

# Cerebral Cavernous Malformations, 3 Genes

## Indications for Ordering

- Confirm diagnosis in an individual with cerebral cavernous malformations (CCM)
- Identify causative gene mutation(s) for familial CCM

## Test Description

- Next generation sequencing
  - Targeted capture of all coding exons and intron/exon junctions followed by massively parallel sequencing
  - Sequence variants reported are confirmed by Sanger sequencing
- Deletion/duplication analysis
  - Custom-designed comparative genomic hybridization array

## Tests to Consider

### Primary test

[Cerebral Cavernous Malformation \(CCM\) Panel, Sequencing and Deletion/Duplication, 3 Genes 2009326](#)

- Preferred test to confirm a clinical diagnosis of and determine an etiology for CCM

### Related tests

[Cerebral Cavernous Malformation \(CCM\) Sequencing, 3 Genes 2009331](#)

- Use to confirm a clinical diagnosis of and determine an etiology for CCM

[Cerebral Cavernous Malformation \(CCM1, CCM2 and CCM3\) Deletion/Duplication 2003172](#)

- Useful if no mutations have been found using sequencing

[Vascular Malformations Panel, Sequencing and Deletion/Duplication, 14 Genes 2007384](#)

- Preferred test to confirm clinical diagnosis of a blood vessel disorder

[Vascular Malformations Sequencing, 14 Genes 2007390](#)

- Acceptable test to confirm clinical diagnosis of a blood vessel disorder

[Familial Mutation, Targeted Sequencing 2001961](#)

- Useful when a familial mutation identifiable by sequencing is known

## Disease Overview

Blood vessel disorder characterized by cavernous malformations in the brain

- Malformations in familial form can increase in number and size over time
- Hyperkeratotic cutaneous capillary-venous malformations (HCCVMs) occur in a small percentage

### Symptoms

- Headaches, seizures, and neurological deficits secondary to intracranial bleed
- ~25% of individuals with CCM remain asymptomatic

### Incidence

- ~1/200 for all CCM
- Familial CCM – 1/2,000-10,000 individuals

### Genetics

**Genes** – see table

**Mutations** – CCM can be sporadic or familial

### Test Interpretation

**Clinical sensitivity** – ~80% for three genes combined

### Results

- Positive – one copy of a pathogenic mutation in the *CCM1/KRIT1*, *CCM2*, or *CCM3/PDCD10* gene detected
  - Predictive of familial CCM
- Negative – no pathogenic mutation detected in the *CCM1*, *CCM2*, or *CCM3* gene in an individual clinically affected with CCM
  - Diagnosis of familial CCM is unlikely but not excluded
- Inconclusive – variants of unknown clinical significance may be identified in any of the 3 genes tested

### Limitations

- Diagnostic errors can occur due to rare sequence variations
- Not determined or evaluated:
  - Deep intronic mutations
  - Regulatory region mutations
  - Breakpoints of large deletions/duplications
  - Mutations in genes not listed
- Small deletions or insertions may not be detected by massively parallel sequencing

## Reference

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Morrison L, Akers A. Cerebral Cavernous Malformation, Familial. 2003 Feb 24 [Updated 2011 May 31]. In: Pagon RA, Adam MP, Ardinger HH, et al., editors. GeneReviews® [Internet]. Seattle (WA): University of Washington, Seattle; 1993-2015 ([www.ncbi.nlm.nih.gov/books/NBK1293/](http://www.ncbi.nlm.nih.gov/books/NBK1293/))

Gene Symbol	Gene Description	NM#	OMIM#	Condition	Inheritance	Familial CCM Attributable to Gene
<i>CCM1/KRIT1</i>	Ankyrin repeat containing	194456	604214	CCM1	AD	~55%
<i>CCM2</i>	Cerebral cavernous malformation 2	031443	607929	CCM2	AD	~ 5%
<i>CCM3/PDCD10</i>	Programmed cell death 10	007217	609118	CCM3	AD	~10%

AD = autosomal dominant