Genome-wide DNA Methylation Analysis of Lung Carcinoma Reveals One Neuroendocrine and Four Adenocarcinoma Epitypes Associated with Patient Outcome

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Abstract

Purpose: Lung cancer is the worldwide leading cause of death from cancer. DNA methylation in gene promoter regions is a major mechanism of gene expression regulation that may promote tumorigenesis. However, whether clinically relevant subgroups based on DNA methylation patterns exist in lung cancer remains unclear.

Experimental Design: Whole-genome DNA methylation analysis using 450K Illumina BeadArrays was performed on 12 normal lung tissues and 124 tumors, including 83 adenocarcinomas, 23 squamous cell carcinomas (SqCC), 1 adenosquamous cancer, 5 large cell carcinomas, 9 large cell neuroendocrine carcinomas (LCNEC), and 3 small-cell carcinomas (SCLC). Unsupervised bootstrap clustering was performed to identify DNA methylation subgroups, which were validated in 695 adenocarcinomas and 122 SqCCs. Subgroups were characterized by clinicopathologic factors, whole-exome sequencing data, and gene expression profiles.

Results: Unsupervised analysis identified five DNA methylation subgroups (epitypes). One epitype was distinctly associated with neuroendocrine tumors (LCNEC and SCLC). For adenocarcinoma, remaining four epitypes were associated with unsupervised and supervised gene expression phenotypes, and differences in molecular features, including global hypomethylation, promoter hypermethylation, genomic instability, expression of proliferation-associated genes, and mutations in \textit{KRAS}, \textit{TP53}, \textit{KEAP1}, \textit{SMARCA4}, and \textit{STK11}. Furthermore, these epitypes were associated with clinicopathologic features such as smoking history and patient outcome.

Conclusions: Our findings highlight one neuroendocrine and four adenocarcinoma epitypes associated with molecular and clinicopathologic characteristics, including patient outcome. This study demonstrates the possibility to further subgroup lung cancer, and more specifically adenocarcinomas, based on epigenetic/molecular classification that could lead to more accurate tumor classification, prognostication, and tailored patient therapy.
Translational Relevance
DNA methylation in gene promoters is a major mechanism of gene expression regulation that may promote tumorigenesis. DNA methylation of specific genes, and/or patterns of DNA methylation in lung cancers have been associated with patient outcome. However, hitherto, neither the existence of reproducible DNA methylation-based subgroups of potential clinical relevance nor the DNA methylation pattern across multiple histologic subgroups has been carefully investigated in lung cancer. On the basis of a multicohort approach, we conducted a comprehensive survey of genome-wide DNA methylation patterns in lung cancer identifying one neuroendocrine and four reproducible adenocarcinoma epitypes. Importantly, epitypes were associated with specific clinicopathologic and molecular characteristics, gene expression phenotypes, and patient outcome. These findings shed light on the epigenetic characteristics and molecular diversity underlying lung cancer. Moreover, they highlight the possibility to further subgroup the disease based on epigenetic/molecular classification, which could lead to improvements in tumor classification, prognostication, and tailored patient therapy.

Materials and Methods

Patient material
DNA and total RNA were extracted from the same tissue piece for 124 tumors and 12 matched normal lung tissue specimens from patients with early-stage lung cancer operated at the Skåne University Hospital (Lund, Sweden; Table 1, discovery cohort). The study was approved by the Regional Ethical Review Board in Lund, Sweden (Registration no. 2004/762 and 2008/702). The 12 normal specimens originated from patients with adenocarcinoma and were mixed in gender (3 males, 9 females), smoking status (6 never-smokers, 6 smokers), and patient age (57–82 years). Three-hundred and seventy three adenocarcinomas from The Cancer Genome Atlas (TCGA) project (11) and 444 NSCLC cases from Sandoval and colleagues (ref. 5; Sandoval cohort) were used as validation cohorts (Table 1).

