<table>
<thead>
<tr>
<th>Title</th>
<th>PTEN-opathies : from biological insights to evidence-based precision medicine</th>
</tr>
</thead>
<tbody>
<tr>
<td>Author(s)</td>
<td>Yehia, Lamis; Ngeow, Joanne; Eng, Charis</td>
</tr>
<tr>
<td>Citation</td>
<td>Yehia, L., Ngeow, J., &amp; Eng, C. (2019). PTEN-opathies: from biological insights</td>
</tr>
<tr>
<td></td>
<td>to evidence-based precision medicine. Journal of Clinical Investigation, 129(2),</td>
</tr>
<tr>
<td></td>
<td>452-464. doi:10.1172/JCI121277</td>
</tr>
<tr>
<td>Date</td>
<td>2019</td>
</tr>
<tr>
<td>URL</td>
<td><a href="http://hdl.handle.net/10220/48638">http://hdl.handle.net/10220/48638</a></td>
</tr>
<tr>
<td>Rights</td>
<td>© 2019 American Society for Clinical Investigation. All rights reserved. This</td>
</tr>
<tr>
<td></td>
<td>paper was published in Journal of Clinical Investigation and is made available</td>
</tr>
<tr>
<td></td>
<td>with permission of American Society for Clinical Investigation.</td>
</tr>
</tbody>
</table>
The tumor suppressor phosphatase and tensin homolog (PTEN) classically counteracts the PI3K/AKT/mTOR signaling cascade. Germline pathogenic PTEN mutations cause PTEN hamartoma tumor syndrome (PHTS), featuring various benign and malignant tumors, as well as neurodevelopmental disorders such as autism spectrum disorder. Germline and somatic mosaic mutations in genes encoding components of the PI3K/AKT/mTOR pathway downstream of PTEN predispose to syndromes with partially overlapping clinical features, termed the “PTEN-opathies.” Experimental models of PTEN pathway disruption uncover the molecular and cellular processes influencing clinical phenotypic manifestations. Such insights not only teach us about biological mechanisms in states of health and disease, but also enable more accurate gene-informed cancer risk assessment, medical management, and targeted therapeutics. Hence, the PTEN-opathies serve as a prototype for bedside to bench, and back to the bedside, practice of evidence-based precision medicine.
PTEN-opathies: from biological insights to evidence-based precision medicine

Lamis Yehia,1 Joanne Ngeow,1,2,3,4 and Charis Eng1,5,6,7

1Genomic Medicine Institute, Lerner Research Institute, Cleveland Clinic, Cleveland, Ohio, USA. 2Lee Kong Chian School of Medicine, Nanyang Technological University, Singapore. 3Cancer Genetics Service, Division of Medical Oncology, National Cancer Centre, Singapore. 4Oncology Academic Program, Duke-NUS Graduate Medical School, Singapore. 5Taussig Cancer Institute, Cleveland Clinic, Cleveland, Ohio, USA. 6Department of Genetics and Genome Sciences, Case Western Reserve University School of Medicine, Cleveland, Ohio, USA. 7Germline High Risk Cancer Focus Group, Case Comprehensive Cancer Center, Case Western Reserve University, Cleveland, Ohio, USA.

The Journal of Clinical Investigation

Introduction

The tumor suppressor phosphatase and tensin homolog (PTEN) classically counteracts the PI3K/AKT/mTOR signaling cascade. Germline pathogenic PTEN mutations cause PTEN hamartoma tumor syndrome (PHTS), featuring various benign and malignant tumors, as well as neurodevelopmental disorders such as autism spectrum disorder. Germline and somatic mosaic mutations in genes encoding components of the PI3K/AKT/mTOR pathway downstream of PTEN predispose to syndromes with partially overlapping clinical features, termed the “PTEN-opathies.” Experimental models of PTEN pathway disruption uncover the molecular and cellular processes influencing clinical phenotypic manifestations. Such insights not only teach us about biological mechanisms in states of health and disease, but also enable more accurate gene-informed cancer risk assessment, medical management, and targeted therapeutics. Hence, the PTEN-opathies serve as a prototype for bedside to bench, and back to the bedside, practice of evidence-based precision medicine.

The tumor suppressor phosphatase and tensin homolog (PTEN) classically counteracts the PI3K/AKT/mTOR signaling cascade. Germline pathogenic PTEN mutations cause PTEN hamartoma tumor syndrome (PHTS), featuring various benign and malignant tumors, as well as neurodevelopmental disorders such as autism spectrum disorder. Germline and somatic mosaic mutations in genes encoding components of the PI3K/AKT/mTOR pathway downstream of PTEN predispose to syndromes with partially overlapping clinical features, termed the “PTEN-opathies.” Experimental models of PTEN pathway disruption uncover the molecular and cellular processes influencing clinical phenotypic manifestations. Such insights not only teach us about biological mechanisms in states of health and disease, but also enable more accurate gene-informed cancer risk assessment, medical management, and targeted therapeutics. Hence, the PTEN-opathies serve as a prototype for bedside to bench, and back to the bedside, practice of evidence-based precision medicine.

Conflict of Interest: The authors have declared that no conflict of interest exists.

Reference information: J Clin Invest. https://doi.org/10.1172/JCI121277.
The identification of germline PTEN mutations allowed for the comprehensive elucidation of component cancers and associated diagnostic criteria (31). Finally, somatic mutations in components of the PTEN signaling cascade occurring in postnatal somatic tissue can drive a vast array of sporadic cancers (32–35).

Overgrowth syndromes are important to diagnose, not only for timely disease management, but also because several of these conditions are associated with elevated risks of cancer. Here, we utilize the PTEN-opathies, particularly PHTS, as a model to examine how perturbation of the PTEN signaling pathway leads to a spectrum of heterogeneous clinical phenotypes. We discuss the genetic, functional, and mechanistic insights that put forth why some organs overgrow but never turn malignant while others develop malignancies. Importantly, the elucidation of the underlying mechanisms is of clinical importance since it promotes the implementation of evidence-based medical management and preventative and therapeutic approaches.

