Clinical features:
Hyperparathyroidism is caused by overactivity of one or more of four parathyroid glands in the body. This increase in parathyroid activity leads to increased levels of parathyroid hormone (PTH) in the bloodstream, which results in abnormal calcium levels in the blood and organs. Primary hyperparathyroidism is caused by enlargement of one of the parathyroid glands, which results in overproduction of PTH and hypercalcemia. Individuals with primary hyperparathyroidism are typically treated with surgery. Patients who have hyperparathyroidism due to another underlying condition are said to have secondary hyperparathyroidism. These individuals initially have low levels of calcium in the body, and over time an increase in PTH is seen. Common presenting symptoms of patients with hyperparathyroidism are skeletal abnormalities/fragility and kidney stones. Hyperparathyroidism can also affect organs other than the skeleton and kidneys. Neuromuscular, gastrointestinal, cardiovascular, and psychiatric abnormalities have all been noted in patients with primary hyperparathyroidism (1).

Our Hyperparathyroidism Sequencing Panel includes the 8 genes listed below:

| Hyperparathyroidism Sequencing Panel |
|-----------------|-----------------|-----------------|
| AP2S1            | CDC73           | GNA11           |
|                 |                  | PTH1R           |
| CASR            | CDKN1B          | MEN1            |
|                 |                  | RET             |

Molecular genetics:
Heterozygous mutations in CASR, GNA11 and AP2S1 are associated with familial hypocalciuric hypercalcemia (FHH) types 1, 2, and 3, respectively. This condition is similar to primary hyperparathyroidism in presentation, but is not correctable by surgery. FHH type 1, caused by loss-of-function mutations in the CASR gene, is the most common form of this condition. Mutations in GNA11 and AP2S1 are less common, but mutations in AP2S1 have been reported to more severely affect calcium homeostasis when compared to individuals with CASR mutations (2). Homozygous inactivating mutations in the CASR gene cause a severe form of neonatal hyperparathyroidism. This form of hyperparathyroidism typically manifests within the first 6 months of life with severe hypercalcemia, bone demineralization and failure to thrive. Parathyroidectomy can be considered for these patients, based on the severity of their symptoms. Dominant CASR mutations have been reported in a small number of patients with neonatal hyperparathyroidism (3).

Multiple endocrine neoplasia (MEN) types 1, 2A, and 4 are caused by heterozygous mutations in MEN1, RET, and CDKN1B, respectively. The most common presenting feature in patients with MEN1 is primary hyperparathyroidism, which affects nearly 100% of affected individuals by age 50. Tumors of the parathyroid, pancreatic islets, duodenal endocrine cells, and the pituitary gland are common, with a 94% penetrance by age 50. Patients with MEN1 are at risk for a range of other tumors throughout the body, which are, with the exception of gastrinomas, non-metastasizing (4). Multiple endocrine neoplasia type 4 includes patients with a MEN1-like phenotype caused by dominant mutations in the CDKN1B gene. Studies have indicated that approximately 3% of individuals with MEN1-associated tumors carry heterozygous CDKN1B mutations. (5).

MEN2A is caused by heterozygous mutations in the RET gene. Patients with MEN2A have a 100% of developing medullary thyroid carcinoma (MTC) by age 70; the presence of MTC is the defining characteristic of MEN2A. Pheochromocytomas are present in 50% of affected patients, and 15-30% develop primary hyperparathyroidism (HPT). HPT in patients with MEN2A is typically mild, and may range from a single adenoma to marked hyperplasia (6).

Heterozygous mutations in CDC73 gene (also known as HRPT2) are associated with a range of parathyroid abnormalities including familial isolated hyperparathyroidism, hyperparathyroid-jaw tumor syndrome and sporadic parathyroid carcinoma. Studies suggest that up to 7% of individuals with familial isolated hyperparathyroidism have heterozygous pathogenic variants in CDC73. A distinct syndrome known as hyperparathyroid-jaw tumor...
syndrome (HPT-JT) is characterized by primary hyperparathyroidism, typically caused by a single parathyroid adenoma or parathyroid carcinoma. Ossified fibrous tumors of the jaw are present in 30-40% of patients with HPT-JT syndrome. Kidney lesions and uterine rumors are also more common in individuals with CDC73-related HPT-JT syndrome.

Heterozygous mutations in \textit{PTH1R} are associated with Murk Jansen type metaphyseal chondrodysplasia. This condition is characterized by severe short stature with bowed limbs, clinodactyly, prominent upper face and small mandible. Patients with this condition have normal or undetectable levels of parathyroid hormone. However, laboratory findings are very similar to hyperparathyroidism, and include: hypercalcemia, hypophosphatemia and increased renal excretion of phosphate, cAMP and hydroxyproline (8-10). Most cases of \textit{PTH1R}-related Jansen metaphyseal dysplasia are de novo; however, familial cases of the condition have been reported (11).

**Test methods:**
Comprehensive sequence coverage of the coding regions and splice junctions of all genes in this panel is performed. Targets of interests are enriched and prepared for sequencing using the Agilent SureSelect system. Sequencing is performed using Illumina technology and reads are aligned to the reference sequence. Variants are identified and evaluated using a custom collection of bioinformatic tools and comprehensively interpreted by our team of directors and genetic counselors. All pathogenic and likely pathogenic variants are confirmed by Sanger sequencing. The technical sensitivity of this test is estimated to be >99% for single nucleotide changes and insertions and deletions of less than 20 bp. Deletion/duplication analysis of the panel genes is performed by oligonucleotide array-CGH. Partial exonic copy number changes and rearrangements of less than 400 bp may not be detected by array-CGH. Array-CGH will not detect low-level mosaicism, balanced translocations, inversions, or point mutations that may be responsible for the clinical phenotype. The sensitivity of this assay may be reduced when DNA is extracted by an outside laboratory.

**Hyperparathyroidism Sequencing Panel (sequence analysis of 8 genes)**

<table>
<thead>
<tr>
<th>Sample specifications:</th>
<th>3 to10 cc of blood in a purple top (EDTA) tube</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cost:</td>
<td>$2500</td>
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<tr>
<td>CPT codes:</td>
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<tr>
<td>Turn-around time:</td>
<td>4 weeks</td>
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*Note: We cannot bill insurance for the above test.*

**Results:**
Results, along with an interpretive report, will be faxed to the referring physician. Additional reports will be provided as requested. All abnormal results will be reported by telephone.

For more information about our testing options, please visit our website at dnatesting.uchicago.edu or contact us at 773-834-0555.

**References:**


Committed to CUSTOMIZED DIAGNOSTICS, TRANSLATIONAL RESEARCH & YOUR PATIENTS’ NEEDS