

Genetic and Clonal Dissection of Murine Small Cell Lung Carcinoma Progression by Genome Sequencing

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SUMMARY

Small cell lung carcinoma (SCLC) is a highly lethal, smoking-associated cancer with few known targetable genetic alterations. Using genome sequencing, we characterized the somatic evolution of a genetically engineered mouse model (GEMM) of SCLC initiated by loss of *Trp53* and *Rb1*. We identified alterations in DNA copy number and complex genomic rearrangements and demonstrated a low somatic point mutation frequency in the absence of tobacco mutagens. Alterations targeting the tumor suppressor *Pten* occurred in the majority of murine SCLC studied, and engineered *Pten* deletion accelerated murine SCLC and abrogated loss of Chr19 in *Trp53*; *Rb1*; *Pten* compound mutant tumors. Finally, we found evidence for polyclonal and sequential metastatic spread of murine SCLC by comparative sequencing of families of related primary tumors and metastases. We propose a temporal model of SCLC tumorigenesis with implications for human SCLC therapeutics and the nature of cancer-genome evolution in GEMMs.

INTRODUCTION

Human tumors are believed to arise through reiterated Darwinian cycles of spontaneous mutation and selection (Nowell, 1976). By the time a tumor is clinically detected, individual tumor cells harbor numerous acquired mutational events under selection (“drivers”) and an even greater number of events offering no selective advantage (“passengers”). The identification of driver mutations in human cancers remains a major obstacle for cancer genome sequencing efforts. Although several approaches have been recently described, the statistical power

of these approaches is critically dependent on large sample numbers in part due to high-observed mutation frequencies, particularly in mutagen-associated cancers (Lawrence et al., 2013).

As an example of these challenges, two recent small-cell lung carcinoma (SCLC)-sequencing studies identified distinct novel putative driver alterations (Peifer et al., 2012; Rudin et al., 2012). Whether this reflects true biological differences in the tumor cohorts or differences in analytical methods is unknown. A limitation of these and many human cancer-genome characterization studies to date is the lack of rigorous in vivo functional validation. Studies that include functional data largely rely upon cultured cells, which lack many hallmark features of naturally arising tumors (Hanahan and Weinberg, 2011).

SCLC is nearly always associated with extended tobacco use and has lagged behind other solid tumors with respect to identification of targetable driver mutations (Califano et al., 2012; Jackman and Johnson, 2005). In addition, patients usually present with highly advanced, metastatic disease. Although there is often a significant response to systemic chemotherapy, the disease invariably relapses and the median 5-year overall survival is less than 5%. Moreover, surgical resection is rarely performed, and the consequent lack of available SCLC tissue is a significant barrier to molecular studies. Human SCLC harbor mutations in *TP53* and *RB1* at very high frequency; therefore, a mouse model of SCLC was generated by lung-specific compound deletion of *Trp53* and *Rb1* (hereafter referred to as “PR mSCLC” for *p53*, *Rb1* mutant murine SCLC; Meuwissen et al., 2003). In the absence of tobacco-associated mutagens, these animals develop SCLC that progresses from small neuroendocrine bodies (NEBs) and recapitulates many features of the human disease, including frequent distant metastases to sites commonly seeded by human SCLC.

We hypothesized that several features of the PR mSCLC model were well-suited for a comparative cancer genome sequencing study. First, unlike many models, mSCLC is initiated by engineered deletion of two tumor suppressors (*Rb* and *p53*).

In addition, somatic tumor-genome evolution, including the conserved oncogenic DNA copy number amplifications of *Myc11* and *Nfib*, has been demonstrated during tumor progression in mSCLC (Calbó et al., 2005; Dooley et al., 2011). The long latency (12–14 months) and high frequency of metastases in this model also mirrors the progression of most adult-onset human cancers that are believed to evolve over many years (Jones et al., 2008). We also predicted that the absence of tobacco mutagens would reduce the background mutation frequency and improve statistical power to detect recurrent driver mutations. Here, we characterize a panel of PR mSCLC primary and metastatic tumors at single-nucleotide resolution using exome and genome sequencing in order to elucidate mechanisms of tumor progression and identify conserved acquired somatic drivers of SCLC.

RESULTS

Murine SCLCs Harbor Complex Genomes

We generated a PR mSCLC tissue bank consisting of primary tumors and metastases as previously described (Dooley et al., 2011; Table S1A available online). Exome sequencing was performed on 27 SCLC primary tumors and metastases isolated from six individual animals with matched control DNA isolated from tail clippings (total of 33 exomes). Fourteen tumors and paired control DNA also underwent whole-genome sequencing (WGS; total 18). Raw data were processed through a mouse-specific analysis pipeline (Extended Experimental Procedures).

Considering the role of previously characterized acquired DNA copy number alterations in this model, we first identified recurrent somatic DNA copy number alterations in primary mSCLC tumors (Extended Experimental Procedures; Tables S1B–S1D; Beroukhi et al., 2007; Mermel et al., 2011). As shown in Figures 1A–1C, the most frequent alterations in somatic DNA copy number were whole chromosomal alterations, including losses of Chr19 (9 of 17 primary tumors; GISTIC q value: $<1 \times 10^{-15}$), followed by gain of Chr4 (6/17 primary tumors; GISTIC q value: $<1 \times 10^{-15}$). mSCLC tumors also harbored recurrent loss of Chr8, Chr12, Chr14, and Chr16 (GISTIC q value: 8.34×10^{-7} ; $<1 \times 10^{-15}$, $<1 \times 10^{-15}$, and 8.34×10^{-7} , respectively) and gain of Chr16 (q value 1.6×10^{-6}). In all cases, whole chromosome losses were hemizygous.

We also detected focal Chr4 amplifications that harbored well-established oncogenes previously described in PR mSCLC, including *Myc11* (8/17 tumors; GISTIC q value: 3.7×10^{-7}) and *Nfib* (4/17 tumors; GISTIC q value 1.0×10^{-4} ; Figure 1C; Calbó et al., 2005; Dooley et al., 2011). We identified a recurrent focal deletion encompassing *Mir200a/Mir200b* and the hairy enhancer of split (*Hes2*, *Hes3*, and *Hes5*) family of transcriptional effectors of the Notch signaling pathway (q value 2.39×10^{-5}). Whether these amplified and deleted regions drive progression of mSCLC remains to be tested, but analysis with GISTIC demonstrates that these alterations occurred more frequently than expected by chance, suggesting these events provide selective advantage during tumor progression.

We identified genomic rearrangements in 14 mSCLC tumors by WGS (Table S1E; Extended Experimental Procedures). No

specific classes of rearrangements were enriched in these samples, nor were recurrent rearrangements identified in mSCLC (Figure S1A). However, the vast majority of events occurred on Chr4 (Figure S1B). We investigated the process underlying the complex amplifications on Chr4 by reconstruction of individual Chr4 maps (Figure S1C). This suggested that serial rearrangement cycles, rather than a single event (i.e., chromothripsis), led to generation of the Chr4 oncogenic amplifications in a punctuated manner (Baca et al., 2013; Korbel and Campbell, 2013). Interestingly, the tumor-suppressor loci *Cdkn2a* and *Cdkn2b* are located between *Nfib* and *Myc11* on Chr4 and therefore may pose a selective pressure against whole chromosomal gain or chromothripsis of Chr4 as a mechanism to amplify *Myc11* and *Nfib* function in this setting. PCR-based validation of a subset of putative rearrangements suggested a high degree of confidence in rearrangement calls (Figure S1D; Experimental Procedures). We detected rearrangements with putative function, including a focal deletion of *Magi2*, an upstream component of the phosphatase and tensin homolog (PTEN)/phosphatidylinositol 3-kinase (PI3K) signaling network (Wu et al., 2000; Zmajkovicova et al., 2013). We also noted intrachromosomal rearrangements generating in-frame fusions of Abl1 kinase (*Abl1-Nup214*) and transcriptional regulators *Cited4* (*Cited4-Asap3* and *9030409GRik-Cited4*; Figure S1E).

We next identified point mutations in the exonic sequences of 27 primary tumor and metastasis using muTect (Cibulskis et al., 2013). Exome sequencing revealed a mean of 0.91 protein-altering point mutations per Mb sequenced, or 27.9 protein-altering mutations per tumor (Figure S2A; Table S1F). Given the general lack of experience with these methods in model organisms, we performed two independent validation exercises that suggested these methods were accurate and estimates of mutation frequencies were valid (see Extended Experimental Procedures; Table S1G; Figure S2B).

To begin cross-species analysis of human cancer and murine SCLC genomes, we first compared the overall frequencies of DNA copy number alterations, point mutations, and rearrangements observed in mSCLC to several human tumor types (Extended Experimental Procedures). Interestingly, mSCLCs exhibited a comparable frequency of genomic rearrangements and copy number alterations compared to human cancers but harbored a significantly lower number of point mutations (Figures 1D–1F). Although the mechanisms underlying these observations remain unclear, the low point mutation frequency is likely in part a result of the absence of tobacco-associated mutagens. The high frequency of rearrangements, including complex punctuated rearrangements of Chr4, may be in part a reflection of p53 loss (Rausch et al., 2012). In order to specifically search for shared driver genes in SCLC, we also compared recurrently amplified or deleted regions within mSCLC genomes to available data from human SCLC genome-sequencing studies (Table S1H; Extended Experimental Procedures; Peifer et al., 2012; Rudin et al., 2012). Regions within Chr4 amplification and Chr14 loss in mSCLC were conserved in human SCLC. The region of recurrent amplification on Chr4 encompassing *Myc11* corresponded to a region of amplification on Chr1 in human SCLC harboring *MYCL1*. In addition, a set of genes frequently deleted within the Chr3p region in human SCLC, including the

