Activation of MET via Diverse Exon 14 Splicing Alterations Occurs in Multiple Tumor Types and Confers Clinical Sensitivity to MET Inhibitors

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ABSTRACT
Focal amplification and activating point mutation of the MET gene are well-characterized oncogenic drivers that confer susceptibility to targeted MET inhibitors. Recurrent somatic splice site alterations at MET exon 14 (METex14) that result in exon skipping and MET activation have been characterized, but their full diversity and prevalence across tumor types are unknown. Here, we report analysis of tumor genomic profiles from 38,028 patients to identify 221 cases with METex14 mutations (0.6%), including 126 distinct sequence variants. METex14 mutations are detected most frequently in lung adenocarcinoma (3%), but also frequently in other lung neoplasms (2.3%), brain glioma (0.4%), and tumors of unknown primary origin (0.4%). Further in vitro studies demonstrate sensitivity to MET inhibitors in cells harboring METex14 alterations. We also report three new patient cases with METex14 alterations in lung or histiocytic sarcoma tumors that showed durable response to two different MET-targeted therapies. The diversity of METex14 mutations indicates that diagnostic testing via comprehensive genomic profiling is necessary for detection in a clinical setting.

SIGNIFICANCE: Here we report the identification of diverse exon 14 splice site alterations in MET that result in constitutive activity of this receptor and oncogenic transformation in vitro. Patients whose tumors harbored these alterations derived meaningful clinical benefit from MET inhibitors. Collectively, these data support the role of METex14 alterations as drivers of tumorigenesis, and identify a unique subset of patients likely to derive benefit from MET inhibitors. Cancer Discov; 5(8); 1–10. ©2015 AACR.

See related commentary by Ma, p. 802.
See related article by Paik et al., p. 842.

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Note: Supplementary data for this article are available at Cancer Discovery Online (http://cancerdiscovery.aacrjournals.org/).

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INTRODUCTION

Personalized medicine offers great promise in cancer treatment by matching patients with targeted therapies that act based on the specific molecular alterations present in their tumors. Targeted therapies have the potential to be more effective than conventional cytotoxic chemotherapies, often with fewer side effects (1). Consequently, the identification of new subsets of patients likely to benefit from targeted therapy is critically important for improving cancer patient care.

The hepatocyte growth factor (HGF) receptor, encoded by the MET oncogene, is a receptor tyrosine kinase that plays a fundamental role in regulating development and cell growth. Upon stimulation, MET induces a cellular program known as invasive growth, which promotes mitogenesis, motility, invasion, and morphogenesis. Pathologic activation of MET, through both gene copy-number amplification and point mutation, is a well-characterized driver of oncogenesis that occurs in many different types of tumors. In cancer, activation of MET promotes tumor proliferation, invasive growth, and angiogenesis (2).

Accumulating evidence suggests that patients with tumors harboring MET alterations can benefit from targeted therapies (3). A number of drugs have been developed that repress MET activation and/or signaling, including small-molecule kinase inhibitors and monoclonal antibodies targeting MET or its ligand, HGF. For example, treatment with crizotinib has benefited patients with tumors containing high-level MET amplifications, including non–small cell lung carcinoma (NSCLC), gastroesophageal cancer, glioblastoma, and carcinoma of unknown primary origin (4–8), and the dual MET/VEGFR2 inhibitor foretinib provided benefit to patients with MET-mutated papillary renal cell carcinoma (9). MET-targeting antibodies onartuzumab and MetMAb have elicited responses in patients with MET-amplified NSCLC and gastric cancer (10, 11). In addition, high MET expression has been suggested to predict the response of patients with gastro-esophageal junction carcinoma to a therapy regimen involving rilotumumab, a monoclonal HGF-targeting antibody (12).

Somatic mutations affecting splice sites of exon 14 of the MET gene (METex14) were first reported in primary lung cancer specimens and in a lung cancer cell line (13–15). These METex14 alterations were shown to promote RNA-splicing–based skipping of MET exon 14, which results in activation of MET kinase activity through a unique mechanism. The portion of the protein encoded by exon 14, most prominently Y1003 in a DpYR motif, is required for efficient recruitment of the ubiquitin ligase CBL, which targets MET for ubiquitin-mediated degradation (16–18). Loss of MET exon 14 maintains the reading frame and leads to increased MET stability and prolonged signaling upon HGF stimulation, leading to increased oncogenic potential (19, 20). Inclusion of MET exon 14 into an oncogenic TPR–MET fusion, in which exon 14 is conspicuously excluded, leads to reduction of TPR–MET oncogenic potential (21). Thus, in cancer, genomic alterations that promote METex14 skipping lead to oncogenic MET activation.

