 and TSC2-null xenografts (HCC25-0705A and HCC01-0207) do not harbor any genetic lesions in TSC2 gene, suggesting the existence of nongenetic mechanisms of TSC2 loss in those HCC samples. It has been reported that promoter methylation was responsible for silencing of TSC2 gene in other cancer types (24, 25). In addition, posttranslational mechanisms such as phosphorylation and acetylation could lead

Table 2. Patient profile, treatment arm and survival outcome of 15 EVOLVE-1 trial HCC patients with TSC2-null/low tumors by IHC

<table>
<thead>
<tr>
<th>Patient ID</th>
<th>TSC2 IHC H-score</th>
<th>Randomized treatment</th>
<th>OS (months)</th>
<th>Race</th>
<th>Gender</th>
<th>HBV</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>60</td>
<td>Placebo</td>
<td>1.25</td>
<td>Asian</td>
<td>M</td>
<td>+</td>
</tr>
<tr>
<td>2</td>
<td>100</td>
<td>Placebo</td>
<td>1.35</td>
<td>Caucasian</td>
<td>M</td>
<td>-</td>
</tr>
<tr>
<td>3</td>
<td>120</td>
<td>Placebo</td>
<td>3.61</td>
<td>Other</td>
<td>M</td>
<td>N.A.</td>
</tr>
<tr>
<td>4</td>
<td>120</td>
<td>Placebo</td>
<td>5.59</td>
<td>Asian</td>
<td>M</td>
<td>+</td>
</tr>
<tr>
<td>5</td>
<td>90</td>
<td>Placebo</td>
<td>18.23</td>
<td>Asian</td>
<td>M</td>
<td>+</td>
</tr>
<tr>
<td>6</td>
<td>50</td>
<td>Everolimus</td>
<td>0.76</td>
<td>Other</td>
<td>M</td>
<td>-</td>
</tr>
<tr>
<td>7</td>
<td>50</td>
<td>Everolimus</td>
<td>2.27</td>
<td>Other</td>
<td>M</td>
<td>-</td>
</tr>
<tr>
<td>8</td>
<td>40</td>
<td>Everolimus</td>
<td>4.63</td>
<td>Asian</td>
<td>M</td>
<td>+</td>
</tr>
<tr>
<td>9</td>
<td>110</td>
<td>Everolimus</td>
<td>5.85</td>
<td>Asian</td>
<td>M</td>
<td>+</td>
</tr>
<tr>
<td>10</td>
<td>100</td>
<td>Everolimus</td>
<td>9.53</td>
<td>Caucasian</td>
<td>F</td>
<td>-</td>
</tr>
<tr>
<td>11</td>
<td>10</td>
<td>Everolimus</td>
<td>9.56</td>
<td>Asian</td>
<td>M</td>
<td>+</td>
</tr>
<tr>
<td>12</td>
<td>0</td>
<td>Everolimus</td>
<td>18.96</td>
<td>Caucasian</td>
<td>M</td>
<td>-</td>
</tr>
<tr>
<td>13</td>
<td>40</td>
<td>Everolimus</td>
<td>25.00</td>
<td>Asian</td>
<td>M</td>
<td>+</td>
</tr>
<tr>
<td>14</td>
<td>0</td>
<td>Everolimus</td>
<td>28.02</td>
<td>Asian</td>
<td>M</td>
<td>-</td>
</tr>
<tr>
<td>15</td>
<td>100</td>
<td>Everolimus</td>
<td>52.72</td>
<td>Caucasian</td>
<td>M</td>
<td>-</td>
</tr>
</tbody>
</table>