**PTEN dysfunction and cancer**

The identification of germline PTEN mutations allowed for the comprehensive elucidation of component cancers and associated

---

**Table 1. Germline mutation frequencies of PTEN pathway genes in the PTEN-opathies**

<table>
<thead>
<tr>
<th>Syndrome (OMIM)</th>
<th>Gene</th>
<th>Germline mutation frequency</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cowden syndrome, CS (158350)</td>
<td>PTEN</td>
<td>25%–85%</td>
<td>41, 60, 83</td>
</tr>
<tr>
<td></td>
<td>AKT1</td>
<td>2%</td>
<td>167</td>
</tr>
<tr>
<td></td>
<td>PIK3CA</td>
<td>9%</td>
<td>167</td>
</tr>
<tr>
<td>Bannayan-Riley-Ruvalcaba syndrome, BRRS (153480)</td>
<td>PTEN</td>
<td>60%</td>
<td>83, 84, 168, 169</td>
</tr>
<tr>
<td>Macrocephaly-autism spectrum disorder, macro-ASD (605309)</td>
<td>PTEN</td>
<td>10%–20%</td>
<td>71, 108–111</td>
</tr>
<tr>
<td>Proteus and Proteus-like syndromes, PS (176920)</td>
<td>PTEN</td>
<td>7%–67%</td>
<td>23–25, 44, 170</td>
</tr>
<tr>
<td>Megalencephaly-capillary malformation syndrome, MCAP (602501)</td>
<td>PIK3CA</td>
<td>8%</td>
<td>171</td>
</tr>
<tr>
<td>Megalencephaly-polygyria-polydactyly-hydrocephalus syndrome, MPPH (603387)</td>
<td>PIK3R2</td>
<td>Up to 41%</td>
<td>172</td>
</tr>
<tr>
<td></td>
<td>AKT3</td>
<td>Up to 29%</td>
<td>172</td>
</tr>
</tbody>
</table>
The Journal of Clinical Investigation

REVIEW SERIES: BIOLOGY OF FAMILIAL CANCER PREDISPOSITION SYNDROMES

3

lipid phosphatase activity only (4, 46, 47). Interestingly, several PTEN mutations retain partial or even complete catalytic activity (48), suggesting alternative mechanisms for compromised PTEN function. For example, catalytically active mutant PTEN p.Lys-289Glu is characterized by a nuclear import defect due to loss of monoubiquitination at p.Lys289 (49). Nuclear PTEN is thought to be protected from polyubiquitination and subsequent proteasome-mediated degradation in the cytoplasm; therefore, it is able to dampen AKT signaling and induce p53-independent apoptosis (49). In support of these observations, nuclear exclusion of PTEN has been associated with more aggressive, advanced-stage cancers (50–54). Relatedly, the N-terminal phosphatase domain contains two ATP-binding motifs, critical for regulating PTEN exit from the nucleus (55). Expectedly, ATP-binding motif mutants (e.g., p.Lys62Arg, p.Tyr65Cys, p.Lys125Glu) do not bind ATP efficiently, resulting in nuclear PTEN mislocalization. This subsequently leads to increased cellular proliferation, reduced/abrogated apoptosis, and increased anchorage-independent growth (56, 57).

PTEN has also been shown to be SUMOylated at Lys266 within the C2 domain, which facilitates PTEN binding to the plasma membrane through electrostatic interactions and subsequent suppression of PI3K/AKT signaling, both in vitro and in vivo (58). Additionally, germline PTEN mutations have been observed at Lys254 (Figure 3), a residue that is also SUMOylated to enhance PTEN nuclear import to then function in DNA repair (59). Therefore, mutations at Lys254 result in nuclear exclusion of PTEN and compromised DNA repair mechanisms.

Aside from intragenic mutations, approximately 10% of CS patients harbor germline PTEN promoter mutations (60). Patho-

lifetime risks (36). Three independent studies revealed elevated risks for breast, thyroid, endometrial, kidney, and colon cancers and melanoma in PHTS (36–38). Similarly to other hereditary cancer syndromes, the risk for bilateral and multifocal cancer is elevated (22). Relatedly, individuals with PHTS have a 7-fold increased risk of developing second malignant primary neoplasms (39). Collectively, these cancer risk assessment studies inform clinical surveillance recommendations and medical management of individuals with germline PTEN mutations (36), with the aim of detecting malignancies at the earliest, most manageable stages (Table 2).

PTEN comprises nine exons canonically encoding a 403–amino acid protein (1, 40). Broadly, PTEN mutations could impact the abundance of PTEN protein, resulting in haploinsufficiency; result in reduced or lost phosphatase activity; act in a dominant-negative manner; and/or result in aberrant localization and function (21). The germline mutation spectrum in PHTS is broad, with mutations affecting all nine exons of PTEN (refs. 36, 39, 41, 42, and Figure 3). Approximately two-thirds of germline PTEN mutations occur in exons 5, 7, and 8 (41). Interestingly, up to 40% of all germline PTEN mutations are located in exon 5, encoding the core catalytic motif, although this exon represents only 20% of the coding sequence (41, 43, 44). Relatedly, two distinct Alu elements have been reported in two unrelated CS patients with identical break points within exon 5, suggesting that this exon is a possible retrotransposition hotspot (45). Mutations within the core catalytic motif typically abrogate pan-phosphatase (lipid and protein) activity, such as mutations affecting p.Cys124, but rarely, mutations such as p.Gly129Glu result in abrogation of lipid phosphatase activity only (4, 46, 47). Interestingly, several PTEN mutations retain partial or even complete catalytic activity (48), suggesting alternative mechanisms for compromised PTEN function. For example, catalytically active mutant PTEN p.Lys-289Glu is characterized by a nuclear import defect due to loss of monoubiquitination at p.Lys289 (49). Nuclear PTEN is thought to be protected from polyubiquitination and subsequent proteasome-mediated degradation in the cytoplasm; therefore, it is able to dampen AKT signaling and induce p53-independent apoptosis (49). In support of these observations, nuclear exclusion of PTEN has been associated with more aggressive, advanced-stage cancers (50–54). Relatedly, the N-terminal phosphatase domain contains two ATP-binding motifs, critical for regulating PTEN exit from the nucleus (55). Expectedly, ATP-binding motif mutants (e.g., p.Lys62Arg, p.Tyr65Cys, p.Lys125Glu) do not bind ATP efficiently, resulting in nuclear PTEN mislocalization. This subsequently leads to increased cellular proliferation, reduced/abrogated apoptosis, and increased anchorage-independent growth (56, 57).