METex14 alterations have since been shown to occur in approximately 3% of lung adenocarcinoma cases (15, 22–26) and have also been observed in neuroblastoma and gastric cancer cell lines (27, 28). In total, fewer than 20 distinct METex14 sequence variants have been described, and their full diversity and prevalence across tumor types have not been characterized (Supplementary Table S1).

In vitro preclinical studies indicate that MET-targeted agents can counteract oncogenesis resulting from MET exon 14
loss (14, 17). This suggests that targeted therapies inhibiting MET signaling would be beneficial for patients with MET\textsuperscript{ex14} alterations. Recently, three case reports have demonstrated clinical response to crizotinib, a tyrosine kinase inhibitor, in lung carcinoma patients with MET\textsuperscript{ex14} alterations (29–31).

We present a large series of genomic profiles of advanced cancers, assayed in the course of clinical care, with MET\textsuperscript{ex14} alterations. We also present in vitro studies, further demonstrating the oncogenic potential of MET\textsuperscript{ex14} alterations. Finally, we report durable responses to MET-targeted therapy in three patients with tumors harboring MET\textsuperscript{ex14} alterations.

RESULTS

Comprehensive cancer genome profiling (32) was performed on 38,028 tumor specimens from unique patients in the course of routine clinical care, in a Clinical Laboratory Improvement Amendments (CLIA)–certified laboratory, between April 2012 and February 2015. Base substitution, indel, copy-number alteration, and rearrangement alterations were examined to identify those likely to affect splicing of exon 14 of the MET gene (MET\textsuperscript{ex14} alterations). In total, 224 distinct MET\textsuperscript{ex14} alterations were identified, occurring in 221 specimens. These alterations displayed remarkably diverse sequence composition, with 126 different genomic sequence variants represented. The alterations comprised base substitutions (n = 2) and indels (n = 33) at splice acceptor sites, base substitutions (n = 102) and indels (n = 31) at splice donor sites, and base substitutions (n = 2) and indels (n = 49) in the ∼25 bp intronic noncoding region immediately adjacent to the splice acceptor site (Fig. 1A).

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We also identified five samples with whole exon deletions of MET exon 14 (Fig. 1A and B). Indels were predominantly deletions, but several insertions and complex indels were detected (Supplementary Table S2).

MET\textsuperscript{ex14} alterations were detected in 221 cases and were distributed among primary disease sites as lung adenocarcinoma [3%; 131/4,402; 95% confidence interval (CI), 2.5%–3.5%], other lung neoplasms (2.3%, 62/2,669; 1.8%–3%), brain glioma (0.4%; 6/1,708; 0.1%–0.8%), tumors of unknown primary origin (0.4%; 15/3,376; 0.3%–0.7%), and other tumor types (<0.1%; 7/25,873). MET\textsuperscript{ex14} alterations were not found in tumors of the female reproductive system (n = 7,436), colon and rectum (n = 3,714), pancreas (n = 1,424). We did...
Exon 14 Alterations Confer Response to Targeted Therapy

Figure 2. Comprehensive genomic profiling of 4,402 lung adenocarcinomas. A, co-mutation plot of frequently altered genes. The known clinically relevant driver genes and other most frequently altered genes are shown. The type of mutation is indicated by colors described in the key. Data for this figure are available in Supplementary Table S4. B–D, co- and anti-occurrence of genes containing known driver and other frequently occurring alterations in lung adenocarcinoma. Statistically significant (FDR < 5%) co- and anti-occurrence was tested using the Fisher exact test with FDR correction for multiple-hypothesis testing and is indicated with *. Color scale, fold change of enrichment (red) or exclusivity (green), versus random assortment. CDKN2A and CDKN2B are shown in gray because they occur in close proximity on chromosome 9 and both are frequently affected within a single homozygous copy-number deletion. To reduce outlying signal, the least significant boundary of a 50% binomial confidence interval around measured co-occurrence counts was used for plotting enrichment.

not observe a statistically significant difference among the rates of METex14 alterations in the various subtypes of lung carcinoma. In addition, the distribution of the genomic position and type (base substitution, deletion, insertion, or complex indel) of METex14 alterations did not vary significantly among the different sites of tumor primary origin.

