

Rational Combination of a MEK Inhibitor, Selumetinib, and the Wnt/Calcium Pathway Modulator, Cyclosporin A, in Preclinical Models of Colorectal Cancer

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Abstract

Purpose: The mitogen-activated protein kinase (MAPK) pathway is a crucial regulator of cell proliferation, survival, and resistance to apoptosis. MEK inhibitors are being explored as a treatment option for patients with KRAS-mutant colorectal cancer who are not candidates for EGFR-directed therapies. Initial clinical results of MEK inhibitors have yielded limited single-agent activity in colorectal cancer, indicating that rational combination strategies are needed.

Experimental Design: In this study, we conducted unbiased gene set enrichment analysis and synthetic lethality screens with selumetinib, which identified the noncanonical Wnt/Ca⁺⁺ signaling pathway as a potential mediator of resistance to the MEK1/2 inhibitor selumetinib. To test this, we used shRNA constructs against relevant WNT receptors and ligands resulting in increased responsiveness to selumetinib in colorectal cancer cell lines. Further, we evaluated the rational combination of selumetinib and WNT pathway modulators and showed synergistic antiproliferative effects in *in vitro* and *in vivo* models of colorectal cancer.

Results: Importantly, this combination not only showed tumor growth inhibition but also tumor regression in the more clinically relevant patient-derived tumor explant (PDTX) models of colorectal cancer. In mechanistic studies, we observed a trend toward increased markers of apoptosis in response to the combination of MEK and WntCa⁺⁺ inhibitors, which may explain the observed synergistic antitumor effects.

Conclusions: These results strengthen the hypothesis that targeting both the MEK and Wnt pathways may be a clinically effective rational combination strategy for patients with metastatic colorectal cancer. *Clin Cancer Res*; 19(15); 4149–62. ©2013 AACR.

Introduction

Activating mutations in the *KRAS* proto-oncogene are present in up to 40% to 50% of colorectal cancer patient

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Note: Supplementary data for this article are available at Clinical Cancer Research Online (<http://clincancerres.aacrjournals.org/>).

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doi: 10.1158/1078-0432.CCR-12-3140

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tumors, whereas another 10% are reported to have BRAF V600E mutations (1–3). Retrospective clinical studies have confirmed the lack of benefit of epidermal growth factor receptor (EGFR)-directed therapy in patients with KRAS mutations, limiting treatment options to standard chemotherapeutics with or without VEGF pathway-targeted agents (4–8). This creates an urgent need to test new targeted agents such as inhibitors of the MAPK/MEK/ERK pathway. MEK is central to the pathogenesis of colorectal cancer as a downstream effector of mutant KRAS as well as in mediating effects of cell surface receptors such as the EGFR and IGF-1R (9–11). Despite the entry of MEK inhibitors into Phase I and II trials, single-agent activity has been limited in colorectal cancer, suggesting that targeting resistance pathways through rational combination strategies may lead to greater efficacy (12–15). Previous studies in our laboratory (16) have identified the Wnt signaling pathway as a resistance mechanism to selumetinib, a selective inhibitor of MEK1/2 (AZD6244; ARRAY-142886; AstraZeneca, Inc), that has been investigated as monotherapy and is currently in the

Translational Relevance

There is an urgent need for the development of novel, individualized therapies for patients with advanced treatment-refractory colorectal cancer to advance progress in the treatment of this disease. The recent development of genome-wide screening approaches and integrative bioinformatics methods has accelerated the discovery of clinically relevant pathway interactions and mechanisms of drug resistance in numerous cancer types. In this study, we used two powerful and complementary molecular genetic approaches, gene set enrichment analysis and synthetic lethality screens, to identify potential resistance mechanisms to the MEK inhibitor, selumetinib which yielded a dual targeting strategy of the Wnt/Ca²⁺ pathway and MEK, resulting in robust anti-tumor activity and tumor regression in preclinical models of colorectal cancer. These findings strongly support further clinical studies to test the efficacy of the combination of MEK and Wnt inhibitors in patients with

clinic evaluating efficacy in combination with chemotherapy for several cancer types (12, 14, 17–20). The wingless/integrated (Wnt) signaling pathway has been described as canonical or noncanonical based on β -catenin dependence (21). The canonical pathway signals via the frizzled (FZD) family of G-protein-coupled receptors resulting in the stabilization and cytoplasmic accumulation of β -catenin, which then translocates to the nucleus and interacts with TCF-Lef transcription factors to regulate genes involved in proliferation, migration, and survival (21). The noncanonical pathways, also termed β -catenin independent, Wnt/Ca²⁺ or planar cell polarity, are also activated by Wnt/FZD ligands and receptors, leading to the release of intracellular calcium. Increased calcium leads to the activation of the serine/threonine phosphatase, calcineurin (CN; refs. 22, 23). Calcineurin induced de-phosphorylation of Nuclear Factor of Activated T-cells (NFAT) results in its translocation to the nucleus and transcriptional regulation of NFAT-dependent genes (21). We initially studied the role of Wnt signaling in mediating resistance to MEK inhibitors based upon the observation of high levels of Wnt pathway gene expression in selumetinib-resistant KRAS-mutant colorectal cancer cell lines (16).

Recent advances in genome-wide screening technologies have resulted in the identification of new combination targets through the use of synthetic lethality for a number of clinical anticancer agents (24–26). The aim of the current study was to test the hypothesis that pharmacologic modulation of the Wnt signaling pathway, discovered through gene set enrichment analysis (GSEA) and synthetic lethality as mediating resistance to MEK inhibition, would result in synergistic antitumor effects against *in vitro* and *in vivo* models of colorectal cancer when combined with MEK blockade. On the basis of these preclinical results, this rational combination could lead to a promis-

ing new therapeutic strategy for patients with advanced colorectal cancer.

Materials and Methods

Gene Set Enrichment Analysis

GSEA (27) was conducted on 26 colorectal cancer cell lines using the GSEA software as previously reported (16). See Supplementary Methods for details.

Synthetic Lethality Screen Analysis

The Synthetic Lethality Screen (SLS) Analysis was conducted using the SW480 (KRAS mutant) and RKO (BRAF V600E mutant) colorectal cancer cell lines. A lentiviral-expressed genome-wide human short-hairpin RNA (shRNA) library obtained from Systems Biosciences was used. The library contains 3 to 5 shRNAs per target gene, targeting 47,000 human transcripts. For the screen, the colorectal cancer cell lines were infected with the lentiviral shRNA library and subjected to puromycin selection for 2 weeks to obtain a pure population of shRNA expressing cells, and to eliminate shRNAs that targeted essential genes. The cells were then divided into 6 populations: 3 untreated, and 3 treated for 72 hours with selumetinib at a dose equivalent to 1 μ m/L. Total RNA was isolated from each group of cells, reverse-transcribed and PCR amplified. The PCR products were then deep-sequenced by the Illumina Genome Analyzer_{1.5}. Sequences obtained from the sequencer were analyzed by the BiNGS!SL-seq system (28) to identify shRNAs that were depleted in the treated samples, as previously described and validated (26, 29, 30).

Patient-derived tumor explant models

Animal studies were conducted in accordance with the NIH guidelines for the care and use of laboratory animals in a facility accredited by the American Association for Accreditation of Laboratory Animal Care, and approved by the University of Colorado Institutional Animal Care and Use Committee before initiation. Patient-derived tumor explant (PDTX) establishment and treatment protocols were conducted under previously described procedures (16, 31). See Supplementary Methods for details.

In vitro effects of MEK and Wnt inhibitors

Cell culture, proliferation assays, shRNA knockdowns, quantitative reverse transcription PCR (qRT-PCR), immunoblot analysis, clonogenic assay, caspase-3/7 assay, Annexin V assay, 3D cell culture, luciferase assay were conducted as previously described (16, 29, 31, 32). See Supplementary Methods for details.

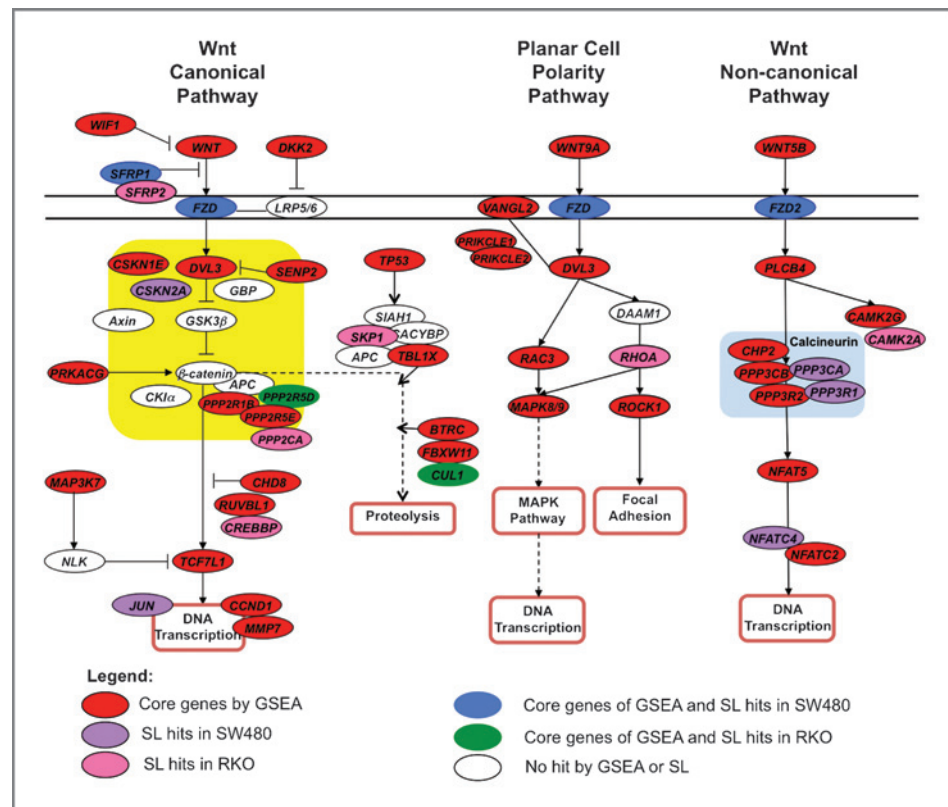
In vivo effects of MEK and Wnt inhibitors

Immunohistochemistry and pharmacokinetic analysis of PDTX tumors were conducted as previously described (16, 31, 33–35). See Supplementary Methods for details.

