



PRODUCTS AND SERVICES 2024

Celemics

Beyond the boundaries of
what's possible in the world of NGS



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1. Target Enrichment

Celemics NGS Targeted Sequencing Solutions

Outstanding Targeted Sequencing
Performance Supported by
Celemics Core Technologies

Key Features

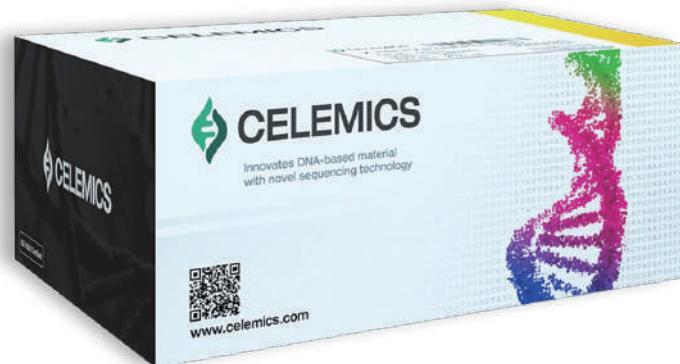
- Flawless design with industry-leading performance
- Robust result even in areas difficult to analyze or challenging samples
- Provision of molecular barcoded kits and bioinformatics solution
- Gene add-on service for expanding the existing panels or designing customized NGS panels
- Flexible integration on various sequencing platforms
- No need for heavy instrument

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Celemics NGS Targeted Sequencing Solution

Our target enrichment panel uses hybridization-based capture technology to enable the core process of targeted sequencing, which is the separation and analysis of specific regional sequences of entire genomes. It can also accurately analyze all types of mutations, such as SNV, Indel, CNV, and rearrangement. Celemics' target enrichment panel utilizes our exclusive core technologies; intrinsic probe design, rebalancing, and molecular barcode technologies. These technologies ensure our targeted sequencing solutions to efficiently analyze not only hard-to-capture areas such as GC-rich and homologous regions but also tiny amounts of damaged DNA or RNA originated from circulating tumor cells or FFPE samples with strong ability to assess all types of mutations with high sensitivity and specificity.



Celemics Core Technologies

Probe Design Technology

Celemics presents unique approach in the industry; performance verification for all designed probes. Currently, it is impossible to predict DNA capture level and affinity through in-silico method. Once the probe is designed, the actual validation run must be done to verify and confirm the capture performance. To ensure Celemics' designed probe performance, we first utilize our Big Data based probe design process to select best probe combinations with respect to optimal capturing region, including hard-to-capture region. Then, after the proper validation run, we finalize the probe sets through 'rebalancing' to ensure exceptional coverage and uniformity.

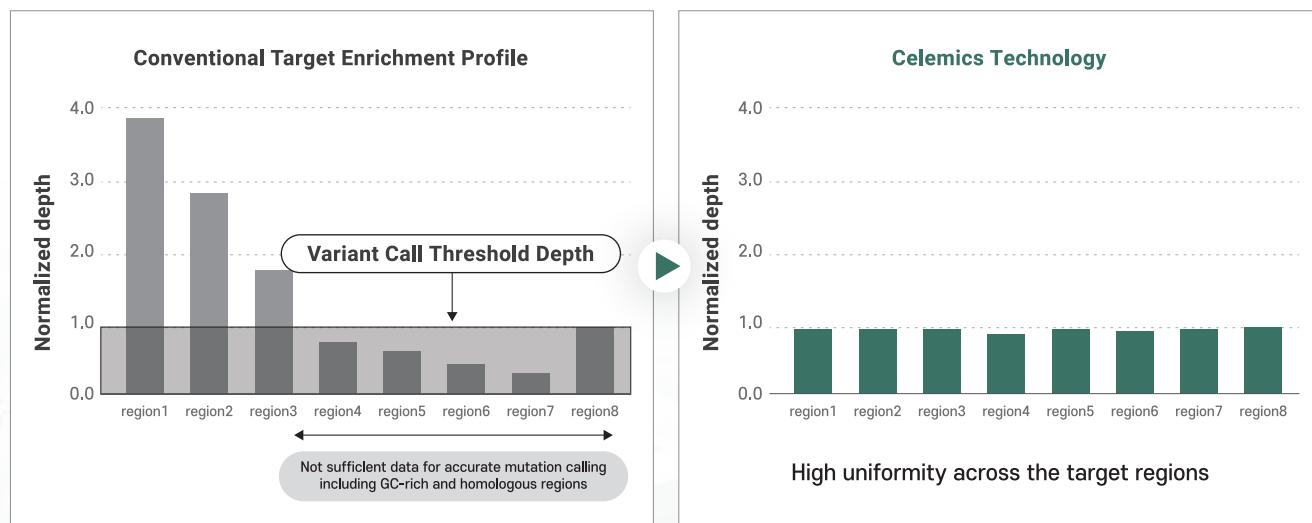


Figure 1. Current NGS Market problem and how Celemics provides the solution through probe design technology.

Probe Manufacturing Technology

All Celemics designed probes are manufactured in specific ways; we achieve cost-effective and high performance set of low-biased probes through our proprietary synthesis technology. This will accomplish superior lot-to-lot uniformity of the probe sets, guaranteeing the desirable reproducibility, especially for repeated orders. Moreover, Celemics operates thorough validation and optimization for enhanced probe affinity.

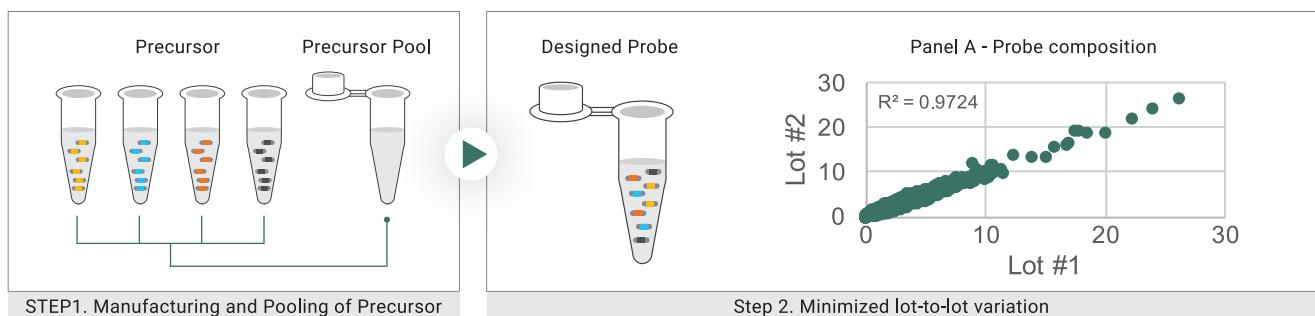


Figure 2. Celemics exclusive Probe manufacturing technology. In-house manufactured oligonucleotides for faster TAT.

Optimization Technology

Celemics provides robust NGS solution by custom-fit assay development and exclusive technology for chemistry optimization. This includes not only the control of enzymes and buffers, but we also introduce our proprietary technology for designing special blocker. Celemics has proprietary approach for design species-specific and sequencer-specific blockers; we can provide different blockers pertaining to your sample type, whether it is human or animal-derived, or sequencer-specific blockers for the NGS instrument of your choice. Along with these exclusive blockers, Celemics has the ability to fine-tune the chemistry to control the binding specificity and affinity of our in-house designed probes and kit, which would lead to stabilized sequencing reaction and thus provide market-leading quality of on-target ratio and uniformity.

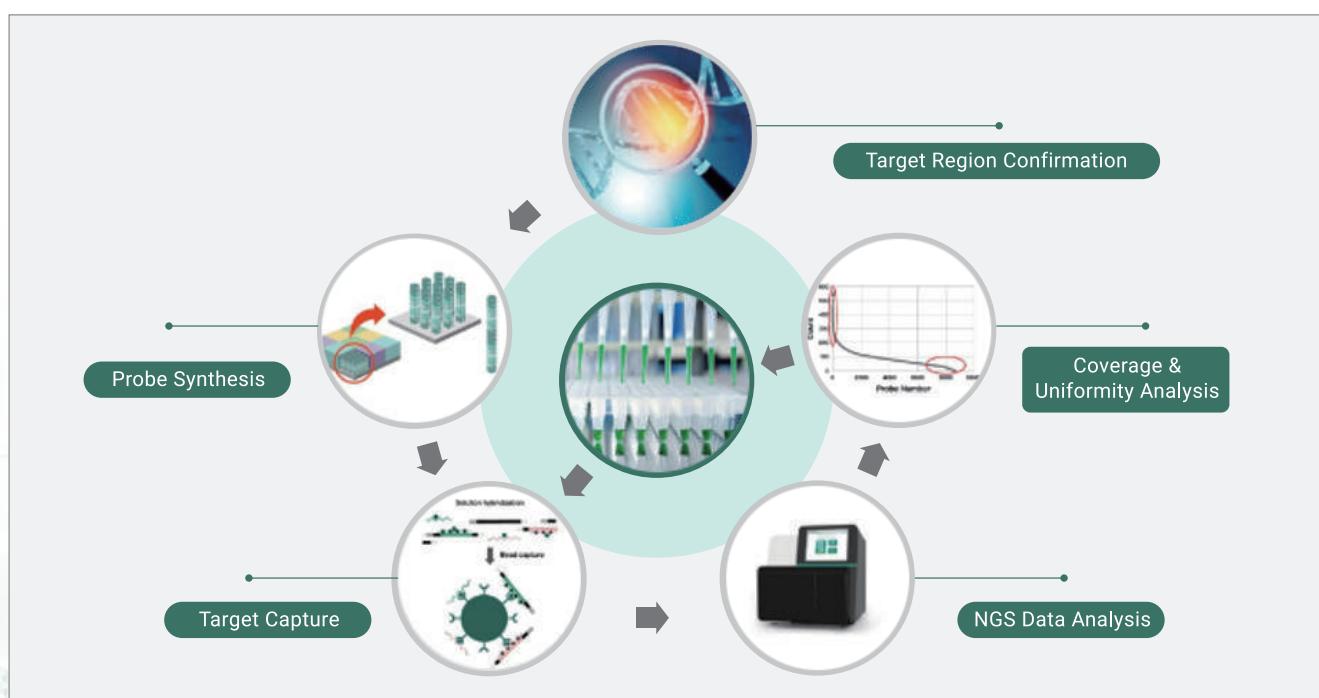


Figure 3. Overview of Celemics Rebalancing Technology.

Celemics Library Preparation Kit

Celemics provides library preparation kits that are highly optimized for efficient usage with Celemics ready-to-use panels and/or customized panels. The kits are designed to be compatible with different types of sequencing instruments, paired with corresponding indices. There are two methods for library preparation step, Standard Library Preparation Kit (LP Kit) and Enzymatic Library Preparation Kit (EP Kit). Both kits include all set of enzymes needed for high quality and quantity of NGS libraries regardless of sample types.

LP Kit		EP Kit
Option 1. Sonication	Option 2. Fragmentase	
Bead Purification & Quantification		FER/A
ER/A		
Adapter Ligation		
Bead Purification		
Index PCR		
Target Enrichment		

Figure 4. Celemics library preparation kit option chart.

Celemics Bioinformatics Solution

As a part of Celemics' intellectual property, a unique NGS bioinformatics pipeline is developed to process and analyze massive amounts of genomic data into a readable format with clinically significant biomarkers obtained through Next Generation Sequencing. From FASTQ to VCF and interpretation; we can provide all types of variants, including SNV, Indel, CNV, rearrangement, MSI, TMB, or any other ultra-low variants of you wish to discover. Along with the purchase of Celemics' panels and kits, customer will be provided with built-in service for analysis. In addition to this, customer may choose to customize analysis options or request different tiers of analysis for further clinical interpretation.

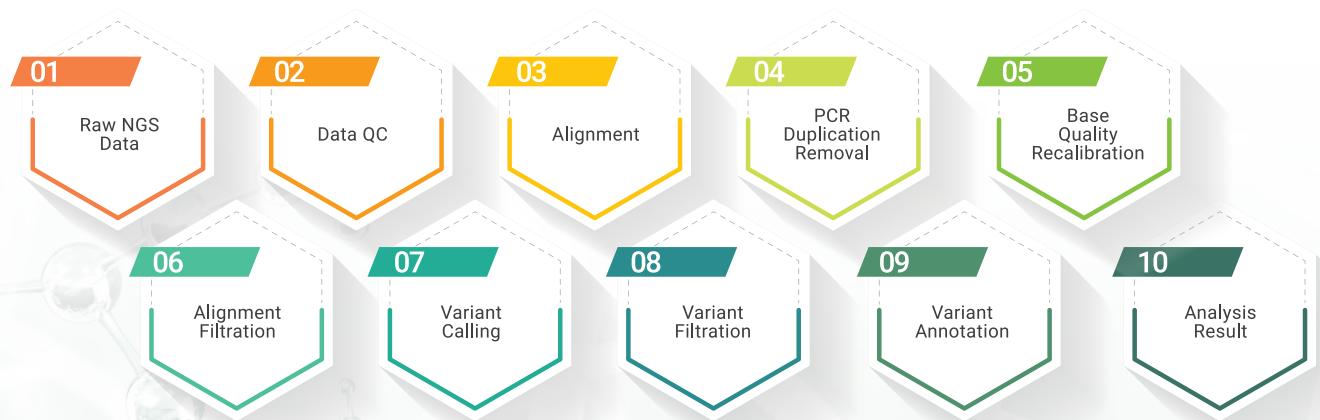
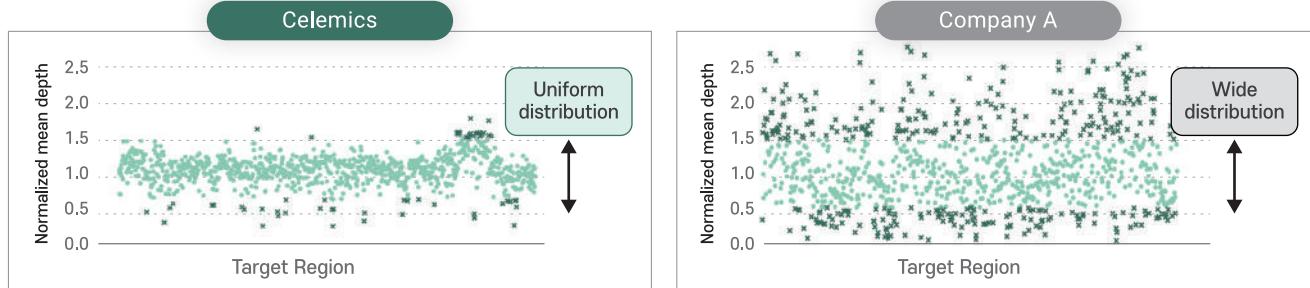


Figure 5. NGS data analysis pipeline.

Celemics NGS Targeted Sequencing Performance Data

On-target ratio and uniformity

Celemics has technology to optimize binding capacity with strong RNA probe to provide industry-leading on-target ratio and uniformity.



* This comparison study was performed with same target region, same data amount, and same analysis method.

Figure 6. Comparison of capture uniformity between Celemics and Company A.

Hard-to-capture region; GC-rich

Celemics' probe affinity demonstrates superior capture capacity even in hard-to-capture region.

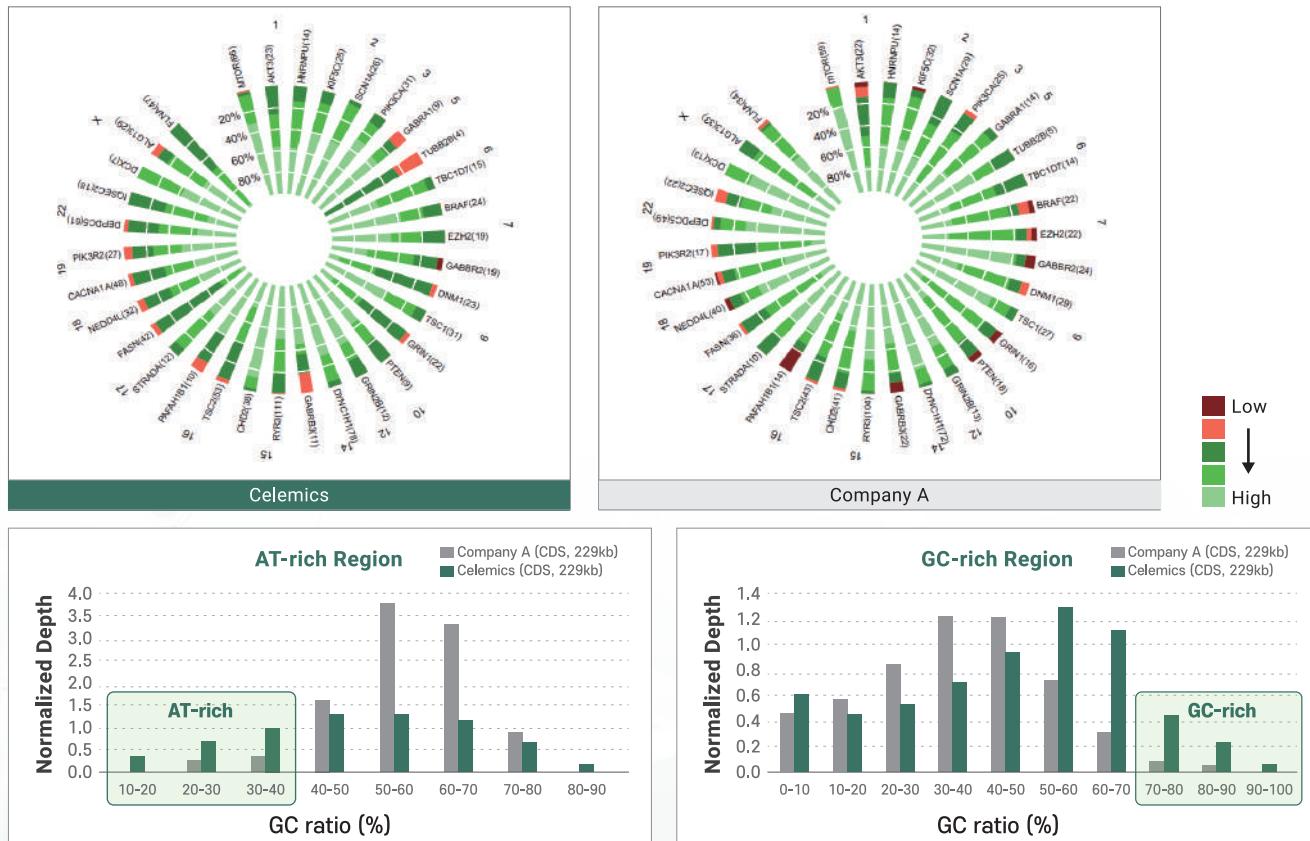


Figure 7. Hard-to-capture region coverage data comparison.

Celemics NGS Targeted Sequencing Performance Data

Hard-to-capture region; GC-rich

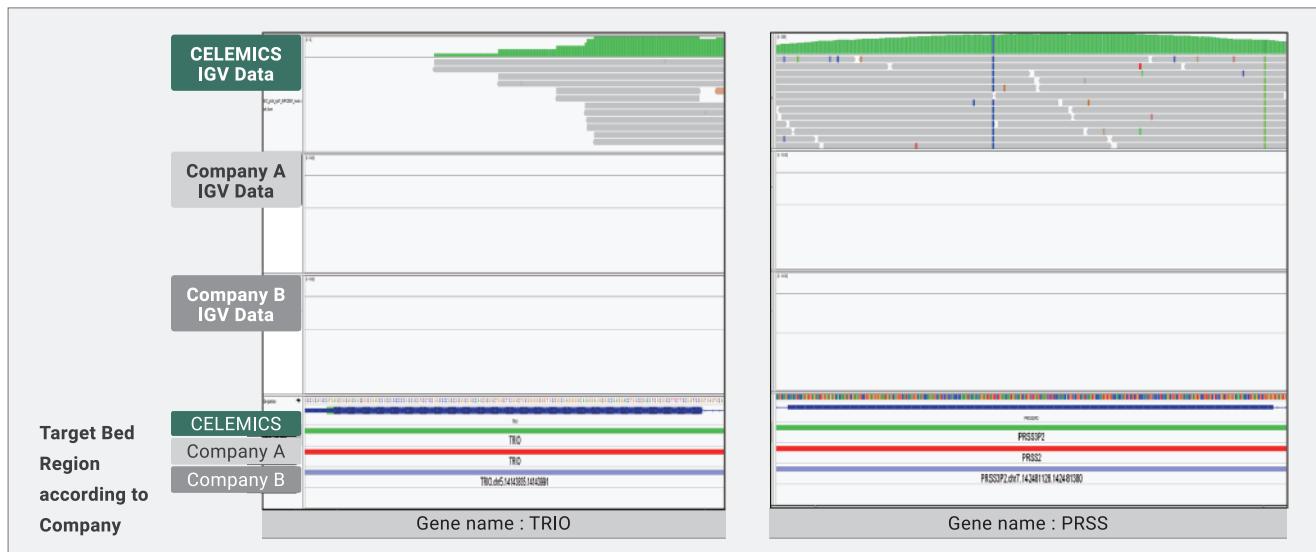


Figure 8. Comparison of IGV plots for TRIO and PRSS genes show superior capture performance of Celemics designed probe sets.

Hard-to-capture region; Masking region

Unlike other companies, Celemics does not mask hard-to-capture regions to increase the overall data performance metrics as our exclusive probe design and rebalancing technologies ensure to capture all targeted regions.

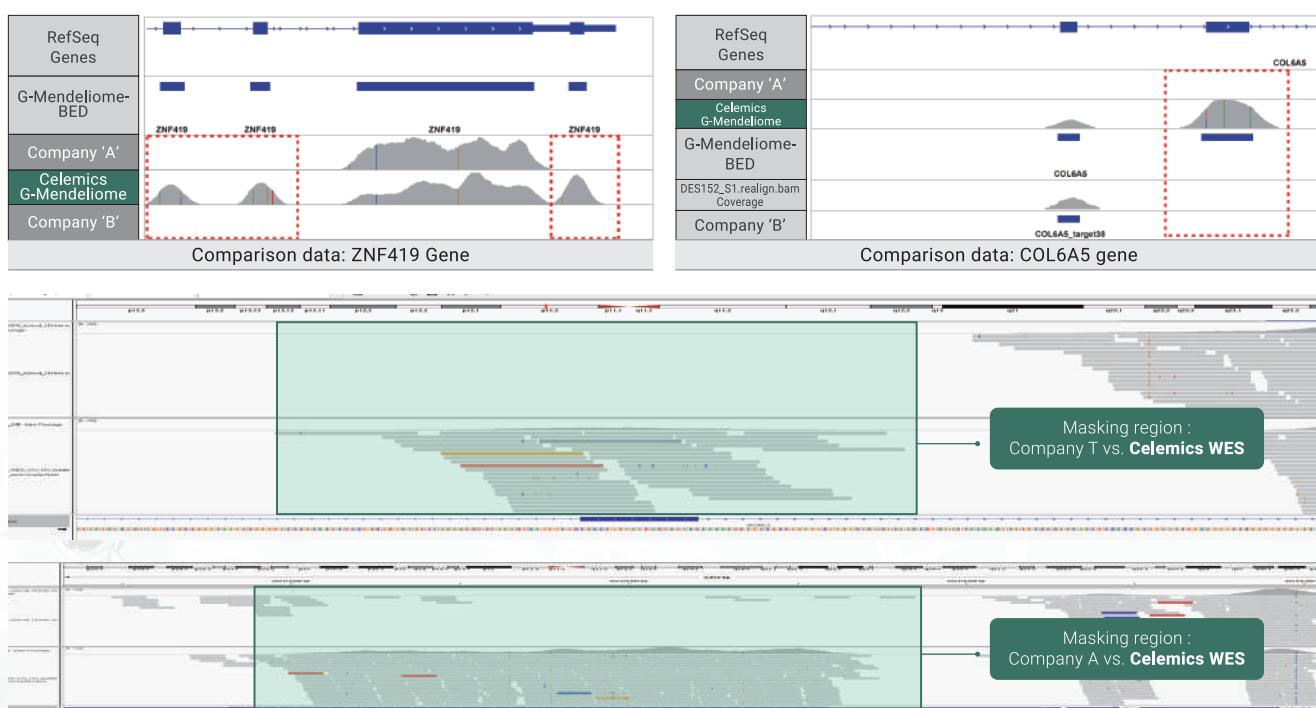
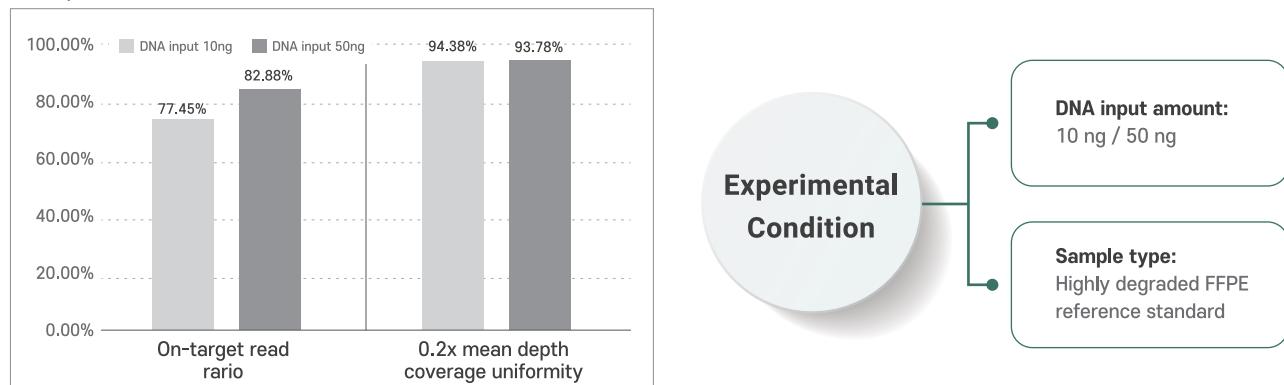


Figure 9. Comparison of capture data of 'masking regions' between Celemics and other competitor products.

Celemics NGS Targeted Sequencing Performance Data

Accurate detection with difficult samples

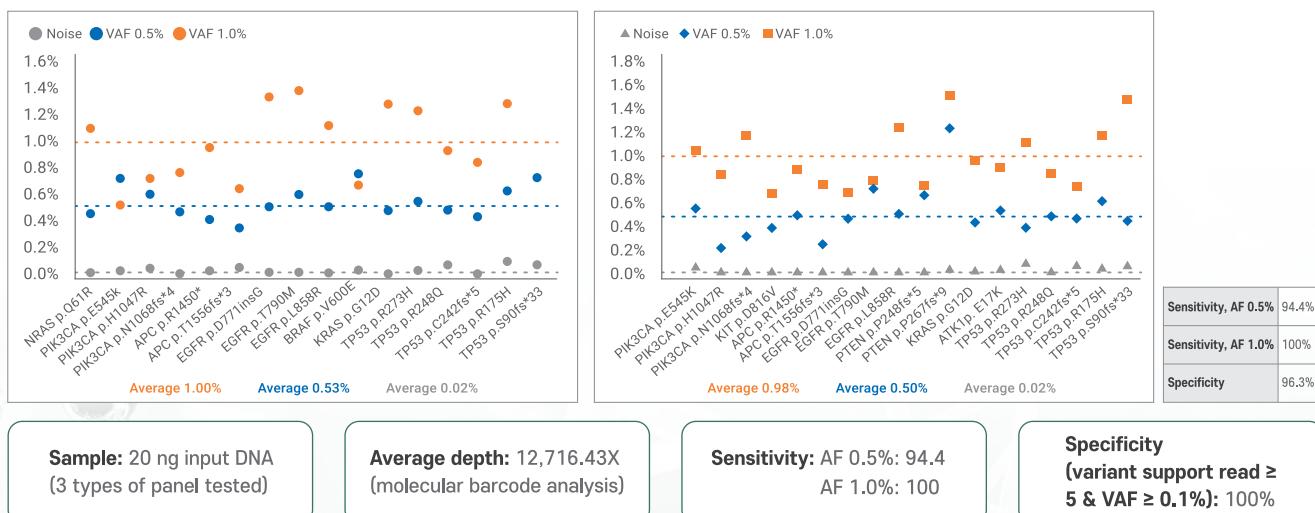
Celemics' optimized chemistry and probe sets allow accurate detection in low-yield, severely damaged FFPE DNA samples.