PTEN comprises nine exons canonically encoding a 403–amino acid protein (1, 40). Broadly, PTEN mutations could impact the abundance of PTEN protein, resulting in haploinsufficiency; result in reduced or lost phosphatase activity; act in a dominant-negative manner; and/or result in aberrant localization and function (21). The germline mutation spectrum in PHTS is broad, with mutations affecting all nine exons of PTEN (refs. 36, 39, 41, 42, and Figure 3). Approximately two-thirds of germline PTEN mutations occur in exons 5, 7, and 8 (41). Interestingly, up to 40% of all germline PTEN mutations are located in exon 5, encoding the core catalytic motif, although this exon represents only 20% of the coding sequence (41, 43, 44). Relatedly, two distinct Alu elements have been reported in two unrelated CS patients with identical break points within exon 5, suggesting that this exon is a possible retrotransposition hotspot (45). Mutations within the core catalytic motif typically abrogate pan-phosphatase (lipid and protein) activity, such as mutations affecting p.Cys124, but rarely, mutations such as p.Gly129Glu result in abrogation of lipid phosphatase activity only (4, 46, 47). Interestingly, several PTEN mutations retain partial or even complete catalytic activity (48), suggesting alternative mechanisms for compromised PTEN function. For example, catalytically active mutant PTEN p.Lys-289Glu is characterized by a nuclear import defect due to loss of monoubiquitination at p.Lys289 (49). Nuclear PTEN is thought to be protected from polyubiquitination and subsequent proteasome-mediated degradation in the cytoplasm; therefore, it is able to dampen AKT signaling and induce p53-independent apoptosis (49). In support of these observations, nuclear exclusion of PTEN has been associated with more aggressive, advanced-stage cancers (50–54). Relatedly, the N-terminal phosphatase domain contains two ATP-binding motifs, critical for regulating PTEN exit from the nucleus (55). Expectedly, ATP-binding motif mutants (e.g., p.Lys62Arg, p.Tyr65Cys, p.Lys125Glu) do not bind ATP efficiently, resulting in nuclear PTEN mislocalization. This subsequently leads to increased cellular proliferation, reduced/abrogated apoptosis, and increased anchorage-independent growth (56, 57).

PTEN comprises nine exons canonically encoding a 403–amino acid protein (1, 40). Broadly, PTEN mutations could impact the abundance of PTEN protein, resulting in haploinsufficiency; result in reduced or lost phosphatase activity; act in a dominant-negative manner; and/or result in aberrant localization and function (21). The germline mutation spectrum in PHTS is broad, with mutations affecting all nine exons of PTEN (refs. 36, 39, 41, 42, and Figure 3). Approximately two-thirds of germline PTEN mutations occur in exons 5, 7, and 8 (41). Interestingly, up to 40% of all germline PTEN mutations are located in exon 5, encoding the core catalytic motif, although this exon represents only 20% of the coding sequence (41, 43, 44). Relatedly, two distinct Alu elements have been reported in two unrelated CS patients with identical break points within exon 5, suggesting that this exon is a possible retrotransposition hotspot (45). Mutations within the core catalytic motif typically abrogate pan-phosphatase (lipid and protein) activity, such as mutations affecting p.Cys124, but rarely, mutations such as p.Gly129Glu result in abrogation of lipid phosphatase activity only (4, 46, 47). Interestingly, several PTEN mutations retain partial or even complete catalytic activity (48), suggesting alternative mechanisms for compromised PTEN function. For example, catalytically active mutant PTEN p.Lys-289Glu is characterized by a nuclear import defect due to loss of monoubiquitination at p.Lys289 (49). Nuclear PTEN is thought to be protected from polyubiquitination and subsequent proteasome-mediated degradation in the cytoplasm; therefore, it is able to dampen AKT signaling and induce p53-independent apoptosis (49). In support of these observations, nuclear exclusion of PTEN has been associated with more aggressive, advanced-stage cancers (50–54). Relatedly, the N-terminal phosphatase domain contains two ATP-binding motifs, critical for regulating PTEN exit from the nucleus (55). Expectedly, ATP-binding motif mutants (e.g., p.Lys62Arg, p.Tyr65Cys, p.Lys125Glu) do not bind ATP efficiently, resulting in nuclear PTEN mislocalization. This subsequently leads to increased cellular proliferation, reduced/abrogated apoptosis, and increased anchorage-independent growth (56, 57).

PTEN has also been shown to be SUMOylated at Lys266 within the C2 domain, which facilitates PTEN binding to the plasma membrane through electrostatic interactions and subsequent suppression of PI3K/AKT signaling, both in vitro and in vivo (58). Additionally, germline PTEN mutations have been observed at Lys254 (Figure 3), a residue that is also SUMOylated to enhance PTEN nuclear import to then function in DNA repair (59). Therefore, mutations at Lys254 result in nuclear exclusion of PTEN and compromised DNA repair mechanisms.

Figure 2. The classic PTEN pathway and associated PTEN-opathies. The PTEN-opathies encompass a spectrum of disorders with mutations within genes encoding proteins belonging to the PTEN pathway. PIK3CA-related overgrowth spectrum (PROS) includes distinct clinical entities with phenotypic overlap among the different syndromes. These overgrowth disorders are typically associated with postzygotic somatic mosaic PIK3CA mutations in affected tissues and are characterized by segmental overgrowth affecting the body (e.g., CLOVES syndrome, fibroadipose hyperplasia) or the brain (e.g., megalencephaly–capillary malformation syndrome [MCAP], hemimegalencephaly). PIK3CA encodes the catalytic p110α subunit protein of PI3K. Similarly to PTEN dysfunction, PIK3CA activation results in phosphorylation and activation of AKT, ultimately resulting in overgrowth-promoting downstream effects within the PI3K/AKT/mTOR signaling pathway downstream of PTEN. Expectedly, these syndromes show clinical phenotypic overlap with PHTS, including megalencephaly, vascular malformations, overgrowth, and neurocognitive deficits.
and can be detected in human serum and plasma. PTEN-L has also been shown to interact with canonical PTEN to regulate mitochondrial function and energy production (64). More recently, another N-terminal extended PTEN isoform, named PTEN\(\beta\), has been identified (65). PTEN\(\beta\) translation is initiated from an AUU codon upstream of the AUG initiation codon for canonical PTEN. This isoform specifically localizes in cell nucleoli, and regulates ribosomal DNA (rDNA) transcription and cellular proliferation. As these newly identified PTEN protein isoforms are characterized by distinct subcellular localizations and biological functions, further studies are warranted to better understand how these isoforms contribute to carcinogenesis. Importantly, since PTEN-L and PTEN\(\beta\) share the canonical PTEN sequence, mutations that impact canonical PTEN would be expected to impact these isoforms as well. However, mutations within the N-terminal extended regions of PTEN-L and PTEN\(\beta\) can have downstream effects independent of canonical PTEN. An intriguing hypothe-