Statistical analyses

Statistical calculations were carried out using Microsoft Excel and GraphPad Prism Software version 5.0. For comparisons of 2 groups unpaired *t* test was conducted. When

Figure 1. Canonical (A) and noncanonical (B) Wnt signaling pathway represented by KEGG analysis. Red ovals represent core genes in the Wnt pathway with increased expression in colorectal cancer cells resistant to selumetinib. Purple and pink ovals represent synthetically lethal genes for SW480 and RKO colorectal cancer cell lines, respectively. Blue and green ovals represent top-scoring genes in both GSEA and SLS analyses for SW480 and RKO, respectively.



comparisons of multiple groups were needed an ANOVA was conducted. The specific tests applied are included in the figure legends.

Results

Integrative analysis of GSEA and SLS

To identify pathways enriched in selumetinib-resistant colorectal cancer cell lines, we previously conducted an unbiased GSEA analysis of a panel of 26 colorectal cancer cell lines (16). Within the 20 pathways identified as enriched in selumetinib-resistant lines (Supplementary Table S1), the Wnt signaling pathway was one of the top scoring pathways ($P = 0.03$). As depicted in Fig. 1, core genes involved in the canonical and noncanonical Wnt signaling pathways were enriched, consistent with our previous published gene expression analysis on 11 KRAS-mutant colorectal cancer cell lines (16). Next, we employed a complementary approach and conducted an unbiased genome-wide SLS on 2 colorectal cancer cell lines (SW480 and RKO) to identify genes and pathways that when inhibited may increase response to selumetinib. Interestingly, we found that this functional genomic approach independently identified shRNAs in the canonical and noncanonical Wnt pathway as being synthetically lethal for selumetinib (Fig. 1). Of note, concordant with previously published data, *FZD2* was identified as a top-scoring gene in both GSEA and SLS analyses (16, 36).

Wnt pathway inhibition modulates responsiveness to selumetinib in colorectal cancer cell lines.

To test the hypothesis that components of the Wnt pathway mediate resistance to selumetinib, shRNA knockdown (KD) experiments were conducted to modulate Wnt pathway gene expression. Four Wnt pathway genes, *FZD2*, *FZD3*, *Wnt2B*, and *Wnt5B*, were knocked down in the selumetinib-resistant colorectal cancer cell lines SW480 and RKO. These genes, receptors, and ligands were identified by GSEA to be upregulated in selumetinib-resistant colorectal cancer cell lines. Moreover, *FZD2* was one of the top scoring SL hits in the screen. The relative expression levels of *FZD2* and *Wnt5B* mRNA were significantly reduced relative to a control in the RKO colorectal cancer cell line, as measured by qRT-PCR (Supplementary Fig. S1A). Moreover, shRNAs targeting the Wnt pathway receptor *FZD3* significantly reduced relative levels of this mRNA in both RKO and SW480 colorectal cancer cell lines. However, when we attempted to knock down the Wnt pathway ligand, *Wnt2B*, we observed a significant reduction in this mRNA only in SW480 cells (Supplementary Fig. S1B and S1C). Possibly due to the low basal expression levels of Wnt ligands and FZD receptors, immunoblot analysis showed only modest or no reduction of Wnt receptors and ligands at the protein level (Supplementary Fig. S1D).

To evaluate the effect of these knockdown experiments on drug responsiveness, proliferation assays were conducted in parental, and shRNA transfected RKO and SW480 colorectal

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cancer cell lines treated with selumetinib. Knockdown of Wnt pathway receptors, *FZD2* and *FZD3* consistently resulted in statistically significant increases in percent inhibition in response to selumetinib in RKO and SW480 cell lines. In addition, knockdown of *Wnt2B* showed a trend toward increased percent inhibition that was not statistically significant, whereas no increase in responsiveness to selumetinib in the *Wnt5B* knockdown cells was observed (Supplementary Fig. S2). Interestingly, when the same genes were knocked down in the selumetinib-sensitive SW620 colorectal cancer cell line, no increase in responsiveness was observed, reinforcing our hypothesis that modulation of sensitivity through Wnt signaling may be restricted to the resistant colorectal cancer cell lines (data not shown). To further evaluate the role of Wnt signaling in resistance to selumetinib, we tested the effects of stable expression of *Wnt5B*, *Wnt2B*, *FZD2*, *FZD3*, or a dominant negative *TCF4* on sensitivity in the selumetinib sensitive colorectal cancer cell lines, LS513 and SW620. As depicted in Supplementary Fig. S3, we did not observe a significant change in sensitivity when these lines were exposed to increasing concentrations of selumetinib. These results are perhaps not surprising as our hypothesis is that colorectal cancer cell lines that are sensitive to selumetinib exhibit low levels of Wnt pathway activation and thus overexpression of a single component of the pathway is not sufficient to elicit a phenotypic change. Likewise, expression of a dominant negative *TCF4* construct resulted in no significant increase in resistance to selumetinib. Again, this could be the result of low Wnt signaling in these selumetinib sensitive cell lines, whose main pathway addiction is likely the Ras/MAPK pathway and not Wnt.

Synergistic antiproliferative effects of selumetinib and the Wnt inhibitors cyclosporin A (CsA) and TNP-470 in colorectal cancer cell lines. Recent reports have shown that the noncanonical Wnt pathway confers resistance to Bcr-Abl inhibition in leukemia models (32). Moreover, our genomic screens and mechanistic studies have shown that this β -catenin independent pathway may mediate responsiveness to MEK inhibitors in colorectal cancer. As there are currently no selective noncanonical Wnt inhibitors available, we used TNP-470 and CsA, as noncanonical Wnt pathway probes. These compounds have been previously investigated as Wnt inhibitors, although they also exhibit other functions as well (32, 37). Appropriate doses of CsA (0–5 $\mu\text{mol/L}$) and TNP-470 (0–10 $\mu\text{mol/L}$) were obtained by exposing a panel of 15 colorectal cancer cell lines to the each agent and assessing antiproliferative effects by the sulforhodamine B (SRB) method (data not shown). On the basis of previously published data, three selumetinib-resistant (SW480, RKO, and NCI-H508) and one selumetinib-sensitive (SW620) colorectal cancer cell lines were chosen for further combination studies (16). After exposure to selumetinib and CsA, synergistic antiproliferative effects were observed at most of the combination doses in RKO and SW480 cells (Fig. 2A; Supplementary Table S2). In contrast, the combination of selumetinib and TNP-470 resulted in synergistic antiproliferative effect in RKO, but not in the SW480

colorectal cancer cell line perhaps due to the strong single agent effect of TNP-470. Of note, the dose range of selumetinib used in these combination studies was reduced at least 50% compared with the IC_{50} of single-agent selumetinib for SW480 and RKO cell lines, as determined by SRB.

To further evaluate the synergistic antiproliferative effect of selumetinib in combination with inhibitors of the Wnt signaling pathway, and to test the activity of TNP-470 as a noncanonical Wnt inhibitor in a more tumor-like, nonangiogenic environment, three-dimensional (3D) spheroid assays were conducted. As depicted in Fig. 2B, synergy was detected with the combination of selumetinib and TNP-470. These data suggest that *in vitro*, the synergistic antiproliferative effects were the result of inhibition of the MEK and Wnt signaling pathways rather than effects of TNP-470 on angiogenic targets.

Furthermore, these synergistic antiproliferative were confirmed with a clonogenic assay using the SW480 colorectal cancer cell line. Cells were exposed to selumetinib, CsA, or the combination, stained with crystal violet or allowed to regrow in fresh media for an additional 72 hours before staining and analysis. At 72 hours, there was a clear combination effect which was even more pronounced after the recovery growth period of an additional 72 hours (Fig. 2C). These results suggest a cytotoxic effect of the combination rather than cytostatic.