Sample No.	Sample Name	DNA input (ng)	On-target read ratio	Mean Depth	0.2x mean depth coverage uniformity	1x coverage	20x coverage
1	Severe damaged reference standard #1	10	77.45%	186.42	94.38%	99.98%	98.16%
2	Severe damaged reference standard #2	50	82.88%	293.87	93.78%	99.98%	99.08%

Figure 10. Sequencing data using low-yield, severely damaged FFPE DNA samples (Quantitative Multiplex Reference Standard fcDNA (Horizon Discovery)).

Use of Celemics' designed molecular barcode maximizes the data retrieval and accuracy even for ultra-low VAF, especially for ctDNA-related applications.



* Reference material used: Seraseq® ctDNA Reference Material v2 AF0.5% / AF1.0%

Figure 11. Exceptional performance evaluation of Celemics ctDNA panels, demonstrating accurate detection of variants with low VAF using Seraseq® ctDNA Reference Material v2 AF0.5% / AF1.0% (SeraCare).

Celemics NGS Targeted Sequencing Performance Data

Targeted RNA Sequencing

Celemics Targeted RNA sequencing panel is much more cost-effective compared to total RNA sequencing. It provides full coverage of mRNA of targeted genes and applicable in various types of sample, such as low-yield FFPE, fresh or frozen tissues and other biological samples.

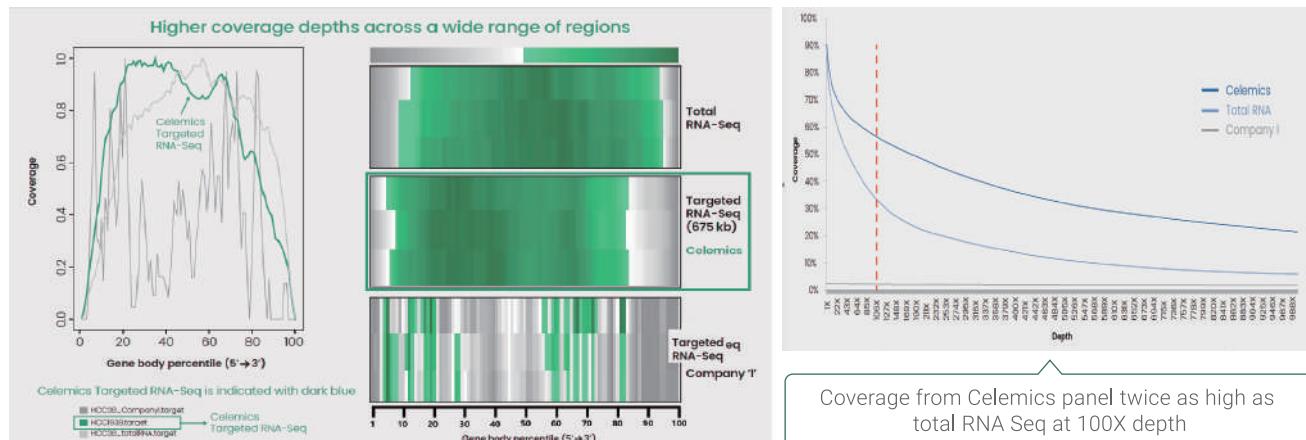


Figure 12. Celemics targeted RNA sequencing solution compared with total RNA sequencing.

Fusion Detection

Our proprietary probe design and highly optimized enzymes allows effective fusion detection.



Figure 13. Precisely designed and rebalanced probes effectively capturing fusion region.



2. Ready-to-use Panel

Celemics Whole Exome Sequencing

Extensive Exonic Coverage
with Exceptional Performance

Key Features

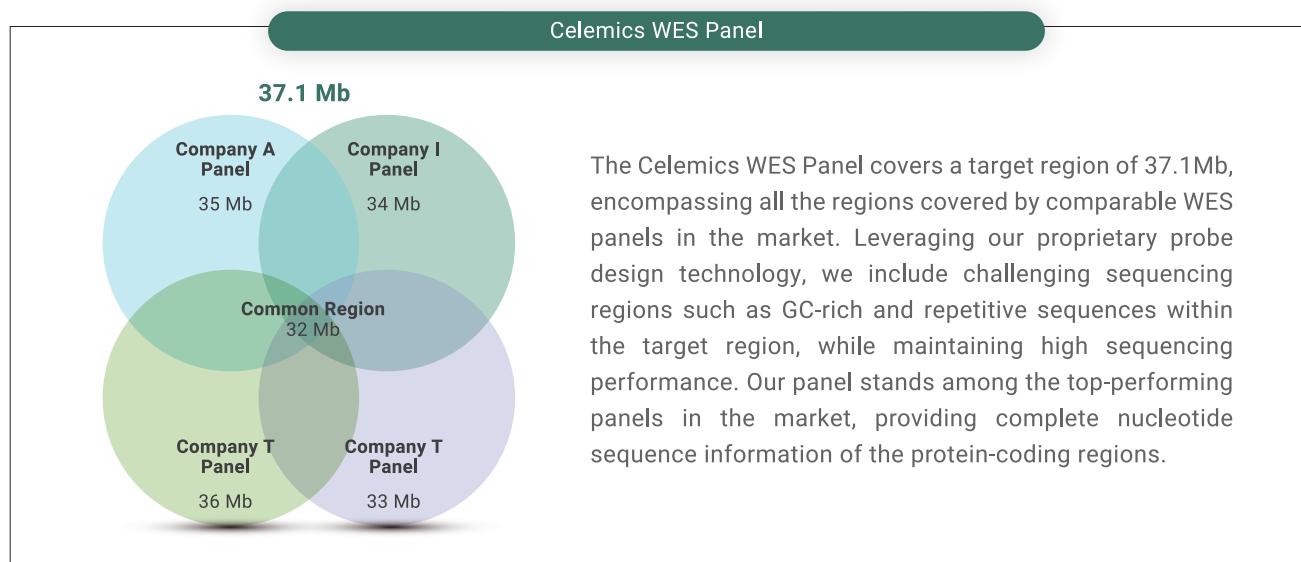
- Complete Whole Exome Coverage
- Rapid Single Day Workflow
- No Need of Heavy Instruments
- FASTQ to Clinical Interpretation Capability

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Celemics Whole Exome Sequencing Panel

What differentiates the Celemics Whole Exome Sequencing Panel from other WES panels in the market? Most researchers look for complete coverage especially when it comes to WES. However, most WES panels in the market vary in their target regions and some compromise with coverage, even deleting hard-to-capture regions in order to enhance performance. Celemics has developed a WES panel that covers the regions of all four major WES panels in the market, spanning the coding regions from RefSeq, CCDS and GENCODE. The Celemics WES Panel provides the most comprehensive coverage of protein-coding regions, thereby enabling marker discovery to diagnostics.



Specification

Covered region	CCDS, RefSeq, Genecode	
Target size	37.1 Mb	
Multiplexing option	Up to 12 Plex enrichment	
Platform	Illumina, Thermo Fisher, and MGI	
Uniformity	gDNA	FFPE
	> 96%	> 95%
On-target	gDNA	FFPE
	> 90%	> 90%
Bioinformatics Support	Primary Analysis: FASTQ to annotated VCF Secondary Analysis: CNV, Large Indel, and TMB Tertiary Analysis: Clinical interpretation, Visualization Curation	

Performance Data

Market-leading panel performance

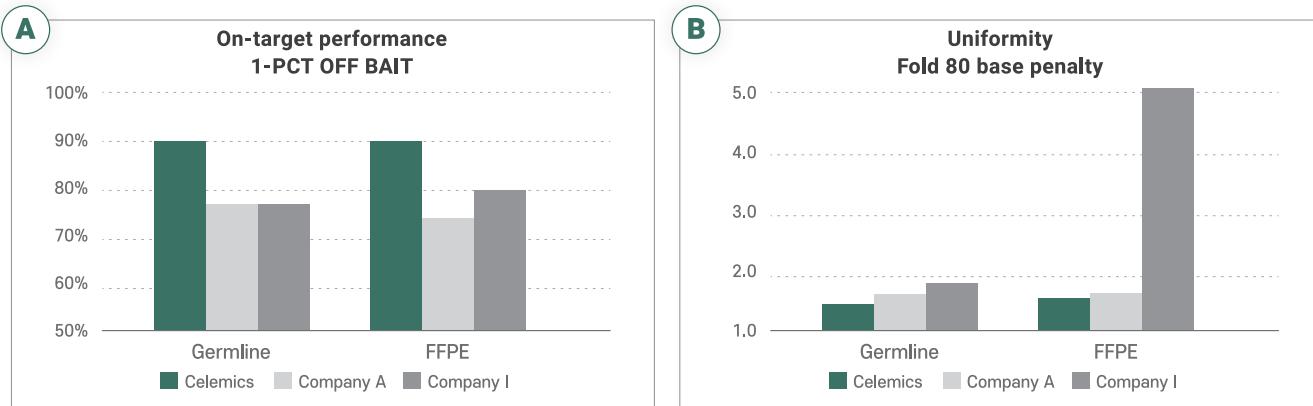


Figure 1. Superior Performance in the Market. Celemics WES Panel shows exceptional performance compared to other competitor products in both germline and FFPE analysis, measured by (A) 1-PCT OFF BAIT (higher the better), (B) Fold 80 base penalty (lower the better). Third-party laboratories (Certified Service Providers) conducted a comparison study between the Celemics WES Panel, Company A and Company I panels. Reference materials NA12878, NA12891, NA12892 for germline analysis, and HD832 for FFPE analysis were used with same amount. Illumina instruments were used for the sequencing. The data from the three panels was downsampled to an equal size of 5.4 GB to eliminate effects caused by different sequencing amounts.

Superior target capture performance

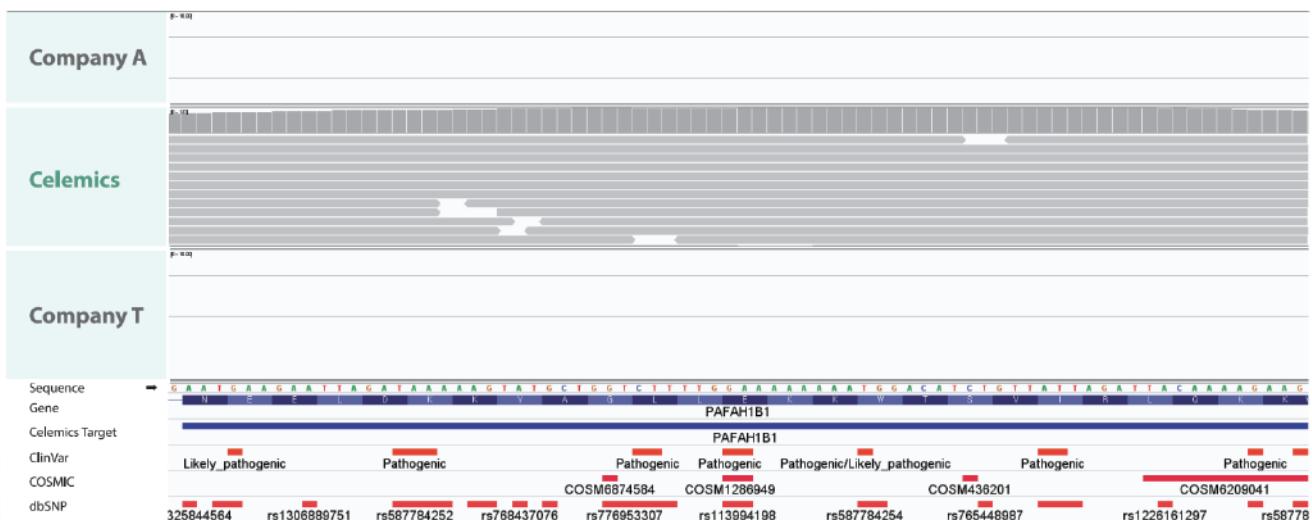


Figure 2. Superior Capture Performance and Coverage. A mutation in PAFAH1B1 causes Isolated Lissencephaly Sequence (ILS) & Miller-Dieker syndrome. While other competitor panels fail to capture the A-T rich regions in the gene, the Celemics WES Panel successfully covers the region.

With Celemics' proprietary probe and assay design technology, we are competent to provide a robust WES panel with market-leading on-target ratio and uniformity. For all panels that we design and manufacture, we always validate the panel and sequencing performance by fine-tuning the probe sets and reagents to ensure exceptional capture performance even in 'hard-to-capture' region to maximize the efficiency and provide the highest quality possible sequencing data for all our customers.

Performance Data

Comparison of uniformity with competitor panels

Coverage uniformity measures how evenly sequencing data is distributed across target regions. Ideally, all target regions should have similar and high coverage, which is important for consistently detecting all genetic variations. A high coverage uniformity ensures accurate identification of genetic mutations across all positions within the target regions.

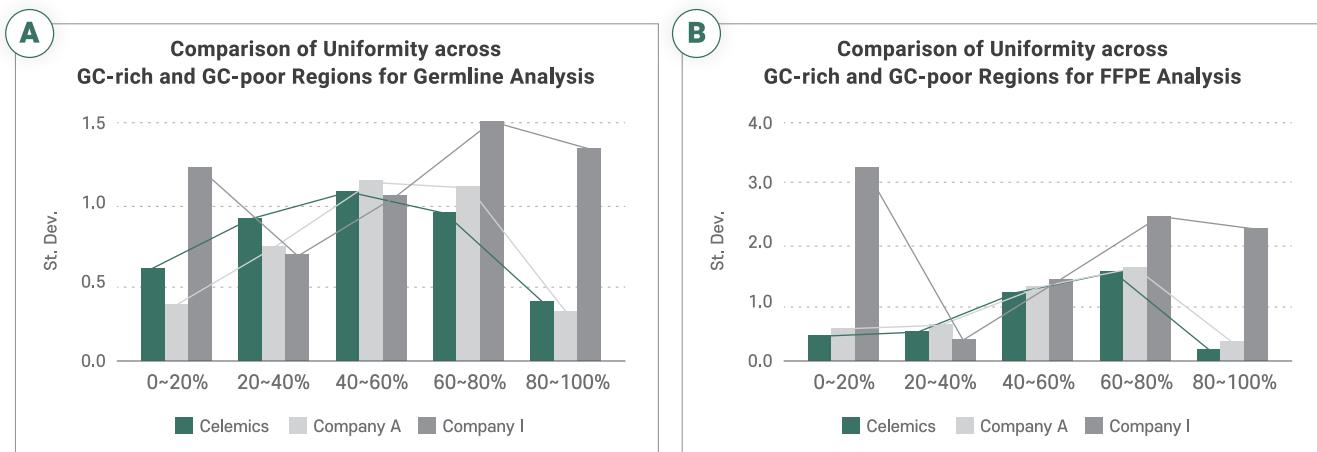


Figure 3. Exceptional Uniformity across Low and High GC Regions. (A) The Celemics WES Panel demonstrates minimal deviation, yielding 0.166 standard deviations (lower the better) across GC-rich and AT-rich regions in comparison to competitor products yielding 0.199 and 0.356 standard deviations. (B) The Bar graphs shown in different GC ratios also illustrate the consistent uniformity of Celemics WES Panel in comparison to the competitor products.

Comparison of coverage with competitor panels

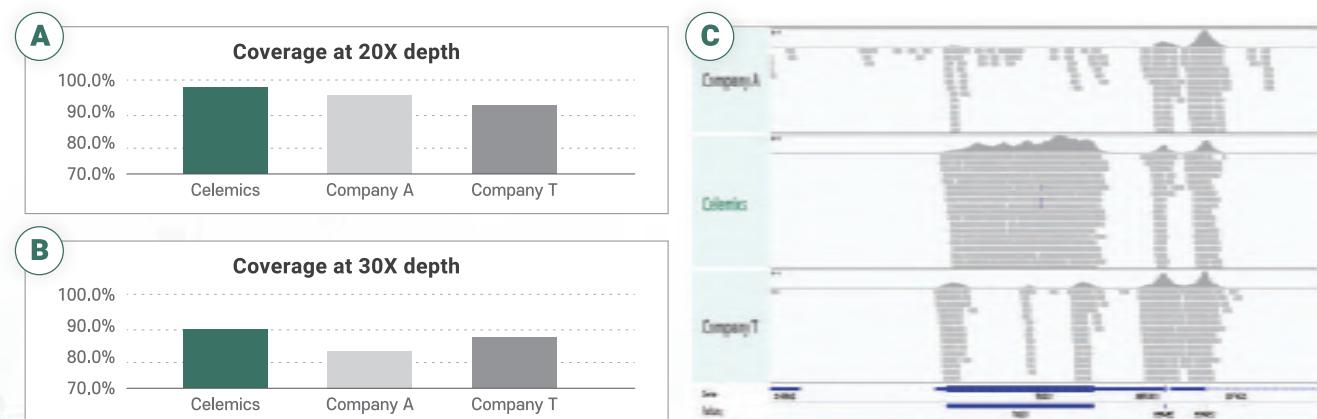


Figure 4. Exhaustive Coverage for Each Gene. (A) The Celemics WES Panel covers each gene with thorough coverage in comparison to competitor products. The bar graphs indicate the percentage of genes that are covered at (A) 20X depth and (B) 30X depth. The data from the three panels was downsampled to an equal size of 5.4 GB to eliminate effects caused by different sequencing amounts. (C) The IGV figure demonstrates the superior coverage performance of the Celemics Whole Exome Sequencing Panel against the TGID1 gene compared to other competitor products.

Simple Gene Add-on Customization

Flexible customization with Gene Add-on Service

The Celemics WES Panel offers the Gene Add-on Service, which allows for the expansion of the panel. Areas such as introns and mitochondria, which are typically not sequenced as part of standard WES panels in the market, can be included through the Gene Add-on Service, in addition to the core Celemics WES panel. Celemics has extensive experience in designing and developing custom Target Enrichment panels. As a company capable of manufacturing Target Enrichment panels in-house, we have the expertise to expand the target region without compromising the performance of the panel. Whether it's introns, mitochondria, or any other region of interest that falls outside the default analysis range, we can incorporate those regions into the panel through target region expansion, enabling sequencing and analysis. We are committed to meeting the exact requirements of our customers and delivering panels with enhanced value.



Target Gene Selection

Gene Add-On Service



Elaborate Design of the Capture Probe

Integration of Celemics proprietary technologies for the best panel performance



Synthesis of The Capture Probe

Advanced technology for probe synthesis and reagent optimization

Rapid Single Day Workflow

The Hybridization capture method offers the advantage of stable and reliable results. However, it is known for its complex experimental process and longer turnaround time. With the Celemics WES Panel, what used to take more than 20 hours can be completed within 8 hours, allowing researchers to initiate NGS sequencing on the single day as the experiment. This accelerated turnaround time enables faster access to sequencing data, accelerating research and discovery processes.

Conventional workflow ► 20 hours

Library Prep

Target Capture



Single Day workflow ► 5-8 hours

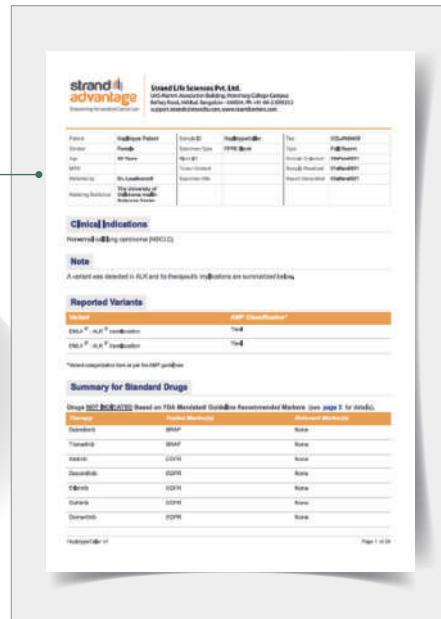
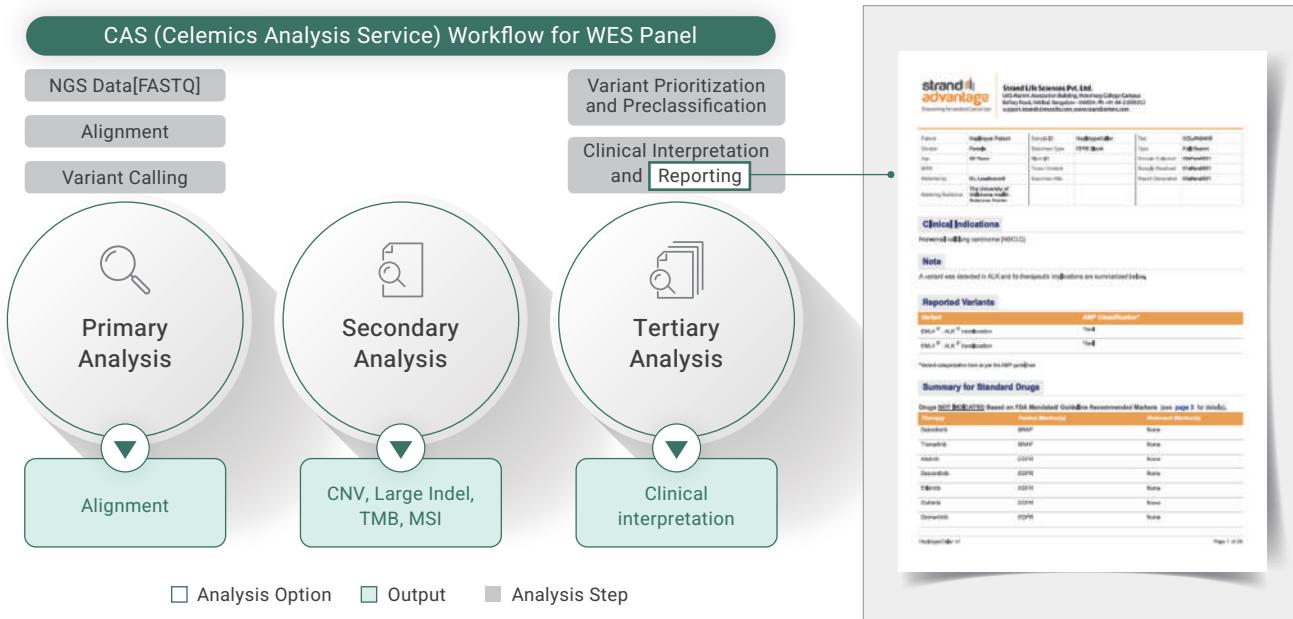
Library Prep

Target Capture

Simplify your workflow with alternative methods for sample shearing, concentrating, and even QC and expedite your exome sequencing without compromising data quality.

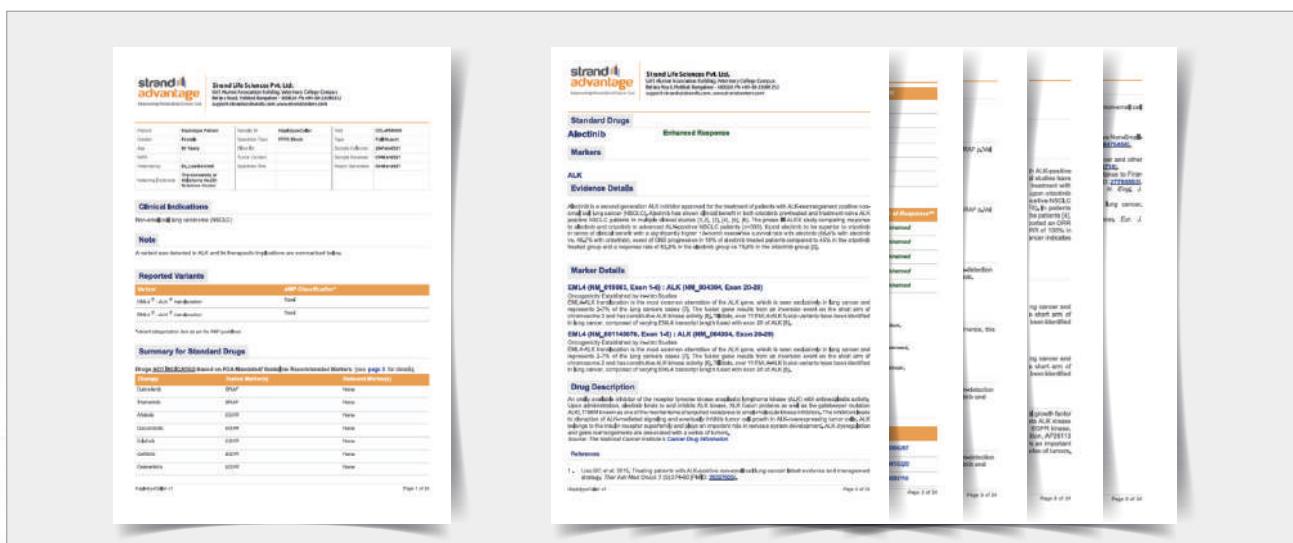
Full Bioinformatics Capability: FASTQ to Clinical Interpretation

Bioinformatics Support through CAS



CAS provides easy data transmission by single-click and automated uploads. Due to the complete support from Celemics bioinformatics experts, CAS does not require separate third-party bioinformaticians. CAS also supports real-time troubleshooting throughout primary to tertiary analysis and client-specific customization.

Clinical Interpretation Report

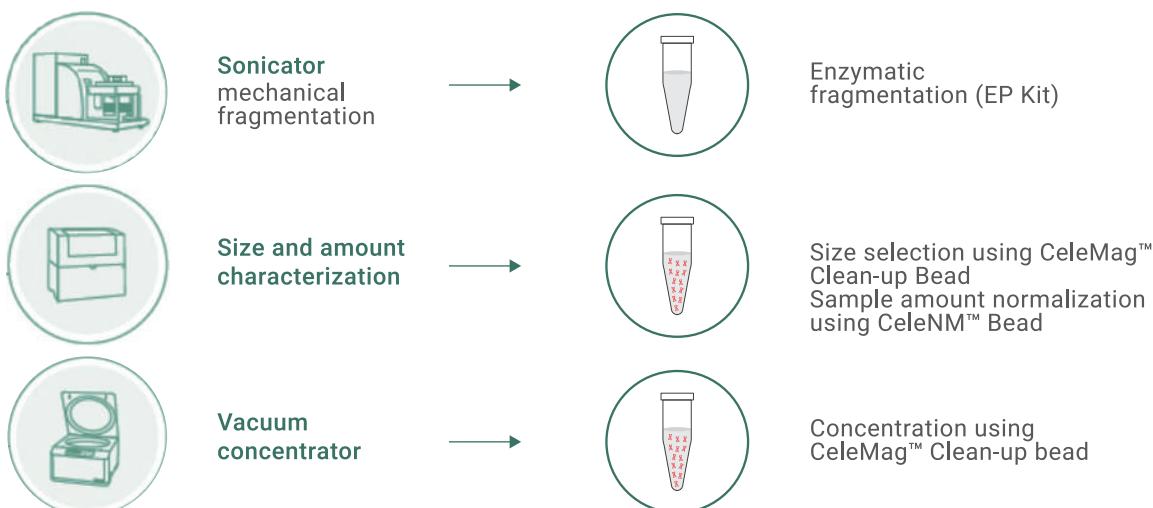


Celemics provides robust clinical interpretation services through a CAP-accredited partner that combines bioinformatics algorithms, public data from external sources/knowledge databases, visualization interfaces and reporting capabilities. The report includes pathogenicity and drug associated information.

