Noonan Syndrome and Related Disorders: Sequencing Panel

Test Code: MN001
Turnaround time: 8 weeks
CPT Codes: 81311 x1, 81405 x1, 81406 x1

Condition Description

The Ras/mitogen activated protein kinase (MAPK) pathway is involved in the control of the cell cycle and differentiation. Because of this critical role, a disruption in the pathway results in congenital developmental conditions. A class of human genetic syndromes, called the rasopathies, are caused by germline mutations in the genes in this pathway. The rasopathies, while distinct syndromes, share some overlapping features such as craniofacial dysmorphism, varying degrees of neurocognitive impairments, cutaneous, ocular, and musculoskeletal abnormalities, and cardiac malformations. Some syndromes have an increased risk of cancer.

Noonan Syndrome
Noonan syndrome (NS) is an autosomal dominant disorder characterized by congenital heart defects, short stature, developmental delay, distinctive craniofacial features that change with age, broad or webbed neck, unusual chest shape, apparently low-set nipples and cryptorchidism. About one third of individuals with NS have mild intellectual disability. Individuals with NS have an increased risk for cancer.

There are seven genes known to be cause NS; PTPN11, SOS1, RAF1, KRAS, NRAS, BRAF, and MAP2K1. Approximately 50% of NS cases are caused by mutations in the PTPN11 gene, 10-13% by the SOS1 gene, 3-17% by the RAF1 gene, and fewer than 5% by the KRAS. Fewer than 1% of cases are caused by mutations in the NRAS, BRAF, and MAP2K1 genes.

LEOPARD Syndrome
LEOPARD syndrome (LS) is an autosomal dominant disorder characterized by features that make up the acronym LEOPARD. They are lentigens, EKG abnormalities, ocular hypertelorism, pulmonary valve stenosis, abnormal genitalia, retardation of growth, and sensorinervual deafness. Like NS, up to one third of individuals with LS have mild intellectual disability.

Three genes are known to cause LS; PTPN11, RAF1, and BRAF. Approximately 90% of LS cases are caused by mutations in the PTPN11 gene. Fewer than 5% of LS cases are caused by mutations in the RAF1 or the BRAF gene.

Cardiofaciocutaneous Syndrome
Cardiofaciocutaneous (CFC) syndrome is an autosomal dominant disorder characterized by features in three primary systems: cardiac, craniofacial, and cutaneous; however, other systems may be involved as well. Cardiac abnormalities can include pulmonary valve stenosis, abnormal genitalia, retardation of growth, and sensorinervual deafness. Like NS, up to one third of individuals with CFC have mild intellectual disability. Ectodermal features include skin findings, such as xerosis, hyperkeratosis, ichthyosis, keratosis pilaris, ulerythema oophorogenes, eczema, pigmented moles, palmoplantar hyperkeratosis; hair findings such as sparse, curly, fine or thick, woolly, or brittle hair, and possible absent eyelashes and eyebrows; and the nails may be dystrophic or fast growing. Cognitive delay (ranging from mild to severe) is seen in all affected individuals. Neoplasias have been reported in some individuals with CFC.

There are four genes known to be associated with CFC; BRAF, MAP2K1, MAP2K2, and KRAS. Mutations in the BRAF gene account for ~75% of cases, MAP2K1 and MAP2K2 account for ~25% of cases, and KRAS accounts for <2% of cases.

Costello Syndrome
Costello syndrome is an autosomal dominant disorder characterized by developmental delay, intellectual disability, diffuse hypotonia, failure to thrive in infancy (due to severe postnatal feeding difficulties), short stature, coarse facial features (full lips, large mouth); curly or sparse, fine hair; loose, soft skin, and tight Achilles tendons. Cardiac features include cardiac hypertrophy, congenital heart defect, and arrhythmias. Individuals with Costello syndrome have an approximately 15% lifetime risk for malignant tumors. The solid tumors rhabdomyosarcoma and neuroblastoma occur most frequently in young children. Adolescents and young adults are at risk for transitional cell carcinoma of the bladder.