Modulation of NFAT promoter activity by CsA and TNP-470

To assess the activity of CsA on the noncanonical Wnt signaling pathway, SW480, RKO, SW620, and NCI-H508 colorectal cancer cell lines were transduced with an NFAT-Luc reporter construct and treated with selumetinib, CsA, or TNP-470 as single agents or in combination. Experiments were conducted in the presence or absence of the calcium ionophore, ionomycin, as a positive control for activation of the Wnt calcium pathway and to increase the dynamic range of the luciferase assay. As depicted in Fig. 3A, a statistically significant decrease in luciferase light units was measured between vehicle-treated RKO cells and those treated with CsA alone or in the combination group (P value ≤ 0.02). Similar results were observed in NCI-H508 cells treated with TNP-470 ($P < 0.01$; Fig. 3B). To varying degrees, luciferase activity was reduced by CsA alone in the other 2 other cell lines (SW480 and SW620), which was maintained in the combination (Fig. 3A). To verify transduction efficiency, immunoblotting of the E2A protein, an immediate early gene product of adenoviral infection, was assessed. As depicted in Fig. 3C, E2A was present only in transduced cells, as compared with the nontransduced parental cells, and its expression did not change in response to treatment, suggesting relatively equal transfection efficiency between groups. Of note, exposure to single agent selumetinib was associated with luciferase activity that was either comparable, or induced, relative to the control in the RKO, SW480, or SW680 cell lines (Fig. 3A). Moreover, as an additional approach to verify that the Wnt pathway probes were acting via a β -catenin independent mechanism,

subcellular localization of NFAT1 and β -catenin was determined by immunoblot analysis. As depicted in Fig. 3D, in the presence of TNP-470, NFAT1 was retained in the cytoplasm, whereas β -catenin was equally distributed between the cytoplasmic and nuclear compartments. The distribution of NFAT1 to the cytoplasm was also pronounced in the combination group. These results suggest that TNP-470 preferentially inhibits the noncanonical Wnt signaling pathway preventing the nuclear translocation of NFAT1 from the cytoplasm while having no effect on β -catenin localization. Finally, to exclude the possibility that CsA and TNP-470 were acting on the canonical Wnt signaling pathway, we conducted a promoter reporter assay using the β -catenin–dependent TOP-FLASH reporter plasmid. As depicted in Fig. 3E, no change in luciferase activity was observed in the treatment groups as compared with control, in the SW480 colorectal cancer cell line.

In vivo antitumor activity of selumetinib and CsA

As a means of translating our observations into a clinically relevant model, *in vivo* studies were conducted using colorectal cancer PDX models in nude mice. Interestingly, we observed that FZD2 expression, as measured by qRT-PCR, increased significantly in the selumetinib-treated group compared with baseline levels in 3 of 5 previously defined selumetinib-resistant patient-derived colorectal cancer tumors (ref. 16; Supplementary Fig. S4A). Of note, PDX CRC021 and CRC027 showed no significant change in FZD2 expression upon treatment with selumetinib, indicating the presence of other resistance mechanisms. Therefore, we selected CRC006 and CRC007 for the *in vivo* combination drug studies. CRC006 is derived from peritoneal metastases of a patient with colon cancer carrying a G12D KRAS activating mutation and WT PI3K. CRC007 is derived from the primary site of a colorectal cancer tumor, and harbors the G13D KRAS and the 3'UTR PI3K mutations. After 62 days of treatment, CRC006 showed no tumor growth inhibitory effect to single agent selumetinib or CsA, as expected (TGI 30% and 16%, respectively). However, the combination of selumetinib and CsA led to a statistically significant tumor growth inhibition (82% TGI; $P < 0.0001$), showing a dramatic synergistic effect (Fig. 4A). These results were confirmed in PDX model CRC007, which also showed significant antitumor activity in the combination group as compared with the vehicle and single agents (Fig. 4A). To further confirm and characterize the activity of MEK blockade and Wnt modulation, at the end of the initial study, selumetinib was added to the CsA single agent group, and CsA was added to the selumetinib single agent group in both PDX models (Fig. 4B). The introduction of the respective drugs to either single agents resulted in a striking tumor regression, showing that this combination can also cause tumor volume reduction in addition to tumor growth inhibition. In addition, in the CRC006 study, after 200 days of treatment, drugs were withdrawn to monitor tumor re-growth kinetics. Notably, no tumor re-growth was observed up to 65 days after drug withdrawal indicating a sustained antitumor response (Supplementary Fig. S4B). No animals

in these studies exhibited obvious signs of toxicity as indicated by outward morbidity or weight loss compared with vehicle controls or single agents, indicating that the combination of selumetinib and CsA was well tolerated in mice.

Tumor and plasma measurement of selumetinib

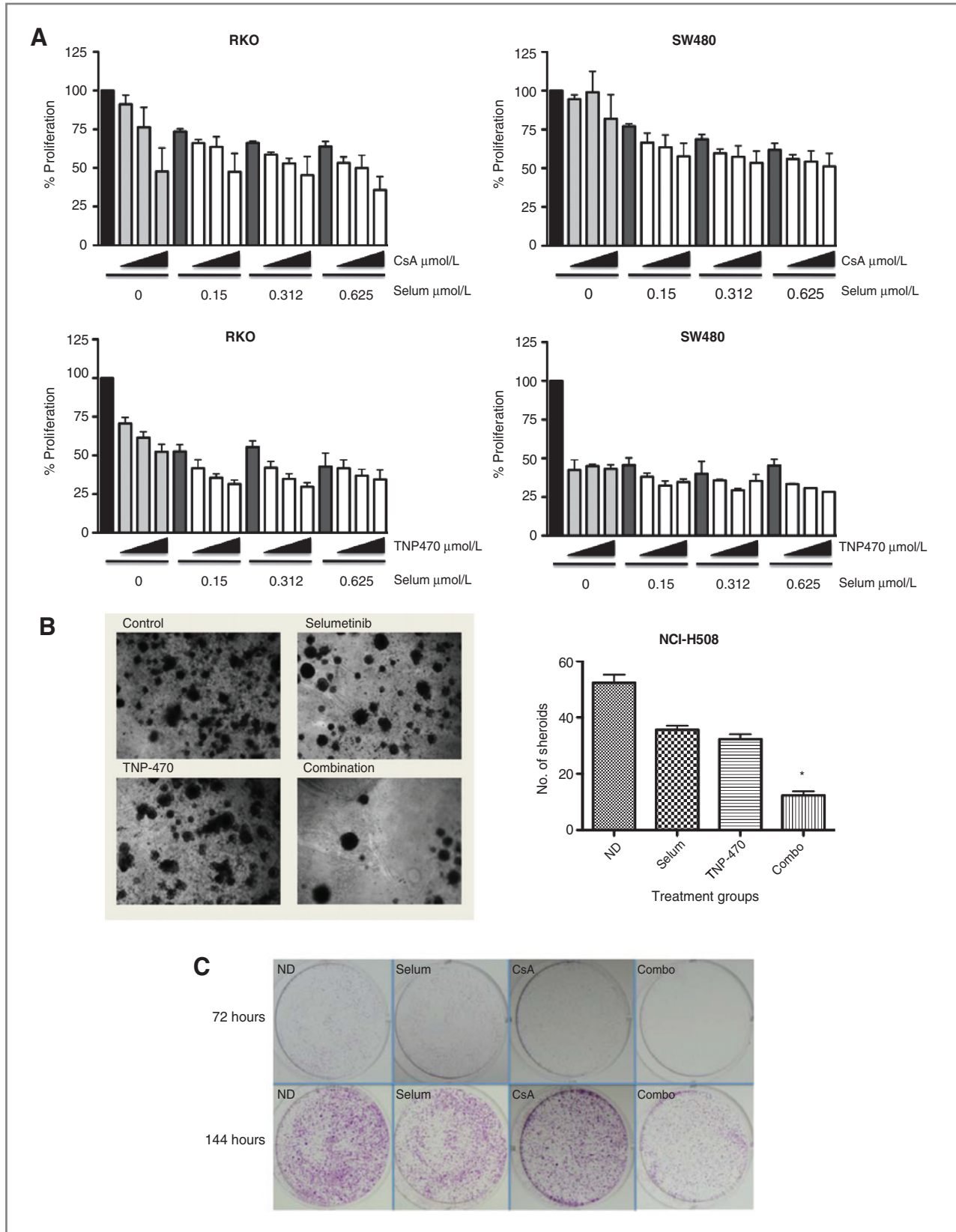
CsA has been shown to inhibit P-glycoprotein (Pgp) drug efflux pumps, which could lead to prolonged intracellular exposure to pharmaceutical compounds (38). To verify that the potent antitumor activity of selumetinib and CsA was due to the dual targeting of the MAPK and Wnt pathways and not enhanced selumetinib exposure, liquid chromatography tandem mass spectrometry analysis was conducted on plasma, tumor, and liver at the end of the study (day 62). Because selumetinib is metabolized via *N*-demethylation to an active compound that inhibits cellular growth *in vitro* at approximately 3 times the potency of the parent (data not shown), *N*-desmethylselumetinib was measured as well. As shown in Fig. 5, the plasma (A), liver (B), and tumor (C) concentrations of selumetinib were not significantly different when compared with single agent samples. Specifically, no significant differences were measured in any of the compartments at 1-hour posttreatment and at the 8-hour trough time point for both selumetinib and its metabolite *N*-desmethyl selumetinib versus combinations.

Pharmacodynamics and antitumor effects of selumetinib and CsA on PDX models

To evaluate downstream effectors in response to treatments, tumor samples from PDX models CRC006 and CRC007 were collected at end of study for immunoblot and immunohistochemical (IHC) analyses. As shown in Fig. 6A, immunoblotting of CRC006 showed a modest decrease in pERK in the combination group only. The pERK inhibition was more pronounced in CRC007 in both the selumetinib single agent and combination groups (Fig. 6B). These results are concordant with our previous findings (16), and show that resistance is not simply a result of the inability of selumetinib to inhibit its target (MEK 1/2).

