MAYO CLINIC LABORATORIES

Test Definition: PRKSG

PRKAR1A Full Gene Sequencing with Deletion/Duplication, Varies

Overview

Useful For

Providing a genetic evaluation for patients with a personal or family history suggestive of Carney Complex (CNC) or acrodysostosis-1 with hormone resistance

Establishing a diagnosis of CNC or acrodysostosis-1 with hormone resistance

Genetics Test Information

This test utilizes next-generation sequencing to detect single nucleotide and copy number variants in one gene associated with Carney Complex (CNC): *PRKAR1A.* See Method Description for additional details.

Identification of a disease-causing variant may assist with diagnosis, prognosis, clinical management, familial screening, and genetic counseling for CNC.

Prior Authorization is available for this assay.

Special Instructions

- Informed Consent for Genetic Testing
- Blood Spot Collection Card-Spanish Instructions
- Blood Spot Collection Card-Chinese Instructions
- Informed Consent for Genetic Testing (Spanish)
- PRKAR1A-Related Disorders Patient Information
- Blood Spot Collection Instructions
- PRKAR1A Full Gene Analysis (PRKSG) Prior Authorization Ordering Instructions

Method Name

Sequence Capture and Targeted Next-Generation Sequencing followed by Polymerase Chain Reaction (PCR) and Sanger Sequencing

NY State Available

Yes

Specimen

Specimen Type

Varies

Ordering Guidance

Testing for the *PRKAR1A* gene as part of a customized panel is available. For more information CGPH / Custom Gene

Panel, Hereditary, Next-Generation Sequencing, Varies.

Targeted testing for familial variants (also called site-specific or known mutations testing) is available for variants identified in the *PRKAR1A* gene. See FMTT / Familial Mutation, Targeted Testing, Varies. To obtain more information about this testing option, call 800-533-1710.

Shipping Instructions

Specimen preferred to arrive within 96 hours of collection.

Necessary Information

Prior Authorization is available for this test. **Submit the required form with the specimen.**

Specimen Required

Patient Preparation: A previous bone marrow transplant from an allogenic donor will interfere with testing. Call 800-533-1710 for instructions for testing patients who have received a bone marrow transplant.
Specimen Type: Whole blood
Container/Tube:
Preferred: Lavender top (EDTA) or yellow top (ACD)
Acceptable: Any anticoagulant
Specimen Volume: 3 mL
Collection Instructions:
1. Invert several times to mix blood.
2. Send whole blood specimen in original tube. **Do not aliquot.**
Specimen Stability Information: Ambient (preferred)/Refrigerated

Forms

1. **New York Clients-Informed consent is required.** Document on the request form or electronic order that a copy is on file. The following documents are available:
-Informed Consent for Genetic Testing (T576)
-Informed Consent for Genetic Testing (Spanish) (T826)
2. PRKAR1A-Related Disorders Patient Information (T820)
3. PRKAR1A Full Gene Analysis (PRKSG) Prior Authorization Ordering Instructions

Specimen Minimum Volume

1 mL

Reject Due To

All specimens will be evaluated at Mayo Clinic Laboratories for test suitability.

Specimen Stability Information

Specimen Type	Temperature	Time	Special Container
Varies	Varies		

Clinical & Interpretive

Clinical Information

Carney complex (CNC) is an autosomal dominant disorder caused by heterozygous germline inactivating variants in the *PRKAR1A* gene. This condition has also been designated by the following acronyms: NAME (nevi, atrial myxomas, ephelides) and LAMB (lentigines, atrial myxoma, blue nevi). CNC is characterized by skin pigmentary abnormalities, myxomas, endocrine tumors, and schwannomas. The most common presenting feature of CNC is unusual skin pigmentation, including brown skin spots called lentigines or blue-black moles called blue nevi. Myxomas are noncancerous (benign) tumors that can occur in the heart (cardiac myxoma), skin, breast, and other internal organs. Cardiac myxomas can occur at a young age and may block blood flow through the heart, causing serious complications or sudden death. Approximately 25% of affected individuals will develop primary pigmented nodular adrenocortical disease (PPNAD), which can lead to development of Cushing syndrome. Large-cell calcifying Sertoli cell tumors occur in most affected male patients and may develop in the first decade of life in about one third of cases. Multiple thyroid nodules are present in as many as 75% of affected individuals. Pituitary adenomas resulting in clinically evident acromegaly occur in approximately 10% of adults with CNC. Another 10% of affected individuals have psammomatous melanotic schwannomas, which are typically benign but may be malignant.(1-4)