No Need of Heavy Instruments

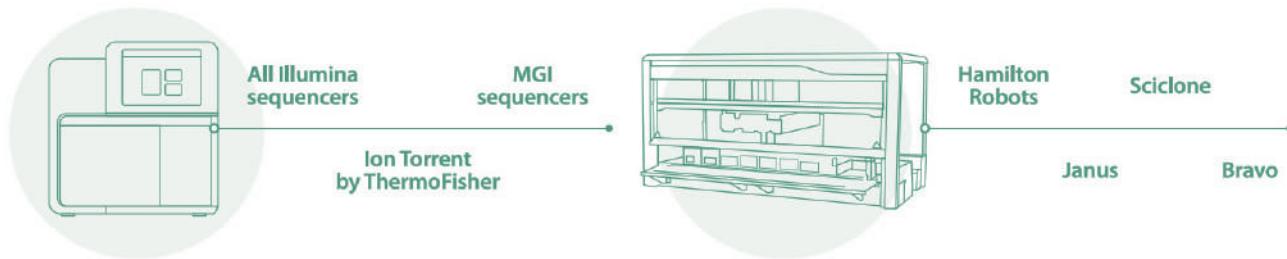
In order to perform Library Preparation prior to Target Enrichment and Sequencing, it is often required to have heavy instruments (such as vacuum concentrator or sonicator, etc.), which are barriers against complete automation. Even with an automation protocol, using these heavy instruments is inevitable and is often burdensome to the users. Celemics has successfully eliminated the need for heavy instruments by substituting them with a more convenient solution of enzymes and beads. After rigorous validation that consistently showed reliable performance, we have optimized this workflow to enable the benefit of a complete walkaway solution.

Replace the heavy instruments with:



Celemics has developed and optimized an enzymatic fragmentation, bead-based concentration, and normalization process, which eliminates the requirements for heavy instruments such as a sonicator (mechanical fragmentation), vacuum concentrator, size and amount characterization device, etc.

Flexible Integration with NGS Sequencers & Complete Walkaway Automation



The Celemics WES panel is seamlessly integrated with all NGS instruments from Illumina, MGI, and Thermo Fisher. Since there are no heavy instruments required, the experiment can be carried out with complete automation.

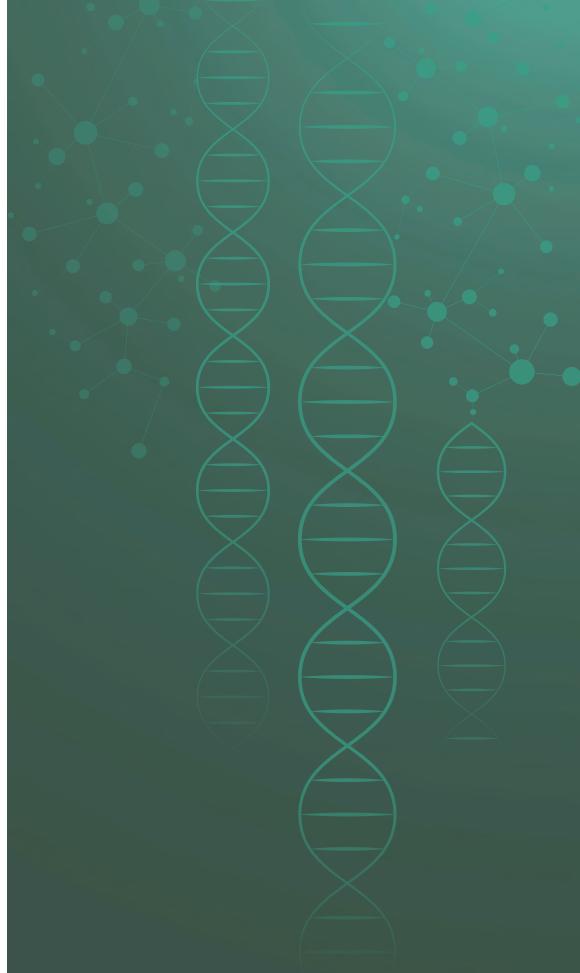


Celemics Clinical Exome Sequencing Panel

Focused On Sequencing of
Clinically Important Genes
Which Are Associated With
Various Genetic Diseases

Key Features

- Comprehensive genome profiling of a variety of genetic diseases
- Cost-effectiveness by compact target size compared to WES



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Celemics Clinical Exome Sequencing

Celemics' G-Mendeliome Clinical Exome Sequencing (CES) Panel is designed to overcome the limitations of analyzing clinical diseases with conventional whole-exome sequencing. The CES panels aim to only include clinically significant regions specifically related to inherited diseases.

Targeted sequencing of clinically important genes is a valuable approach for diagnosing and managing a wide range of genetic diseases, including inherited conditions, cancer predisposition syndromes, and other genetic disorders. It allows for efficient and focused analysis, increasing the likelihood of finding disease-causing variants and providing patients and healthcare providers with actionable information for medical decision-making.



Specification

Panel	Clinical Exome Sequencing - Standard	Clinical Exome Sequencing – Expanded
Gene Count	5,516	7,563
Covered region	CDS, Hotspots, Mitochondrial genome	
Target size	13.8 Mb	19.6 Mb
Mutation type	SNV, Indel, CNV	
Sample type (Amount)	Blood (>50 ng of fragmented DNA)	
Platform	All sequencers from Illumina, Thermo Fisher, and MGI	
Bioinformatics Support	Primary Analysis: FASTQ to annotated VCF Secondary Analysis: CNV, Large Indel Tertiary Analysis: Clinical interpretation, Visualization Curation	

*Gene Add-On Service: Genes can be added by customer's request.

G-Mendeliome Clinical Exome Sequencing (CES) Panel

Comprehensive Genomic Profiling of a Variety of Genetic Diseases

CES panel includes wide range of 7,000 genes associated with clinically significant genetic diseases, even including all clinically significant regions that are not covered by competitors panels.

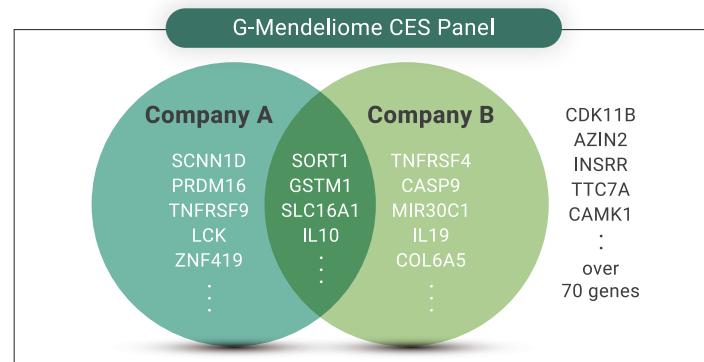
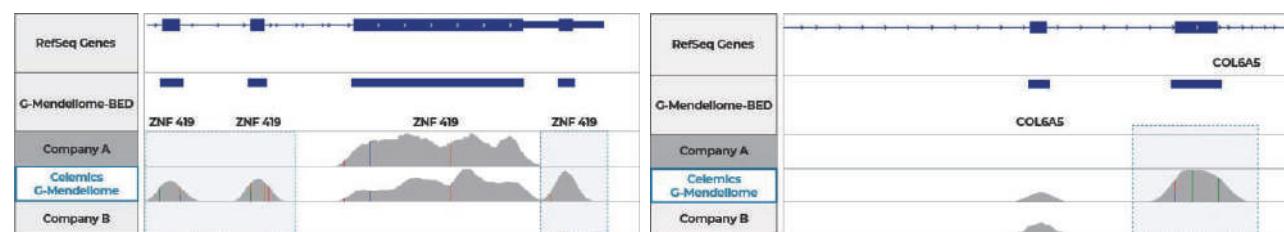


Figure 1. G-Mendeliome CES Panel. The G-Mendeliome CES panel, developed in collaboration with GC Genome, the largest clinical NGS service provider in South Korea, to solve the problems of poor diagnostic rates and high costs. This panel includes a wide range of genes, including those relevant to clinical testing and of significant medical importance. It encompasses many genes that clinicians find interesting and valuable in medical practice.

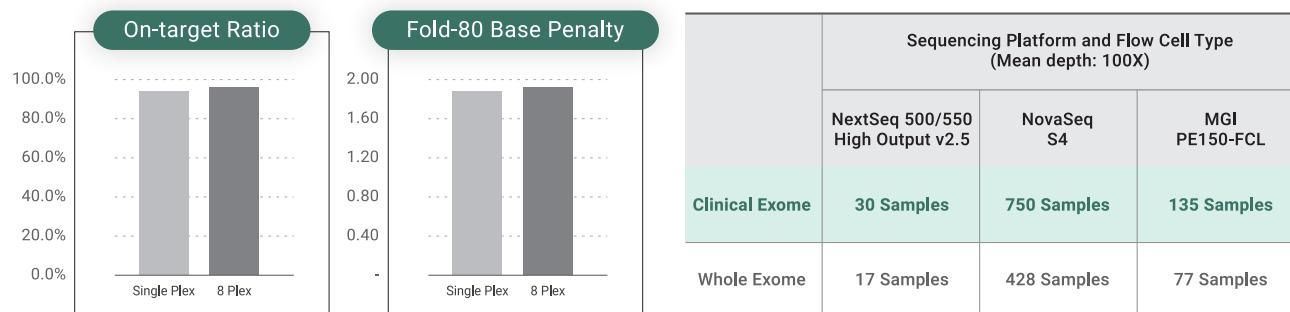
Comparison data for Hard-to-Capture region between Celemics G-Mendeliome and competitor panels



Through the in-house manufacturing and probe design system of Celemics, customers can request the sequencing of homologous regions as well as hard-to-capture regions

The comparison data showed obtained sequencing reads for ZNF419 and COL6A5 genes, which are commonly masked in other panels.

High Effective Sequencing for Clinical-associated Genes



The G-Mendeliome CES panel offers a more efficient solution to analyze clinical associated biomarkers in terms of key metrics such as the on-target ratio and fold-80 base penalty, even during multiplexing. Compact size of G-Mendeliome CES Panel compared to whole exome sequencing allows more cost-effective analysis.

List of Diseases Assessed by G-Mendeliome CES Panel

Category	Related Diseases
Cardiology	Aortopathy and connective tissue disorders
	Arrhythmia
	Cardiomyopathy
	Congenital heart defect
	Dyslipidemia
	Other cardiovascular diseases
Dermatology	Adams-Oliver syndrome
	Albinism
	Cardiofaciocutaneous syndrome
	Cutis laxa
	Dyskeratosis congenita
	Ectodermal dysplasia
	Ehlers-Danlos syndrome
	Epidermolysis bullosa
	Hereditary acrodermatitis enteropathica
	Hermansky-Pudlak syndrome
	Hypotrichosis
	Ichthyosis
	Neurofibromatosis
	Pachyonychia congenita
	Palmoplantar keratoderma
	Progeria and Progeroid Syndromes
	Skin cancer
	Tuberous sclerosis
	Waardenburg syndrome
	Xeroderma pigmentosum
Endocrinology	Adrenal hyperplasia
	Diabetes
	Hyperinsulinism
	Hyperparathyroidism
	Hypothyroidism
	Kallmann syndrome
	Multiple endocrine neoplasia
	Obesity
	Pancreatitis
	Premature ovarian failure
ENT	Hearing loss
GI/Hepatology	Cholestasis
	Congenital diarrhea
	Congenital hepatic fibrosis
	Gastrointestinal atresia
	Hirschsprung disease
	Polycystic liver disease
Hematology	Anemia
	Bleeding&Thrombotic disorder
	Bone marrow failure
	Congenital neutropenia
	Hemochromatosis
	RBC membrane disorder

List of Diseases Assessed by G-Mendeliome CES Panel

Category	Related Diseases
Immunology	Antibody deficiencies
	Autoinflammatory disorders
	Combined T/B cell deficiencies
	Complement deficiencies
	Defects in intrinsic and innate immunity
	Immune dysregulation
	Phagocytic defects
Metabolism	Aminoacidopathies
	Carbohydrate disorders
	Congenital disorders of glycosylation
	Creatine biosynthesis disorders
	Fatty acid oxidation defects
	Lipodystrophy
	Lysosomal storage disorders
	Organic acidemias
	Peroxisomal disorders
	Porphyria
	Purine/Pyrimidine metabolism disorders
	Pyruvate metabolism and tricarboxylic acid cycle defects
	Urea cycle disorders
Nephrology	Bartter syndrome
	Ciliopathies
	Diabetes insipidus
	Hemolytic uremic syndrome
	Hypokalemia
	Hypomagnesemia
	Hypophosphatemic rickets
	Nephrolithiasis
	Nephrotic syndrome/Focal glomerulonephrosis
	Pseudohypoaldosteronism
	Renal malformation
	Renal tubular acidosis
Neurology	Autism
	Movement disorders
	Neurodegenerative disorders
	Neuromuscular disorders
	Neuropathies and related disorders
	Seizures and Brain abnormalities

List of Diseases Assessed by G-Mendeliome CES Panel

Category	Related Diseases
Oncology	Breast and gynecological cancer
	Colorectal cancer
	Endocrine cancer
	Gastrointestinal cancer
	Hematologic malignancy
	Lung cancer
	Nervous system/brain cancer
	Pancreatic cancer
	Prostate cancer
	Renal cancer
	Sarcoma
	Skin cancer
Ophthalmology	Albinism
	Cataract/Ectopia lentis
	Corneal dystrophy
	Glaucoma
	Microphtalmia/Anophthalmia
	Nystagmus
	Ophthalmoplegia/Oculomotor apraxia
	Optic atrophy
	Retinal dystrophy
	Retinoblastoma
Pulmonology	Bronchiectasis
	Central hypoventilation/Apnea
	Cystic fibrosis
	Cystic lung disease
	Hermansky-Pudlak syndrome
	Interstitial lung disease
	Primary ciliary dyskinesia
	Surfactant dysfunction
Skeletal disorders	Amelogenesis imperfecta
	Arthrogryposes
	Cleft lip/palate
	Craniosynostosis
	Exostosis
	Facial dysostosis
	Macrocephaly/Overgrowth syndrome
	Osteopetrosis
	Short stature syndrome

OncоБioRisk

Comprehensive and
Specialized Hereditary
Cancer Panel

Key Features

- Effective analysis of inherited cancer
- Enable CNV analysis
- Provide genetic information for precision medicine



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OncoRisk Panel

Celemics' OncoRisk panel is designed to analyze 31 well-known oncogenes that are selected by Contract Research Organizations and numerous research studies. The genes included in this panel are all focused on hereditary cancers, making it highly valuable for researchers interested in this field. Furthermore, our gene add-on service allows adding specific genes of interest in this panel, enabling sequencing at a lower cost compared to whole exome sequencing (WES) or whole genome sequencing (WGS). With the industry-leading performance, we provide cost-effective and high quality sequencing results to every customer.



Specification

Gene count*	31 Genes
Covered region	CDS
Target size	96 Kb
Mutation type	SNV, Indel, and CNV
Sample type	Blood (> 50 ng of fragmented DNA), Fresh-Frozen, and FFPE
Platform	All sequencers from Illumina, Thermo Fisher, MGI
Sensitivity	97.9%
Specificity	> 99%
Bioinformatics Support	Primary Analysis: FASTQ to annotated VCF Secondary Analysis: CNV, Large Indel Tertiary Analysis: Clinical interpretation

*Gene Add-On Service: Genes can be added by customer's request.

Gene List

APC	ATM	BARD1	BLM	BMPR1A	BRCA1	BRCA2	BRIP1
CDH1	CDK4	CDKN2A	CHEK2	EPCAM	MLH1	MRE11A	MSH2
MSH6	MUTYH	NBN	PALB2	PMS2	PRSS1	PTEN	RAD50
RAD51C	RAD51D	SLX4	SMAD4	STK11	TP53	VHL	

Performance Data

Example of variants and CNV analysis results

We provide precise variant information based on high quality sequencing results. OncoRisk panel can detect all types of mutations with robust performance (over 95% of sensitivity at 5% variant allele frequency (VAF); 99.9% and 99.5% of specificity for SNV and Indel). Based on its excellent performance, the panel can accurately determine the genetic characteristics of patients, helping in the development of effective treatment plans. This can assist in formulating strategies for precise and targeted therapies. All validation tests are performed using reference samples (NA12878, NA12891, and NA12892) from Coriell Institute.

Gene	Mutation Type	Amino Acid Change	Variant Allele Frequency
APC	Syn	p.S1738S	41.17%
ATM	Non-Syn	p.D1853N	52.04%
BARD1	Non-Syn	p.R658C	47.53%
BMPR1A	Non-Syn	p.P2T	50.08%
BRCA1	Syn	p.S1389S	42.64%
BRCA2	Syn	p.V2171V	100.00%
BRIP1	Syn	p.Y1137Y	99.53%
PMS2	Non-Syn	p.K541E	100.00%
PRSS1	Syn	p.N246	100.00%
RAD51D	Non-Syn	p.L1521L	100.00%

Table 1: Example of variants analysis results. This example of variant analysis results include AA change, mutation type, total sequencing depth, allele frequency, etc.

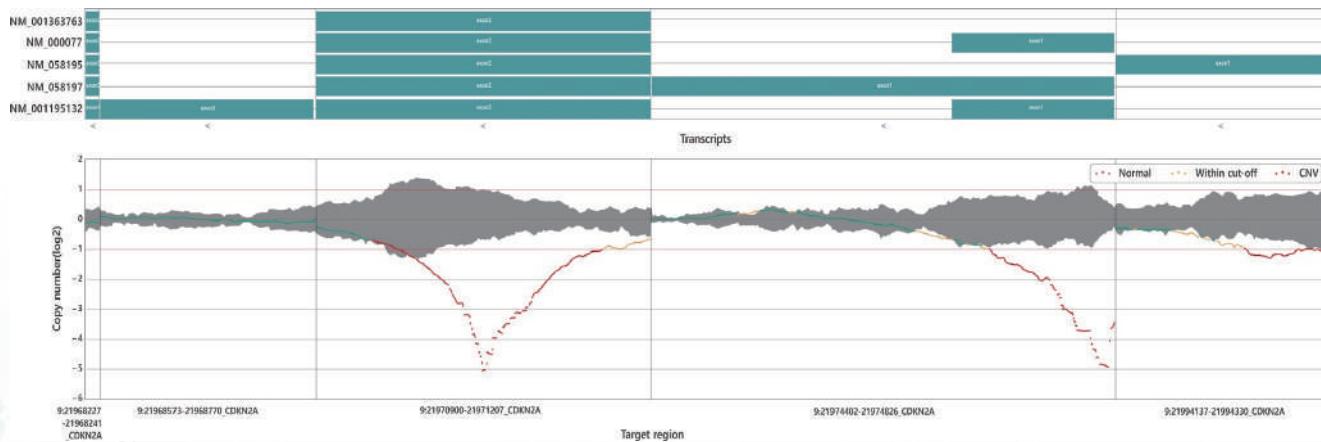


Figure 1: PN170 CDKN2A CNV plot. Example of CNV analysis results (CDKN2A) for specific target regions. In Celemics, two primary methods are used for accurate CNV analysis. One is the Read Depth Methods, and the other is the Comparison to a Reference Analysis. Celemics recommended to use a minimum of 10 or more samples for CNV analysis in research or clinical studies. However, the required number of samples may vary depending on the analysis' objectives, research topic, budget, and other factors. It is essential to consult with experts relevant to the analysis' goals to determine the optimal number of samples.

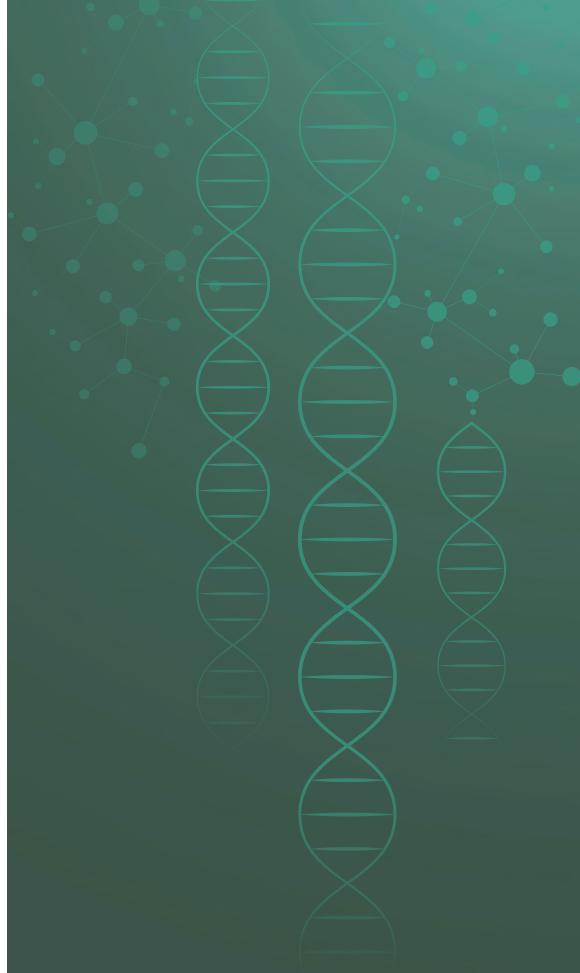


Celemics CancerScreen Focus Panel

Accurate Detection of Genetic
Markers Associated with
Companion Diagnostics

Key Features

- Includes set of genetic markers applicable for Companion Diagnostics
- Provides options for panel selection depending on the type of marker desired
- Provides genetic information of HRR related genes



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CancerScreen Focus Panel

The CancerScreen Focus Panel is designed to assess the genetic markers for targeted cancer drugs used in companion diagnostics. With Celemics' exclusive technologies, the panel demonstrates high performance not only in genomic DNA (gDNA) samples but also in samples extracted from Formalin-Fixed Paraffin-Embedded (FFPE) tissues and even in low-yield clinical samples. The versatility and robustness of CancerScreen Focus panel can consistently deliver reliable performance even during sample pooling, offering remarkable cost-effectiveness.



Product Specification

Panel	CancerScreen Focus - DNA	CancerScreen Focus - RNA	CancerScreen Focus - HRR
Gene Count	22	9	15
Target size	73.4 Kb	32.1 Kb	69.4 Kb
Covered region	CDS		
Mutation type	SNV, Indel, Rearrangement (RNA Panel)		
Sample type (Amount)	Blood, Fresh-Frozen, FFPE		
Platform	All sequencers from Illumina, Thermo Fisher, and MGI		
Bioinformatics Support	Primary Analysis: FASTQ to annotated VCF Secondary Analysis: CNV, Large Indel Tertiary Analysis: Clinical interpretation, Visualization Curation		

*Gene Add-On Service: Genes can be added by customer's request.

Performance Data

CancerScreen Focus DNA Panel

The CancerScreen Focus DNA Panel is designed to detect genetic mutations associated with companion diagnostics. The panel identifies cancer-related genetic mutations through a patient's genetic profile analysis to support personalized treatment decisions.

Gene	Related Drug	Mutation
KRAS and NRAS	Vectibix	KRAS wild-type and NRAS wild type
PIK3CA	Pigray	C420R, E542K, E545A, E545D, E545G, E545K, Q546E, Q546R, H1047L, H1047R, and H1047Y
KIT	Gleevec	D816V
EGFR (HER1)	Erbtitux	EGFR (HER1) protein expression
EGFR (HER1)	Exkivity	Exon 20 insertion mutations
MET	Tabrecta	MET single nucleotide variants and indels that lead to MET exon 14 skipping
BRAF	Braftovi in combination with Mektovi	V600E or V600K
BRAF	Cotellic in combination with Zelboraf	V600E or V600K
KRAS	Erbtitux	G12A, G12D, G12R, G12C, G12S, G12V, G13D
KRAS	Krazati	KRAS G12C
FLT3 (ITD/TKD)	Xospata	ITD mutations and TKD mutations D835 and I836
BRCA1 and BRCA2	Lynparza	Mutations
BRCA1 and BRCA2	Rubraca	Mutations
TP53	Venclexta	Deletion chromosome 17p (17p-)

Table 1. Example of relation between drugs and genes included in Celemics Focus DNA Panel. Sequencing can be performed by using Celemics Focus DNA Panel for all genes mentioned in the table above as examples of genetic associations for FDA-approved drugs.

Chromosome	Gene	Ref Allele	Alt Allele	Mutation	Reference DNA	CancerScreen Focus DNA
1	NRAS	G	T	Q61K	12.5 %	10.7 %
3	PIK3CA	G	A	E545K	9.0 %	9.5 %
3	PIK3CA	A	G	H1047R	17.5 %	16.9 %
4	KIT	A	T	D816V	10.0 %	8.2 %
4	KIT	G	C	L862	7.5 %	6.4 %
7	EGFR	G	A	G719S	24.5 %	22.2 %
7	EGFR	AGG..AGC	A	ΔE746 - A750	2.0 %	0.5 %
7	EGFR	G	A	Q787Q	15.0 %	11.6 %
7	EGFR	C	T	T790M	1.0 %	0.7 %
7	EGFR	T	G	L858R	3.0 %	2.4 %
7	MET	GT	G	-	7.0 %	6.2 %
7	MET	G	A	A1339A	7.0 %	6.9 %
7	BRAF	A	T	V600E	10.5 %	9.1 %
12	KRAS	C	T	G13D	15.0 %	13.5 %
12	KRAS	C	T	G12D	6.0 %	6.0 %
13	FLT3	GGA	G	-	10.0 %	7.7 %
13	BRCA2	CA	C	K1691Nfs*15	32.5 %	29.3 %
17	TP53	G	C	P72R	92.5 %	92.4 %

Table 2. Detection accuracy results of CancerScreen Focus DNA Panel using reference DNA. Validation experiment is performed by using the CancerScreen Focus DNA Panel with the reference sample of OncoSpan FFPE (Horizon Discovery). The validation results indicate that CancerScreen Focus DNA Panel is able to obtain values closely resembling the allele frequencies of known genetic mutations, and successfully detected all mutations of interest (Sensitivity > 99%; Specificity > 99%).

Performance Data

Available in low-throughput platform

The panel consists of size up to 74kb (DNA Panel), therefore suitable for sequencing even with low-throughput instrument. Sequencing at a depth of 500X for the analysis of mutations at the 1% level using the MiSeq Reagent V2 allows for the analysis of up to 50 samples in a single run.

Sequencing Platform	MiSeq Reagent Kit v2		Ion GeneStudio S5		DNBSEQ-G400	
Throughput	5.1 Gb		15 Gb		55 Gb	
Mean Depth	500 X	1,000 X	500 X	1,000 X	500 X	1,000 X
Sequencing Amount per Sample	100 Mb	200 Mb	100 Mb	200 Mb	100 Mb	200 Mb
Estimated Samples per run	50	25	150	75	500	250

CancerScreen Focus RNA Panel

The CancerScreen Focus RNA Panel is designed to detect fusion mutations associated with companion diagnostics. The panel identifies well-known fusion breakpoints for cancer to support personalized treatment decisions.

Gene	Related Drug	Mutation
ROS1	Rozlytrek	ROS1 fusion
NTRK1, NTRK2, and NTRK3 fusions	Rozlytrek	NTRK1/2/3 fusions
RET	Gavreto	RET fusions

Table 3. Example of fusion genes associated with medication in CancerScreen Focus RNA Panel. Sequencing can be performed by using Celemics Focus RNA Panel for all genes mentioned in the table above as examples of genetic associations for FDA-approved drugs.



Figure 1. Result of gene fusion detection (TACC3 and FGFR3) and list of applicable fusion analysis. Performance data of CancerScreen Focus RNA Panel using Seraseq® FFPE Tumor Fusion RNA v4 Reference Material (SeraCare). (A) The validation experiment result indicate that the panel can successfully detect gene fusion between TACC3 and FGFR3. (B) Other 12 companion diagnostics associated fusion genes known to be present in the reference sample from Seraseq® FFPE Tumor Fusion RNA v4 Reference Material (SeraCare) also successfully detected (Data not shown).

Provision of Genetic Information for Homologous Recombination Repair (HRR)

The CancerScreen Focus HRR Panel is designed to assess the level of genomic instability and homologous recombination deficiency in cancer cells. This specific panel can be beneficial for patients interested in Genomic Instability Assessment, Homologous Recombination Deficiency (HRD), and Tumor Profiling.

