**Li-Fraumeni Syndrome: TP53 Gene Sequencing**

**Test Code:** QX  
**Turnaround time:** 4 weeks  
**CPT Codes:** 81405 x1

### Condition Description

Li-Fraumeni Syndrome (LFS) is an autosomal dominant cancer predisposition syndrome associated with soft-tissue sarcoma, breast cancer, leukemia, osteosarcoma, melanoma, and cancer of the colon, pancreas, adrenal cortex, and brain [1]. Tumors frequently appear in childhood and affected individuals may experience multiple primary tumors during their lifetime. The cancer risk is estimated to be 90% by age 60.

Classic LFS is defined as a proband with a sarcoma before the age of 45 years and a first-degree relative with any cancer before the age of 45 years, and one additional first- or second-degree relative in the same lineage with any cancer before the age of 45 years or a sarcoma at any age.

Li-Fraumeni-Like Syndrome (LFL) is defined alternately as a proband with any childhood cancer, or a sarcoma, brain tumor, or adrenocortical tumor before the age of 45 years, plus a first- or second-degree relative in the same lineage with a typical LFS tumor at any age, and an additional first- or second-degree relative in the same lineage with any cancer before the age of 60 years (Birch [2]); or two first- or second-degree relatives with any LFS-related cancer at any age (Eeles [3]).

The **TP53** gene (17p13.1) has 10 exons and is a tumor suppressor gene. Approximately 70% of LFS cases and 40% of LFL cases contain germline mutations in **TP53**. 95% of mutations can be detected by sequence analysis. Some genotype-phenotype correlations have been found: brain tumors seem to be associated with missense **TP53** mutations located in the DNA-binding loop that contact the minor groove of DNA, whereas adrenal gland carcinomas are associated with missense mutations located in the loops opposing the protein-DNA contact surface. In addition, mutations likely to result in a null phenotype (absence of the protein or loss of function) are associated with earlier onset brain tumors. A few families with LFS or LFL have been found to have mutations in the **CHEK2** gene. The specific contribution of **CHEK2** mutations to LFS and LFL-associated cancer risks has yet to be defined.

Sequencing of the **TP53** gene is recommended after a clinical diagnosis consistent with Li-Fraumeni syndrome, and provides a complementary method to confirm the presence of mutations in a proband, identify at-risk individuals among the proband’s relatives, and provide prenatal diagnosis in families with known mutations.

For patients with suspected LFS or LFL, sequence analysis is recommended as the first step in mutation identification. For patients in whom mutations are not identified by full gene sequencing, deletion/duplication analysis is appropriate.

Please click here for the GeneTests summary on this condition.

### References:


### Genes

**TP53**

### Indications

This test is indicated for:

- Confirmation of a suspected diagnosis of LFS or LFL.
- Individuals at-risk for LFS or LFL due to family history.

### Methodology

PCR amplification of 10 exons contained in the **TP53** gene is performed on patient genomic DNA. Direct sequencing of amplification products is performed in both forward and reverse directions using automated fluorescence deoxy sequencing methods. The patient's gene sequences are then compared to a normal reference sequence. Sequence variations are classified as mutations, benign variants unrelated to disease, or variations of unknown clinical significance. Variants of unknown clinical significance may require further studies of the patient and/or family members. This assay does not interrogate the promoter region, deep intronic regions, or other regulatory elements, and does not detect large deletions.

### Detection

An estimated 70% of families with the clinical diagnosis of LFS will have a detectable **TP53** mutation. Sequence analysis of the coding region of the **TP53** gene detects approximately 95% of disease-causing mutations. Mutations in the promoter region, some mutations in the introns or other regulatory element mutations, and large deletions cannot be detected by this analysis.

Analytical Sensitivity: ~99%.
Results of molecular analysis should be interpreted in the context of the patient's clinical presentation and family history.

**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**

Please submit copies of pedigree or other family history information along with the sample. 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 form.

**Related Tests**

- **Li Fraumeni Syndrome:** TP53 Gene Deletion/Duplication (QY) is available for those individuals in whom sequence analysis is negative.
- **Known Mutation Analysis (KM)** is available to family members if mutations are identified by sequencing.
- 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.