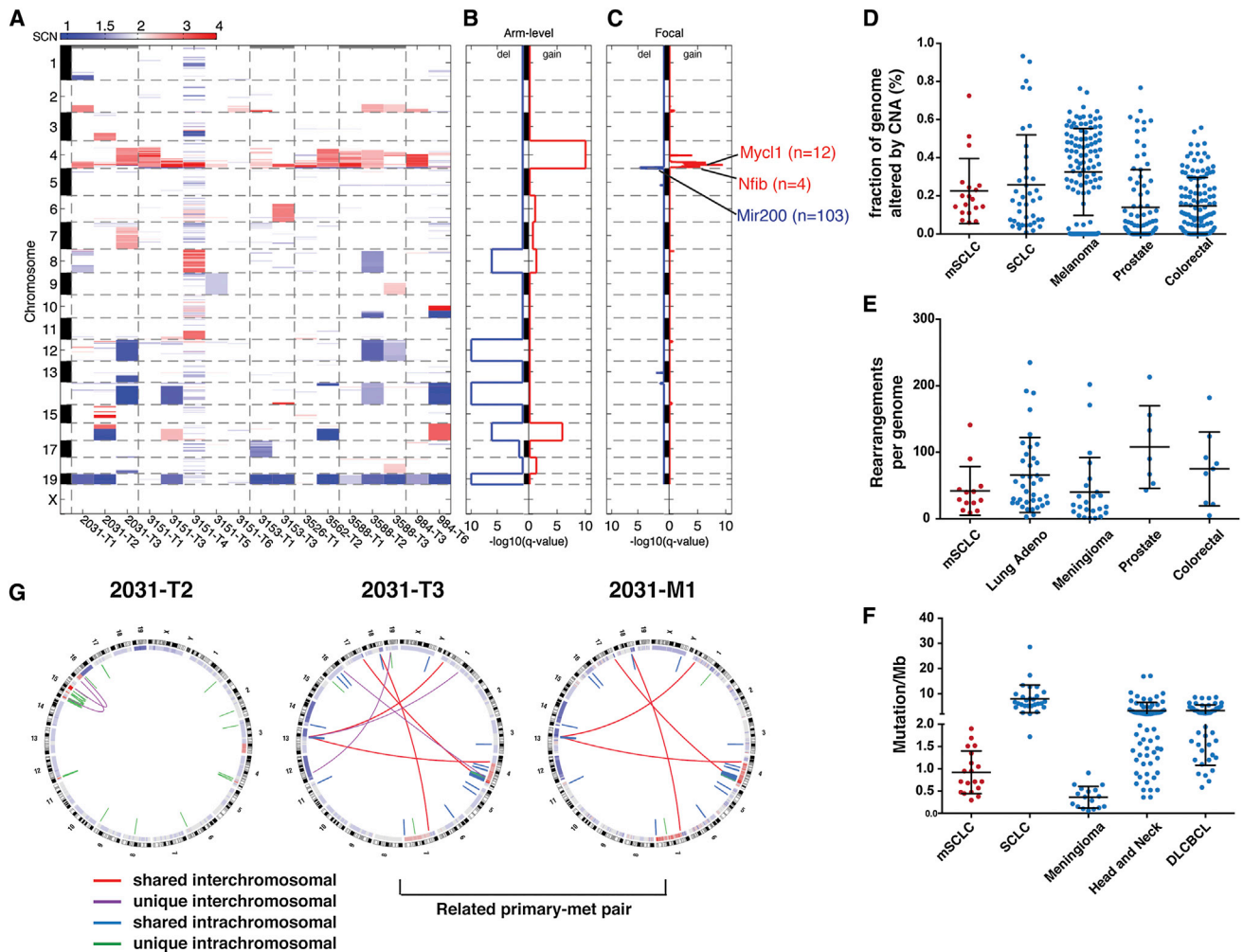


Figure 1. Genome Remodeling during mSCLC Progression

(A) Global DNA copy number alterations (CNAs) shown for mSCLC primary tumors. Blue represents copy loss; red represents copy gain. Individual tumors shown horizontally, chromosomes depicted on vertical axis.

(B) GISTIC analysis of recurrent whole-chromosome CNAs in mSCLC identifies recurrent loss of Chr19, Chr12, Chr14, and Chr16 and recurrent gain of Chr4.

(C) GISTIC analysis of recurrent focal CNAs identifies six recurrent amplification peaks on Chr4 and a single area of recurrent copy number loss on Chr4. Genes of interest are listed next to focal gains and losses, and the number of genes in the peak of the CNA is shown in parentheses.

(D) Comparison between mSCLC and human cancers with respect to the fraction of the genome altered by CNAs.

(E) Comparison of mSCLC and human cancers with respect to the number of rearrangements per tumor.

(F) mSCLCs exhibit a lower point mutation frequency compared to human cancers.

(G) Circos diagrams depicting whole-genome sequencing of mSCLC. Shared rearrangements between primary tumors and metastases identify lineage relationships. Outer band represents metaphase banding pattern; inner track shows DNA copy number alterations. Intrachromosomal rearrangements are shown as blue (shared between multiple tumors) or green (unique); interchromosomal events are shown as red lines (shared between multiple tumors) or purple (unique). See also [Figure S1](#) and [Table S1](#). Error bars (D–F) represent mean and SD.

putative tumor suppressor FHIT, was syntenic to murine Chr14, which was subject to recurrent hemizygous loss ([Wistuba et al., 2001](#)).

The mechanisms that give rise to point mutations in this model are not the focus of this work; however, we observed a noteworthy mutation signature in mSCLC that would bear further investigation ([Figures S2C and S2D](#)). This signature was also dominant in the set of validated mutations ([Extended Experimental Procedures](#)). Interestingly, the signature was not de-

tected in a *Kras*^{G12D}; p53-null driven mouse model of lung adenocarcinoma (data not shown; D.G.M, G.G., and T.J., unpublished data). This suggested the mSCLC signature is unique to this model and not a universal feature of genetically engineered models or p53-null murine cancer cells. These mutations did not occur preferentially in regions of DNA copy number alteration or near rearrangement breakpoints (data not shown), and therefore, we suggest that this mutational signature is the product of an as yet unknown mechanism.

Tsou et al., 1998). We also identified recurrent nonsynonymous mutations in genes encoding other Pten signaling components: Magi1, a scaffolding protein involved in shuttling Pten to the plasma membrane; Eef2k, a downstream PI3K effector involved in the regulation of translation elongation; and Ikbkb, a gene product linking nuclear factor κ B to PI3K signaling (Häcker and Karin, 2006; Kotelevets et al., 2005; Zmajkovicova et al., 2013). Each of these genes was mutated in two clonally independent tumors. This suggests that disruption of Pten signaling at multiple points in the pathway may promote tumor progression in mSCLC. Indeed, ingenuity pathway analysis of all protein-altering point mutations identified in mSCLC revealed enrichment of the PI3K/PTEN networks (Table S1J). In addition, *PTEN* alterations have been reported in human SCLC, further supporting a conserved tumor-suppressive role (Dacic et al., 2002; Forgacs et al., 1998; Yokomizo et al., 1998).

In addition to alterations in Pten signaling, we detected recurrent mutations in the semaphorin (*Sema5b*, *Sema3c*, and *Sema4f*) and ephrin (*Epha5* and *Epha7*) gene families, which regulate cellular migration during embryonic development. Interestingly, axonal guidance pathways have been implicated as drivers in pancreatic cancer by recent cross-species sequencing and transposon-based screens in pancreatic cancer (Biankin et al., 2012).

We also compared genes mutated in mSCLC to two recent human-SCLC-sequencing reports (Peifer et al., 2012; Rudin et al., 2012). Because the mutational burden in human SCLC was high, we analyzed genes mutated in mSCLC relative to the published significantly mutated, hot spot, and clustered genes from both studies (Table S1K). Several genes were mutated in both mSCLC and human SCLC, including *PTEN* and *EPHA7*. However, whether this is the product of the high mutation frequency observed in human SCLC or reflects a conserved functional role for shared events remains to be determined. Of note, only one gene besides *TP53* and *RB1*, *TMEM132D*, was reported as significantly mutated by both human studies. This highlights the challenges associated with genomic analysis of highly mutated human cancer genomes.

The genomic location of *Pten*, Chr19 28.14cM, also raised the possibility that Chr19 loss, the most frequent observed alteration in DNA copy number in mSCLC, may be driven primarily by impairment of Pten function. All tumors harboring *Pten* point mutations also exhibited evidence for loss of Chr19, suggesting that complete loss of Pten function may be advantageous and occur via multiple mechanisms in mSCLC.

To further define the frequency and timing of Pten loss in mSCLC, we examined Pten expression by immunohistochemistry (IHC) in early neuroendocrine bodies and in advanced tumors (Figures 2B–2D). Qualitative analysis of Pten staining revealed that the majority of high-grade mSCLCs exhibit complete loss of Pten as compared to precursor neuroendocrine bodies (Figure S2G), supporting the notion that Pten loss may facilitate tumor outgrowth. We also observed several mSCLC tumors with a mixed Pten status (Figure 2D). Although PI3K independent functions of Pten have been demonstrated, a hallmark of Pten loss is activation of the canonical PI3K/AKT signaling pathway. Therefore, we assessed Pten status and PI3K signaling by IHC for Pten and phospho-Akt (pAktS473).

Pten-negative areas showed a reciprocal increase in pAkt staining by IHC (Figures 2D and 2E), implicating canonical PI3K signaling as a major output of Pten loss during mSCLC progression. In addition, a tumor harboring an inactivating *Pten* point mutation (T131P), and another sample with a *Magi2* deletion, did not show loss of Pten IHC staining but exhibited increased pAkt staining (data not shown).

To test whether mutations in upstream signaling components impact canonical PI3K signaling in SCLC, we depleted Magi1 using small hairpin RNAs (shRNAs) in mSCLC cell lines. Consistent with this model, Magi1 knockdown resulted in increased pAkt signaling uniquely in cells with wild-type *Pten* status (Figure S3A). We detected modestly diminished cellular growth in response to Magi knockdown in mSCLC cells, independent of *Pten* status, suggesting that Magi1 was required for PI3K-independent functions in mSCLC cells, consistent with prior studies (Wegmann et al., 2004).

Pten Deletion in mSCLC Accelerates Tumorigenesis

In order to define the role of Pten loss in mSCLC, we crossed a cre-regulated, conditional *Pten* allele into the PR mSCLC model (hereafter referred to as PRPt for *p53*, *Rb1* and *Pten*; Lesche et al., 2002). To assess tumor growth kinetics in living animals, a cohort of PRPt animals also harbored a cre-activated luciferase reporter allele. We initiated tumors in PRPt (*Trp53^{FL/FL}; Rb1^{FL/FL}; Pten^{FL/FL}*), PRPt/+ (*Trp53^{FL/FL}; Rb1^{FL/FL}; Pten^{FL/+}*), and PR (*Trp53^{FL/FL}; Rb1^{FL/FL}; Pten^{+/+}*) animals by intratracheal administration of adenovirus expressing cre recombinase under the control of the neuroendocrine-specific CGRP promoter in order to selectively delete *Rb1*, *Trp53*, and *Pten* in pulmonary neuroendocrine cells (Sutherland et al., 2011). Measurement of in vivo luciferase activity at 4, 5, and 6 months posttumor induction revealed acceleration of tumor growth in PRPt versus PR animals (Figures 3A and 3B).

We also assessed tumor burden in cohorts of PR, PRPt/+, and PRPt animals 5 months following tumor induction using small-animal MRI. We detected significantly greater tumor volume in PRPt animals (Figures 3C and 3D). Furthermore, we observed a significant reduction in mSCLC tumor latency and significantly reduced overall survival in PRPt (6.3 months) and PRPt/+ (8.3 months) compared to PR animals (17.5 months; Figure 3E). We confirmed the in vivo imaging results in cohorts of PR, PRPt/+, and PRPt animals at 5 months postinduction using quantitative histology, which showed a striking difference in tumor burden (Figure 3F). To ensure a change in tumor spectrum did not underlie the acceleration of tumor progression in PRPt animals, we performed histological analysis of tumor-bearing lung sections. The majority of the tumors identified displayed neuroendocrine features and stained positive for the neuroendocrine marker CGRP, consistent with a role for Pten loss as a driver of SCLC progression (Figures S3B, S3E, and S3H).