The HRAS gene is the only gene currently known to be associated with Costello syndrome. In patients with a clinical diagnosis of Costello syndrome, 80-90% of mutations in the HRAS gene can be identified.

Noonan-Like Syndrome with Loose Anagen Hair
Noonan-like syndrome with loose anagen hair (NS/LAH) is an autosomal dominant disorder characterized by facial features similar to Noonan syndrome, reduced growth, intellectual disability, distinctive hyperactive behavior, and hair anomalies. The hair is typically sparse, thin, easily pluckable, and slow growing. Additional features include hairless skin that is darkly pigmented, eczema or ichthyosis, sparse eyebrows, thin or dystrophic nails, hypernasal or hoarse voice, and cardiac anomalies.

The SHOC2 gene in the only gene known to be associated with NS/LAH.

References:

- GeneReviews

Genes

- BRAF, CBL, HRAS, KRAS, MAP2K1, MAP2K2, NRAS, PTPN11, RAF1, RIT1, SHOC2, SOS1, SPRED1

Indications

Disclaimer: This information is confidential and subject to change without notice. It may not be reproduced in whole or part unless authorized in writing by an authorized EGL representative.
Confirmation of a clinical diagnosis of Noonan syndrome or a related disorder.

**Methodology**

**Next Generation Sequencing:** In-solution hybridization of all coding exons is performed on the patient's genomic DNA. Although some deep intronic regions may also be analyzed, this assay is not meant to interrogate most promoter regions, deep intronic regions, or other regulatory elements, and does not detect single or multi-exon deletions or duplications. Direct sequencing of the captured regions is performed using next generation sequencing. The patient's gene sequences are then compared to a standard reference sequence. Potentially causative variants and areas of low coverage are Sanger-sequenced. Sequence variations are classified as pathogenic, likely pathogenic, benign, likely benign, or variants of unknown significance. Variants of unknown significance may require further studies of the patient and/or family members.

**Detection**

Clinical Sensitivity: Noonan syndrome - 70-88%, Leopard syndrome – 95%, CFC - unknown , Costello syndrome – 80-90%, NS/LAH - unknown. Mutations in the promoter region, some mutations in the introns and other regulatory element mutations cannot be detected by this analysis. Large deletions will not be detected by this analysis. Results of molecular analysis should be interpreted in the context of the patient's clinical and/or biochemical phenotype.

Analytical Sensitivity: ~99%

**Specimen Requirements**

*Submit only 1 of the following specimen types*

**Type: DNA, Isolated**

**Specimen Requirements:**
- Microtainer
- 8µg

Isolation using the Perkin Elmer™ Chemagen™ Automated Extraction method or Qiagen™ Puregene kit for DNA extraction is recommended.

**Specimen Collection and Shipping:**
Refrigerate until time of shipment in 100 ng/µL in TE buffer. Ship sample at room temperature with overnight delivery.

**Type: Saliva**

**Specimen Requirements:**
- Oragen™ Saliva Collection Kit

Orangen™ Saliva Collection Kit used according to manufacturer instructions. Please contact EGL for a Saliva Collection Kit for patients that cannot provide a blood sample.

**Specimen Collection and Shipping:**
Please do not refrigerate or freeze saliva sample. Please store and ship at room temperature.

**Type: Whole Blood (EDTA)**

**Specimen Requirements:**
- EDTA (Purple Top)
  - Infants and Young Children (2 years of age to 10 years old): 3-5 ml
  - Older Children & Adults: 5-10 ml
- Autopsy: 2-3 ml uncotted cord or cardiac blood

**Specimen Collection and Shipping:**
Ship sample at room temperature for receipt at EGL within 24 hours of collection. Do not refrigerate or freeze.

**Related Tests**

- Single gene sequencing and deletion/duplication analysis are available for the PTPN11, SOS1, RAF1, KRAS, HRAS, BRAF, MAP2K1, MAP2K2, SHOC2 and NRAS genes.
- A next generation sequencing panel is available for short stature.
- Custom diagnostic mutation analysis (KM) is available to family members if mutations are identified by targeted mutation testing or sequencing analysis.