Global methylation analysis
All cases were analyzed by the Illumina Human Methylation 450K v1.0 platform (Illumina) according to manufacturer’s instructions (Supplementary Materials and Methods). Signal intensities were obtained from GenomeStudio (Illumina), converted to β-values, filtered, and normalized to remove biases between Infinium I and II probes (Supplementary Materials and Methods). CpG probes with aberrant methylation in tumors compared with normal lung tissue in the discovery set were identified as described in Supplementary Materials and Methods (Supplementary Fig. S1A), and annotated through the human embryonic stem cell (H1hESC) chromatin state track (12) and the Illumina CpG island track. CpGs in repetitive elements were identified through the “repeats_rmsk_hg19” table from the UCSC Genome Browser. Unsupervised class-discovery was performed using bootstrap clustering (ref. 13; Supplementary Materials and Methods). Principal component analysis (14), including clinicopathologic and technical factors, and comparison of bisulfite conversion plate and beadchip id against unsupervised bootstrap clusters were performed to assess that no technical artifacts influenced methylation data, or bootstrap groups, for the 124-sample discovery cohort (Supplementary Fig. S1B–S1D). DNA methylation centroids representing bootstrap clusters were created from the average β-value for each CpG probe in respective cluster. Samples in validation cohorts were assigned to the centroid with the smallest Euclidean distance for matching CpGs. Methylation data for the discovery cohort is available as GSE60645 (15).

Copy number analysis
Log2 copy number estimates and CNAs for CpG probes in the discovery and Sandoval cohorts were generated and identified as described in Supplementary Materials and Methods from 450K methylation beadchip data. For the TCGA cohort, copy number estimates and CNAs were obtained from level 3 Affymetrix SNP6 data as described (16, 17). Complex arm-wise aberration index (CAAI) scores were calculated similar to Russnes and colleagues (ref. 18; Supplementary Materials and Methods).
Global gene expression analysis

Gene expression analysis was performed on 117 tumors from the discovery cohort using Illumina Human HT-12 V4 microarrays, available as GSE60645 (15). TCGA adenocarcinoma expression data were obtained as RNASeq V2 data. Six correlated gene expression modules in lung cancer, representing different tumor and/or tumor environment associated processes, were derived as originally described by Fredlund and colleagues in GSE29016 (refs. 19, 20; Supplementary Materials and Methods; Supplementary Table S1). These expression modules included an immune response, a neuroendocrine, and a stroma/extra cellular matrix module. Data processing steps, including adenocarcinoma and SqCC molecular subtype classification (9, 21), correlation of methylation and expression data, and calculation of different expression metagenes are further described in Supplementary Materials and Methods.

Functional classification

Gene Ontology enrichment were performed using the DAVID Functional Annotation Tool (22) with the default human population background and a Bonferroni-adjusted $P < 0.05$ as significance threshold.

Results

Genome-wide DNA methylation patterns in lung cancer

We analyzed 124 lung tumors from five histologic subgroups for global DNA methylation patterns using Illumina 450K methylation arrays (Table 1, discovery cohort). Overall, DNA methylation in the tumors followed a distinct pattern along the gene coding sequence, with low methylation levels near the transcription start site and high methylation levels at gene bodies, 3'UTRs, and intergenic regions (Fig. 1A). Correlation analyses of DNA methylation and gene expression revealed a pattern of negative correlations at transcription start sites and more positive correlations in

The table below provides patient characteristics and clinicopathologic data for included cohorts.

<table>
<thead>
<tr>
<th></th>
<th>Lund cohort</th>
<th>Sandoval et al. (5)</th>
<th>TCGA (11)</th>
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<td>KRAS-mutated</td>
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<tr>
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**NOTE:** X, data available for analysis.

²Nonsilent mutations from Mutation Annotation Format (MAF) file.

bOS, overall survival; RFS: relapse-free survival. Number of patients with outcome data (NSCLC/adenocarcinoma).

cOnly CN-FGA.
Figure 1. DNA methylation patterns in lung cancer. A, distribution of average β-values for 473864 CpGs stratified by Illumina gene location across the 124 tumors in the discovery cohort. TSS, transcription start site. B, Spearman correlation of DNA methylation and gene expression for 9,334 gene matching CpGs in 77 adenocarcinomas from the discovery cohort, stratified by Illumina gene location. Top axis indicates number of CpGs per group. C, Spearman correlation for the 9334 CpGs grouped according to the human embryonic stem cell (H1hESC) chromatin state track (12). (Continued on the following page.)
open sea/heterochromatin regions and gene bodies (Fig. 1B and C; Supplementary Table S2). We identified 4136 CpGs with aberrant methylation in >10% (n = 13) of tumors compared with normal lung tissue, including multiple HOX genes, Wnt signaling pathway genes, APC, CDH13, GATA4, GATA5, and RASSF1 consistent with previous studies (3, 6) (Supplementary Fig. S1A; Supplementary Table S2). Hypomethylated CpGs in tumors were enriched in open sea/heterochromatin regions, whereas hypermethylated CpGs were typically located in transcription start sites, CpG islands, and poised promoters in human embryonic stem cells, H1hESC cells, consistent with previous reports (refs. 6, 23; Fig. 1D and E). Hypomethylated CpGs were enriched in repetitive regions (LINE, SINE, LTR elements) compared with hypermethylated CpGs (21% vs. 4%, respectively, Fisher exact P = 9e–54). Importantly, changing the number of CpGs with aberrant methylation by lowering or increasing the number of required tumors with aberrant methylation (n = 2–20 tumors equaling CpG sets between ~1,000 and 44,000 CpGs; Supplementary Fig. S1A) yielded the same enrichment pattern of hypomethylated and hypermethylated CpGs.