The state of PI3K signaling was assessed using phospho-specific IHC for Akt. High levels of pAkt were present in PRPt tumors at 6 months posttumor induction (Figures S3D and S3G). Pten loss and activated Akt signaling are known to promote proliferation and oppose apoptosis. Therefore, we assayed apoptosis and proliferation by IHC. We detected a significant

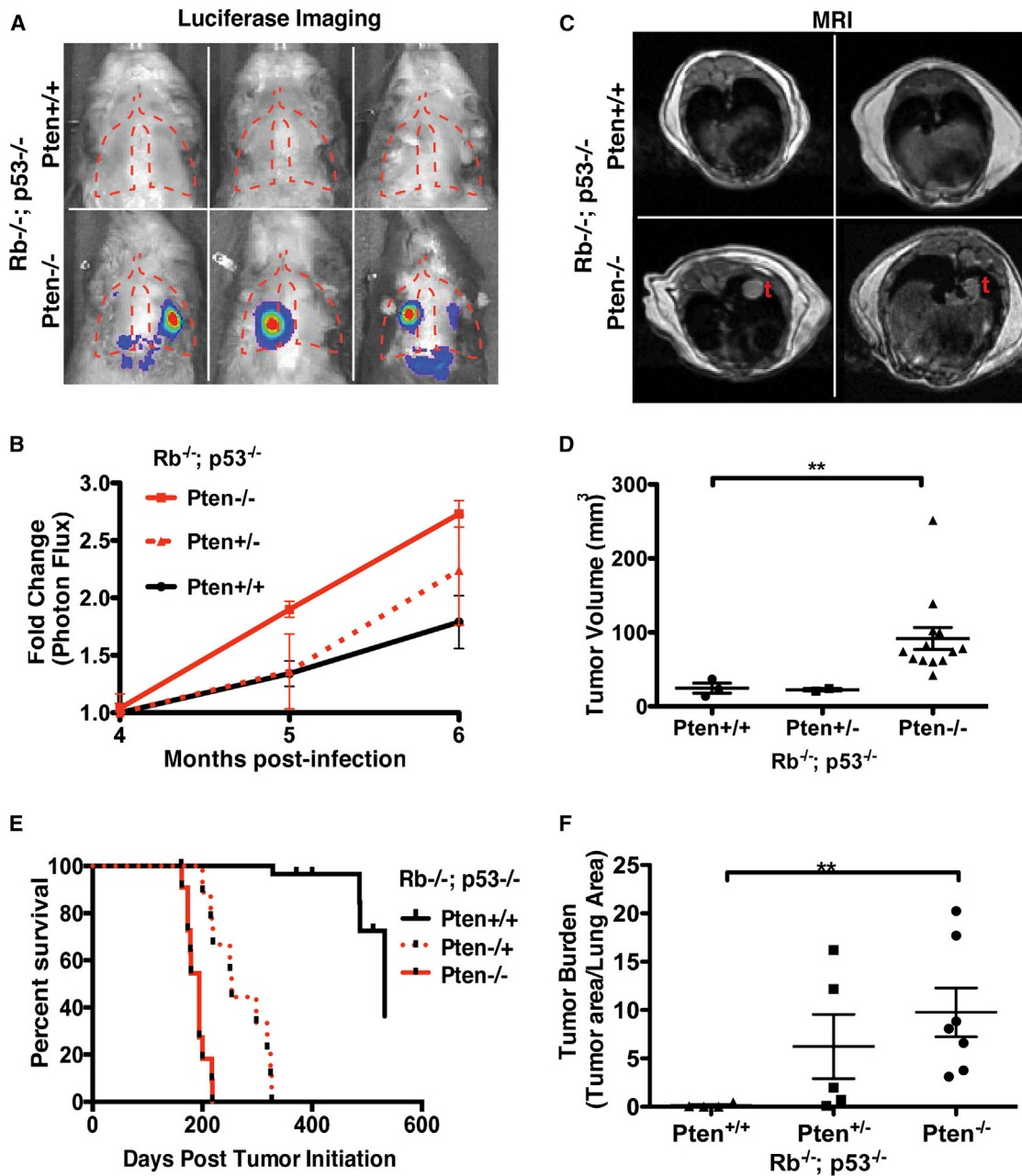


Figure 3. Pten Deletion Accelerates mSCLC Progression

(A) Representative bright field/luminescence images.

(B) Quantitation of luminescence (photon flux) of PR and PRPt animals. Relative photon flux calculated by normalizing all time points per animal to initial measurements at 4 months postinfection.

(C) Representative axial MRI sections of PR and PRPt animals at 5 months postinfection.

(D) MRI tumor volume measurements (mm³).

(E) Overall survival of SCLC cohorts.

(F) Relative tumor burden determined by quantitative hematoxylin and eosin staining microscopy. **p < 0.01.

(B, D, and F) Mean and SEM shown by error bars. See also [Figure S3](#) and [Table S1](#).

increase in phospho-histone H3, a mitotic marker, in the PRPt as compared to PR tumors 6 months after tumor initiation ([Figure S3I](#)). Conversely, we observed a decrease in the levels of cleaved caspase-3, a marker of apoptosis, in *Pten*-null tumors

([Figure S3J](#)). These data support the tumor-suppressive role of *Pten* in mSCLC and provide evidence that loss of *Pten* can drive tumor progression, in part through increased proliferation and diminished apoptosis.

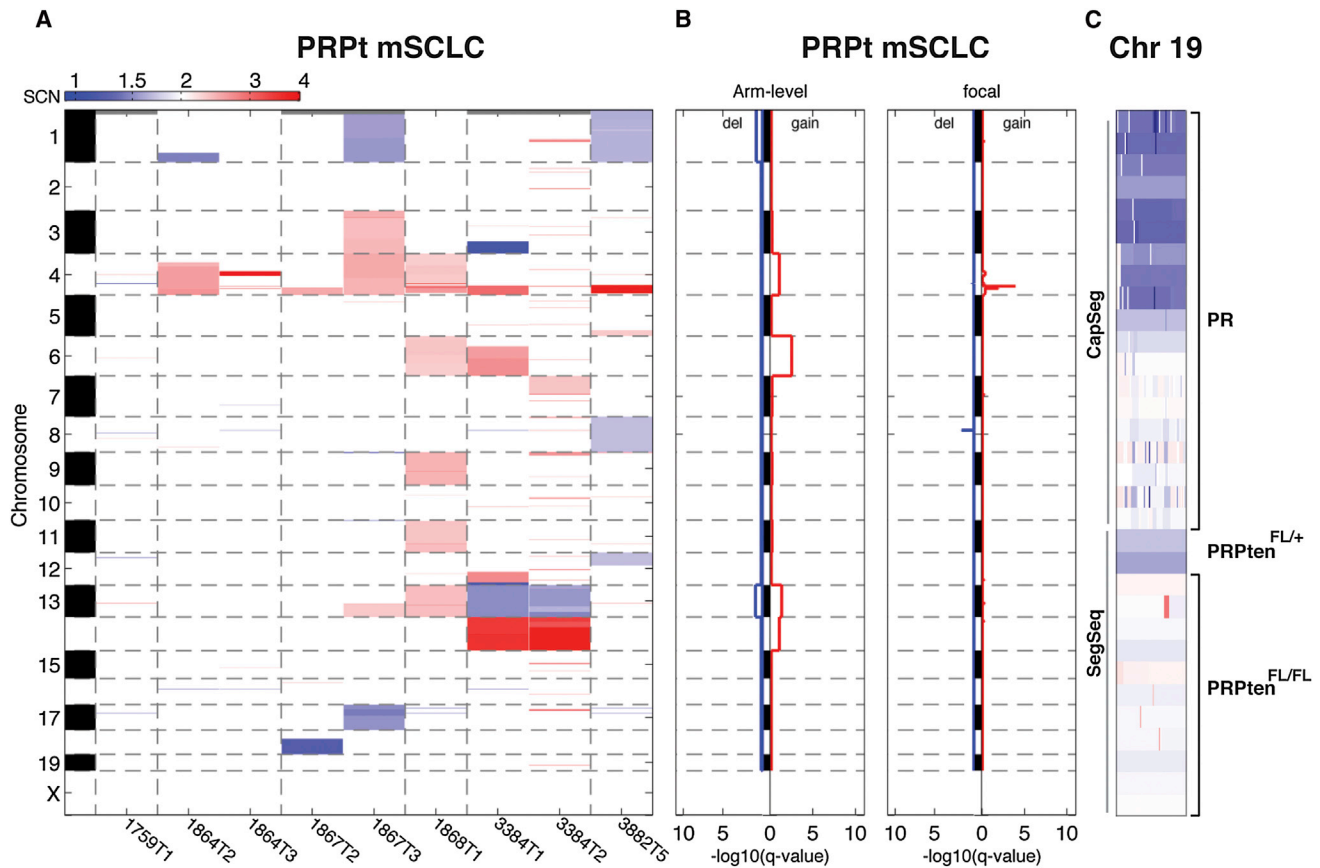


Figure 4. Pten Deletion Alters Genome Evolution in mSCLC

(A) CNA heatmap for PRPt mSCLC tumors analyzed by SegSeq.

(B) GISTIC results for recurrent CNAs. Note the absence of Chr19 deletion and presence of Chr4 focal amplification.

(C) Chr19 copy number map for all primary tumors analyzed. Genotype is listed to the right. Analysis method (CapSeg or SegSeq) listed to the left.

See also [Figure S4](#) and [Table S1](#).

Combinations of Engineered Events Alter the Path of mSCLC Genomic Evolution

Detection of recurrent *Pten* point mutations and the in vivo functional studies provide evidence that *Pten* loss is a crucial event during mSCLC tumor progression. It is therefore reasonable to hypothesize that *Pten* mutation is the driving force behind Chr19 loss in PR mSCLC. To test this notion, we utilized PRPt triple-mutant mSCLC to characterize tumor-genome evolution in the context of *Pten* loss at the time of tumor initiation. We performed low-read-depth whole-genome sequencing of 11 PRPt (nine primary tumors and two metastases) and two PRPt/+ mSCLC tumors to characterize acquired DNA copy number alterations. These tumors were of similar size and histologic grade to PR tumors used in our initial analyses. Consistent with the hypothesis that selective advantage of *Pten* impairment underlies loss of Chr19 in this model, all PRPt mSCLC exhibited a DNA copy number of two for Chr19 ([Figures 4A](#) and [4B](#); [Table S1L](#)). Therefore, deletion of a single exon of *Pten* provided the selective advantage for loss of an entire chromosome in this model. Interestingly, two PRPt/+ tumors exhibited hemizygous

loss of Chr19, and review of the sequencing reads demonstrated that the mutant chromosome 19 was retained, suggesting additional selective advantage of complete *Pten* loss ([Figure 4C](#)).

Despite the decreased tumor latency and absence of Chr19 loss in the PRPt mSCLC tumors, we detected recurrent focal amplifications on Chr4 in these samples ([Figure 4B](#); [Table S1M](#)). Although GISTIC analysis did not show *Myc1* within the predicted amplification peak, our sequencing read depth was designed to detect whole-chromosome gains and losses rather than focal alterations. Therefore, we used quantitative PCR to assess *Myc1* amplification in these samples. *Myc1* copy number was amplified in these tumors, suggesting an important role for *Myc1* amplification during the initial outgrowth of mSCLC ([Figure S4](#)).

Intratumoral Clonal Heterogeneity in mSCLC

We established tumor lineage relationships between primary tumors and metastases from individual mice by identification of shared DNA rearrangements and point mutations (example, [Figure 1G](#)). Using this approach, we identified related

primary-metastasis pairs from six animals, including three tumor families from which we sequenced multiple metastatic lesions (Table S1N). Although shared somatic mutations can identify basic lineage relationships between tumors, more sophisticated methods are required to reconstruct the clonal architecture of tumor progression. We first examined the allelic fraction of somatic mutations in mSCLC tumors. The observed distribution of allelic fractions for all somatic mutations observed in primary tumors revealed an abundance of mutations with low allelic fraction. However, metastases exhibited a greater proportion of mutations with high allelic fraction, consistent with a clonal bottleneck during metastatic seeding (Figures S5A and S5B).

The allelic fraction of a mutation depends on tumor purity, local DNA copy number, and the fraction of cells in a tumor that harbor the mutation. Therefore, in order to systematically characterize the clonal structure of PR mSCLC tumors, we used ABSOLUTE, a method that utilizes the copy number of DNA in the vicinity of a mutation and tumor purity to estimate the fraction of cancer cells harboring a given mutation, called the cancer cell fraction (CCF) (Carter et al., 2012; Landau et al., 2013). ABSOLUTE analysis confirmed the presence of clonal heterogeneity in all mSCLC tumors, with a range of two to five subclones within individual tumors (Tables S1O–S1Q). We compared the CCF for individual mutations between primary tumors and metastases using two-dimensional plots in order to define the clonal structure of mSCLC (Figure 5). Clonal lineages were identified by clustering mutations exhibiting shared CCF (Landau et al., 2013). As a tumor subclone colonizes metastatic sites, it passes through population bottlenecks in which the preexisting mutations are enriched and additional mutations are subsequently acquired. We denote clonal lineages by a common nomenclature (for example, clone 1a is a descendent of clone 1 and clone 1b is a descendent of clone 1a, whereas clone 2 is a related, but independent, sibling of clone 1). The number of mutations delineating each clonal transition is shown in Figure 5, and all mutations in the tumor families detailed below are annotated with the CCF and subclone assignment in Tables S1O–S1Q.

