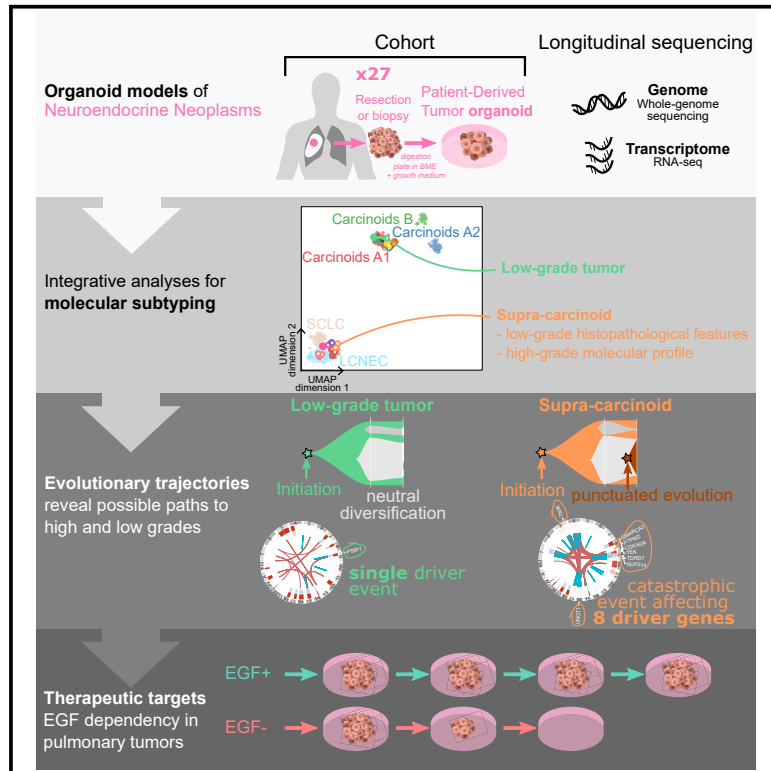


Druggable growth dependencies and tumor evolution analysis in patient-derived organoids of neuroendocrine neoplasms from multiple body sites

Graphical abstract



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In brief

Dayton et al. established patient-derived tumor organoids (PDTOs) from neuroendocrine neoplasms including low-grade pulmonary neuroendocrine tumors. Multi-omic molecular analyses show that PDTOs retain parental tumor intra-tumoral heterogeneity. Phenotypic growth analyses reveal EGF dependency of a subset of pulmonary neuroendocrine tumors, indicating a therapeutic vulnerability in these tumors.

Highlights

- PDTOs of NETs and LCNEC from multiple sites were established
- PDTOs recapitulate intra-tumoral heterogeneity and evolution of parental tumors
- Drug assays reveal therapeutic vulnerabilities and biomarkers
- Pulmonary NET PDTOs are dependent on EGF



Article

Druggable growth dependencies and tumor evolution analysis in patient-derived organoids of neuroendocrine neoplasms from multiple body sites

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SUMMARY

Neuroendocrine neoplasms (NENs) comprise well-differentiated neuroendocrine tumors (NETs) and poorly differentiated neuroendocrine carcinomas (NECs). Treatment options for patients with NENs are limited, in part due to lack of accurate models. We establish patient-derived tumor organoids (PDTOs) from pulmonary NETs and derive PDTOs from an understudied subtype of NEC, large cell neuroendocrine carcinoma (LCNEC), arising from multiple body sites. PDTOs maintain the gene expression patterns, intra-tumoral heterogeneity, and evolutionary processes of parental tumors. Through hypothesis-driven drug sensitivity analyses, we identify *ASCL1* as a potential biomarker for response of LCNEC to treatment with BCL-2 inhibitors. Additionally, we discover a dependency on EGF in pulmonary NET PDTOs. Consistent with these findings, we find that, in an independent cohort, approximately 50% of pulmonary NETs express EGFR. This study identifies an actionable vulnerability for a subset of pulmonary NETs, emphasizing the utility of these PDTO models.

INTRODUCTION

Neuroendocrine neoplasms (NENs) show features of neuroendocrine differentiation, have the highest incidence in the lung and gastroenteropancreatic (GEP) system, and comprise what

are considered two distinct entities, neuroendocrine tumors (NETs) and neuroendocrine carcinomas (NECs). The latter are poorly differentiated, high-grade tumors with a median life expectancy of less than 1 year.¹ NECs are further subdivided into small cell NECs and large cell NECs (LCNECs). NENs are



distinguished from adenocarcinoma and squamous cell carcinomas by a combination of morphological features and expression of at least one of the three standard neuroendocrine markers: chromogranin A, synaptophysin, and CD56/NCAM. Morphological features of NETs include rosettes, solid nesting architecture, and trabeculae. NECs show sheet or nodular growth with extensive necrosis and apoptosis.¹

Small cell NECs are most common in the lung. Small cell lung cancers (SCLCs) account for ~15% of all lung cancers and are better studied than other NECs. LCNEC is more common in the GEP. Irrespective of tissue site, guidelines for treating patients with LCNEC remain rudimentary. Whether the therapeutic guidelines for SCLC can be applied to patients with LCNEC is unclear.²

NETs are well-differentiated, predominantly low-grade tumors (G1 and G2). The WHO criteria for the diagnosis of low-grade NET is a maximum mitotic count of 10 mitoses per 2 mm² for pulmonary NETs, or a Ki67 positivity rate of less than 20% for GEP NETs.¹ Pulmonary NETs are referred to as typical carcinoids (TC) if G1 and atypical carcinoids (AC) if G2. Although low-grade NETs are generally associated with a favorable prognosis, up to 35% of patients with NETs present with metastases, leading to a significant drop in overall survival rates.³ The 10-year disease-specific survival for patients with metastatic G2 pulmonary NETs is 18% and it is unknown what the best treatment strategy is for these patients.⁴

Molecular analyses of pulmonary NETs have identified three groups: less aggressive carcinoids A1 and A2, and more aggressive carcinoids B.^{5,6} In their study, Alcala et al. identify a subgroup of pulmonary NETs termed supra-carcinoids, highly aggressive tumors with the histopathological profile of low-grade NETs but the molecular profile of LCNEC. Pointing to their clinical relevance, supra-carcinoids are associated with a lower 10-year overall survival compared to G1/G2 pulmonary NETs. Other analyses of pulmonary NENs have identified subsets of tumors with similar characteristics to supra-carcinoids and there are several published reports of well-differentiated pulmonary NETs showing features of high-grade disease.^{7–10} Currently, little is known about the biology of supra-carcinoids.

The lack of a clear standard of care for patients with LCNEC or clinically aggressive NETs underscores a clinical unmet need.^{4,11,12} Whereas SCLC research has benefited from multiple models of the disease, LCNEC and NET research has been hindered by a paucity of preclinical models to test hypotheses about potential therapeutic targets and mechanisms of progression for NENs.^{13–18}

Patient-derived tumor organoids (PDTOs) are 3D cultures of tumor cells that can be expanded long-term and are representative of their parental tumor tissue.^{19–22} To date, a handful of PDTOs has been derived from high-grade NENs including SCLC, pulmonary LCNEC, and G3 GEP NETs and NECs.^{23–27} In this study, we establish a collection of NEN PDTOs, including PDTOs of low-grade pulmonary NETs (LNET) and of LCNEC from multiple tissue sites. We also describe short-term cultures of small intestine NETs (SINET) PDTOs. Through multi-omic and phenotypic analyses, we confirm the fidelity of NEN PDTOs to their parental tumors and show that they preserve intra-tumoral heterogeneity and active evolutionary processes. Using this platform, we uncover a potentially actionable therapeutic vulnera-

bility in a subset of pulmonary NETs, suggesting that growth factor dependence may be a feature of these tumors that can be exploited for therapeutic benefit.

RESULTS

Establishment of patient-derived tumor organoids (PDTOs) of understudied NEN subtypes

To generate PDTO models of understudied NEN subtypes, tissue samples from patients undergoing surgical resection or biopsy for NET or LCNEC were obtained, subjected to enzymatic digestion, and the resulting cell suspensions embedded in basement membrane extract (BME) and submerged in culture medium (see STAR methods). When PDTOs formed, they were expanded and used for downstream analyses (Figure 1A).

A panel of 11 LNET (lung NET) and 6 LCNEC PDTO lines was generated (Table S1), along with short-term PDTO cultures (up to passage 4) of 9 small intestine NETs (SINETs). We also further characterized an LCNEC PDTO, LCNEC4, generated and reported in a previous study from our lab.²⁴ All LCNEC and LNET PDTOs showed long-term growth in culture (Figure 1B). One line derived from a metastasis with unknown primary, mLCNEC23 (metastasis of LCNEC23), was established from a fine needle biopsy, showing the feasibility of establishing LCNEC PDTOs from small amounts of patient material. Multiple pathologists confirmed the diagnosis of NET or LCNEC of samples included in this study. NEN PDTOs displayed a variety of morphologies, ranging from dense structures to grape-like cell clusters (Figures 1C and S1A). Consistent with differences in their malignancy and proliferation, LCNEC PDTOs were readily established (75%; 6 out of 8), while LNET PDTOs showed an estimated success rate of 37% (11 out of 30; growth beyond 4 passages and/or 1 year) (Figure S1B).

NEN PDTOs recapitulate disease-specific growth phenotypes

Through histopathological analyses of PDTOs (13 out of 27 samples) (Table S1), we showed that PDTOs captured the histological features of their matching tumor of origin (Figures 2A–2C and S2A–S2C). Immunohistochemical (IHC) staining for the neuroendocrine markers chromogranin A (CHGA), synaptophysin (SYP), and CD56/NCAM1 on NEN PDTOs confirmed their neuroendocrine origin (Figures 2B, S2B, and S2D). Successful subcutaneous xenotransplantation of 4 LCNEC PDTO lines into immunocompromised mice (27 out of 30 injections; Table S1) confirmed tumorigenicity. Xenografted tumors stained positive for at least 1 out of 3 neuroendocrine markers (Figures 2A–2C, S2E; Table S1) and were confirmed to be LCNEC by pathologist assessment based on morphology, NE marker staining, and Ki67 positivity (Table S1).

A distinguishing feature of low-grade NETs is their low proliferation index.¹ IHC staining for the proliferation marker, Ki67 showed similar numbers of Ki67+ cells per field of view in NEN PDTOs and their matched parental tumors (Figure 2C and S2C). In line with these data, all PDTOs presented *MKI67* expression levels within what has been reported in their respective histopathological type^{5,28,29} (Figure 2D).

As expected, LCNEC and LNET PDTOs had distinct *in vitro* growth rates. The average number of days it took for PDTOs of tumors of different grades (G1, G2, or G3/LCNEC) to be

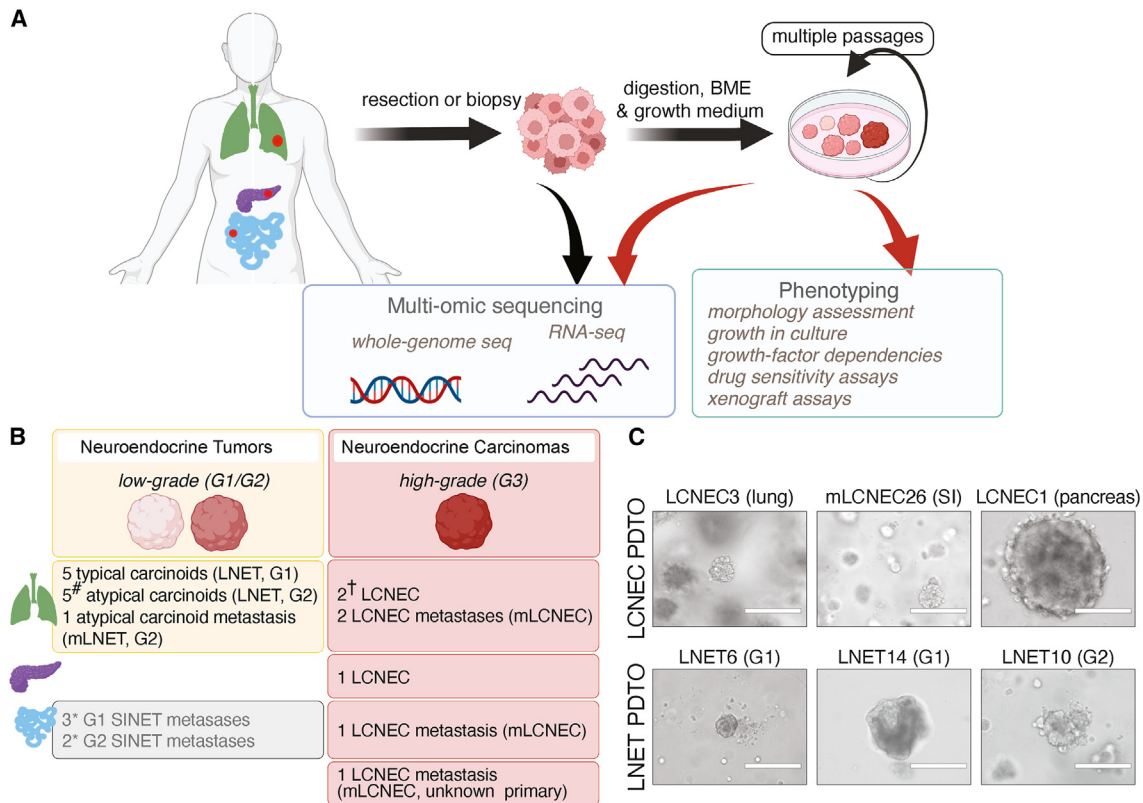


Figure 1. Establishment of NET and LCNEC patient-derived tumor organoids (PDTOs)

(A) Schematic of experimental design.

(B) Overview of established LNET and LCNEC PDTOs and short term SINET organoid cultures. LCNEC: large cell NEC; mLCNEC: metastasis of LCNEC; LNET: lung neuroendocrine tumor; mLNET: metastasis of LNET; SINET: small intestinal neuroendocrine tumor; G1: grade 1; G2: grade 2; G3: grade 3. LNET PDTOs without long-term growth were not included. #: 1 line from a presumed supra-carcinoid; *no growth beyond passage 4; †: 1 line previously reported.

(C) Representative bright-field images of NEN PDTOs. Scale bar: 200 μ m. SI: small intestine. A and B. Made with biorender.com. See also [Figure S1](#) and [Table S1](#).

passaged five times (P5) revealed a clear pattern of decreased average time to P5 with increasing tumor grade (Figures 2E and 2F). We did not observe a temporal trend toward deceleration or acceleration of passage time in PDO lines (Mann-Kendall test q -values > 0.18, Table S1). We did not perform this analysis on SINET PDTOs, as they could not be propagated past passage 4. Altogether, these data argue that PDO culture did not alter the NEN subtype-defining phenotype of tumor growth rate. Of note, one LNET PDO (LNET10) showed a remarkable growth rate compared to other LNETs (~150 days to P5, similar to LCNEC); as we will demonstrate in the following text, this tumor has other unique traits.

