# Pulmonary Hypertension Panel: Sequencing and CNV Analysis

**Test Code:** MM098  
**Turnaround time:** 6 weeks  
**CPT Codes:** 81405 x1, 81406 x1

## Condition Description

Pulmonary hypertension (PH) is increased pulmonary pressure in the absence of common causes such as lung, heart, or thromboembolic chronic diseases. It is thought that both genetic and environmental factors that alter vascular structure and function contribute to the pathogenesis of PH.

Familial cases of PH are usually inherited in an autosomal dominant manner. With the identification of pathogenic variants in genes known to cause PH, what was previously thought to be idiopathic PH is now known to be genetic. A pathogenic variant in the *BMPR2* gene causes ~70% of hereditary cases of pulmonary arterial hypertension (PAH) and in 10-40% of idiopathic PAH. Other genes with pathogenic variants implicated in PH include: *CAV1, GDF2, RASA1, SMAD4,* and *SMAD9.*

Heterozygous pathogenic variants in the *ENG* and *ACVRL1* (previously known as *ALK1*) genes cause hereditary hemorrhagic telangiectasia (HHT). HHT is an autosomal dominant vascular disorder characterized by acquired cutaneous telangiectasias and arteriovenous malformations that can lead to the development of PAH.

References:
- OMIM

## Genes

*ACVRL1, BMPR2, CAV1, ENG, GDF2, RASA1, SMAD4, SMAD9*

## Indications

This test is indicated for:
- Confirmation of a clinical diagnosis of pulmonary hypertension.
- Carrier testing in adults with a family history of pulmonary hypertension.

## 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.

**Copy Number Analysis:** Comparative analysis of the NGS read depth (coverage) of the targeted regions of genes on this panel was performed to detect copy number variants (CNV). The accuracy of the detected variants is highly dependent on the size of the event, the sequence context and the coverage obtained for the targeted region. Due to these variables and limitations a minimum validated CNV size cannot be determined; however, single exon deletions and duplications are expected to be below the detection limit of this analysis.

## Detection

**Next Generation Sequencing:** Clinical Sensitivity: A pathogenic variant in the *BMPR2* gene can be identified in ~70% of hereditary cases of pulmonary arterial hypertension and in 10-40% of idiopathic PAH. The clinical sensitivity for *ENG, ACVRL1,* and *CAV1* is 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. Results of molecular analysis should be interpreted in the context of the patient’s clinical and/or biochemical phenotype.

Analytical sensitivity for sequence variant detection is ~99%.

**Copy Number Analysis:** The sensitivity and specificity of this method for CNV detection is highly dependent on the size of the event, sequence context and depth of coverage for the region involved. The assay is highly sensitive for CNVs of 500 base pairs or larger and those containing at least 3 exons. Smaller (~500 base pairs) CNVs and those that involving only 1 or 2 exons may or may not be detected depending on the sequence context, size of exon(s) involved and depth of coverage.

## Specimen Requirements

**Submit only 1 of the following specimen types**

**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 unclotted cord or cardiac blood

Specimen Collection and Shipping:
Ship sample at room temperature for receipt at EGL within 72 hours of collection. Do not freeze.

Type: Saliva

Specimen Requirements:
Oragene™ Saliva Collection Kit
Oragene™ 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: DNA, Isolated

Specimen Requirements:
Microtainer
15µg
Isolation using the Perkin Elmer™Chemagen™ 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.

Related Tests

- Comprehensive cardiomyopathy panel
- Pulmonary Hypertension: Deletion/Duplication Panel