Parallel Seeding of Multiple Liver Metastases in mSCLC

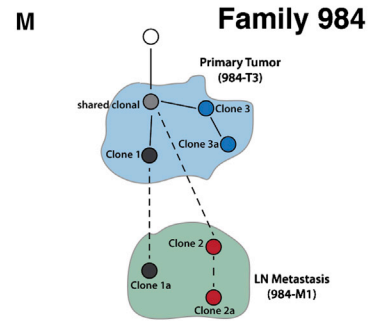
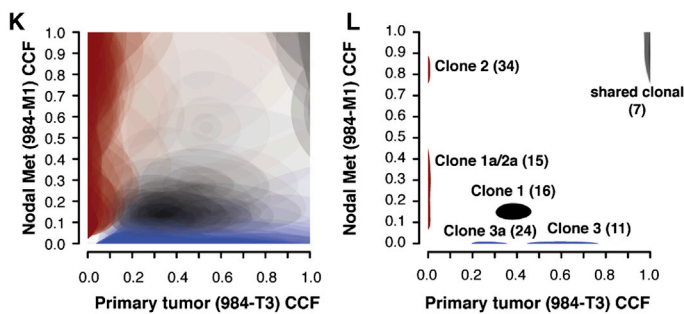
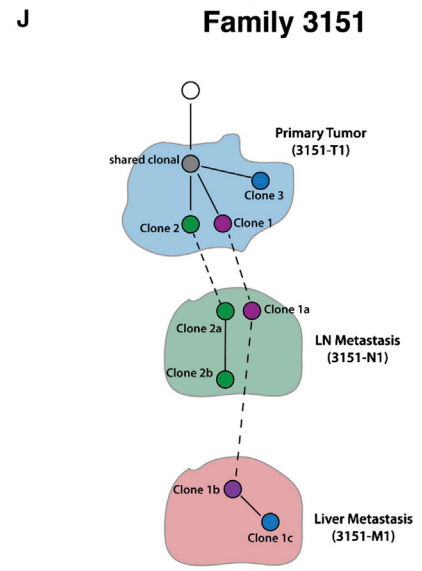
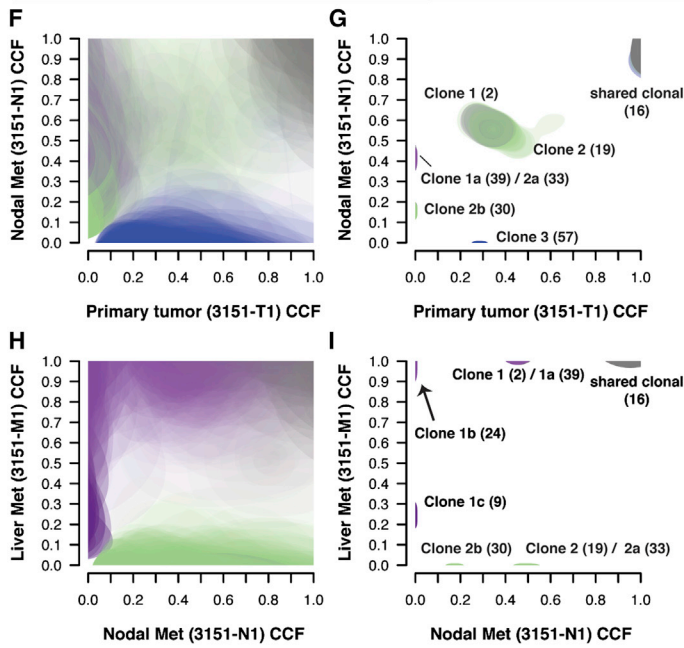
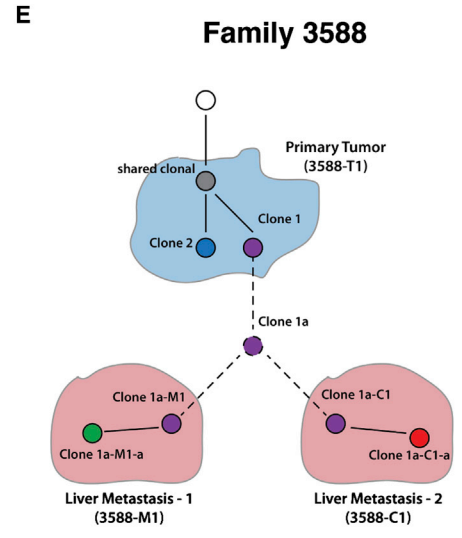
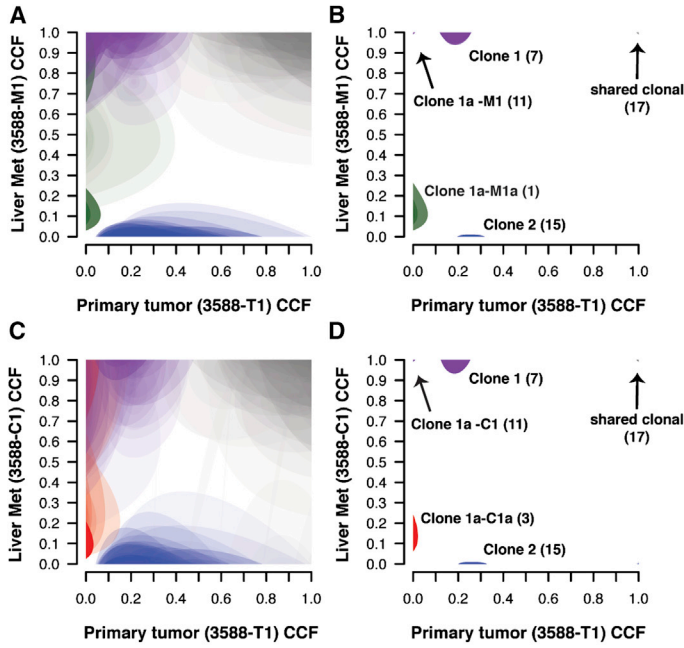
From animal 3588, we sequenced three primary tumors and two independent liver metastases (Figures 5A–5E; Table S1O). Both liver metastases (3588-C1 and 3588-M1) shared 17 clonal mutations with one primary tumor, 3588-T1, demonstrating that these arose from a single primary tumor. 3588-T1 harbored two independent subclones existing at approximately 0.2 CCF (clone 1, purple) and 0.25 CCF (clone 2, blue; see Figures 5B–5D). Interestingly, both liver metastases originated from closely related subclones (clone 1a-M1 and clone 1a-C1) that were descended from a common ancestor (clone 1a). Clone 1a was a descendent of clone 1, as demonstrated by the enrichment of the CCF of clone 1 mutations in both descendent metastases (Figures 5B and 5D, purple clusters). We could not discriminate if clone 1a was present in the primary tumor outside of the sampled region or below the level of detection or whether it first seeded another site prior to founding the liver metastases. Each metastatic lesion also continued to evolve during outgrowth as evidenced by acquisi-

tion of subclonal mutations (clone 1a-M1-a, green, and clone 1a-C1-a, red; Figures 5B, 5D, and 5E).

Polyclonal Seeding of Local Lymph Node Metastases in mSCLC

We sequenced five primary tumors, one thoracic lymph node metastasis, and one liver metastasis from animal 3151. Again, in this case, both metastases shared acquired clonal mutations with one primary tumor, confirming their shared origin (light gray clusters, Figures 5G and 5I; Table S1P). Comparison of the primary tumor (3151-T1) and lymph node metastasis (3151-N1) revealed a large cluster of mutations (green-light purple central cluster, Figure 5G) present at subclonal CCF in both the primary tumor and metastasis. A single-cell-origin model would require mutations to become clonal in a descendent metastasis. Therefore, these data were inconsistent with monoclonal origin of the lymph node metastasis (Figures 5F–5J). Comparison of the lymph node and liver metastases (3151-M1) revealed that only a subset of mutations in this cluster was shared with the liver metastasis (Figures 5H and 5I; clone 1 mutations). In addition, mutations in clone 1a from the nodal metastasis (3151-N1) were enriched to a clonal CCF (1.0) in the distant liver metastasis (Figure 5I). We therefore concluded that two related primary tumor subclones (clone 1, light purple, and clone 2, green; Figure 5G) seeded the lymph node metastasis and gave rise to clones 1a and 2a (Figure 5G). However, only one of these clones spread to the liver (clone 1b, a direct descendent of clone 1a from the lymph node metastasis; Figure 5J). Clone 1b was the founding clone of the liver metastasis and was a recent descendent of clone 1a, as shown by the enrichment of clone 1a CCF (~0.5 to 1.0) in the distant liver metastasis (3151-M1; Figure 5I). We cannot formally exclude the possibility that two highly related clone 1 cells spread directly from the primary tumor to both the lymph node and liver metastasis. However, in this scenario, we would not have expected all clone 1a mutations to be shared with the liver metastasis, as we observed. Therefore, the most parsimonious explanation for the observed data is that two primary tumor subclones first seeded the nodal metastasis and that clone 1a further evolved into clone 1b and founded a tertiary liver metastasis.

Two primary tumors and one lymph node metastasis were sequenced from animal 984. Shared somatic mutations demonstrated that primary tumor 984-T3 founded the lymph node metastasis 984-M1 (Table S1Q). Analysis of this relationship using ABSOLUTE revealed that clone 1 (dark gray, Figures 5K and 5L) was present at subclonal CCF in both the primary tumor and metastasis. This pattern is also inconsistent with monoclonal origin of the nodal metastasis and indicated that multiple primary tumor (984-T3) subclones (clone 1, dark gray, and clone 2, red) spread to the local draining lymph node. Although clone 2 mutations were not detected in the primary tumor, the presence of shared clonal mutations between 984-T3 and 984-M1 (light gray cluster, Figure 5L) confirmed that both subclones within the local lymph node arose from a single primary tumor (984-T3; Figure 5M). In each of these analyses, although we identified specific mutations present within individual subclones, our data did not address whether individual mutations acted as drivers or passengers.



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DISCUSSION

Comparative Genomics to Identify Driver Genes in Cancer

A longstanding goal of cancer genetics has been to exploit the evolutionary conservation of the major tumor-suppressive and proto-oncogenic cellular pathways between humans and mice for biological discovery and preclinical modeling. Recently, this has included analysis of acquired mutations in the genomes of mouse cancer models. For example, focused DNA sequencing of known proto-oncogenes in genetically engineered mouse models initiated by “weak” cancer initiators has identified somatically acquired activating mutations in *Hras* and *Notch1* (O’Neil et al., 2006; Podsypanina et al., 2004). In addition, small-scale exome and genome sequencing of murine models of leukemia and breast cancers has identified conserved somatic *Jak1* and *Trp53* mutations (Wartman et al., 2011; Yuan et al., 2012).

The present study is to our knowledge the most complete description of the somatic genome of a genetically engineered mouse cancer model to date and also quantitatively assesses intratumoral clonal heterogeneity and clonal evolution during metastatic colonization. In the absence of tobacco mutagens, we detected relatively few somatic point mutations compared to human SCLC and mutagen-induced murine tumors (Matsushita et al., 2012). The reduced mutational “noise” facilitated identification of *Pten* loss as an important driver of tumor progression in mSCLC. We detected recurrent somatic alterations targeting *Pten*, including point mutations previously described in human cancer and Cowden syndrome. In addition, we detected acquired point mutations in other components of the PTEN/PI3K pathway, including *Magi1*, *Eef2k*, *Ikbkb*, *Insr*, and *Bcar1*. The majority of PR mSCLC tumors harbor a mutation in this pathway and/or Chr19 loss. We also provide a functional validation of the role of *Pten* by compound deletion of *Pten* in the autochthonous mSCLC model. These results are consistent with a prior publication, suggesting engineered *Pten* loss accelerates early tumorigenesis in a similar SCLC model (Song et al., 2012), and we additionally characterize the effect of *Pten* deletion at all stages of SCLC progression, including a dramatic decrease in survival of PRPt animals.