High-purity NEN PDTOs mirror the gene expression of their parental tumors

We assessed whether NEN PDTOs maintained the gene expression profiles of their parental tumors using bulk RNA sequencing (RNA-seq) (Figures 3A and S3A; Table S2). First, we examined the levels of expression for 3 canonical markers of neuroendocrine differentiation (*CHGA*, *CD56/NCAM1*, and *SYP*), and 3 neuroendocrine lineage transcription factors (*ASCL1*, *INSM1*, and *NEUROD1*)¹³ (Figures 3B and S3B). For 15 out of the 21 parental-tumor PDO families, expression levels for these markers were similar in PDTOs and their parental tumors and within the range of expres-

sion observed in reference samples (Figure 3B). Short-term SINET PDO cultures had expression levels of the common therapeutic target, somatostatin receptor 2 (SSTR2), consistent with those observed in their parental tumors (Figure S3C).

The remaining 6 parental-tumor PDO families, all derived from G1 or G2 LNETs, showed lower levels of expression for the examined neuroendocrine markers in the PDO (Figure S3B). We performed IHC staining for the neuroendocrine marker CHGA in 3 of these LNET PDTOs and found that they consisted of CHGA+ tumor cells and undefined CHGA- cells (Figure S3D). We hypothesized that some PDO lines contain both healthy and tumor cells, while others contain primarily tumor cells. To assess tumor purity of PDTOs, we categorized them as either “mixed” or “high-purity” based on a combination of molecular and IHC criteria (see STAR methods; Figure S3D; Table S3).

Transcriptomic analysis of high-purity PDTOs and their parental tumors, and a comparison with transcriptomes of NEN reference samples from previously published datasets, showed that they captured the molecular group of their parental tumor^{5,28,30} (Figures 3C and 3D). Embedding and clustering by UMAP using genes representative of known molecular groups of pulmonary NENs and SINETs showed that PDTOs and their parental tumors clustered together with the reference NEN tissue samples of the expected molecular group. Although LCNEC1

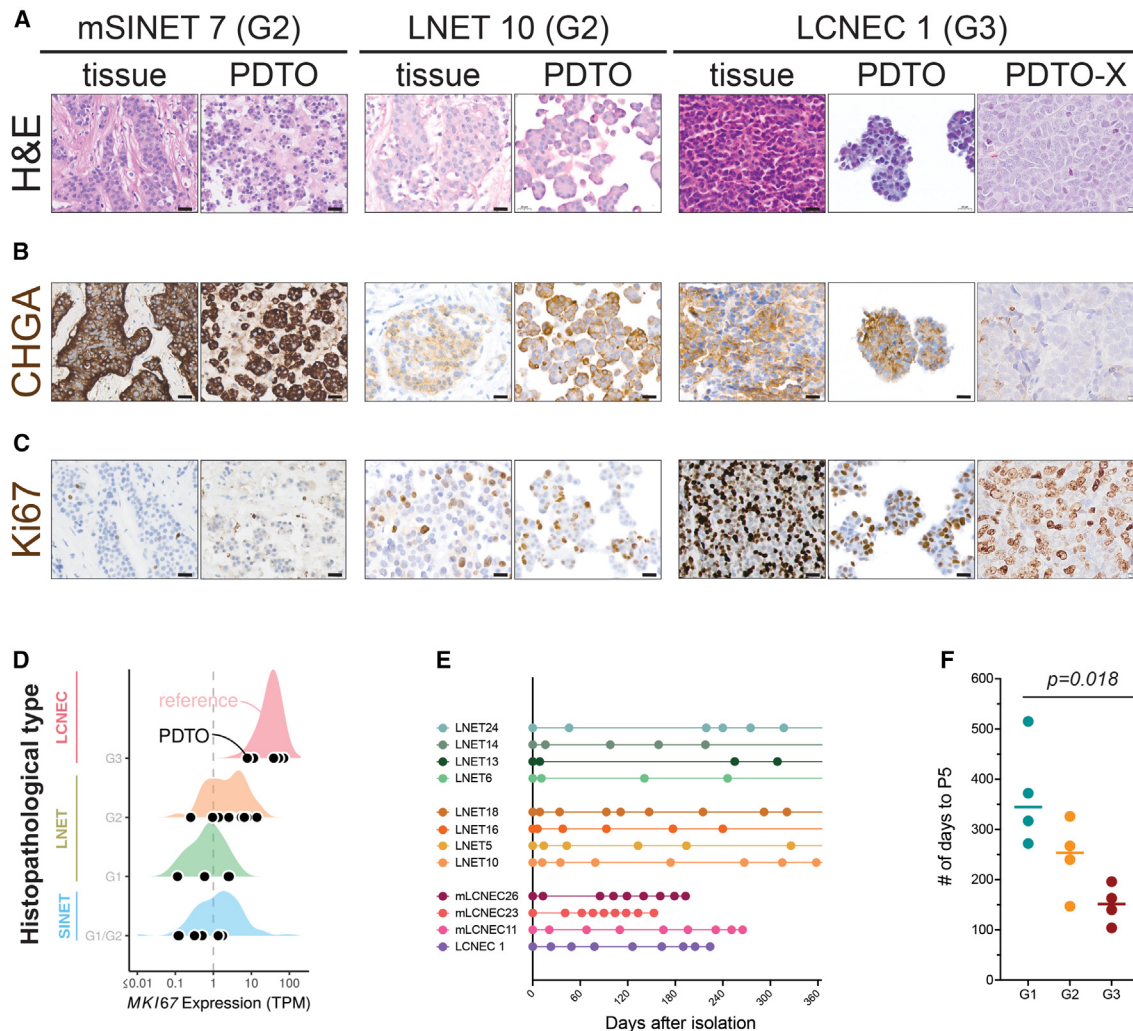


Figure 2. NET and LCNEC PDTOs retain histologic features and relative growth-rate of parental tumor subtypes

(A–C) Representative images of (A) hematoxylin and eosin (H&E) staining and immunohistochemical staining for (B) the neuroendocrine marker, chromogranin A (CHGA) and (C) the proliferation marker Ki67 of PDTOs, PDO-xenotransplants (PDO-X), and their parental tumor tissue. Scale bar: 20 μm except for PDO-X images where scale bar is 10 μm mSINET: metastasis of small intestine NET; LNET: lung NET; LCNEC: large cell NEC.

(D) mRNA expression of *MK167* in transcripts per million (TPM) in PDTOs and reference samples.^{5,28,29} Colored densities: distribution of reference sample expression values. Black dots: PDTOs.

(E) Number of days in between each passage over the course of one year following isolation for LCNEC and LNET PDTOs. Each dot represents a passage. Data shown up to passage 8 or current passage number if lower than 8. mLCNEC: metastasis of LCNEC.

(F) Average cumulative number of days between date of isolation and passage 5 for PDTOs from tumors of different grades; $p = 0.018$, ANOVA. See also Figure S2 and Table S1.

and mLCNEC23 were from extrapulmonary LCNEC tumors (pancreas and unknown primary), both their parental tumors and PDTOs clustered with the reference pulmonary LCNECs, suggesting that LCNECs in different tissue sites share similar expression profiles.

The parental tumor and PDTOs from LNET10 clustered with LCNEC samples. From the reference datasets an additional three LNET samples, all previously reported as supra-carcinoids, also fell into the LCNEC cluster⁵ (Figure 3C). Consistent with the hypothesis that LNET10 is a supra-carcinoid, the parental tumor and PDTOs displayed high expression of immune checkpoint genes and low expression of the putative prognostic marker, *OTP*^{5,31,32} (Figure S3E). The clinical data of the patient with

LNET10 was consistent with the diagnosis of supra-carcinoid: multiple metastases and recurrence following targeted therapy. The high *in vitro* growth rate for this PDO (Figure 2E) is also consistent with this diagnosis.

To identify markers that distinguish PDTOs from their parental tumors, we performed Partial Least Squares (PLS) analyses of all PDO lines and their matched parental tumor (Figure S3F). Gene set enrichment analysis (GSEA) on the identified markers showed that they are mostly immune-related, consistent with observations in PDTOs of other tumor types³³ (Figure S3G). These data support the notion that PDTOs contain the tumoral and epithelial components but not the stromal components of their parental tumors.

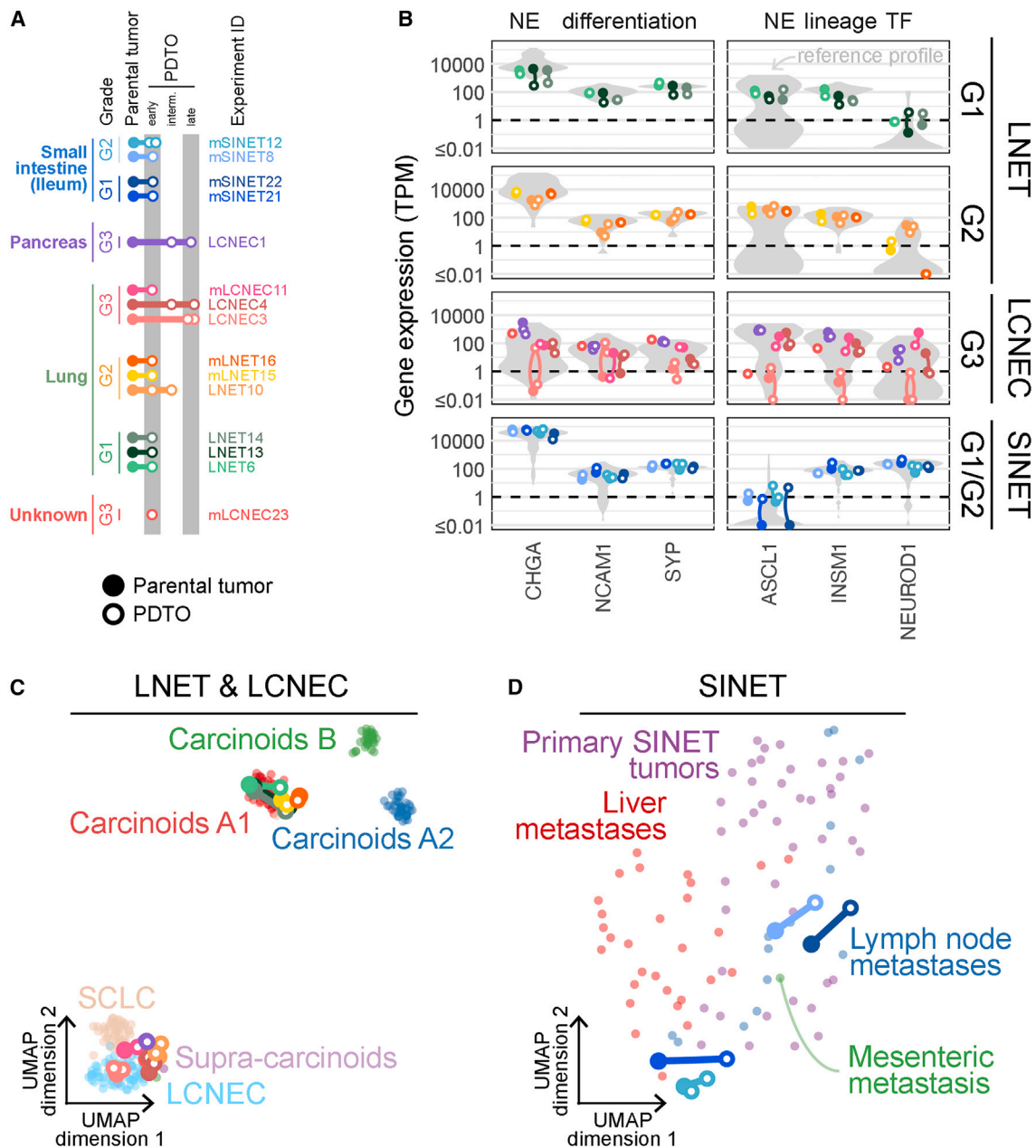


Figure 3. High-purity NEN PDOs recapitulate the gene expression of original tumors

(A) Overview of high-purity PDOs and parental tumors for which RNA-seq data were generated. Filled circles: parental tumors; empty circles: PDOs (early passage: 1–3; intermediate passage: 4–7; late passage: 8+).

(B) Expression of neuroendocrine and transcription factor markers in PDOs and parental tumors, in transcripts per million (TPM). Gray violin plots represent reference profiles with matching histological type and grade (n = 75 for G1 LNET, n = 40 for G2 LNET, n = 69 for LCNEC, n = 88 for SINET).

(C and D) Two-dimensional representation of the molecular profiles of PDO within reference profiles from different molecular groups (point colors; n = 239 LNET & LCNEC, 88 SINET) using UMAP. (C) LNET and LCNEC for a set of 1055 core genes⁵; (D) small intestine NETs for a set of 519 genes (master regulators identified in Alvarez et al. Nature Genetics 2018). See also Figure S3 and Tables S2 and S3.

NEN PDOs retain the genomic profile of their parental tumors

To determine whether NEN PDOs recapitulate the genomic landscape of their parental tumors, we performed whole genome sequencing (WGS) in 10 parental-tumor PDO families representing all tumor types and grades in the collection, and

including multiple time points in culture for 2 LCNEC lines (Figures 4A and S4A; Table S4).

