




















6 Molecular Characterization and Clinical Outcomes of Pancreatic Neuroendocrine Neoplasms Harboring PAK4-NAMPT Alterations

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ABSTRACT

PURPOSE The mammalian target of rapamycin (mTOR) inhibitor everolimus is US Food and Drug Administration–approved for advanced pancreatic neuroendocrine neoplasms (pNENs), yet resistance is common, necessitating the identification of resistance mechanisms for effective treatment strategies. Previous studies suggest that targeting the aberrant expression of mTOR regulators p21-activated kinase 4 (PAK4) and nicotinamide phosphoribosyl transferase (NAMPT) sensitizes pNENs to everolimus. In this study, we queried a large real-world data set of pNENs, characterizing the molecular and immune landscapes, as well as the clinical outcomes associated with aberrant PAK4 and NAMPT expression.

METHODS Two-hundred and ninety-four pNEN cases were analyzed using next-generation sequencing and whole-exome/whole-transcriptome sequencing. We stratified patients into clusters on the basis of median cutoff.

RESULTS High expression of genes activated in response to mTOR activation was found in NAMPT-high and PAK4-high groups. Enrichment of PI3K/AKT/mTOR and glycolysis pathways was observed in these tumors. Higher mutation rates in multiple endocrine neoplasia type 1, alpha thalassemia/mental retardation syndrome X-linked, TSC2, SETD2, and CCNE1 were observed in high NAMPT and PAK4 clusters. Immune analysis revealed enrichment in inflammatory response pathways, IL2/STAT5 signaling, and immune checkpoint genes. Increased neutrophils, natural killer cells, and macrophages were found in PAK4-high/NAMPT-high tumors. Analysis of real-world patient data revealed that high PAK4 ($P = .0428$) or NAMPT ($P = .0002$) expression individually correlated with lower overall survival in all neuroendocrine neoplasms (NEN) cohorts, while the combined high expression of both was associated with the worst outcomes ($P = .0002$). Similar trends were observed in pancreatic NEN cohorts.

CONCLUSION Our study demonstrates that PAK4-high/NAMPT-high pNENs are associated with distinct molecular and immune profiles. Further investigation is warranted to determine if dual PAK4 and NAMPT blockade enhances the efficacy of immunotherapeutics.

ACCOMPANYING CONTENT

 Appendix

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INTRODUCTION

According to the American Cancer Society's estimate, over 4,300 individuals will be diagnosed with pancreatic neuroendocrine neoplasms (pNENs) in 2023 (SEER Statistics).¹ The survival for pNENs is relatively long, which makes the prevalence of this disease high at any given time. Patients with well and moderately differentiated pNENs can remain

asymptomatic for many years and present only at an advanced stage. The management of pNENs remains clinically challenging due in part to the heterogeneity of the disease.² Over the past decades, improvements in the identification of actionable molecular targets or systemic treatments for pNENs have been modest at best. Therefore, pNENs remain a significant unmet clinical problem in urgent need of newer therapeutics.

CONTEXT

Key Objective

We aimed to characterize the molecular and immune landscapes of pancreatic neuroendocrine neoplasms (pNENs) with aberrant p21-activated kinase 4 (PAK4) and nicotinamide phosphoribosyl transferase (NAMPT) expression and delineate their impact on clinical outcomes.

Knowledge Generated

We identified three distinct clusters on the basis of PAK4/NAMPT expression. We found an association of high PAK4/NAMPT expression with mammalian target of rapamycin activation and glycolytic pathway enrichment, increased mutations in specific genes, and altered immune profiles. High PAK4 or NAMPT expression individually correlated with lower overall survival, and combined high expression resulted in the worst outcomes. These results suggest potential therapeutic strategies for pNENs, especially for those resistant to everolimus.

Relevance (A.R. Parikh)

Everolimus is a well-established therapeutic option for pancreatic neuroendocrine tumors (pNETs) but resistance is common. The authors evaluate the role of PAK4-NAMPT expression for in this pNET and showed distinct molecular and immune profiles in tumors with high expression but also worse outcomes that may lead to future therapeutic strategies.*

Plain Language Summary (M. Lewis)

Everolimus is a well-established therapeutic option for pNETs, but resistance is common. The authors evaluate the role of PAK4-NAMPT expression for pNETs and showed distinct molecular and immune profiles in tumors with high expression of PAK4-NAMPT, but also with this marker, the authors showed worse outcomes and important as targeting this pathway that may lead to future therapies.†

*Relevance section written by JCO Oncology Advances Associate Editor Aparna R. Parikh, MD.

†Plain Language Summary written by JCO Oncology Advances Associate Editor Mark Lewis, MD.

Besides loss of multiple endocrine neoplasia type 1 (MEN1), death domain–associated protein, and alpha thalassemia/mental retardation syndrome X-linked (ATRX) genes, the hyperactivation of PI3K/Akt/mammalian target of rapamycin (mTOR) through loss of tumor suppressor PTEN has been well documented as one of the main drivers in pNENs.³ This was the basis for targeting the mTOR pathway. Furthermore, the mTOR inhibitor everolimus is approved by the US Food and Drug Administration (FDA) for patients with pNENs and shows an improvement in median overall survival of 11.1 months compared with 4.4 months with a placebo.⁴ Nevertheless, primary or acquired resistance to mTOR inhibitors is observed in the majority of patients.⁵ There are several mechanisms of everolimus resistance, including incomplete inhibition of the mTOR pathway, as everolimus is only specific toward mTORC1 and not mTORC2 in the mTOR complex.⁵

p21-activated kinase 4 (PAK4) is a group II PAK family member that controls invadopodia and migratory behavior.⁶ PAK4 is a node protein linking different MAPK downstream pathways.⁷ PAK4 regulates several substrates in the PI3K/AKT/mTOR signaling pathway through phosphorylation that regulates the pathogenesis and evolution of pNENs.⁸ Studies show that PAK4 is a key effector of the Rho GTPases that directly regulates mTORC2 and its downstream effectors (such

as pS6K, 4EBP1, and eIF4E), thereby promoting everolimus resistance.⁹ In this direction, it was shown earlier that PAK4 is aberrantly overexpressed in pNENs and that RNAi knockdown or chemical inhibition of PAK4 resensitizes pNENs to everolimus and other pNEN therapies.¹⁰ Thus, PAK4 cross-talks with pNEN driver pathways, making this kinase an attractive target for this treatment-refractory disease.

Deregulated metabolism is a hallmark of all cancers, and NENs are no exception. Tumor cells rely on high glycolysis, pentose, and fatty acid biosynthesis.¹¹ Deregulated tumor energetics result in tumors turning to alternative energy sources, especially the nicotinamide adenine dinucleotide (NAD) pool.¹² Studies have shown that the NAD biosynthetic pathway is deregulated in pNENs, making it an attractive therapeutic target.¹³ Nicotinamide phosphoribosyl transferase (NAMPT) is the rate-limiting enzyme in the NAD salvage pathway, which is one of the major sources of NAD in eukaryotes.¹⁴ In neuroendocrine tumors, NAMPT has been identified as a mechanistic dependency and an attractive therapeutic target.¹⁵ Given the significance of PAK4 and NAMPT in the biology of NENs, in this study, we queried the importance of the expression of these genes in a large real-world data set of pNENs. Our goals were to study the association between PAK4/NAMPT and clinical outcomes, especially in patients treated with everolimus, and to

characterize the molecular and immune landscapes associated with PAK4/NAMPT expression.

METHODS

Tissue Samples

pNEN specimens were sequenced for genomic (DNA-592 gene panel/whole-exome sequencing) and transcriptomic (whole-transcriptomic sequencing) analyses by Caris Life Sciences (Phoenix, AZ) as part of routine comprehensive molecular profiling. Before molecular testing, tumor enrichment was achieved by harvesting targeted tissue using manual microdissection techniques.