We examined the other genomic alterations co-occurring with METex14, focusing on the cohort of 4,402 lung adenocarcinoma specimens (Fig. 2A; Supplementary Table S3). Multiple other receptor tyrosine kinase or MAPK pathway driver mutations in lung adenocarcinoma have been described, including activating mutations in KRAS, EGFR, ERBB2, BRAF, and MET as well as gene fusions involving ALK, RET, and ROS1 (25, 33, 34). Examining co-occurrence among mutations in each of these genes, we observed that they were mutually exclusive (Fig. 2B). This exclusivity of lung adenocarcinoma driver alterations has been observed previously and is confirmed in this large cohort of lung adenocarcinoma specimens. Tumors with METex14 alterations rarely harbored the other known drivers of lung adenocarcinoma, as has been previously observed in other cohorts (23–26), supporting the role of METex14 alterations as oncogenic driver mutations. We also observed that mutations in KRAS, EGFR, ERBB2, and MET each frequently co-occurred with copy-number amplification of the same gene, highlighting the cumulative effect of gene activation by both mutation and amplification.

We next examined co-occurrence of other frequently occurring genomic alterations in lung adenocarcinoma (Fig. 2C and D). In addition to their mutual exclusivity, each of the driver mutations had a distinct pattern of co-occurring alterations, further supporting the hypothesis that they define
distinct molecular subtypes of lung adenocarcinoma. Notably, METex14 splicing alterations were strongly coincident with amplification of MDM2 and CDK4 on chromosome 12q. Unlike METex14 alterations, copy-number amplifications of MET were not significantly coincident with MDM2/CDK4 amplification. We also observed strong and statistically significant co-occurrence of mutations in several pairs of genes, some of which have been described previously (35, 36), most notably KRAS/STK11, STK11/KEAP1, and PIK3CA/RB1. We observed significant anti-occurrence between CDKN2A/RB1 and KRAS/STK11, STK11/KEAP1. Many other statistically significant gene occurrence interactions were observed (Supplementary Table S4).

In addition to the METex14 alterations, we observed two cases with MET p.Y1003N (c.3007T>A) alterations. This alteration has been observed previously (37) and likely activates MET in a fashion similar to METex14 alterations, by preventing CBL-mediated degradation of MET. Interestingly, both of these cases were NSCLC, harbored copy-number amplifications of MDM2 and CDK4, and lacked other characteristic NSCLC driver alterations, such as KRAS, EGFR, ERBB2, BRAF, ALK, RET, and ROS.

We sought to further characterize the function of MET exon 14 skipping using cell line models. To model METex14 alterations occurring in human patient samples, human MET cDNA with exon 14 deleted (METΔ14), and mouse Met with the homologous exon 15 deleted (MEx15) were generated through site-directed mutagenesis. In the human embryonic kidney cell line HEK293, transient expression of METΔ14 activated MEK–ERK signaling, as indicated by increased ERK activation phosphorylation under both 10% FBS and serum starvation condition (Fig. 3A).

In the mouse fibroblast cell line NIH3T3, we generated clones with stable ectopic expression of wild-type MET (METWT) and METΔ15 as well as HRASG12V and red fluorescent protein (RFP) control. Expression of METWT, METΔ14, and METΔ15 was confirmed by immunoblotting. The sum of colonies from 5 random fields at week 3 is reported as the mean of duplicates (±SD).

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Figure 3. Human METΔ14 and the equivalent mouse METΔ15 transform cells and confer MET-dependent growth, at least partially through activation of the MEK–ERK pathway. A, transient expression of FLAG-tagged human METWT or exon 14 deletion (Δ14) mutant in HEK293 cells. Expression and phosphorylation of MET (pY1234/1235) and ERK1/2 (pT202/Y204) were measured by immunoblotting. B, anchorage-independent growth was assessed by soft-agar assay comparing NIH3T3 cells expressing mouse METWT, METΔ15, or HRASG12V or red fluorescent protein (RFP) control. Expression of METWT, METΔ14, and METΔ15 was confirmed by immunoblotting. The sum of colonies from 5 random fields at week 3 is reported as the mean of duplicates (±SD).