Tumor mutational burden (TMB) was similar between PDOs and their parental tumor (Figures 4B and S4B). Consistent with previous observations, TMB was lower for NET than LCNEC (mean 1.26 and 11.5, respectively).^{5,34–36} The spectrum of

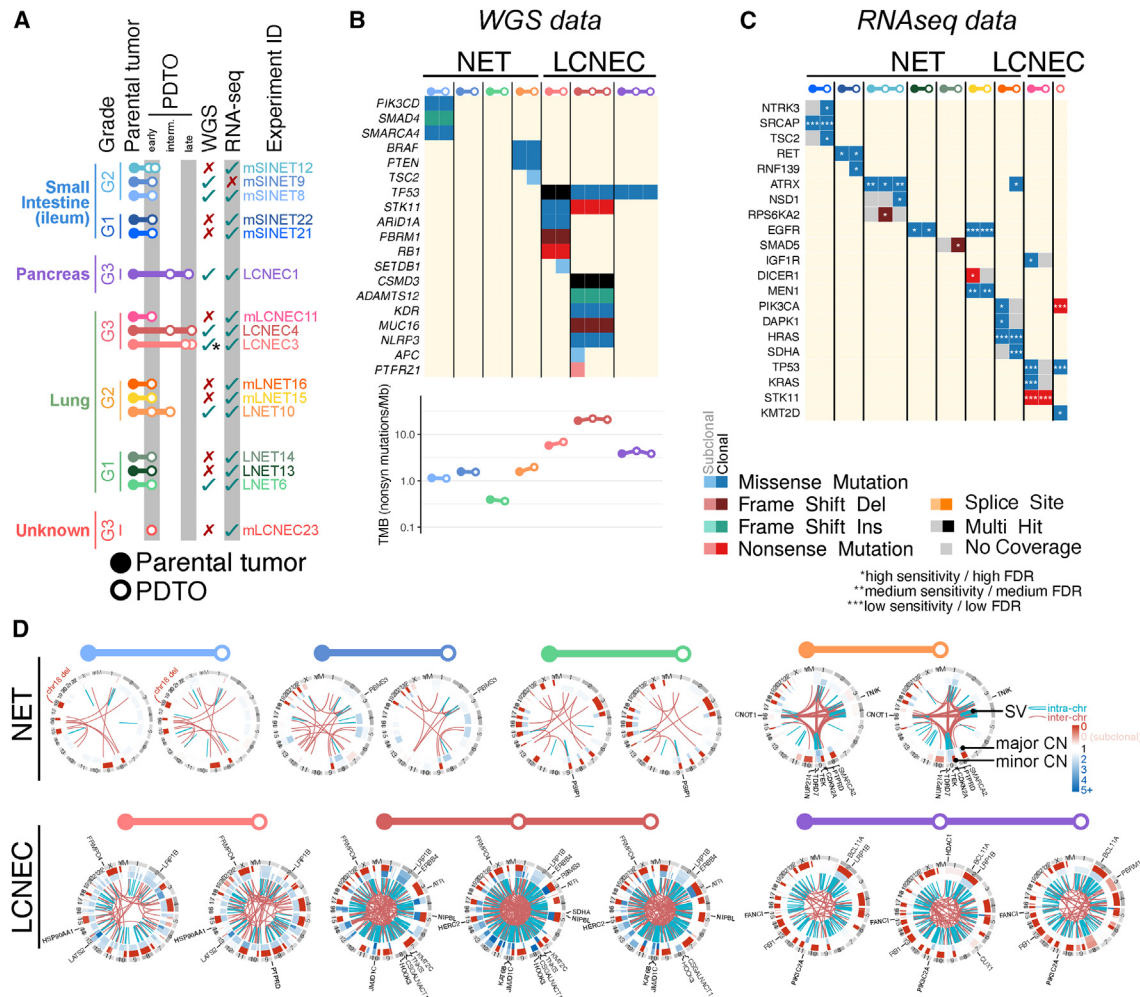


Figure 4. NEN PDTOs retain genomic features of parental tumors

(A) Overview of high-purity PDTOs and parental tumors for which whole genome sequencing (WGS) and/or RNA-seq data were generated. Filled circles: parental tumors; empty circles: PDTOs (early passage: 1–3; intermediate passage: 4–7; late passage: 8+). *LCNEC3: WGS data were generated for 1 passage, RNAseq data for 2 passages.

(B and C) Summary of putative pathogenic somatic alterations detected by (B) WGS or (C) RNA-seq in genes reported to be recurrently mutated in LCNEC, LNET, and SINET. Colors represent variant classes and clonality (light: subclonal; solid: clonal). In (B), the lower panel represents the Tumor Mutational Burden (TMB), the number of nonsynonymous mutations per megabase. In (C), light gray represents genes without enough coverage to detect variants. The EGFR mutation in LNET13, L135Q, has not been reported in the COSMIC database and is unlikely to be an oncogenic alteration. The EGFR mutation in mLNET15, G828E, COSMIC ID COSV51784752, has been reported in 4 samples and has unknown significance.

(D) Structural variants in PDTOs and parental tumors. Inner layer: chromosomal rearrangements; central layer: major copy number (CN); outer layer: minor CN. Structural variants damaging genes that have been previously reported as recurrently mutated in LCNEC, LNET, or SINET are annotated in black. Subclonal CN alterations (non-integer CN) are indicated with intermediate colors (e.g., light red for subclonal CN loss). See also Figure S4 and Table S4.

mutationally altered genes observed recapitulated genomic alterations previously reported in NENs.^{5,7,28,34,36–41} NET PDTOs presented fewer single nucleotide variants (SNVs) and insertions and deletions (indels) in known driver genes than LCNEC PDTOs (average of 1.5 vs. 4), with SINET9 and LNET6 samples showing none (Figures 4B and S4B). For 5 out of 8 high-purity PDTO WGS profiles, the SNVs in putative driver genes observed in the parental tumors were also observed in the corresponding PDTO line, showing a high degree of concordance. In the remaining 3 high-purity PDTO lines, LNET10, LCNEC3, and LCNEC4, discordance between the PDTO and corresponding parental tumor was seen exclusively in subclonal alterations

and in only up to 2 putative driver SNVs (Figure 4B). In the case of the 2 “mixed” LNET PDTO-parental tumor WGS profiles in our dataset, LNET2 and LNET5, we identified somatic driver mutations confirming that they contain tumoral tissue (Figure S4B).

To identify somatic variants in samples for which WGS had not been performed, we used RNA-seq data to call SNVs in genes previously found to be altered in NENs (Figures 4C and S4C). We identified 28+ unique, putatively oncogenic mutations (see STAR methods) in either the PDTOs, parental tumors, or both affecting *MEN1*, *ATRX*, *HRAS*, *TSC2*, *PIK3CA*, and *STK11*^{5,28,34,36} (Figure S4C).

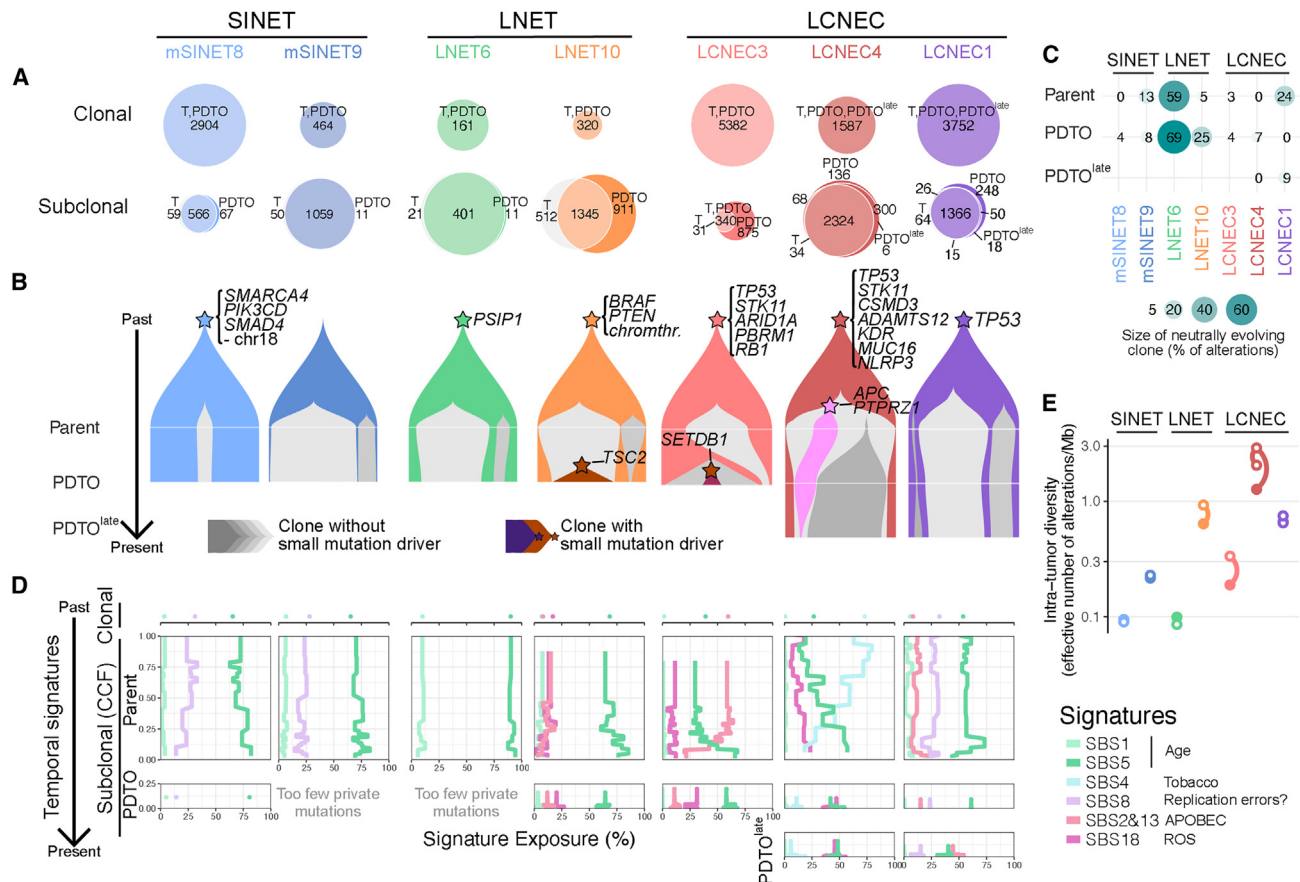


Figure 5. NEN PDOs recapitulate the intra-tumor heterogeneity of the parental tumor

(A) Venn-Euler diagrams of shared and private clonal (top) and subclonal (bottom) somatic small variants.

(B) Fish plots showing clonal reconstruction of tumor and organoid.

(C) Mode of evolution, measured as the size of the neutrally evolving clone in percentage of subclonal alterations (see STAR methods).

(D) Temporal mutational signatures, measured as the signature exposure (the percentage of mutations belonging to each signature), in clonal small variants (top), subclonal small variants present only in the parental tumor (middle), and those only present in the PDO (bottom). The vertical axis corresponds to the cancer cell fraction (CCF), a proxy for the age of the mutation (older alterations: top; high CCF, recent alterations: bottom; low CCF).

(E) Intra-tumor genetic diversity, the effective number of alterations per Mb (see STAR methods). In (A), (B), and (D), columns correspond to PDO/parent families. See also Figure S5.

When coverage of the region of interest for the relevant mutations and samples was sufficient, the mutations identified in the tumor were also found in the corresponding PDO (10/28 mutations and for 9/11 PDO parental-tumor pairs) (Figures 4C and S4C). We identified the oncogenic *HRAS* G13D mutation in all samples from LNET16, including the primary pulmonary NET, its matched metastasis, and the corresponding tumor- and metastasis-derived PDOs. We also identified a somatic mutation in *MEN1*, the most commonly altered gene in pulmonary NETs, in both the tumor and PDO from mLNET15.^{5,34,38} The parental tumor sample from mLNEC11 was found to carry the oncogenic *KRAS* G12V mutation and the PDO of mLNEC23 a predicted oncogenic mutation in the *TP53* gene.

At the level of copy number alterations and structural variants (SVs), PDOs captured both focal events and large-scale chromosomal aberrations (Figures 4D and S4D). As examples of the former, we observed *RBMS3* translocations in SINET9, and a *PSIP1* inversion and a large deletion in LNET6. For the latter, we observed a potential chromothripsis event in LNET10

affecting chromosomes 1, 3, 4, 9, and 16, whole-genome doubling in LCNEC4, and chromosome 18 loss—a known event observed in more than 60% of SINETs—in SINET8.^{42,43} Overall, the patterns of copy number alterations and SVs were conserved between parental tumors and PDOs, and were consistent with patterns previously observed in NENs.

Organoids capture the intra-tumor heterogeneity and evolutionary processes of their parental tumors

To determine whether PDOs capture the fine-scale genetic makeup of their parental tumors, we performed clonal deconvolution and evolutionary analyses. PDOs recapitulate the ratio of clonal and subclonal alterations of each tumor type (Figures 5A, S5A, and S5B), with NETs having predominantly subclonal alterations (from ~400 to ~3200), and LCNECs having predominantly clonal alterations (from ~1500 to ~5300). Subclonal alterations were predominantly present at similar cancer cell fractions in the parental tumor and matched PDOs, and even alterations present in only a small percentage of parental tumor cells were detected in

the PDTO (Figure S5A). As expected, concordance of subclonal mutations between PDTOs and parental tumors was highest in the low-grade NETs (<11% of private alterations in mSINET8, mSINET9, and LNET6). An exception to this was LNET10, the putative supra-carcinoid, which showed more substantial subclonal differences (~40% of private alterations).

These analyses showed that PDTOs preserve the main subclones of their parental tumor (Figures 5B and S5C). In concordance with their lower grade and lower passage time, and consistent with past and present neutral evolution, we did not identify known driver alterations in subclones of SINETS or LNET6 PDTOs but detected neutrally evolving subclones in both parents and PDTOs (MOBSTER method,⁴⁴; Figures 5C and S5D). Interestingly, supra-carcinoid LNET10 had multiple clonal driver mutations (*BRAF*, *PTEN*, a chromothripsis event affecting many genes), consistent with past linear evolution. This sample also had a subclonal *TSC2* mutation that was found at high frequency in the PDTO but was either absent or below the detection limit in the parental tumor, an observation consistent with a possible ongoing selective sweep. LCNEC1, 3, and 4 also show signs of past linear evolution, and possibly ongoing natural selection, due to the presence at low frequency of driver mutations in LCNEC3 (*SETDB1*) and LCNEC4 (*APC* and *PTPRZ1*) PDTOs. These data suggest that both past and present evolution under natural selection are captured by PDTOs.

We reasoned that the mutations that were private to the PDTO could have been generated either by the same mutational processes observed in the parental tumor or by new mutational processes specific to the PDTO and/or the culture conditions. To determine which of these was true, we used the TrackSig method⁴⁵ to reconstruct the temporal trajectory of mutational signatures in tumors and PDTOs.

Mutations appearing in the PDTOs were not only generated by the same processes that were active in the parental tumors, but they also reflected recent shifts in sources of mutation (Figures 5D and S5E). For instance, a signature associated with reactive oxygen species, single base substitution 18 (SBS18), was detected in LCNEC3 and LCNEC4 subclonal alterations and was also found in their PDTOs. Even the quasi-absence of the tobacco smoking-associated SBS4 in LCNEC4 PDTO cells is consistent with a recent drastic decline in this signature in the parental tumor (from 73% of clonal alterations to 18% of “recent” alterations). This shows that PDTOs preserve the endogenous mutational processes operating in the parental tumors.

Finally, we investigated whether PDTOs presented stable levels of intra-tumoral heterogeneity. Interestingly, even late passage PDTOs harbored levels of genetic diversity similar to those observed in parental tumors (Figures 5E and S5F). No sample presented any substantial loss of diversity: LNET6, a low-grade tumor, presented the largest loss but it was minimal (less than 0.02 effective alteration/Mb), potentially indicating that a fraction of tumor cells did not survive in culture. These data argue that PDTOs globally preserve the evolutionary processes at work in their parental tumors: the subtle balance in parental tumors between processes generating genetic diversity, such as mutational processes, and those reducing genetic diversity, such as natural selection and genetic drift, are maintained.