Next Generation Sequencing

Genomic DNA was isolated from formalin-fixed paraffin-embedded (FFPE) samples that underwent microdissection to enrich tumor purity and subjected to next-generation sequencing (NGS) using the NextSeq or NovaSeq 6000 platforms (Illumina, Inc, San Diego, CA). Details of the methods and list of genes assayed can be found elsewhere.¹⁶ The copy-number alteration of each exon was determined by calculating the average depth of the sample along with the sequencing depth of each exon and comparing this calculated result with a precalibrated value, and a copy number of ≥ 6.0 was considered amplified. Tumor mutational burden (TMB) was measured by counting all nonsynonymous missense, nonsense, in-frame insertion/deletion, and frameshift mutations found per tumor that had not been previously described as germline alterations in dbSNP151, Genome Aggregation Database databases, or benign variants identified by Caris's geneticists. TMB-H was defined as ≥ 10 mutations per megabase. For samples profiled by whole exome sequencing, genomic loss of heterozygosity (LOH) was calculated by dividing 22 autosomal chromosomes into 552 segments and calculating the LOH of single nucleotide polymorphisms within each segment, with 99% of segments at least 5 Mb in length and segments spanning $\geq 90\%$ of a whole chromosome or chromosome arm excluded from the calculation. NGS of RNA on FFPE samples was performed using the Agilent SureSelect Human All Exon V7 bait panel (Agilent Technologies, Santa Clara, CA) and the Illumina NovaSeq platform (Illumina, Inc, San Diego, CA) as described previously.¹⁷ Single-sample gene set enrichment analysis (ssGSEA) was performed for hallmark analysis using previously published methods.^{18,19}

Immunohistochemistry

For PD-L1+ expression, multiple antibody clones were used. The antibody clone 22c3 (Dako, Santa Clara, CA) was measured using the tumor proportion score, which is the percentage of viable tumor cells showing partial or complete membrane staining at any intensity, with a positive threshold of $\geq 1\%$. For the 28-8 antibody clone, PD-L1 expression on tumor cells was scored using an FDA-approved test

(pharmDx, Santa Clara, CA) and a positive threshold of $\geq 1+$ stain intensity and $\geq 1\%$ cells stained. For the SP142 antibody clones, PD-L1 expression was scored on tumor cells using a laboratory-developed test and a positive threshold of $\geq 2+$ stain intensity and $\geq 5\%$ cells stained. By contrast, PD-L1 expression on immune cells was scored using an FDA-approved test (Ventana; Roche, Indianapolis, IN) and a positive threshold of $\geq 1+$ stain intensity and $\geq 10\%$ cells stained.

Gene Fusion Detection

Gene fusions were detected by RNA sequencing using either the ArcherDx fusion assay (Archer FusionPlex Solid Tumor panel) or whole-transcriptome sequencing assay (Illumina NovaSeq platform; Illumina, Inc, San Diego, CA). Variants of genes were predetermined for their cancer-related and clinical significance as described previously.²⁰

Real-World Survival Analysis

Overall survival was calculated using a repository of real-world evidence (RWE) insurance claim data, with overall survival defined from the date of biopsy or start of therapy until last contact. Patients who did not have an observed claim within 100 days of the end of available RWE records were presumed to be deceased and uncensored, which was found to be 95% concordant to data obtained from National Death Index data (National Center for Health Statistics, Centers for Disease Control and Prevention). All other patients were censored. Hazard ratios for survival (and 95% CIs) were computed using the Cox proportional hazards model, and overall survival between groups was compared using the log-rank test.

Statistical Analysis

Molecular associations were tested by using chi-square and Fisher's exact tests for categorical variables and Mann-Whitney *U* for continuous variables, where appropriate. Statistical analyses were performed with open-source Python libraries.

Ethics Statement

This study was conducted in accordance with guidelines of the Declaration of Helsinki, Belmont Report, and US Common Rule. In keeping with 45 CFR 46.101(b) (4), this study was performed using retrospective, deidentified clinical data. Therefore, this study was considered IRB-exempt and no patient consent was necessary from the patients.

RESULTS

Association of PAK4 and NAMPT Expression With mTOR and Glycolytic Pathway Genes

Hierarchical agglomerative clustering on the expression of PAK4 and NAMPT was used to stratify 294 cases of pNENs

TABLE 1. Baseline Characteristics of the Study Population

Cohort Characteristic	NAMPT-High Cluster (n = 127)	PAK4-High Cluster (n = 138)	NAMPT PAK4-Low Cluster (n = 29)	Statistic Used	P	q-value
Median age, years (range) (No.)	59 (20-85) (127)	65 (20 to >89) (138)	59 (32-77) (29)	Kruskal-Wallis test	.00025	0.0005
Males	57.5% (73/127)	60.1% (83/138)	55.2% (16/29)	Chi-square test	.843	0.843
Females	42.5% (54/127)	39.9% (55/138)	44.8% (13/29)	Chi-square test	.843	0.843
Smoker	100% (5/5)	100% (13/13)	100% (5/5)	No test performed	NaN	NaN

Abbreviations: NAMPT, nicotinamide phosphoribosyl transferase; NaN, not a number; PAK4, p21-activated kinase 4.

into three clusters: PAK4-low-NAMPT-low (29 cases), PAK4-high (138 cases), and NAMPT-high (127 cases). PAK4-high cluster was associated with tumors biopsied from patients who were older (median age 65 years) compared with those with tumors within NAMPT-high (median age 59 years) or PAK4-low-NAMPT-low (median age 59 years) clusters. The distribution of sex was similar between the three groups and patients were identified as smokers by history (Table 1).

We queried the expression of a panel of genes activated in response to mTOR activation and found that these genes, including Glut1 promoter solute carrier family 2 member 1 (*SLC2A1*; 2.06 to 3.36-fold), glucose regulator phosphofructokinase (*PFKP*; 2.14 to 2.86-fold), monounsaturated fatty acid synthesis enzyme stearoyl-CoA desaturase (*SCD*; 2.75 to 3.97-fold), mevalonate kinase (*MVK*; 2.29 to 3.48-fold), and glucose 6 phosphate dehydrogenase (*G6PD*; 1.75 to 2.63-fold), were all overexpressed in NAMPT-high or PAK4-high compared with the PAK4-low/NAMPT-low tumors (all $q < 0.05$; Figs 1A and 1B). However, the ssGSEA did not reveal a significant enrichment in the PI3K/AKT/mTOR and mTORC1 signaling pathways within the tumors displaying high levels of PAK4 and NAMPT (Appendix Fig A1). Notably, our analysis highlighted that the deviations in mTOR pathway genes were most pronounced in the PAK4-high/NAMPT-high group compared with other groups. Furthermore, the observed enrichment in pathways related to inflammatory responses, such as tumor necrosis factor- α , and IL2/STAT5 signaling pathways (Fig 2A), suggests a significant involvement of these immune and inflammatory pathways in the tumor microenvironment in the NAMPT-high cluster. Although weak, the IL2/STAT5 and inflammatory pathways were positively correlated with NAMPT expression. No such correlation was observed with PAK4 expression (Fig 2B). This enrichment might indicate a proinflammatory environment within these tumors, potentially influencing their progression and response to therapeutic interventions.

Comutations Associated With PAK4 and NAMPT Expression

We next analyzed the co-occurrence of mutations of prominent genes in the mTOR pathway in relation to PAK4 and NAMPT expression in the pNEN cohort under study.

Although not statistically significant, we observed higher rates of mutations in *MEN1*, *ATRX*, *TSC2*, *SETD2*, and *CCNE1* in NAMPT-high and PAK4-high clusters (Fig 3A). Interestingly, mutations in *TSC3*, *SETD2*, and *CCNE2* were not observed in the PAK4-low-NAMPT-low group, while *ATM* mutations were only observed in the NAMPT-high cluster (Fig 3A). However, *RB1* mutations were higher in PAK4-high cluster in comparison with PAK4-low-NAMPT-low cluster. *RB1* mutations were less in the NAMPT-high cluster compared with PAK4-low-NAMPT-low group. More intriguingly, *p53* mutations were less prevalent in the PAK4-high or NAMPT-high clusters versus PAK4-low-NAMPT-low groups (Fig 3B).