Functional annotation analysis of genes with hypermethylated CpGs in the 4136 CpG set showed enrichment of biologic processes such as regulation of transcription, neural development, and cell morphogenesis corroborating previous studies (24, 25), whereas hypomethylated genes showed a much less clear functional enrichment (Supplementary Table S2).

Unsupervised class discovery based on genome-wide DNA methylation patterns identifies five epitypes

Unsupervised bootstrap analysis based on the 4136 CpGs highlighted five tumor clusters in the discovery cohort, hereafter referred to as epitypes (ES1, ES2, ES3, ES4, and ES5; Fig. 2A and Supplementary Fig. S1E). Importantly, epitype association for individual samples was robust across different CpG sets (numbers between 1,282–17,710 CpGs) in exploratory bootstrap analysis (Supplementary Fig. S1F). ES1 showed a global hypomethylation pattern, ES4 a promoter methylation pattern, ES5 a methylation pattern resembling normal lung tissue, whereas ES2 had a pattern in between ES1 and ES4 (Fig. 2). Consistent with the global DNA hypomethylation pattern, ES1 tumors also showed more hypomethylation of CpGs in repetitive elements (Fig. 2C and Supplementary Fig. S1G). Notably, 89% of ES3 cases were either SCLC (n = 2) or LCNEC (n = 6) tumors. Consistent with the dominance of neuroendocrine cases in ES3, we found distinct overexpression of a neuroendocrine gene expression metagene compared with the other epitypes (P = 5e–05, Kruskal–Wallis test). Hence, we refer to ES3 as a neuroendocrine epitype. On the other hand, SqCC tumors clustered in ES1 (17%), ES2 (57%), and ES5 (22%) (Fig. 2A). A distinct association of SqCC cases in ES2 with the reported classicalSqCC gene expression subtype (21) was found, with >86% of classical subtype classified SqCC cases present in this epitype. Adenocarcinomas (n = 83) were divided into ES1 (12%), ES2 (14%), ES4 (36%), and ES5 (37%; Fig. 3A).

Validation of lung cancer epitypes

To validate the identified epitypes from the discovery cohort, we created DNA methylation centroids for each epitype based on the 4136 CpGs. Next, we classified two independent cohorts analyzed by the same methylation platform (Sandoval and TCGA) comprising 122 SqCC tumors and 695 adenocarcinomas (Table 1). Principal component analysis performed in the validation cohorts confirmed that the centroid classification explained most of the total variation in DNA methylation compared with available clinico-pathologic, technical (batch and beadchip data), and molecular factors, including clinical smoking history, sex, tumor stage, tumor size, histology (adenocarcinoma or SqCC), EGFR, KRAS, and TP53 mutations (Supplementary Figs. S2A and S3A–S3C). Notably, most of these factors (e.g., smoking status) contributed little to the total variation in DNA methylation. Moreover, the classification of the validation cohorts was robust across different sets of CpGs, and overlapped extensively with independently derived unsupervised bootstrap groups in these cohorts (Supplementary Figs. S2B–S2D and S3D–S3F).

In both validation cohorts, ≤1% of cases were classified as ES3, supporting that this epitype is highly distinct for lung cancers expressing neuroendocrine marker genes. Similar to the discovery cohort, SqCC tumors in the Sandoval cohort were primarily classified as ES2 (49% of SqCC cases) or ES5 (33%). Although LC, LCNEC, and SqCC tumors were present in different clusters in the discovery set, this cohort is underpowered to robustly claim existence of different epitypes within these histologic subgroups. Moreover, there currently exist no comparable LC, LCNEC, or SCLC cohorts suitable for validation of novel epitypes within these subgroups. Consequently, we hereafter focus the characterization and validation of the epitypes only on lung adenocarcinomas in the three cohorts (excluding ES3), using clinico-pathologic factors, gene expression data, CNAs, and mutational data. Fig. 3A shows the distribution of adenocarcinomas between epitypes in all investigated cohorts.