Hypothesis-driven drug sensitivity testing in PDTOs from clinically aggressive NENs

PDTOs have been shown to have predictive value in cancer therapy.^{21,46–50} We performed dose titration assays to examine the effects of several drugs on 5 LCNEC PDTOs. Given its aggressive clinical course and the evidence that it represents a supra-carcinoid, we included LNET10 PDTOs in these assays.

We first tested the response of organoids to the taxane, paclitaxel, and to the mTOR inhibitor, everolimus. In the clinic, paclitaxel is sometimes used in combination with carboplatin to treat patients with pulmonary LCNEC.³⁸ Everolimus is an approved therapy for low-grade NETs also being tested for the treatment of NECs.^{13,51} We observed differential drug responses of individual PDTO lines to these compounds, with 4 out of 6 of the tested PDTOs showing some response to both drugs (Figures 6A, S6A, and S6B).

We were also interested in determining whether PDTOs could predict patient response to targeted therapies. WGS analysis of the tumor tissue and matched PDTOs from the putative supra-carcinoid, LNET10, identified a *BRAF* V600E mutation (Figure 4B). Some patients with *BRAF*-mutated tumors show clinically significant responses to combined treatment with *BRAF* and MEK inhibitors.^{52,53} We tested the response of LNET10 PDTOs to both single-agent and combination treatment with the *BRAF* inhibitor, dabrafenib and the MEK inhibitor, trametinib (Figures S6C–S6E). As a comparison, we tested the response of *BRAF*-wildtype mLCNEC23 PDTOs to these inhibitors. Whereas mLCNEC23 PDTOs were resistant to both single-agent treatments and their combination, *BRAF*-mutant LNET10 PDTOs were sensitive to all treatments (area under the fitted dose response curve—AUC—for combination, 186 and 96, respectively). We did not observe an improved response of LNET10 PDTOs to combination treatment compared to single-agent treatments. Notably, neither drug nor their combination was able to kill all the cells in LNET10 PDTOs. Anecdotally, treatment of the respective LNET10 patient with this same drug combination led to an initial response followed by tumor relapse and resistance to treatment.

We next sought to identify new therapeutic opportunities for LCNEC patients. Small cell lung cancer (SCLC), the best-studied subtype of NEC,⁵⁴ can be subdivided into molecular groups defined by the differential expression of lineage transcription factors: *ASCL1*, *NEUROD1*, and *POU2F3*.⁵⁵ Preclinical studies suggest that tumors belonging to different SCLC molecular groups have distinct therapeutic vulnerabilities.^{55–60} *ASCL1* and *NEUROD1* are highly expressed in some LCNEC tumors, in the majority of our LCNEC PDTOs, and in LNET10 PDTOs^{36,61–63} (Figure 3B). To determine whether these PDTOs show sensitivities consistent with those identified for *ASCL1*-high or *NEUROD1*-high SCLC, we tested their response to therapies specific for these SCLC molecular groups: the BCL2 inhibitor, navitoclax, and the Aurora kinase inhibitor, alisertib, respectively^{56,59,60} (Figures 6B, S6E, and S6F). While the tested lines did not show a response to treatment with alisertib, we noted a differential response of PDTOs to navitoclax. In agreement with what has been observed for SCLC, PDTOs with high *ASCL1* expression were sensitive to treatment with navitoclax, while lines with low *ASCL1* expression were resistant to the treatment. Although the sample size did not provide sufficient power to definitively

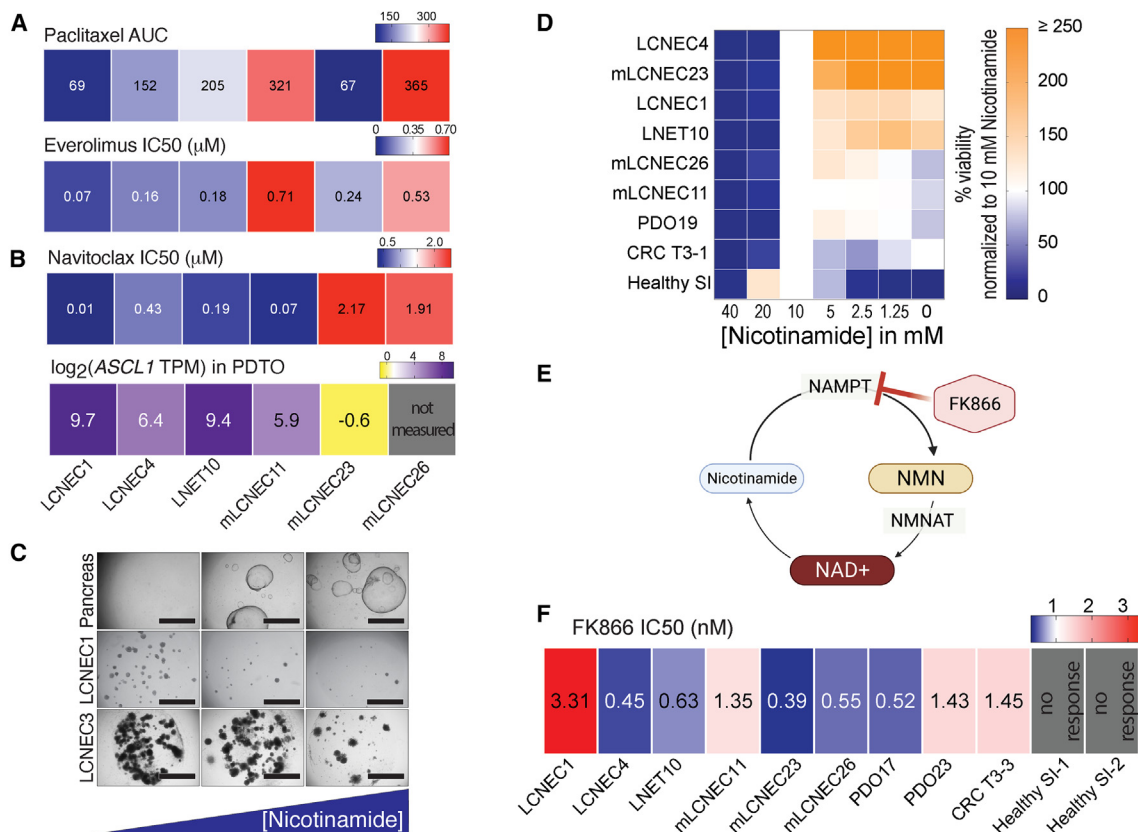


Figure 6. Hypothesis driven drug sensitivity testing in PDTOs from clinically aggressive NENs reveals therapeutic vulnerabilities to approved therapies

(A) Heatmap showing area under the curve (AUC) values for paclitaxel and IC50 values for everolimus of tested PDTO lines. For paclitaxel, the dose-response curve did not allow for IC50 value calculation and AUC is reported instead. Dose-response curves shown in Figures S6A and S6B. (B) Top: Heatmap showing IC50 values for the BCL-2 inhibitor, navitoclax, of PDTOs. Bottom: Heatmap showing expression of *ASCL1* (in log₂ of TPM) in PDTOs. (C) Brightfield images of organoid outgrowth from single cells in media containing increasing concentrations of nicotinamide. Pictures of normal pancreas organoids (top panel) taken on day 7 after plating. Pictures of LCNEC organoids (bottom two panels) taken on day 26 after plating. Concentrations from left to right: 0 mM, 10 mM, 20 mM. Scale bars: 2,000 μm. Magnification: 2×. (D) Quantification of organoid outgrowth from single cells in different concentrations of nicotinamide for LNET 10, 5 LCNEC PDTO lines, colorectal cancer (CRC) PDTO line (T3-1), pancreatic ductal adenocarcinoma line (PDO19), and healthy small intestine (SI) organoids. Cell number was measured by Cell-titer Glo ATP assay. Data are shown relative to outgrowth of the same line in 10 mM nicotinamide. (E) Diagram depicting NAD⁺ salvage biosynthesis pathway. Created using biorender.com. (F) Heatmap showing IC50 values of NEN PDTO lines, a colorectal cancer PDTO line (CRC T3-3), 2 pancreatic ductal adenocarcinoma PDTO lines (PDO17, PDO23), and 2 healthy SI lines for the NAMPT inhibitor, FK866. See also Figure S6.

prove the association, high expression of *BCL2* also appeared to be predictive of a low IC50 value for navitoclax (Spearman's $\rho = -0.8$, one-sided rank test p value = 0.067). These data point to *ASCL1* expression in NENs as a potential general biomarker for therapeutic response to BCL2 inhibitors.

During the medium optimization phase of our study, NEN PDTOs showed the best outgrowth in medium lacking nicotinamide (Figure 6C). This was unexpected because nicotinamide is an essential component of the medium used to culture multiple kinds of organoids.^{19,64} To quantitatively assess the effect of nicotinamide on PDTOs, we tested the outgrowth efficiency of single cell suspensions derived from LCNEC and LNET10 PDTOs, from PDTOs of other tumor types (colorectal cancer and pancreatic ductal adenocarcinoma), and from healthy tissue derived organoids, in different concentrations of nicotinamide (Figure 6D). As previously observed, 10 mM nicotinamide was

optimal or near optimal for outgrowth of the healthy tissue organoid lines and the colorectal cancer PDTO line. This was not the case for NEN PDTOs, where 4 out of 6 NEN PDTOs showed the best outgrowth at either the lowest concentration of nicotinamide, 1.25 mM, or in its complete absence.

Nicotinamide is a precursor of oxidized nicotinamide adenine dinucleotide (NAD⁺).⁶⁵ We speculated that the outgrowth inhibition of nicotinamide on NEN PDTOs implicates a sensitivity of NENs to drugs that influence the conversion of nicotinamide to NAD⁺. To test this possibility, we exposed LCNEC PDTOs, LNET10 PDTOs, PDTOs of other tumor types (colorectal cancer and pancreatic ductal adenocarcinoma), and healthy intestinal tissue organoids to FK866, an inhibitor of nicotinamide phosphoribosyltransferase (NAMPT), the enzyme that catalyzes the rate-limiting step in the NAD⁺ salvage pathway⁶⁵ (Figures 6E–6F and S6G). Consistent with our media assays, while healthy

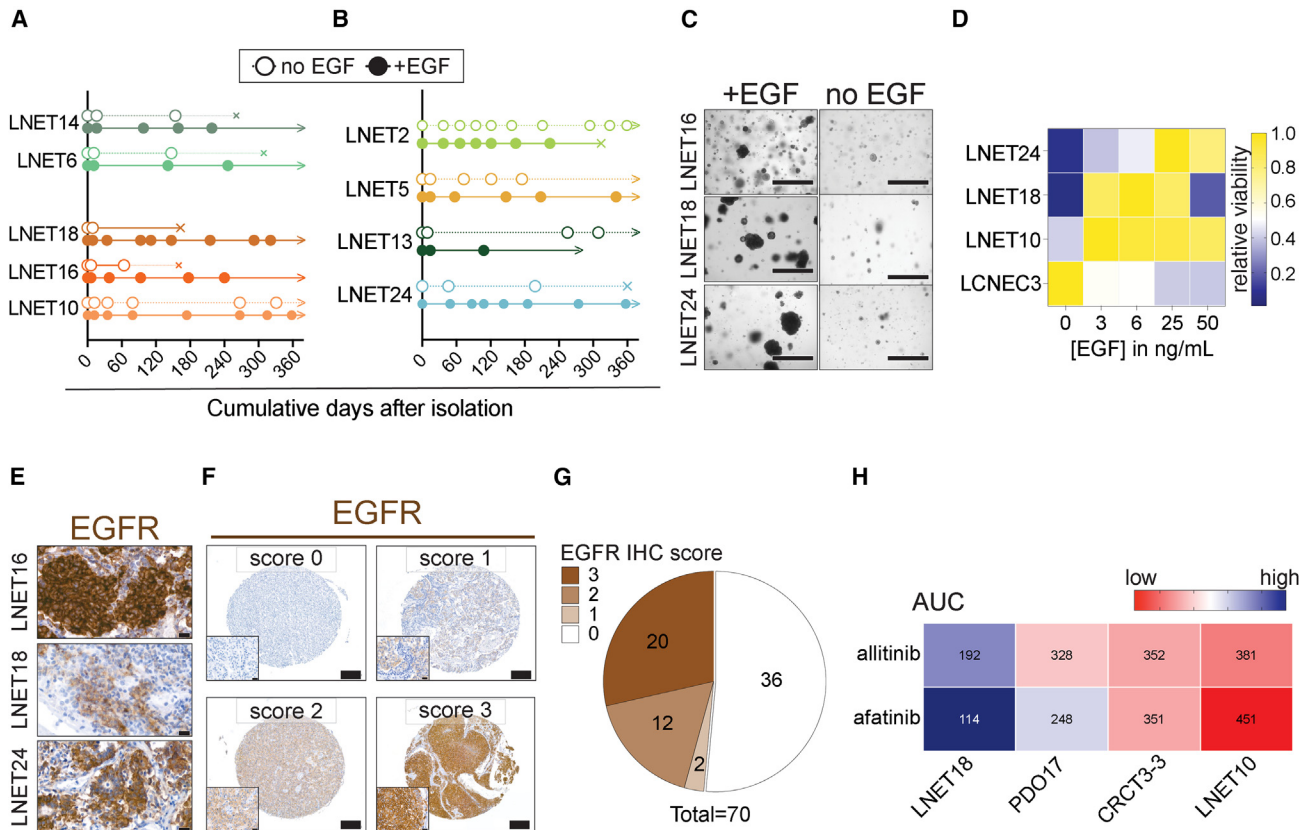


Figure 7. Lung NET PDOs are dependent on EGF and EGFR expression is common in lung NETs

(A and B) Number of days between passages spanning one year (A) following isolation in medium with or without EGF, or (B) following isolation in medium without EGF or thawing into medium with EGF. Each dot represents a passage.

(C) Brightfield images showing growth of LNET PDOs in the presence or absence of EGF, 31 days (LNET16), 42 days (LNET18), or 75 days (LNET24) after plating. Scale bars: 1,000 μ m. Magnification: 4 \times .

(D) Quantification of organoid outgrowth from single cells in different concentrations of EGF for 3 LNET PDOs and 1 LCNEC PDO. Cell number was measured by Cell-titer Glo ATP assay. Data are shown relative to outgrowth of the same line in no EGF and normalized to highest viability value.

(E) Immunohistochemical (IHC) staining for the EGF receptor, EGFR, in parental tumor tissue for the PDOs in C. Scale bar: 20 μ m.

(F) Representative tissue microarray (TMA) cores containing pulmonary NET samples stained for EGFR. An example of each EGFR IHC intensity score is shown (0, negative; 1, weak; 2, medium; 3, strong). See Table S5 for a summary of scores and percent positive tumor cells for TMA cores and tumors. Scale bars: 200 μ m; inset: 20 μ m.

(G) Distribution of EGFR IHC intensity scores for 70 pulmonary NETs from two different TMAs. Each tumor was represented by 3 cores.