Association of PAK4 and NAMPT Expression With Immune Checkpoint Gene Expression and Immune Cell Infiltration

In pNENs characterized by heightened levels of NAMPT or PAK4, a significant enrichment in the expression of immune checkpoint genes was observed compared with the PAK4-low-NAMPT-low group. Specifically, genes such as *LAG3* (2.61 to 3.19-fold), *CD80* (2.93 to 2.78-fold), *IDO1* (3.43 to 2.2-fold), *CD274* (3.75 to 3.62-fold), *CD86* (4.28 to 3.37-fold), *PDCD1LG2* (3.68 to 2.86-fold), and *HAVCR2* (4.09 to 3.99-fold; all $q < 0.05$) exhibited notably elevated expression levels (Fig 4). A moderate positive correlation was observed between the expressions of *HAVCR2* and *CD86* and NAMPT (Appendix Fig A2).

Furthermore, compared with PAK4-low-NAMPT-low tumors, an enrichment in B cells, M1 and M2 macrophages, and neutrophils was observed in tumors belonging to the NAMPT-high cluster (all $q < 0.05$). A similar enrichment in M2 macrophages, neutrophils, and natural killer cells was also observed in the PAK4-high compared with the PAK4-low-NAMPT-low cluster (all $q < 0.05$). No significant differences were observed in CD4+ and CD8+ T cells among the three groups (Fig 5).

Association of PAK4 and NAMPT Expression With Prognosis of NENs

Kaplan-Meier curves showed an association of PAK4 and NAMPT expression with real-world survival data from all

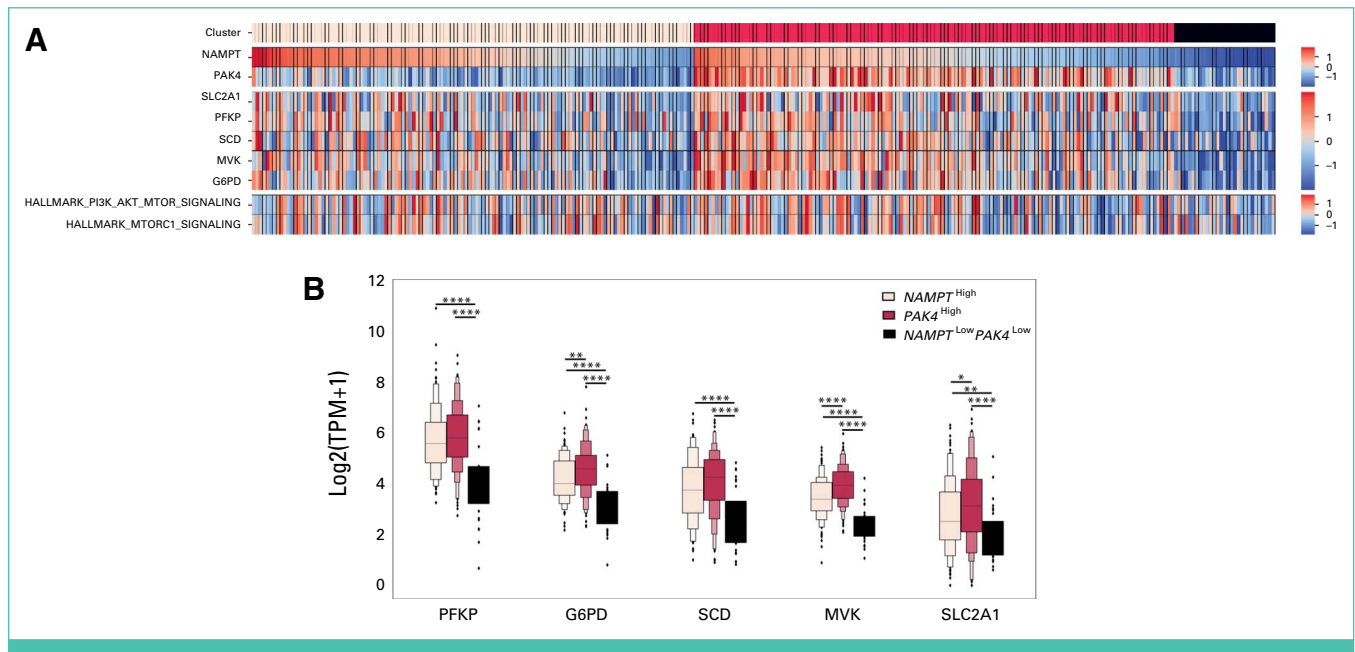


FIG 1. (A) The heat map of the various clusters in the study on the basis of the molecular profiling of pNENs on the basis of PAK4 and NAMPT expression. The entire population is divided into three clusters. NAMPT-high, PAK4-high, and NAMPT, PAK4-low. (B) The box and whisker plots of the panel of genes activated in response to mTOR activation. SLC2A1, PFKP, SCD, MVK, and G6PD were found to be all overexpressed in NAMPT-high or PAK4-high compared with low tumors (all $q < 0.05$). G6PD, glucose 6 phosphate dehydrogenase; mTOR, mammalian target of rapamycin; MVK, mevalonate kinase; NAMPT, nicotinamide phosphoribosyl transferase; pNENs, pancreatic neuroendocrine neoplasms; PAK4, p21-activated kinase 4; PFKP, phosphofructokinase; SCD, stearyl-CoA desaturase; SLC2A1, solute carrier family 2 member 1.

neuroendocrine neoplasms (NEN) and pancreatic NEN patient cohorts (Appendix Fig A3). Patient cohorts were stratified by PAK4 (high v low) and NAMPT (high v low) median expression. Patient cohorts with either high PAK4 or high NAMPT had lower overall survival compared with low PAK4 or low NAMPT cohorts, respectively (Appendix Figs A3A and A3B). In addition, patients with both high PAK4 and high NAMPT had worse survival outcomes compared with PAK4-low and NAMPT-low tumors (Appendix Fig A3C). A subgroup analysis showed no significant difference in survival on everolimus, potentially because of low number of cases. Although not statistically significant, similar survival trends were observed when the pancreatic NEN patient cohorts were stratified on the same lines as mentioned above (Appendix Figs A3D–A3H).

Dual Targeting of PAK4 and NAMPT Decreases Viability of pNEN Cells

Our previous studies have shown that the dual inhibition of PAK4 and NAMPT either by siRNA or small molecule KPT-9274 inhibits pNEN cellular and in vivo xenograft models.¹⁰ Here, we overexpressed PAK4 in BON-1 pNEN cells (Appendix Fig A4A). PAK4 and NAMPT dual inhibition resulted in significant loss of cell viability, which was rescued by PAK4 overexpression (OE; Appendix Fig A4B). Similarly, PAK4 OE reduced the response to everolimus (Appendix Fig A4C). OE of NAMPT or niacin treatment rescued the response

to KPT-9274, indicating NAMPT-specific response to KPT-9274 (Appendix Figs A4D–A4F). Additionally, we evaluated the expression of PAK4 in pNEN tumors compared with matched normal control using immunohistochemistry staining, which showed higher intensity of staining in tumor tissues (Appendix Fig A5). Overall, these data show the dependency of pNEN cells on PAK4 and NAMPT for their survival and growth.

DISCUSSION

In this article, we characterize the impact of high PAK4 and NAMPT on pNEN mutation, metabolic, and immune landscapes. Our findings offer extensive insights into the molecular and immune landscapes. The significance of these aberrations in pNENs have implications for the treatment strategies and potentially the efficacy of existing therapies.