CancerScreen Core,50,100,400

Highly Optimized NGS Panel
for Somatic Cancer

Key Features

- Up to 407 somatic cancer-related genes
- Exceptional sensitivity and specificity
- Analysis results with SNV, InDel, Genomic rearrangement, CNV, and TMB
- Maximized cost-effectiveness

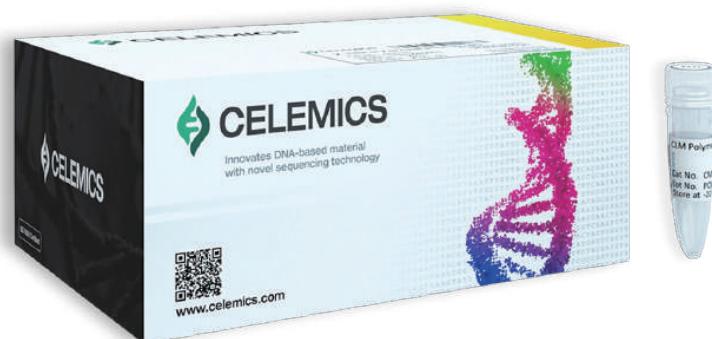


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CancerScreen Core / 50 / 100 / 400 Panel

CancerScreen panel is designed to detect all types of variants for up to 407 somatic cancer-related genes. With its exceptional sensitivity and specificity, Celemics CancerScreen panel offers maximized cost-effectiveness to customers. Celemics provides full exclusive bioinformatics support. The generated report consists of the primary, secondary, and tertiary results for the in-depth understanding and interpretation of sequencing data. Also, if the gene of interest does not exist in the panel, it can be added separately through our gene add-on service.



Specification

Panel	CancerScreen Core	CancerScreen 50	CancerScreen 100	CancerScreen 400
Gene count*	13	54	99	407
Covered region	Whole CDS Rearrangement	Whole CDS Rearrangement	CDS	CDS
Target size	61 Kb	197 Kb	299 Kb	1,123 Kb
Mutation type	SNV, Indel, CNV, Rearrangement, and TMB			
Sample type	Blood, Fresh-frozen, and FFPE			
Platform	All sequencers from Illumina, Thermo Fisher, and MGI			
Bioinformatics Support	Primary Analysis: FASTQ to annotated VCF Secondary Analysis: CNV, Large Indel Tertiary Analysis: Clinical interpretation			

*Gene Add-On Service: Genes can be added by customer's request.

Performance Data

Market-leading performance

The CancerScreen panels boast market-leading performance with high values in on-target ratio and coverage uniformity, ensuring the accurate detection of genetic mutations occurring in target genes.

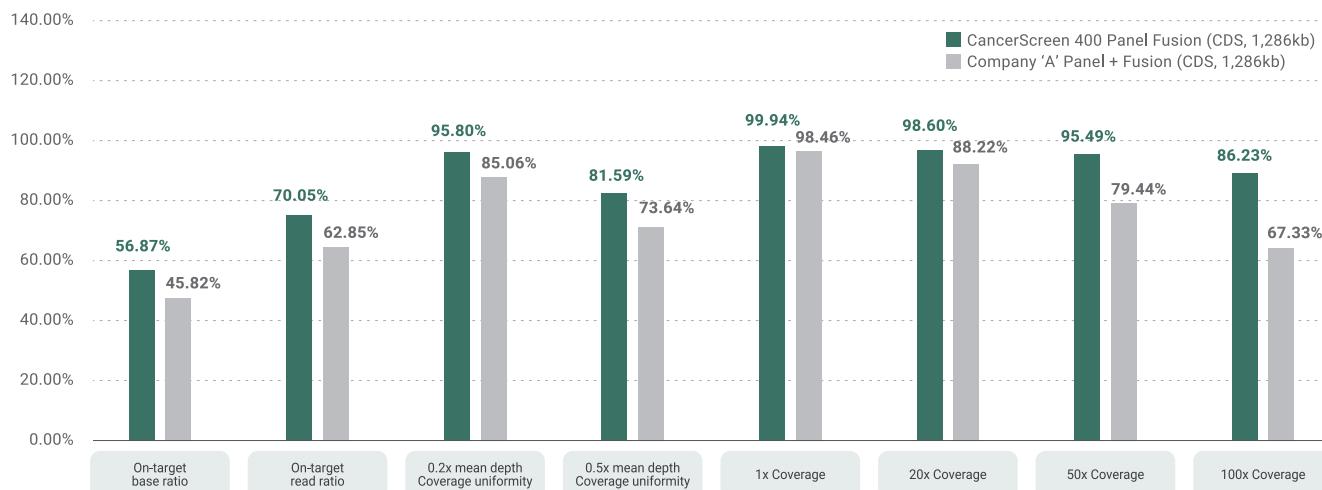


Figure 1: Comparison between CancerScreen 400 and competitor panel. Higher on-target ratio, uniformity, coverage at 100X compared to competitor product over the target regions.

Performance Comparison over Hard-to-Capture Regions

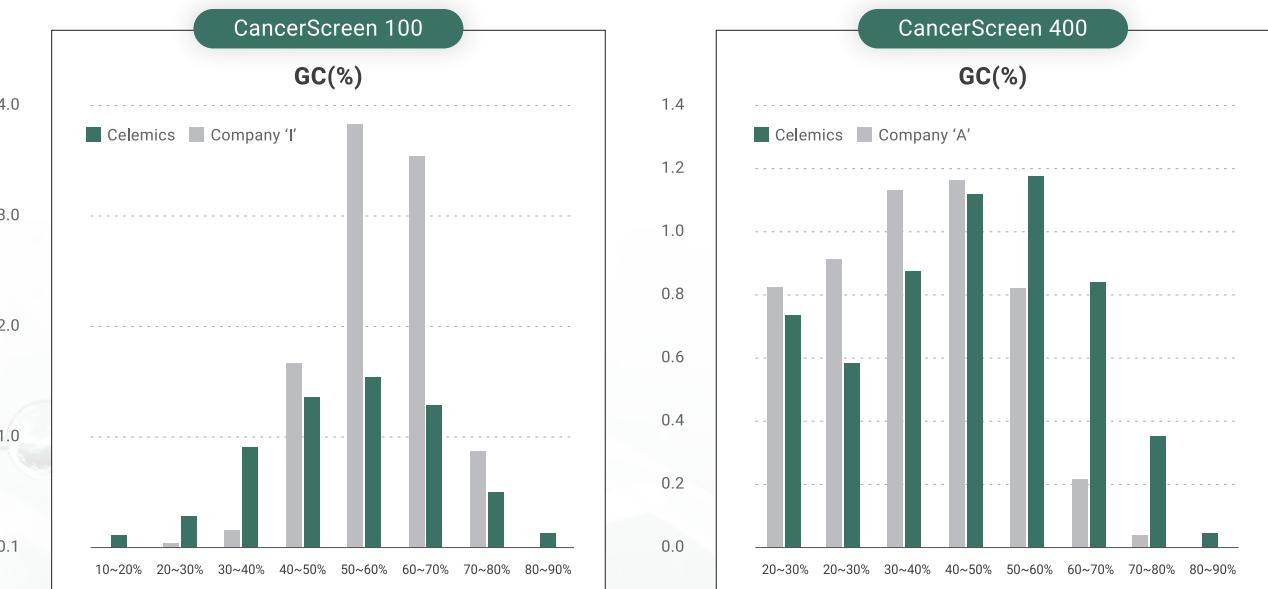


Figure 2: Comparison with competitor panels. A high coverage uniformity ensures accurate identification of genetic mutations across all positions within the on-target regions. Celemics panels shows high uniformity in target regions with high GC rate compared to other competitor products.

Gene List

CancerScreen Core								
ALK	APC	BRAF	EGFR	ERBB2	KRAS	MET	NRAS	PIK3CA
RET	ROS1	SMAD4	TP53					

CancerScreen 50								
ABL1	AKT1	ALK	APC	ATM	BRAF	BRCA1	BRCA2	CDH1
CDK4	CDK6	CDKN2A	CSF1R	CTNNB1	DDR2	EGFR	ERBB2	ERBB4
ESR1	FGFR1	FGFR2	FGFR3	GNA11	GNAQ	GNAS	HRAS	IDH1
IDH2	JAK2	KDR	KIT	KRAS	MAP2K1	MET	MLH1	MTOR
MYC	MYCN	NOTCH1	NRAS	NTRK1	PDGFRA	PIK3CA	PTCH1	PTEN
PTPN11	RB1	RET	ROS1	SMAD4	SMO	SRC	STK11	TP53

CancerScreen 100								
ABL1	AKT1	AKT2	AKT3	ALK	APC	ARID1A	ARID1B	ARID2
ATM	ATRX	AURKA	AURKB	BARD1	BCL2	BLM	BMPR1A	BRAF
BRCA1	BRCA2	BRIP1	CDH1	CDK4	CDK6	CDKN2A	CHEK2	CSF1R
CTNNB1	DDR2	EGFR	EPCAM	EPHB4	ERBB2	ERBB3	ERBB4	EZH2
FBXW7	FGFR1	FGFR2	FGFR3	FLT3	GNA11	GNAQ	GNAS	HNF1A
HRAS	IDH1	IDH2	IGF1R	ITK	JAK1	JAK2	JAK3	KDR
KIT	KRAS	MDM2	MET	MLH1	MPL	MRE11	MSH2	MSH6
MTOR	MUTYH	NBN	NF1	NOTCH1	NPM1	NRAS	NTRK1	PALB2
PDGFRA	PDGFRB	PIK3CA	PIK3R1	PMS2	PRSS1	PTCH1	PTCH2	PTEN
PTPN11	RAD50	RAD51C	RAD51D	RB1	RET	ROS1	SLX4	SMAD4
SMARCB1	SMO	SRC	STK11	SYK	TERT	TOP1	TP53	VHL

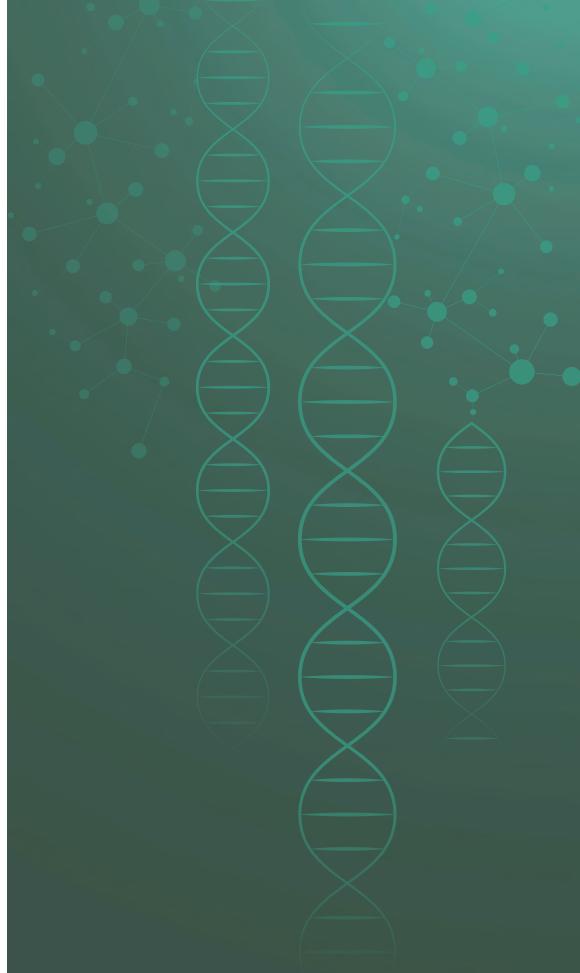
Gene List

CancerScreen 400								
ABL1	ABL2	ADGRA2	AKT1	AKT2	AKT3	ALK	AMER1	APC
APCDD1	APEX1	APOB	APOBEC1	AR	ARAF	ARFRP1	ARID1A	ARID1B
ARID2	ASXL1	ATM	ATP11B	ATR	ATRX	AURKA	AURKB	AXIN1
AXL	B2M	B3GAT1	BACH1	BAP1	BARD1	BCL2	BCL6	BCL9
BCOR	BCR	BIRC2	BIRC3	BLM	BRAF	BRCA1	BRCA2	BRD2
BRD3	BRD4	BRIP1	BTG1	BTK	BTLA	CARD11	CASP5	CASP8
CBFB	CBL	CD274	CDK12	CDK4	CDK6	CDK8	CDKN1A	CDKN1B
CDKN2A	CDKN2B	CDKN2C	CDX2	CEBPA	CHD1	CHD2	CHD4	CHEK1
CHEK2	CHUK	CIC	CRBN	CREBBP	CRKL	CRLF2	CSF1R	CSF2
CSF2RA	CSF2RB	CSNK2A1	CTCF	CTLA4	CTNNA1	CTNNB1	CUL3	CUL4A
CUL4B	CXCL10	CXCL11	CXCL9	CXCR3	CYLD	CYP17A1	DAXX	DCUN1D1
DDR2	DICER1	DIS3	DNMT1	DNMT3A	DOCK2	DOT1L	EGFR	ELMO1
EML4	EMSY	EP300	EPHA3	EPHA5	EPHA6	EPHA7	EPHB1	EPHB4
EPHB6	ERBB2	ERBB3	ERBB4	ERCC1	ERCC2	ERG	ERRFI1	ESR1
ETV1	ETV4	ETV5	ETV6	EWSR1	EYA2	EZH2	FANCA	FANCC
FANCD2	FANCE	FANCF	FANCG	FANCI	FANCL	FANCM	FAS	FAT1
FAT3	FBXW7	FGF1	FGF10	FGF12	FGF14	FGF19	FGF2	FGF23
FGF3	FGF4	FGF6	FGF7	FGFR1	FGFR2	FGFR3	FGFR4	FH
FLCN	FLT1	FLT3	FLT4	FOXA1	FOXL2	FOXO3	FOXP3	FRS2
FUBP1	GABRA6	GAS6	GATA1	GATA2	GATA3	GATA4	GATA6	GID4
GLI1	GNA11	GNA13	GNAQ	GNAS	GRIN2A	GRM3	GSK3B	GUCY1A2
GZMA	GZMB	GZMH	H3F3A	HGF	HIST1H3B	HNF1A	HOXA3	HRAS
HSD3B1	HSP90AA1	IDH1	IDH2	IDO1	IDO2	IFITM1	IFITM3	IFNA1
IFNB1	IFNG	IGF1	IGF1R	IGF2	IGF2R	IKBKE	IKZF1	IL12A
IL12B	IL2	IL23A	IL6	IL7R	INHBA	INPP4B	INSR	IRF2
IRF4	IRS2	ITGAE	ITK	JAK1	JAK2	JAK3	JUN	KAT6A
KDM5A	KDM5C	KDM6A	KDR	KEAP1	KEL	KIT	KLF4	KLHL6
KMT2A	KMT2B	KMT2C	KNSTRN	KRAS	LAG3	LMO1	LRP1B	LRP6
LTK	LYN	LZTR1	MAGI2	MAGOH	MAML1	MAP2K1	MAP2K2	MAP2K4
MAP3K1	MAP3K13	MAPK1	MAX	MCL1	MDM2	MDM4	MED12	MEF2B
MEN1	MET	MITF	MLH1	MPL	MRE11	MSH2	MSH6	MTOR
MUTYH	MYB	MYC	MYCL	MYCN	MYD88	MYO18A	NCOA3	NCOR1
NF1	NF2	NFE2L2	NFKBIA	NOTCH1	NOTCH2	NOTCH3	NOTCH4	NPM1
NRAS	NSD1	NSD3	NTRK1	NTRK2	NTRK3	NUP93	NUTM1	PAK3
PAK5	PALB2	PARP1	PARP2	PARP3	PARP4	PAX5	PBRM1	PDCD1
PDCD1LG2	PDGFRA	PDGFRB	PDK1	PGR	PHF6	PHLPP2	PIK3C2B	PIK3C3
PIK3CA	PIK3CB	PIK3CG	PIK3R2	PKHD1	PLCG1	PLCG2	PMS2	PNP
PNRC1	POLD1	POLE	PPARG	PPP2R1A	PRDM1	PREX2	PRF1	PRKAR1A
PRKCI	PRKDC	PRPF40B	PRSS8	PTCH1	PTCH2	PTEN	PTK2	PTPN11
PTPRC	PTPRD	QKI	RAB35	RAC1	RAC2	RAD17	RAD50	RAD51
RAD52	RAD54L	RAF1	RANBP2	RARA	RB1	RBM10	REL	RET
RHEB	RHOA	RHOB	RICTOR	ROBO1	ROBO2	ROS1	RPA1	RPS6KB1
RPTOR	RUNX1	RUNX1T1	RUNX3	SDHA	SDHB	SDHC	SDHD	SEMA3A
SEMA3E	SET	SETBP1	SETD2	SF3A1	SF3B1	SH2B3	SKP2	SLIT2
SMAD2	SMAD3	SMAD4	SRSF2	SRSF7	STAG2	STAT3	STAT4	TERT
TET2	TP53							



Celemics CancerScreen Comprehensive

Highly accurate and
comprehensive NGS panel
for somatic cancer



Key Features

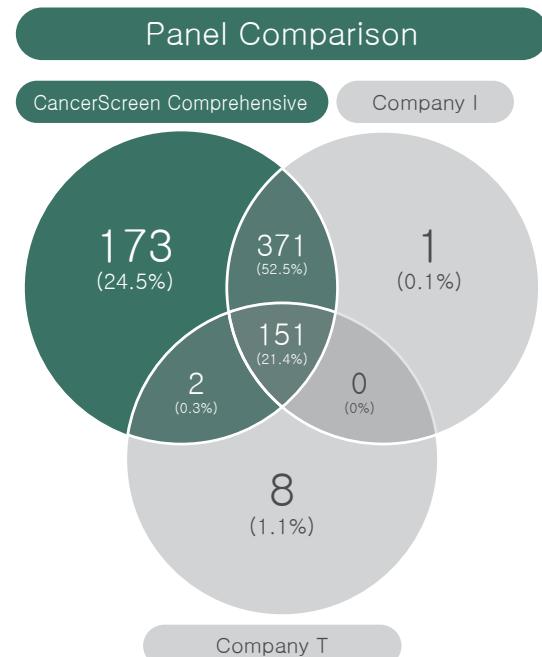
- Comprehensive analysis of most common genes related to solid tumors in a single NGS run
- Sensitive detection with only 10 ng of gDNA
- NGS panel applicable for companion diagnostics and drug therapy
- Cost-effective methodology leading to excellent result quality
- Superior capture performance even in hard-to-capture region, such as GC/AT-rich and homologous regions
- Flexible integration on various sequencer, including Illumina, Ion Torrent, and MGI

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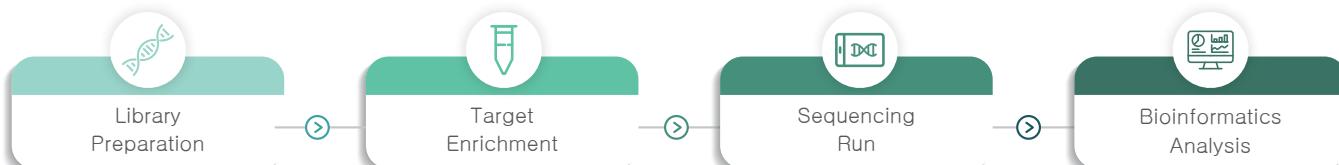
CancerScreen Comprehensive

The CancerScreen Comprehensive panel is designed to detect all variant types and the immuno-oncology markers, microsatellite instability (MSI), and other possible relevant variants, which are crucial biomarkers for cancer immunotherapy. The panel consists of 697 genes for DNA and 68 genes for RNA associated with cancer, and also designed to detect Epstein-Barr Virus (EBV) and Human Papillomaviruses (HPV), and Copy Number Variation (CNV) allowing for in-depth analyses. With Celemics' exclusive probe design and assay optimization technologies, the panel ensures superior performance in terms of detection sensitivity and specificity, enabling time-saving and cost-effective NGS in various oncology-related applications. Along with the panels and reagents, Celemics also offers client-specific full bioinformatics support, with the report consisting of primary, secondary, and tertiary analysis for in-depth understanding and interpretation of sequencing data. Also, Celemics offers flexible customization of the ready-to-use panels; if the gene of interest does not exist in the panel or if you wish to expand the target region of interest, it can be added separately through our gene add-on service and can be integrated onto various sequencing platforms, such as Illumina, Ion Torrent, and MGI.

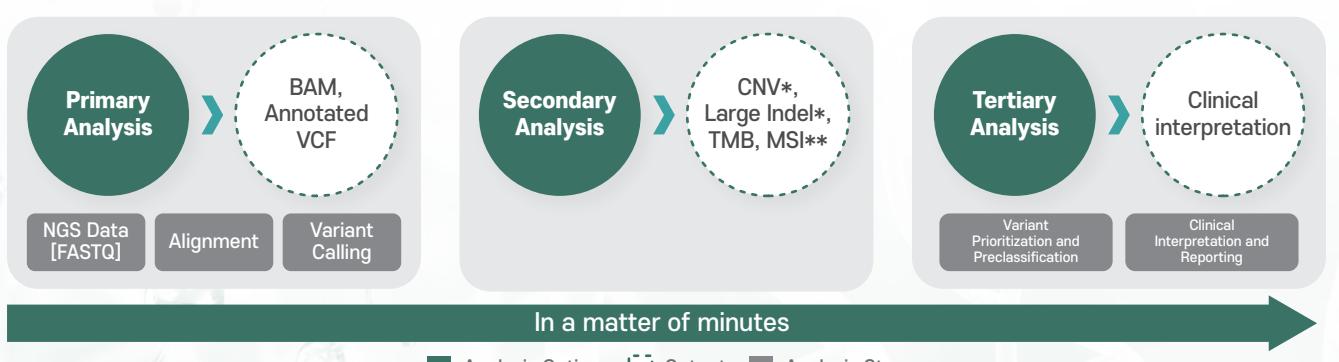


*Gene Add-On Service: Genes can be added by customer's request.

Sequencing Workflow



Celemics Analysis Service (CAS) Workflow



Celemics Analysis Service (CAS) can provide client-specific BI solutions; ranging from simple annotated VCF even to complete clinical interpretations.

Product Specification

CancerScreen Comprehensive	
Gene Numbers	706 genes (697 genes for DNA, 68 genes for RNA)
Target Regions	CDS, Hotspot variant, UTR, Intronic, Intergenic regions, and MSI markers
Variant Types	SNV, Indel, CNV, Fusion, MSI, TMB
Target Size	2.32 Mb (DNA) & 201 Kb (RNA)
Sample Types	Blood and Tissue (FFPE, Frozen Tissue)
Min. Input Amount of DNA	> 10 ng
NGS Platform	All Illumina, Thermo Fisher, MGI Platforms

Performance Data

CancerScreen Comprehensive - DNA

	On target read ratio	Uniformity (St. Dev)
Single-plex Sample	84.72%	0.56
8-plex Sample	84.53%	0.57

Table 1. CancerScreen Comprehensive DNA performance statistics. DNA panel demonstrated on-target ratio of 84.72 and 84.53% for single-plex and 8-plex sample, respectively, showing reproducible results regardless of single-plex and 8-plex sample library with robust uniformity. The data was generated using OncoSpan FFPE (Horizon Discovery) sample for Table 1 and Figure 1.

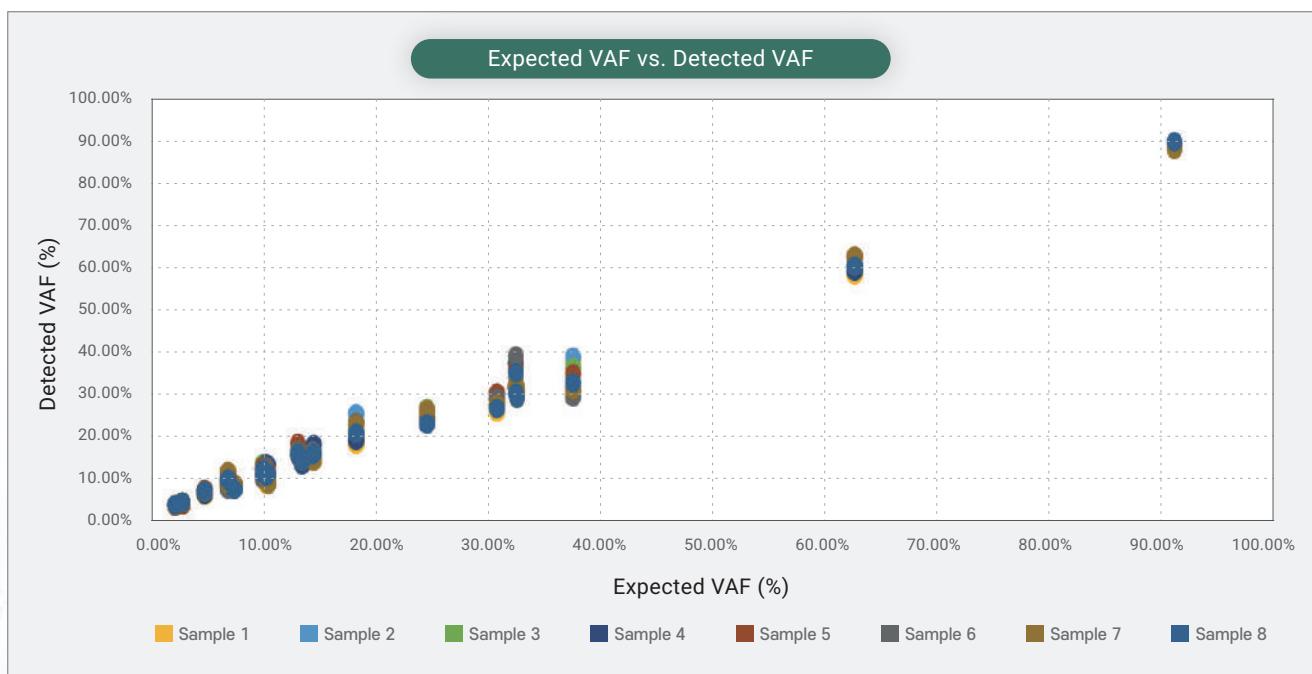


Figure 1. Expected VAF vs. Detected VAF correlation comparison. Each sample consists of 8-plex sample libraries. The actual VAF showed relative concordance for the corresponding target genes, demonstrating the detection capability and reproducibility of the panel, regardless of the single or pooled sample libraries.

	Expected AF % (at COA)	Actual AF %		Expected AF % (at COA)	Actual AF %
NRAS p.Q61K	12.11	14.39	EGFR p.L858R	3.80	4.34
ALK 3'UTR insertion	9.23	9.44	MET p.L238fs*25	5.82	7.03
PIK3CA p.H1047R	17.36	19.63	BRAF p.V600E	12.45	12.38
EGFR p.E746_A750 (15bp del)	1.66	1.56	KRAS p.G12D	5.73	7.09
EGFR p.T790M	1.02	1.09	TP53 p.P72R	90.92	91.41

Table 2. Comparison of Expected and Detected VAF values. The provided table illustrates few of selected variants were assessed to have relatively similar allele frequencies.

CancerScreen Comprehensive - RNA

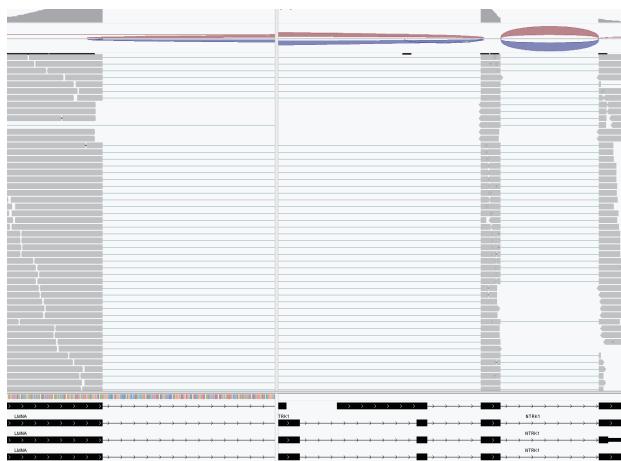


Figure 2. Fusion breakpoint IGV.