Adenocarcinoma epitypes are associated with reproducible clinicopathologic characteristics including smoking history, EGFR, and KRAS mutations

The epitypes showed differences in the composition of never-smokers and smokers. ES5 was enriched for never-smokers in both the discovery and Sandoval cohorts (63–68% of all never-smokers), while less in the TCGA cohort.

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Figure 2. Identification of five DNA methylation subtypes in the discovery cohort. A, DNA methylation subtypes in 124 lung cancers based on bootstrap clustering of 4,136 variant CpGs. Heatmap displays beta values (rows) from unmethylated (blue) to methylated (yellow) for three sample groups (columns): 124 tumors divided into five subtypes by bootstrap clustering, 12 matched normal lung tissues, and blood leukocytes, with associated clinical characteristics and reported adenocarcinoma (AC) and SqCC gene expression phenotypes (9, 21). Left hand CpG tracks, CpG island track; black, island; gray, shore/shelf; white, open sea, H1hESC track (ref. 12; embryonic stem cell chromatin state): purple, poised promoter; red, active promoter; yellow, enhancer; green, transcribed; blue, insulator; white, heterochromatin. Sample annotations: black, yes; gray = no. B, global promoter hypermethylation (left) and global hypermethylation (right) score for methylation clusters (based on all filtered CpGs on the platform). C, box plots of DNA methylation for 629 CpGs matching repetitive elements from the set of 4,136 for each tumor in the discovery cohort across epitypes. Tumors are colored according to epitype as in A, with exception for ES5 (gray).
Gene expression signatures associated with adenocarcinoma epitypes

The epitypes were associated with consistent differences in various gene expression metagenes in both the discovery and TCGA cohorts. For instance, ES1 had the highest expression of proliferation-associated genes (the CIN70; ref. 26, metagene), while ES5 the lowest (P = 0.00005 in the discovery cohort and P = 9e–17 in TCGA, Kruskal–Wallis test). The opposite pattern was found for expression of a terminal respiratory unit (TRU; ref. 27) gene signature (P = 0.0002 and P = 6e–18, respectively, Kruskal–Wallis test). The epitypes also differed in expression of an immune response–associated metagene and a stroma/extracellular matrix–associated metagene. Notably, the expression of these two gene modules likely relates to infiltration of immune or stromal cells in the analyzed macrodissected tissue. ES1 consistently showed the lowest and ES5 the highest expression of both metagenes (Fig. 3F, data not shown for the TCGA cohort). These results suggest that ES5 is an epitype with considerable infiltration of nonmalignant cells consistent with the observed methylation pattern being more similar to normal lung tissue. In contrast, ES1 would represent tumors with high tumor cell content. ES2 showed a different pattern for these two metagenes compared with the other epitypes (Fig. 3F). Expression of the stromal metagene was similar in ES2, ES4, and ES5, whereas expression of the immune metagene was lower in ES2 compared with ES4 and ES5, but higher compared with ES1. Supporting these observations, we found similar patterns of stromal and immune expression scores between the epitypes using the Estimation of Stromal and Immune Cells in Malignant Tumors (ESTIMATE) method (28) in both cohorts (data not shown). Together, this suggests that differences in the cellular type and amount of infiltrating nonmalignant cells may exist between the epitypes.

To further investigate biologic processes differing between the epitypes, we identified differentially expressed genes between adenocarcinomas stratified by epitype in the discovery (n = 1,824 expression probes) and TCGA (n = 5,726 genes) cohorts (Supplementary Materials and Methods). Functional analysis revealed enrichment of biologic processes involved in immune response, cell proliferation, and cell adhesion (Supplementary Table S3), consistent with results from the metagene analyses (Fig. 3).

The mutational spectrum of adenocarcinoma epitypes

To further characterize the mutational spectrum in the epitypes, we analyzed whole-exome sequencing data for TCGA adenocarcinomas. Overall, ES1 cases harbored the highest number of mutations and ES5 the least (Fig. 4A), independent of patient smoking status. Moreover, the epitypes showed differences in the type of mutation transitions when stratified by smoking status (Supplementary Fig. S4). The largest differences were observed in the distributions of C>T and C>A transitions (recognized as a smoking-related signature; ref. 29), between the ES1 (more C>A, less C>T) and ES5 epitypes (less C>A, more C>T). Consistently, overlapping ES1 cases were more often classified as transversion-high (89%) in the recent TCGA study compared with the other epitypes (55%–70%, Fisher exact P = 0.03; ref. 3).