The hyperactivation of PI3K/Akt/mTOR through loss of tumor suppressor PTEN has been well documented as a main driver in pNENs. This led to the introduction of mTOR inhibitor everolimus for the treatment of low-grade pNENs.⁴ Nevertheless, responses to everolimus have been modest at best and resistance to everolimus is universal.²¹ There are several factors associated with resistance to mTOR inhibition²² including incomplete inhibition of mTOR as well as compensatory reactivation of mTORC2 feeding forward the

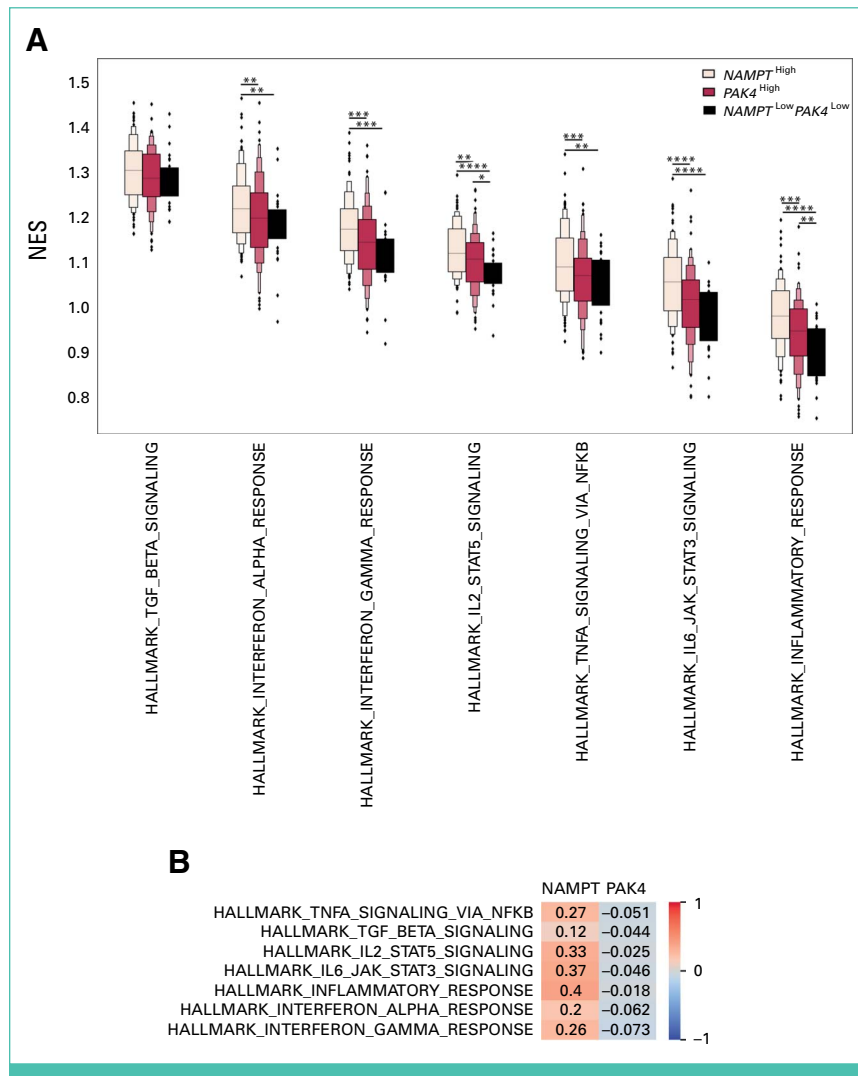


FIG 2. Box and whisker plots show enrichment analysis of inflammatory signaling pathways in pNENs. (A) TNF- α and IL2/STAT5 signaling pathways in the tumor microenvironment of the NAMPT-high cluster. (B) No such correlation of the inflammatory signals with PAK4 expression. NAMPT, nicotinamide phosphoribosyl transferase; NES, normalized enrichment score; PAK4, p21-activated kinase 4; pNENs, pancreatic neuroendocrine neoplasms; TNF, tumor necrosis factor.

mTOR signaling.²³ Therefore, identification of the mechanisms of mTOR inhibition resistance is of utmost importance to design strategies that could enhance the response to everolimus in patients with pNENs.

Earlier studies have shown that Rho GTPase effectors such as RAC can regulate mTORC1 and mTORC2.²⁴ PAK4 is a key effector of the Rho GTPases that directly regulate several mTORC2 downstream effectors (such as pS6K, 4EBP1, and eIF4E), thereby promoting everolimus resistance.²⁵ PAK4 is an effector of the Rho GTPases signaling pathway²⁶ and is known as a core molecule linking Ras/Erk, Wnt/ β -catenin, and androgen receptor–/estrogen receptor–dependent pathways.²⁷ Thus, PAK4 interacts with pNEN driver pathways, making this kinase an attractive target for resistant

pNENs. We also showed that PAK4 is aberrantly overexpressed in pNENs and that RNAi knockdown or chemical inhibition of PAK4 resensitizes pNENs to everolimus and other pNEN therapies.^{10,28}

Deregulated metabolism is a hallmark of cancer, including NENs and pNENs.²⁹ Several metabolites shed by neuroendocrine cells have been identified to engage in cellular signaling and have paracrine effects on tumor cell proliferation.²⁹ Deregulated tumor energetics also drive tumors to seek alternative energy sources, especially the NAD pool. NAD is produced through the de novo pathway using tryptophan.¹² However, tumors depend on other NAD-producing mechanisms such as Preiss–Handler and salvage pathways.¹² Nicotinate phosphoribosyltransferase (NAPRT) is the rate-

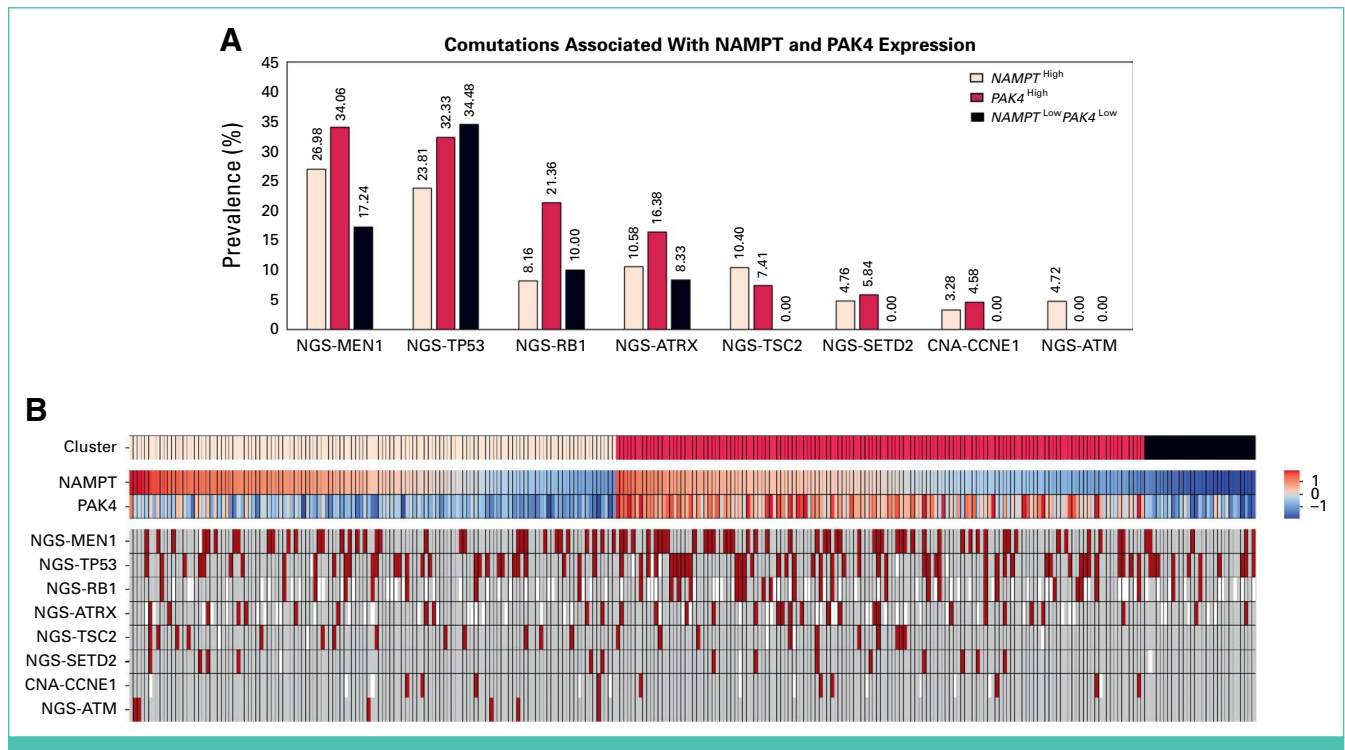


FIG 3. Comutations associated with PAK4 and NAMPT expression in pNENs. (A) Bar diagram showing higher rates of mutations in MEN1, ATRX, TSC2, SETD2, and CCNE1 in the NAMPT-high and PAK4-high clusters ($P = >.05$). (B) The heat map of the same. ATM mutations were identified only in NAMPT-high clusters, while RB1 was higher in the PAK4-high cluster. P53 mutations were less prevalent in the PAK4-high or NAMPT-high clusters versus low groups. NAMPT, nicotinamide phosphoribosyl transferase; PAK4, p21-activated kinase 4; pNENs, pancreatic neuroendocrine neoplasms.