(H) Heatmap showing sensitivity of LNET 18, LNET 10, PDO17, and CRCT3-3 to the EGFR inhibitors allitinib and afatinib, as measured by area under the curve (AUC). Numerical values for AUC are shown. Red indicates high AUC values, blue indicates low AUC values. The dose-response curve did not allow for IC50 value calculation and AUC is reported instead. PDO17: pancreatic ductal adenocarcinoma PDO, CRC T3-3, colorectal cancer PDO. See also Figure S7 and Table S5.

tissue organoids showed no response to treatment with FK866, 4 out of 6 NEN PDO lines showed subnanomolar IC50 values. In all cases, the IC50 values were below the steady state plasma concentrations for FK866 (14 nM) reported in a Phase I clinical trial, suggesting clinical relevance of these results.^{66,67} Pancreatic ductal adenocarcinoma and colorectal cancer PDOs showed IC50 values for FK866 within the same range as the tested NEN PDO lines. These results indicate that PDO media requirements can be used to identify potential therapeutic vulnerabilities.

A subset of lung NET PDOs are dependent on EGF and expression of the EGF receptor is common in lung NETs

To identify dependencies in NEN PDOs, we tested the requirement for growth factors commonly used in organoid culture: EGF

or FGF7 and FGF10. When sufficient tissue was available, we cultured a portion of the cell suspension in base NEN PDO media, a portion in media supplemented with FGF7 and FGF10, and a portion in media supplemented with EGF. Consistent with the notion that high-grade tumors acquire growth-factor independence, 5 out of 7 LCNEC PDOs showed no discernible difference in growth with the additional growth factors (Figure S7A).

Pulmonary NET PDOs appeared to be EGF-dependent. Starting at the time of organoid isolation, we directly compared the outgrowth of five LNET PDOs in media containing EGF and media lacking EGF (Figure 7A). In all cases, better outgrowth was observed in media containing EGF. In 4 out of 5 cases, the omission of EGF precluded growth beyond 3 passages. The short-term PDO cultures of SINETS did not grow beyond passage 4 and were not tested for growth factor dependencies.

Given that LNET PDOs were dependent on EGF, we asked whether LNET PDO lines that had shown suboptimal growth in medium without EGF might be similarly dependent on EGF. We thawed frozen vials of 4 LNET PDO lines (LNET2, LNET5, LNET13, and LNET24), directly into media containing EGF and compared their outgrowth over time to the outgrowth dynamics we had observed for the same lines in media without EGF (Figure 7B). 2 out of these 4 PDO lines (LNET5 and LNET24), could be expanded more times within a 1-year time frame than when they had been grown for the same length of time without EGF. LNET24 displayed the most striking difference; without EGF it could only be passaged 3 times, but with the addition of EGF, it was passaged 7 times. In line with these observations, withdrawal of EGF from lines grown in EGF media, or addition of EGF to lines that had been grown in the absence of EGF, revealed improved expansion in the EGF-containing media (Figure 7C).

To quantitatively assess EGF-dependency in LNET PDOs, we performed an EGF dose response outgrowth assay (Figure 7D). EGF improved the expansion of LNET18 and LNET24 PDOs in a dose-dependent manner. While 2 out of 3 LNET PDOs showed similar expansion at 25 ng/ μ L and 50 ng/ μ L, LNET18 PDOs showed reduced expansion at 50 ng/ μ L of EGF compared to even 3 ng/ μ L of EGF. It is possible that for LNET18, at the highest concentrations of EGF, the internalization rate for the EGF receptor, EGFR, exceeded the rate at which it could be recycled back to the plasma membrane. Indeed, culturing head and neck cancers PDOs at low EGF concentrations led to increased expression of membrane EGFR.⁶⁸ LCNEC3 PDOs were not dependent on EGF, and we noted the best expansion in the absence of EGF. Given that LNET10 tumor tissue and PDOs harbor a *BRAF*^{V600E} mutation, which leads to EGF-independent activation of the MAPK pathway, we were surprised to observe increased expansion of LNET10 PDOs in all of the tested EGF concentrations compared to without EGF. Adaptive feedback activation of MAPK signaling has been observed in *BRAF*-mutant colon cancers treated with *BRAF* inhibitors, suggesting that EGF-mediated MAPK activation can promote the growth of EGFR-expressing *BRAF*-mutant tumors.^{69,70}

We next analyzed RNA-seq data from PDOs and parental tumors and from previously published datasets of pulmonary NET tissue⁵ (Figure S7B). *EGFR* expression was present in most tumors and PDOs in these datasets. IHC staining for EGFR confirmed membrane EGFR protein expression in 11 out of 13 LNET parental tumors (Figures 7E and S7C; Table S5). In line with the observation that LNET2 PDOs were not dependent on EGF and that LNET19 PDOs could not be propagated long-term in EGF-containing media, EGFR staining of LNET2 and LNET19 parental tumor tissue was negative. mLNET15 and LNET20 parental tumor tissue showed some staining for EGFR but their PDO growth stopped at passage 3, suggesting that factors other than EGF contribute to *in vitro* growth of some EGFR-expressing tumors.

To ask whether EGFR expression is a common feature of pulmonary NETs, we performed IHC staining for EGFR on pulmonary NET tumor tissue microarrays containing a total of 216 cores from 73 pulmonary NETs (Figure 7F). We assigned each stained core a membrane EGFR staining intensity score and used this to assign a score to the pulmonary NETs on the array. 48% of tumors expressed membrane EGFR, most of which

showed very strong staining (Figure 7G). Altogether, these data show that a subset of close to half of pulmonary NETs expresses membrane EGFR.

Our data imply that some pulmonary NETs might be sensitive to treatment with EGFR inhibitors. To begin to test this possibility, we treated 1 EGF-independent (LNET10) and 1 EGF-dependent (LNET18) PDO line with EGFR inhibitors (Figure 7H). As we did not observe activating mutations in EGFR in our LNET PDOs, we chose EGFR inhibitors that target the wild-type receptor, allitinib and afatinib. As a reference for EGFR sensitivity, we simultaneously tested 2 PDO lines which have previously been shown to be respectively sensitive (PDO17) and resistant (CRC T3-3/P3.T2.1) to treatment with afatinib.^{71,72} Consistent with the observation that it was dependent on EGF for growth in culture, LNET18 PDOs showed the lowest AUC values of all the tested lines (LNET18 192 and 227, PDO17 328 and 248 for allitinib and afatinib, respectively). LNET10 PDOs, which have a downstream activating mutation, and CRC T3-3 PDOs both had AUC values > 300. EGF-dependent LNET18 PDOs were also sensitive to inhibition of EGFR downstream signaling, via treatment with the MEK inhibitor, trametinib (Figure S7D). We also tested LCNEC1 and LNET10 and found both lines were sensitive to MEK inhibition, indicating that MAPK signaling might be important for some NENs independent of tumor grade. Collectively, these data are consistent with the notion that a subset of pulmonary NETs is dependent on EGF growth-factor signaling and provide a rationale for further investigating the potential for treating these tumors with EGFR or MAPK-targeted therapies.

DISCUSSION

In this study, we established a biobank of human NEN PDOs that fully recapitulates the spectrum of malignancy observed for NENs, encompassing both slow growing tumors and highly proliferative, metastatic carcinomas. Our biobank includes models of an understudied subtype of high-grade NEN, LCNEC, PDOs of low-grade pulmonary NETs, and a PDO derived from a supra-carcinoid, a clinically aggressive pulmonary NET. Other NEN organoid biobanks were recently reported.^{25,26} These biobanks contain primarily GEP NECs or GEP G3 NETs and lack models of low-grade NETs and pulmonary LCNEC. Lung NENs account for 25% of all NENs and even low-grade pulmonary NETs show a significant rate of metastasis.^{3,13} Thus, the inclusion of low-grade pulmonary NET PDOs in our collection represents a valuable addition to the cell models currently available for NEN research. The development of these models enabled the clinically relevant discovery that a subset of pulmonary NETs is dependent on EGF. Altogether, our NEN PDO biobank will provide opportunities for investigating carcinogenesis and therapeutics across the broad spectrum of aggressiveness for NENs.

A hurdle in the development of NET PDOs has been the lack of clarity regarding their potential growth-factor dependencies. Our discovery of EGF dependence in some pulmonary NET PDOs has significant clinical implications. Pulmonary NETs expressing membrane EGFR might respond to the therapies targeting EGFR or EGFR-mediated downstream signaling that are currently approved for the treatment of other tumor types. There are other reports of EGFR expression in pulmonary NETs, but

these studies were unable to demonstrate a functional role for receptor expression in promoting the growth or survival of these tumors.^{73–76} Our data argue that EGFR expression is indicative of EGF-dependence. The patient population most likely to benefit from EGFR-targeted or EGFR pathway-targeted treatments could be identified through immunohistochemistry for EGFR. Not all the EGFR-expressing tumors in our study could be propagated as PDOs in EGF-containing medium, therefore research to identify additional biomarkers of EGF-dependence is needed.

The EGF-dependence of some pulmonary NET PDOs raises a broader question: are NETs generally growth-factor dependent? We hypothesize that the identification of additional NET growth-factor dependencies could enable the generation of PDOs from additional NET subtypes, such as SINETs, which we were not able to propagate long-term in this study. Consistent with this idea, a mouse xenograft study suggests that some pancreatic NETs are dependent on the growth factor, HGF.⁷⁷ Beyond model generation, the identification of growth-factor dependencies for NETs could point to new therapeutic strategies aimed at targeting growth-factor mediated pathways in specific patient populations.

Our comprehensive analysis of the genomic features of NEN PDOs highlights both the fidelity and utility of these models for research on intra-tumoral heterogeneity and tumor evolution. PDOs not only retain most of the intra-tumoral heterogeneity of their parental tumors, but they also recapitulate the evolutionary forces at work and subclonal dynamics. Our experiments spanned more than a year, and we found that the late passage G3 PDOs show changes in subclonal composition, while low-grade tumors show no such turnover (e.g., passage 2 of SINET8). The supra-carcinoid PDO showed a turnover speed similar to that of LCNEC, in line with other evidence suggesting a more aggressive disease.⁵ These data argue that PDOs can be harnessed to study subclonal tumor cell dynamics and tumor evolution. This is critical to accurately model disease treatment resistance and relapse, which is often driven by either pre-existing, low-frequency subclones or novel subclones appearing after the onset of therapy.⁷⁸

Despite our low sample size, our molecular analyses of NEN PDOs and their parental tumors shed light on NET biology. We saw that evolutionary trajectories can strongly vary across LNETs of different grades and molecular groups. Low-grade tumors such as LNET6 can initiate with a single driver alteration (e.g., a *PSIP1* structural variant³⁴) and slowly accumulate neutral (non-driver) alterations due to weak age-related endogenous mutational processes. At the other end of the spectrum, supra-carcinoids like LNET10 can evolve following catastrophic chromosomal events such as chromothripsis, involving multiple cancer genes and fueled by more diverse mutational processes spanning small variants and large structural rearrangements. This is a textbook example of punctuated evolution, where tumor evolution can be stagnant for a few years before undergoing a “leap” due to a catastrophic event.^{79,80} Interestingly, LNET10 seems to experience a subsequent selective sweep and to undergo a fast allelic turnover. A recent case study from the Dutch MEN1 Study Group supports this model of progression via punctuated evolution; a pulmonary NET showing an indolent course for six years unexpectedly progressed to aggressive disease likely driven by an activating mutation in *PIK3CA*.⁹ Further

studies will be needed to determine whether these observations can be generalized and to what degree they represent how slow growing tumors can unexpectedly become clinically aggressive.

Here, we report case studies in LCNEC and supra-carcinoid PDOs that highlight their utility in the identification of novel therapeutic strategies and biomarkers of treatment response. Consistent with studies showing that solid tumors with a neuroendocrine phenotype show increased sensitivity to an inhibitor of the NAD salvage pathway, FK866, we found that NEN PDOs are sensitive to this inhibitor.⁸¹ It is tempting to speculate that the neuroendocrine phenotype, associated with the biosynthesis of hormones and neuropeptides, creates targetable metabolic vulnerabilities.

We also identified high expression of *ASCL1* as a potential biomarker for therapeutic response to BCL2 inhibitors. Although the link between *ASCL1* expression and sensitivity to BCL2 inhibitors has been observed in SCLC, it has not previously been explored in LCNEC. We did not see the same link between *NEUROD1* expression and sensitivity to Aurora kinase inhibition as has been observed for SCLC, arguing that not all SCLC therapies and biomarkers apply to LCNEC, and underscoring the need for more preclinical *in vitro* models of LCNEC for hypothesis testing.

Limitations of the study

While *ASCL1* is associated with pulmonary NENs, its overexpression has been reported in some GEP and prostate NECs and our data show that expression of this neuroendocrine transcription factor may have clinical relevance for both pulmonary and extrapulmonary LCNECs.^{25,62,82} The questions that follow are, to what degree are LCNECs from different tissue sites similar and might LCNECs across different tissue sites share therapeutic vulnerabilities and biomarkers of response? The LCNEC PDO samples in this study are not enough to make such a broad generalization, but our data support the idea, and further research is warranted. The ability to classify LCNECs according to shared gene expression profiles, irrespective of tissue site, could aid in overcoming the fact that LCNEC, when divided according to tissue site, is very rare at each site. Another limitation of the study is that we were only able to test the response to EGFR inhibition of one relevant LNET PDO line. Studies in additional PDO lines are warranted.

In conclusion, analysis of the unique media dependencies and drug responses of PDOs in our biobank, combined with a comprehensive examination of their genomic features provide insights into the biology of NENs. We identified potentially actionable vulnerabilities for both low-grade and high-grade disease, highlighting the importance of preclinical models for the entire spectrum of NEN malignancy. Our pulmonary NET PDOs represent an important resource for the study of this disease and enable studies aimed at identifying mechanisms of disease progression and factors predictive of this progression.

STAR★METHODS

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SUPPLEMENTAL INFORMATION

Supplemental information can be found online at <https://doi.org/10.1016/j.ccell.2023.11.007>.

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AUTHOR CONTRIBUTIONS

T.L.D., N.A., L.F.-C., and H.C. designed and conceived the study. T.L.D. generated the organoids. T.L.D., L.dH., and V.G. cultured and curated organoid lines and performed related experiments. T.L.D., V.G., and A.F.M.D. performed drug sensitivity assays. V.G. and J.V. performed xenotransplantation experiments. J.B. and J.D. contributed to study design. L.Mo., L.L., W.M.H., and L.B. performed histological stains, acquired images, and performed related analyses. N.A. processed the sequencing data. T.L.D. and N.A. analyzed and interpreted the data and generated figures. J.V. and H.B. embedded organoids and cut slides for immunohistochemistry staining. S.J. generated novel reagents. L.H., L.B., and S.L. performed pathological assessments. N.A., C.V., and A.vH. curated sequencing data. L.Ma. contributed to analysis of sequencing data. L.Mo., J.D., S.L., R.S.vL., L.B., and K.S. provided samples, curated patient data, and provided pathology information. N.F.M.K., K.J.H., H.M.K., I.H.M.B.R., A.-M.D., G.V., M.R.V., W.B., J.vdB., and M.T. provided clinical feedback. J.D., M.R.V., G.D.V., J.vdB., and M.T. coordinated clinical aspects of the study. L.F.-C. and M.F. supervised N.A., L.Ma., C.V., and A.S.-O. E.-J.S. and J.D. supervised L.Mo. and L.L. H.C. directed the study.

