The University of Chicago Genetic Services Laboratories

5841 S. Maryland Ave., Rm. G701, MC 0077, Chicago, Illinois 60637
Toll Free: (888) UC GENES (888) 824 3637
Local: (773) 834 0555 FAX: (773) 702 9130
ucgslabs@genetics.uchicago.edu dnatesting.uchicago.edu
CLIA #: 14D0917593 CAP #: 18827-49

Next Generation Sequencing Mesothelioma Panel

Malignant Mesothelioma (MM) is an aggressive cancer. It is associated with a history of asbestos exposure, though germline genetics may also influence the risk of develping MM. Some studies have found that up to 12% of patients with MM carry germline gene mutations in cancer susceptibility genes[1,2]. Moreover, germline mutations in DNA repair genes may increase the susceptibility to asbestos in exposed individuals[3,4]. However, at present, the relative contribution of germline mutations to the development of MM remains uncertain. Genetic testing for germline mutations in a broad range of DNA repair and related genes has been recommended for mesothelioma patients at diagnosis, as the information obtained can be important for treatment, prognosis, and surveillance for additional cancers for patients, as well as for cancer screening and prevention for their families [1,2].

The Mesothelioma Panel includes sequence and deletion/duplication analysis of the 28 genes listed below. Please contact us for additional details and questions.

Comprehensive Cancer Panel gene list					
APC	ATM	BAP1	BRCA1	BRCA2	CDKN2A
CHEK2 (CHK2)	FANCA	FANCC	FANCD2	FANCF	FANCI
FANCM	MLH1	MRE11A	MSH6	MUTYH	NF2
PALB2	PMS1	POT1	PTEN	SDHA	SLX4
TMEM127	TP53	VHL	WT1		

Mesothelioma Panel

Sample specifications:	3 to10 cc of blood in a purple top (EDTA) tube; or 2 T-25 flasks of cultured skin fibroblasts or DNA extracted from fibroblasts if the patient has a history of MDS/leukemia. **NOTE:** Peripheral blood samples are not accepted for patients with a history of MDS/leukemia.
Cost:	$3,000
CPT codes:	81162, 81321, 81405, 81292, 81406
Turn-around time:	6 weeks

Test methods:
Comprehensive sequence coverage of the coding regions and splice junctions of all genes in this panel is performed. Targets of interests are enriched and prepared for sequencing using the Agilent SureSelect system. Sequencing is performed using Illumina technology and reads are aligned to the reference sequence. Variants are identified and evaluated using a custom collection of bioinformatic tools and comprehensively interpreted by our team of directors and genetic counselors. All novel and/or potentially pathogenic variants are confirmed by Sanger sequencing. The technical sensitivity of this test is estimated to be >99% for single nucleotide changes and insertions and deletions of less than 20 bp. Our CNV detection algorithm was developed and its performance determined for the sole purpose of identifying deletions and duplications within the coding region of the gene(s) tested. Partial exonic copy number changes and rearrangements of less than 400 bp may not be detected by this methodology. Regions of high homology and repetitive regions may not be analyzed. This methodology will not detect low level mosaicism, balanced translocations, inversions, or point

mutations that may be responsible for the clinical phenotype. The sensitivity of our deletion/duplication assay may be reduced when DNA extracted by an outside laboratory is provided.

Results:

Results, along with an interpretive report, will be faxed to the referring physician. Additional reports will be provided as requested. All abnormal results will be reported by telephone.

For more information about our testing options, please visit our website at dnatesting.uchicago.edu or contact us at 773-834-0555.

Committed to CUSTOMIZED DIAGNOSTICS, TRANSLATIONAL RESEARCH & YOUR PATIENTS' NEEDS

1. Panou V., Gadiraju M., Wolin A., Weipert C.M., Skarda E., Husain A.N., Patel J.D., Rose B., Zhang S.R., Weatherly M., et al. Frequency of Germline Mutations in Cancer Susceptibility Genes in Malignant Mesothelioma. J. Clin. Oncol. 2018: Jco2018785204.

2. Hassan R., Morrow B., Thomas A., Walsh T., Lee M.K., Gulsuner S., Gadiraju M., Panou V., Gao S., Mian I., et al. Inherited predisposition to malignant mesothelioma and overall survival following platinum chemotherapy. Proc. Natl. Acad. Sci. USA. 2019; 116:9008–9013. doi: 10.1073/pnas.1821510116.

3. Betti M, Casalone E, Ferrante D, et al: Germline mutations in DNA repair genes predispose asbestos-exposed patients to malignant pleural mesothelioma. Cancer Lett 405:38-45, 2017.

4. Betti M, et al. (2018) Sensitivity to asbestos is increased in patients with mesothelioma and pathogenic germline variants in BAP1 or other DNA repair genes. Genes Chromosomes Cancer 57:573–583.