limiting enzyme in the Preiss-Handler pathway that converts niacin to nicotinic acid mononucleotide (NAMN) that in turn is converted into nicotinic acid adenine dinucleotide before NAD production by NAD synthetase.¹² As a tumor metabolic liability, NAMPT is often lost in cancer due to hypermethylation³⁰; thus, the salvage pathway is the major source of NAD synthesis by tumors, creating dependency on NAMPT. Our previous work has established that NAMPT is overexpressed in pNEN tissue and can be targeted using PAK4-NAMPT dual inhibitor.^{10,28}

Notably, the current analysis revealed distinct profiles among the different groups stratified on the basis of PAK4 and NAMPT expression. The PAK4-high, NAMPT-high groups exhibited elevated expression of genes associated with mTOR activation, glycolysis, and pathways linked to PI3K/AKT/mTOR. These findings strongly suggest a convergence of the PAK4-mTOR-NAD axis within pNENs. The heightened activity in these pathways implies a potential strategy for effectively targeting these tumors. Specifically, the dual targeting of PAK4 and NAMPT could be an effective approach, particularly in sensitizing tumors that have shown resistance to everolimus. These observations suggest a robust association between PAK4/NAMPT expression and the dysregulation of these pivotal oncogenic pathways in pNENs.

Furthermore, this study sheds light on the immune landscape, revealing enrichment in various immune checkpoint genes and signaling pathways, such as those involved in the inflammatory response and IL2/STAT5 pathways, within the PAK4-high and NAMPT-high tumors. The increased expression of immune checkpoint genes and altered immune cell infiltration in NAMPT-high and PAK4-high tumors suggests potential immunotherapeutic vulnerabilities or opportunities for treatment intervention. It is notable that several recent studies have implicated PAK4 and NAMPT in immune surveillance.^{31,32} For example, Tang and colleagues have shown using pan-cancer analysis the immunologic and prognostic role of PAK4.³³ Similarly, PAK4 has been suggested to regulate multiple aspects of immune biology and has been termed as an immune evasion target for cancer.³⁴ Several groups have demonstrated that PAK4 inhibition can enhance the antitumor activity of immune checkpoint blockade³⁵⁻³⁷ and sensitize tumors to CAR-T therapy.³⁸

Also, many investigations have pointed to the role of NAD metabolism in immune modulation.³⁹ High NAD⁺ metabolism has been shown to maintain inducible PD1 levels resulting in immune evasion.⁴⁰ Extracellular NAMPT has been shown to promote M2 macrophage polarization in hematologic malignancies.⁴¹ NAMPT has also been shown to be critical for promoting tumor angiogenic activity of

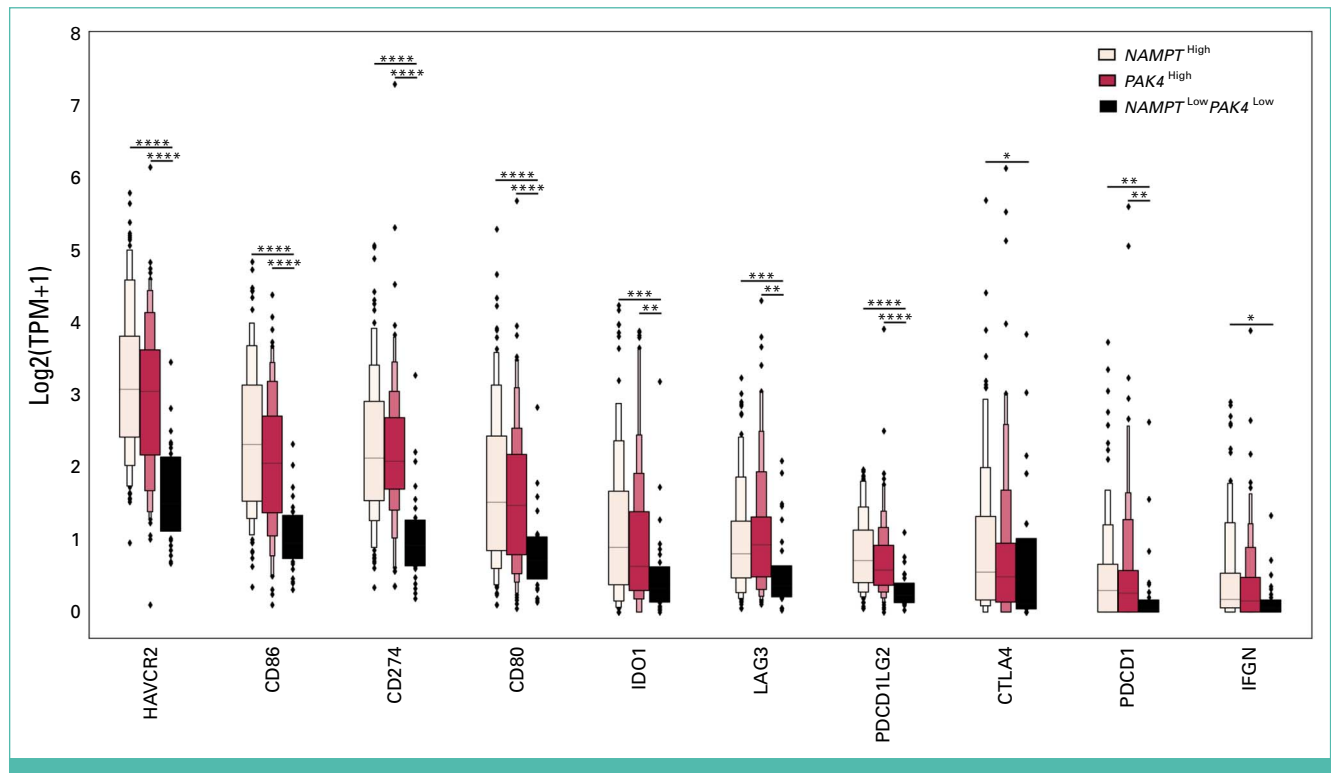


FIG 4. Box and whisker plots demonstrating the effect of PAK4 and NAMPT alterations on the expression of immune checkpoint genes in pNENs. Genes such as LAG3, CD80, IDO1, CD274, CD86, PDCD1LG2, and HAVCR2 were richly expressed in PAK4/NAMPT-high clusters compared with PAK4/NAMPT-low clusters and it is statistically significant ($q < 0.05$). NAMPT, nicotinamide phosphoribosyl transferase; PAK4, p21-activated kinase 4; pNENs, pancreatic neuroendocrine neoplasms.

neutrophils.⁴² It is not surprising to note that local targeting of NAD⁺ signaling including enzymes such as NAMPT can enhance the efficacy of immunotherapies in several solid tumors.⁴³⁻⁴⁵

In our analysis, the identification of distinct immune profiles in PAK4-high, NAMPT-high pNENs offers clues for the development of potential targeted therapeutic approaches in the combination setting. Given the known role of mTOR inhibitors, such as everolimus, in pNEN treatment and the observed sensitivity of pNENs with aberrant PAK4/NAMPT expression to mTOR inhibition, the study implies a potential for enhanced efficacy of mTOR inhibitors in this specific subgroup. Additionally, the findings raise intriguing questions regarding the potential responsiveness of PAK4/NAMPT-aberrant pNENs to immunotherapeutic interventions. The observed immune landscape alterations in these tumors suggest a possible relationship between the PAK4/NAMPT axis and immunotherapeutic response, which warrants further investigation.