To assess the *in vivo* mechanism of the synergy, we evaluated proliferation in response to drug treatments in the PDX model, using Ki67 as a marker of mitotic cells. As depicted in Fig. 6C, a dramatic reduction in tumor cell nuclear staining of Ki67 was observed in the combination group (20%) as compared with either single agents selumetinib (75%) and CsA (85%), and vehicle group where 90% of the cells exhibited proliferation (staining intensity: 2–3/3).

To further explore the mechanistic effects of modulation of the Wnt and MAPK pathways, we conducted gene array analysis on tumors from the CRC007 PDX model, treated with selumetinib, CsA, or the combination. As depicted in Fig. 6D, a heatmap of the relative expression of MEK activity and CsA target genes showed inhibition of the MAPK pathway by single agent selumetinib, which was enhanced in the combination group. CsA single agent also inhibited its target genes, IRF9 (interferon regulatory factor 9), ABCB1,



and PPP3R2. Moreover, IRF9 inhibition was also maintained in the combination group. CsA alone inhibited the ABCB1 multidrug resistance pump expression as has been well-documented (38), although in our study we did not observe increased intratumoral selumetinib concentrations. On the basis of our *in vitro* findings, we hypothesized that differentially expressed genes in the CsA and combination arms would be enriched with NFAT-signaling target genes. Thus, we used the NFAT binding motif of the genes (+2Kb, -2Kb), to conduct an enrichment analysis on the differentially expressed genes (defined as \geq or \leq 1.5-fold change compared with control). Interestingly, we found that approximately 7% (55/808) of the differentially expressed genes in the combination arm contained the NFAT binding motif. Some of the differentially expressed genes in the selumetinib group also contained this motif, and their expression levels were either maintained or enriched in the combination arm, reinforcing the hypothesis of cross-talk between the 2 pathways, as has been previously described (refs. 39–41; Supplementary Fig. S5). To further confirm modulation of MAPK and Wnt pathways in our treatment groups, we compared gene signature patterns observed after dual inhibition of RAS and Wnt and showed similar transcriptional modifications of Wnt, RAS, and apoptotic pathways (ref. 42; Supplementary Fig. S5). In addition, we found that expression of the MYC oncogene was downregulated in the combination treatment arm as compared with single agents (Supplementary Fig. S5).

Induction of apoptosis

To further evaluate the mechanism behind the synergistic antiproliferative effects of the dual inhibition of MEK and Wnt pathways, *in vitro* and *in vivo* induction of apoptosis was evaluated through caspase-3/7 activation, immunoblot and immunohistochemical analyses for apoptotic markers. Although caspase-3/7 activity in SW480 was not significantly elevated after treatment with single agent selumetinib or CsA or the combination, a maximum 1.5-fold increase in caspase-3/7 activity was observed in RKO cells treated with the combination (Supplementary Fig. S6A). Immunoblotting of these cell lines revealed an increase of cleaved PARP in SW480 cells (Supplementary Fig. S6B). We also assessed apoptotic activity by Annexin V staining and flow cytometry in RKO and SW480 cell lines at 24 and 72 hours posttreatment, but did not observe either single-agent or combination effects (data not shown). To assess apoptosis *in vivo*, protein extracts were prepared from tumors in both PDTX models at end of study for immunoblot analysis. As shown in Supplementary Fig. S6C, cleaved caspase-3 was apparent but not increased by combination treatment as compared

with single agents, perhaps reflecting the long duration of exposure of the drugs in these *in vivo* models.

Discussion

Small-molecule MEK 1/2 inhibitors have been evaluated in both preclinical and clinical studies as a potential therapeutic option for patients with advanced colorectal cancer carrying KRAS-activating mutations (12, 14, 16, 36, 43). However, single-agent efficacy has been limited, potentially due to inherent resistance mechanisms. The multiple gene abnormalities and molecular alterations that are a hallmark of cancer affect proliferation and survival may be specifically targeted by novel anticancer agents (44–46). Previous studies have shown that identification of signal transduction pathways mediating resistance can be used to identify effective drug combination treatments (47–49). However, recent data have shown that the cancer phenotype may be defined by changes in expression of groups of genes, which result in pleiotropic responses to specific drugs (16, 31, 50). Gene array analysis in conjunction with GSEA is a powerful strategy to identify interconnected signaling pathways that maintain cancer cell growth and may lead to new rational combination treatments (16, 31, 50). In our study, we conducted baseline GSEA and found that Wnt pathway-related genes were upregulated in selumetinib-resistant colorectal cancer cell lines. However, as these pathways may not necessarily be overexpressed in resistant tumors, a synthetic lethality approach was used. SLS has emerged as a powerful platform to systematically search for cancer addiction pathways and clinically relevant interactions and mechanisms of drug resistance in cancer cells (26, 29, 51, 52). Moreover, this approach identifies genes, which, when suppressed, mediate response to a specific treatment, leading to actionable targets. In our study, combining these novel, complementary approaches we found that several genes involved in the Wnt signaling pathway may be mediators of responsiveness to the MEK inhibitor selumetinib.

The significance of these results is highlighted by the crosstalk between the MAPK and Wnt signaling pathways identified by others and suggests a role for Wnt in maintaining colorectal cancer cell survival and escaping MEK inhibition. A report by Horst and colleagues showed that both colorectal cancer cell line xenografts and patient-derived colorectal cancer tumor xenografts were heterogeneous with respect to β -catenin expression, and that these areas colocalized with pERK expression (39). Moreover, a recent report described a KRAS-dependent gene signature in colorectal cancer models that was characterized by enhanced Wnt activity through activation of BMP-7 and

Figure 2. Antiproliferative effects of selumetinib (Selum) in combination with CsA or TNP-470 in SW480, RKO, and NCI-H508 cells. A, results of SRB proliferation assay after 72 hours of exposure to indicated concentrations of selumetinib alone or in combination with CsA (1.25, 2.5, and 5 $\mu\text{m}/\text{mL}$), or TNP-470 (2.5, 5, and 10 $\mu\text{m}/\text{mL}$) as indicated by triangles. Data are expressed as percent proliferation compared with no drug controls \pm SD. B, representative images of 3D cultures of NCI-H508 colorectal cancer cell line spheroids treated with selumetinib and TNP-470 for 3 weeks, as described in Materials and Methods. Antiproliferative effects for each treatment group were quantified by averaging the number of spheroids in 4 separate fields per chamber at $\times 4$ magnification. Bar graph depicts mean of 3 separate experiments \pm SD. C, representative images of clonogenic assays of SW480 cell line treated with either single agents selumetinib (0.3 $\mu\text{m}/\text{mL}$) or CsA (5 $\mu\text{m}/\text{mL}$), or in combination for 72 hours. Cells were then stained with crystal violet at 72 hours (top) or allowed to regrow for an additional 72 hours before staining (144 hours; bottom).