Generated with STAR-Fusion for known rearrangement LMNA & NTRK1 pair. The IGV plot illustrates the successful capture and data generation of CancerScreen Comprehensive from one of the rearrangements included in Seraseq® FFPE Fusion RNA Reference Material v4.

Gene 1	Gene 2	Gene 1	Gene 2
CCDC6	RET	LMNA	NTRK1
CD74	ROS1	NCOA4	RET
EGFR	SEPTIN14	PAX8	PPARG
EML4	ALK	SLC34A2	ROS1
ETV6	NTRK3	SLC45A3	BRAF
FGFR3	BAIAP2L1	TFG	NTRK1
FGFR3	TACC3	TMPRSS2	ERG
KIF5B	RET	TPM3	NTRK1
EGFR exon 2-7 skipping		MET exon 14 skipping	

Table 3. List of fusion for RNA panel.

CancerScreen Comprehensive RNA panel can detect above listed fusion points, included in Seraseq® FFPE Fusion RNA Reference Material v4, for assessing RNA variants associated with somatic cancer.

Performance Data

Microsatellite Instability (MSI)

Celemics' CancerScreen Comprehensive panel is also designed to include analysis of MSI biomarkers in a single NGS run for in-depth and comprehensive assessment.

Sample	MSI_Score	MSI_Assign
MSI-High #1	0.3077	H
MSI-High #2	0.3396	H
MSI-High #3	0.3208	H

Sample	MSI_Score	MSI_Assign
MSI-S #1	0.1923	S
MSI-S #2	0.2264	S
MSI-S #3	0.2308	S
MSI-S #4	0.1538	S
MSI-S #5	0.2075	S

Sample	MSI_Score	MSI_Assign
MSI-S #6	0.1154	S
MSI-S #7	0.3077	S
MSI-S #8	0.1667	S
MSI-S #9	0.2037	S

Table 4. Microsatellite Instability (MSI) Analysis. For microsatellite instability (MSI) interpretation, Seracare Seraseq® gDNA MSI-High Mix (MSI-H) and HapMap sample (MSI-S) were selected for MSI analyses.

Copy Number Variation (CNV) Analysis

Copy Number Variation (CNV) Analysis of specific genes can also be done using CancerScreen Comprehensive panel for in-depth somatic cancer-associated studies.

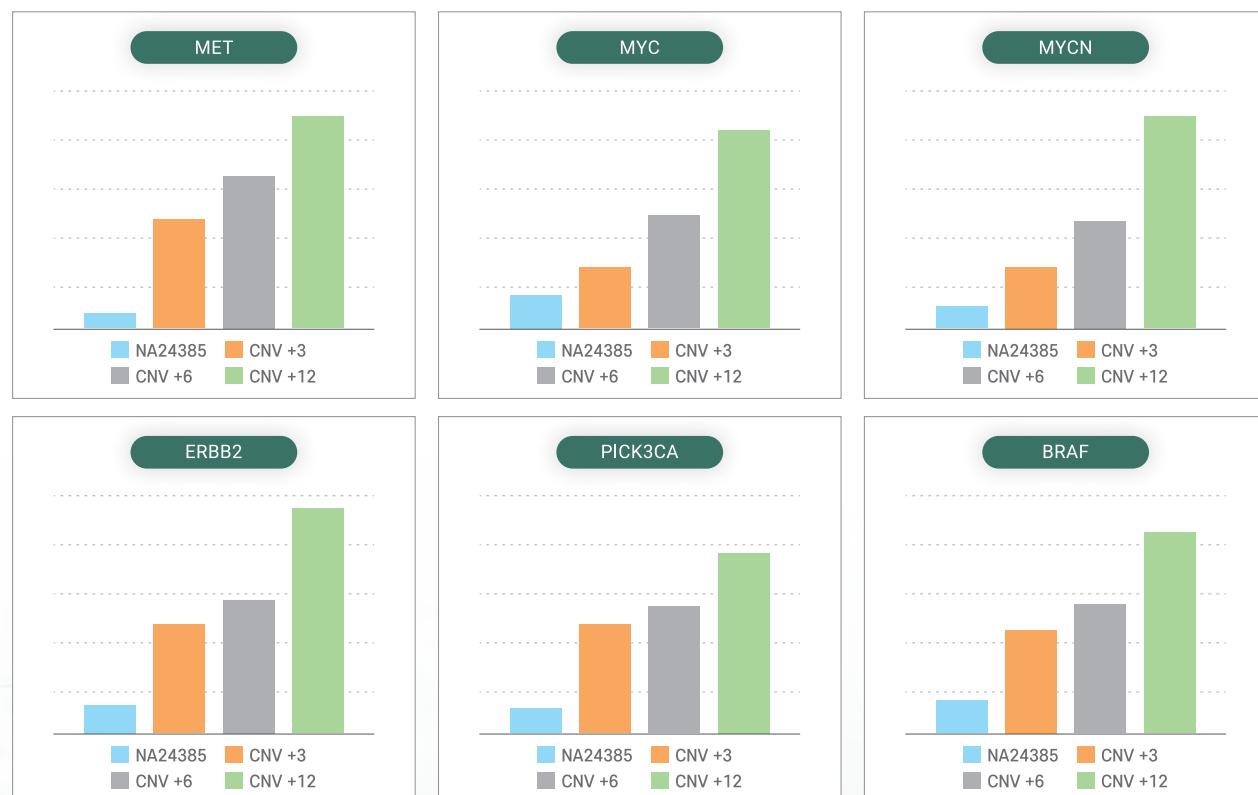


Figure 3. Copy Number Variation (CNV) analysis using CancerScreen Comprehensive Panel. The CNV detection ability was assessed using reference sample, NA24385, and Seraseq® Solid Tumor CNV Mix, +3 copies, +6 copies, +12 copies, showing CancerScreen Comprehensive can detect the changes in copy numbers for target genes of interest.

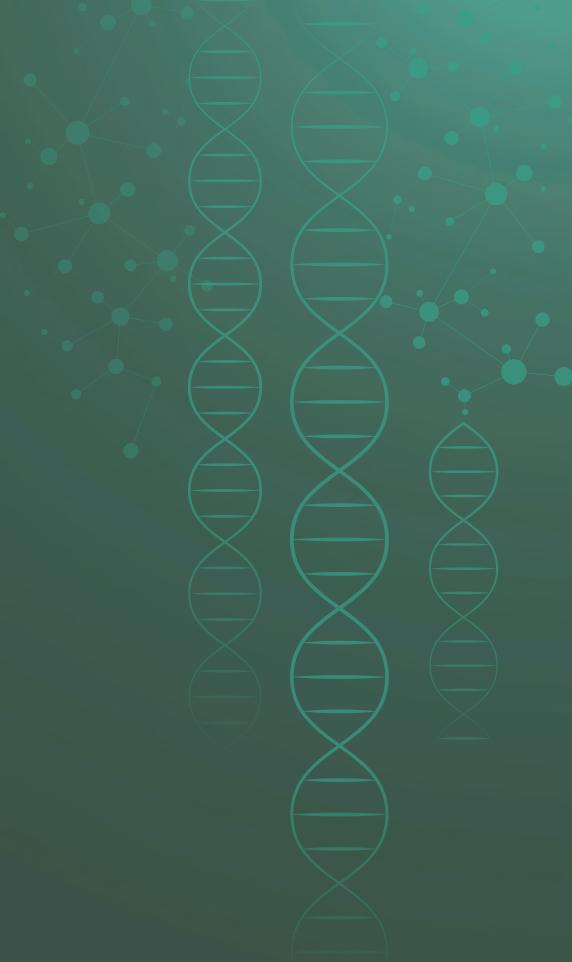


Celemics Liquid Biopsy Panel

Accurate ctDNA Analysis
with Market-leading Specificity
and Sensitivity

Key Features

- Small amount of sample requirement
- Market-leading specificity and sensitivity
- Accurate analysis by molecular barcode

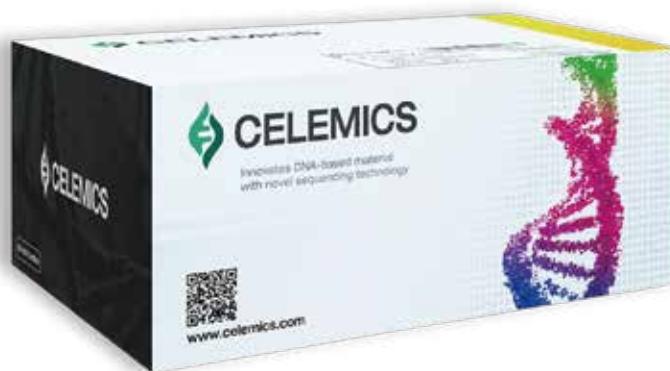


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Liquid Biopsy Panel

Celemics has developed NGS-based ctDNA kits for colon, breast, and lung cancer assays through collaborative research with Seoul National University Hospital since 2017. We have integrated our market-leading proprietary technologies including hybridization probe design algorithms, noise removal techniques, and reagent optimization. The use of molecular barcodes allows for the identification and tracking of individual DNA molecules throughout the sequencing process, minimizing errors and enabling the precise detection of rare genetic variants.



Specification

	Colorectal Cancer	Breast Cancer	Lung Cancer
Gene Count	15	27	28
Covered region	Whole CDS	Whole CDS	Whole CDS for 8 genes and Hotspot exonic region for 20 genes
Target size	49 Kb	99 Kb	47 Kb
Mutation type	SNV, Indel		
Sample type (Amount)	Plasma (>20 ng of cfDNA)		
Platform	All sequencers from Illumina		
Bioinformatics Support	1. Primary Analysis: FASTQ to annotated VCF 2. Secondary Analysis: CNV, Large Indel 3. Tertiary Analysis: Clinical interpretation, Visualization Curation <small>* Linux-based consensus read generation software</small>		

*Gene Add-On Service: Genes can be added by customer's request.

Performance Data

Celemics ctDNA Panels

ctDNA analysis has revolutionized the field of oncology by offering a non-invasive and highly informative method for diagnosing and managing cancer. Celemics ctDNA Colorectal, Breast, and Lung Cancer Panel allows for more precise and personalized approaches to treatment, improving patient outcomes. Our NGS panels enable healthcare providers to tailor treatments to individual patients based on the genetic characteristics of their tumors, ultimately improving the management and outcomes of cancers.

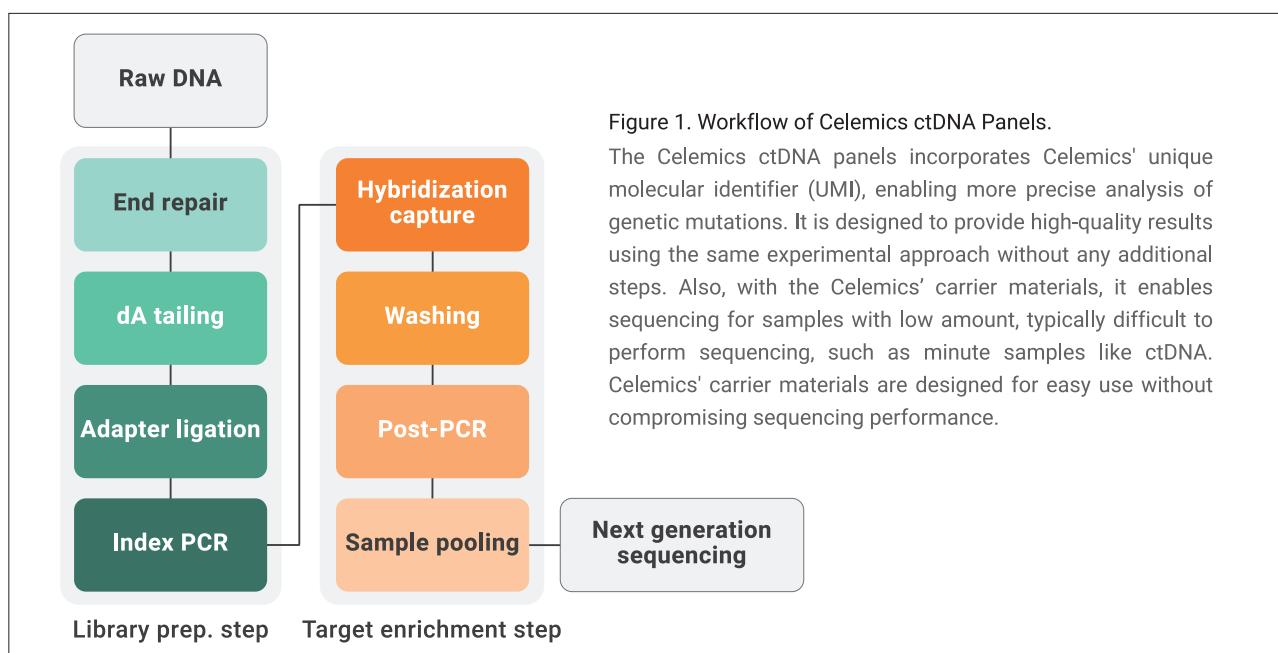


Figure 1. Workflow of Celemics ctDNA Panels.

The Celemics ctDNA panels incorporates Celemics' unique molecular identifier (UMI), enabling more precise analysis of genetic mutations. It is designed to provide high-quality results using the same experimental approach without any additional steps. Also, with the Celemics' carrier materials, it enables sequencing for samples with low amount, typically difficult to perform sequencing, such as minute samples like ctDNA. Celemics' carrier materials are designed for easy use without compromising sequencing performance.

Increased Sequencing Depth with Celemics UMI

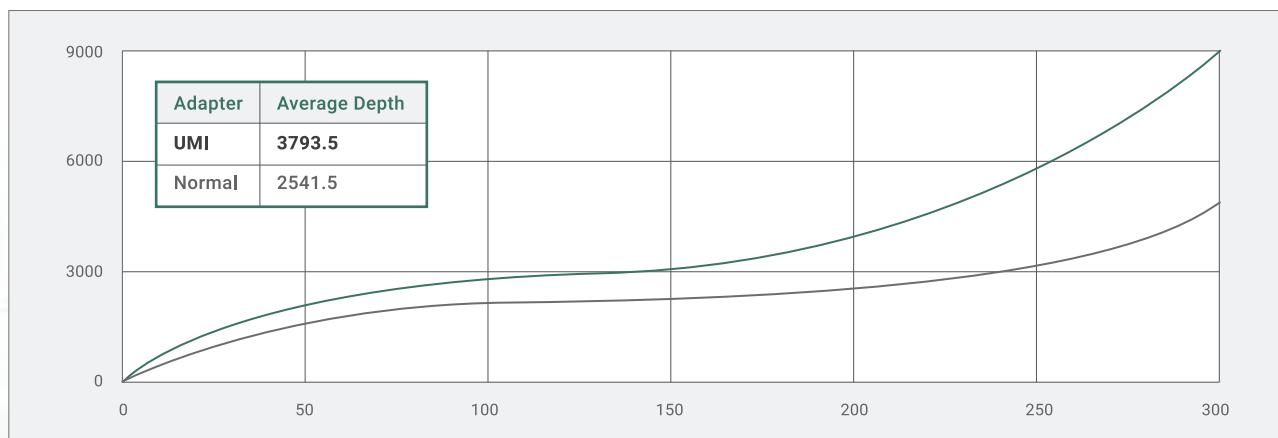


Figure 2. Comparison of sequencing depth when using normal and UMI in Celemics ctDNA Colorectal Cancer Panel. The average sequencing depth was 3793.5 when using UMI, and 2541.5 when using a normal adapter. It was confirmed that when using UMI, the average sequencing depth was more than 1200 depth higher than when using a normal adapter.

Performance Data

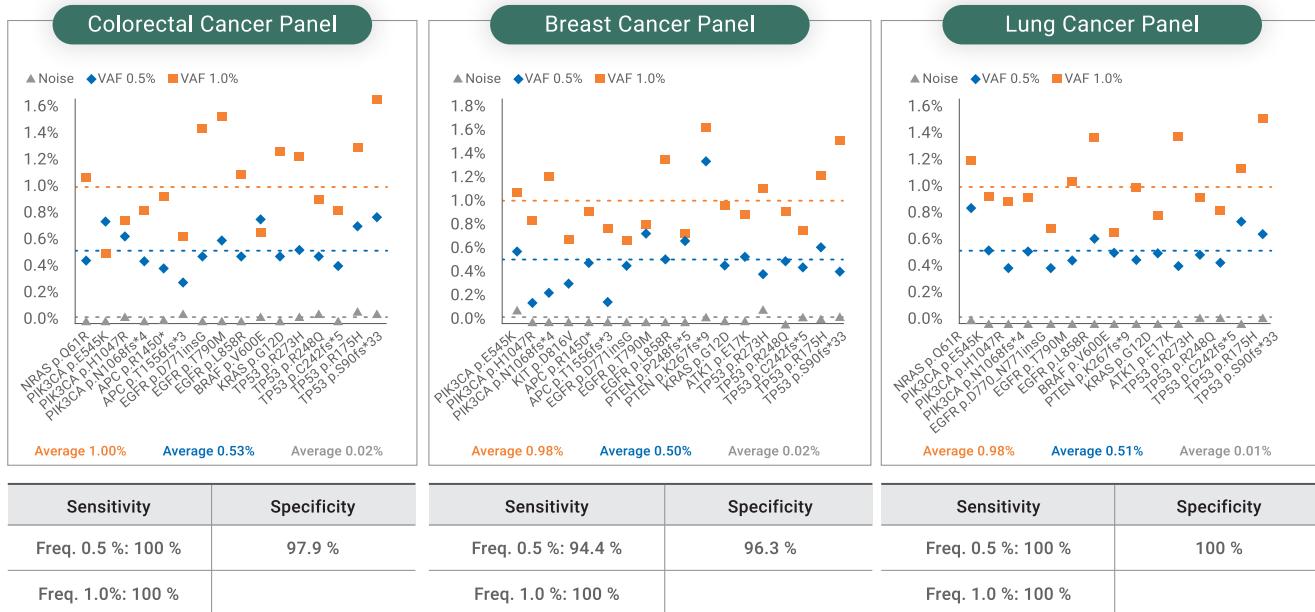


Figure 3. Analysis results for Celemics ctDNA Panels. Celemics' ctDNA Panel is designed to detect the markers in 15, 27, and 28 key genes associated with Colorectal, Breast, and Lung cancer respectively. Our panel achieves more than 94% of analytical sensitivity both of allele frequency of 0.5% and 1.0% with more than 96% of specificities in all tested panels. The tests are performed by using Seraseq® ctDNA Reference Material v2 AF1%, Seraseq® ctDNA Reference Material v2 AF0.5%, and Seraseq® ctDNA Mutation Mix v2 WT.

Gene List

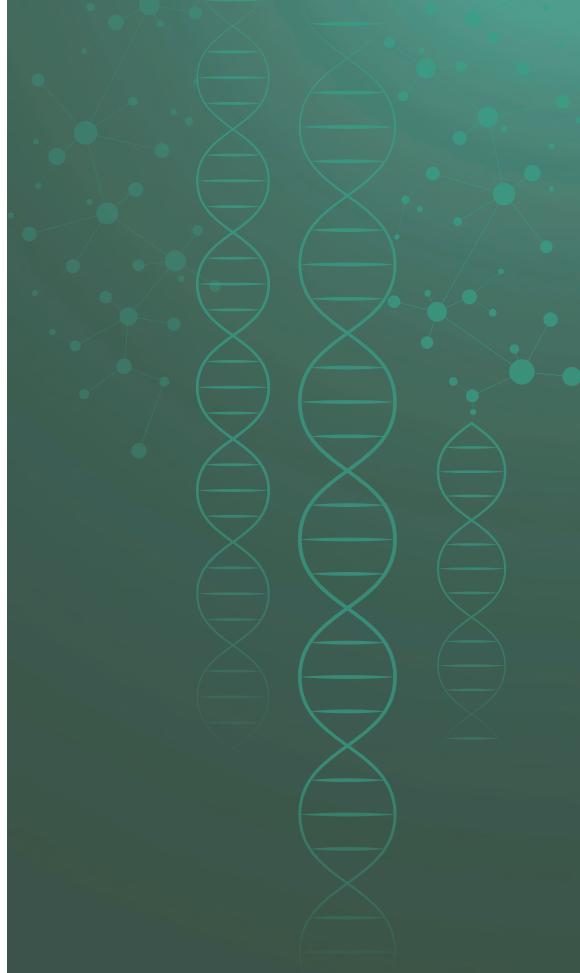
Gene List of ctDNA Colorectal Cancer Panel				
APC	ATM	BRAF	EGFR	ERBB2
FBXW7	KRAS	MET	NRAS	PTEN
PDGFRA	PIK3CA	SMAD4	TCF7L2	TP53

Gene List of ctDNA Breast Cancer Panel				
AKT1	APC	AR	BRCA1	BRCA2
CCND1	CDH1	EGFR	ERBB2	ESR1
FGFR1	FGFR2	GATA3	IGF1R	KIT
KRAS	MAP2K4	MAP3K1	MDM2	MYC
NF1	PIK3CA	PIK3R1	PTEN	RB1
TOP2A	TP53			

Gene List of ctDNA Lung Cancer Panel				
AKT1	ALK	ARAF	ARID1A	BRAF
CBL	CDKN2A	EGFR	ERBB2	HRAS
KEAP1	KRAS	MAP2K1	MET	MTOR
NF1	NRAS	NTRK1	NTRK2	PIK3CA
PTEN	RB1	RIT1	ROS1	SETD2
STK11	TP53	U2AF1		

Celemics Mitochondrial DNA Panel

High Uniformity and
Complete Coverage of
Human Mitochondrial Genome



Key Features

- Specifically designed for sequencing relatively small target sizes of mitochondrial genome
- High-fidelity sequencing
- Flexible customization

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Celemics Mitochondrial DNA Sequencing Panel

Celemics' mtDNA panel is specifically developed for the analysis of the whole mitochondrial genome. Not only can it be used as a standalone panel for mtDNA analysis, but it can also be spike-in to other panels, allowing for the simultaneous analysis of mitochondrial DNA alongside other genomic regions of interest. This flexibility and versatility make the mtDNA panel from Celemics a powerful tool for mitochondrial genome analysis in various research and diagnostic applications.



Specification

Covered region	Whole mitochondrial genome
Target size	16.6 Kb
Mutation type	SNV, Indel
Sample type (Amount)	Blood, FFPE, Fresh-frozen tissue
Platform	All sequencers from Illumina, Thermo Fisher, and MGI
Bioinformatics Support	<ol style="list-style-type: none"> Primary Analysis: FASTQ to annotated VCF Secondary Analysis: Large Indel

*Gene Add-On Service: Genes can be added by customer's request.

Performance Data

High-fidelity Sequencing Panel for Whole Mitochondrial DNA

The Celemics mtDNA sequencing panel is designed to accurately capture whole mitochondrial genome. Whether used as a stand-alone panel or spike-in with other panels, it performs consistently, and it particularly does not interfere with the capture performance of other panels when used simultaneously. This ensures obtaining intact results even when used concurrently with other panels.

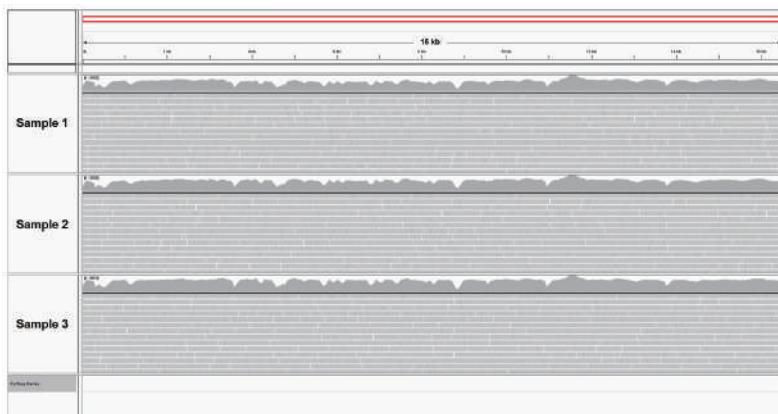


Figure 1: IGV Example of Celemics mtDNA Sequencing Panel used as a spike-in method.

Celemics mtDNA Sequencing Panel shows over 99% with high uniformity. Celemics' mtDNA sequencing can be performed in two different ways, depending on how the library is prepared. The hybridization-based panel is performed by using specifically designed capture probes. Our own proprietary rebalancing technologies provide sequencing results with complete and consistent coverage of the mtDNA whole genome.

Consistent sequencing depth can be secured through Gene Add-on

Celemics' mtDNA sequencing panel can be effectively enhanced using the Gene Add-on method. This method allows for achieving a uniform sequencing depth across different sequencing regions while not interfering with the sequencing results of other panels.

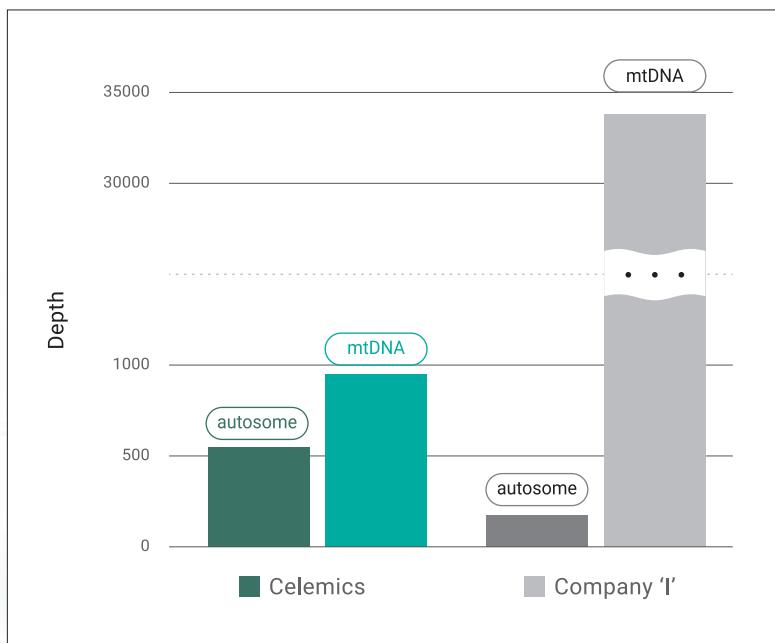


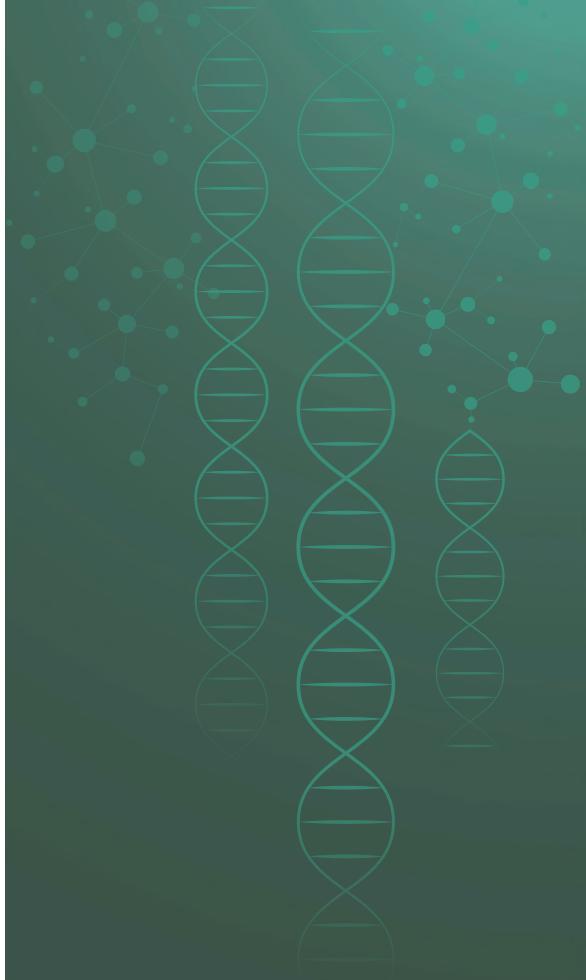
Figure 2: Comparison of Mitochondria Sequencing Depth between Celemics and Competitor Panel: Gene Add-on Method.