Some of the study limitations include that this a retrospective study that lacks granular clinical information. Patient outcome data have been extracted from RWE insurance claim data. Such data have been collected for purposes other than research, and thus have some limitations including

increased likelihood of missing data, and variables in assessing exposures and outcomes. One limitation is that the use of deidentified data omits crucial details of the pathology (grade of differentiation and stage) that potentially could affect patient outcome. The second limitation of the study is the lack of treatment timeline that might have had a bearing effect on outcomes. The timing of tissue collection (at the time of diagnosis *v* post-treatment) and site (primary *v* metastatic) could alter the disease's biological characteristics and likely affect the PAK4 and NAMPT pathways, as metastatic sites often exhibit more aggressive traits. Unfortunately, the effect of these confounding factors on the overall survival outcomes in our cohort cannot be completely excluded. Also, in our cohort of patients, there are patients with TP53 and RB1 mutations. These mutations are rare in well-differentiated pNENs but are strongly linked to high-grade neuroendocrine carcinoma of the pancreas. Because we do not have the granular information on the grade in the commercially available tissue sets, this would confound results, given the stark biological differences between high-grade NEN and well-differentiated NENs, including survival rates and cell signaling behaviors, especially within mTOR-associated pathways. Nonetheless, the fact that we present a large data set for a rare group of malignancies using molecular analysis performed by the same NGS provider makes it relevant. Furthermore, the data presented in this report

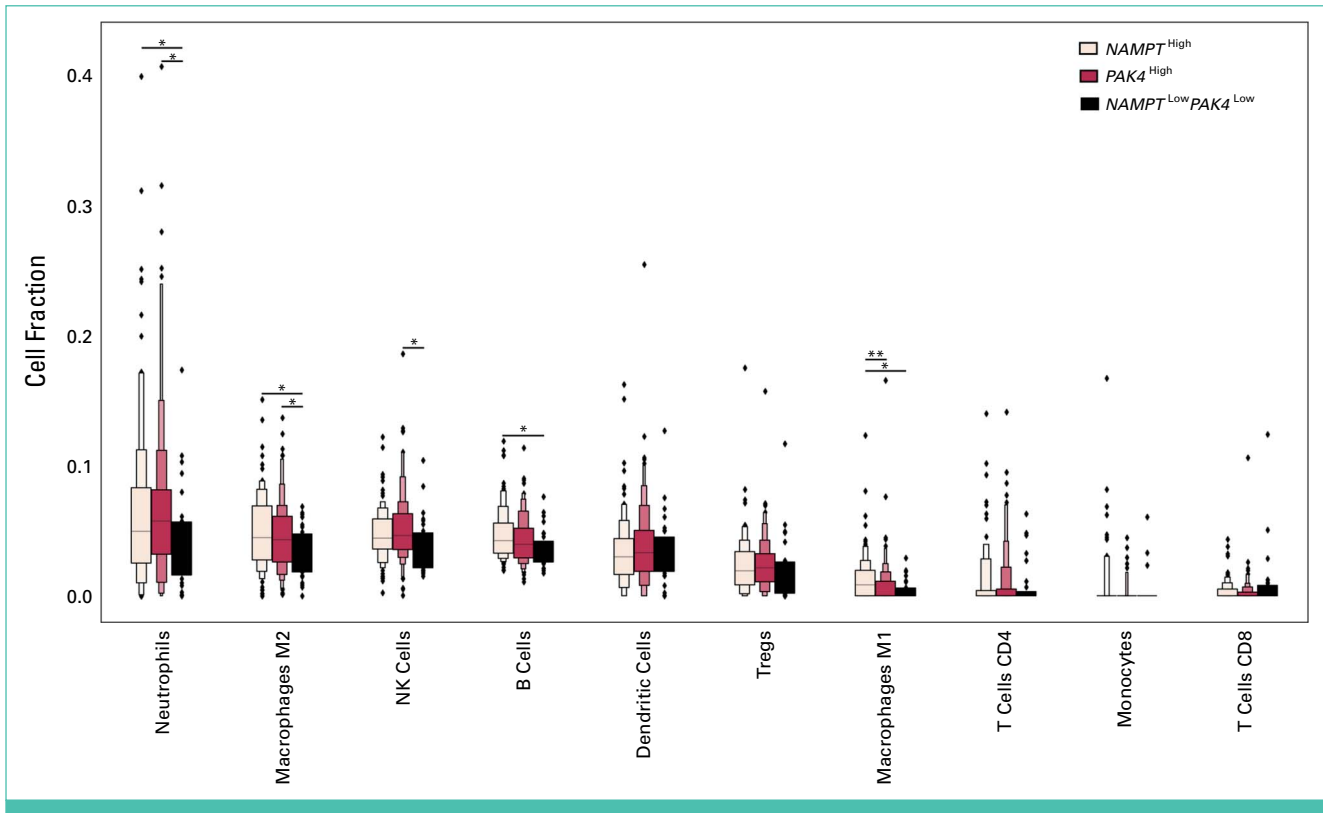


FIG 5. Box and whisker plots demonstrating the effect of PAK4 and NAMPT alterations on immune cell infiltration in pNENs. Enrichment of B cells, neutrophils, and M1 and M2 macrophages is observed in NAMPT-high and PAK4-high clusters ($q < 0.05$); however, no difference was noticed in CD4+ and CD8+ T cells across all three clusters. NAMPT, nicotinamide phosphoribosyl transferase; PAK4, p21-activated kinase 4; pNENs, pancreatic neuroendocrine neoplasms.

suggest that a sizable fraction of pNENs have high expression levels of PAK4 and NAMPT. Overall, this study potentially opens new avenues for personalized therapeutic strategies in low-grade pNENs for which there are no effective therapies, indicating the potential for tailored treatment regimens on the basis of the distinct molecular and immune profiles associated with PAK4 and NAMPT expression. PAK4-NAMPT dual inhibitor KPT-9274 has

shown potent antitumor activity in preclinical models of pNENs. The drug has shown activity as a single agent or in combination with everolimus. KPT-9274 has also been shown to overcome everolimus resistance in pNEN xenograft. The findings underscore the need for further exploration and clinical trials to validate the efficacy of targeted therapies and immunotherapeutic interventions in this specific pNEN subgroup.

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APPENDIX

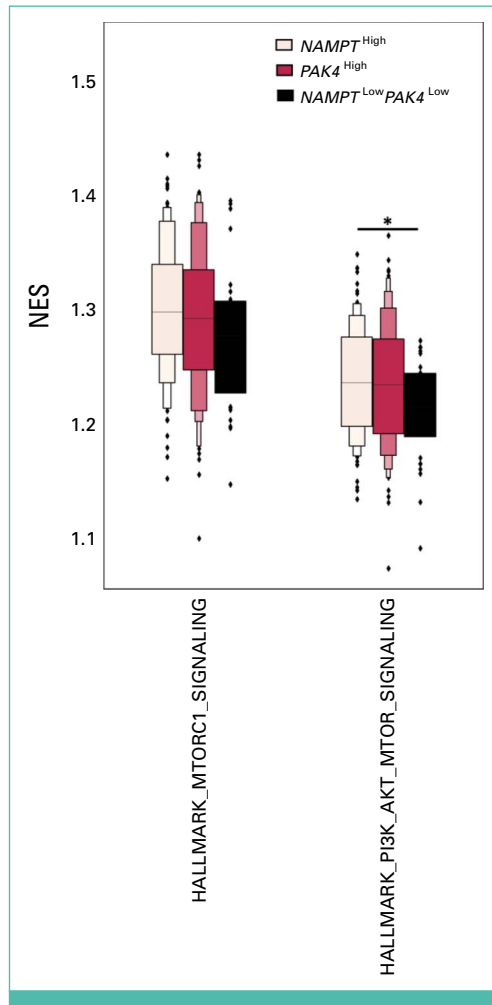


FIG A1. Box and whisker plots representing single-set enrichment analysis representing changes in hallmark (MTORC1) and hallmark PI3K mTOR signaling in NAMPT-high, PAK4-high versus NAMPT-low and PAK4-low groups. It was found that there is no statistically significant difference between the groups. mTOR, mammalian target of rapamycin; NAMPT, nicotinamide phosphoribosyl transferase; NES, normalized enrichment score; PAK4, p21-activated kinase 4.