To search for individual mutations associated with the epitypes, we performed a permutation-based screen of 174 genes identified by MutSigCV (30) analysis of 402 TCGA adenocarcinomas as described in ref. (31). This analysis identified seven genes with false discovery rate ≤10%, including four well-known tumor suppressor genes (KEAP1, TP53, STK11, and SMARCA4) and three genes appearing as either false positives (COL11A1, and LRRRC3), or with <10% mutation frequency in any epitype (SNRPN). For TP53, STK11, KEAP1, and SMARCA4, we observed notable differences in the mutation frequencies between the epitypes (Fig. 4B), but no differences in mutation type (missense, truncating, or in-frame indel; χ² P > 0.05). The latter result may partly be related to the overall low number of specific mutations, for example, 86% of SMARCA4 mutations in ES4 were missense mutations compared with 30% to 50% in ES1, ES2, or ES5. In these analyses, KRAS mutations were borderline nonsignificantly associated with the epitypes, whereas the association of EGFR mutations with the epitypes was less strong (see Fig. 3C).
Figure 3. Clinicopathologic and gene expression characteristics of adenocarcinoma epitypes. A, distribution of adenocarcinomas in epitypes in the discovery, Sandoval, and TCGA cohorts. B, distribution of never-smokers with adenocarcinoma in epitypes in the discovery, Sandoval, and TCGA cohorts. P values calculated using the Fisher exact test. C, distribution of EGFR (left) and KRAS mutations (right) in the epitypes in the discovery and TCGA cohorts. D, association of reported gene expression adenocarcinoma (AC) subtypes (bronchioid, magnoid, and squamoid; ref. 9) with epitypes in the discovery (top) and TCGA (bottom) cohorts. Combinations with clear enrichment highlighted in red. P values were calculated using the χ² test. (Continued on the following page.)
Materials and Methods.

associated with relapse-free survival (log-rank for NSCLC stage I tumors from Sandoval, the epitypes were
epitype. B, association of specific mutations (only nonsilent) with epitypes in TCGA adenocarcinomas. Mutations were identified by a permutation-based approach applied to a list of significant mutations in adenocarcinoma identified through MutSigCV analysis as described in ref. (31) and Supplementary Materials and Methods. P values were calculated using the Fisher exact test.

Figure 4. Association of adenocarcinoma epitypes with mutations. A, total number of mutations (silent and nonsilent) for TCGA adenocarcinomas stratified by epitype. B, association of specific mutations (only nonsilent) with epitypes in TCGA adenocarcinomas. Mutations were identified by a permutation-based approach applied to a list of significant mutations in adenocarcinoma identified through MutSigCV analysis as described in ref. (31) and Supplementary Materials and Methods. P values were calculated using the Fisher exact test.

Epitypes of Lung Carcinoma

Adenocarcinoma epitypes are associated with patient outcome

The four epitypes were associated with patient outcome (overall survival or relapse-free survival) in the discovery and Sandoval cohorts for NSCLC in general, and adenocarcinoma specifically (Fig. 5). Convincingly, in both cohorts, the ES2 and ES5 epitypes were associated with the best outcome in adenocarcinomas, whereas ES1 and ES4 were associated with the worst outcome. For stage I adenocarcinomas, the epitypes were associated with overall survival in the discovery cohort (relapse-free survival, log-rank $P < 0.005$), while borderline nonsignificant in the Sandoval cohort (relapse-free survival, log-rank $P = 0.06$). However, for NSCLC stage I tumors from Sandoval, the epitypes were associated with relapse-free survival (log-rank $P = 0.04$).

In univariate analysis of epitype association, patient age, smoking history, sex, EGFR, and KRAS mutation status in stage I adenocarcinomas from the discovery cohort, the epitypes were the only significant factor for overall survival ($P < 0.05$). In multivariate analysis including all these factors, the ES2 and ES5 epitypes remained significant ($P < 0.05$). In multivariate analysis of stage I adenocarcinomas from the Sandoval cohort, none of the factors (age, smoking history, gender, and epitype) reached significance.