<table>
<thead>
<tr>
<th>Component</th>
<th>Risk (SEER)</th>
<th>Lifetime Risk</th>
<th>Screening/Surgical Guidelines</th>
<th>Age to Start</th>
<th>Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>Breast (female)</td>
<td>12%</td>
<td>67%–85%</td>
<td>Breast awareness and self-exam: report changes to health care provider</td>
<td>18</td>
<td>Consistent</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Clinical breast exam</td>
<td>25(\delta)</td>
<td>Every 6–12 months</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Mammogram with consideration of tomosynthesis and breast MRI with contrast</td>
<td>30–35(\delta)</td>
<td>Every 12 months</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Discuss mastectomy</td>
<td>Personalized</td>
<td>As needed</td>
</tr>
<tr>
<td>Thyroid</td>
<td>1%</td>
<td>6%–38%</td>
<td>Thyroid ultrasound</td>
<td>Time of PHTS diagnosis, including childhood</td>
<td>Every 12 months</td>
</tr>
<tr>
<td>Kidney</td>
<td>1.6%</td>
<td>2%–34%</td>
<td>Consider renal ultrasound</td>
<td>40</td>
<td>Every 1–2 years</td>
</tr>
<tr>
<td>Endometrium</td>
<td>2.5%</td>
<td>21%–28%</td>
<td>Encourage patient education and prompt response to symptoms (e.g., abnormal bleeding)</td>
<td>Not applicable</td>
<td>Not applicable</td>
</tr>
<tr>
<td>Kidney</td>
<td>1.6%</td>
<td>2%–34%</td>
<td>Consider screening via endometrial biopsy</td>
<td>Not applicable</td>
<td>Every 1–2 years</td>
</tr>
<tr>
<td>Kidney</td>
<td>1.6%</td>
<td>2%–34%</td>
<td>Transvaginal ultrasound in postmenopausal women at the clinician’s discretion</td>
<td>Not applicable</td>
<td>As needed</td>
</tr>
<tr>
<td>Kidney</td>
<td>1.6%</td>
<td>2%–34%</td>
<td>Discuss hysterectomy with completion -of childbearing</td>
<td>Personalized</td>
<td>As needed</td>
</tr>
<tr>
<td>Colon</td>
<td>5%</td>
<td>9%–17%</td>
<td>Colonoscopy</td>
<td>35(\delta) unless symptomatic</td>
<td>Every 5 years or more frequently depending on whether patient is symptomatic or polyps are found</td>
</tr>
<tr>
<td>Dermatologic(\delta)</td>
<td>2%</td>
<td>2%–6%</td>
<td>Dermatologic exam</td>
<td>Personalized</td>
<td>Clinician’s recommendation</td>
</tr>
<tr>
<td>Developmental</td>
<td>NA</td>
<td>NA</td>
<td>Consider psychomotor assessment in children</td>
<td>Time of PHTS diagnosis</td>
<td>Clinician’s recommendation</td>
</tr>
<tr>
<td>Brain MRI if symptomatic</td>
<td>Time of PHTS diagnosis</td>
<td>Clinician’s recommendation</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

\(\delta\)Cancer lifetime risks calculated to age 70 by Tan et al. (36) and Bubien et al. (37), and to age 60 by Nieuwenhuis et al. (38). Cancer risk percentage ranges reflect lowest and highest frequencies reported in all three studies. \(\delta\)Annual comprehensive physical examination starting at age 18 years or 5 years before the youngest age of diagnosis of a component cancer in the family (whichever comes first), with particular attention to thyroid examination. Encourage patient education regarding the signs and symptoms of cancer. \(\delta\)Cancer screening should begin 5–10 years before the earliest known component cancer in the family or according to the ages listed in the table, whichever comes first. \(\delta\)Lifetime cancer risk estimates of skin cutaneous melanoma. SEER, surveillance, epidemiology, and end results; PHTS, PTEN hamartoma tumor syndrome. Adapted with permission from the NCCN Clinical Practice Guidelines in Oncology (NCCN Guidelines) for Genetic/Familial High-Risk Assessment: Breast and Ovarian V.1.2019.
sis is the tissue-specific expression of various PTEN protein isoforms, which could, in turn, predispose PHTS individuals to different phenotypes in a genotype-dependent manner. Indeed, the complex interplay among the PHTS family proteins could partly explain why a wide spectrum of clinical phenotypes are observed in the PTEN-opathies, with implications for the precise clinical management of these disorders.

PTEN dysfunction in PHTS offers important biological insights in the context of common sporadic cancers. Indeed, PTEN is one of the most frequently somatically mutated genes in cancer (66–68). The experimental data, in turn, offer insights regarding how germline PTEN mutations cause the clinical manifestations observed in PHTS. Cell survival, growth, apoptosis, migration, and genomic instability represent processes that influence cell fate and reflect overgrowth and cancer-related phenotypes. In time, it became evident that PTEN is also critical for normal development and physiology (11, 69). These findings help explain the occurrence of neurodevelopmental disorders such as megalencephaly, autism spectrum disorder (ASD), and developmental delay in individuals with PHTS (70–72). Importantly, germline PTEN mutations have been reported in previously undiagnosed individuals with isolated PHTS-related phenotypes, indicating that the syndrome is indeed undiagnosed (71, 73–79). Certainly, utilizing knowledge about PHTS pathogenesis aids in establishing a molecular diagnosis, itself critical both for understanding the pathomechanisms behind and for subsequent medical management of the observed phenotypes.

