EGL Genetics | Eurofins Clinical Diagnostics
2460 Mountain Industrial Boulevard | Tucker, Georgia 30084
Phone: 470-378-2200 or 855-831-7447 | Fax: 470-378-2250
eglgenetics.com

Renal Cancer Panel: Sequencing and CNV Analysis

Test Code: MM206
Turnaround time: 4 weeks
CPT Codes: 81298 x1, 81317 x1, 81321 x1, 81404 x1, 81292 x1, 81295 x1, 81405 x1, 81406 x1, 81407 x1

Condition Description

Renal cancer is a multifarious and heterogeneous disease with a varied spectrum of malignant subtypes and clinical presentation. A number of gene mutations have been reported in the literature. Renal cell carcinoma (RCC) tumor subtypes include clear cell or conventional (70-80%); papillary type 1 and type 2 (10-15%); chromophobe (3-5%) and collecting duct (1%). The general population's lifetime risk to develop RCC is 1.5%. RCC is the seventh and eighth most common cancer in men and women respectively. Approximately 3-5% of RCC cases are hereditary and occur as a result of an inherited mutation. Unlike sporadic RCC cases, hereditary RCC is often categorized by earlier disease onset and/or multifocal or bilateral tumors.

References:

- Altekruse, S., et al. (2009). Seer cancer statistics review, 1975-2007, National Cancer Institute. http://seer.cancer.gov/statfacts/html/kidrp.html#risks. Accessed June 13, 2013.
- Rini, B., et al. (2006). Renal cell carcinoma. *Curr Opin in Onc*, 18(3):289-296.
- Rosner, I., et al. (2009). The clinical implications of the genetics of renal cell carcinoma. *Urologic Oncology*, 27(2):131-136.
- Coleman, J., and Russo, P. (2009). Hereditary and familial kidney cancer. *Curr Opin Urol*, 19:478-485.

Genes

BAP1, BUB1B, CDC73, CDKN1C, FH, FLCN, GPC3, MET, MLH1, MSH2, MSH6, PALB2, PMS2, PTEN, SDHB, SDHC, SDHD, SMARCB1, TP53, TSC1, TSC2, VHL, WT1

Indications

The test is indicated for:

- Individuals with a clinical or suspected diagnosis of renal cancer.

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: Unknown. Mutations in the promoter region, some mutations in the introns and other regulatory element mutations cannot be detected by this analysis. Results of molecular analysis should be interpreted in the context of the patient's clinical/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: DNA, Isolated

Specimen Requirements:
Microtainer
8µg
Isolation using the Perkin Elmer™Chemagen™ Chemagen™ Automated Extraction method or Qiagen™ Puregene kit for DNA extraction is

2460 Mountain Industrial Boulevard | Tucker, Georgia 30084
Phone: 470-378-2200 or 855-831-7447 | Fax: 470-378-2250
eglgenetics.com

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.

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
Orangene™ 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.

Special Instructions

This test is for germline mutation analysis. DNA isolated from FFPE tumor samples is not suitable for this test.

Related Tests

- Hereditary Cancer Syndrome: Sequencing Panel.
- Renal Cancer: Deletion/Duplication Panel.