Discussion

In the current study, we have explored the landscape of genome-wide DNA methylation across the major histologic subgroups of lung cancer, identifying five epitypes of tumors linked to different gene expression phenotypes. We demonstrate that aberrant DNA methylation in lung cancer is consistent with the classical view of hypermethylation in CpG islands, and hypomethylation in heterochromatin regions, including repetitive elements (32). Hypermethylated genes were enriched for developmental and differentiation-associated processes and polycomb targets pre-marked by histone H3K27 trimethylation in embryonic cells (24, 25). These results are consistent with a hypothesis that DNA methylation in lung cancer preferentially targets genes involved in morphogenetic processes and late stage differentiation of the lung epithelium, potentially contributing to establishment of an early undifferentiated cancer phenotype (24).

Through a multicohort approach, we demonstrate that LCNEC and SCLC tumors with neuroendocrine features represent a distinct lung cancer epitype compared with NSCLC, consistent with a similar association based on copy number and transcriptional alterations (33). Supporting ES3 as a distinct neuroendocrine epitype, centroid classification of 69 NSCLC cell lines (7) classified only the known LCNEC cell line, NCI-H1155, as ES3. Remaining cell lines were predominantly classified as ES1 (58%) or ES4 (36%). In both the discovery cohort and the Sandoval NSCLC validation cohort, DNA methylation epitypes identified by unsupervised bootstrap analysis comprised of a mix of adenocarcinomas and SqCCs. On the transcriptional and CNA level, adenocarcinomas and SqCCs display large differences (16, 27, 33). Here, additional studies (larger cohorts) are needed to pinpoint DNA methylation alterations that could explain such histology or cell type–specific expression patterns.

In the discovery cohort, we divided adenocarcinomas (91% stage I tumors) into four epitypes (ES1, ES2, ES4, and ES5), with marked differences in molecular and clinicopathologic characteristics, including patient outcome. Although resected stage I NSCLC patients have the most...
favorable prognosis, the 5-year survival rate is 52% to 89% (34). Thus, improved molecular subclassification of early-stage NSCLC is highly relevant. To date, only a few studies have reported DNA methylation epitypes in NSCLC or adenocarcinoma specifically (3–7). However, thorough validation of the reported epitypes has not been performed in any of these studies. In contrast, we validated our epitypes in 695 adenocarcinomas from two independent cohorts showing that they (i) provide powerful explanations of the total variation in DNA methylation compared with other clinicopathologic and molecular factors; (ii) are robust across a wide range of CpGs; (iii) have consistent clinicopathologic and molecular features in different cohorts; and (iv) could be recovered in validation cohorts by independent unsupervised analysis.

On the basis of extensive promoter hypermethylation, overrepresentation of KRAS-mutated adenocarcinomas, and poor patient outcome, the ES4 epitype shares features with the Shinjo and colleagues (4) adenocarcinoma CIMP-high phenotype. Supporting this association, 89% of all matching CIMP-high cases in the recent TCGA study were classified as ES4, whereas the remaining 11% were classified as ES1 (3). However, in contrast with the Shinjo and colleagues (4) CIMP-high phenotype, the ES4 epitype included never-smokers, EGFR mutations, and was not associated with gender (similar to the CIMP-high group in ref. 3; Fig. 3). These discrepancies may be because the CIMP definition in lung cancer is not standardized, illustrated by the differences in CIMP-high frequency between the TCGA and Shinjo and colleagues’ studies (20.4% and 7.8%, respectively; refs. 3, 4). Notably, the enrichment of KRAS-mutated adenocarcinomas in a promoter hypermethylated cluster is consistent with previous reports (4, 6). This enrichment is intriguing given that KRAS-mutated adenocarcinomas have been reported to display less distinctive mRNA and CNA patterns compared with, for example, EGFR-mutated adenocarcinomas (17, 35). However, KRAS mutations have not been found to be the driver of such a promoter hypermethylated epitype in either lung adenocarcinoma or colorectal cancer, suggesting a more complex underlying mechanism (6, 36).

The ES1 epitype was characterized by global hypomethylation, distant from CpG islands, hypomethylation of CpGs in repetitive elements, high expression of proliferation-associated genes, a non-TRU–like expression pattern, association with the magnoid subtype, a high
mutational burden including TP53, KEAP1, and STK11 mutations, strong association with smoking, and poor patient outcome in both discovery and validation cohorts (Figs. 2–5). Hypomethylation in cancer have been associated with different repetitive elements that could contribute toward genomic instability (refs. 37, 38; and references therein). Accordingly, we found that ES1 tumors displayed not only more CNAs, but also that these alterations appeared more complex compared with the other epitypes based on the complex arm-wise aberration index (CAAI; ref. 18; Supplementary Fig. S5A–S5C). We also found that copy number breakpoints occurring in repetitive elements for copy number gain or loss regions were hypomethylated to a greater extent in ES1 tumors (Supplementary Fig. SSD and S5E). Together, these clinicopathologic and molecular characteristics suggest that tumor progression in ES1 may be primarily driven by genomic instability and less by classical oncogene activation (exemplified by a lower EGFR and KRAS mutation frequency). The latter is supported by the fact that ES1 cases were less often denoted oncogene-positive compared with tumors from other epitypes based on data from the recent TCGA study (P = 0.02, Fisher exact test; ref. 3).