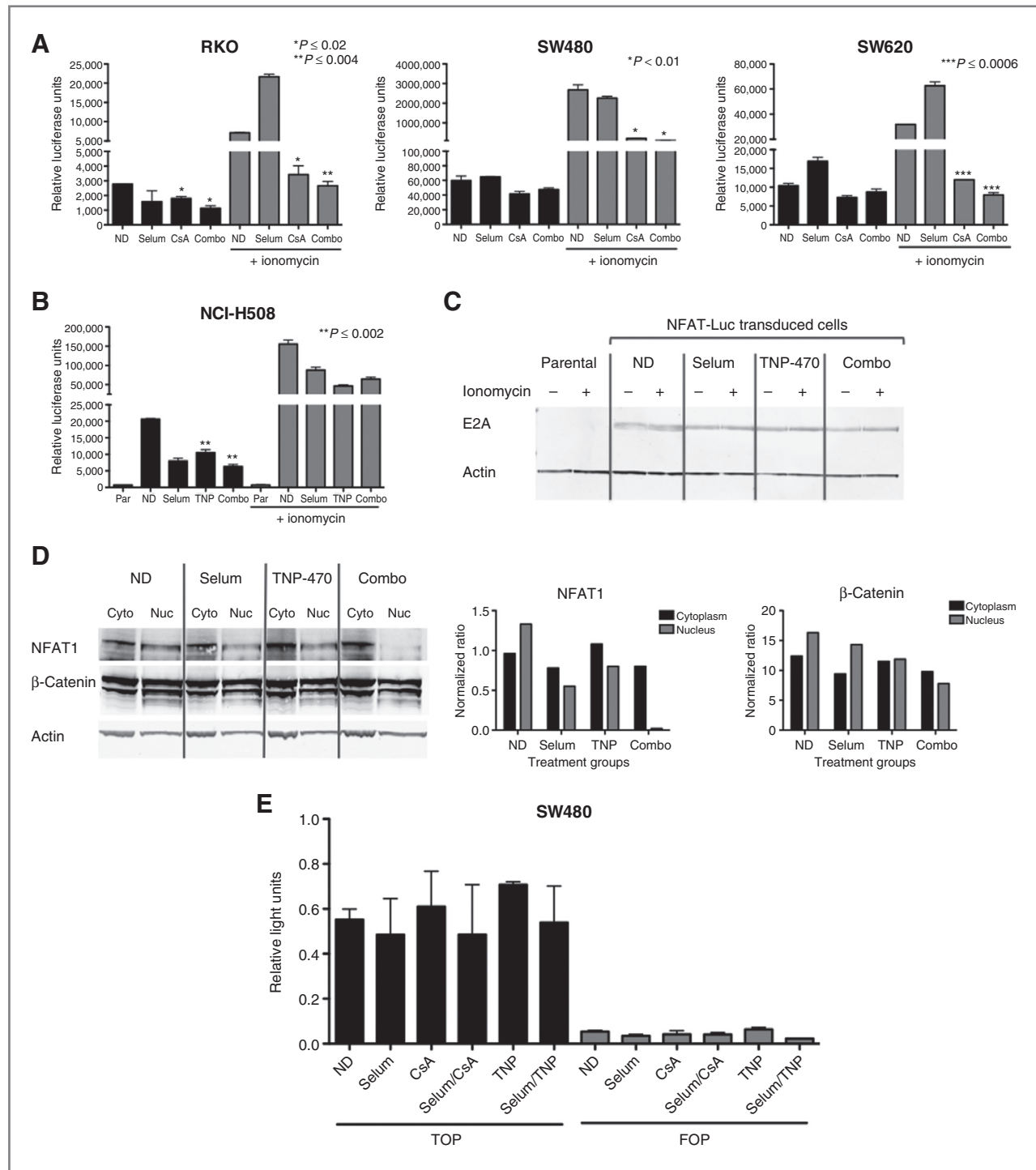


Figure 3. Treatment of colorectal cancer cells with CsA and TNP-470 results in inhibition of the noncanonical Wnt pathway. **A**, CsA inhibits activity of the noncanonical Wnt-associated *NFAT* promoter in SW480, RKO, and SW620 colorectal cancer cell lines. Bar graphs represent average relative luciferase light units \pm SD in each respective cell line ($n = 3$). **B**, left: effects of TNP-470 on *NFAT* promoter activity in NCI-H508 cells treated with single agents selumetinib (0.3 μ mol/mL), TNP-470 (5 μ mol/mL) and in combination, alone or in the presence of ionomycin (1 μ g/mL) for 24 hours. Bar graphs represent average relative luciferase light units \pm SD ($n = 3$). Par = parental nontransfected control. Right: immunoblot analysis of early adenoviral E2A protein as a readout of transduction efficiency. **C**, immunoblot analysis of NFAT1 protein levels in the cytoplasm and nucleus in response to TNP-470 in NCI-H508 cells. C, cytoplasmic fraction; N, nuclear fraction. **D**, treatment with selumetinib, CsA, or TNP-470 has no effect on the Wnt β -catenin-dependent TOPflash (TOP) promoter construct. The FOPflash (FOP) promoter contains a mutation in the β -catenin binding element as a control for specificity.

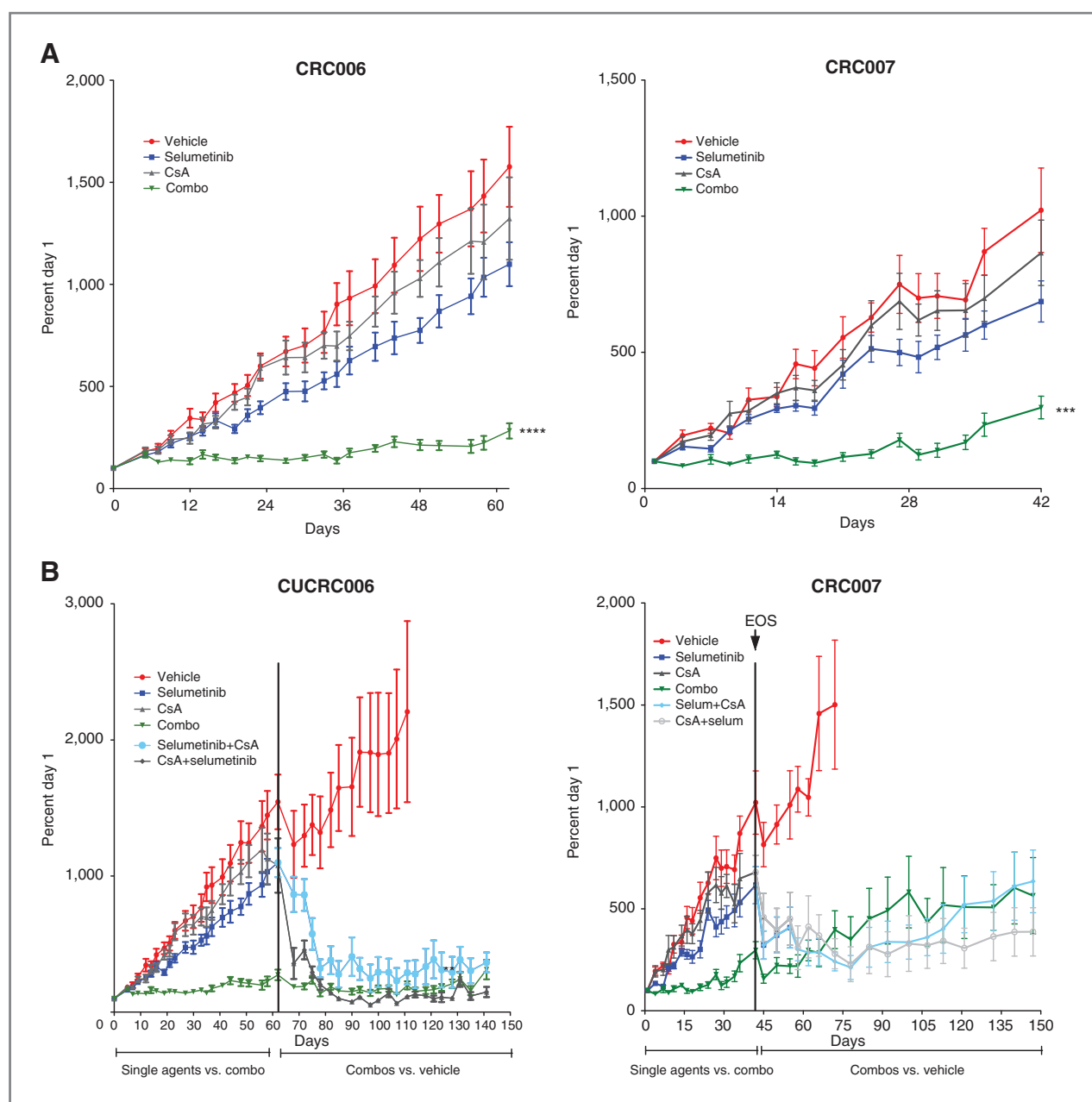


Figure 4. Antitumor activity of selumetinib and CsA on PDTX models of colorectal cancer. **A**, mice bearing tumors from CRC006 and CRC007 were treated with single agents selumetinib (25 mg/kg BID), CsA (25 mg/kg QD), and the combination. Tumor growth index (TGI) was calculated by relative tumor growth of treated mice divided by relative tumor growth of control mice $\times 100$. **B**, tumor regressive effects of the addition of respective combination agents to single agent arms in CRC006 and CRC007 PDTX models at end of study (EOS: days 62 and 42, respectively). Potent antitumor effects were maintained up to 200 days in CRC006 and 150 days in CRC007 after the switch to combination treatments in the single agent arms. EOS, end of study.

TAK-1 kinase (49). Indeed, we observed that inhibition of MAPK signaling with selumetinib led to decreased expression of NFAT-dependent genes in a PDTX model of colorectal cancer, providing further evidence that these 2 pathways are interconnected.

While the β -catenin-dependent Wnt pathway and its dysregulation in colorectal cancer is well studied, the noncanonical Wnt pathway is largely uncharacterized in mammalian cells, and its role in oncogenesis still remain

controversial (53). We found that the shRNA-mediated inhibition of numerous components of the Wnt signaling pathway, which were either upregulated or synthetically lethal in colorectal cancer cell lines, enhanced responsiveness to selumetinib. Because the noncanonical Wnt pathway is less characterized as a therapeutic target, there are presently no clinically selective Wnt/ Ca^{++} pathway inhibitors available for clinical use. Although CsA and TNP-470 have been described as immunosuppressant and

