Retinitis Pigmentosa: Sequencing Panel

**Test Code:** MM233

**Turnaround time:** 6 weeks

**CPT Codes:** 81404 x1, 81406 x1, 81408 x1

### Condition Description

Retinitis pigmentosa (RP) is a heterogeneous group of inherited diseases that commonly result in a progressive retinal degeneration. Over 90 forms of RP have been identified. RP can be syndromic or nonsyndromic and can be inherited in an autosomal dominant, autosomal recessive, or X-linked manner. RP is characterized by progressive visual field loss, night blindness, and abnormal or nonrecordable electroretinogram (ERG). Fundus changes include pigment deposition in the retina along the blood vessels with optic nerve pallor and arteriolar narrowing in early stages advancing to characteristic “bone spicule” pigmented pattern in later stages. Please note that RPGR orf15 analysis is not included in this test.


**References:**

- OMIM
- GeneReviews

### Genes

ABCA4, APLI1, BBS1, BEST1, C10TNFS, C2orf71, C8orf37, CA4, CERKL, CHM, CLN3, CLRN1, CNGA1, CNGB1, CRB1, CRX, CYP4V2, DHDDS, EYS, FAM161A, FLVCR1, FSCN2, GUC1A1, GUCY2D, IDH3B, IMDH1, IMPG2, KNL1, LRRD1, MAK, MERTK, NCR2E3, NLR, OFD1, PDE5A, PDE6B, PDE6G, PRCD, PROM1, PRPF3, PRPF31, PRPF46, PRPF8, PRPB, RBP3, RBP4, RDH12, RGR, RHO, RLBP1, ROM1, RP1, RP2, RP9, RP65, RPGR, RPGRIP1, SAG, SEMA4A, SNRP200, SPATA7, TOPORS, TTC8, TULP1, USH2A, ZNF513

### Indications

This test is indicated for:

- Confirmation of a clinical diagnosis of retinitis pigmentosa.
- Carrier testing in adults with a family history of retinitis pigmentosa.

### 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:** Unknown. Pathogenic variants in the promoter region, some pathogenic variants in the introns and other regulatory element pathogenic variants 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:** 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: Ship sample at room temperature with overnight delivery.
Type: Isolated DNA

Specimen Requirements:

In microtainer: 60 ug

Isolation using the Qiagen™ Puregene kit for DNA extraction is recommended.

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

Special Instructions

Please include fundus photographs, electroretinogram (ERG) findings, visual field findings, and visual acuity, if available, for expert review and clinical correlation with test results.

Related Tests

- Eye Disorders: Comprehensive Sequencing and Deletion/Duplication Panels.
- Retinitis Pigmentosa: Deletion/Duplication Panel.