Moreover, from the same study, ES1 cases showed higher tumor purity and tumor ploidy compared with the other epitypes (Kruskal–Wallis P < 0.0001). Thus, ES1 appears to represent a poorly differentiated, aneuploid, and aggressive subset of adenocarcinomas with high tumor cellularity, less driven by oncogene activation. A smaller fraction of ES1 cases showed concomitant global hypomethylation and promoter methylation (more evident in the larger validation cohorts, Supplementary Figs. S2E and S3G). This subset of cases may better resemble the Shinjo and colleagues (4) CIMP-high group, as they were all smokers and did not harbor any EGFR mutations (data not shown).

Irrespectively, our results support that a CIMP phenotype can occur in adenocarcinomas with markedly different epigenetic, transcriptional, and genetic make-up.

DNA methylation patterns may act as a fingerprint for different cell types (39). Compared with the DNA methylation pattern of ES1, the ES2 epitype appears more infiltrated by nonmalignant cells. Consistently, we observed differences in gene expression of metagenes associated with immune response and stroma/extracellular matrix between ES1 and ES2. Intriguingly, despite indicators of poor prognosis, including frequent CNAs, higher expression of proliferation-related genes, association with the magnoind expression subtype, and a high mutational burden (including TP53, STK11, and KEAP1 mutations), ES2 adenocarcinoma cases (together with ES5 cases) showed the best outcome. While the generally better prognosis of ES5 cases may be attributable to their lower proliferation rate, the better prognosis of ES2 patients compared with ES1 could, hypothetically, be related to an altered and/or reduced immune cell infiltration in ES1, which have been shown to confer a poorer prognosis in multiple cancer types (19, 40–42). Whether the ES2 epitype represents an intermediate/transition state to ES1 for adenocarcinomas remains to be investigated. Although somatic alterations in specific epigenetic regulators were recently found in a notable proportion of adenocarcinomas, there were no associations with global DNA methylation patterns (3).

Here, the association of SMARCA4 (a nucleosome remodeler) mutations with ES2 is intriguing and warrants further investigation.

In contrast with the other epitypes, ES5 showed a DNA methylation pattern with similarities to blood leukocytes and normal lung tissue. Together, with its more TRU-like expression pattern, lower expression of proliferation-related genes, higher expression of immune and stroma-related metagenes, high frequency of bronchioid classified tumors, enrichment of never-smokers, and better patient outcome, ES5 matches a proposed TRU type of adenocarcinoma (43) but also shares characteristics with the CIMP-negative epitype reported by Shinjo and colleagues (4). Importantly, ES5 cannot be dismissed as an epitype merely due to sampling issues, as the analyzed tumor DNA carried both CNAs and mutations. For instance, for the 25 cancer hallmark genes defined by Imielinski and colleagues (44), 78% of ES5 cases in the TCGA cohort carried at least one alteration (mutation or CNA). Moreover, the lack of NSCLC cell lines classified as ES5 or ES2 (see above) does not dismiss these epitypes in clinical tumor specimens, as for instance the well established intrinsic molecular subtypes in breast cancer are not reproduced exactly in breast cancer cell lines (45).

DNA methylation of smaller sets of CpGs/metagenes (e.g. CDKN2A, FHIT, APC, and RASSF1A) have been associated with smoking in both genome-wide and gene-focused studies of lung cancer (6, 38, 46) (and references therein).

