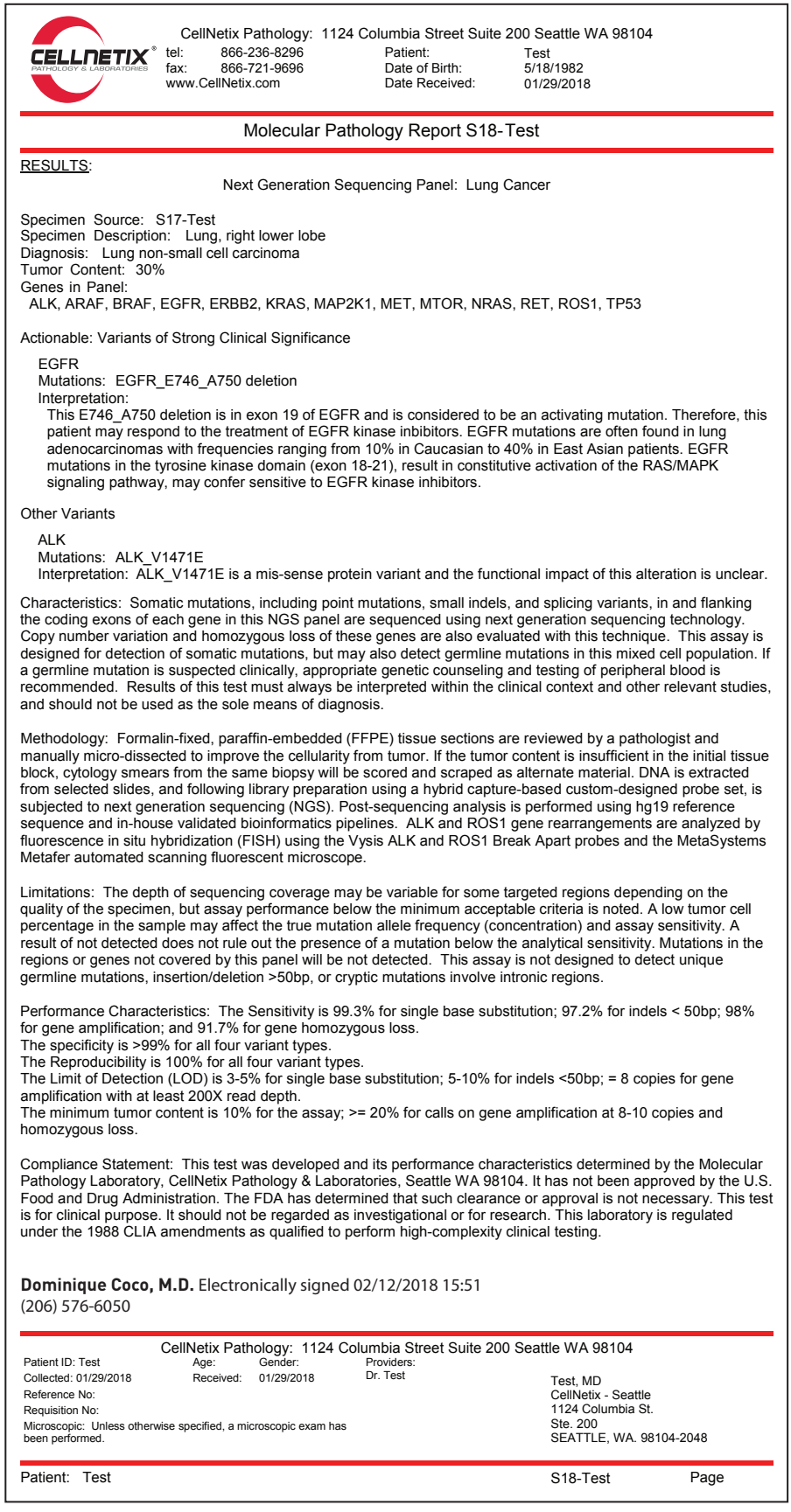
A Guide to Your Report Page

To help you understand how to find information on your SymGene Focus Pathology Report page, below are descriptions and corresponding annotations of the different sections that may appear.