Finally, because it is technically challenging to functionally interrogate all germline and somatic PTEN mutations, research efforts have focused on devising high-throughput methods to evaluate pathogenicity. Surprisingly, several residues within the catalytic pocket are shown to be tolerant to mutations, with solvent exposure playing a critical role in dictating tolerance (80). Moreover, several uncharacterized PTEN variants result in decreased PTEN thermodynamic stability and abundance, thus expanding the list of potentially functional variants (81). Collectively, such efforts foster evidence-based, functionally relevant classification of PTEN mutations into more clinically actionable categories. Predictably, meta-analysis of outputs coupled with clinical phenotypic correlations will likely yield more robust classifications. Such analyses culminated in a recently completed effort through ClinGen’s PTEN Variant Curation Expert Panel (82).

**Genotype-phenotype correlations and modifiers of cancer risks**

As with other inherited cancer syndromes, while it is possible to risk-assess increased organ-specific cancer probabilities, it is still impossible to predict at an individual level who will go on to develop any particular component cancer during his or her lifetime. Hence, multiple studies have attempted to find predictive PTEN genotype-

---

**Figure 3. PTEN structure and germline mutation spectrum in PHTS.** (A) PTEN germline mutation spectrum from 431 PHTS patients. PTEN is canonically a 403–amino acid protein. Different types of mutations are depicted in the lollipop plot overlaying the PTEN protein structure. The frequency of mutations correlates with the heights of the vertical lines representing each lollipop. PTEN comprises a PIP2-binding domain (PBD), a phosphatase domain, a C2 domain, and a C-terminal tail including a PDZ-binding domain. The active site is included within amino acid residues 123 and 130. (B) PTEN consists of 9 exons that encode the 403–amino acid protein. The exons are overlaid to match the protein domains in A. Intronic regions are not represented. The colored bars represent large deletions (abbreviated as del) and duplications (abbreviated as dup) annotated by affected exon numbers and the number of affected patients in parentheses. Figure adapted with permission from ref. 174.
it is predicted that PTEN phosphatase activity is retained in individuals with ASD, versus malian stable or primary cell lines, partial hypomorphic PTEN lipid higher PTEN activity relative to non–ASD-associated mutations studies have shown that ASD-associated mutations tend to retain ing and indeed provide an important dimension to consider for assess-
ting contribution to partial opening of the active site (88). Such effects cannot be extrapolated from PTEN’s secondary structure alone and indeed provide an important dimension to consider for assessing PTEN genotype–PHTS phenotype associations. Additionally, studies have shown that ASD-associated mutations tend to retain higher PTEN activity relative to non–ASD-associated mutations (80, 89, 90). Whether assayed in vivo in yeast or in vitro in mammalian stable or primary cell lines, partial hypomorphic PTEN lipid phosphatase activity is retained in individuals with ASD, versus total loss of PTEN lipid phosphatase activity in individuals with more severe PHTS-related phenotypes (80, 89–91). Relatedly, it is predicted that PTEN mutations that result in the accumulation of stable inactive PTEN protein would lead to more severe PHTS-related developmental phenotypes and malignancies (90). Finally, imbalances in PTEN subcellular localization could impact PHTS phenotypic manifestations. A murine model of germline-mislocalized cytoplasm-predominant PTEN exhibits macrocephaly and a neurocognitive profile reminiscent of high-functioning ASD (92, 93). Intriguingly, germline-mislocalized nuclear-predominant PTEN can exist in patients with either cancer or ASD (57, 94). In this context, it is tempting to speculate whether mutant nuclear PTEN plays distinct roles in the affected tissues related to the latter disparate phenotypes.

The lack of absolute PTEN genotype-phenotype correlations suggests that additional factors act as phenotypic modifiers in PHTS. A proof-of-principle study showed that approximately 6% of PTEN mutation–positive CS/CS-like individuals also harbor germline variants in genes encoding three of the four subunits of mitochondrial complex II (SDHB, SDHC, SDHD), which were originally discovered as alternative susceptibility genes in PHTS. Subsequent studies showed that SDHD p.G12S and p.H50R variants directly lead to impaired PTEN subcellular localization and function through SRC-induced oxidation, accompanied by apoptosis resistance and induction of cellular migration (97). Importantly, the selective SRC inhibitor bosutinib could rescue these tumorigenic phenotypes only when wild-type PTEN was present. Similarly, SDHD p.G12S and p.H50R variants result in reduced autophagy in a PTEN-dependent manner (98).

From a clinical perspective, these data provide mechanistic insights that could explain the increased prevalence of thyroid cancer in CS patients with SDHx variants alone compared with those with PTEN mutations alone, as well as the seemingly paradoxical decreased prevalence of thyroid cancer in the setting of coexisting PTEN mutations and SDHx variants.

A hypothesis-generating pilot study further identified microbiomic differences in fecal samples derived from PTEN mutation–positive patients with and without PHTS component cancers (99). Functional metagenomic analysis revealed enrichment of cancer-relevant biological processes such as folate biosynthesis, genetic information processing, and cell growth/death pathways in fecal samples from PHTS cancer patients compared with those without a cancer diagnosis. These data suggest that gut dysbiosis could also play a role as a cancer risk modifier in PHTS patients. Conceivably, with increased sample sizes and independent replication, we suspect that novel associations will be discovered and expanded beyond cancer, toward phenotypes such as ASD and non-neoplastic overgrowth. Collectively, this knowledge will be impactful for more tailored medical management of PHTS patients.