C, NIH3T3 cells from B were treated with increasing concentrations of the MET inhibitor capmatinib or D) MEK inhibitor trametinib for 72 hours, and inhibition of proliferation was determined by cell viability assay (CellTiterGlo). *, P < 0.05, comparing METΔ15 with RFP at 20 nmol/L capmatinib.
MET Exon 14 Alterations Confer Response to Targeted Therapy

METΔ15 increased anchorage-independent colony formation 10-fold, as compared with MET WT (Fig. 3B). These findings are consistent with the previous reports noting the oncogenic nature of MET variants lacking exon 14-mediated CBL binding, and further highlight the evolutionarily conserved role of the MET exon 14-encoded portion of the juxtamembrane domain in attenuation of MET signaling.

Capmatinib (INC280) is a highly selective and potent small-molecule inhibitor of the MET receptor tyrosine kinase (IC50 value of 0.13 nmol/L). It is highly specific, with >10,000-fold selectivity for c-MET in biochemical studies with a panel of human kinases. Capmatinib demonstrates potent activity (IC50 values of 0.2–2 nmol/L) in cell-based biochemical and functional assays that measure c-MET signaling and c-MET–dependent cell proliferation and survival (38, 39).

To determine if METΔ15-expressing cells are sensitive to capmatinib, proliferation was measured by CellTiterGlo assay 72 hours after treatment. NIH3T3 cells expressing METWT or METΔ15 showed dose-dependent inhibition of cell proliferation with capmatinib treatment, and at 20 nmol/L concentration, cell survival rate of METΔ15 is significantly lower than RFP control. Cells expressing either METΔ15 or HRASG12V were sensitive to trametinib, a MEK1/2 inhibitor. In comparison, cells expressing HRASG12V were resistant to capmatinib, suggesting a high selectivity of capmatinib to MET-driven cells (Fig. 3C and D). These in vitro results suggest that genomic alterations resulting in MET exon 14 skipping or loss are oncogenic; cells expressing these forms of MET are dependent on its aberrant signaling, and potentially sensitive to inhibition with MET-selective agents.

Given preclinical evidence suggesting sensitivity to MET inhibitors, the clinical outcomes for patients harboring METex14 alterations were investigated. We were able to successfully identify a small number of patients who had been treated with appropriate targeted therapies. All cases had been subjected to comprehensive genomic profiling in the course of routine clinical care. Although only a subset of cases were available for evaluation, in this limited sampling, the outcomes for those obtaining MET inhibitors tended very strongly to favorable responses.

An 84-year-old female never-smoker had a palpable left upper anterior chest mass incidentally identified during the course of an examination after a minor trauma. Imaging demonstrated a mass 13 cm in the largest dimension traversing the left lung and chest wall, which was deemed to be unresectable, stage III disease. Morphologic and immunohistochemical characterization of a biopsy of the chest wall mass demonstrated histocytic sarcoma (Fig. 4A and B). Comprehensive genomic profiling demonstrated that the tumor harbored a METex14 alteration (c.2888-5_2944del62) as well as TP53 p.R175H and ZMYM3 c.3008-1G>A. The patient was not a candidate for surgical therapy, so systemic treatment options were investigated. After 4 months of treatment with capmatinib, the lesion decreased >60% in volume, deemed a major response to capmatinib.

Figure 4. Histiocytic sarcoma of the thorax harboring a METex14 alteration has a major response to capmatinib. A and B, photomicrographs demonstrate a neoplasm with pleomorphic, polygonal cells with scattered mitotic activity as well as apoptotic cells. Tumor cells were focally positive for CD68 by immunohistochemical staining, consistent with a histiocytic origin. Stains for CD45 and vimentin were positive (data not shown). CK7, CK20, CK5/6, CK AE1/3, CK CAM5.2, p63, CD43, CD30, and smooth muscle actin were negative (data not shown). Contrast-enhanced chest CT images at C 0 months, D 2 months, and E 4 months after therapy with capmatinib. Left anterior chest wall mass (white arrow) demonstrated decrease in bulk and heterogeneity after 2 and 4 months of treatment with capmatinib. At initiation of treatment, the tumor was measured as 13.8 × 11.7 cm, and decreased to 8.9 × 6.5 cm at 4 months, a reduction of >60% volume and a partial response per RECIST 1.1.
partial response under RECIST criteria 1.1 (Fig. 4C–E). The patient experienced minimal toxicity on crizotinib, but did have disease progression as assessed by imaging at 11 months.