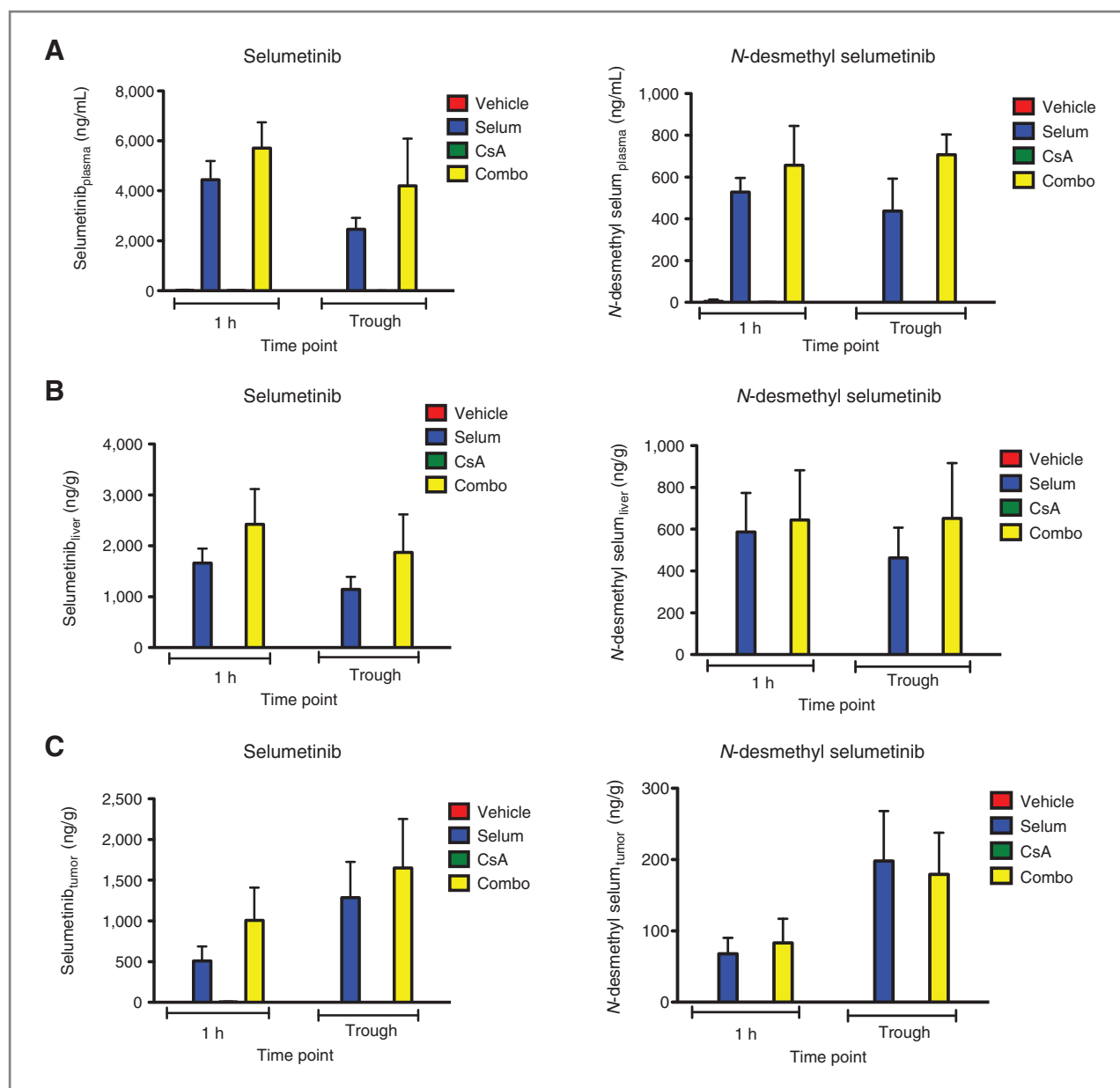


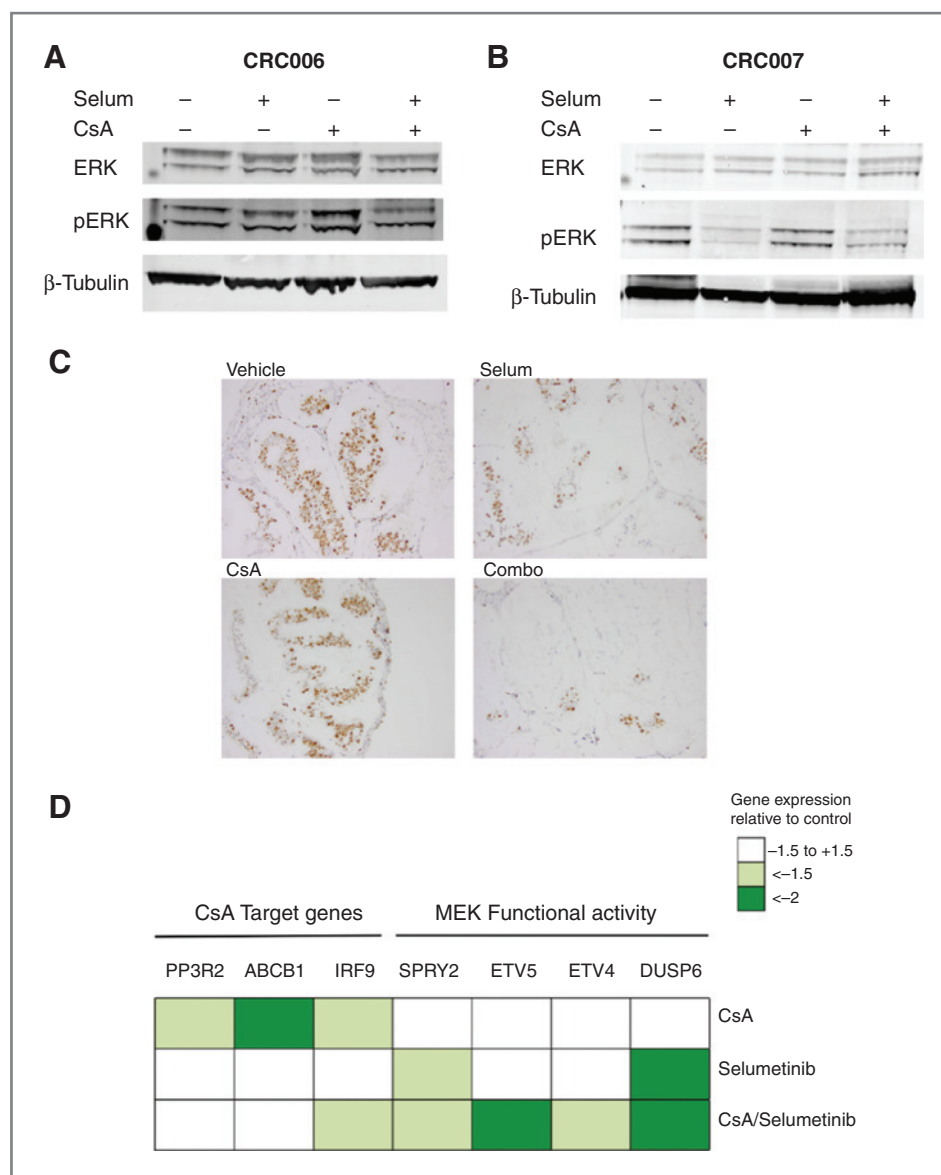
Figure 5. Plasma, tumor, and tissue distribution of selumetinib and selumetinib *N*-desmethyl in mice treated with selumetinib, CsA, or the combination. Mice bearing tumor CRC006 were administered a daily (BID) oral dose of 25 mg/kg selumetinib, as a single agent or in combination with a daily oral dose of CsA (25 mg/kg) for 62 days. Samples of plasma (A), liver (B), and tumor (C) were taken at the indicated time after the last dose (mean, SD; $n = 4$). No significant differences were measured in any of the compartments at 1 hour posttreatment and at the 8-hour trough time point for both selumetinib and its metabolite *N*-desmethyl selumetinib versus combinations ($P > 0.05$).

antiangiogenic agents, respectively, we used them as pharmacologic probes of the Wnt/Ca⁺⁺ pathway. A recent report showed that CsA targets the noncanonical Wnt pathway in mouse Bcr-Abl⁺ leukemia models, which, when combined with dasatinib, resulted in a complete eradication of the leukemia cells, compared with the relapse and mortality observed in mice treated with single-agent dasatinib or CsA (32). Likewise, TNP-470 acts on the β -catenin independent Wnt pathway, targeting a site downstream of FZD2 receptor (37). In our study, we

documented that the combination of selumetinib and CsA, or TNP-470 resulted in a synergistic antiproliferative effect in colorectal cancer cell lines in both 2D and 3D culture conditions, as well as *in vivo* PDTX models where posttreatment gene array analysis showed modulation of CsA and selumetinib target genes.

Several studies have extensively analyzed selumetinib as a single agent against numerous cancer types, and concluded that its anticancer activity is mainly cytostatic (54, 55). These data are concordant with our results, which showed

Figure 6. Pharmacodynamics of selumetinib and CsA on PDTX models at EOS. Inhibition of pERK levels in tumors from CRC006 (A) and CRC007 (B) as measured by immunoblot. C, inhibition of cell proliferation as measured by immunohistochemical staining of Ki-67 in CRC006 PDTX models treated with the indicated agents. D, heatmap depicting relative expression levels of CsA and MEK target genes.



reversible cell growth suppression with single agent selumetinib exposure, but not in the combination groups with CsA or TNP-470. Therefore, the synergy observed with selumetinib and CsA or TNP-470 may be associated with cytotoxicity. In support of these data, selumetinib has been shown to cause tumor regression and induction of apoptosis *in vivo* when combined with docetaxel in preclinical models of melanoma (55, 56). As it has been reported that CsA can inhibit Pgp, it could be hypothesized that the synergistic effects of CsA and selumetinib are due to inhibition of this efflux pump resulting in higher intratumoral concentrations of selumetinib and not on direct inhibition of CN/NFAT activity (38). However, we showed that the synergistic antiproliferative effects are likely due to CsA-mediated CN inhibition, as we did not see accumulation of selumetinib in the presence of CsA.

