TreeCODE
Decoding Life Through Science

CELEMICS

# Celemics Whole Exome Sequencing Service

## Ultimate Exonic Coverage Customizable Bioinformatics

**Launching Promotion!**

No limitation in sample numbers
Free international shipping
Samples to reach Celemics by August 31st 2022

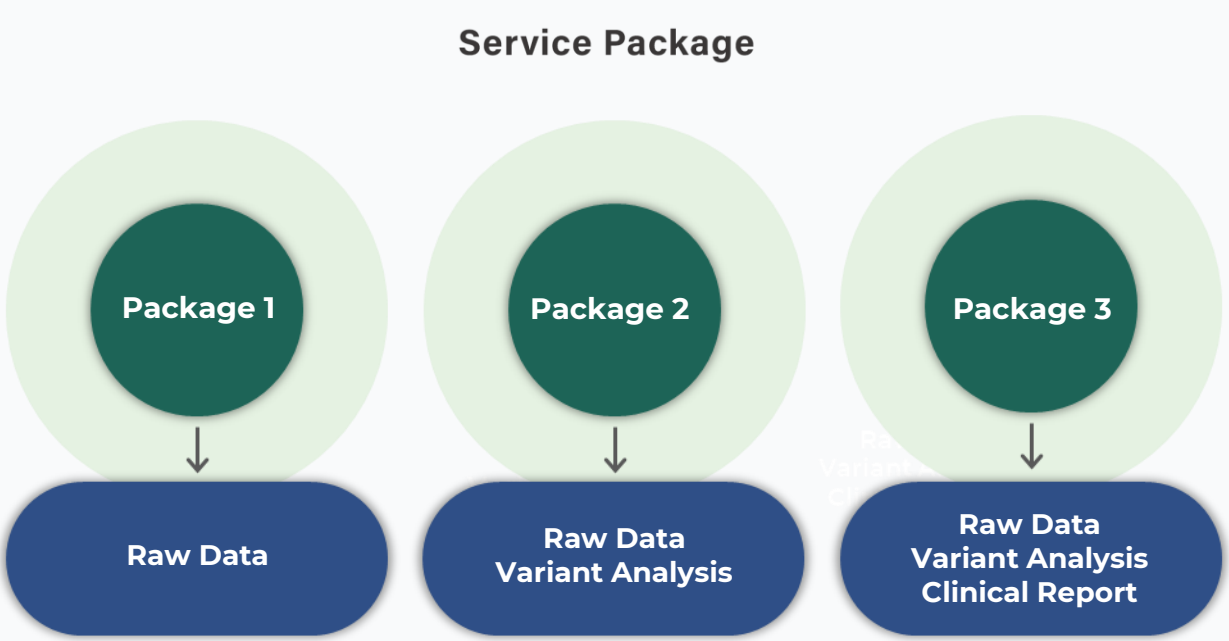
### Key Features of Celemics Whole Exome Sequencing Service

- **Complete Whole Exome Coverage**
  Covering exonic regions of major exome panels (37 Mb) with >98% coverage.
- **Superior Performance in the Market**
  Strong capture performance against GC rich regions as well as higher quality in coverage and uniformity.
- **FASTQ to Clinical Interpretation Support**
  Experience our full bioinformatics support and customizable services.

### Experience the comprehensive exome panel covering all exons of the existing exome panels in the market

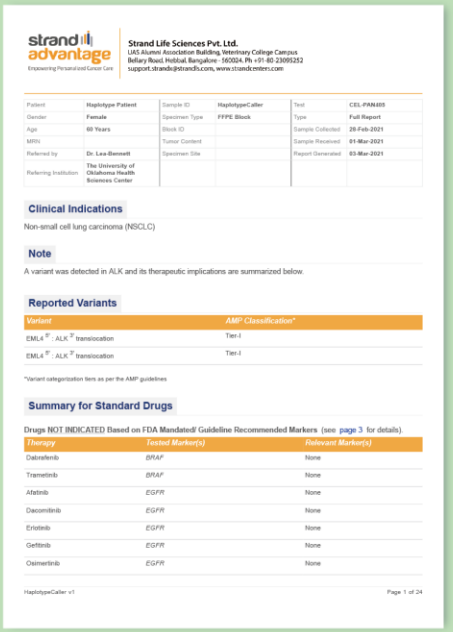
Celemics Whole Exome Sequencing Panel is designed to cover all the exonic regions of major exome panels in the market, allowing us to provide the ultimate coverage of the whole human exome.
We have created a Whole Exome Panel that consistently delivers the highest quality of results to our valued customers. In addition, this advancement allows us to offer cost-effective solutions that the market has never seen before.

### Select your data analysis options from raw data to clinical reports



## Clinical Report Example: Includes pathogenicity and drug associated information

Celemics provides quick reporting of actionable information for the customers who need a quick and clear result interpretation from NGS data. The clinical interpretation report provided through Strand includes pathogenicity and drug associated information.