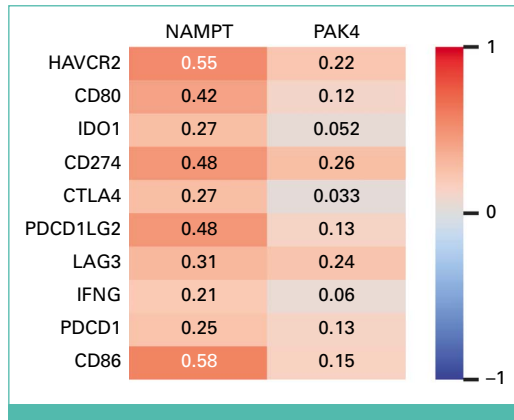


FIG A2. Heat map showing the expression in the association of PAK4 and NAMPT expression with immune checkpoint gene expression and immune cell infiltration. A moderate positive correlation was observed between the expressions of HAVCR2 and CD86 and NAMPT expression change in immune genes in NAMPT-high and PAK4-high groups in contrast to LAG3, CD80, and IDO1 as represented in [Figure 4](#). NAMPT, nicotinamide phosphoribosyl transferase; PAK4, p21-activated kinase 4.

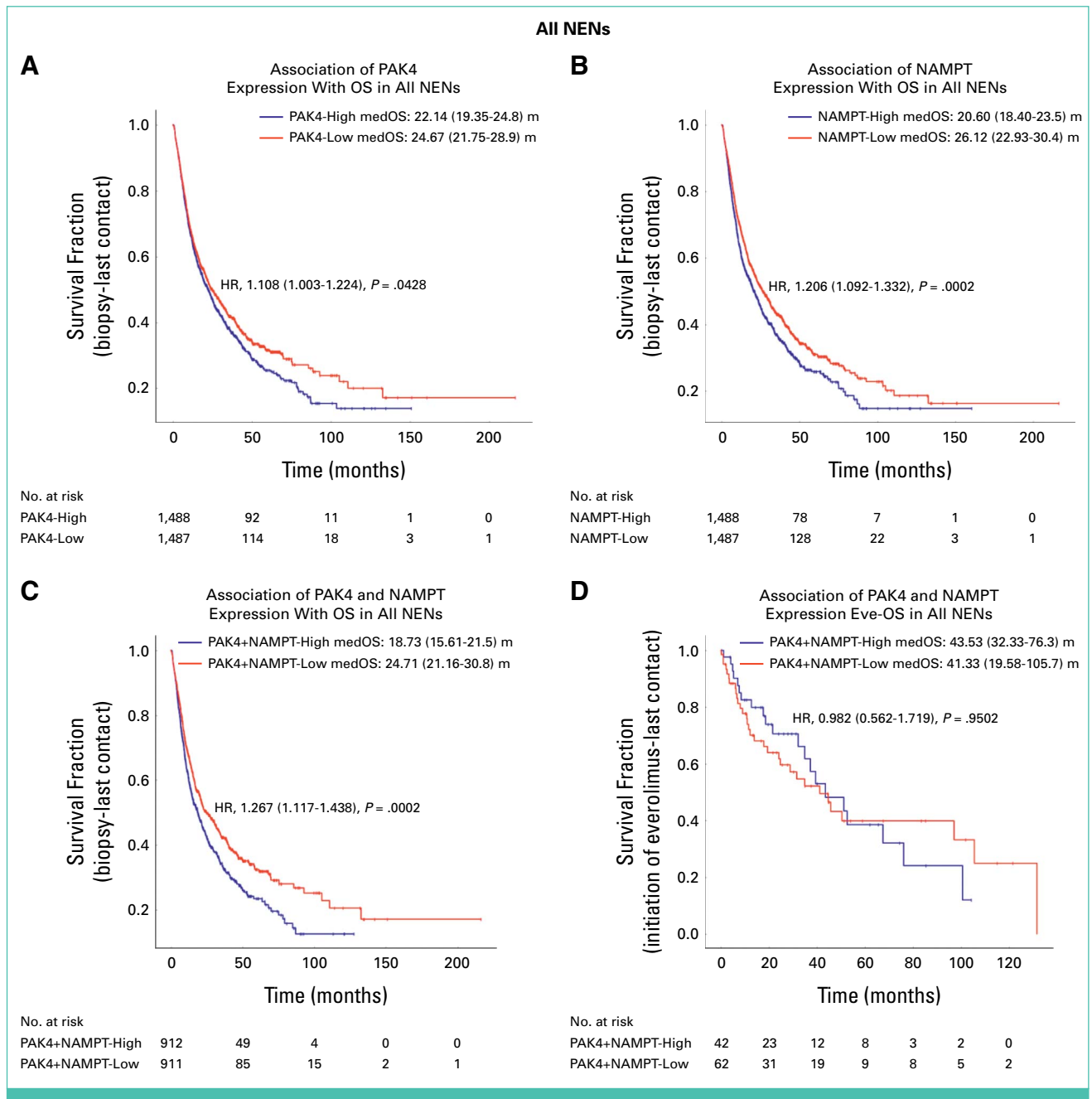


FIG A3. Kaplan-Meier survival analysis of PAK4 and NAMPT expression in NENs. (A-D) In patients with NEN, either high PAK4 or NAMPT is associated with lower overall survival compared with their low-expression cohorts ($P < .05$). However, in pNENs, similar trends are observed but not statistically significant ($P > .05$; E-H). HR, hazard ratio; NAMPT, nicotinamide phosphoribosyl transferase; NENs, neuroendocrine neoplasms; OS, overall survival; PAK4, p21-activated kinase 4; pNENs, pancreatic neuroendocrine neoplasms. (continued on following page)

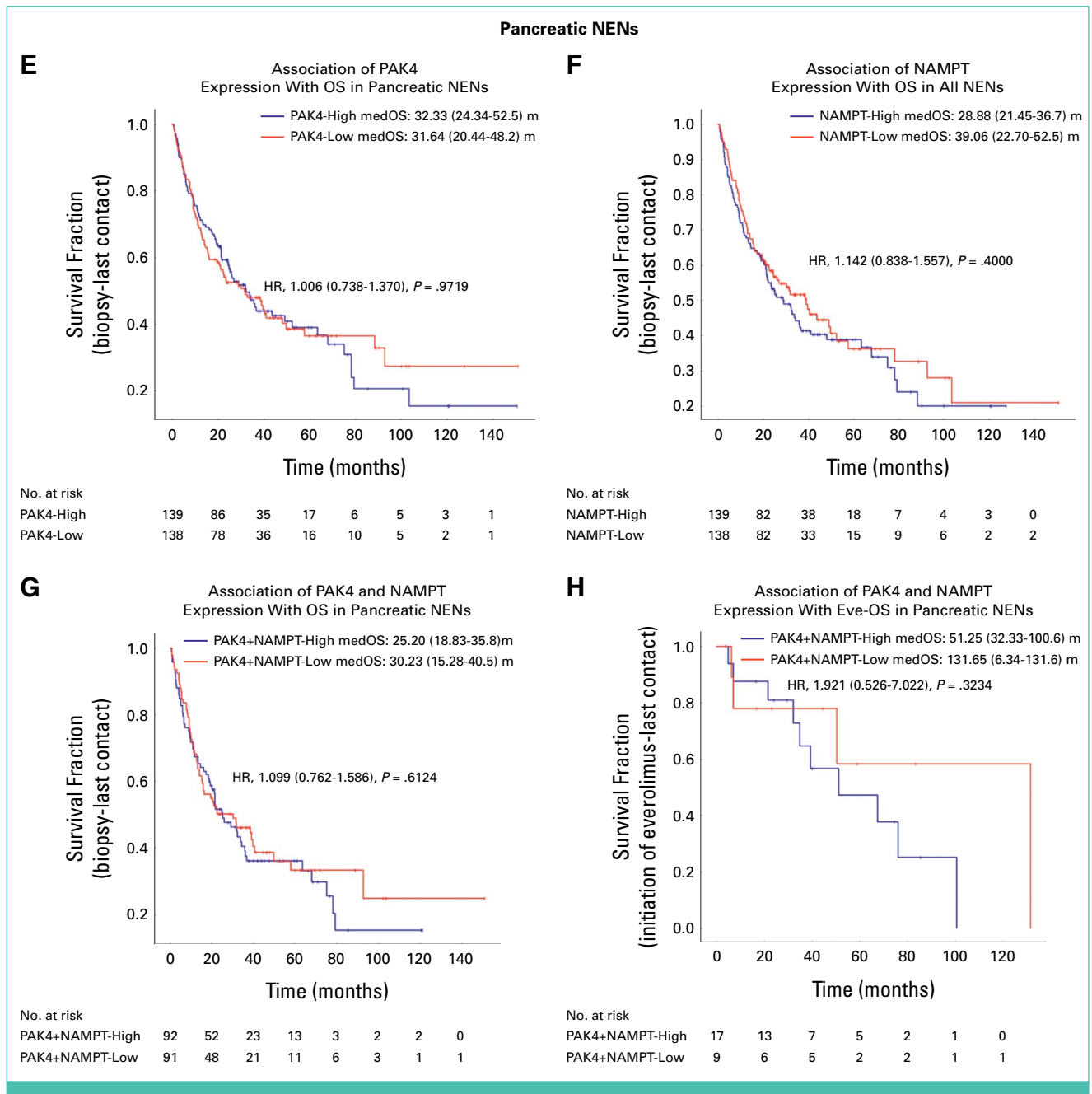


FIG A3. (Continued).