**Germline predisposition – overgrowth versus cancer**

The discovery of PTEN as the Cowden syndrome gene paved the way for understanding how its disruption contributes to disease etiology (1, 3, 4). Functional characterization further established PTEN as a bona fide tumor suppressor gene (Figure 1). Studies in *Drosophila* and mouse models have shown that PTEN and downstream PI3K/AKT/TOR signaling play a central role in regulating cell number and size. Hence, dysfunction of this pathway recapitulates the growth anomalies observed in the PTEN-related human diseases. *Drosophila* PTEN has been shown to regulate cell number and size when mutated, leading to hyperplastic overgrowth in fruit fly mutant tissue (100). Similarly to mammalian signaling pathways, *Drosophila* PTEN regulates growth by antagonizing DDP110 (the *Drosophila* homolog of PI3K), and by acting as a negative regulator of insulin receptor signaling (101–103). With this knowledge of the basic mechanistic principles, what remains elusive, however, is the ability to identify factors that regulate progression from overgrowth to malignancy in a defined set of organs.
The most obvious explanation for organ-specific cancer development could be that the expression of the cancer-related gene, here PTEN, could be limited to the tissues in which malignancies arise. However, PTEN is ubiquitously expressed in all three germ cell layers throughout development, supporting the occurrence of hamartomatous overgrowths and variable multisystem phenotypes in individuals with germline PTEN mutations (11, 69, 104, 105). Homozygous Pten-knockout mice die before birth, further supporting a critical role for PTEN in embryogenesis (11, 105–107). High-level PTEN expression has also been reported during human development in tissues known to be associated with PHTS (104). However, this does not corroborate the tendency of these organs to develop malignancies when PTEN malfunctions. For example, the strongest PTEN protein levels are observed throughout the central and peripheral nervous systems (104), even though brain cancer is not a PHTS component cancer. Nevertheless, neurodevelopmental phenotypes are observed in PHTS, including macrocephaly (about 94% of patients), ASD (108–111), and Lhermitte-Duclos disease (LDD), a pathognomonic hamartomatous overgrowth of the cerebellum (112). Immunohistochemical studies show decreased or absent PTEN expression accompanied by elevated p-AKT in the affected LDD dysplastic gangliocytoma cells (113). Interestingly, murine studies have found that even a subtle reduction in PTEN causes increased tumorigenesis in a tissue-specific manner (114). In humans, reduced PTEN protein dose in CS-derived lymphoblastoid cell lines tends to occur in conjunction with an underlying germline PTEN mutation and to correlate with increasing clinical phenotypic burden (41). Further investigation in CS/CS-like patients with thyroid cancer reveals that low PTEN protein levels from blood-derived lymphoblastoid cells can predict for the presence of a germline PTEN mutation (115). Importantly, low blood PTEN levels correlate with weak or absent PTEN staining in the affected PHTS-derived thyroid tissues. Hence, one possibility is that variable tissue-specific thresh-

### Table 3. Preclinical studies, case reports, and clinical trials using PI3K/AKT/mTOR inhibitors for the treatment of the PTEN-opathies

<table>
<thead>
<tr>
<th>Drug target</th>
<th>Drug</th>
<th>Indication (reference)</th>
<th>Treatments and reported outcomes</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Preclinical studies of patient-derived cells</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>PI3K</td>
<td>Wortmannin, LY294002</td>
<td>PI3CA-related overgrowth spectrum, PROS (173)</td>
<td>Decreased proliferation of primary dermal fibroblasts from skin biopsies of overgrowth lesions and decreased phosphorylation of AKT and p70S6K</td>
</tr>
<tr>
<td>Pan-AKT</td>
<td>ARQ 092</td>
<td>AKT1-related Proteus syndrome (136)</td>
<td>Suppression of AKT and downstream signaling in patient-derived cells and tissues mosaic for the AKT1 somatic gain-of-function p.Glu17Lys mutation</td>
</tr>
<tr>
<td></td>
<td></td>
<td>PROS (137)</td>
<td>Decreased proliferation of primary fibroblasts with PI3CA mutations, decreased phosphorylation of AKT and downstream targets, less cytotoxicity in comparison with rapamycin and wortmannin</td>
</tr>
<tr>
<td><strong>Case reports</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>mTORC1</td>
<td>Sirolimus (rapamycin)</td>
<td>PTEN-related Proteus syndrome (125)</td>
<td>Dose: 0.1 mg/kg/d, divided into 2 doses. Duration: 17+ months. Outcomes: resolution of respiratory and nutritional complications, reduction in soft-tissue masses, reduction in the size of mesenteric lymph nodes, minimal effect on the size or appearance of external subcutaneous lipomata.</td>
</tr>
<tr>
<td></td>
<td>Bannayan-Riley-Ruvalcaba syndrome (126)</td>
<td>Dose: 0.8 mg/m²/dose, twice daily. Duration: 12 months. Outcome: decreased size of the vascular mass.</td>
<td></td>
</tr>
<tr>
<td></td>
<td>PTEN hamartoma tumor syndrome, PHTS (127)</td>
<td>Dose: 0.1 mg/kg/d. Duration: 19 months. Outcomes: transient improvement of somatic growth and reduced thymus volume, absence of clinical benefit.</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Infantile Lhermitte-Duclos disease (128)</td>
<td>Dose: 0.6 mg/kg/d. Duration: 12 months. Outcomes: decreased episodes of decerebrate posturing, regaining of normal appearance of the pituitary stalk, less compression of the brainstem.</td>
<td></td>
</tr>
<tr>
<td>PI3K</td>
<td>BYL719 (p110α)</td>
<td>PROS (138)</td>
<td>Dose: 50–250 mg/d. Duration: 6–18 months. Outcomes: patient-dependent with general improvement of overgrowth; decrease in size of vascular tumors, reduction of hemihypertrophy, attenuation of scoliosis.</td>
</tr>
<tr>
<td><strong>Clinical trials</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>mTORC1</td>
<td>Sirolimus</td>
<td>PHTS/Cowden syndrome, CS</td>
<td>Phase II clinical trial completed and results forthcoming (NCT00971789)</td>
</tr>
<tr>
<td></td>
<td>Everolimus</td>
<td>PHTS with neurocognitive deficits</td>
<td>Phase I/II clinical trial currently recruiting (NCT02991807)</td>
</tr>
<tr>
<td>PI3K/mTOR</td>
<td>BGT226</td>
<td>CS patients with advanced solid malignancies</td>
<td>Phase II clinical trial completed and results forthcoming (NCT00600275)</td>
</tr>
<tr>
<td></td>
<td>BEZ235</td>
<td></td>
<td>Phase I/II clinical trial completed and results forthcoming (NCT00620594)</td>
</tr>
<tr>
<td>Pan-AKT</td>
<td>ARQ 092</td>
<td>Patients with overgrowth diseases and/or vascular anomalies</td>
<td>Phase I/II clinical trial currently recruiting (NCT03094832)</td>
</tr>
</tbody>
</table>
Intriguingly, despite the fact that germline PTEN mutations result in component cancers within a restricted set of organs (36), PTEN somatic driver mutations are enriched in multiple sporadic cancer types that are not components of the PHTS spectrum, including prostate cancer, glioblastoma multiforme, and others (1). Moreover, identical germline PTEN mutations often result in apparently disparate phenotypes (e.g., cancer versus non-malignant overgrowths), including in an intrafamilial manner (116). These observations suggest that additional factors act as overgrowth versus cancer phenotypic modifiers in PHTS. Indeed, while germline PTEN mutations predispose PHTS patients to cancer, it is the landscape of acquired somatic alterations that likely governs cancer initiation and progression. Hence, although the germline PTEN mutations affect all cells of PHTS patients, the tissue-restricted pattern of particular modifying factors could explain the nonrandom progression to malignancy in specific organs. Additionally, the type of germline PTEN mutation could also influence eventual cell fates. For example, germline PTEN mutations such as C-terminal deletions that result in genomic instability could prime tissues that are particularly sensitive to DNA damage for progression to malignancy (117). Finally, the immune system has been recognized as a major determinant of cancer development (118–120). PTEN loss promotes resistance to tumor immune cell infiltration through the production of inhibitory cytokines, hence resulting in immune escape (121). Interestingly, pregnant mice treated with low-dose lipopolysaccharide to induce maternal inflammation produce offspring with brain overgrowth (122). This phenotype is more pronounced in Pten-heterozygous mice compared with wild type, indicating evident crosstalk between genetic susceptibility and the inflamed microenvironment mediated through ROS signaling. Importantly, ROS cause oxidation and subsequent inactivation of PTEN, a mechanism observed in a subset of CS/CS-like patients (97,123). Hence, the manifestation of a cancer phenotype does represent a complex interplay among predisposing factors, genetic and epigenetic confounders, tissue-specific signaling networks, oncogenic signaling pathways, and microenvironmental context (124).