NOTE: TSC2 status in the tumors was determined by TSC2 IHC performed at PhenoPath Laboratories. Note that patient 6, 7, and 8 were only treated with everolimus for 2–6 weeks due to various reasons described in the article.
TSC2 protein degradation. Although no TSC1 inactivation can lead to TSC2 loss, TSC2 can be phosphorylated by AKT, ERK, AMPK, and GSK3β at distinct sites and these phosphorylation events inactivate TSC2 (16). Both AKT- and ERK-dependent phosphorylation of TSC2 have been shown to disrupt its interaction with TSC1 and destabilize TSC2 (32, 33). Recently, arrest defective protein 1 (ARD1) was shown to acetylate and stabilize TSC2 and loss of heterozygosity (LOH) of ARD1 has been observed in breast, lung, pancreatic, and ovarian cancer samples (34). It is also noteworthy to point out that TSC1 inactivation can lead to TSC2 protein degradation. Although no TSC1 mutations were identified in any of our HCC samples, a TSC1 mutation has been identified by high-resolution characterization of one hepatocellular carcinoma genome (35). The exact mechanisms of nonepigenetic loss of TSC2 in HCC remain to be determined.

In agreement with our findings, mutations in TSC1/2 as putative biomarkers that predict efficacy of mTORC1 inhibitors have emerged recently from whole-genome or exome sequencing analyses of tumor samples from patients who had experienced extraordinary benefit from mTORC1 inhibitor treatments. Solit and colleagues showed that TSC1 loss-of-function mutations were present in one metastatic bladder cancer patient with a durable (>2 years) complete response and four with partial response or stable disease after receiving everolimus, but in only 1 of 9 patients with disease progression (36). Similarly, Voss and colleagues found inactivating mutations in TSC1 or TSC2, or activating mutations in MTOR, in 4 of 6 renal cell carcinoma patients who had durable response to either everolimus or temsirolimus, but not in patients who progressed rapidly on the same treatments (37). Recently, TSC2 (Q1178X) loss-of-function mutation was identified in one thyroid cancer patient who achieved a complete response that lasted for 18 months when treated with everolimus (38). Despite lacking placebo arms for comparison in those studies, the remarkable clinical efficacy of mTORC1 inhibitors in distinct types of TSC1/TSC2-mutated tumors (bladder, kidney, thyroid, and liver cancer) suggests a strong correlation between TSC1/TSC2 loss-of-function and clinical efficacy of mTORC1 inhibitors such as everolimus. This link is consistent with the preclinical observation that the loss of TSC complex gave rise to high levels of constitutive mTOR activation and is not surprising given the large number of signaling inputs regulating mTOR through the TSC1/TSC2 complex (16). Interestingly, the prevalence of mutations in TSC1 versus TSC2 seems to vary among tumor types.

In this study, we also developed a TSC2 IHC assay to be used with primary HCC samples in the clinic. The IHC approach is superior to the sequencing assay for the cases of missense TSC2 mutations with unknown functional consequences and it can also capture TSC2 loss by all types of mechanisms. However, as for all IHC assays, it was challenging to define the H-score cutoff for TSC2-null or low need to be better determined by...
correlating with TSC2 mutations, TSC2 levels in immunoblot and more importantly, everolimus clinical response in more patients. In this study, we identified 15 TSC2-null/low tumors from 139 EVOLVE-1 samples. By analyzing the patient ethnicity of those samples, we found that TSC2 loss is more common in Asian than in Caucasian HCC. The cause of such ethnic difference in TSC2 loss is unknown but may be related to the distinct etiologies of Caucasian HCC (HCV and alcohol) and Asian HCC (HBV). Additional epidemiology studies in non-Asian populations using our IHC assay are warranted and may better inform the broad utility of TSC2 loss as a patient selection biomarker in HCC.