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support.strandx@strandls.com, www.strandcenters.com

| | | | | | |
|---|---|---|---|---|---|
| Patient | Haplotype Patient | Sample ID | HaplotypeCaller | Test | CEL-PAN405 |
| Gender | Female | Specimen Type | FFPE Block | Type | Full Report |
| Age | 60 Years | Block ID | | Sample Collected | 28-Feb-2021 |
| MRN | | Tumor Content | | Sample Received | 01-Mar-2021 |
| Referred by | Dr. Lea-Bennett | Specimen Site | | Report Generated | 03-Mar-2021 |
| Referring Institution | The University of Oklahoma Health Sciences Center | | | | |

**Clinical Indications**

Non-small cell lung carcinoma (NSCLC)

**Note**

A variant was detected in ALK and its therapeutic implications are summarized below.

**Reported Variants**

| Variant | AMP Classification* |
|---|---|
| EML4 $^{E}$ : ALK $^{F}$ translocation | Tier-I |
| EML4 $^{E}$ : ALK $^{F}$ translocation | Tier-I |

*Variant categorization tiers as per the AMP guidelines

**Summary for Standard Drugs**

Drugs NOT INDICATED Based on FDA Mandated/ Guideline Recommended Markers (see page 3 for details).

| Therapy | Tested Marker(s) | Relevant Marker(s) |
|---|---|---|
| Dabrafenib | *BRAF* | None |
| Trametinib | *BRAF* | None |
| Afatinib | *EGFR* | None |
| Dacomitinib | *EGFR* | None |
| Erlotinib | *EGFR* | None |
| Gefitinib | *EGFR* | None |
| Osimertinib | *EGFR* | None |

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**Standard Drugs**

**Alectinib** Enhanced Response

**Markers**

ALK

**Evidence Details**

Alectinib is a second generation ALK inhibitor approved for the treatment of patients with ALK-rearrangement positive non-small cell lung cancer (NSCLC). Alectinib has shown clinical benefit in both crizotinib pre-treated and treatment naive ALK positive NSCLC patients in multiple clinical studies [1,2], [3], [4], [5], [6]. The phase III ALEX study comparing response to alectinib and crizotinib in advanced ALK-positive NSCLC patients (n=303), found alectinib to be superior to crizotinib in terms of clinical benefit with a significantly higher 12-month event-free survival rate with alectinib (68.4% with alectinib vs. 48.7% with crizotinib), event of CNS progression in 18% of alectinib treated patients compared to 45% in the crizotinib treated group and a response rate of 82.9% in the alectinib group vs 75.5% in the crizotinib group [2].

**Marker Details**

**EML4 (NM_019063, Exon 1-6) : ALK (NM_004304, Exon 20-29)**
Oncogenicity Established by in-vitro Studies
EML4-ALK translocation is the most common aberration of the ALK gene, which is seen exclusively in lung cancer and represents 2-7% of the lung cancers cases [7]. The fusion gene results from an inversion event on the short arm of chromosome 2 and has constitutive ALK kinase activity [8]. Till date, over 11 EML4-ALK fusion variants have been identified in lung cancer, composed of varying EML4 transcript length fused with exon 20 of ALK [9].

**EML4 (NM_001145076, Exon 1-6) : ALK (NM_004304, Exon 20-29)**
Oncogenicity Established by in-vitro Studies
EML4-ALK translocation is the most common aberration of the ALK gene, which is seen exclusively in lung cancer and represents 2-7% of the lung cancers cases [7]. The fusion gene results from an inversion event on the short arm of chromosome 2 and has constitutive ALK kinase activity [8]. Till date, over 11 EML4-ALK fusion variants have been identified in lung cancer, composed of varying EML4 transcript length fused with exon 20 of ALK [9].

**Drug Description**

An orally available inhibitor of the receptor tyrosine kinase anaplastic lymphoma kinase (ALK) with antineoplastic activity. Upon administration, alectinib binds to and inhibits ALK kinase, ALK fusion proteins as well as the gatekeeper mutation ALKL1196M known as one of the mechanisms of acquired resistance to small-molecule kinase inhibitors. The inhibition leads to disruption of ALK-mediated signaling and eventually inhibits tumor cell growth in ALK-overexpressing tumor cells. ALK belongs to the insulin receptor superfamily and plays an important role in nervous system development. ALK dysregulation and gene rearrangements are associated with a series of tumors.
*Source: The National Cancer Institute's Cancer Drug Information*

**References**

1. Liao BC *et al.* 2015. Treating patients with ALK-positive non-small cell lung cancer: latest evidence and management strategy. *Ther Adv Med Oncol.* 7 (5):274-90 [PMID: 26327925].

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## Specifications

| | |
|---|---|
| **Target size** | 37 Mb |
| **Covered region** | CCDS, RefSeq, Gencode |
| **Sample types** | Genomic DNA, Cell-free DNA, FFPE, Fresh frozen tissue |
| **Sequencing depth** | Standard : 100x |
| **Turnaround time** | Package 1 and 2: 9 weeks, Package 3: 11 weeks |
| **Deliverables** | Package 1 : FASTQ, Summary report<br>Package 2 : FASTQ, BAM, Stat file, Annotated VCF, Summary report<br>Package 3 : FASTQ, BAM, Stat file, Annotated VCF, Summary and clinical reports |

Note Please contact us for the following information:
* Pricing for each package
* Sample requirement for different sample type

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