Molecularly targeted therapeutics

Altered PI3K/AKT/mTOR signaling in the PTEN-opathies implies that PI3K, AKT, and mTOR are germane targets for therapeutic intervention (Table 3). Proof-of-principle case reports demonstrate the use of the mTORC1 inhibitor sirolimus (rapamycin) to alleviate the symptoms and overgrowth manifestations of individuals with PHTS (125–128). Indeed, sirolimus has been used in a phase II open-label clinical trial in individuals with PHTS. Additionally, a double-blind drug-placebo, crossover trial with the mTORC1 inhibitor everolimus is currently accruing PHTS patients with ASD (22). Notably, mTORC1 inhibitors have been used in patients with tuberous sclerosis complex (TSC) (129–132) and Peutz-Jeghers syndrome (PJS) (133). TSC1/2 and STK11/LKB1, the susceptibility genes for TSC and PJS, respectively, are not only upstream of mTOR (9,134) but are also downstream of PTEN signaling (135).

In addition to mTORC1 inhibition, upstream components of the PTEN signaling pathway, such as PI3K and AKT, also serve as candidates for pharmacologic inhibition in the PTEN-opathies (Table 3). As such, AKT and PIK3CA inhibitors have been used in PS and PIK3CA-related overgrowth spectrum (PROS) disorders (136–138). PIK3CA encodes the p110a catalytic subunit protein of PI3K. Preclinical studies using the allosteric pan-AKT inhibitor ARQ 092 revealed suppression of AKT and downstream signaling in cells and tissues from PS patients, mosaic for the AKT1 somatic gain-of-function p.Glu17Lys mutation (136). ARQ 092 treatment of primary fibroblast cells from PROS patients also showed promising results; compared with sirolimus and the PI3K inhibitor wortmannin, ARQ 092 resulted in higher antiproliferative activity and lower cytotoxicity, at least in vitro (137). Relatedly, a recent proof-of-principle study demonstrated the successful usage of the PIK3CA inhibitor BYL719 (alpelisib) in a preclinical murine model of PROS and subsequently for the treatment of 19 patients with severe PROS disorders (138). Importantly, in these PTEN-opathies, all patients harbored somatic mutations; the ultimate goal from treatment is to continuously reduce progrowth signals in affected tissues with minimal toxicity toward normal wild-type cells. However, this becomes more challenging in the germline context, such as PHTS, where a high therapeutic index becomes even more critical since all cells harbor the underlying PTEN mutation. Moreover, constitutional PTEN pathway dysfunction would theoretically necessitate some type of chronic treatment regimen. However, lifelong mTOR and PIK3CA inhibition might not be feasible because of immunosuppressive effects, disruption of systemic glucose homeostasis, and the critical role the PTEN pathway plays in normal tissue and organ development (11,69,139,140). Although isolated case reports and studies (125, 126, 128, 138) show promise for the therapeutic management of the PTEN-opathies, longitudinal studies are necessary to evaluate long-term safety and efficacy.

Another major caveat to molecular targeting of the PI3K/AKT/mTOR pathway is feedback activation of collateral oncogenic signaling pathways, causing resistance. This led to the investigation of combinatorial therapies that would, in theory, effectively target the growth-promoting signals without loss of feedback controls. Indeed, inhibiting mTORC1 has been shown to result in feedback activation of upstream signaling components such as AKT through insulin receptor substrate 1 (IRS1) or through direct phosphorylation at Ser473 by mTORC2 (141). However, experimental studies show promise in that the rebound upregulation of AKT during mTORC1 inhibition can be abrogated by pre-treatment or cotreatment with resveratrol, at least in vitro (142). Moreover, PI3K inhibition can result in therapeutic resistance in PIK3CA-mutant cell lines due to a rebound insulin-dependent feedback mechanism (140), or failure to suppress CDK4/6 as evidenced through persistent RB phosphorylation (143). In these contexts, the combination of various PI3K inhibitors with anti-glycemic therapies or CDK4/6 inhibitors, respectively, results in the attenuation of the progrowth feedback signaling cascades, hence overcoming resistance. Interestingly, NVP-BEZ235, a dual PI3K/mTOR inhibitor, has been shown to selectively inhibit the growth of a subset of androgen receptor–positive (AR+) breast cancer cell lines (144). AR is positively correlated with PTEN expression in breast cancer, owing to direct PTEN transcription that is mediated by an androgen response element in the PTEN promoter.
Mechanistically, the beneficial effect of AR activation in combination with PI3K/AKT/mTOR inhibition in AR+/ER+ breast cancers can be explained, at least partially, through PTEN upregulation and MYC suppression (144). Interestingly, the converse phenomenon has been extensively studied in prostate cancer and has been shown to be context-dependent (147-149). As such, PTEN-deficient prostate cancer cells have decreased AR transcription, and PI3K pathway inhibition activates AR signaling by alleviating the feedback inhibition on HER2/3 kinases (148). Therefore, the crosstalk between PTEN and AR signaling will likely be genotype- and context-dependent.