The development of more reliable preclinical models is a crucial step toward improving the success rate of novel cancer therapeutics in the clinic. PDTX models in nude mice may represent a more clinically relevant model as they more accurately reflect the complex molecular, genetic, and histologic heterogeneity of patient tumors as compared with standard cell line xenografts (57). Our *in vivo* studies using PDTX models of KRAS-mutant colorectal cancer showed that selumetinib combined with CsA was a potent inhibitor of tumor growth and could induce tumor regression in models that are resistant to single-agent selumetinib. Previous studies have shown that dual inhibition of Wnt and KRAS signaling pathways resulted in a distinct gene expression signature with respect to alterations involved in Wnt, RAS, and apoptosis pathways (42). Interestingly, we observed similar gene expression modulation in our PDTX

models after combination treatment with selumetinib and CsA. The MYC oncogene has been recently shown to play a key role in activating Wnt signaling (58). Consistent with this finding, we also observed MYC downregulation in the combination arm as compared with both single agents suggesting a MYC-mediated suppression of Wnt targeted genes.

To our knowledge, this is the first study in which the combination of MEK blockade and Wnt pathway modulation has shown synergistic antiproliferative effects in both *in vitro* and *in vivo* preclinical colorectal cancer models. While we focused our studies largely on the KRAS/BRAF-mutant colorectal cancer population, this does not exclude activity in KRAS wide-type tumors, which deserves further study. Interestingly, although the data are limited, several studies have suggested that the results of treatment of explant models correlates with actual clinical outcome, providing early clinical validation of this approach (35, 57, 59).

In summary, we used an unbiased molecular genetic approach to identify rational combination partners for MEK inhibitors in colorectal cancer. These genetic screens yielded a dual targeting strategy of the Wnt pathway and MEK, which resulted in robust antitumor activity and tumor regression in preclinical models of colorectal cancer. The results of these studies further validate our previous findings (16) and support our hypothesis that cotargeting of resistance pathways may result in more effective personalized medicine strategies. While we acknowledge the challenges in using a promiscuous agent such as CsA to definitively elucidate the crosstalk between the MEK and Wnt pathways, nonetheless the data are supportive of further preclinical studies in this area, particularly using more selective Wnt inhibitors, which is ongoing in our lab. These findings have led to the design of a phase I/IB clinical trial exploring the combination of selumetinib and CsA with an expanded

cohort of patients with advanced treatment-refractory colorectal cancer.

Disclosure of Potential Conflicts of Interest

S.G. Eckhardt received commercial research grant from AstraZeneca. No potential conflicts of interest were disclosed by the other authors.

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Acknowledgments

The authors would like to thank Drs. Paul D. Smith, Christopher Porter, Erica L. Bradshaw-Pierce, and Ms. Michelle VanScoyk for their helpful discussions and scientific review of this manuscript. We would also like to thank AstraZeneca, Inc. for supplying selumetinib for these studies.

Grant Support

A. Spreafico, Astra Zeneca post-doctoral fellowship. S.G. Eckhardt, grants CA106349 and CA046934.

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Received October 10, 2012; revised May 2, 2013; accepted June 3, 2013; published OnlineFirst June 11, 2013.

References

- Chresta CM, Davies BR, Hickson I, Harding T, Cosulich S, Critchlow SE, et al. AZD8055 is a potent, selective, and orally bioavailable ATP-competitive mammalian target of rapamycin kinase inhibitor with *in vitro* and *in vivo* antitumor activity. *Cancer Res* 2010;70:288–98.
- Fransen K, Klintenas M, Osterstrom A, Dimberg J, Monstein HJ, Soderkvist P. Mutation analysis of the BRAF, ARAF and RAF-1 genes in human colorectal adenocarcinomas. *Carcinogenesis* 2004;25:527–33.
- Vaughn CP, Zobel SD, Furtado LV, Baker CL, Samowitz WS. Frequency of KRAS, BRAF, and NRAS mutations in colorectal cancer. *Genes Chromosomes Cancer* 2011;50:307–12.
- Amado RG, Wolf M, Peeters M, Van Cutsem E, Siena S, Freeman DJ, et al. Wild-type KRAS is required for panitumumab efficacy in patients with metastatic colorectal cancer. *J Clin Oncol* 2008;26:1626–34.
- Bokemeyer C, Van Cutsem E, Rougier P, Ciardiello F, Heeger S, Schlichting M, et al. Addition of cetuximab to chemotherapy as first-line treatment for KRAS wild-type metastatic colorectal cancer: pooled analysis of the CRYSTAL and OPUS randomised clinical trials. *Eur J Cancer* 2012;48:1466–75.
- Karapetis CS, Khambata-Ford S, Jonker DJ, O'Callaghan CJ, Tu D, Tebbutt NC, et al. K-ras mutations and benefit from cetuximab in advanced colorectal cancer. *N Engl J Med* 2008;359:1757–65.
- Lievre A, Bachet JB, Le Corre D, Boige V, Landi B, Emile JF, et al. KRAS mutation status is predictive of response to cetuximab therapy in colorectal cancer. *Cancer Res* 2006;66:3992–5.
- Loupakis F, Ruzzo A, Cremolini C, Vincenzi B, Salvatore L, Santini D, et al. KRAS codon 61, 146 and BRAF mutations predict resistance to cetuximab plus irinotecan in KRAS codon 12 and 13 wild-type metastatic colorectal cancer. *Br J Cancer* 2009;101:715–21.
- Bertrand FE, Steelman LS, Chappell WH, Abrams SL, Shelton JG, White ER, et al. Synergy between an IGF-1R antibody and Raf/MEK/ERK and PI3K/Akt/mTOR pathway inhibitors in suppressing IGF-1R-mediated growth in hematopoietic cells. *Leukemia* 2006;20:1254–60.
- Corcoran R, Settleman J, Engelman J. Potential therapeutic strategies to overcome acquired resistance to BRAF or MEK inhibitors in BRAF mutant cancers. *Oncotarget* 2011;2:336–46.
- Turke AB, Song Y, Costa C, Cook R, Arteaga CL, Asara JM, et al. MEK inhibition leads to PI3K/AKT activation by relieving a negative feedback on ERBB receptors. *Cancer Res* 2012;72:3228–37.
- Adjei AA, Cohen RB, Franklin W, Morris C, Wilson D, Molina JR, et al. Phase I pharmacokinetic and pharmacodynamic study of the oral, small-molecule mitogen-activated protein kinase kinase 1/2 inhibitor AZD6244 (ARRY-142886) in patients with advanced cancers. *J Clin Oncol* 2008;26:2139–46.