DECLARATION OF INTERESTS

Where authors are identified as personnel of the International Agency for Research on Cancer/World Health Organization, the authors alone are responsible for the views expressed in this article and they do not necessarily represent the decisions, policy or views of the International Agency for Research on Cancer/World Health Organization.

H.C.'s full disclosure is given at <https://www.uu.nl/staff/JCClevers/>. H.C. is inventor of several patents related to organoid technology, cofounder of Xilis Inc. and currently an employee of Roche, Basel.

INCLUSION AND DIVERSITY

We support inclusive, diverse, and equitable conduct of research.

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STAR★METHODS

KEY RESOURCES TABLE

| REAGENT or RESOURCE | SOURCE | IDENTIFIER |
|--|--------------------------|-----------------------------|
| Antibodies | | |
| Mouse monoclonal anti-Chromogranin A (LK2H10) | Thermo Scientific | MA5-13096 |
| Mouse monoclonal anti-human Ki67 antigen (MIB-1) | Agilent-Dako | GA62661-2; RRID: AB_2687921 |
| Mouse monoclonal anti-human Synaptophysin | Dako | GA660 |
| Mouse monoclonal anti-human NCAM1/CD56 (clone 123C3) | Dako | IR628 |
| Rabbit monoclonal anti-EGFR (EP22) | Cell Marque | CMC41432010 |
| Chemicals, peptides, and recombinant proteins | | |
| DNase I | Sigma-Aldrich | Catalog #DN25 |
| Collagenase | Sigma | C9407 |
| red blood cell lysis buffer | Roche | 11814389001 |
| Dispase II | Thermo Fisher | Cat# 17105041 |
| RNALater Stabilization Solution | Thermo Fisher | AM7020 |
| Advanced DMEM/F12 | Thermo Fisher scientific | 12634-010 |
| DMEM + GlutaMAX | | 31966-021 |
| B-27 Supplement | | 17504044 |
| GlutaMAX | | 35050061 |
| HEPES | | 15630080 |
| Penicillin-Streptomycin | | 15140122 |
| Noggin-Fc fusion protein | ImmunoPrecise | Cat# N002 |
| R-spondin1 conditioned medium | made in house | |
| N-acetyl-L-cysteine | Sigma-Aldrich | A1965 |
| Nicotinamide | Sigma-Aldrich | N0636 |
| Human EGF | Peptotech | AF-100-15 |
| A83-01 | Tocris | 2939 |
| Prostaglandin E2 | Tocris | 2296 |
| SB 202190 (p38 inhibitor) | Sigma-Aldrich | S7076 |
| Y-27632 dihydrochloride (ROCK inhibitor) | Abmole | M1817 |
| Primocin | Invivogen | ant-pm-2 |
| Cultrex Basement Membrane Extract (BME), Growth Factor Reduced, Type 2 | R&D Systems, Bio-Techne | 3533-010-02 |
| Formaldehyde Solution 4% | Sigma-Aldrich | 1.00496 |
| TrypLE Express | Thermo Fisher Scientific | 12605010 |
| CHIR (Chir99021) | Stemgent | Cat# 04-0004-10 |
| FGF2 | Peptotech | Cat# 100-18B |
| FGF7 | Peptotech | Cat# 100-19 |
| FGF10 | Peptotech | Cat# 100-26 |
| Staurosporine | Sigma Aldrich | S4400 |
| Paclitaxel | Selleckchem | S1150 |
| Everolimus (RAD001) (1 mL 10 mM in DMSO) | Selleckchem | S1120 |
| Trametinib | MedChem Express | HY-10999 |
| Dabrafenib (1 mL 10 mM in DMSO) | Selleckchem | S2807 |
| Navitoclax (ABT-263) (1 mL 10 mM in DMSO) | Selleckchem | S1001 |

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| REAGENT or RESOURCE | SOURCE | IDENTIFIER |
|--|---|---|
| Alisertib (MLN8237) (1 mL 10 mM in DMSO) | Selleckchem | S1133 |
| FK-866/Daporinad | Selleckchem | S2799 |
| Allitinib (1 mL 10 mM in DMSO) | Selleckchem | S2185 |
| Afatinib (1 mL 10 mM in DMSO) | Selleckchem | S1011 |
| Critical commercial assays | | |
| RNeasy Mini Kit | QIAGEN | Cat# 74104 |
| All-Prep DNA/RNA Kit | QIAGEN | Cat# 80204 |
| RNase-free DNase Set | QIAGEN | Cat# 79254 |
| CellTiter-Glo 3D Cell Viability Assay | Promega | Cat# G9683 |
| MycoAlert mycoplasma detection kit | Lonza | Cat# LT07-318 |
| Qubit dsDNA HS Assay Kit | Thermo Fisher | Cat# Q32854 |
| EnVision FLEX Visualization kit | Dako | K8002 |
| Deposited data | | |
| LUAD and LUSC cohorts somatic mutations (TCGA) | GDC data portal | LUAD; LUSC |
| Next-generation sequencing data of lung NENs (RNA-seq) | Alcala et al. ⁵ | EGA: EGAS00001003699 |
| Next-generation sequencing data of small intestine NETs (RNA-seq) | Alvarez et al. ²⁸ | SRA: SRP107025 |
| Next-generation sequencing data of small intestine NETs (RNA-seq) | Hofving et al. ²⁹ | EGA: EGAS00001003358 |
| Next-generation sequencing data of SCLC (RNA-seq) | George et al. ⁸³ | EGA: EGAS00001000925 |
| Next-generation sequencing data for PDOs and their matched original tumors (WGS and RNA-seq) | this study | EGA: EGAS00001005752 |
| Experimental models: Cell lines | | |
| NEN patient-derived tumor organoids | this study | Table S1 |
| Pancreatic ductal adenocarcinoma PDOs | Driehuis et al. ⁷¹ | PDO17, PDO23, PDO19 |
| Colorectal Cancer PDOs | Roerink, Sasaki, Lee-Six et al. ⁷² | CRC T3-3/P3.T2.1, CRC T3-1/P3.T4.1 |
| Software and algorithms | | |
| Nextflow version 20.10.0.5430 | Seqera labs ⁸⁴ | https://www.nextflow.io/ |
| GATK version 4.1.7.0 | Broad institute | https://gatk.broadinstitute.org/hc/en-us |
| bwa2 version 2.0 | Vasimuddin et al. ⁸⁵ | https://github.com/bwa-mem2/bwa-mem2 |
| Trim-galore version 0.6.5 | Babraham Institute | https://www.bioinformatics.babraham.ac.uk/projects/trim_galore |
| STAR version 2.7.3a | Dobin et al. ⁸⁶ | |
| ABRA2 version 2.22 | Mose et al. ⁸⁷ | |
| StringTie version 2.1.2 | Pertea et al. ⁹⁵ | |
| Strelka2 version 2.9.10 | Kim et al. ⁸⁸ | |
| SVaba version 1.1.0 | Wala et al. ⁹⁹ | |
| Delly version 0.8.7 | Rausch et al. ¹⁰⁰ | |
| Manta version 1.6.0 | Chen et al. ¹⁰¹ | |
| SURVIVOR version 1.0.7 | Jeffares et al. ¹⁰³ | |
| PURPLE version 2.52 | Shale et al. ⁸⁹ | https://github.com/hartwigmedical/hmftools/tree/master/purple |
| SigProfilerExtractor version 1.1.3 | Islam et al. ⁹⁰ | |
| Cytoscape version 3.9.1 | Shannon et al. ⁹¹ | https://cytoscape.org/ |
| Pyclone-VI | Gillis et al. ⁹² | |

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Continued

| REAGENT or RESOURCE | SOURCE | IDENTIFIER |
|--|----------------------------|---|
| R version 4.1.2 | R CRAN | |
| R package trend version 1.1.4 | R CRAN | |
| R package ggridges version 0.5.3 | R CRAN | |
| R package umap version 0.2.8.0 | R CRAN | |
| R package mixOmics version 6.18.1 | Bioconductor ⁹³ | |
| R package ActivePathways version 1.1.0 | R CRAN ⁹⁴ | |
| R package maftools version 2.2.10 | R CRAN ¹¹⁰ | |
| R package DPclust version 2.2.8 | Github ¹¹² | https://github.com/Wedge-lab/dpclust |
| R package dpclust3p version 1.0.8 | github | https://github.com/Wedge-lab/dpclust3p |
| R package eulerr version 6.1.1 | R CRAN | https://github.com/jolars/eulerr |
| R package mobster version 1.0.0 | Github ⁴⁴ | |
| R package circlize version 0.4.13 | R CRAN ¹¹¹ | |
| R package ggpointdensity version 0.1.0 | R CRAN | |
| R package copynumber version 1.20.0 | R CRAN | |
| R package TrackSig version 0.2.0 | Github ⁴⁵ | https://github.com/morrislab/TrackSigFreq |
| R package clonevol version 0.99.11 | Github ¹¹³ | https://github.com/hdng/clonevol |
| R package fishplot version 0.5.1 | Github ¹¹⁴ | https://github.com/chrisamiller/fishplot |
| Biorender | Biorender | http://biorender.com (agreement number PO2499GT9Q) |

Other

| | | |
|-------------------------------------|---------------------|---------------------|
| Agilent2100 Bioanalyzer | Agilent | |
| Bioanalyzer2100 RNA Nano 6000 chips | Agilent | Cat# 5067-1511 |
| Multi-drop Combi Reagent Dispenser | Thermo Fisher | |
| D300e Digital Dispenser | Tecan | |
| Spark multimode microplate reader | Tecan | |
| Link 48 Autostainer Platform | Dako | |
| SpinVessel 50 mL conical tubes | V&P Scientific, Inc | VP 830SV-50CB |
| SpinVessel | V&P Scientific, Inc | VP 418SV2-2-50CB-CC |

RESOURCE AVAILABILITY

Lead contact

Further information and requests for resources and reagents should be directed to and will be fulfilled by the Lead Contact, Hans Clevers (h.clevers@hubrecht.eu).

Materials availability

Organoid lines reported in this manuscript can be requested from the lead author, h.clevers@hubrecht.eu and/or from talya.dayton@embl.es. Distribution of organoids to third parties will have to be authorized by the relevant ethical committee and a complete MTA will be required to ensure compliance with the Dutch ‘medical research involving human subjects’ act. Use of organoids is subjected to patient consent; upon consent withdrawal, distributed organoid lines and any derived material will have to be promptly disposed of.

Data and code availability

The raw and processed next-generation sequencing data generated for this study were deposited on the European Genome-phenome Archive (EGA) (accession code EGA: EGAS00001005752). We also used public RNA-seq datasets available on EGA, for lung NENs (accession code EGA: EGAS00001003699), small intestine NETs (accession code EGA: EGAS00001003358), small cell lung cancer (accession code EGA: EGAS00001000925), and a dataset of small intestine NETs available from the short reads archive (SRA, accession code SRA: SRP107025). We retrieved a public list of somatic mutations in lung adenocarcinoma (LUAD) and squamous cell carcinoma (LUSC) from the TCGA project using the GDC data portal. All bioinformatic processing pipelines are open-source and freely accessible via Github at <https://github.com/IARCBioinfo/>. Analysis scripts used to analyze the sequencing data and produce the related figures are available via Github at https://github.com/IARCBioinfo/MS_panNEN_organoids.

EXPERIMENTAL MODELS AND STUDY PARTICIPANT DETAILS

Approval of studies involving human and patient-informed consent

The collection of patient data and tissue for the generation and distribution of normal and NEN organoids was performed according to the guidelines of the European Network of Research Ethics Committees (EUREC) following European, national and local law. The protocols were approved by the medical ethical committee (METC) corresponding to the respective hospitals where patients were treated: Verenigde Commissies Mensgebonden Onderzoek of the St. Antonius Hospital Nieuwegein, Z-12.55; UMC Utrecht, METC 12-093 HUB-Cancer; NKI Institutional Review Board (IRB), M18ORG/CFMPB582; Maastricht University Medical Center, METC 2019-1061, and 2019-1039. All patients participating in this study signed informed consent forms and could withdraw their consent at any time.

NEN tissue processing

On arrival, NEN tissues were cut into 3–5 mm³ pieces. Two or three random pieces were placed in RNAlater solution and stored at –80°C for DNA and RNA isolation, one random piece was fixed in formalin for histopathological analysis and immunohistochemistry, and the remainder were processed for organoid derivation. For organoid derivation: tissue was minced, collected with 10 mL DMEM containing antibiotics, and transferred to a 15 mL conical tube. To dissociate the minced tissue further, 200 µL of collagenase solution (20 mg mL⁻¹) was added to the tissue/DMEM solution and the tube was placed on an orbital shaker at 37°C for 25 min. After digestion, 50 µL of DNase I solution (10 mg/mL) was added. The digested tissue suspension was sheared using 5 mL plastic pipettes, strained over a 100 µm filter. Large tissue pieces that remained after digestion were presumed to be necrotic or fibrotic and discarded. The filtered tissue suspension was centrifuged at 1,000 r.p.m. and the supernatant was removed. In case of a visible red pellet, erythrocytes were lysed in 50–300 µL of red blood cell lysis buffer (depending on pellet size) for 5 min at room temperature and then washed twice with 13 mL DMEM containing antibiotics. Finally, the pellet was resuspended in appropriate volume of BME for plating in 30 µL droplets on preheated suspension plates (Greiner).

Tumor organoid culture

NEN patient-derived tumor organoids were grown in 30 µL drops of BME in suspension culture plates, overlaid with growth medium. The growth medium consisted of Advanced DMEM/F12 supplemented with 1x GlutaMAX, 10 mM HEPES, penicillin-streptomycin, Primocin (InvivoGen, Cat# N001), 1% Noggin conditioned medium (U-Protein Express, Cat# N002), 20% of RSPO3 conditioned medium (made in-house), 1x B27 supplement (GIBCO, Cat# 175044), 1.25 mM n-Acetylcysteine (Sigma, Cat# A9165), 3 µM CHIR (Stemgent, Cat# 04-0004-10), 1 µM Prostaglandin E2 (Tocris, Cat# 2296), 0.005 µg/mL FGF2 (Peprotech), 10 µM ROCK inhibitor (Abmole, Cat# Y27632), 500 nM A83-01 (Tocris, Cat# 2939), 3 µM p38 inhibitor SB202190 (Sigma, Cat# 7067). Note that the primary difference of this medium compared to published media is the addition of CHIR and FGF2, with CHIR making a clear difference in supporting organoid growth while FGF2 impact was not entirely clear. All lung NET organoids and some LCNEC organoids were grown in media additionally supplemented with 0.05 µg/mL EGF (Peprotech, Cat# AF-100-15). Media was changed once a week.