PRKAR1A encodes for cyclic AMP-dependent protein kinase type I-alpha regulatory subunit. *PRKAR1A* functions as a canonical tumor-suppressor gene, with biallelic inactivation in tumors resulting in constitutive activation of protein kinase A. Approximately 70% of individuals with a diagnosis of CNC have an affected parent, while approximately 30% have a *de novo* disease-causing variant. CNC is a highly penetrant disorder, with approximately 95% of those with a disease-causing *PRKAR1A* variant developing disease by age 50 years. The proportion of probands with a disease-causing variant detectable by sequence analysis is approximately 60% but can be higher (approximately 80%) in individuals presenting with Cushing syndrome caused by PPNAD.(4)

While the majority of reported disease-causing *PRKAR1A* gene variants are associated with CNC, this gene is also associated with an autosomal dominant condition called acrodysostosis-1 with hormone resistance. This condition is characterized by multiple hormone resistance, short stature, brachycephaly, and short broad hands with short metacarpals and phalanges, among other features. This phenotype results from disease-causing *PRKAR1A* variants in one of the protein's cyclic AMP-binding domains and has a different mechanism of disease than CNC.(5)

Reference Values

An interpretive report will be provided.

Interpretation

All detected variants are evaluated according to American College of Medical Genetics and Genomics recommendations.(6) Variants are classified based on known, predicted, or possible pathogenicity and reported with interpretive comments detailing their potential or known significance.

Cautions

Clinical Correlations:
Test results should be interpreted in the context of clinical findings, family history, and other laboratory data. Misinterpretation of results may occur if the information provided is inaccurate or incomplete.

If testing was performed because of a clinically significant family history, it is often useful to first test an affected family

member. Detection of a reportable variant(s) in an affected family member would allow for more informative testing of at-risk individuals.

To discuss the availability of additional testing options or for assistance in the interpretation of these results, contact the Mayo Clinic Laboratories genetic counselors at 800-533-1710.

Technical Limitations:
Next-generation sequencing may not detect all types of genomic variants. In rare cases, false-negative or false-positive results may occur. The depth of coverage may be variable for some target regions; assay performance below the minimum acceptable criteria or for failed regions will be noted. Given these limitations, negative results do not rule out the diagnosis of a genetic disorder. If a specific clinical disorder is suspected, evaluation by alternative methods can be considered.

There may be regions of genes that cannot be effectively evaluated by sequencing or deletion and duplication analysis as a result of technical limitations of the assay, including regions of homology, high guanine-cytosine (GC) content, and repetitive sequences. Confirmation of select reportable variants will be performed by alternate methodologies based on internal laboratory criteria.

This test is validated to detect 95% of deletions up to 75 base pairs (bp) and insertions up to 47 bp. Deletions-insertions (delins) of 40 or more bp, including mobile element insertions, may be less reliably detected than smaller delins.

Deletion/Duplication Analysis:
This analysis targets single and multi-exon deletions/duplications; however, in some instances single exon resolution cannot be achieved due to isolated reduction in sequence coverage or inherent genomic complexity. Balanced structural rearrangements (such as translocations and inversions) may not be detected.

This test is not designed to detect low levels of mosaicism or to differentiate between somatic and germline variants. If there is a possibility that any detected variant is somatic, additional testing may be necessary to clarify the significance of results.

For detailed information regarding gene specific performance and technical limitations, see Method Description or contact a laboratory genetic counselor.

If the patient has had an allogeneic hematopoietic stem cell transplant or a recent blood transfusion, results may be inaccurate due to the presence of donor DNA. Call Mayo Clinic Laboratories for instructions for testing patients who have received a bone marrow transplant.

Reclassification of Variants:
At this time, it is not standard practice for the laboratory to systematically review previously classified variants on a regular basis. The laboratory encourages healthcare providers to contact the laboratory at any time to learn how the classification of a particular variant may have changed over time.

Variant Evaluation:
Evaluation and categorization of variants is performed using published American College of Medical Genetics and

Genomics and the Association for Molecular Pathology recommendations as a guideline. Other gene-specific guidelines may also be considered.(6) Variants are classified based on known, predicted, or possible pathogenicity and reported with interpretive comments detailing their potential or known significance. Variants classified as benign or likely benign are not reported.

Multiple in silico evaluation tools may be used to assist in the interpretation of these results. The accuracy of predictions made by in silico evaluation tools is highly dependent upon the data available for a given gene, and periodic updates to these tools may cause predictions to change over time. Results from in silico evaluation tools should be interpreted with caution and professional clinical judgment.