However, on a genome-wide level our results suggest an overall less dominant effect of clinical smoking history on the DNA methylation landscape in primary adenocarcinomas, despite the enrichment of never-smokers in specific epitypes. This conclusion may be exemplified by results from the principal component analyses, the presence of never-smokers in all epitypes with exception of ES1, the low number of smoking associated CpGs in both the current and previous studies (6, 46), and that the patterns of global and promoter hypermethylation between epitypes were similar irrespective of smoking status (Figs. 2A, S1B, S2A, S3A and S6A and B). Combined with similar findings of intrinsically heterogeneous gene expression and CNA patterns in smoking-defined adenocarcinoma subgroups (20, 31), our results question whether never-smokers can be identified as a molecular subgroup of its own with transcriptional, DNA methylation, and CNA patterns clearly different from tumors arising in smokers. Instead, our study further supports that a majority of adenocarcinomas arising in never-smokers together with a specific subset of tumors from smokers represent a more distinct and relevant molecular/biologic entity of less aggressive and potentially more smoking-unrelated disease (20, 31). The clinical smoking definitions are intrinsically problematic due to their self-reported nature, but also because they do not capture the intensity and duration of cigarette exposure,
and the exposure to environmental tobacco smoke and other pollutants for never-smokers. Interestingly, the few TCGA never-smokers classified as ES1 display smoking characteristic C>A transversion frequencies similar to current-smokers, clearly different from, for example, ES2-classified never-smokers (Supplementary Fig. S4A). Thus, whether these never-smokers are “true” never-smokers remains unclear. This suggests that ES1 is in fact strongly related to patients with a smoking history and, importantly, presumably also distinct underlying tumor biology and/or tumorigenic events.

The question of whether the observed DNA methylation epitypes/alterations are driver or passenger events, and their position and role in the evolutionary tree of a tumor remains to be determined. Promoter hypermethylation of individual genes, notably tumor suppressors like CDKN2A, have been recognized as early events in lung tumorigenesis, while there is a lack of consensus over whether global hypomethylation is an early or late event in lung cancer (see refs. 37, 38). The impact of smoking on epigenetic modifications may further complicate the picture, as certain alterations have been associated with duration or amount of tobacco smoking and may thus be later events in the cancer development and progression (38). Whole-genome bisulfite sequencing combined with other profiling/sequencing techniques may be one potential way of reconstructing the evolution of a tumor in relation to driver mutations, CNAs, and DNA methylation, as recently described for DNA alterations in breast cancer (47).

Besides describing DNA methylation patterns in lung adenocarcinoma, our study strongly supports a link between adenocarcinoma gene expression phenotypes and genome-wide DNA methylation patterns (9). Importantly, this link brings further insights and explanation to the observed clinicopathologic characteristics, gene expression patterns, mutational signatures, and biologic pathways/processes associated with the epitypes (3, 9, 27, 43). However, the current study also extends the knowledge about genome-wide DNA methylation patterns in the adenocarcinoma gene expression phenotypes, for example, showing that the current definition of these phenotypes comprises of a mix of DNA methylation patterns (Fig. 3D). In contrast with Wilkerson and colleagues (9), we found that the magnoid subtype was strongly associated with a global DNA hypomethylation pattern in both the discovery and TCGA cohorts (Supplementary Fig. S6C and S6D). Furthermore, DNA methylation patterns in and between the epitypes were consistent irrespective of bronchioid, magnoid, or squamoid classification (Supplementary Fig. S6E and S6F). Together, our results suggest that further refinement of both the proposed gene expression phenotypes and the CIMP phenotype in lung adenocarcinoma should be possible through integrated analysis of transcriptional, copy number, and DNA methylation data.

Epigenetic alterations, including DNA methylation, are potentially reversible which offers an interesting therapeutic opportunity. For instance, DNA methyltransferase (DNMT) inhibitors can induce DNA hypomethylation at specific gene loci that can result in sustained gene reactivation (48). Currently, DNMT inhibitors and multiple histone deacetylase (HDAC) inhibitors are in clinical use and/or clinical testing in different malignancies, and a recent phase I/II trial reported an objective response to a combinatorial treatment with DNMT and HDAC inhibitors in recurrent metastatic NSCLC (49). Interestingly, in a recent NSCLC cell line experiment, cell lines with a CIMP-positive phenotype responded with growth inhibition to 5-Aza-dC (a DNMT inhibitor) treatment, while CIMP-negative cell lines did not (4). Whether the proposed epitypes in the current study define patient subgroups likely to benefit or not from such treatments remains to be investigated.

In summary, based on a multicohort approach, we have conducted a comprehensive survey of the genome-wide DNA methylation pattern in lung cancer involving the major histologic subgroups. Together, the current study adds further layers of information about the epigenetic characteristics and molecular diversity in lung cancer. Moreover, it highlights the possibility to further refine disease classification that may ultimately lead to improvements in detection, patient stratification, prognostication, and therapy.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

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References

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