Hereditary Leiomyomatosis and Renal Cell Cancer (HLRCC): \textit{FH} Gene Deletion/Duplication

| Test Code: | VI |
| Turnaround time: | 2 weeks |
| CPT Codes: | 81228 x1 |

### Condition Description

Hereditary leiomyomatosis and renal cell cancer (HLRCC) is an autosomal dominant condition characterized by cutaneous leiomyoma, uterine leiomyoma (fibroids), and/or a single renal tumor. The majority (three-quarters) of individuals with HLRCC present with a single or multiple cutaneous leiomyoma. Cutaneous leiomyoma appear as skin-colored to light brown papules or nodules distributed over the trunk and extremities and occasionally on the face and appear at a mean age of 25 years, increasing in size and number with age. Uterine leiomyomata are present in almost all females with HLRCC and tend to be numerous and large; age at diagnosis ranges from 18 to 52 years; with most women experiencing irregular or heavy menstruation and pelvic pain. The presence of cutaneous leiomyomata correlates with the presence of uterine fibroids in females. Renal tumors causing hematuria, lower back pain, and a palpable mass are usually unilateral, solitary, and aggressive and range from type 2 papillary to tubulo-papillary to collecting-duct carcinomas. They occur in about 10%-16% of individuals with HLRCC; the median age of detection is 44 years. Disease severity shows significant intra- and interfamilial variation.

HLRCC is diagnosed by the presence of multiple cutaneous leiomyomas with at least one histologically confirmed leiomyoma or by a single leiomyoma in the presence of a positive family history of HLRCC. Diagnosis is confirmed by testing of fumarate hydratase enzyme activity in cultured skin fibroblasts or lymphoblastoid cells showing reduced activity (760%) or by molecular genetic testing. The \textit{FH} gene (1q42.1) is the only gene known to be associated with HLRCC. Between 80% and 100% of individuals with HLRCC have identifiable sequence variants in \textit{FH}. No correlation is observed between \textit{FH} mutations and the occurrence of cutaneous lesions, uterine fibroids, or renal cancer of HLRCC. The proportion of cases caused by \textit{de novo} mutations is unknown as subtle manifestation in parents has not been evaluated and genetic testing data are insufficient. Early detection of at-risk individuals affects medical management. In the absence of an increased risk of developing childhood malignancy, however, the American Society of Clinical Oncology (ASCO) recommends delaying genetic testing in at-risk individuals during childhood until individuals reach 18 years of age and are able to make informed decisions regarding genetic testing.

Mutations in the \textit{FH} gene also occur in the autosomal recessive condition fumerase deficiency (FHD), or fumeric aciduria. FHD results from inherited biallelic mutations in \textit{FH}, and is characterized by rapidly progressive neurologic impairment including hypotonia, seizures, and cerebral atrophy. Homozygous or compound heterozygous germline mutations in \textit{FH} are found in individuals with FHD. Leiomyomas and renal cancer have not been reported in FHD. Most individuals with FHD, however, survive only a few months; a very few survive to early adulthood. In one report, a parent (heterozygous carrier) of an individual with fumarase deficiency developed cutaneous leiomyomas similar to those observed in HLRCC.

[Click here](#) for the GeneTests summary on this condition.

### Genes

**\textit{FH}**

### Indications

This test is indicated for:

- Confirmation of a clinical diagnosis of HLRCC in individuals who have tested negative for sequence analysis
- Individuals at-risk for HLRCC due to family history who have tested negative for sequence analysis

### Methodology

DNA isolated from peripheral blood is hybridized to a CGH array to detect deletions and duplications. The targeted CGH array has overlapping probes which cover the entire genomic region.

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Please note that a “backbone” of probes across the entire genome are included on the array for analytical and quality control purposes. Rarely, off-target copy number variants causative of disease may be identified that may or may not be related to the patient’s phenotype. Only known pathogenic off-target copy number variants will be reported. Off-target copy number variants of unknown clinical significance will not be reported.

**Detection**

Detection is limited to duplications and deletions. The CGH array will not detect point or intronic mutations. Results of molecular analysis must be interpreted in the context of the patient's clinical and/or biochemical phenotype.

**Specimen Requirements**

Submit only 1 of the following specimen types

* Preferred specimen type: Whole Blood

**Type: Whole Blood**

Specimen Requirements:

In EDTA (purple top) or ACD (yellow top) tube:
- Infants (2 years): 3-5 ml
- Older Children & Adults: 5-10 ml

Specimen Collection and Shipping: Refrigerate until time of shipment. Ship sample within 5 days of collection at room temperature with overnight delivery.

**Type: Saliva**

Specimen Requirements:

Oragene™ Saliva Collection kit (available through EGL) used according to manufacturer instructions.

Specimen Collection and Shipping: Store sample at room temperature. Ship sample within 5 days of collection at room temperature with overnight delivery.

**Special Instructions**

Submit copies of diagnostic biochemical test results with the sample, if appropriate. Contact the laboratory if further information is needed.

Sequence analysis is required before deletion/duplication analysis by targeted CGH array. If sequencing is performed outside of Emory Genetics Laboratory, please submit a copy of the sequencing report with the test requisition.

**Related Tests**

- Sequencing analysis of the FH gene is available (VI) and is required before deletion/duplication analysis.
- Prenatal testing is available to individuals who are confirmed carriers of mutations. Please contact the laboratory genetic counselor to discuss appropriate testing prior to collecting a prenatal specimen.