Rarely, incidental or secondary findings may implicate another predisposition or presence of active disease. Incidental findings may include, but are not limited to, results related to the sex chromosomes. These findings will be carefully reviewed to determine whether they will be reported.

Clinical Reference

1. Maleszewski JJ, Larsen BT, Kip NS, et al: PRKAR1A in the development of cardiac myxoma: a study of 110 cases including isolated and syndromic tumors. Am J Surg Pathol. 2014 Aug;38(8):1079-1087 doi: 10.1097/PAS.0000000000000202
2. Rhayem Y, Le Stunff C, Abdel Khalek W, et al: Functional characterization of PRKAR1A mutations reveals a unique molecular mechanism causing acrodysostosis but multiple mechanisms causing Carney complex. J Biol Chem. 2015 Nov13;290(46):27816-27828. doi: 10.1074/jbc.M115.656553
3. Salpea P, Horvath A, London E, et al: Deletions of the PRKAR1A locus at 17q24.2-q24.3 in Carney complex: genotype-phenotype correlations and implications for genetic testing. J Clin Endocrinol Metab. 2014 Jan;99(1):E183-E188. doi: 10.1210/jc.2013-3159
4. Stratakis CA, Raygada M: Carney complex. In: Adam MP, Ardinger HH, Pagon RA, et al. GeneReviews [Internet]. University of Washington, Seattle; 2003. Updated August 16, 2018. Accessed September 22, 2021. Available at www.ncbi.nlm.nih.gov/books/NBK1286/
5. Nagasaki K, Iida T, Sato H, et al: PRKAR1A mutation affecting cAMP-mediated G protein-coupled receptor signaling in a patient with acrodysostosis and hormone resistance. J Clin Endocrinol Metab. 2012 Sep;97(9):E1808-E1813. doi: 10.1210/jc.2012-1369
6. Richards S, Aziz N, Bale S, et al: Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. Genet Med. 2015 May;17(5):405-424

Performance

Method Description

Next-generation sequencing (NGS) and/or Sanger sequencing are performed to test for the presence of variants in coding regions and intron/exon boundaries of *PRKAR1A*, as well as some other regions that have known disease-causing variants. The human genome reference GRCh37/hg19 build was used for sequence read alignment. At least 99% of the bases are covered at a read depth over 30X. Sensitivity is estimated at above 99% for single nucleotide variants, above 94% for deletions-insertions (delins) less than 40 base pairs (bp), above 95% for deletions up to 75 bp and insertions up

to 47 bp. NGS and/or a polymerase chain reaction-based quantitative method is performed to test for the presence of deletions and duplications in *PRKAR1A*.

There may be regions of genes that cannot be effectively evaluated by sequencing or deletion and duplication analysis as a result of technical limitations of the assay, including regions of homology, high guanine-cytosine (GC) content, and repetitive sequences.(Unpublished Mayo method)

The reference transcript for *PRKAR1A* gene is NM_002734.4. Reference transcript numbers may be updated due to transcript re-versioning. Always refer to the final patient report for gene transcript information referenced at the time of testing. Confirmation of select reportable variants may be performed by alternate methodologies based on internal laboratory criteria.

PDF Report
Supplemental

Day(s) Performed
Varies

Report Available
28 to 42 days

Specimen Retention Time
Whole blood: 2 weeks (if available); Extracted DNA: 3 months

Performing Laboratory Location
Rochester

Fees & Codes

Fees
- Authorized users can sign in to Test Prices for detailed fee information.
- Clients without access to Test Prices can contact Customer Service 24 hours a day, seven days a week.
- Prospective clients should contact their account representative. For assistance, contact Customer Service.

Test Classification
This test was developed, and its performance characteristics determined by Mayo Clinic in a manner consistent with CLIA requirements. This test has not been cleared or approved by the US Food and Drug Administration.

CPT Code Information
81479

Prior Auhtorization
Insurance preauthorization is available for this testing; forms are available.

Patient financial assistance may be available to those who qualify. Patients who receive a bill from Mayo Clinic Laboratories will receive information on eligibility and how to apply.

LOINC® Information

Test ID	Test Order Name	Order LOINC® Value
PRKSG	PRKAR1A Full Gene Analysis	94214-4

Result ID	Test Result Name	Result LOINC® Value
617436	Test Description	62364-5
617437	Specimen	31208-2
617438	Source	31208-2
617439	Result Summary	50397-9
617440	Result	82939-0
617441	Interpretation	69047-9
617442	Additional Results	In Process
617443	Resources	99622-3
617444	Additional Information	48767-8
617445	Method	85069-3
617446	Genes Analyzed	48018-6
617447	Disclaimer	62364-5
617448	Released By	18771-6