Using the Gene Add-on method with the Celemics mtDNA sequencing panel is a valuable strategy for obtaining reliable and consistent results when studying mitochondrial DNA. It ensures that the mtDNA is sequenced accurately and comprehensively while maintaining the integrity of other sequencing panels or regions in the same experiment. Compared to competing panels, Celemics' panel demonstrates a significant advantage in terms of sequencing depth uniformity between autosomal chromosomes and mtDNA. Specifically, Our mtDNA panel exhibits a consistent sequencing depth of 598 for autosomal chromosomes and 921 for mtDNA.



Celemics CancerScreen CUP

Explore the Unknown
Primary Cancer with
Celemics' Exclusive Technology



Key Features

- Probe specifically designed for methyl-seq
- Compatible with various sample types and C/T conversion method
- Primary cancer differentiation
- Easy to follow protocol and flexible integration on various sequencing platforms

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CancerScreen CUP

Methylation sequencing can identify the locations and levels of methylated DNA in a genome-wide or targeted manner for various applications of epigenetic research. Celemics' solution for DNA methylation sequencing can provide more comprehensive and detailed patterns of specific target region of your choice. Also, Celemics targeted methylation sequencing can provide solutions for the study of Cancer of Unknown Primary (CUP) to classify and originate the metastatic tumors, leading to the precision-driven therapeutic interventions.

Methylation Sequencing Workflow and Probe Design Technology

Probe-specific Methylation Sequencing

With the probes specifically designed for methylation sequencing, Celemics performs comparison analysis of the sequences before and after C/T conversion, enabling accurate detection of methylation sites.

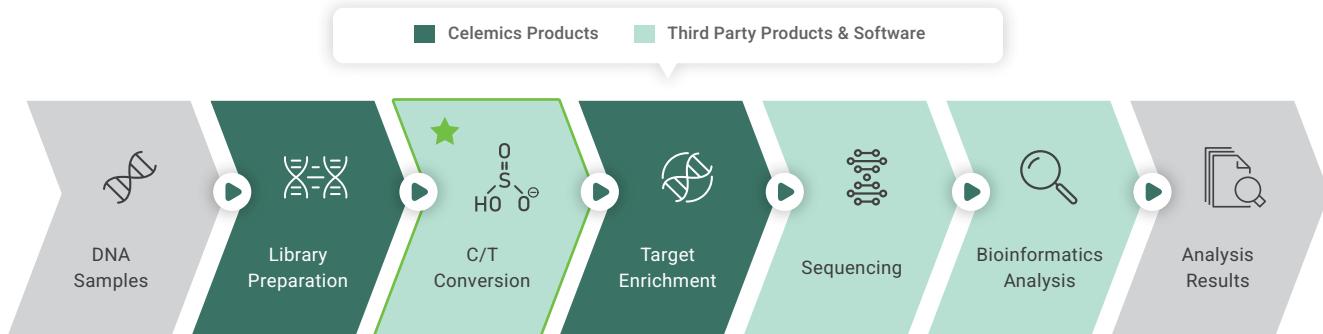


Figure 1. Targeted methylation sequencing workflow. Celemics provides and support easy-to-follow protocol for methylation sequencing.
* C/T Conversion Kit not provided; Celemics can provide optimization services with any C/T conversion kit of choice.

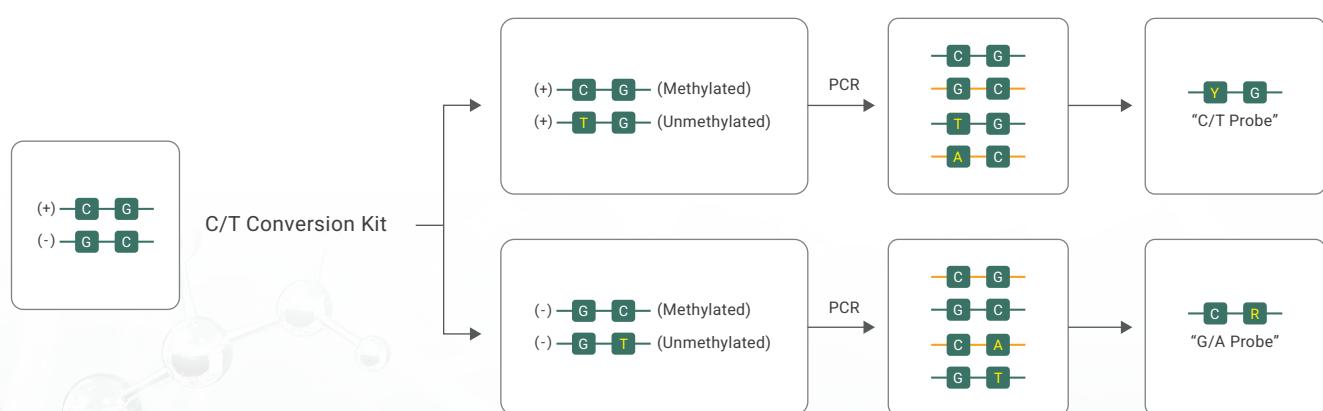


Figure 2. Process for exclusive Celemics' methyl-seq probe design. Celemics introduces exclusive set of probes specifically designed for methylation sequencing, considering the sequence alteration by C/T conversion.

Performance Data

Targeted Methylation Sequencing for Cancer of Unknown Primary (CUP)

Celemics Customized Targeted Methylation Sequencing Panel Solution offers proprietary probe design and a specialized workflow for detecting and classifying the Cancer of Unknown Primary (CUP). The performance data below represents analyses of 14 samples, which comprised cell lines from 5 different cancer types, demonstrating its compatibility and operability for successfully categorizing and identifying the origin of the tumors.

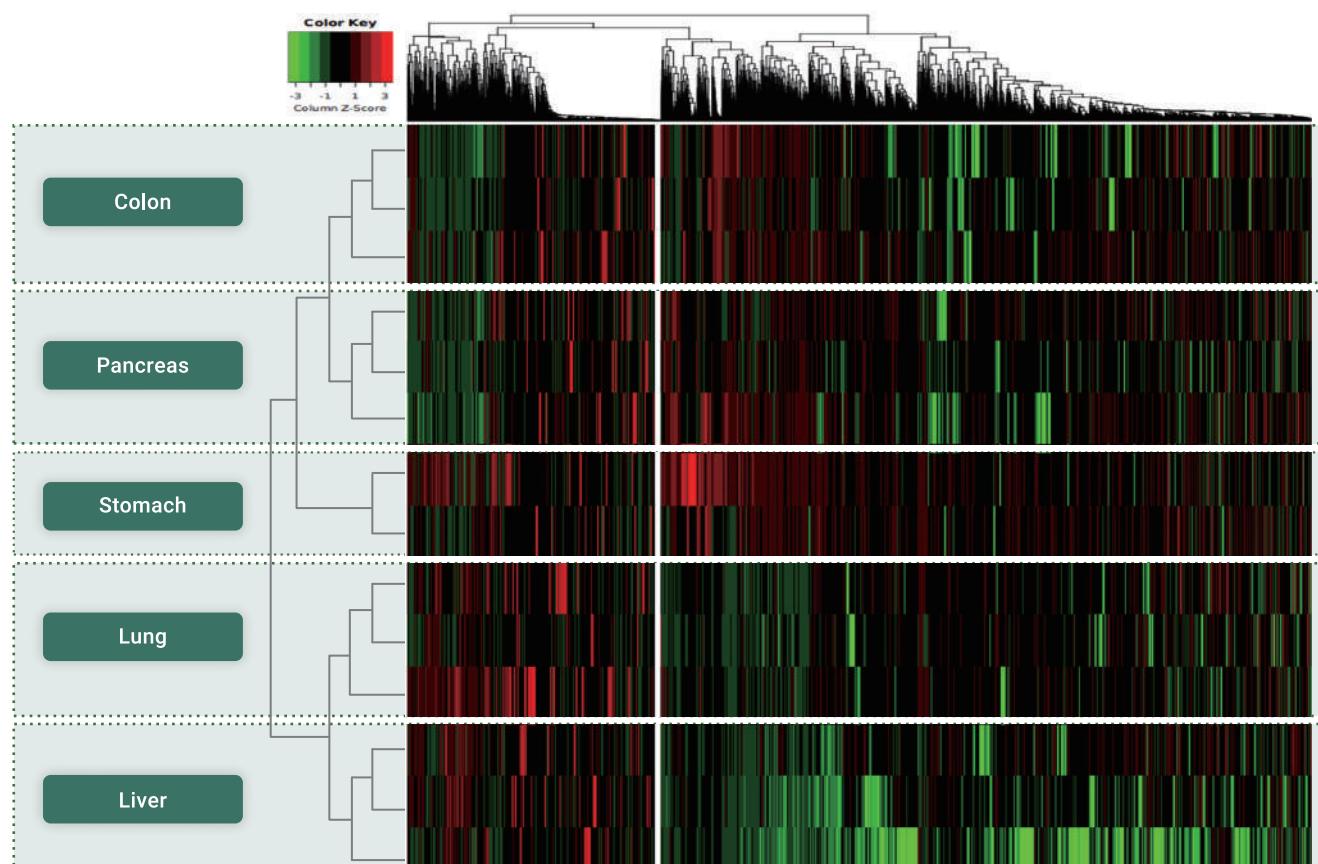


Figure 3. Heatmap and hierarchical clustering results of 14 cancer samples. CancerScreen CUP panel successfully validated and differentiated 14 cancer samples into 5 different cancer types.

ACC	BLCA	BRCA	CESC	CHOL	COAD	DLBC
ESCA	GBM	HNSC	KICH	KIRC	KIRP	LGG
LIHC	LUAD	LUSC	MESO	PAAD	PCPG	PRAD
READ	SARC	SKCM	STAD	TGCT	THCA	THYM
UCEC	UCS	UVM				

Table 1. 31 target cancer types of Celemics CancerScreen CUP Panel.

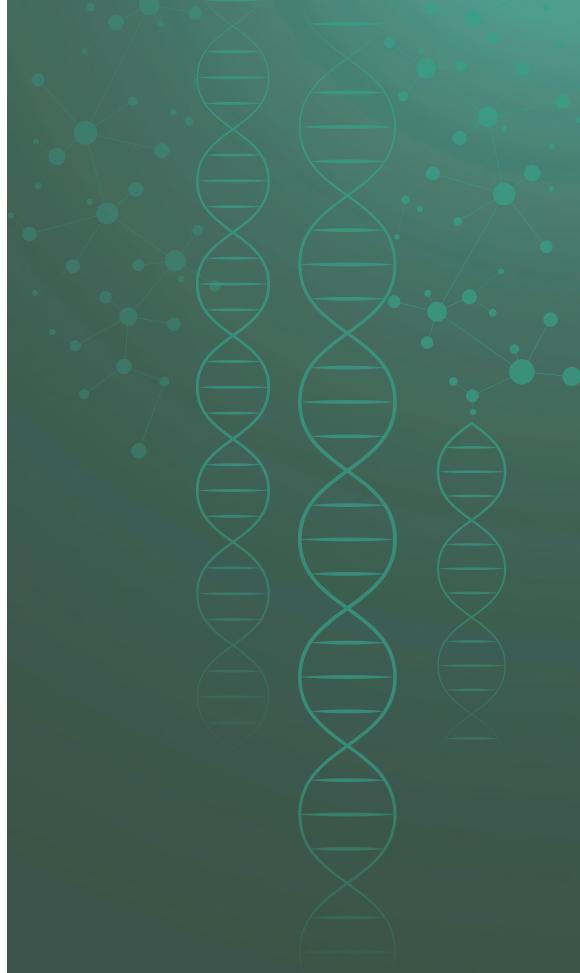


Celemics Comprehensive Respiratory Virus Panel

Superior Success Rate even with
Low Amount of Clinical Sample

Key Features

- Whole genome analysis of 9 different, and 39 different strains of respiratory viruses
- Exceptional variant detection success rate and WGS even in low-viral load clinical sample
- Provision of user-friendly Celemics Virus Verifier Software
- Flexible customization and flawless integrations on various NGS platforms
- Simple workflow with all-inclusive kits



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Celemics Comprehensive Respiratory Virus Panel

Viruses are continuously evolving in ways that make them increasingly infectious and difficult to cure. Thus, the discovery of specific disease-causing viral strains and research into their ability to spread within individuals in a given population have become a paramount public health issue. The Celemics Comprehensive Respiratory Virus Panel (CRV Panel) was developed to detect and sequence respiratory disease-causing viruses in humans using the NCBI RefSeq database as its foundation. It allows for the whole genome sequencing and simultaneous testing of 9 different virus types and its 39 strains of clinically significant and prevalent respiratory viruses, including SARS-CoV-2 and all its relevant mutations and variants.



Workflow of All-inclusive CRV Panel

Celemics' CRV panel includes all set of reagents and panel needed for comprehensive and simultaneous analyses of various viral strains.

Workflow



CRV Panel Specification

Target Virus	9 types / 39 virus strains, including SARS-CoV-2
Target Size	706 Kb
Mutation Analysis	Viral detection, viral mutation (SNV, Indel) from generated Whole Genome Sequence
Sample Type	URT, NP/OP, etc.
Platform	All Illumina and Thermo Fisher Scientific Sequencers
Kit Composition	Double-stranded cDNA synthesis kit, library preparation kit, target enrichment kit, and CVV software
Bioinformatics Pipeline	Stand-alone bioinformatics SW 'Celemics Virus Verifier' (FASTQ to Visual Report)

Pathogen List

Human Adenovirus	Coronavirus	Parainfluenza Virus	Respiratory Syncytial Virus
Human Adenovirus Type 1 (HAdV-C1)	Coronavirus HKU1	Parainfluenza 1 (PIV 1)	Respiratory Syncytial Virus A (RSV A)
Human Adenovirus Type 2 (HAdV-C2)	Coronavirus NL63	Parainfluenza 2 (PIV 2)	Respiratory Syncytial Virus B (RSV B)
Human Adenovirus Type 3 (HAdV-B3)	Coronavirus 229E	Parainfluenza 3 (PIV 3)	Human Metapneumovirus
Human Adenovirus Type 4 (HAdV-E4)	Coronavirus OC43	Parainfluenza 4 (PIV 4) A	
Human Adenovirus Type 5 (HAdV-C5)	SARS-CoV-2	Parainfluenza 4 (PIV 4) B	
Human Adenovirus 7 (HAdV-B7)			
Human Adenovirus 14 (HAdV-B14)		Human Enterovirus	
Human Adenovirus 21 (HAdV-B21)	Influenza A		Human Rhinovirus (A/B/C)
	Influenza A-H7 Virus (Flu A-H7)	EV-C104	Human Rhinovirus A
	Influenza A-H1 Virus (Flu A-H1)	EV-C105	Human Rhinovirus B
Bocavirus 1/2/3/4 (Bov)	Influenza A-H3 Virus (Flu A-H3)	EV-C109	Human Rhinovirus C
Human Bocavirus 1	Influenza A-H3 Virus (Flu A-H3)	EV-C117	
Human Bocavirus 2		EV-C118	
Human Bocavirus 3	Influenza B		CV-A21
Human Bocavirus 4	Influenza B Virus (Flu B)	EV-D68	

Performance Data

The CRV panel ensures to provide superior WGS success rate and pathogen classification even with poor quality specimen, such as low viral load clinical specimen or poor quality environment-originated samples. Using Celemics' CRV panel, you will witness the robust pathogen detection accuracy with significantly reduced gap formation compared to other competitor products.

Low Viral Load Clinical Sample

Sample Type	Coverage (1X)	Coverage (10X)	Coverage (100X)
Clinical specimen	99.95%	99.87%	98.95%

Table 1. Coverage result based on clinical samples using CRV Panel. The performance test results from clinical samples show excellent Whole Genome Coverage

LOD detection (>100 copy)		LOD detection (>100 copy)	
Influenza virus A-H3 H3N2	detected	Human Enterovirus EV-D68	detected
Influenza virus B	detected	Parainfluenza virus 4A	detected
SARS-CoV-2	detected	Influenza virus A-H1 H1N1	detected

Table 2. Virus samples tested with varying degrees of copy numbers. Various types of respiratory viruses were evaluated in respect to changes in copy numbers using Synthetic Viral Control Samples (Twist Bioscience). All types of virus successfully sequenced and detected with detection limit set to 1x coverage higher than 10%.

Celemics Virus Verifier Software

Celemics provides stand-alone software for bioinformatics analysis that allows customers to access the detailed data analysis information and ensures the sequencing data security of sensitive client information.





3. Arigenomics

Celemics Agrigenomics Panels

Innovative NGS Solutions
for Animals, Plants,
and Microorganisms

Key Features

- Includes set of exclusive target organism-specific reagents and optimized assay for enhanced performance
- Maximized sequencing efficiency targeting specific genome of interests
- Flexible customization and flawless integrations on various NGS platforms
- Easy-to-follow protocol

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Celemics Agrigenomics Solutions

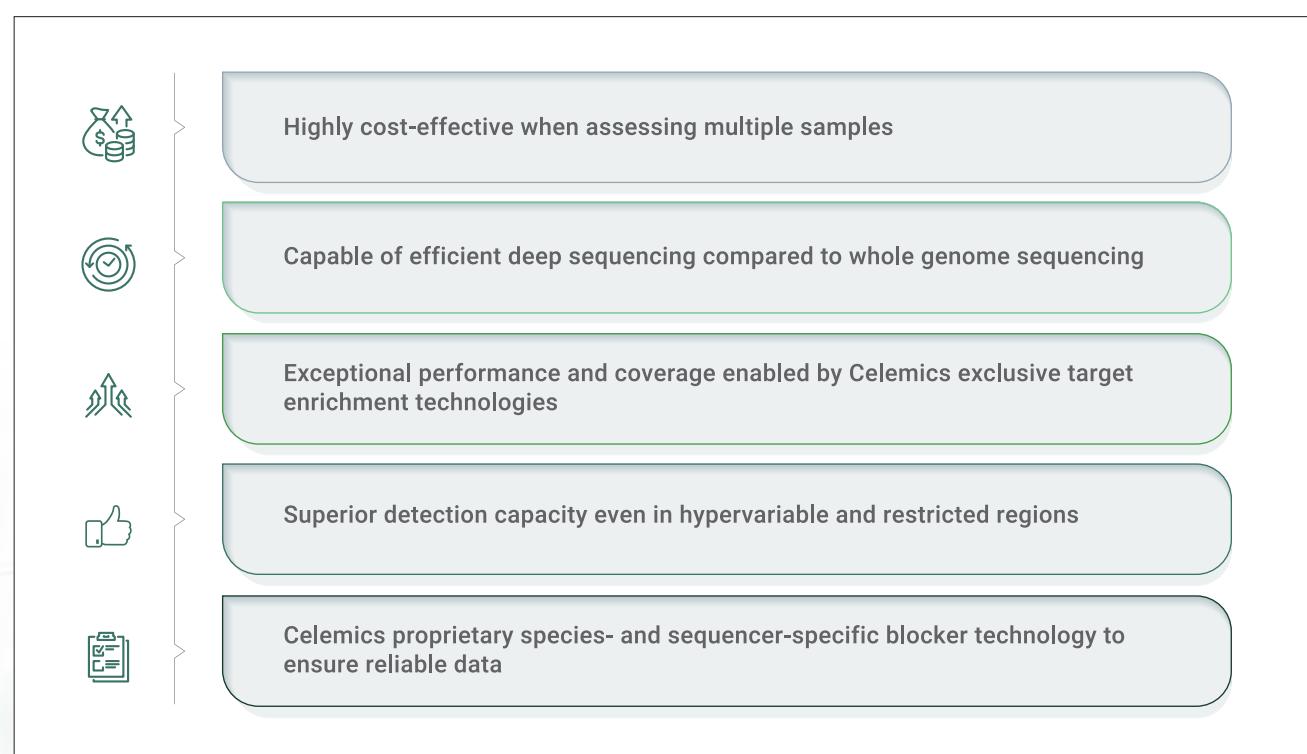
The needs and demand for NGS in agrigenomics and animal research field are exponentially increasing as NGS can provide genetic information at an unprecedented scale and speed compared to conventional genotyping method. To meet the expectations and needs for sequencing animals and plants, Celemics offers range of ready-to-use panels applicable to agrigenomics field as well as an option for developing customized NGS panel that specifically fits individual research purposes. With Celemics' exclusive core technologies, we aim to revolutionize the field of agrigenomics by enabling complex genetic studies and developing new strategies for improving crop and animal productivity and sustainability



Celemics Target Enrichment Solution in Agrigenomics

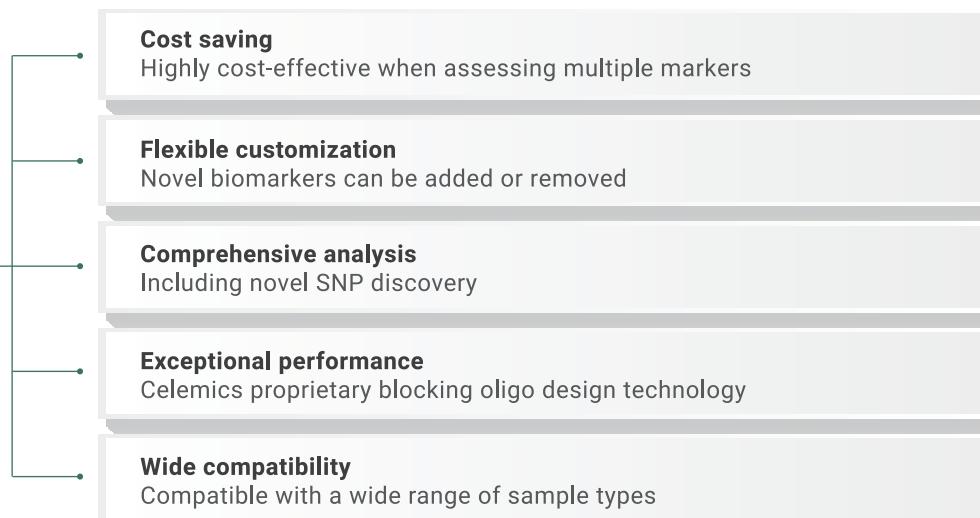
Benefits of target enrichment in Agrigenomics field

Celemics NGS solution can be applied to various agrigenomics applications. All panels are supplemented with species-specific blockers with complete optimization and validation which will result in incomparable benefits when compared to conventional detection and testing methods



Comparison with conventional technologies

	Advantages	Disadvantages
Conventional GBS	Sequencing of multiple samples due to lower amount of data required compared to WGS	Limited biomarkers available due to limited conserved regions, reducing overall resolution Unable to detect SNPs in the restriction sites
Microarray	Higher reproducibility than conventional GBS	Hard to customize new targets (novel biomarkers) Low flexibility to meet various kinds of genotyping
PCR	Cost-effective for low number of markers Easy and fast analysis	Limited number of biomarkers to analyze at once Inappropriate for mass-analysis of biomarkers



Agrigenomics Applications

Celemics NGS solution can be applied to various agrigenomics applications. All panels are supplemented with species-specific blockers with complete optimization and validation.

Animal-borne Pathogen Testing

Whole Viral Genome Sequencing

Virus/bacteria Identification

Molecular Breeding

Mass Genotyping

Metagenomics

Performance Data

Celemics NGS solution for animals

Celemics provides African Swine Fever Virus (ASFV) and Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) Panel for efficient and effective virus detection accompanied by our exclusive in-house designed hybridization probes. It can provide highly accurate results even from swine blood sample, which is considered more challenging due to its lower viral load compared to concentrated culture supernatant or spleen tissue sample. We have optimized the panel and reagents in addition to swine-specific blockers for your convenient and effective testing.

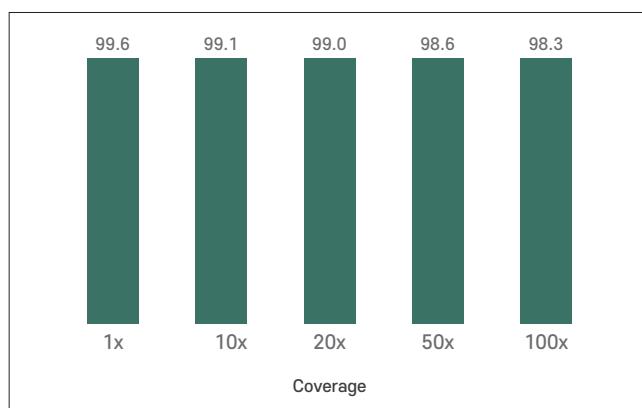


Figure 1. Validated sequencing result shows high coverage at all levels.

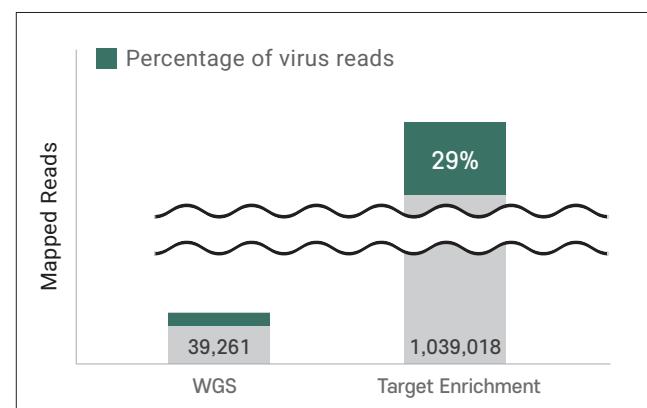


Figure 2. Targeted sequencing ensures significantly higher virus reads compared to the whole genome sequencing method. In addition to targeted sequencing method, proprietary Swine-specific blocking reagent will efficiently filters out repetitive sequences, allowing for the selective retrieval of ASFV sequences.



Figure 3. Visualization of sequencing data mapped to reference genome for PRRSV Target Region. Celemics probe design and assay optimization technology enables accurate detection even in challenging hypervariable regions.

Celemics NGS solution for plants

Celemics offers both ready-to-use panels and customized panels for crops and plants for speciation, biomarker discovery, GMO testing, and more. All panels are supplemented with species-specific blockers with complete optimization and validation.

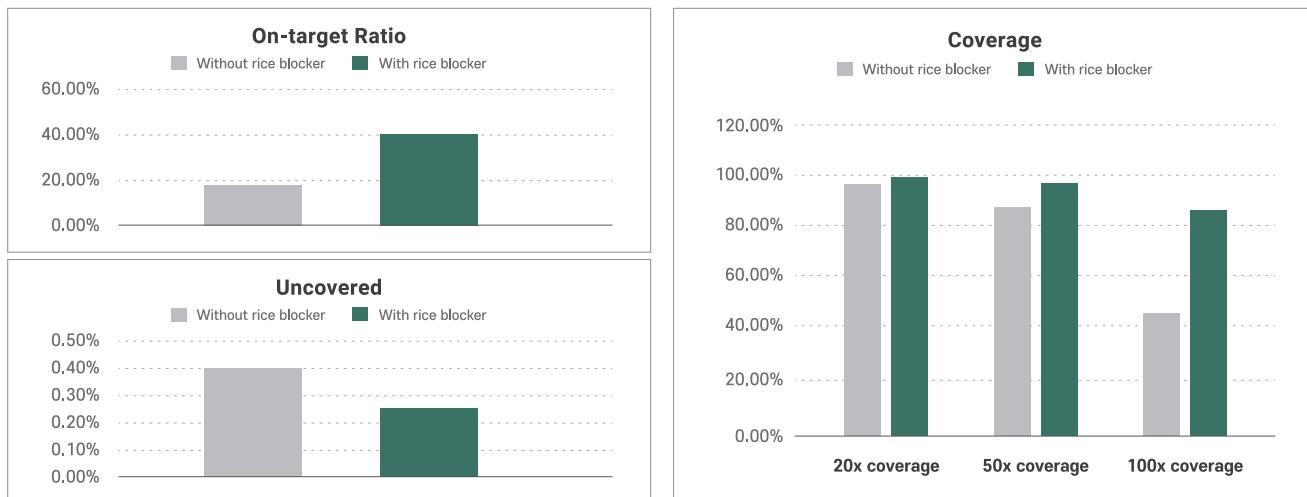


Table 1. Species-specific blocker allows effective detection of biomarkers. The sequencing data of sample with rice-specific blocker and without blocker were compared. The on-target ratio and coverage, especially for 100x, were significantly higher and in sample with rice-specific blocker and showed much lower uncovered rate compared to the sample without the specific blocker.