Recent sequencing of human SCLC identified multiple mutations in the PTEN/PI3K pathway, including *PTEN*, *PIK3CB*, *PIK3R3*, *MAGI1*, and *MAGI2* mutations. Although *PTEN* was not identified as a recurrent target of deletion in SCLC, Chr10 copy number loss encompassing *PTEN* was evident in one study (Peifer et al., 2012). In addition, prior studies have demonstrated *PTEN* alterations in approximately 20% of SCLC (Dacic et al.,

2002; Forgacs et al., 1998; Yokomizo et al., 1998). Therefore, we suggest that PR mSCLC models a subclass of human SCLC harboring alterations in the PTEN pathway.

Our data support a model in which *Pten* acts primarily as a classical, rather than haploinsufficient, tumor suppressor in mSCLC. First, *Pten* protein expression was lost completely in the majority of high-grade SCLC. In addition, all *Pten* point mutations occurred in tumors with copy number loss at Chr19, suggesting that *Pten* function was completely abrogated in these cells. Finally, PRPt/+ animals showed evidence for loss of the wild-type (WT) *Pten* allele, suggesting additional selective advantage of complete *Pten* loss.

Single Locus Control of Chromosomal Alterations in Cancer

Whole-chromosome gains and losses are frequently observed in human cancers, yet it remains unclear whether the selective advantage for these events results from one or multiple loci. Several studies in mouse models have suggested that multiple loci confer selective advantage for whole chromosome gain and loss. For example, *Kras-LA2* animals developed spontaneous lung adenomas, and these tumors frequently exhibited whole-chromosome gains of the *LA2*-bearing mutant Chr6, whereas focal *Kras-LA2* amplifications were uncommon (Sweet-Cordero et al., 2006; To et al., 2011). This led to the speculation that additional oncogenic Chr6 loci are under selection, including other components of Mapk signaling (To et al., 2011). In addition, prior studies of radiation-induced lymphomas from *Trp53*^{+/-} animals identified frequent loss of heterozygosity (LOH) at Chr19 and focal deletions involving *Pten* (Mao et al., 2003). Interestingly, whole-chromosome loss of Chr19 was also noted in *Pten*^{+/-} and *Pten*^{+/-}; *Trp53*^{+/-} lymphomas and was interpreted as evidence for the existence of additional tumor-suppressor loci.

The data presented in this study implicate a single gene, *Pten*, at the driving force behind loss of Chr19 in mSCLC. Of note, Mao et al. (2004) showed frequent whole-chromosome loss of Chr3 in radiation-induced lymphomas in *Trp53*^{+/-} mice and identified *Fbxw7* as a candidate tumor suppressor in a small focal deletion. Heterozygous loss of *Fbxw7* accelerated tumorigenesis and abrogated *Fbxw7* LOH, which was inferred to reflect maintenance of the entire chromosome. However, these studies restricted LOH analysis to the *Fbxw7* locus. The data presented here extend the concept that a selective advantage for impairment of a single locus can drive loss of an entire chromosome and definitively demonstrate retention of Chr19 in PRPt mSCLC using whole-genome methods. The fact that no PRPt tumor analyzed exhibited DNA copy number

Figure 5. Clonal Evolution of mSCLC during Metastatic Spread

Each tier (A–E, F–J, and K–M) shows ABSOLUTE analysis of related primary and metastatic tumors in an individual animal. Left column of plots (A), (C), (F), (H), and (K) shows unclustered CCF results for individual mutations in tumor pairs. Each cloud represents the 95% confidence interval of the predicted CCF for each mutation. Middle plots (B, D, G, I, and L) show the 95% confidence intervals following a Bayesian clustering procedure that groups mutations into predicted subclones. Clonal models based on ABSOLUTE results are shown in (E), (J), and (M). Dashed lines represent assumed transitions that are not directly observed in the data. In all panels, cloud color denotes membership in corresponding node (clone) in the model diagram. (A–D) CCF results demonstrating a single subclone (purple) from the primary tumor seeded two independent liver metastases. (F and G) shows multiple subclones from the primary tumor (clone 1 and clone 2) seeding a lymph node metastasis. Clone 1b (purple), a descendent of clone 1a, seeded a tertiary liver metastasis from the lymph node (H and I). (K and L) CCF results showing polyclonal seeding of a lymph node met (gray, clone 1a, and red, clone 2).

See also Figure S5 and Table S1.

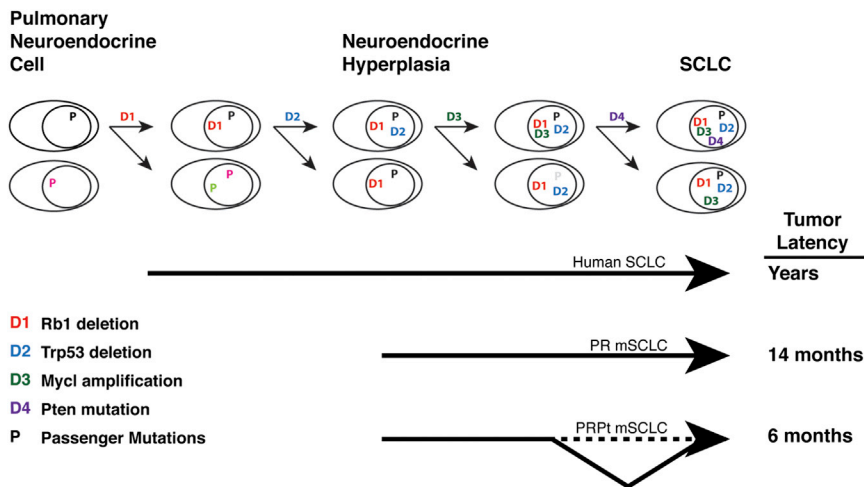


Figure 6. Model of SCLC Tumorigenesis

Stepwise acquisition of recurrent driver mutations identified by comparative SCLC sequencing (D1–D4) promotes murine SCLC progression from the pulmonary neuroendocrine cell to bona fide SCLC. As additional drivers are engineered into the mouse model, tumor latency is reduced and progression is accelerated. P, passenger mutations fixed in the tumor population during progression through the series of bottlenecks.

loss of Chr19 is a powerful demonstration that loss of the *Pten* tumor suppressor is the driving selective mechanism behind loss of Chr19 in PR mSCLC.

Patterns of Clonal Progression in mSCLC

The description of clonal evolution between primary tumors and metastases in solid human malignancies has been achieved primarily by sequencing several distinct tumor regions (Campbell et al., 2010; Gerlinger et al., 2012; Yachida et al., 2010). However, in contrast to most human biopsies, which sample only a small part of a tumor, we utilized approximately 50% of the individual mSCLC tumor mass for nucleic acid preparation. Thus, a large fraction of tumor sampling coupled with a deep sequencing coverage (approximately 100×) may have helped elucidate the patterns of clonal evolution between primary tumors and metastases in the mSCLC model. We also capitalized on the high frequency of macroscopic metastases in the mSCLC model and our ability to harvest these diverse sites of disease at animal necropsy. We believe our finding of spread of multiple primary tumor subclones to a local lymph node metastasis is unprecedented and the first demonstration of polyclonal seeding of metastases using deep sequencing. Considering the role of the metastatic niche in mediating treatment resistance (Gilbert and Hemann, 2010), the fact that multiple tumor subclones establish themselves in environments such as the lymph node may have therapeutic implications.

We provide evidence of spread of a tumor subclone from a lymph node metastasis to a distant site (Figure 5J). Sequential spread of metastasis from one site to another has also been demonstrated in human pancreatic cancer (Campbell et al., 2010; Yachida et al., 2010). These and our data raise the possibility that lymph nodes can act as the site of collection of multiple tumor subclones and may serve as a gateway for distant metastases. These data are consistent with the prognostic implication of sentinel lymph node biopsy in several cancer types (Chen et al., 2006). However, whether seeding of lymph node metastases prior to systemic dissemination is a more uniform property of cancer metastasis will require additional studies. In addition, it will be important to determine if additional genetic and or

epigenetic alterations acquired in the local lymph node microenvironment contribute to systemic dissemination. The ability to illuminate the dynamic clonal architecture within metastatic mSCLC tumors highlights the opportunity to more completely dissect clonal metastatic progression in this experimentally tractable system.

A Model for Tumorigenesis in SCLC

The genomic and functional data presented here begin to establish a framework for tumorigenesis in SCLC (Figure 6). The near-ubiquitous presence of *TP53* and *RB1* mutations in human SCLC suggests that these are among the earliest events in these tumors. In this genetic context, we believe *Myc1* amplification events provide a strong proliferative advantage. Although the clonality analysis described in this study did not allow for characterization of high-level amplifications, the ease of detection of the Chr4 amplifications suggests that these amplifications arise during early outgrowth of the primary tumor. In addition, the occurrence of focal Chr4 amplifications in the setting of engineered *Pten* deletion is a strong demonstration of the requisite nature of *Myc1* amplification in early mSCLC outgrowth. These data also suggest that *Pten* mutations are selected for at later stages of tumor progression, a notion supported by our *Pten* IHC analysis showing tumors with areas both positive and negative for *Pten* expression.

Therapeutic targeting of *Pten* signaling with available high-potency inhibitors of PI3K might therefore be warranted for human SCLC. However, although we detect increased phospho-Akt in advanced mSCLC, it is not certain that the effects of *Pten* loss are entirely mediated via increased PI3K activity. In addition, increased *MYC* DNA copy number or gene expression has been shown to mediate primary resistance to PI3K inhibition (Ilic et al., 2011; Shepherd et al., 2013). Considering the frequent occurrence of Chr4 amplifications involving *Myc1*, combination therapy targeting L-myc or biological effectors of L-myc may be necessary to achieve effective responses.

Implications for Tumor Evolution in Mouse Cancer Models

Characterization of PR tumors by exome and genome sequencing revealed a highly molded somatic genome with a low somatic point mutation frequency relative to human cancers. Interestingly, PRPt tumors exhibited a less-complex tumor

genome by DNA copy number analysis. This may reflect the addition of a third driver event (Pten loss) at tumor initiation that bypasses a critical bottleneck during tumor outgrowth. This notion is supported by previous studies showing recurrent acquisition of activating oncogene mutations in models initiated by transgenes with relatively modest impact on proliferation (Podsypanina et al., 2004). Therefore, although the initiating engineered mutations are often credited with the entire tumor phenotype, somatically acquired events should be considered when interpreting results of both discovery efforts and preclinical studies using mouse cancer models. The work described here demonstrates the potential of harnessing the shared evolution of GEMMs and human cancers using comparative genome sequencing to identify acquired drivers of cancer progression and dissect stepwise tumorigenesis.

EXPERIMENTAL PROCEDURES

Mouse Model

$p53^{fl/fl};Rb^{fl/fl}$ and $p53^{fl/fl};Rb^{fl/fl};Rosa26^{LSL-Luc/LSL-Luc}$ mice have been previously described (Dooley et al., 2011; $Rosa26^{LSL-Luc/LSL-Luc}$ mice are from E. Jackson and T.J., unpublished data). To obtain $p53^{fl/fl};Rb^{fl/fl};Rosa26^{LSL-Luc/LSL-Luc};Pten^{fl/fl}$ mice, we obtained $Pten^{fl/fl}$ animals from Jackson Laboratories ($Pten^{tm1Hwu/j}$; Lesche et al., 2002). Tumors were initiated by adenoviral delivery of Cre, as described previously (DuPage et al., 2009). The Massachusetts Institute of Technology (MIT) Institutional Animal Care and Use Committee approved all animal studies and procedures. Primary tumors and metastases from the mouse model were dissected and snap-frozen for DNA and/or RNA isolation as previously described (Dooley et al., 2011). In parallel, part of each tumor was kept for histology to verify SCLC features. Live-animal imaging was performed using an IVIS Spectrum (PerkinElmer) and Varian 7T/310/ASR MRI system (Varian/Agilent Technologies).