CellNetix Pathology: 1124 Columbia Street Suite 200 Seattle WA 98104
tel: 866-236-8296
fax: 866-721-9696
www.CellNetix.com

Patient: Test
Date of Birth: 5/18/1982
Date Received: 01/29/2018

Molecular Pathology Report S18-Test

RESULTS:

Next Generation Sequencing Panel: Lung Cancer

Specimen Source: S17-Test
Specimen Description: Lung, right lower lobe
Diagnosis: Lung non-small cell carcinoma
Tumor Content: 30%
Genes in Panel:
ALK, ARAF, BRAF, EGFR, ERBB2, KRAS, MAP2K1, MET, MTOR, NRAS, RET, ROS1, TP53

Actionable: Variants of Strong Clinical Significance

EGFR
Mutations: EGFR_E746_A750 deletion
Interpretation:
This E746_A750 deletion is in exon 19 of EGFR and is considered to be an activating mutation. Therefore, this patient may respond to the treatment of EGFR kinase inbibitors. EGFR mutations are often found in lung adenocarcinomas with frequencies ranging from 10% in Caucasian to 40% in East Asian patients. EGFR mutations in the tyrosine kinase domain (exon 18-21), result in constitutive activation of the RAS/MAPK signaling pathway, may confer sensitive to EGFR kinase inhibitors.

Other Variants

ALK
Mutations: ALK_V1471E
Interpretation: ALK_V1471E is a mis-sense protein variant and the functional impact of this alteration is unclear.

Characteristics: Somatic mutations, including point mutations, small indels, and splicing variants, in and flanking the coding exons of each gene in this NGS panel are sequenced using next generation sequencing technology. Copy number variation and homozygous loss of these genes are also evaluated with this technique. This assay is designed for detection of somatic mutations, but may also detect germline mutations in this mixed cell population. If a germline mutation is suspected clinically, appropriate genetic counseling and testing of peripheral blood is recommended. Results of this test must always be interpreted within the clinical context and other relevant studies, and should not be used as the sole means of diagnosis.

Methodology: Formalin-fixed, paraffin-embedded (FFPE) tissue sections are reviewed by a pathologist and manually micro-dissected to improve the cellularity from tumor. If the tumor content is insufficient in the initial tissue block, cytology smears from the same biopsy will be scored and scraped as alternate material. DNA is extracted from selected slides, and following library preparation using a hybrid capture-based custom-designed probe set, is subjected to next generation sequencing (NGS). Post-sequencing analysis is performed using hg19 reference sequence and in-house validated bioinformatics pipelines. ALK and ROS1 gene rearrangements are analyzed by fluorescence in situ hybridization (FISH) using the Vysis ALK and ROS1 Break Apart probes and the MetaSystems Metafer automated scanning fluorescent microscope.

Limitations: The depth of sequencing coverage may be variable for some targeted regions depending on the quality of the specimen, but assay performance below the minimum acceptable criteria is noted. A low tumor cell percentage in the sample may affect the true mutation allele frequency (concentration) and assay sensitivity. A result of not detected does not rule out the presence of a mutation below the analytical sensitivity. Mutations in the regions or genes not covered by this panel will be not detected. This assay is not designed to detect unique germline mutations, insertion/deletion >50bp, or cryptic mutations involve intronic regions.

Performance Characteristics: The Sensitivity is 99.3% for single base substitution; 97.2% for indels < 50bp; 98% for gene amplification; and 91.7% for gene homozygous loss.
The specificity is >99% for all four variant types.
The Reproducibility is 100% for all four variant types.
The Limit of Detection (LOD) is 3-5% for single base substitution; 5-10% for indels <50bp; = 8 copies for gene amplification with at least 200X read depth.
The minimum tumor content is 10% for the assay; >= 20% for calls on gene amplification at 8-10 copies and homozygous loss.

Compliance Statement: This test was developed and its performance characteristics determined by the Molecular Pathology Laboratory, CellNetix Pathology & Laboratories, Seattle WA 98104. It has not been approved by the U.S. Food and Drug Administration. The FDA has determined that such clearance or approval is not necessary. This test is for clinical purpose. It should not be regarded as investigational or for research. This laboratory is regulated under the 1988 CLIA amendments as qualified to perform high-complexity clinical testing.

Dominique Coco, M.D. Electronically signed 02/12/2018 15:51
(206) 576-6050

CellNetix Pathology: 1124 Columbia Street Suite 200 Seattle WA 98104

Patient ID: Test
Collected: 01/29/2018
Reference No:
Requisition No:
Microscopic: Unless otherwise specified, a microscopic exam has been performed.

Age:
Gender:
Received: 01/29/2018

Providers:
Dr. Test

Test, MD
CellNetix - Seattle
1124 Columbia St.
Ste. 200
SEATTLE, WA. 98104-2048

Patient: Test S18-Test Page

Patient information

Specimen and panel information

Actionable mutations detected for approved therapies

Alterations types could be detected by this assay

Method details for the detection

Limitations of this assay

Sensitivity, specificity, and limit of detection of this assay

Direct contact information for follow up or questions.

 ©2018 CellNetix