Celemics NGS solution for virus and bacteria

Celemics offers both ready-to-use panels and customized panels for analyzing diverse viruses and bacteria for both human and non-human. Celemics' exclusive kits and panels allow rapid and accurate sequencing of whole viral genome, viral speciation and strain identification, along with variant tracking on any targeted region of interest.



Figure 4. Vibrio panel for pathogen-specific NGS panel.

Celemics Agrigenomics Solutions

Celemics offers flexible customization of agrigenomics panels and assays to meet our customers' research and diagnostic requirements. Please inquire for any additional information regarding ready-to-use and customized solutions.

Celemics Agrigenomics Panels

African Swine Fever Virus (ASFV) Panel

Target Info	Whole genome of ASFV 26 strains
Target Size	192 Kb
Sequencing Platform	Illumina, Thermo Fisher, and MGI

Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) Panel

Target Info	Whole genome of PRRSV
Target Size	16 Kb
Sequencing Platform	Illumina, Thermo Fisher, and MGI

PEDV Panel

Target Info	Whole genome of PEDV
Target Size	28 Kb
Sequencing Platform	Illumina, Thermo Fisher, and MGI

Vibrio Panel

Target Info	2,566 SNP biomarkers
Target Size	156 Kb
Sequencing Platform	Illumina, Thermo Fisher, and MGI

* For other panels and customizing options, please contact your local Celemics representative.



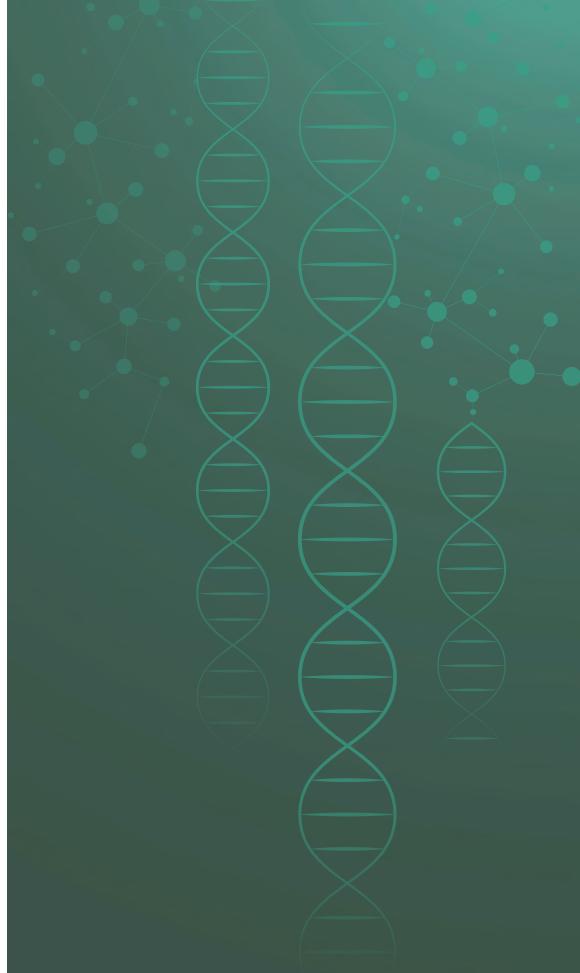
4. Customized NGS Solution

Celemics Customized NGS Solution

Taking NGS Customization
to the Next level

Key Features

- Provision of end-to-end customized NGS solution
- Industry-leading on-target ratio and uniformity of hybridization-based target enrichment
- Robust performance of assessing DNA and RNA across various specimen quality
- Provision of white-labeled customized product for supporting customer's business expansion
- Simple and rapid workflow



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Celemics Customized NGS Panel



Celemics target enrichment panel employs hybridization-based capture technology to enable targeted sequencing, facilitating the analysis of specific regional sequences of entire genomes. It accurately analyzes various types of mutations, including single nucleotide variants (SNVs), insertions/deletions (Indels), copy number variations (CNVs), and rearrangements. Celemics' target enrichment panel utilizes our proprietary probe design, rebalancing, blocker, and assay optimization technologies to efficiently analyze not only hard-to-capture areas such as GC-rich and homologous regions, but also tiny amounts of damaged DNA or RNA originated from circulating tumor cells or FFPE samples. Celemics has successfully developed and delivered over 1,000 custom panels. Our target enrichment approach specifically isolates genomic regions of interest, leading to enhanced sensitivity in detecting genetic mutations through increased coverage with cost-effectiveness.

Customized NGS panel design and manufacture workflow

Celemics' core technologies are incorporated when designing and manufacturing exclusive customized NGS panels. For every panel Celemics designed, we perform the actual validation NGS run to confirm the panel performance. After our validation run, probe sets are rebalanced and optimized, if necessary, through feedback cycle, and thereby provide robust customized NGS panel with outstanding performance and maximized sequencing efficiency.

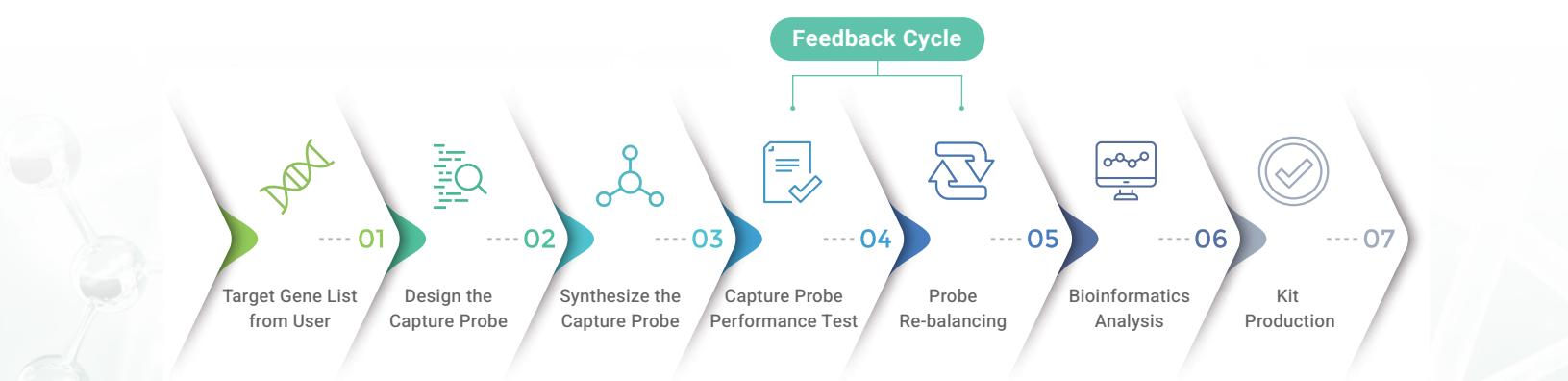


Figure 1. Celemics panel design and manufacturing process.

Custom Assay Development



We, as NGS experts, provide extensive NGS solutions for new insights into various clinical or research fields. With proprietary probe design and manufacturing technology, Celemics takes Customization to the next level; we offer customized NGS solution for any types of sample you wish to analyze. From simple gene add-on from our existing ready-to-use panel to discovering new targets that you were unable to analyze using current commercially available solutions, we can develop complete set of assay with optimized reagent and buffer for your target of interest. The process of developing and optimizing custom assay will include not only the customizing the panel design but also designing species-specific or sequencer-specific blockers, followed by reagent and buffer conditioning depending on the customer's experiment condition and sequencing platform. Celemics provides tailored-fit customize assay development from designing to validation run; optimizing the custom assay to perfection.

	Species	Sample type	Sequencing Platform	Library Preparation	Multiplexing	Hybridization
Options & Components	Human Plant Animal Fungi Virus Bacteria Etc.	DNA/RNA from Blood, Tissue, FFPE, Saliva, etc.	Illumina	Celemics LP	CeleNM™ Bead	Standard Hybridization
		Liquid Biopsy (cfDNA, cfRNA)				
		Environmental Specimen	ThermoFisher	Celemics EP	Conventional Multiplexing	Enhanced Hybridization
		Etc.				

Table 1. Options and components for custom assay development.

High-throughput Genotyping



Celemics provides the solution with our high-throughput genotyping panel. We have utilized NGS and hybridization-based capture technology, whereby a high number of regions of interest are simultaneously enriched using specifically designed probe, to provide genotyping results with maximized analytical efficiency in your area of interest. With our exclusive technologies, we can provide NGS-based target enrichment sequencing assay for comprehensive and highly accurate analyses.

Comparison with Conventional Technologies

	Advantages	Disadvantage
Conventional GBS	Sequencing of multiple samples due to lower amount of data required compared to WGS	Limited biomarkers available due to limited conserved regions, reducing overall resolution Unable to detect SNPs in the restriction sites
Microarray	Higher reproducibility than conventional GBS	Hard to customize new targets (novel biomarkers) Low flexibility to meet various kinds of genotyping
PCR	Cost-effective for low number of markers Easy and fast analysis	Limited number of biomarkers to analyze at once Inappropriate for mass-analysis of biomarkers
Celemics Target Enrichment	Cost saving : Highly cost-effective when assessing multiple markers Flexible customization : Novel biomarkers can be added or removed Comprehensive analysis : Including novel SNP discovery Exceptional performance : Celemics proprietary oligo design technology Wide compatibility : Compatible with a wide range of sample type	

Business Model Consultations from Celemics

Celemics is CE-IVD, ISO 9001, ISO 13485 and KGMP accredited to provide support and consultations for our customers. Through our experience and accreditations, we are eligible to support all kinds of business models including IVD regulation, clinical trial procedures, OEM and ODM, White-labeled products, and technical transfer consults. We can also assist in customers requiring other specific accreditation (CAP, GCLP, and more) upon client's request. For more inquiries regarding prospective consultations, please contact us at cs@celemics.com



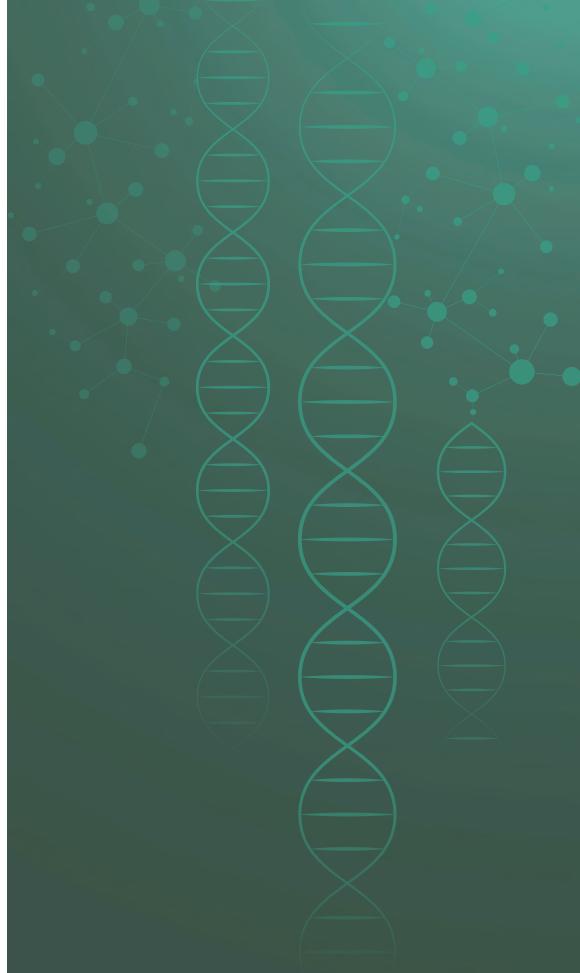
5. Modular Accessories

Celemics Library Preparation Kit (LP / EP)

Optimized for High-efficiency
Celemics Panels

Key Features

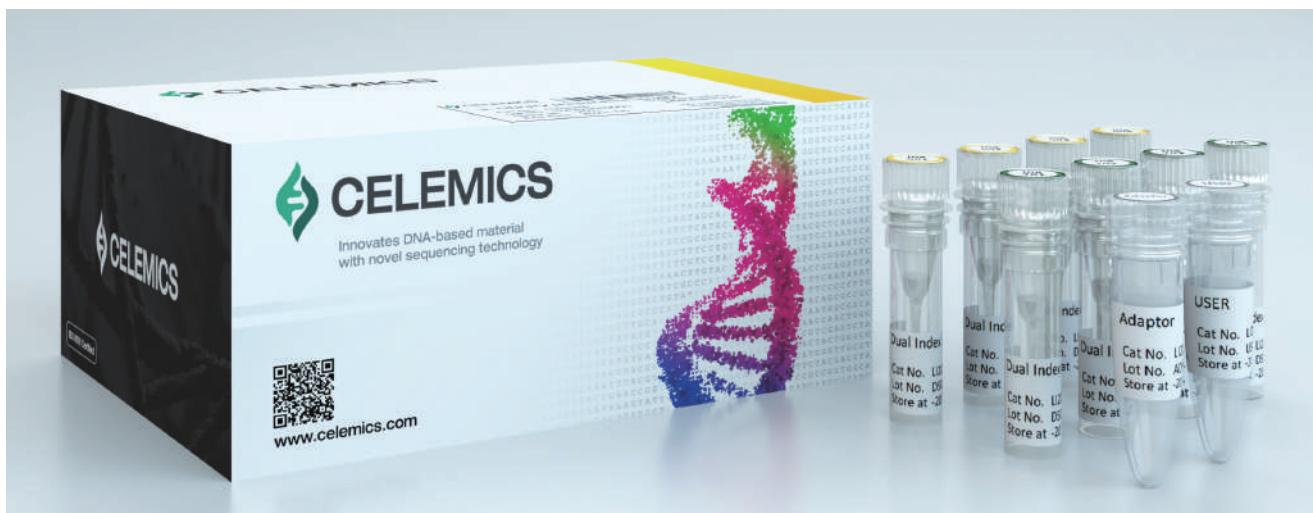
- Includes optimized set of enzymes needed for high-efficiency library preparation
- Easy-to-follow protocol
- Robust and reproducible NGS libraries
- Flexible integration with NGS panels from various vendors



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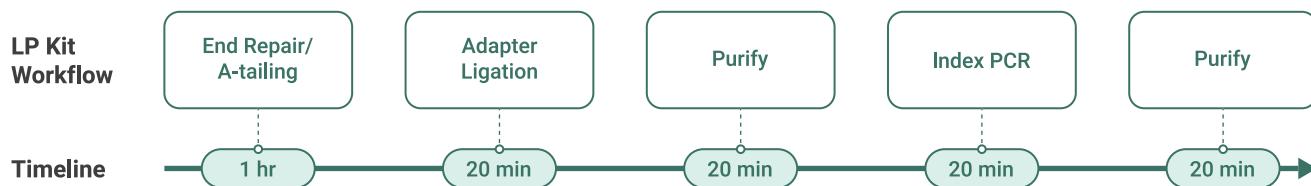
Celemics Library Preparation Kit



All Celemics library preparation kits are highly optimized for efficient usage with Celemics' ready-to-use or customized panels. Both the Standard (LP) and Enzymatic Preparation (EP) kits include end-repair and A-tailing enzyme mix as well index primers, adapters and buffers

Celemics Library Preparation Kit - LP

For standard method of Library Preparation Kit (denoted as LP Kit), customers can use ultra-sonication devices or fragmentase for DNA fragmentation.



Reproducibility Data using LP Kit

No.	Input amt (ng)	PCR cycle	Conc. (ng/uL)	Yield (ng)
1	100	8	55.6	1668
2	100	8	56.2	1686
3	100	8	54.4	1632
4	100	8	51.3	1539
5	100	8	51.6	1548
6	100	8	44.6	1338

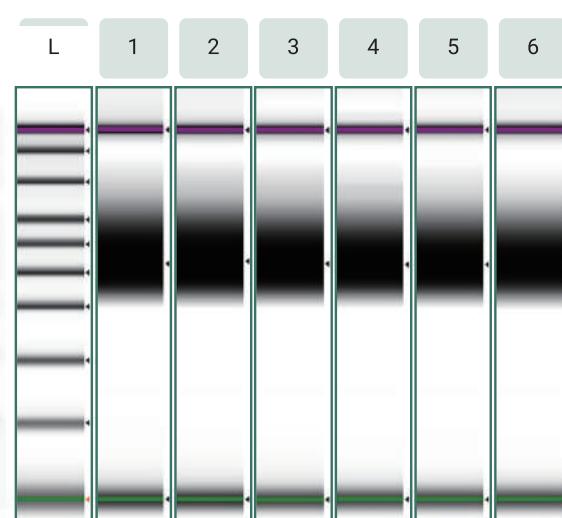


Table 1 & Figure 1. Reproducibility of Celemics' Library Preparation Kit (LP). 100 ng input of NA12878 with Celemics LP kit showed highly reproducible result, relatively similar concentration and the total yield, for all 6 of replicated samples.

Celemics Library Preparation Kit - LP

Performance Comparison Data

The amplified yield of DNA libraries using Celemics' LP kit was compared with other major vendors. The results showed that Celemics' LP kit presented the highest yield with robustness when compared with other vendors' kits, regardless of the input DNA amount.

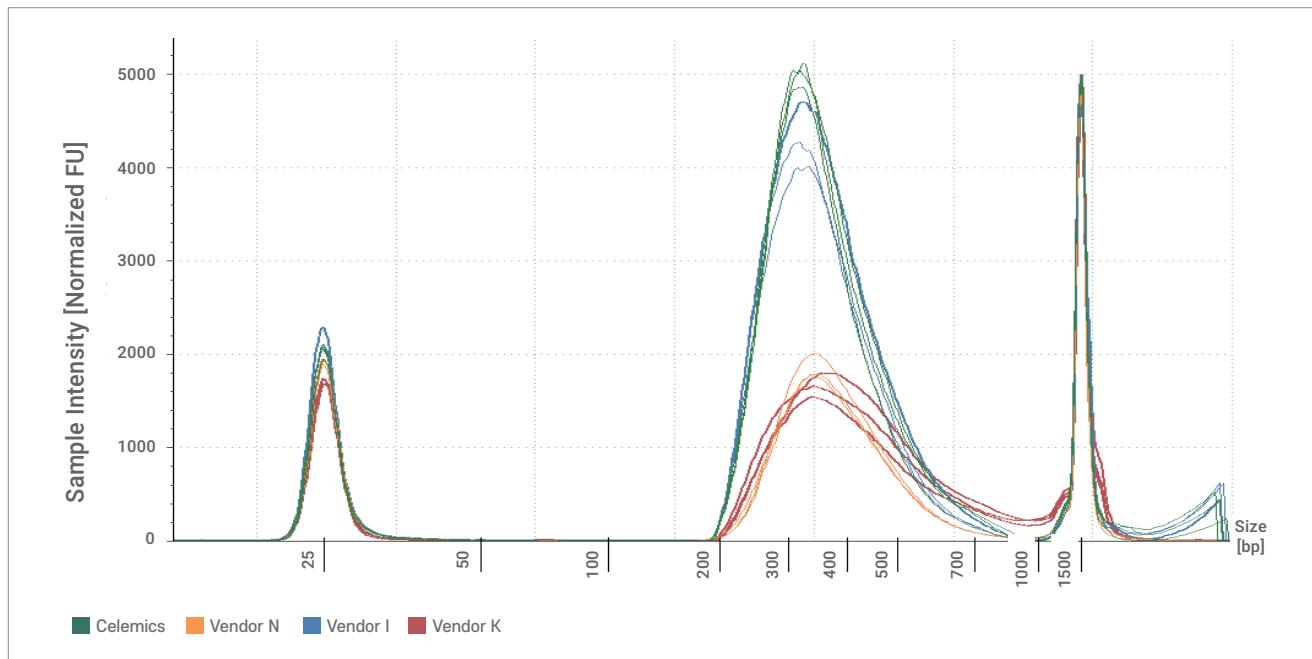


Figure 2. Reproducibility and overall yield for Celemics LP Kit was compared with three other vendors. For all library kits, 10 ng of DNA were equally used and the result shows that Celemics LP kit provides the highest yield and reproducible data compared to other vendors kits.

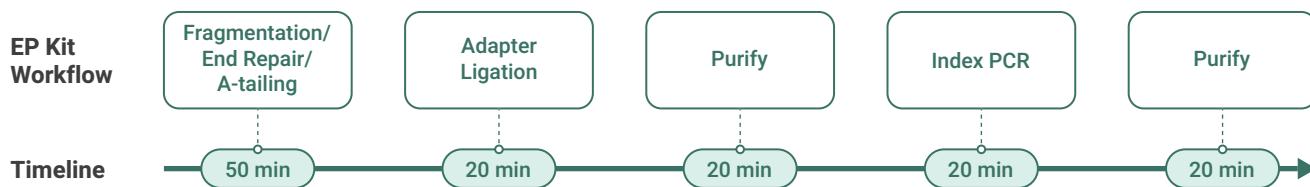
Sequencing Performance Matrix

	Duplication ratio	On-target ratio	Fold 80 base penalty	Mean depth over target region	1x coverage	10x coverage	20x coverage	50x coverage	100x coverage
Celemics LP	3.83%	86.85%	1.44	478.48	100.00%	99.98%	99.94%	99.76%	99.12%
Vendor I	4.63%	84.73%	1.49	469.42	100.00%	99.97%	99.92%	99.69%	98.62%

Table 2. Sequencing performance comparison. The prepared libraries using Celemics' LP kit and Vendor I were sequenced for performance comparison. The overall sequencing quality and result of Celemics LP kit outperformed those of Vendor I.

Celemics Library Preparation Kit - EP

The Enzymatic Library Preparation Kit (denoted as EP Kit) includes all set of reagents needed from enzymatic fragmentation to ER/A in a single reaction enabling convenient workflow. EP kit offers effortless workflow with minimal risk of DNA loss.



Reproducibility Data using EP Kit

No.	Input amt (ng)	PCR cycle	Conc. (ng/uL)	Yield (ng)
1	100	6	61.0	1830
2	100	6	56.4	1692
3	100	6	61.5	1845
4	100	6	56.7	1701
5	100	6	57.1	1713
6	100	6	59.6	1788
7	100	6	60.8	1824
8	100	6	59.5	1785

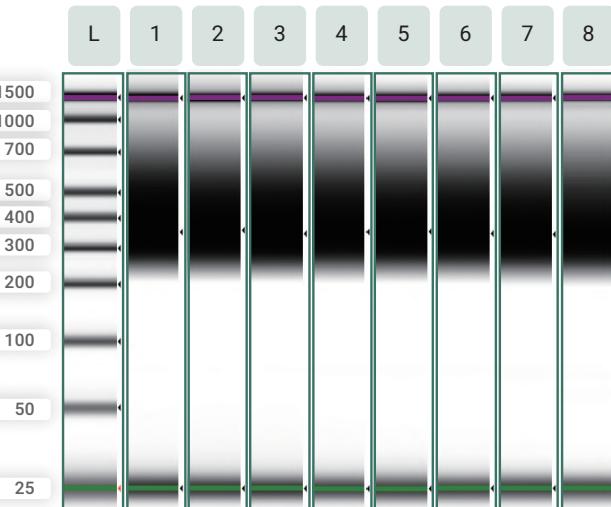


Table 2 & Figure 3. Reproducibility of Celemics' Library Preparation Kit (EP). 100 ng input of NA12878 with Celemics EP kit showed highly reproducible result, relatively similar concentration and the total yield, for all 8 of replicated samples.

Performance Comparison Data

The amplified yield of DNA libraries using Celemics' EP kit was compared with other major vendors. The results showed that Celemics' EP kit presented the highest yield with robustness when compared with other vendors' kits, regardless of the input DNA amount.

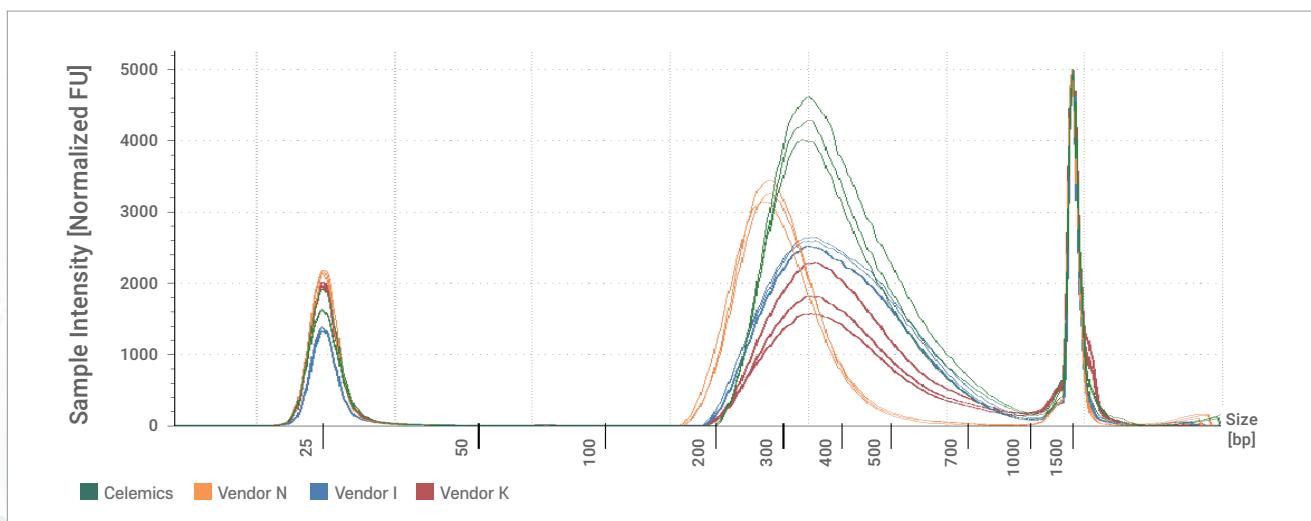


Figure 4. Reproducibility and overall yield for Celemics EP Kit was compared with three other vendors. For all library kits, 100 ng of DNA were equally used and the result shows that Celemics EP kit provides the highest yield and reproducible data compared to other vendors kits.

Celemics Library Preparation Kit - EP

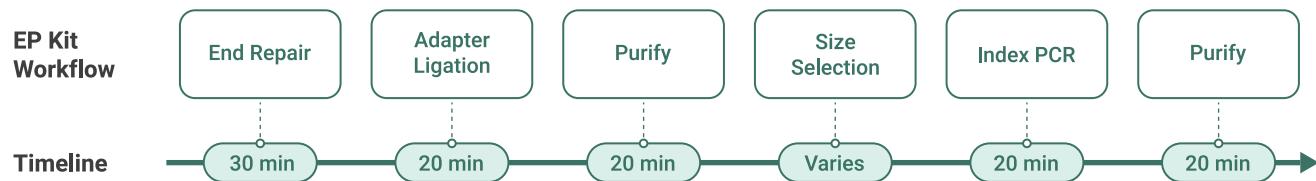
Sequencing Performance Matrix

	Duplication ratio	On-target ratio	Fold 80 base penalty	Mean depth over target region	1x coverage	10x coverage	20x coverage	50x coverage	100x coverage
Celemics EP	5.01%	88.58%	1.51	471.21	100.00%	99.95%	99.89%	99.56%	98.75%
Vendor I	4.20%	88.88%	1.53	465.64	100.00%	99.97%	99.95%	99.81%	99.20%

Table 3. Sequencing performance comparison. The prepared libraries using Celemics' EP kit and Vendor I were sequenced for performance comparison. The results were comparable to one another for on-target and duplication ratio, with fold-80 base penalty (lower the better) of Celemics kit lower than the Vendor I

Celemics Library Preparation Kit – LP for Ion Torrent

Celemics provides the optimized library preparation kit for Ion Torrent platform users. The user may choose either sonicator or fragmentase for DNA fragmentation.



