

# Celemics Whole Exome Sequencing Kit

Ultimate Exonic Coverage  
Simplified One-Day Protocol  
Customizable Bioinformatics

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

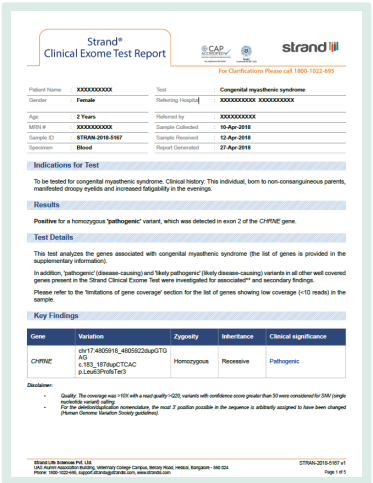
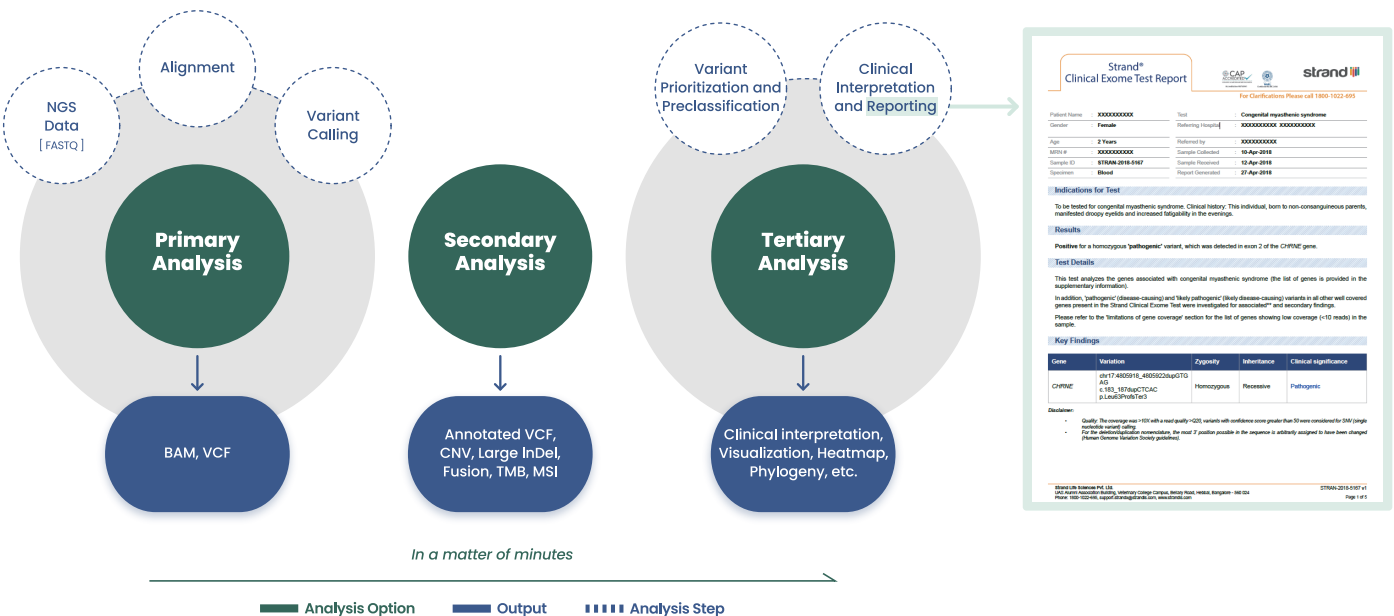
Celemics Whole Exome Sequencing Panel is designed to cover all the exonic regions of major exome panels in the market, allowing us to provide the ultimate coverage of the whole human exome. We have created a Whole Exome Panel that consistently delivers the highest quality of results to our valued customers.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

## Streamline library preparation and hybridization for a one-day workflow with no heavy instruments

The Hybridization Enhancer developed by Celemics drastically shortens the hybridization time with no compromise on coverage and uniformity performance. Celemics' alternative methods to library preparation steps do not require heavy instruments such as a sonicator and a vacuum concentrator, allowing for convenient workflow and automation support.

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

### CAS (celemics Analysis Service) Workflow



## Key Features

- **Complete Whole Exome Coverage**

Covering exonic regions of major exome panels (37 Mb) with greater than 98% coverage.

- **Superior Performance in the Market**

Strong capture performance against GC rich regions with high coverage and uniformity.

- **Gene Add-On Service**

Use your tailored exome panel by adding spike-in mtDNA or any regions of interest.

- **FASTQ to Clinical Interpretation Support**

Experience our full bioinformatics support and customizable services.

- **Rapid One-Day Protocol**

Expedite exome sequencing with no compromise on data quality.

- **No Need for Heavy Instruments**

Simplify your workflow with alternative methods for sample shearing, concentrating, and QC.

- **Complete Walkaway Automation**

Automate from sample preparation to hybridization on Hamilton, Bravo, or Sciclone, etc.

- **Flexible Integration with NGS Sequencers**

Seamlessly integrated with Illumina and MGI sequencers.

## Specifications

<b>Target size</b>	37 Mb
<b>Covered region</b>	CCDS, RefSeq, Gencode
<b>Multiplexing option</b>	4-plex enrichment
<b>Platform</b>	All Illumina and MGI platforms
<b>Bioinformatics</b>	Primary, secondary, and tertiary analysis via CAS
<b>Uniformity</b>	93% (0.2x mean depth coverage uniformity)
<b>On-target (1-PCT OFF BAIT)</b>	90%

## Related Products

Product name	Target size	#of genes	Covered region
G-Mendeliome CES Standard	13.8 Mb	5,508	CDS, hotspots
G-Mendeliome CES Expanded	19.6 Mb	7,513	CDS, hotspots, mitochondrial genome
G-Mendeliome Disease-Specific Panels	37-1,159 Kb	14-293	Whole CDS, hotspots

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