13. Balmanno K, Chell SD, Gillings AS, Hayat S, Cook SJ. Intrinsic resistance to the MEK1/2 inhibitor AZD6244 (ARRY-142886) is associated with weak ERK1/2 signalling and/or strong PI3K signalling in colorectal cancer cell lines. *Int J Cancer* 2009;125:2332–41.
14. Bennouna J, Lang I, Valladares-Ayerbes M, Boer K, Adenis A, Escudero P, et al. A Phase II, open-label, randomised study to assess the efficacy and safety of the MEK1/2 inhibitor AZD6244 (ARRY-142886) versus capecitabine monotherapy in patients with colorectal cancer who have failed one or two prior chemotherapeutic regimens. *Invest New Drugs* 2011;29:1021–8.
15. Corcoran RB, Dias-Santagata D, Bergethon K, Iafrate AJ, Settleman J, Engelman JA. BRAF gene amplification can promote acquired resistance to MEK inhibitors in cancer cells harboring the BRAF V600E mutation. *Sci Signal* 2010;3:ra84.
16. Tentler JJ, Nallapareddy S, Tan AC, Spreafico A, Pitts TM, Morelli MP, et al. Identification of predictive markers of response to the MEK1/2 inhibitor selumetinib (AZD6244) in K-ras-mutated colorectal cancer. *Mol Cancer Ther* 2010;9:3351–62.
17. Bekaii-Saab T, Phelps MA, Li X, Saji M, Goff L, Kauh JS, et al. Multi-institutional phase II study of selumetinib in patients with metastatic biliary cancers. *J Clin Oncol* 2011;29:2357–63.
18. Hayes DN, Lucas AS, Tanvetyanon T, Krzyzanowska MK, Chung CH, Murphy BA, et al. Phase II efficacy and pharmacogenomic study of Selumetinib (AZD6244; ARRY-142886) in iodine-131 refractory papillary thyroid carcinoma with or without follicular elements. *Clin Cancer Res* 2012;18:2056–65.
19. Jänne PA, Shaw AT, Pereira JR, Jeannin G, Vansteenkiste J, Barrios C, et al. Selumetinib plus docetaxel for KRAS-mutant advanced non-small-cell lung cancer: a randomised, multicentre placebo-controlled, phase 2 study. *Lancet Oncol* 2013;14:38–47.
20. O'Neil BH, Goff LW, Kauh JS, Strosberg JR, Bekaii-Saab TS, Lee RM, et al. Phase II study of the mitogen-activated protein kinase 1/2 inhibitor selumetinib in patients with advanced hepatocellular carcinoma. *J Clin Oncol* 2011;29:2350–6.
21. Staal FJ, Luis TC, Tiemessen MM. WNT signalling in the immune system: WNT is spreading its wings. *Nat Rev Immunol* 2008;8:581–93.
22. Jessen JR. Noncanonical Wnt signaling in tumor progression and metastasis. *Zebrafish* 2009;6:21–8.
23. Wang Y. Wnt/Planar cell polarity signaling: a new paradigm for cancer therapy. *Mol Cancer Ther* 2009;8:2103–9.
24. Martin SA, Hewish M, Sims D, Lord CJ, Ashworth A. Parallel high-throughput RNA interference screens identify PINK1 as a potential therapeutic target for the treatment of DNA mismatch repair-deficient cancers. *Cancer Res* 2011;71:1836–48.
25. Mendes-Pereira AM, Sims D, Dexter T, Fenwick K, Assiotis I, Kozarewa I, et al. Genome-wide functional screen identifies a compendium of genes affecting sensitivity to tamoxifen. *Proc Natl Acad Sci U S A* 2012;109:2730–5.
26. Porter CC, Kim J, Fosmire S, Gearheart CM, van Linden A, Baturin D, et al. Integrated genomic analyses identify WEE1 as a critical mediator of cell fate and a novel therapeutic target in acute myeloid leukemia. *Leukemia* 2012;26:1266–76.
27. Subramanian A, Tamayo P, Mootha VK, Mukherjee S, Ebert BL, Gillette MA, et al. Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. *Proc Natl Acad Sci U S A* 2005;102:15545–50.
28. Kim J, Tan AC. BiNGS!SL-seq: a bioinformatics pipeline for the analysis and interpretation of deep sequencing genome-wide synthetic lethal screen. *Methods Mol Biol* 2012;802:389–98.
29. Sullivan KD, Padilla-Just N, Henry RE, Porter CC, Kim J, Tentler JJ, et al. ATM and MET kinases are synthetic lethal with nongenotoxic activation of p53. *Nat Chem Biol* 2012;8:646–54.
30. Casas-Selves M, Kim J, Zhang Z, Helfrich BA, Gao D, Porter CC, et al. Tankyrase and the canonical Wnt pathway protect lung cancer cells from EGFR inhibition. *Cancer Res* 2012;72:4154–64.
31. Pitts TM, Tan AC, Kulikowski GN, Tentler JJ, Brown AM, Flanigan SA, et al. Development of an integrated genomic classifier for a novel agent in colorectal cancer: approach to individualized therapy in early development. *Clin Cancer Res* 2010;16:3193–204.
32. Gregory MA, Phang TL, Neviani P, Alvarez-Calderon F, Eide CA, O'Hare T, et al. Wnt/Ca2+/NFAT signaling maintains survival of Ph+ leukemia cells upon inhibition of Bcr-Abl. *Cancer Cell* 2010;18:74–87.
33. Davies BR, Logie A, McKay JS, Martin P, Steele S, Jenkins R, et al. AZD6244 (ARRY-142886), a potent inhibitor of mitogen-activated protein kinase/extracellular signal-regulated kinase 1/2 kinases: mechanism of action in vivo, pharmacokinetic/pharmacodynamic relationship, and potential for combination in preclinical models. *Mol Cancer Ther* 2007;6:2209–19.
34. Denton CL, Gustafson DL. Pharmacokinetics and pharmacodynamics of AZD6244 (ARRY-142886) in tumor-bearing nude mice. *Cancer Chemother Pharmacol* 2011;67:349–60.
35. Morelli MP, Tentler JJ, Kulikowski GN, Tan AC, Bradshaw-Pierce EL, Pitts TM, et al. Preclinical activity of the rational combination of selumetinib (AZD6244) in combination with vorinostat in KRAS-mutant colorectal cancer models. *Clin Cancer Res* 2012;18:1051–62.
36. Dry JR, Pavey S, Pratilas CA, Harbron C, Runswick S, Hodgson D, et al. Transcriptional pathway signatures predict MEK addiction and response to selumetinib (AZD6244). *Cancer Res* 2010;70:2264–73.
37. Zhang Y, Yeh JR, Mara A, Ju R, Hines JF, Cirone P, et al. A chemical and genetic approach to the mode of action of fumagillin. *Chem Biol* 2006;13:1001–9.
38. Illmer T, Schaich M, Platzbecker U, Freiberg-Richter J, Oelschlagel U, von Bonin M, et al. P-glycoprotein-mediated drug efflux is a resistance mechanism of chronic myelogenous leukemia cells to treatment with imatinib mesylate. *Leukemia* 2004;18:401–8.
39. Horst D, Chen J, Morikawa T, Oginio S, Kirchner T, Shivdasani RA. Differential WNT activity in colorectal cancer confers limited tumorigenic potential and is regulated by MAPK signaling. *Cancer Res* 2012;72:1547–56.
40. Kim D, Rath O, Kolch W, Cho KH. A hidden oncogenic positive feedback loop caused by crosstalk between Wnt and ERK pathways. *Oncogene* 2007;26:4571–9.
41. Wang IC, Snyder J, Zhang Y, Lander J, Nakafuku Y, Lin J, et al. Foxm1 mediates cross talk between Kras/mitogen-activated protein kinase and canonical Wnt pathways during development of respiratory epithelium. *Mol Cell Biol* 2012;32:3838–50.
42. Mologni L, Brussolo S, Ceccon M, Gambacorti-Passerini C. Synergistic effects of combined Wnt/KRAS inhibition in colorectal cancer cells. *PLoS ONE* 2012;7:e51449.
43. Yoon J, Koo KH, Choi KY. MEK1/2 inhibitors AS703026 and AZD6244 may be potential therapies for KRAS mutated colorectal cancer that is resistant to EGFR monoclonal antibody therapy. *Cancer Res* 2011;71:445–53.
44. Di Nicolantonio F, Martini M, Molinari F, Sartore-Bianchi A, Arena S, Saletti P, et al. Wild-type BRAF is required for response to panitumumab or cetuximab in metastatic colorectal cancer. *J Clin Oncol* 2008;26:5705–12.
45. Kwak EL, Bang YJ, Camidge DR, Shaw AT, Solomon B, Maki RG, et al. Anaplastic lymphoma kinase inhibition in non-small-cell lung cancer. *N Engl J Med* 2010;363:1693–703.
46. Lievre A, Bachet JB, Boige V, Cayre A, Le Corre D, Buc E, et al. KRAS mutations as an independent prognostic factor in patients with advanced colorectal cancer treated with cetuximab. *J Clin Oncol* 2008;26:374–9.
47. Gioeli D, Wunderlich W, Sebolt-Leopold J, Bekiranov S, Wulfkühle JD, Petricoin EF III, et al. Compensatory pathways induced by MEK inhibition are effective drug targets for combination therapy against castration-resistant prostate cancer. *Mol Cancer Ther* 2011;10:1581–90.
48. Shi H, Kong X, Ribas A, Lo RS. Combinatorial treatments that overcome PDGFRbeta-driven resistance of melanoma cells to V600E-BRAF inhibition. *Cancer Res* 2011;71:5067–74.
49. Singh A, Sweeney MF, Yu M, Burger A, Greninger P, Benes C, et al. TAK1 inhibition promotes apoptosis in KRAS-dependent colon cancers. *Cell* 2012;148:639–50.
50. Jimeno A, Tan AC, Coffa J, Rajeshkumar NV, Kulesza P, Rubio-Viqueira B, et al. Coordinated epidermal growth factor receptor pathway gene overexpression predicts epidermal growth factor receptor inhibitor sensitivity in pancreatic cancer. *Cancer Res* 2008;68:2841–9.

51. Luo J, Emanuele MJ, Li D, Creighton CJ, Schlabach MR, Westbrook TF, et al. A genome-wide RNAi screen identifies multiple synthetic lethal interactions with the Ras oncogene. *Cell* 2009;137:835–48.
52. Whitehurst AW, Bodemann BO, Cardenas J, Ferguson D, Girard L, Peyton M, et al. Synthetic lethal screen identification of chemosensitizer loci in cancer cells. *Nature* 2007;446:815–9.
53. Pukrop T, Binder C. The complex pathways of Wnt 5a in cancer progression. *J Mol Med* 2008;86:259–66.
54. Ball DW, Jin N, Rosen DM, Dackiw A, Sidransky D, Xing M, et al. Selective growth inhibition in BRAF mutant thyroid cancer by the mitogen-activated protein kinase kinase 1/2 inhibitor AZD6244. *J Clin Endocrinol Metab* 2007;92:4712–8.
55. Haass NK, Sproesser K, Nguyen TK, Contractor R, Medina CA, Nathanson KL, et al. The mitogen-activated protein/extracellular signal-regulated kinase kinase inhibitor AZD6244 (ARRY-142886) induces growth arrest in melanoma cells and tumor regression when combined with docetaxel. *Clin Cancer Res* 2008;14:230–9.
56. Holt SV, Logie A, Odedra R, Heier A, Heaton SP, Alferez D, et al. The MEK1/2 inhibitor, selumetinib (AZD6244; ARRY-142886), enhances anti-tumour efficacy when combined with conventional chemotherapeutic agents in human tumour xenograft models. *Br J Cancer* 2012;106:858–66.
57. Tentler JJ, Tan AC, Weekes CD, Jimeno A, Leong S, Pitts TM, et al. Patient-derived tumour xenografts as models for oncology drug development. *Nat Rev Clin Oncol* 2012;9:338–50.
58. TCGA. Comprehensive molecular characterization of human colon and rectal cancer. *Nature* 2012;487:330–7.
59. Hidalgo M, Bruckheimer E, Rajeshkumar NV, Garrido-Laguna I, De Oliveira E, Rubio-Viqueira B, et al. A pilot clinical study of treatment guided by personalized tumorgrafts in patients with advanced cancer. *Mol Cancer Ther* 2011;10:1311–6.