In a separate clinical trial (NCT01324479), two NSCLC cases with \( \text{MET} \text{ex14} \) alterations were identified by comprehensive genomic profiling. This trial is a phase I open-label, dose-escalation study with expansion to assess the safety and tolerability of the investigational MET inhibitor capmatinib in patients with MET-dependent advanced solid tumors. Both patients received capmatinib, described in detail above, and were treated at Sarah Cannon Research Institute, Nashville, TN.

An 82-year-old female, with a 25 pack-year smoking history, was diagnosed with stage IV large cell lung carcinoma with right hilar node metastases. Initial therapy included complete surgical resection; the patient declined perioperative chemotherapy and was monitored until recurrence of disease 3 years and 3 months later. The patient declined treatment with standard-of-care chemotherapy regimens and instead elected to enter the clinical trial above. Comprehensive genomic profiling was performed on the primary resection and demonstrated that the tumor harbored a \( \text{MET} \text{ex14} \) alteration (c.3028G>C) and \( \text{TP53} \) p.N30fs*14. MET gene copy number was six, in a triploid cancer genome, as measured by next-generation sequencing based comprehensive genomic profiling. MET IHC performed on the same specimen was 3+ (H-score 270). MET FISH was not performed. The patient was treated with capmatinib for more than 5 months and had a tumor reduction of 53%, a partial response (Fig. 5A and B).

A 66-year-old female, with a 4 pack-year smoking history, was diagnosed with stage 1b poorly differentiated squamous cell carcinoma of lung (LSCC), which was resected and followed immediately with adjuvant gemcitabine and carboplatin, which were discontinued after a single cycle due to toxicity. The patient was then monitored only. After 9 months, her disease recurred in the soft tissue of the axilla and chest wall; she was also later noted to have central nervous system, bone, and renal metastases. The patient then underwent several courses of palliative radiotherapy including whole brain radiotherapy, weekly paclitaxel and carboplatin for 4 months, and subsequently was enrolled in a phase I clinical trial for a CHK1 inhibitor, but progressed after 2 months on this therapy. Upon enrollment into the capmatinib study, comprehensive genomic profiling demonstrated the LSCC harbored a \( \text{MET} \text{ex14} \) alteration (c.3028+1G>T) and no other known alterations. MET gene copy number was four. Additional molecular testing indicated \( \text{MET} \) FISH 13.8 copy number (\( \text{MET}:\text{CEBP7} \) ratio 2.3) and IHC 3+ (H-score 300). The patient was treated with capmatinib for 13 months with tumor reduction of 61%, a partial response. On disease progression, the patient’s tumor burden remained significantly decreased from baseline, and disease-related pain did not recur (Fig. 5C and D).
DISCUSSION

METex14 alterations are important recurrent alterations that are clinically and therapeutically relevant, occurring in approximately 3% of lung adenocarcinomas, 2% of other lung neoplasms, 0.5% of brain gliomas, and 0.5% of carcinomas of unknown primary origin. Consequently, the assessment of METex14 alteration status will be appropriate for many advanced cancer patients. In the context of NSCLC, the demonstration of mutual exclusivity between METex14 alterations and other oncogenic drivers is consistent with METex14 itself being such a driver. Three cases with durable responses to MET-targeted therapy presented in this study included response to crizotinib, an FDA-approved inhibitor targeting MET and ALK, as well as capmatinib, a highly selective and potent small-molecule MET inhibitor that is in clinical development.

In addition, three other such reports of response to targeted therapy in cases with METex14 alterations have been recently published, further extending the evidence of potential clinical benefit (29–31). As there are no clinical trials at present focusing on the METex14 advanced cancer population, the accumulation of clinical responses presented in this article is only evidence of the potential clinical benefit of MET inhibitors in lung cancer patients. Although it is interesting that in two of our clinical cases, as well as in one recently published case (29), a METex14 alteration was accompanied by MET overexpression by IHC, with one of those cases also containing an apparent MET gene copy-number amplification. In the third presented case, neither IHC nor FISH analysis was performed. In preclinical studies, lack of CBL binding to both human and murine MET exon 14 regions (Met exon 15 in mouse), such as via skipping of MET exon 14, has been shown to impair MET downregulation and degradation, leading to increased MET protein expression (14, 17, 19, 20). Indeed, MET overexpression has been previously noted in lung tumors with METex14 alterations, and MET variants lacking exon 14 were noted to be preferentially overexpressed in those cases rather than the full-length MET (14). As mentioned above, MET amplification, presumably leading to MET overexpression, has been shown to confer sensitivity to MET inhibitors in a variety of tumor types. Thus, the functional basis for MET inhibitor sensitivity may be similar in patients with METex14 alterations and MET amplification in their tumors.