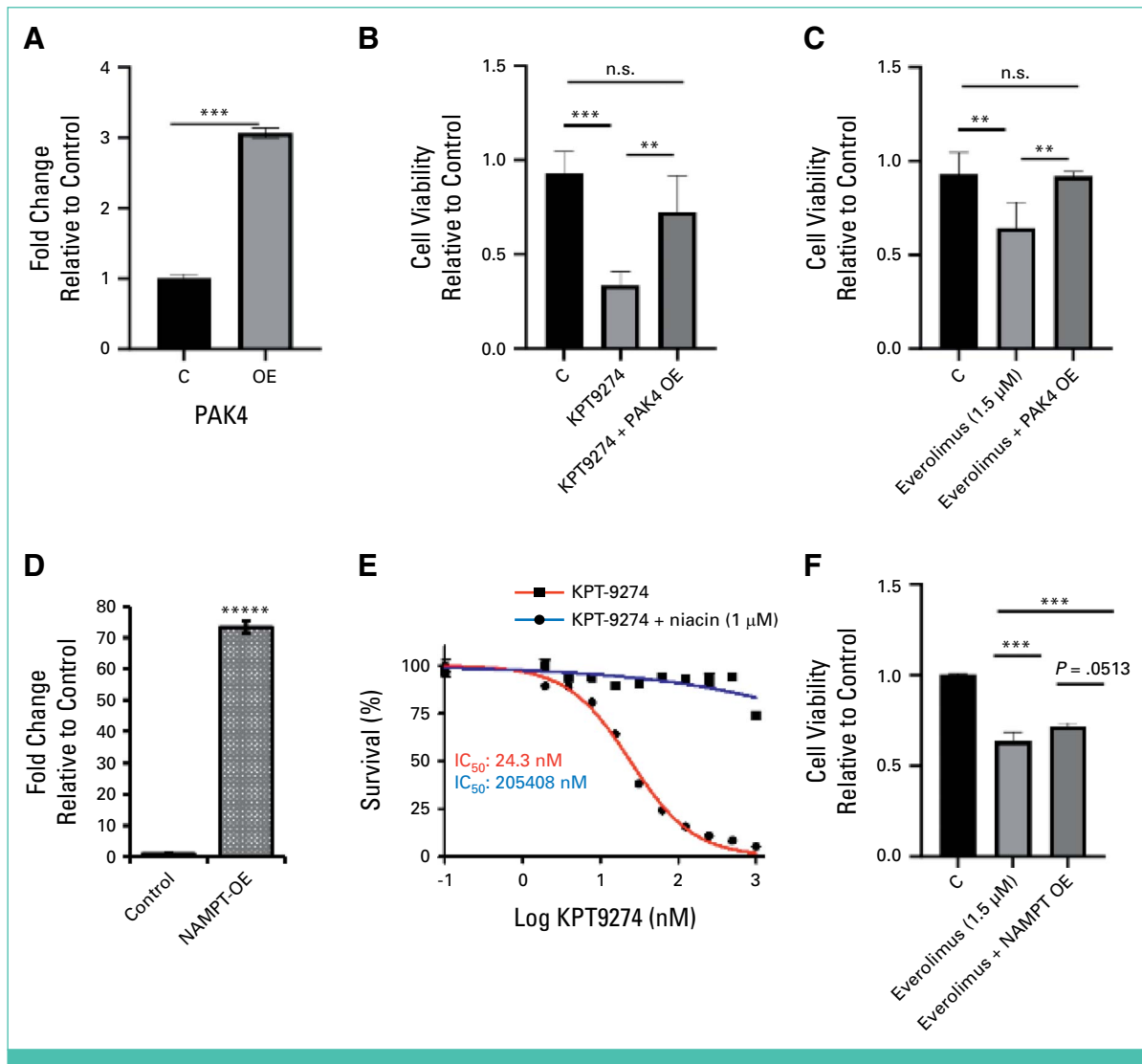


FIG A4. (A) RT-PCR showing OE of PAK4 in BON-1 cells after plasmid introduction. (B) MTT assay at 72 hours showing statistically significant reduced response to KPT-9274 in PAK4 OE cells. (C) MTT assay at 72 hours showing statistically significant low response to everolimus. (D) RT-PCR showing OE of NAMPT after plasmid introduction. (E) MTT assay at 72 hours showing lack of growth inhibition when KPT9274 was coadministered with niacin. (F) MTT assay at 72 hours showing diminished activity of everolimus in NAMPT overexpressing cells. MTT, 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide; NAMPT, nicotinamide phosphoribosyl transferase; OE, overexpression; PAK4, p21-activated kinase 4; RT-PCR, reverse transcriptase polymerase chain reaction. ** $P < .05$, *** $P < .01$, **** $P < .0001$.

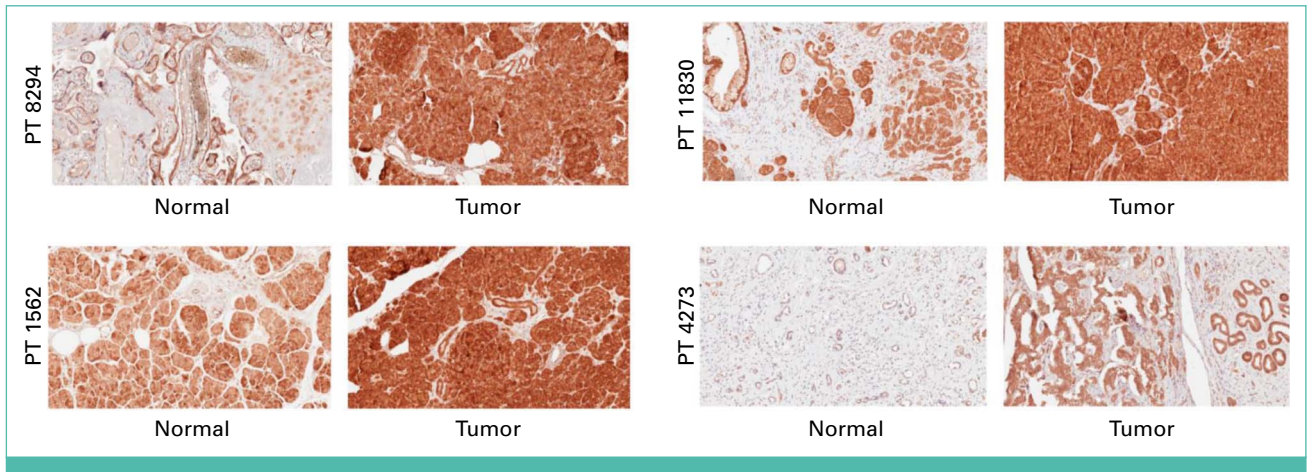


FIG A5. Immunohistochemistry staining preparations showing expression of PAK4 in pNEN tumors. It represents a higher intensity of staining of PAK4 in pNEN compared with matched control. PAK4, p21-activated kinase 4; pNENs, pancreatic neuroendocrine neoplasms.