Genome, Exome Sequencing

Whole-exome sequencing was performed as previously described (Gnirke et al., 2009). Whole-genome sequencing was performed using a protocol developed for human whole-genome studies (Berger et al., 2011). Low-coverage whole-genome sequencing and DNA copy number analysis was performed as previously described (Dooley et al., 2011). Mutations were identified using MuTect (Cibulskis et al., 2013). Recurrence was assessed using MutSig 1.0 with minor modifications for mouse data (Berger et al., 2011; Getz et al., 2007). All somatic mutations were reviewed manually, and validation of selected mutations was performed by targeted resequencing using microfluidic PCR (Access array system; Fluidigm) and the MiSeq sequencing system (Illumina). Genomic rearrangements were identified by dRanger (Berger et al., 2011). DNA copy number alterations were identified from exome data using CapSeg (A.M., B. Hernandez, M. Meyerson, G.G., and S.L.C., unpublished data), and GISTIC 2.0 was used to identify recurrent alterations (Beroukhir et al., 2010; Mermel et al., 2011). SegSeq was used to identify copy number alterations (CNAs) from WGS data (Chiang et al., 2009). See [Extended Experimental Procedures](#) for additional details.

Immunohistochemical Analysis

IHC was performed on formalin-fixed paraffin-embedded 4 μ m sections using the ImmPRESS Peroxidase Polymer Detection Kit (Vector Laboratories) with recommended dilutions of primary antibodies (see [Extended Experimental Procedures](#)).

Murine SCLC Cell Line Functional Experiments

Murine SCLC cell lines were maintained as previously described (Dooley et al., 2011). Broad TRC shRNAs (shMagi1_83: TRCN0000079083, shMagi1_83: TRCN0000079084) were used for Magi1 knockdown. Following infection with Magi1 or control shRNA-expressing lentiviruses, cells were selected

using puromycin (Sigma). After puromycin selection, cells viability was assessed by Cell Titer Glo (Promega).

ABSOLUTE Analysis and Deductive Logic of Clonal Evolution Mapping

ABSOLUTE was performed as previously described (Carter et al., 2012; Landau et al., 2013). All mutations that define clonal lineages underwent extensive manual review using IGV (Robinson et al., 2011) to ensure models were generated using high-confidence mutations.

ACCESSION NUMBERS

The NCBI BioProject accession number for the sequences reported in this paper is PRJNA223640.

SUPPLEMENTAL INFORMATION

Supplemental Information includes Extended Experimental Procedures, five figures, and one table and can be found with this article online at <http://dx.doi.org/10.1016/j.cell.2014.02.031>.

AUTHOR CONTRIBUTIONS

D.G.M., T.J., and G.G. designed the study, and D.G.M. wrote the manuscript. D.G.M. and T.P. equally contributed to biological interpretation of sequencing results and performed experiments. A.T.-W. and C.S. contributed equally to analysis of sequencing data. S.C. performed ABSOLUTE analysis of sequencing data. Inference of clonal evolution was performed by S.C., D.G.M., T.P., and A.T.-W. G.G. and T.J. supervised data analysis and experiments.

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EXTENDED EXPERIMENTAL PROCEDURES

Exome and Genome Sequencing

To isolate DNA from tumors and normal tissue, samples were digested in 800 $\mu\text{g}/\text{mL}$ proteinase K overnight at 55°C and phenol/chloroform-extracted and alcohol precipitated using standard techniques. Tumor RNA was isolated using RNAqueous kit (Life technologies, CA). Sequencing was performed as previously described (Blumenstiel et al., 2010; Costello et al., 2013; Fisher et al., 2011; Gnirke et al., 2009). Briefly, 0.5–3 μg of DNA from each sample was used for library preparation, which included shearing and ligation of sequencing adaptors. Exome capture was performed using the Agilent SureSelect XT Mouse All Exon Kit. DNA was sequenced using the Illumina HiSeq platform, and paired-end sequencing reads of length 76bp and average fragment lengths of 150bp (range 104–168bp) were generated for each sample. Samples were multiplexed and sequenced on multiple Illumina HiSeq flow cells to average target exome coverage of 105.7x in tumor DNA and 85.8x in normal tissue DNA sampled from the tail. WGS reads were of length 101bp with average fragment lengths of 335bp (range 216 to 361bp per library) to an average depth of coverage of 136.2x for tumor samples and 55.4x for normal samples. Alignments to mm9 (<http://www.ncbi.nlm.nih.gov/assembly/165668/>) using bwa (Li and Durbin, 2010) version 0.5.9-r16 and quality control were performed using the Picard (<http://picard.sourceforge.net/>) and Firehose (<http://dx.doi.org/10.7908/C180514N>) pipelines at the Broad Institute. Firehose is a framework combining workflows for the analysis of cancer sequencing data. The workflows perform quality control, local realignment, mutation calling, small insertion and deletion identification, rearrangement detection, and coverage calculations, among other analyses. Although the pipeline was developed for human cancer analysis, modifications to the pipeline enabled the analysis of mouse sequence data.

Mutation Calling

The MuTect algorithm (<http://www.broadinstitute.org/cancer/cga/mutect>) was used to identify somatic mutations in targeted exons and whole-genome data (Cibulskis et al., 2013). MuTect identifies candidate somatic mutations by Bayesian statistical analysis of bases and their qualities in the tumor and normal BAM files at a given genomic locus. The lowest allelic fraction at which somatic mutations could be detected on a per-sample basis was estimated based on cross-contamination level of 2%. All somatic mutations were reviewed manually from their respective BAM files using the Integrative Genomics Viewer (Robinson et al., 2011).

Mutation Significance Analysis

For the purpose of discovering recurrently mutated genes, we used the MutSig 1.0 algorithm (<http://www.broadinstitute.org/cancer/cga/mutsig>), as described (Berger et al., 2011; Chapman et al., 2011; Getz et al., 2007; Lee et al., 2012) with slight modifications for mouse data. In short, this method builds a background model of mutational processes, which takes into account the genome-wide variability in mutation rates. Each gene is assigned a p value quantifying how consistent the observed mutations are relative to the background mutation rate. The false detection rate is then estimated from the p values (Benjamini and Hochberg, 1995) and the genes are ranked according to the significance of the excess of nonsilent mutations beyond the background mutation rate. Compared to MutSig CV (Lawrence et al., 2013) MutSig 1.0 does not consider many covariates, several of which are not readily available for model organisms, such as replication time or tissue-specific expression, but its relative simplicity is well suited for analysis of low mutation rate tumors such as the mouse SCLC model. To preclude “double-counting” of shared mutations in related primary tumor-metastasis pairs, we compressed mutations across related samples, keeping only the event occurring in the primary tumor.

Identification of Rearrangements

The dRanger algorithm (Baca et al., 2013; Berger et al., 2011; Chapman et al., 2011; Hodis et al., 2012; Imielinski et al., 2012) was used to detect genomic rearrangements by identifying instances where the two read pairs mapped to distinct regions of the genome or mapped in a manner that suggested another structural event such as an inversion. Candidate somatic rearrangements were queried in both the matched normal genome and a panel of nontumor genomes to remove germ-line events. The Breakpointer algorithm (Drier et al., 2013) (<http://www.broadinstitute.org/cancer/cga/breakpointer>) scanned for split read supporting evidence at the sites of all candidate rearrangements. To compensate for the low number of normal mouse WGS samples, and the lower coverage within those samples, we required a more stringent standard of evidence than those used for human studies. For each rearrangement site found within a tumor or corresponding met sample, at least one of the samples must have a dRanger score ≥ 7 (observed in at least 7 read pairs) as well as Breakpointer confirmation were required in this analysis.

Tumor Purity

Tumor purity was estimated based on the degree of remaining normal read coverage within the engineered Trp53 deletion. For each sample the observed count of uniquely mapped reads within the deleted region (chr11:69396589–69404536) was tallied for tumor as well as for normal samples. Read depth was also measured for all other genomic locations in bins of 10Mb. For each tumor sample, coverage was linearly fit to the corresponding normal coverage. Outlier bins were removed from the fit to minimize the effect of large somatic copy alternations in the tumor sample. The linear fit provided the expected number of tumor reads (N_{exp}) as a function of normal read coverage, which was then compared to the observed number of tumor reads in the Trp53 region (N_{obs}). The estimated tumor purity is then $\text{purity} = 1 - N_{\text{obs}}/N_{\text{exp}}$, with confidence intervals based on the Poisson error in N_{exp} , as well as the uncertainty of the linear fit.

Somatic Copy Number Alternation Detection

Somatic copy number alterations (SCNAs) were identified from the whole exome data from the ratio of tumor read depth to the expected read depth derived from a panel of normal samples using the CapSeg program (A.M., B. Hernandez, M. Meyerson, G.G., and S.L.C., unpublished data). The SegSeq program (Chiang et al., 2009) was used for SCNA detection in WGS data. We utilized GISTIC 2.0 to identify recurrent events in primary mSCLC tumors to avoid over-representing shared events between related primary tumor-metastasis pairs. The GISTIC2 program (Beroukhim et al., 2010) was adapted for mouse analysis based on CapSeg SCNAs.

Validation

Validation of selected mutations was performed by targeted resequencing using microfluidic PCR (Access array system, Fluidigm) and the MiSeq sequencing system (Illumina). In total, 322 putative mutations were validated by this approach, including 100 mutations chosen at random and an additional 222 mutations of biological interest. Tumor and matched normal samples were selected based on the presence of the indicated mutations by whole exome sequencing. Target specific primers were designed to flank sites of interest and produce amplicons of 200 bp \pm 20 bp. Molecularly barcoded, Illumina-compatible specific oligos, containing sequences complementary to the primer tails were added to the access array chip in the same well as the genomic DNA samples (20–50 ng of input) such that all amplicons for a given genomic sample share the same index. PCR was performed on the Fluidigm access array according to the manufacturer's instructions. Indexed libraries were recovered for each sample in a single collection well from the Fluidigm chip, quantified using picogreen, and then normalized for uniformity across libraries. Resulting normalized libraries were loaded on the MiSeq instrument and sequenced using paired end 150 bp sequencing reads (Lohr et al., 2012). These data revealed that 84% of calls that were adequately covered in the experiment passed validation (Table S1G). Second, overlapping exome and whole genome sequencing data for 14 samples for which both data sets were obtained revealed a 95% validation rate for exome calls (Figure S2B). In addition, all Pten mutations that were identified by whole exome sequencing were validated by direct sequencing: Pten exons were amplified from tumor DNA and corresponding normal tissue by Primestart HT polymerase using primers flanking the point mutations (Exon 1 - T26P, Exon 5 - T131P, Exon7 - splice_site). PCR products were purified using ExoSAP-IT (Affymetrix). The purified products were directly sequenced using a 3730 Capillary DNA sequencer with Big Dye Terminator Cycle sequencing kit (Applied Biosystems). Sequencing data were visualized using 4Peaks software. Genomic rearrangements were selected for validation by a) manual review of sequencing reads, b) if the rearrangement generated a putative fusion protein, and c) biological interest. PCR oligonucleotides were designed to span the breakpoint and to span the wild-type locus. PCR was then performed using mouse tail DNA as a germline control and tumor DNA. PCR products were resolved on agarose gels, and positive products were sequenced directly to confirm the presence of the putative breakpoint.