Although most therapeutic strategies are aimed at attenuating downstream oncogenic signaling consequent to PTEN dysfunction, strategies to enhance PTEN levels and/or activity represent promising therapeutic modalities. This is particularly pertinent for the cell-permeable PTEN-L (63) that would theoretically allow the restoration of PTEN levels in the context of PTEN haploinsufficiency. Moreover, PTEN expression and/or activity could also be enhanced through modulating negative and positive regulators of PTEN (e.g., transcription factors, miRNAs, protein ubiquitination machinery, etc.). Certainly, these approaches are context-dependent with respect to baseline endogenous PTEN levels and activity, tissue specificity, and the requisite of establishing long-term effects, among many other factors. Importantly, restoring wild-type PTEN in the context of a stable mutant PTEN protein could worsen the condition owing to dominant-negative effects (150). Another plausible approach is through gene editing of mutant PTEN alleles to restore or even enhance PTEN function (e.g., increased phosphatase activity or recruitment to the plasma membrane) (151). While gene editing poses many challenges, including off-target effects and activation of adaptive immune responses (152, 153), recent advances show promise in mitigating these outcomes (154-156). Undoubtedly, gene editing will be exceptionally challenging in the germline setting where the whole organism is targeted for editing.

Finally, given the broad spectrum and diverse functional consequences of germline PTEN mutations, targeting the PI3K/AKT/mTOR signaling pathway may not be effective in all contexts, e.g., when disease-associated PTEN mutations impact lipid phosphatase–independent functions. One possible approach could be to target the vulnerabilities caused by patient-specific germline PTEN mutations. For example, because PTEN plays a vital role in maintaining genomic integrity in the nucleus, it is possible to therapeutically use PARP inhibitors (157). Moreover, patients with germline PTEN mutations within the C-terminal region could benefit from proteasome inhibitors to mitigate PTEN degradation (158). Indeed, treatment with the proteasome inhibitor MG-132 can restore both nonsense and missense mutant PTEN protein levels in vitro (159). However, restoring missense mutant PTEN levels in the presence of the wild-type allele can also result in dominant-negative effects, and could worsen the condition (150). Predictably, in the era of precision medicine, cancer prevention is key and determining context-specific therapeutic indices will be vital for the effective management of the PTEN-opathies.

**Immunotherapy**

The PI3K/AKT/mTOR pathway is an important regulator of immunity (160, 161). Since PTEN is a master regulator of this pathway, it is therefore not surprising that PTEN disruption can result in immune dysregulation. The latter is germane in carcinogenesis, whereby immune surveillance, evasion of immune recognition, and a chronically inflamed microenvironment represent major immune hallmarks of cancer (118). Additionally, PI3K/AKT/mTOR pathway activation has been shown to modulate responses to immunotherapy. Loss of PTEN in the sporadic context has been associated with resistance to anti–PD-1 therapy in melanoma (121), a CS component cancer, and more recently in a case study of metastatic uterine leiomyosarcoma (162). Interestingly, activation of the PI3K/AKT/mTOR pathway has been shown to drive expression of PD-1/PD-L1 in a subset of solid tumors, causing immunoresistance (163-165). Indeed, because PTEN seems to be a major immunotherapeutic response predictor, multiple questions arise regarding the promising utility of immunotherapeutic agents in individuals with germline PTEN mutations and cancer. Studies have shown that a subset of individuals with PHTS have autoimmune phenotypes as well as B and T cell–related immune dysfunctions (161, 166). Importantly, reduction in peripheral lymphocyte numbers in comparison with control subjects, including decreased CD4+ cell numbers and hence absolute FOXP3+ Treg numbers, would suggest that these individuals will have a different response to immunotherapy compared with individuals with normal immune systems.

**Perspective**

The PTEN-opathies represent a paradigm whereby one pathway appears etiologic for a wide spectrum of clinically distinct phenotypes. The recognition and characterization of the PTEN-opathies allow for significant advances in understanding how clinical phenotypic manifestations result from underlying molecular and cellular processes to then guide risk assessment, therapeutics, and preventative strategies. Preclinical studies and clinical trials show promise for the treatment of a subset of the PTEN-opathies. However, this becomes more complex in the germline context, where a high therapeutic index is mandatory, yet exceptionally challenging. Indeed, individuals with germline PTEN mutations have a lifelong predisposition to PHTS-related signs and symptoms, necessitating prolonged treatments that could impact normal growth and development and cause nontargeted cytotoxicity. One of the most serious complications of the PTEN-opathies, particularly PHTS, is the increased lifetime risk for cancer. Although PTEN-enabled organ-specific cancer risk estimates and management guidelines are part of the routine clinical armamentarium of precision care, it remains virtually impossible to absolutely predict which individual (versus a probability) will develop which component malignancy. Nonmalignant component phenotypes of PHTS, such as ASD and severe vascular malformations, can be chronically debilitating and affect quality of life for patients and their families. Intriguingly, identical germline PTEN mutations are observed in patients with these seemingly disparate phenotypes (e.g., cancer versus ASD), indicating that additional factors may act as phenotypic modifiers in PHTS. Hence, future studies elucidating absolute modifiers of disease manifestations and associated signaling networks will be key to define more precise and effective preventative and therapeutic strategies for the individual at risk.
Acknowledgments
We are grateful to our patients and families who have participated in our research studies for over two decades. We are also grateful for our funding sources, including the National Cancer Institute (P01CA124570 and R01CA118989), American Cancer Society (RPG-02-151-01-CCCE and Clinical Research Professorship), the National Institute of Neurological Disorders and Stroke (U54NS092090), Breast Cancer Research Foundation, Doris Duke Distinguished Clinical Scientist Award and the Zaccconi Center of PTEN Research Excellence (all to CE). LY is an Ambrose Monell Foundation Cancer Genomic Medicine Fellow at the Cleveland Clinic Genomic Medicine Institute. CE is the Sondra J. and Stephen R. Hardis Chair of Cancer Genomic Medicine at the Cleveland Clinic and an American Cancer Society Clinical Research Professor.

Address correspondence to: Charis Eng, Cleveland Clinic Genomic Medicine Institute, 9500 Euclid Avenue NE50, Cleveland, Ohio 44195, USA. Phone: 216.444.3440; Email: engc@ccf.org.


83. Nilsson E, et al. Neural transcriptome of constitu-