TSC2 mutations were not reported in recent next-generation sequencing studies of HCC (39–42) and there is only one report finding a TSC1 mutation in HCC (35). The different patient ethnicity (Caucasian HCC) and HCC etiology (HCV for Japan HCC) in those studies may account for the differences between those and our results. In fact, the HCC mutation spectrums in those papers significantly differed from each other. For those studies with Asian HBV+ HCC samples, only a small discovery set was subjected to whole-genome or -exome sequencing and TSC2 mutations may not be represented in their initial discovery set. Finally, the targeted exon sequencing assay used in our study is more sensitive than the whole-genome or -exome sequencing method for a particular gene. The sequencing depth at TSC2 locus in our assay (median exon coverage ranging from 496 to 1043) is much higher than that expected from the whole-genome or -exome sequencing. Previously, the challenge of using TSC1/TSC2 lesions as patient selection biomarkers was that somatic TSC1/2 mutations in cancer are generally rare. TSC1/2 mutations are estimated to be less than 2% in several major cancer types, including kidney cancer, based on TCGA (The Cancer Genome Atlas) studies and other large-scale deep sequencing efforts (36, 43). Only recently, bladder cancer was found to have a high frequency of PI3K–mTOR pathway alterations with approximately 8% TSC1 mutations and approximately 2% TSC2 mutations (44). Identifying tumor types with reasonable frequency of TSC1/2 mutations will enable TSC status to be used as a biomarker in the clinic for practical reasons. On the basis of our TSC2 IHC survey of 239 Asian HCC tumors, the frequency of TSC2 loss is estimated to be around 20% in Asian HBV+ HCC. China alone accounts for more than 80% of HCC cases in China are HBV+. Therefore, Asian HBV+ HCC represents nearly half of the total cases of HCC worldwide. This epidemiology data strongly support TSC2 loss as a potential patient selection biomarker for Asian HBV+ HCC likely to benefit from everolimus therapy and further exploration of the prognostic value of TSC2 loss.

If the high frequency of TSC2 loss can be confirmed and its prognostic significance can be established in larger and more diverse Asian HCC populations, an everolimus clinical trial focused on the Asian patients will be justified and we recommend TSC2 loss defined by IHC as the patient enrollment criterion. Like other predictive biomarkers, it will always be certain that not all TSC2-null tumors will respond to everolimus treatment. It will be important to examine the additional genetic lesions or clinical features of TSC2-null tumors to enhance the predicting specificity of this biomarker and to enable drug combinations with everolimus to achieve better antitumor efficacy, such as PI3K inhibitors as suggested by a previous report (46). In addition, TSC lesion is unlikely to explain all cases of everolimus response in HCC patients and other predictive biomarkers for everolimus responders, such as activating mutations in MTOR or RHEB, remain to be identified.

Disclosure of Potential Conflicts of Interest
S.L. Chan is a consultant/advisory board member for Novartis. D. Sellami has ownership interest in Novartis stocks. R. Schlegel and A. Huang have ownership interest in the Novartis Institutes for BioMedical Research stocks. No potential conflicts of interest were disclosed by the other authors.

Authors’ Contributions

Acknowledgments
The authors thank Jingsheng Liang, Xiaoyan Li, Yan Chen, and Angela Tam for technical assistance. The authors also thank Hui-Qin Wang, Fang Li, Qing Sheng, Ensar Halilovic, John Monahan, and Joseph Lehar for advice and helpful discussions.

Grant Support
This work was supported by Novartis Pharmaceutical Company to both Novartis authors and authors from other institutions. The costs of publication of this article were defrayed in part by the payment of page charges. This article must therefore be hereby marked advertisement in accordance with 18 U.S.C. Section 1734 solely to indicate this fact.

Received October 27, 2014; revised February 4, 2015; accepted February 17, 2015; published OnlineFirst February 27, 2015.

References
Molecular Cancer Therapeutics

Loss of Tuberous Sclerosis Complex 2 (TSC2) Is Frequent in Hepatocellular Carcinoma and Predicts Response to mTORC1 Inhibitor Everolimus

Hung Huynh, Huai-Xiang Hao, Stephen L. Chan, et al.

Mol Cancer Ther 2015;14:1224-1235. Published OnlineFirst February 27, 2015.