Comparison of mSCLC Alterations to Human SCLC

To assess the overlap of somatic copy number alterations between human studies and our mouse model, we selected two comprehensive papers in the field and compared their reported recurrent focal and arm level somatic copy number alterations with our GISTIC focal and arm level results (Peifer et al., 2012; Rudin et al., 2012). We mapped mouse gene identifiers to hg19 symbols using the Jackson Laboratory homology table (<http://www.informatics.jax.org/homology.shtml>). Next, we converted the human symbols to hg19 and subset both mouse and human data sets so that we only compared genes that had a homology mapping. We then used this map to compare our two sets and visualized our data set using Venny (<http://bioinfogp.cnb.csic.es/tools/venny>). To determine the significance of the overlap between studies we constructed two (amplifications and deletions) 2x2 Fishers contingency tables for each paper. We also compared somatic mutations found in the papers with our mouse model. We again, mapped the mouse gene identifiers to hg19 symbols using the Jackson Laboratory homology table and converted all human symbols to hg19. In this comparison we used all "significantly mutated," "hotspot," and "clustered mutations" from Rudin et al. and Peifer et al. We considered mutations as a shared event regardless of position with the gene. For comparisons to human data shown in Figure 1, we compared the frequency of events in mSCLC to published human data sets (Bass et al., 2011; Berger et al., 2011; Beroukhim et al., 2010; Chapman et al., 2011; Greenman et al., 2007; Lohr et al., 2012; Stransky et al., 2011).

Antibodies for IHC

IHC was performed using the following antibodies: CGRP (C8198, Sigma, 1:5000) pAKT(S473) (#9271, Cell Signaling, 1/100), Pten (#9188, Cell Signaling, 1/100), Cleaved Caspase-3 (#9661, Cell Signaling, MA, 1/100) and phospho-histone3 (#9701, Cell Signaling, 1/100). Sections were developed with DAB and counterstained with hematoxylin. Tumor size (mm²), apoptotic (number of cleaved caspase-3 cells/mm²) and mitotic index (number of phospho-H3 cells/mm²) of PR, PRPt and PRPt/+ tumors were quantified using a Nikon 80i scope and the NIS-Elements Software (Nikon, NY). Haematoxylin and eosin staining was performed using standard methods.

Live Animal Imaging

For bioluminescence imaging of tumors expressing a conditional luciferase allele, mice were scanned for 60 s under isoflurane anesthesia using an IVIS Spectrum imaging system (Perkin Elmer) and signal (Total Flux; photons/Sec) in the lung was quantified using Living Image (Perkin Elmer). For MRI imaging isoflurane anesthetized animals were scanned using a Varian 7T/310/ASR-whole

mouse MRI system (Varian/Agilent). FSEMS (fast spin echo multi-slice) images were acquired with parameters: 2000ms TR; 12ms TE; 256X256 binning; 20 slices at 1mm thickness. Respiratory movement artifacts were minimized by using respiratory gating (Model 1025T, SA Instruments). Tumor volumes (mm³) were measured using Varian VnmrJ 2.3A software to generate regions of interest around tumors from consecutive 1mm thick slices.

Immunoblotting

Anti-pAKT(S473) (Cell Signaling, 1: 1000), anti-pAKT(T308) (Cell Signaling, 1: 1000), anti-Akt (Cell Signaling, 1: 1000) were used for western blotting following standard methods.

RNA Purification, Reverse Transcription, and Real-Time PCR

RNA was isolated following manufacturer's instructions for TRIzol (Invitrogen). 1.5 µg of RNA was reverse transcribed following manufacturer's instructions for High-Capacity cDNA Reverse Transcription (Applied Biosystems). cDNA was then diluted 1:10 for real time PCR reactions. Real time PCR reactions on genomic DNA were performed using 10 ng (mouse tumor) of DNA. All cDNA and genomic DNA real time PCR reactions were performed using SYBR green and Taqman (Life Technologies) respectively. Reactions were performed in triplicate and normalized to the levels of an internal control and analyzed using the comparative Ct method. *Genomic DNA Primers: mycl1* Mm00558485_cn, Control/Reference *Tfrc* and *Tert*. *cDNA primers: Magi1* F: 5' GGAAGGCTCAA CAAGGACCTA, *Magi1* R: 5' GGTAGAGGTTGCCCTTATGGT, *Gapdh* F: 5' TTTGATGTTAGTGGGGTCTCG, *Gapdh* R: 5' AGCTTGTCATCAACGGGAAG.

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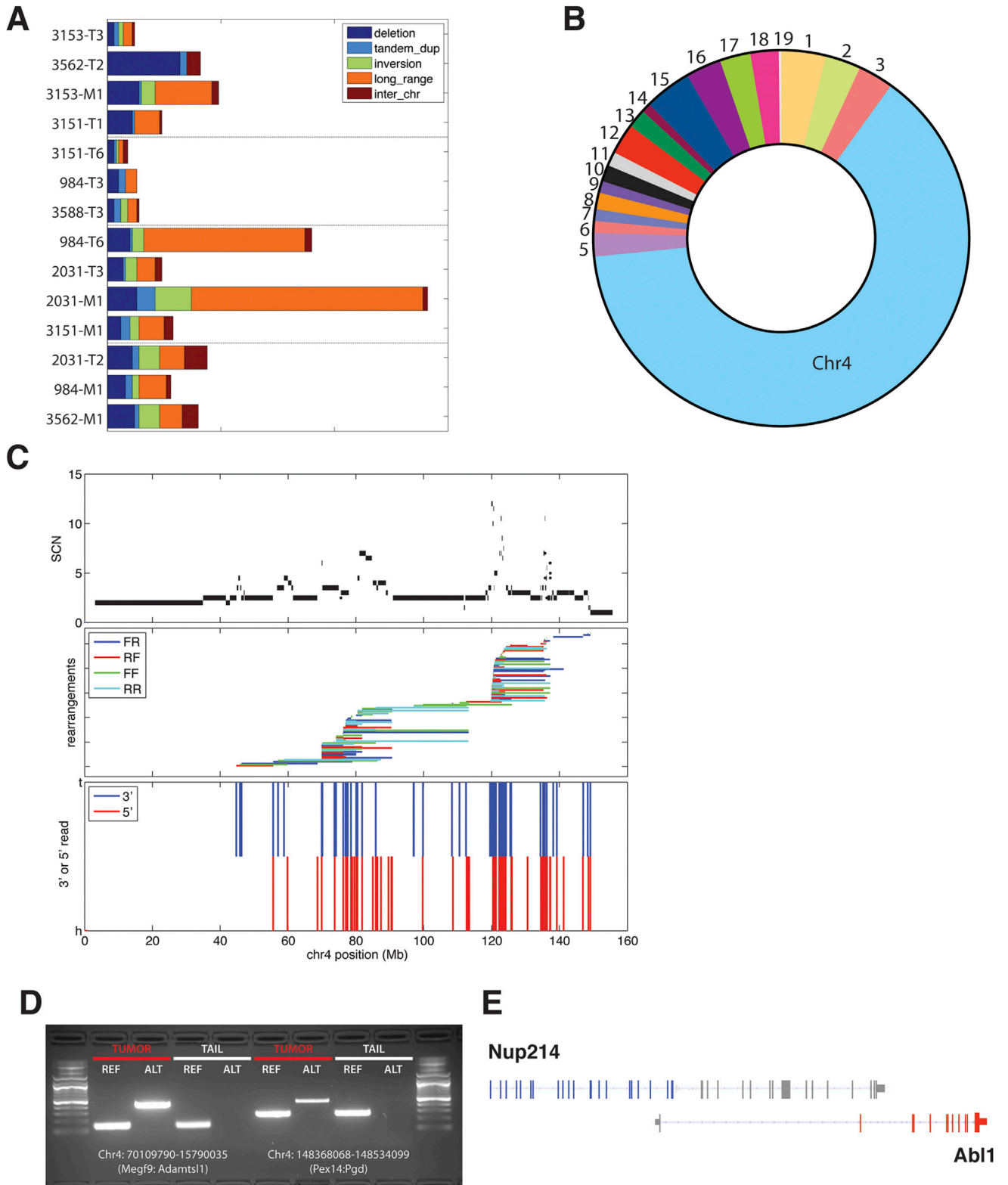


Figure S1. Whole-Genome Sequencing Identifies Highly Rearranged mSCLC Genomes, Related to Figure 1

(A) Types of genomic rearrangements detected by individual tumor.

(B) Chromosomal distribution of rearrangements. Note Chr4 rearrangements account for the majority of all events.

(legend continued on next page)

(C) Top: DNA copy number alteration level across Chr4 for tumor AD3151-T1 from CapSeg exome read depth. Middle: Pattern of rearrangements showing the start and end coordinates of each event based on alignments of the supporting WGS read fragments. Events are color-coded to indicate the read pair orientation. "FR" is a "forward-reverse" pair orientation consistent with a deletion event. "RF" or "reverse-forward" is consistent with a tandem duplication, and "FF" or "RR" are consistent with inversion events. Bottom: Pattern of 3' and 5' ends of rearrangements. An alternating pattern of 3' and 5' ends is characteristic of chromothripsis; however, the pattern shown here is suggestive of punctuated overlapping rearrangements.

(D) Example of PCR validation of putative genomic rearrangement. Note the presence of alternate band in tumor material, but absence in tail DNA sample.

(E) Putative fusion of Nup214 and Abl1 kinase.

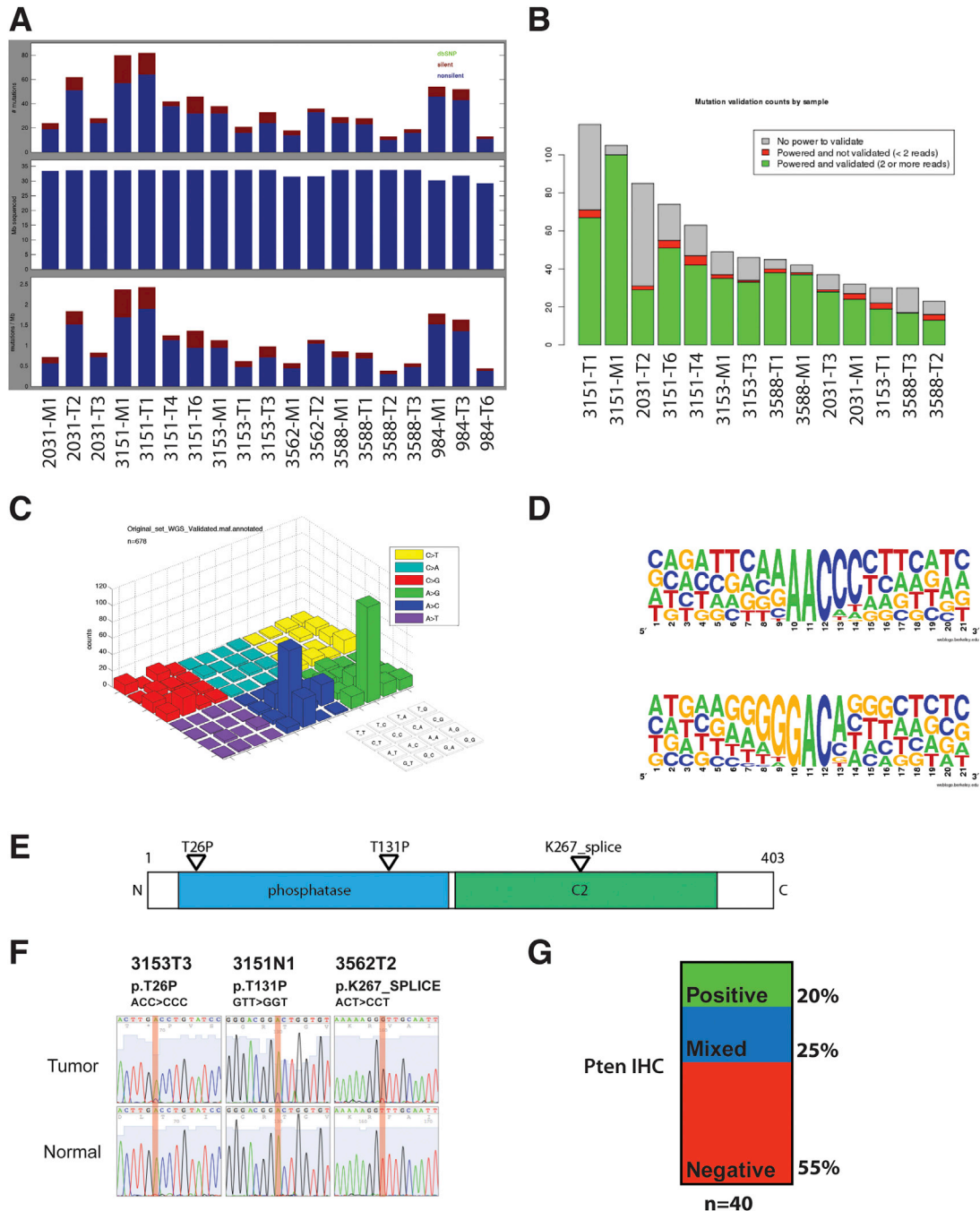


Figure S2. Acquired Mutations in mSCLC, Related to Figure 2

(A) Upper panel shows the number of silent and nonsynonymous mutations per sample. Center panel shows adequately covered Mb sequenced per sample (minimum 8X normal control and 14X tumor coverage). Lower panel depicts the mutations/Mb of covered sequence.