The levels of MET protein lacking exon 14 compared with full-length MET in the tumors of the 3 patients who achieved responses to MET inhibitors are not known. Therefore, the possibility of overexpression of full-length MET being a driver alteration responsible for sensitivity to MET inhibitors cannot be excluded. However, the lack of detectable MET amplification in two of the three sensitive tumors, the report of MET variants lacking exon 14 being preferentially expressed over full-length MET in lung cancer samples (14), and the oncogenic nature of METex14 alterations all suggest that the inhibition of MET variants lacking exon 14 contributed to the observed clinical responses.

It is also interesting to note that none of the three responders in our cohort had either MDM2 or CDK4 amplification in their tumors. As mentioned above, gene copy-number amplification of MDM2, and less frequently of CDK4, is highly coincident with METex14 alterations. Whether amplification of either MDM2 or CDK4 might affect sensitivity of tumors with METex14 alterations to MET inhibitors is currently unclear. Among the three recently published case studies, a patient with a METex14 alteration and amplification of MDM2 and CDK4 in their tumor (29) exhibited the shortest response to a MET-targeted agent of the six responses known to date, but a patient with a METex14 alteration and amplification of MDM2, but not of CDK4, in their tumor exhibited a major response (31). However, it is difficult to draw conclusions regarding the effect of MDM2 or CDK4 amplification on the responsiveness to MET inhibitors at this time. Because numerous inhibitors of MDM2 and CDK4 are currently being clinically evaluated in a variety of cancer types, including the CDK4/6 inhibitor palbociclib, which has been FDA approved for the treatment of breast cancer, the efficacy of combined MET and MDM2/ CDK4 inhibition in preclinical models is worth investigating.

In summary, these results demonstrate that METex14 alterations occur in multiple tumor types, particularly lung carcinoma, and can confer clinical sensitivity to targeted therapies. Identification of this new patient population is an important step toward making appropriate targeted therapies available for all cancer patients.

METex14 alterations pose a challenge for diagnostic testing. They exhibit highly diverse sequence composition, many are novel, and more than half are indel mutations (up to 3 kb in length), which are challenging to detect with high sensitivity and specificity. Consequently, assessing METex14 alteration status requires appropriate laboratory and analytic methods that are capable of accurate sequencing, statistical detection, annotation, and reporting of this diverse class of alterations.

As the number of targeted therapies and molecular alterations that are relevant for routine cancer patient treatment continues to grow, comprehensive genomic profiling will be increasingly required to accurately stratify patients for appropriate therapy. Finally, the diversity of METex14 alterations highlights the need for profiling of large numbers of cancer genomes to identify and fully elucidate cancer driver mutations that have degenerate genomic sequence signatures.

METHODS

Comprehensive Cancer Genome Profiling

Comprehensive cancer genomic profiling was performed using the FoundationOne test. The laboratory and computational methods employed in the FoundationOne DNA assay have been described in...
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Disclosure of Potential Conflicts of Interest

G.M. Frampton has ownership interest (including patents) in Foundation Medicine. S. Jaeger, A. Huang, R. Schlegel, R. Yelensky, J.S. Ross, E. Collisson, M. Peters, P.J. Stephens, V.A. Miller


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Other (submitted clinical images in support of the data): J.A. Bufill

Acknowledgments

The authors thank Salil Soman for assistance with radiological figure preparation.

Grant Support

X. Lu and E. Collisson were supported by Uniting Against Lung Cancer grant P0503003.

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Received March 11, 2015; revised May 7, 2015; accepted May 11, 2015; published OnlineFirst May 13, 2015.
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Cancer Discovery  Published OnlineFirst May 13, 2015.

Updated version  Access the most recent version of this article at: doi:10.1158/2159-8290.CD-15-0285

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