For splitting, a 2 min incubation in TrypLE at 37°C was followed by mechanical shearing through a p10 tip attached a fire-polished plugged glass pipettes (Fisher Scientific, Cat# 11506973) was used to break organoids up into small clusters of cells. Following isolation, LCNEC lines were consistently passaged at an approximate splitting ratio of 1:12 every 14 days. Pulmonary NET lines show a high degree of variability in their growth rates and required passaging at a split ratio of 1:2 or 1:3 every 2 months for lines derived from grade 2 tumors and once every 3 months of lines derived from grade 1 tumors. SI NET PDTOs showed a similar growth rate as pulmonary NET PDTOs but could not be passaged more than 4 times. All organoid lines tested negative in the MycoAlert mycoplasma detection kit (Lonza, LT07-318).

PDTO models

All NEN PDTO models were generated as described for this study. Pancreatic Adenocarcinoma PDTO lines, PDO17, PDO19, and PDO23 were generated and reported in a previous study.⁷¹ Colorectal Cancer PDTO lines, CRC T3-3/P3.T2.1 and CRC T3-1/P3.T4.1, were generated and reported in a previous study.⁷²

Mice

For PDTO xeno-transplantations, NOD.Cg-Prkdcscid Il2rgtm1Wjl/SzJ (NSG) mice were used. Transplantation experiments were performed after institutional review by the Animal Ethics Committee of the Royal Netherlands Academy of Arts and Sciences (KNAW) with project license of AVD8010020209924 and research protocol HICLe9924.22.02.

METHOD DETAILS

Xenotransplantation of tumor organoids

NEN PDTOs were collected for transplantation 7 to 10 days after splitting. On the day of transplantation, organoids were released from the basement membrane extract (BME) and a small portion of the total sample was dissociated into single cells to estimate the cellular density of each sample. Approximately 100 000 cells were suspended in 100 µL of medium mixed with BME at a 1:1 ratio. Subcutaneous injections were performed into opposite flanks of all 3–4 NSG mice per line (2 flanks per mouse, 100 000 cells per location). The mice were sacrificed 73–108 days after injections. Tumor measurements were taken by digital calipers (RS PRO,

Cat# 841–2518) and volumes estimated by formula: tumor volume = (length x width²)/2, where length represents the largest tumor diameter and width the perpendicular tumor diameter. All tumors were subjected to immunohistochemical analysis.

Histological analyses

Tissue and organoids were fixed overnight in 4% paraformaldehyde and subsequently dehydrated, paraffin embedded, and sectioned. Standard H&E staining was performed and stained sections were blindly analyzed by a pathologist specialized in NENs. WHO 2021 criteria for NENs were applied. Immunohistochemistry was performed using antibodies against Chromogranin A (Thermo Scientific, clone: LK2H10) dilution 1:1000, Ki67 clone MIB-1 (DAKO, 'ready to use'), Synaptophysin (DAKO, 'ready to use'), CD56/NCAM1 (DAKO, 'ready to use'), and EGFR (Cell Marque, EP22, 1:200). All stainings were performed using the DAKO Link 48 Autostainer Platform and the EnVision FLEX Visualization kit (DAKO, cat# K8002) according to standard diagnostic routine protocols and manufacturer instructions. Immunohistochemical stainings were evaluated by pathologists (L. Brosens, or L.M. Hillen and S. Lantuejoul), who were blinded for all clinical, histopathological, and sequencing data. Slides were scanned using a Panoramic 1000 slide scanner (3DHISTECH Ltd) and images were acquired using the CaseViewer software (3DHISTECH Ltd).

Tissue microarray analysis

EGFR expression in human pulmonary neuroendocrine tumors was analyzed in two tissue microarrays (TMA) from the Maastricht University Medical Center (MUMC+), jointly containing cores derived from 70 tumors. Each tumor on the TMAs was represented by 3 cores derived from both central and peripheral tumor regions. Each TMA core was independently scored for EGFR IHC intensity and membrane localization and given a score of either high, medium, low, or absent EGFR membrane expression, where at least 20% of tumor cells were positive. In the majority of positive cases 70 to 100% of tumor cells were positive. Subsequently, tumors were assigned an overall score. In cases where cores from the same tumor were given a different EGFR IHC score, the tumor was assigned the score consistent between at least 2 out of the 3 cores (see [Table S5](#)).

RNA and DNA isolation

RNA was isolated from NEN organoids using the RNeasy Mini Kit (QIAGEN, Cat# 74104) following the manufacturer's instructions including DNaseI treatment (QIAGEN, Cat# 79254). RNA and DNA were isolated from the same sample of NEN organoids and/or tissue using the All Prep DNA/RNA Mini Kit (QIAGEN, Cat # 80204) following the manufacturer's instructions.

Classification of NEN PDOs as “high-purity” or “mixed”

Established NEN PDO lines were classified as either “high-purity” or “mixed” according to available data derived from: morphological/histological analyses and molecular analyses. The term “high-purity” was applied to PDO lines for which there was no discernible contamination in the organoids from non-tumor cells as identified by either histology or molecular analyses. The term “mixed” was applied to PDOs for which histology and/or molecular analyses provided evidence for the presence of both tumor cells and non-tumor cells. The following criteria were defined as evidence of tumor cells in the culture: 1) presence of neuroendocrine marker-expressing cells identified by immunohistochemical staining (CHGA, SYP, or CD56/NCAM); 2) levels of neuroendocrine marker expression within the range observed for corresponding subtype in reference dataset ([Figures 3 and S3; Table S2](#)); 3) UMAP clustering of organoid sample together with corresponding parental tumor tissue ([Figures 3 and S3](#)); 4) identification of shared genetic driver or NEN-associated alterations in PDO and parental tumors by WGS (when available); 5) identification of genetic driver or NEN-associated alterations in RNAseq reads (applied when WGS data were not available) ([Figures 4 and S4; Table S4](#)).

In all cases, a sample was defined as “pure” by criteria 1 when 60% or more of cells were NE-marker positive, and “mixed” when less than 60% of cells were NE-marker positive. For lines that were defined as “mixed” by criteria 1, evidence of tumor cell content by criterias 2–5 were used to determine whether the NE-marker+ cells were likely to be tumor cells (i.e., criteria 2–5 were used to classify lines for which criteria 1 showed less than 60% of cells were NE-marker+). When WGS data were available, tumor purity was estimated jointly with the copy number alterations using software PURPLE (see “[copy number variant calling](#)” paragraph below). One sample, LNET2Np7, derived from tumor adjacent normal tissue of LNET2 patient was assessed using this criteria. However, WGS analyses were inconclusive with regards to tumor cell content. Given the concurrent diagnosis of diffuse idiopathic pulmonary neuroendocrine cell hyperplasia (DIPNECH) in this patient and the high likelihood of DIPNECH cells in the “normal adjacent tissue,” this sample was removed from downstream analyses.

Nicotinamide assays

Single cells (4,000) were plated in 5 μ L of BME in the wells of a 96 well plate and overlaid with media containing different concentrations of nicotinamide. Following expansion and organoid formation (one to four weeks depending on the line), ATP levels were measured using the CellTiter-Glo 3D Reagent (Promega, catalog no. G9681) according to the manufacturer's instructions, and luminescence was measured using a Spark multimode microplate reader (Tecan). Results for each line were normalized to the value for that line in 10 mM nicotinamide, the standard concentration used in organoid culture (100%).

Quantitation of EGF dependency in lung NET organoids

Single cells (4,000) were plated in 5 μ L of BME in the wells of a 96 well plate and overlaid with media containing different concentrations of EGF. Following expansion and organoid formation (one to ten weeks depending on the line), ATP levels were measured using

the CellTiter-Glo 3D Reagent (Promega, catalog no. G9681) according to the manufacturer's instructions, and luminescence was measured using a Spark multimode microplate reader (Tecan). Results for each line were normalized to the value for that line in media lacking EGF (100%). Values shown in the graph were then normalized across rows by dividing by the highest viability value.

Drug sensitivity tests

Prior to the start of the drug screen, TrypLE was used to disrupt organoids into single cells and small clusters of cells that were then plated in 30 μ L drops BME in the wells of a 6 well plate. Organoids were then grown in the appropriate media as for regular expansion. Seven to ten days later, organoids were collected from the BME by the addition of 1 mg/mL dispase II (Sigma-Aldrich, catalog no. D4693) to the medium of the organoids. Organoids were incubated for 90 min at 37°C to digest the BME. Following collection of organoids and washing with DMEM to remove dispase, organoids were filtered using a 70-mm nylon cell strainer (BD Falcon), counted, and resuspended in 5% BME/growth medium (12,500 organoids/mL) and transferred to SpinVessel 50 mL conical bottom tubes. The SpinVessel tubes containing the organoid solution were placed on a SpinVessel machine and rotated at speed setting 25 so as to keep organoids in a homogeneous solution. Finally, 40 μ L volume of organoid solution was dispensed (Multidrop Combi Reagent Dispenser, Thermo Scientific, catalog no. 5840300) in 384-well plates (Corning, catalog no. 4588).

Drugs were added 3 days after plating using the Tecan D300e Digital Dispenser (Tecan). The time in between plating and addition of drugs was maintained to allow organoids to recover after plating. All drugs in the assays were dissolved in DMSO and all wells were normalized for DMSO percentage, which never exceeded 1%. Drug exposure was performed in triplicate for each concentration shown and drug assays were repeated at least once for all drugs. When available drugs were purchased as 1 mL of a 10 mM solution in DMSO (See reagents table). For FK866 5 mM solution was made in DMSO and further diluted to reach the assay concentrations. 10 mM solutions in DMSO were prepared of staurosporin, trametinib, and paclitaxel.

Seven days after adding the drugs, ATP levels were measured using the CellTiter-Glo 3-D Reagent (Promega, catalog no. G9681) according to the manufacturer's instructions, and luminescence was measured using a Spark multimode microplate reader (Tecan). Results were normalized to vehicle (100%) and baseline control (Staurosporin 1 μ mol/L; 0%). For each line, when viability did not go above 70% or below 30%, an additional screen was performed for that particular drug with an adjusted dose of this drug for this organoid line. Screen quality was determined by checking Z factor scores for each plate following this formula:

$$Z = \frac{(3 \times SD(DMSO\ control)) + (3 \times SD(staurosporin\ control))}{(Average(DMSO\ control)) - (Average(staurosporin\ control))}$$

The average Z factor score for all assays included in the manuscript was 0.7 (ranging from 0.40 to 0.81), which is consistent with an experimentally robust assay.

Whole-genome sequencing

Lab work

DNA was isolated from tumor tissue and organoid samples using the All Prep DNA/RNA Mini Kit (QIAGEN, Cat # 80204) following the manufacturer's instructions. For a blood germline reference, isolation of DNA from blood samples donated by corresponding patients was performed by USEQ (Utrecht Sequencing Facility) using the QIAGEN QIASymphony SP. Quality and quantification of DNA samples were checked with Qubit (DNA BR). DNA integrity and RNA contamination was assessed by using TapeStation DNA screens (Genomic screen) and Nanodrop (260/280 ratio). Per sample, 500–1,000 ng of DNA was used for DNA library preparation by USEQ using the TruSeq DNA Nano kit. Whole-genome sequencing was performed on NovaSeq 6000 to an average coverage of 30x for germline reference samples, and 60x to 90x for tumor tissue and organoid samples (see Table S4).

Early passage was defined as passages 1 to 3, intermediate passage as 4 to 6, and late passage as passages 7 and beyond.

Processing

Raw reads were processed using our in-house whole-genome sequencing processing workflow <https://github.com/IARCBioinfo/alignment-nf> v 1.2, which uses software bwa to align reads to reference genome GRCh38 with decoy genome and alt contigs, and GATK to perform base quality score recalibration. We performed quality controls using fastQC for raw reads and qualimap for aligned reads (using workflow <https://github.com/IARCBioinfo/qualimap-nf> v. 1.1), and confirmed that files of a same experiment came from the same individual using NGSCheckMate (using workflow <https://github.com/IARCBioinfo/NGSCheckMate-nf> v. 1.1a).

RNA sequencing

Lab work

We performed paired-end bulk RNA sequencing (RNA-seq) across 20 patients, including 1 patient with both primary tumor and metastasis, for a total of 18 parental tumor samples and 21 NEN PDTO lines that had been in culture for 6 to 67 weeks (Table S2). For 5 PDTO lines we captured expression patterns from 2 separate time points in culture. RNA was isolated as described above. RNA integrity was measured using the Agilent RNA 6000 Nano kit with the Agilent 2100 Bioanalyzer and RNA concentrations were determined using the Qubit RNA HS Assay Kit. RIN values of organoid RNA samples were typically 9–10 and only samples with RIN >8 were used for library preparation. RIN values of tissue RNA samples were typically 8–10, with 5 samples showing an RIN between 6.3 and 7.4, and only samples with RIN >6 were used for library preparation. RNA libraries were prepared using TruSeq Stranded mRNA polyA kit (Illumina) and sequenced on either an Illumina Nextseq 2000 (paired-end, 2 x 150 bp) or an Illumina NovaSeq 6000 (paired-end, 2 x 150 bp). Library preparation and sequencing was performed by USEQ (Utrecht Sequencing Facility).

Processing

Processing of 47 RNA-seq from the experiments and public data for 210 RNA-seq from LLEN,⁵ 30 LNETs,⁶ and 88 RNA-seq from SINET^{28,29} were all done using our RNA-seq pre-processing workflow (<https://github.com/IARCbioinfo/RNAseq-nf> v. 2.4) to ensure mitigation of potential batch effects between cohorts due to differences in processing (software, version, or operating system); as described in Gabriel et al.,³⁰ this workflow uses trimalore to trim reads for adapter sequences and STAR to map reads to reference genome GRCh38. Base quality scores were then recalibrated to improve subsequent variant calling using GATK (<https://github.com/IARCbioinfo/BQSR-nf> v. 1.1), and alignments were realigned locally using ABRA2 to improve their quality, in particular at splicing junctions (<https://github.com/IARCbioinfo/abra-nf> v. 3.0).

Expression Quantification

Gene expression quantification was performed with Stringtie,⁹⁵ in one-pass mode, using our workflow <https://github.com/IARCbioinfo/RNAseq-transcript-nf> v 2.2 with the gencode v33 comprehensive gene annotation as reference, providing expression in raw read count and TPM formats. We also processed the SINET RNA-seq datasets EGA: EGAS00001003358 and SRA: SRP107025^{28,29} with the same workflows, which is also the version that was used to process the LLEN data by Gabriel and colleagues,³⁰ allowing integration of the different datasets with minimal batch effects.