(B) Cross-platform validation of mutations using whole genome and exome data sets. Bars show the number of exome mutation calls covered by WGS data. Grey represents mutations calls not covered by at least two reads. Red are exome mutations covered by at least two reads in the WGS data that fail to identify the variant. Green represents exome variants covered by at least two reads in which the variant is confirmed by at least one read in the WGS data.

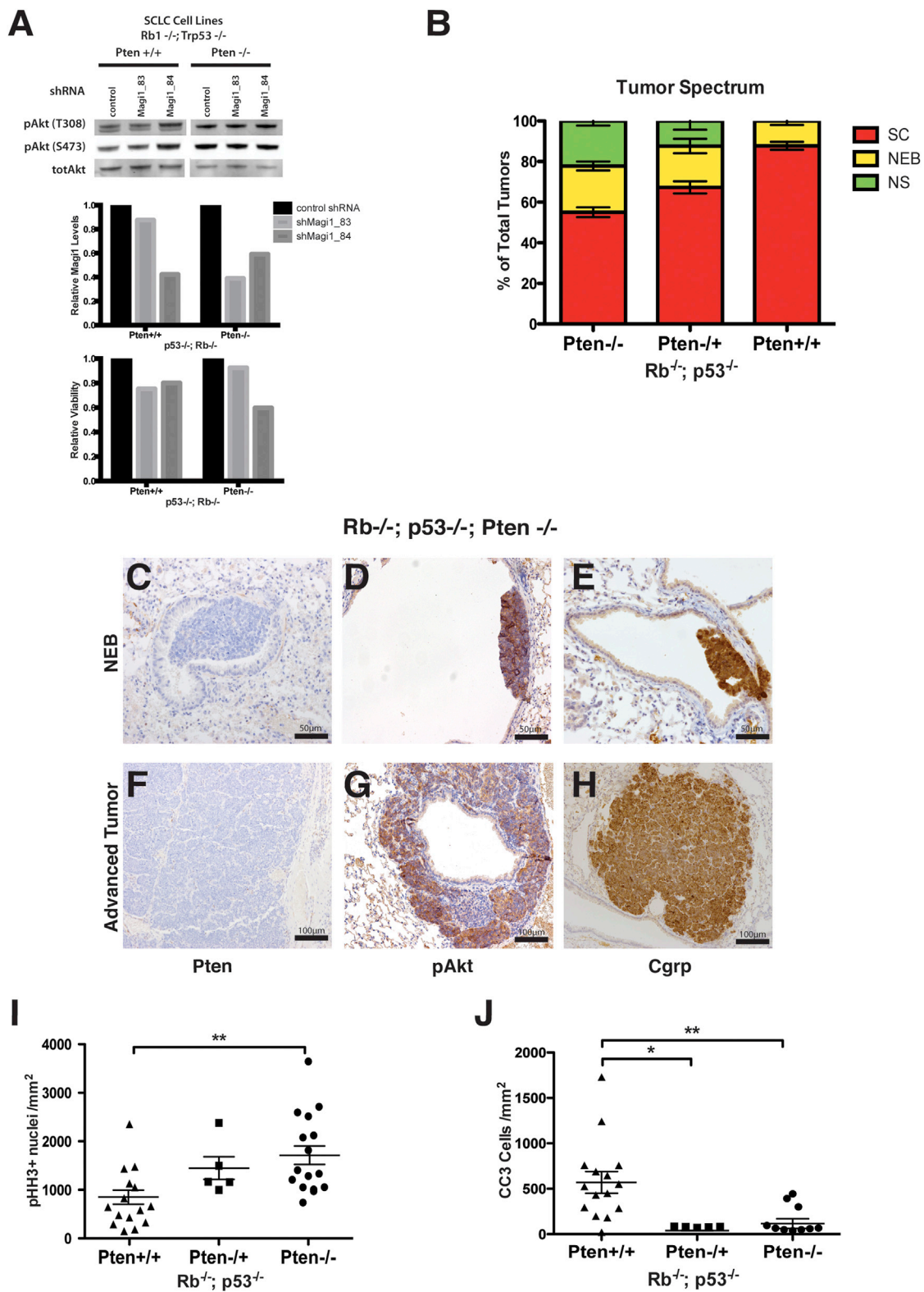
(C) Distribution of mutation signature in mSCLC. Z-axis bars represent mutation counts observed in all samples. Colored sections represent type of mutation, divided into bars representing the three-base context of events.

(D) expanded mutation signature of the dominant mutation signatures in mSCLC.

(E) mSCLC *Pten* mutations mapped onto *Pten* polypeptide sequence.

(F) Sanger sequence traces validating acquired *Pten* mutations. D) Parts of whole chart showing distribution of positive, negative, and mixed *Pten*-positive advanced mSCLC by IHC.

(G) Stacked bar chart showing distribution of positive, negative, and mixed *Pten*-positive advanced mSCLC by IHC.



(legend on next page)

Figure S3. Pten Pathway Disruption in mSCLC, Related to Figure 3

(A) Stable expression of indicated control or Magi1 shRNAs (83 and 84) in Pten WT (left) and null (right) mSCLC cell lines: Immunoblot analysis (top panel) of total Akt, phosphoAkt T308 and S473. Relative expression levels of Magi1 (Middle Panel) in shMagi1 treated compared to control shRNAs. Relative viability (Bottom panel) of cells expressing Magi1 hairpins.

(B) Histological analysis of tumor spectrum of Small Cell Lung Cancer (SC), Neuroendocrine Bodies (NEB) and Non-Small Cell Lung Cancer (NS).

(C–H) Immunohistochemistry of PRPt NEBs (top) and advanced mSCLC tumors (bottom) for: Pten (C,F), pAkt-S473 (D,G), and CGRP (E,H).

(I) phospho-Histone H3 positive nuclei per mm² and J) Cleaved Caspase-3 cells per mm² from histologically advanced mSCLC tumors. *p < 0.05 **p < 0.01
Panels B, I, J: Mean and standard error of the mean shown.

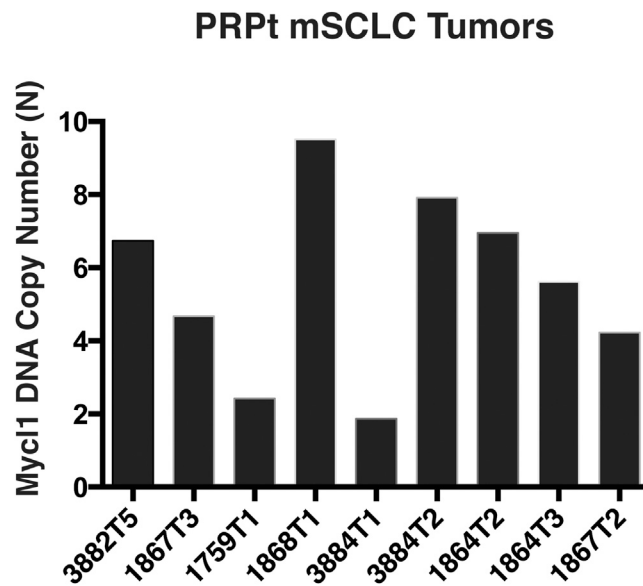


Figure S4. *Mycl1* DNA Copy Number in PRPt Tumors, Related to Figure 4

qPCR amplification of *Mycl1* in PRPt samples. Y Axis is DNA copy content normalized to normal tail DNA control (2N = tail *Mycl1* DNA content). x axis shows PRPt samples analyzed.

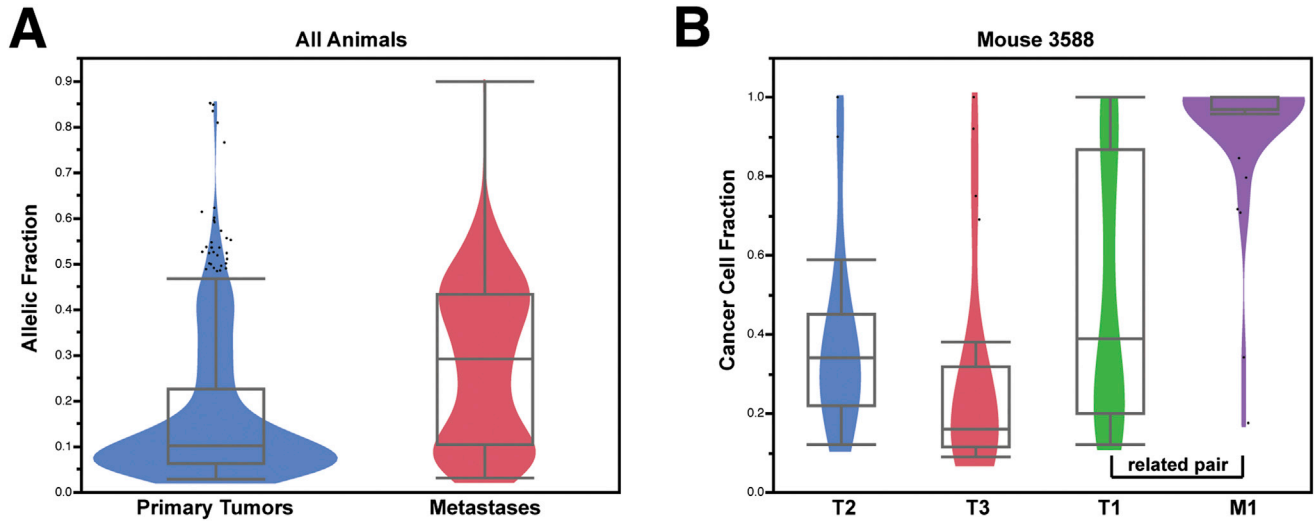


Figure S5. Clonal Heterogeneity in mSCLC, Related to Figure 5

(A) Violin plot of allelic fraction of all somatic mutations in primary mSCLC isolated from lungs and metastases. Low allelic fraction mutations predominate primary tumors whereas metastases are relatively enriched for high allelic fraction events.

(B) Violin plot of cancer cell fraction (CCF) values from ABCSOLUTE in multiple primary tumors and a metastasis from a single mouse. Primary tumor T1 and metastasis M1 share overlapping point mutations and genomic rearrangements indicating shared clonal origin. Note the increased CCF values in M1, indicating clonal selection during metastatic seeding.

Boxes represent the median and interquartile range (IQR), and error bars extend 1.5X IQR from the boxes.