Familial Adenomatous Polyposis: APC Gene Sequencing

**Test Code:** TV  
**Turnaround time:** 4 weeks  
**CPT Codes:** 81201 x1

### Condition Description

*APC*-associated polyposis conditions result from a mutation in the *APC* gene and cause a predisposition for colon cancer. Disorders in this category include familial adenomatous polyposis (FAP), attenuated FAP (AFAP), Gardner syndrome, and Turcot syndrome.

FAP is an autosomal dominant disorder characterized by the development of hundreds to thousands of adenomatous colonic polyps, usually beginning during early adolescence. 95% of affected individuals develop polyps by age 35; without surgical intervention, these polyps will inevitably progress to colorectal cancer by the early forties. Extracolonic manifestations may occur, including:

- dental anomalies  
- polyps of the gastric fundus and duodenum  
- congenital hypertrophy of the retinal pigment epithelium (CHRPE)  
- osteomas  
- desmoid tumors  
- soft tissue tumors  
- other associated cancers

Attenuated FAP differs in that the overall polyp burden tends to be less (average of 30) and polyps are also more proximally located. Colorectal cancer generally occurs at a later age. Gardner syndrome is associated with colon polyps typical of FAP in conjunction with osteomas, desmoid tumors, and other neoplasms. Turcot syndrome consists of colon polyps and central nervous system tumors.

The diagnosis of *APC*-associated polyposis conditions relies primarily on clinical findings. Molecular genetic testing of *APC* detects disease-causing mutations in up to 90% of individuals with typical FAP. Molecular genetic testing is most often used to confirm the diagnosis of FAP or attenuated FAP in individuals with equivocal findings (e.g., more than 100 adenomatous polyps) and to provide early diagnosis of at-risk family members. Phenotype variations may correlate with the specific location of the *APC* gene mutation. *APC*-associated polyposis conditions are inherited in an autosomal dominant manner. Approximately 75%-80% of individuals with *APC*-associated polyposis conditions have an affected parent.

The *APC* gene (5q21-q22) has 15 exons. The specific function of the *APC* gene is the object of much research and tumor suppressor activity is suspected.

Sequencing of the *APC* gene is recommended after a clinical diagnosis consistent with FAP or an *APC*-associated polyposis 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 FAP or an *APC*-associated polyposis condition, 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.

### Genes

**APC**

### Indications

This test is indicated for:

- Confirmation of a clinical diagnosis of FAP or an *APC*-associated polyposis syndrome.  
- Individuals at-risk for FAP or an *APC*-associated polyposis syndrome due to family history.

### 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:** Sequence analysis of the *APC* gene detects disease-causing mutations in approximately 90% of individuals with typical FAP. Mutations in the promoter region, some mutations in the introns and 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/or tumor pathology.
Specimen Requirements

Submit only 1 of the following specimen types

* Preferred specimen type: Whole Blood

**Type: Whole Blood**

Specimen Requirements:

In EDTA (purple 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 EGL Genetics, please submit a copy of the sequencing report with the test requisition.

**Related Tests**

- **Familial Adenomatous Polyposis: APC Gene Deletion/Duplication (QP)** is available for those individuals in whom sequence analysis is negative.
- **MYH-Associated Polyposis: MYH Common Mutation Panel (TW)**, **MYH-Associated Polyposis: MYH Gene Sequencing (QV)**, and **MYH-Associated Polyposis: MYH Gene Deletion/Duplication (QW)** may be indicated for individuals with a clinical diagnosis of FAP or AFAP who do not have a detectable APC mutation.
- **Known Mutation Testing (KM)** is available to family members if mutations are identified by sequencing.
- Prenatal testing is available to couples who are confirmed carriers of mutations. Please contact the laboratory genetic counselor to discuss appropriate testing prior to collecting a prenatal specimen.