Unsupervised analyses

Analyses were performed separately on (i) lung and pancreatic NENs, and (ii) on small intestine NETs. Raw counts from all samples were normalized using the variance stabilization transform (R package DESeq2) to provide approximately normally distributed values, separately for (i) and (ii) and using the “blind” mode so each tumor type is processed in an independent and completely unsupervised manner (samples can have their own variance/mean relationship) but biologically meaningful differences between SINETS and other NENs are not removed. UMAP was then performed separately on (i) and (ii), using features known to be informative about molecular groups, and setting the number of neighbors to the maximal value (number of samples) so that both short- and long-distance relationships between samples are preserved, as in our recent integrative study.³⁰ The subset of genes for the lung and pancreatic NENs (i) were extracted from a published list of “core” genes that are differentially expressed between all pairs of lung NEN molecular groups,⁵ excluding genes that were discarded between gencode v19 and v33 or that changed ENSEMBL ID between the releases (54/1459 genes). Cluster annotations were extracted from Gabriel et al.³⁰ (<https://github.com/IARCbioinfo/DRMetrics/data/Attributes.txt.zip>), assuming as shown in the article that clusters A1, A2, and B from Alcala et al.⁵ respectively correspond to clusters LC1, LC3, and LC2 from Simbolo et al.,⁸ and grouping together under the term LCNEC (resp. SCLC) LCNEC and LCNEC-like SCLC (resp. SCLC and SCLC-like LCNEC). The subset of genes for the SINET samples (ii) included all 520 genes from Alvarez et al.²⁸ except *NME1-NME2*, which is a readthrough transcription between neighboring genes *NME1* and *NME2* that was not quantified by StringTie.

Supervised analyses

A Partial Least Squares (PLS) analysis was performed on matched parental tumors (“parent” group) and PDTOs (“organoid” group) in order to find genes whose expressions are altered by the PDTO formation process, using the pls function from R package mixOmics in “regression” mode and selecting the first 10 components of the expression matrix (named X in the PLS framework, while the group matrix is Y), after running the variance stabilization transform on the entire dataset simultaneously using a design comparing the “parent” and “PDTO” groups, so differences between the groups is not removed during the transformation. PLS components separating parents and PDTOs were identified using ANOVA *F*-tests with each of the ten components as a function of the groups. We found only two components associated with the groups (*F*-tests, component 1, $p < 2.2 \times 10^{-16}$, component 2, $p = 0.01293$, other components $p > 0.35$).

To understand which genes were responsible for the separation between parents and PDTOs, we computed the Pearson correlation between the expression of each gene and each of the two PLS components associated with the groups and performed integrated gene set analysis on the correlation *p* values using the ActivePathways R package with GO terms as gene sets. ActivePathways allows combining *p* values from multiple sources (here components 1 and 2) to find which pathways are associated with each source separately and in combination. We found 108 significantly enriched pathways (see results in [Figure S3G](#); [Table S2](#)). Pathways were then aggregated into super-pathways using the EnrichmentMap module of cytoscape, which forms a network of pathways based on their similarity in terms of shared genes, using the default cutoff of 0.375 similarity to connect two pathways. Results are presented [Figure S3H](#), and show a vast majority (89/108) of pathways belonging to immune-related pathways and pathways sharing genes with these immune-related pathways. We also found two additional super pathways—one comprising four blood-vessel-related pathways and one comprising five synaptic-related pathways—a small group of 3 pathways and 6 additional isolated pathways.

Somatic alteration calling

Small variants calling

Single nucleotide variants were called from WGS data using software Mutect2 from GATK4 (using our workflow <https://github.com/IARCbioinfo/mutect-nf> v. 2.2b), and indels and multinucleotide variants were called using the intersection of Mutect2 and strelka2 calls (using our workflow <https://github.com/IARCbioinfo/strelka2-nf> v. 1.2a) in order to filter out false positive calls, more numerous in indels than in SNVs. Annotations were performed with ANNOVAR (using our workflow https://github.com/IARCbioinfo/table_annovar-nf v. 1.1.1). To ensure comparisons with previous studies on NETs^{5,34} and common cancers,⁹⁶ that mostly relied on whole-exome sequencing, tumor mutational burdens were computed using the exonic ranges from the SureSelect Human All

Exon v7 panel from Agilent (bed file downloaded from the manufacturer's website, approximately covering 36Mb), and focusing on non silent mutations (nonsynonymous SNVs, nonsense mutations, nonstop mutations, and indels).

Small variants were called from RNA-seq data in the samples without WGS data using software Mutect2 from GATK4 as for WGS, but in tumor-only mode (also using our workflow <https://github.com/IARCbioinfo/mutect-nf> RNAseq branch) and annotated using ANNOVAR as described above. In addition, calls were further filtered using a random forest algorithm. See Alcalá et al. (submitted) for a complete benchmarking of the algorithm using samples for which both RNA-seq and WGS was performed.⁹⁷ In summary, in the benchmarking, we show that around 40% of the driver mutations presented in Figures 4B and S4B were also present in the RNAseq (26/68), including at least one driver detected for all patients with at least one driver mutation detected from WGS. We used a machine learning approach to classify these 40% of variants detected in RNA-seq data as somatic or non-somatic (germline or sequencing artifact). We show that RNA-seq is sufficient to call somatic alterations with very good precision (up to 100%, see Figure 6 from Alcalá et al. (submitted)).⁹⁷ Because of the trade-off between sensitivity and specificity, we report variants with three levels of confidence. The high-sensitivity (73%) set, denoted by “***” in Figures 4C and S4C, has the interesting property of being likely to contain most somatic variants, but at the expense of being less specific (98%). The medium-sensitivity (62%) set, denoted by “**”, is a compromise between sensitivity and specificity. Finally, the low-sensitivity (38%) set, denoted by “*”, has the interesting property of likely only containing true somatic variants, but at the expense of missing a majority of actual somatic variants. Whenever a variant was found in either parental tumor or a PDTO, the corresponding position in the matched PDTO or parental tumor was classified as “no_coverage” whenever the read depth was 9 or less, below recommended depth for variant detection.⁹⁸

Structural Variant Calling

Structural variants (SVs) were called from WGS data using a two-step ensemble method combining results from 3 software: SVaba,⁹⁹ Delly,¹⁰⁰ and Manta.¹⁰¹ In the discovery step, following Mangiante et al.,¹⁰² we independently called SVs in each of the 23 tumor samples with WGS data using the SURVIVOR consensus calling,¹⁰³ merging SVs within a distance of 1 kb and requiring either agreement between 2 SV callers or a strong support by a single caller (at least 15 reads), as implemented in our workflow (https://github.com/IARCbioinfo/sv_somatic_cns, v. 1.0). This step led to a list of high-quality SVs. In the subsequent recovery step, for each experiment and each SV that was not detected in all samples from this experiment, we checked whether one of the SV callers found reads supporting this SV with breakpoints within 1 kb of those detected (SVs marked as “recovered” in Table S4), in unfiltered calls from SVaba and Manta, and initial calls from DELLY (no unfiltered calls are reported by the software). SVs were annotated based on their type (inversion, translocation, duplication, deletion), the position of their breakpoints (intergenic, within exons or introns) and their strands as described in Mangiante et al. (2021), using the gencode v33 annotation.

Copy Number Variant calling

Copy number variants (CNVs) were called from WGS data using software PURPLE using our custom workflow <https://github.com/IARCbioinfo/purple-nf> (branch dev_multi-sample). This workflow relies on the recommended PURPLE workflow using AMBER for B-allele frequency (BAF) estimation and COBALT for read depth ratio (RDR) estimation (<https://github.com/hartwigmedical/hmftools/tree/master/purple>), but relying on multi-sample segmentation of using the multipcf function from R package copynumber¹⁰⁴ instead of the simple pcf function used in the recommended workflow; this allows to infer more consistent breakpoints across samples from the same experiment. In addition, we used the option to include the list of SNVs called by Mutect2 (see above) to improve the CNV estimation by using the variant allelic fractions.

Analyses

We identified as damaging mutations the nonsynonymous mutations predicted as damaging by REVEL (score greater than or equal to 0.5) which combines multiple other damage predictions to maximize the evidence of pathogenicity,¹⁰⁵ along with stop gains, stop losses, indels, and splicing mutations. We retrieved driver gene lists from a literature search of lung and SI neuroendocrine neoplasms^{7,34,36,38–41,106–109} (see Table S4 for the complete list). The waterfall plots (Figures 4B and 4C) were produced using R package maftools.¹¹⁰ Circos plots were produced using R package circlize.¹¹¹

Mutational signatures

Small variants

Signatures were extracted from the VCFs using SigProfilerExtractor, comparing decompositions with 2–10 *de novo* signatures and using the number of signatures maximizing stability while minimizing cosine differences in signature reconstruction. Temporal signature activities were reconstructed using R package TrackSig separately on public (present in both parent and PDTO) and private alterations (present only in one sample). All signatures are reported in Figure S5 and Table S4, and signatures known to be due to sequencing artifacts were removed and signature contributions normalized to sum to 100% for Figure 5.

Evolutionary analyses

Mutation clustering and clonality

Somatic alterations were clustered and classified as clonal or subclonal using deconvolution of VAF distributions with R package DPclust.¹¹² Input files were prepared using R package dpclust3p, focusing on alterations with good coverage (above the target depth, 30X or 60X depending on the samples; see Table S4) and in clonal CNVs regions with consistent CN estimates in at least 2 samples from the same line for more accurate reconstructions. We used 5000 iterations after a burn-in phase of 1000 iterations. DPclust computed cancer cell fractions (CCFs) based on VAF and CN states and provided a likelihood that each alteration belongs to each cluster. In order to obtain high-confidence clonal reconstruction, we assigned alterations to a given cluster only if their

likelihood to belong to this cluster was greater than or equal to 95%; other alterations were classified as “Uncertain” clustering. Clusters with less than 2.5% of assigned alterations were excluded. Clusters with an estimated location above a CCF of 0.95 in all samples were considered clonal. We summed up the likelihoods of belonging to each subclonal cluster, and considered alterations with a likelihood sum greater than or equal to 95% as subclonal. Venn-euler diagrams of shared clonal and subclonal alterations in Figure 5A were computed using R package *eulerr*.

Clonality of driver small variant alterations not included in the DPclust model fit was subsequently assessed by finding the closest cluster in terms of CCF considering only alterations with the same CN as the focal driver variant. Clonality of CNVs was assessed using PURPLE estimated allelic fractions, with CNVs with both minor and major allele copy number estimates close to an integer value (with a threshold of 0.2) considered clonal, and the rest as subclonal. Clonality of structural variants was assessed by averaging the variant allelic fraction reported by each of the three callers and comparing with the expected clonal allelic fraction given the tumor purity. Clonality of the chromothripsis event in LNET10 was assessed using the clonality of the involved CNV segments (in particular in chr1 and chr9) and the allelic fractions of structural variants estimated from the proportion of supporting reads in the structural variants clustered in the involved regions (chr1, chr4, chr9, and chr16).

Phylogenies and fishplots

We used *clonevol*¹¹³ to reconstruct tumor phylogenies between clusters. In order to account for the uncertainty in estimating the centroid of mutation clusters from CCF distributions, for each cluster we randomly sampled centroid positions from normal distributions centered on the estimated value and with a standard deviation equal to the observed standard deviation of CCF values for this cluster. We then ran *clonevol* independently on each randomly sampled centroid, and selected 20 resulting possible phylogenies; we selected the replicate with the CCF centroids closest to the point estimate for visualization. We plotted the results using R package *fishplot*.¹¹⁴ Because no clonal cluster and alterations were identified for LNET2, we used a polyclonal model; for all other samples, a clonal cluster was found and we used a monoclonal model. Note that alterations absent from a sample but that cluster with alterations at a non-zero frequency in this sample are thus inferred as part of a subclone detected in the focal sample; such mutations usually have a lower coverage in the focal sample, explaining the detection failure. In particular, although absent from sample LCNEC4 organoids, the *APC* and *PTPRZ1* mutations reported in Figure 4B were detected at a very low allelic fraction (6 and 7%, respectively) and were assigned to cluster 2 from Figure S5A, which is at low but non-zero frequency in the PDOs (Figure 5B), and indeed coverage at their positions in the PDOs were lower than in the original tumor (59 and 24 vs. 89 for *APC*, and 96 and 24 vs. 109 for *PTPRZ1*), making failure of detecting them if present in this cluster likely. Similarly, the *ERCC6L* mutation in LNET2 and the *SMARCA4*, *ATR*, and *NTRK3* mutations were all assigned to low frequencies clones even though undetected in the corresponding sample.

Diversity summary statistics

Levels of intra-tumor genetic diversity were computed using the effective number of alleles Δ ,¹¹⁵ a measure widely used in ecology and conservation genetics to monitor the level of genetic diversity in species of conservation interest.¹¹⁶ In the case of biallelic markers such as somatic small variants, Δ is a genetic diversity metric which ranges from 1 (no diversity) to 2 (maximal diversity) and captures how many alleles are effectively segregating in the population at a given polymorphic site; for example, given a polymorphic site with two alleles, A at a high frequency 0.999 and B at a low frequency 0.001, although two alleles are present, because allele B is only present in a fraction of individuals, the *effective* number of alleles is $1.002 \approx 1$. In order to obtain a quantity analogous to the tumor mutational burden, we rather focus on $\Delta-1$, the effective number of *alternative* alleles (i.e., not taking into account the reference allele), and compute its sum across all polymorphic sites:

$$\Delta_T = \sum_i (\Delta_i - 1),$$

where $\Delta_i = 1/(CCF_i^2 + (1-CCF_i)^2)$ and CCF_i is the cancer cell fraction of the alternative allele at site i . We name this metric “effective number of alterations”, and further divide it by the size of the genomic ranges (in Mb) from which the alternative alleles were called. The resulting quantity ranges from 0, when there are no subclonal alterations or when all subclonal alterations have infinitesimal values, to the subclonal TMB when all clonal alterations are present in exactly half of the tumor cells ($CCF = 0.5$, the situation maximizing diversity). All diversity statistics were computed using Nei and Chesser’s estimators.¹¹⁷

Mode of evolution

Neutral evolution was detected from the distribution of subclonal alterations using R package MOBSTER.⁴⁴ MOBSTER uses a mixture model to identify a “neutral tail” in the distribution of CCF indicating the presence of a neutrally evolving subclone. For each sample, we filtered out alterations with a CCF below 5% and independently fitted models with and without neutral tails and with up to 4 additional subclones, and chose the best model using the reduced reduced Integrated Classification Likelihood (relCL) statistic.

QUANTIFICATION AND STATISTICAL ANALYSES

Temporal trends in passage times were tested using Mann-Kendall trend tests as implemented in the R package *trend*, for each sample individually. Resulting p values were adjusted for multiple testing using the Benjamini-Hochberg procedure.¹¹⁸