Reproducibility for Celemics LP kit for Ion Torrent

Sample Name	Input amount (ng)	PCR cycle	Conc. (ng/uL)	Yield (ng)
1	200	12	29.2	876.0
2	200	12	29.6	888.0
3	200	12	30.6	918.0
4	200	12	29.5	885.0
5	200	12	30.1	903.0
6	200	12	31.1	933.0
7	200	12	29.1	873.0
8	200	12	29.7	891.0

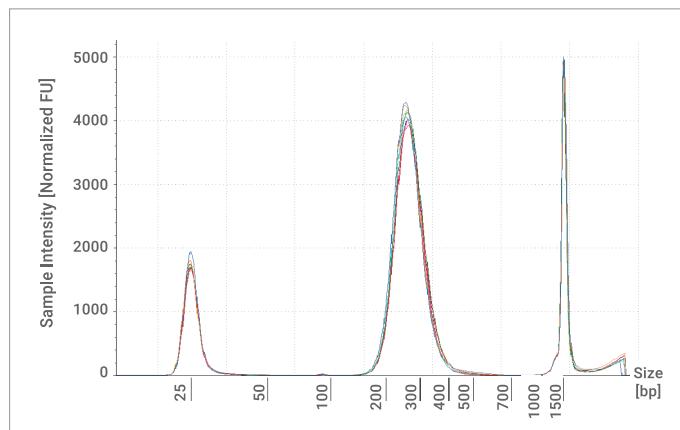


Table 1 & Figure 1. Reproducibility of Celemics' Library Preparation Kit (LP) for Ion Torrent. 200 ng input of NA12878 with Celemics LP kit showed highly reproducible result, relatively similar concentration and the total yield, for all 8 of replicated samples.

Comparison data for Celemics LP kit for Ion Torrent

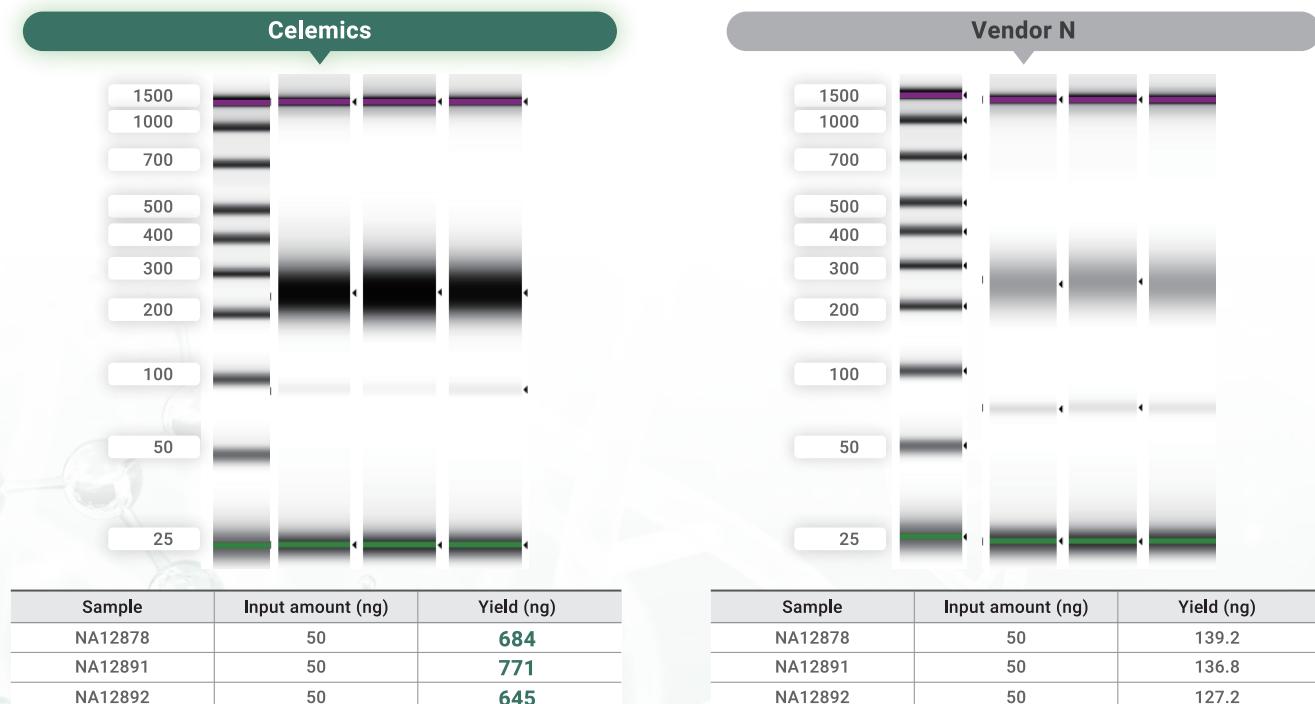


Figure 2. Comparing the library yield between Celemics LP kit and product from Vendor N for Ion Torrent. Using 50 ng input amount, Celemics LP kit showed significantly higher yield compared to those amplified with Vendor N.

Celemics Library Preparation Kit – LP for Ion Torrent

Comparison data for Celemics LP kit for Ion Torrent

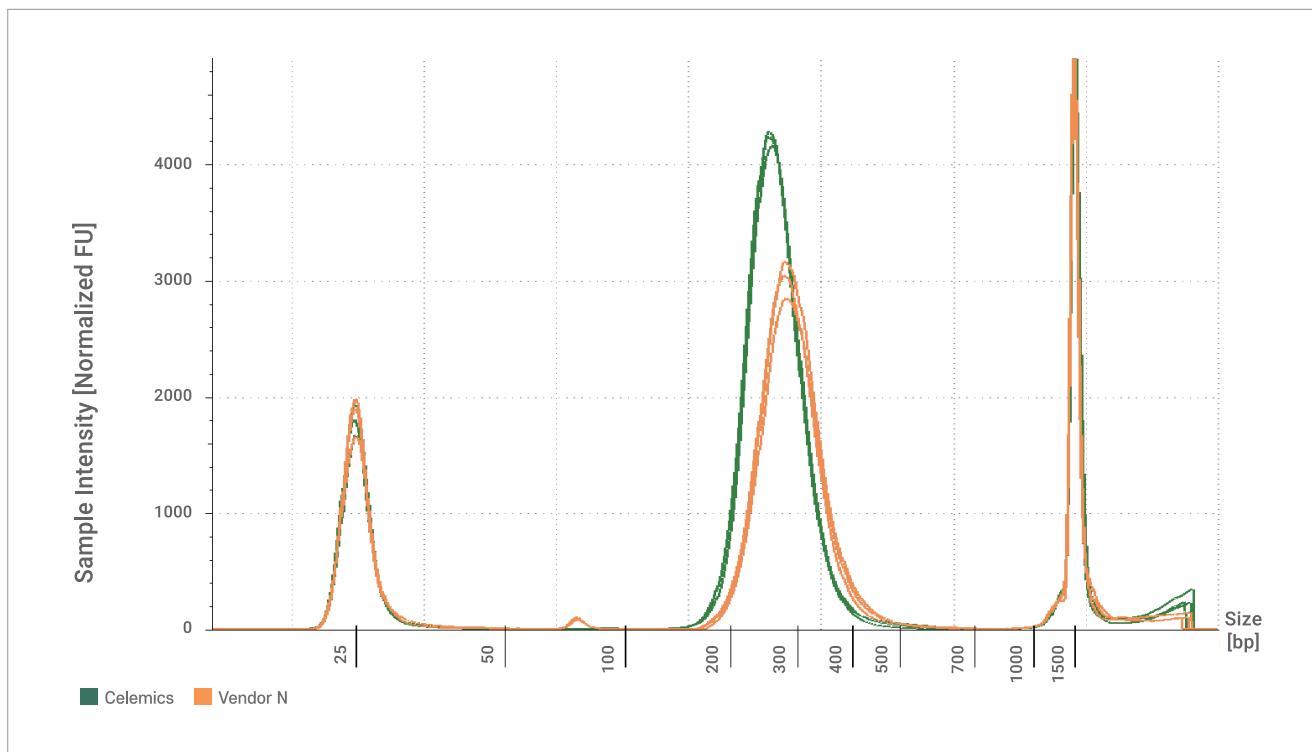
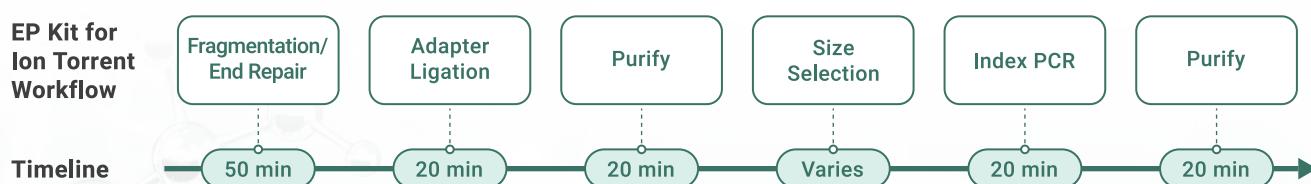


Figure 3. Comparing yield between Celemics LP kit for Ion Torrent and Vendor N. The input amount was set to 200 ng of reference DNA, NA12878, for both groups and the results showed that Celemics kit showed significantly higher yield with better reproducibility compared to Vendor N.

Celemics Library Preparation Kit – EP for Ion Torrent

Celemics also provides the Enzymatic Library Preparation Kit (EP Kit) for Ion Torrent platform users. EP Kit eliminates the need for heavy instruments for fragmentation, such as sonicator, and user can prepare high-yield libraries with easy to follow protocols.



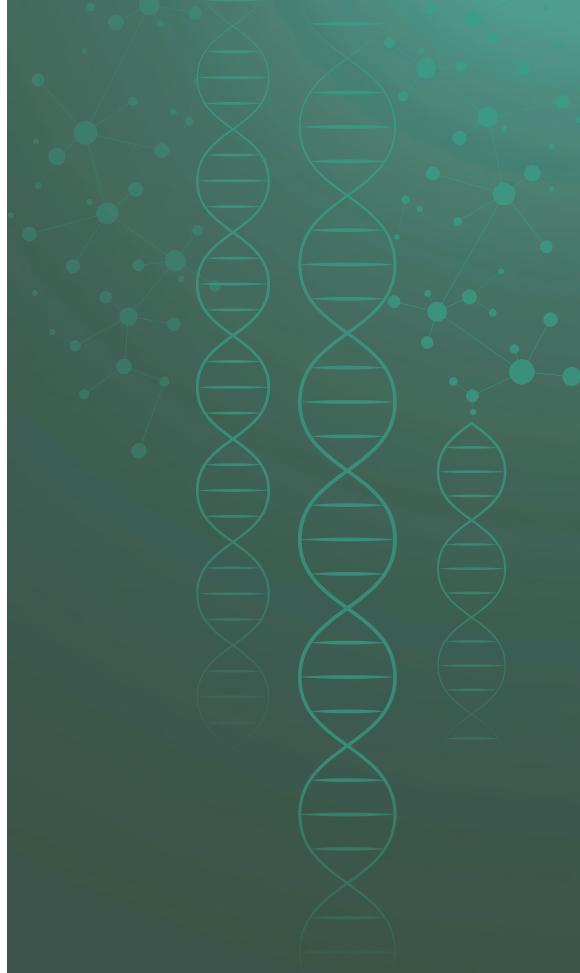


Celemics Double-stranded cDNA Synthesis Kit

Stabilize RNA to
Double-stranded cDNA
for Unquestionable Performance

Key Features

- Includes all components needed from RNA fragmentation to double-stranded cDNA synthesis suitable for NGS-quality
- Easy-to-follow protocol
- Robust and reproducible NGS libraries



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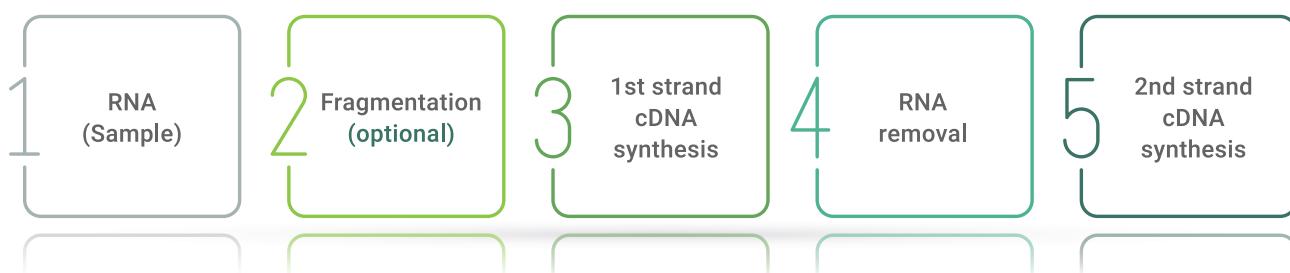
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Celemics Double-stranded cDNA Synthesis Kit

Celemics' Double-stranded cDNA Synthesis Kit is designed to provide the optimized for template for NGS-based RNA sequencing. The kit includes all components from RNA fragmentation to double stranded cDNA synthesis for NGS library preparation. The undeniable stability and performance of the kit allows for the cDNA synthesis even from low amounts of RNA samples with high accuracy and reduced reaction time.



Double-stranded cDNA synthesis workflow



Performance Data

The robustness of Celemics Double-stranded cDNA Synthesis Kit was tested by generating 6 replicated sample using 100 ng of Universal Human RNA (Agilent Technologies, USA)

Reproducibility Data

No.	Input amt (ng)	PCR cycle	Conc. (ng/uL)	Yield (ng)
1	100	10	60.1	1803
2	100	10	63.3	1899
3	100	10	59.8	1794
4	100	10	58.2	1746
5	100	10	58.4	1752
6	100	10	59.4	1782

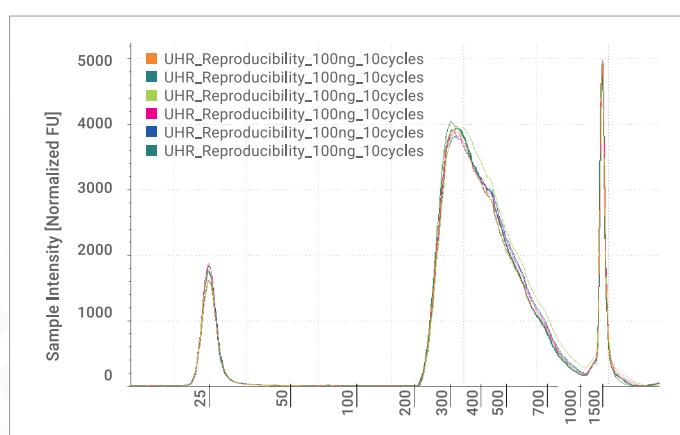


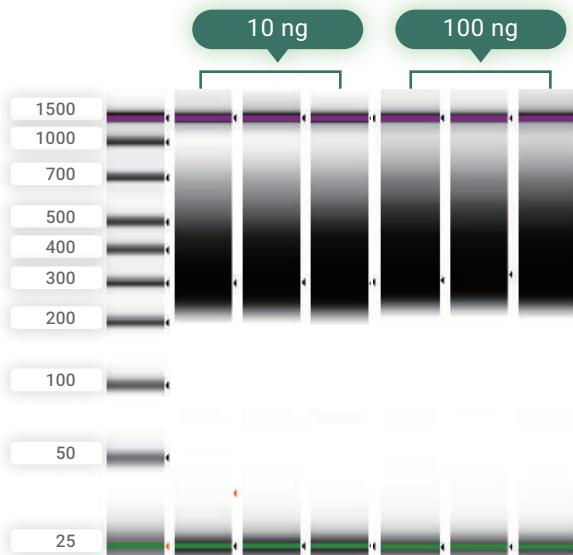
Table 1 & Figure 1. Reproducibility of Celemics' double-stranded cDNA synthesis kit. 100 ng input of Universal Human RNA (UHR) with Celemics kit showed highly reproducible result, relatively similar concentration and the total yield, for all 6 of replicated samples.

Performance Data

Performance Comparison Data

The amplified yield with synthesized cDNA were compared with our major competitors' in the market. The data generated using Celemics Double-stranded cDNA Synthesis Kit provided significantly higher yield than those of competitors' products.

Celemics				
No.	Input amt (ng)	PCR cycle	Conc. (ng/uL)	Yield (ng)
1	10	12	54.3	1629
2	10	12	56.7	1701
3	10	12	65.7	1971
4	100	10	66.9	2007
5	100	10	63.4	1902
6	100	10	65.4	1962



Vendor K				
No.	Input amt (ng)	PCR cycle	Conc. (ng/uL)	Yield (ng)
1	10	12	31.0	930
2	10	12	29.9	897
3	10	12	25.1	753
4	100	10	44.8	1344
5	100	10	46.0	1380
6	100	10	46.6	1398

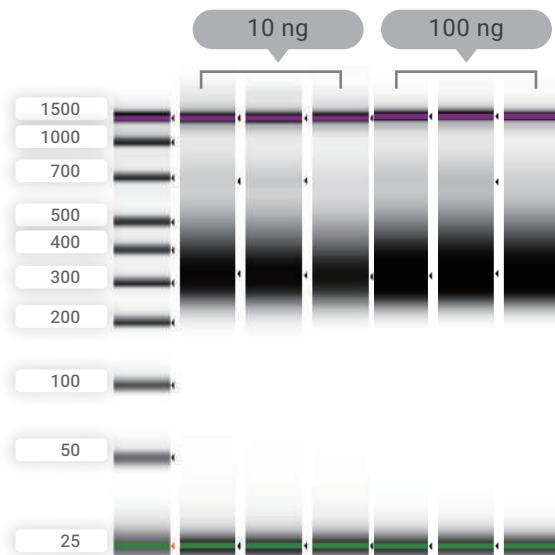


Table 2 & Figure 2. Comparison of the amplified yield using Celemics and Vendor K's double-stranded cDNA synthesis kit. For both 10 ng and 100 ng input of UHR, the overall yields generated with Celemics kit were significantly higher than those generated with Vendor K's product.

Celemics				
No.	Input amt (ng)	PCR cycle	Conc. (ng/uL)	Yield (ng)
1	100	10	66.9	2007
2	100	10	63.4	1902
3	100	10	65.4	1962

Vendor K				
No.	Input amt (ng)	PCR cycle	Conc. (ng/uL)	Yield (ng)
1	100	10	48.6	1458
2	100	10	44.9	1347
3	100	10	48.3	1449

Table 3. Comparison of the amplified yield using Celemics and Vendor N's double-stranded cDNA synthesis kit. Using 100 ng input amount of UHR, the Celemics kit provided higher yield compared to the competitor product.



Celemics CLM Polymerase

Market-leading Performance
with Minimized PCR Bias

Key Features

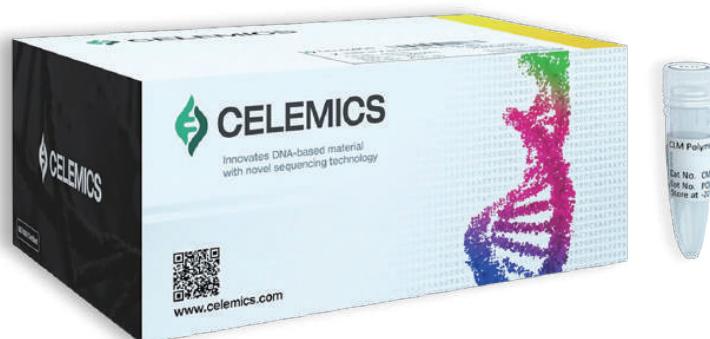
- Market-leading performance
- Optimized performance for NGS
- High yield and accuracy
- Minimized PCR bias

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CLM Polymerase

The role of polymerase is critical in Next Generation Sequencing (NGS) process. Due to the complexity of the library, high performance polymerase is obligatory for high uniformity and yields. As an innovative leader in NGS industry, Celemics has been providing CLM polymerase with market-leading performance, exhibiting high yield and accuracy with minimized PCR bias. The high-fidelity CLM polymerase will always ensure a low PCR error rate with high degree of accuracy in the replication of DNA of interest. The product includes all reaction components for PCR with easy-to-follow protocols.



Performance Data

Amplified DNA Yield

The ability of CLM Polymerase to efficiently amplify the DNA libraries depending on the input amount have been tested and compared with other major competitor brands in the market.

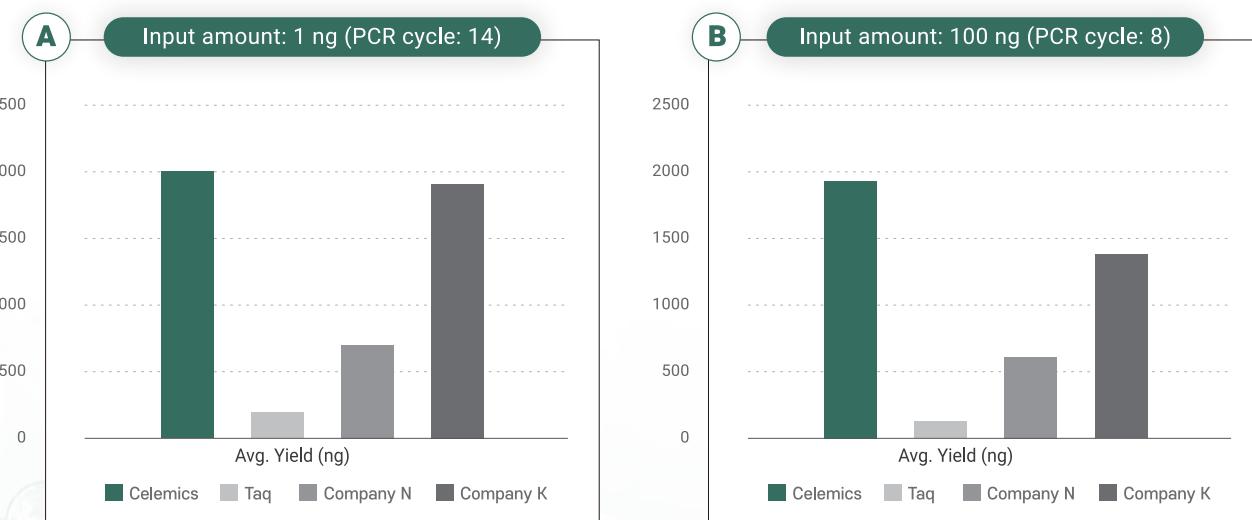


Figure 1A. refers to the comparison of amplification efficiency of input DNA library amount of 1 ng. The average yield of DNA libraries after 14 cycles for Celemics was 1,997 ng, which is the highest among the comparing groups, Company K, Company N and Taq polymerase. Figure 1B. shows comparison graph with DNA library input amount of 100 ng. The average yield of Celemics' CLM polymerase was the highest (1,918 ng) compared to other competitors' enzymes, showing the robust amplification efficiency of chemically optimized Celemics' polymerase.

Performance Data

PCR Error Rate

The highly engineered and optimized reagent condition of CLM Polymerase ensures lower PCR error rates compared to other parties.

Polymerase	Sub_ratio	Indel_ratio	Err_ratio
Celemics	0.068%	0.041%	0.109%
Company K	0.068%	0.048%	0.116%
Taq	0.112%	0.040%	0.153%

Table 1. Calculated PCR error rate for CLM Polymerase and other competitor products. Of the comparing groups, Celemics' CLM Polymerase showed the lowest error ratio of 0.109%.

Reproducibility

CLM polymerase ensures consistent and reproducible amplification results regardless of input amount or sample types.

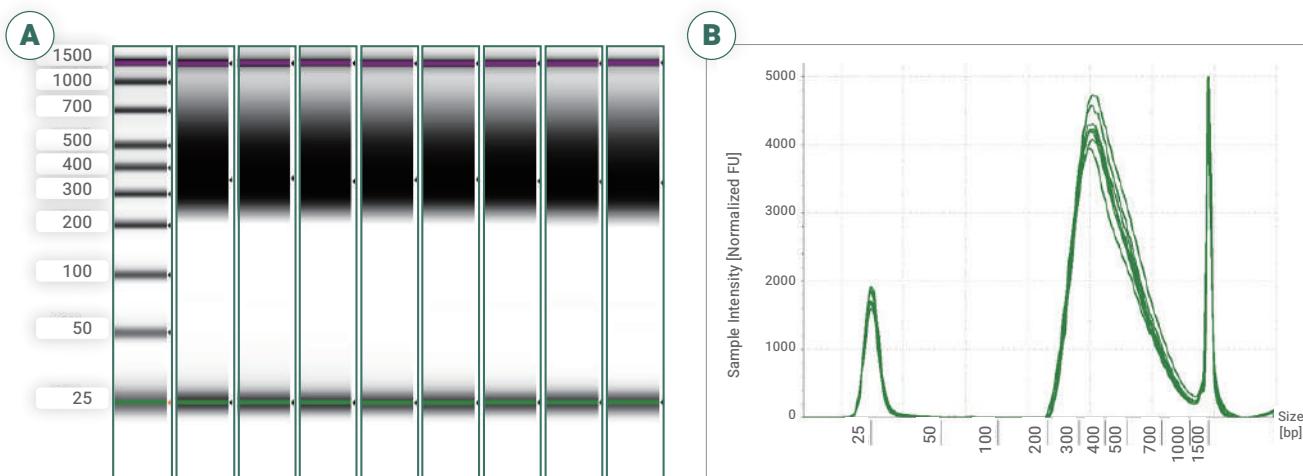


Figure 2. Polymerase reproducibility data. The concentration of 8 replicates of 100 ng of input DNA showed reproducible result. A) represents the gel images of 8 replicates and B) is the electropherogram of those 8 replicates. Total of 6 PCR cycles were performed and bead ratio of 1x was chosen for purification. Overall yields were greater than 1500 ng for all samples.

Uniform amplification in both high-GC and low-GC regions

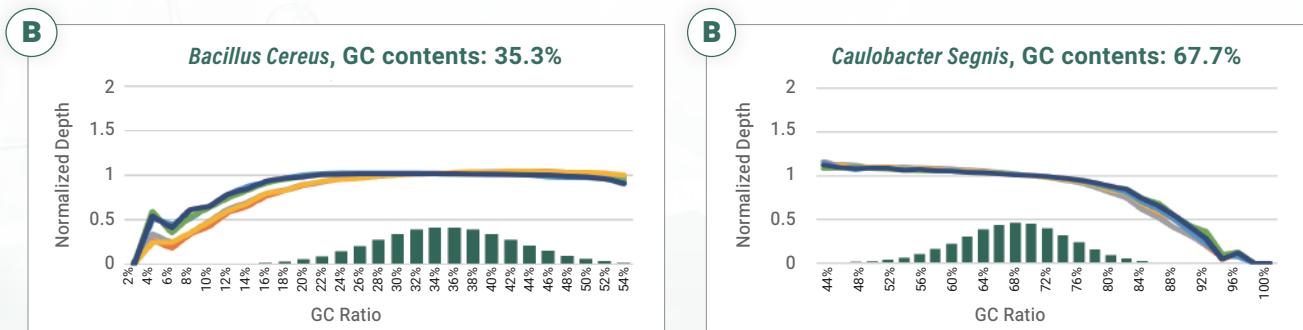


Figure 3A and 3B. The amplification of high-GC and low-GC region using CLM Polymerase. The amplification capacity was tested using bacterial sample with known GC contents. The result shows that optimized and high quality polymerase that allows steady and uniform amplification without PCR bias for both high-GC and low-GC regions.

Performance Data

Sequencing Data Comparison

Sample Name	On-target ratio	Fold 80 base penalty	Mean depth over target region	1x coverage	20x coverage
Celemics	86.38%	1.98	602.74	100.00%	99.95%
Taq	80.93%	2.62	570.43	99.96%	99.47%
Company N	81.12%	2.33	597.19	99.99%	99.82%
Company K	77.97%	1.80	540.94	100.00%	99.94%

Table 2. Comparison of sequencing data. 100 ng of NA12878 genomic DNA (Coriell Institute, USA) was used to prepare DNA libraries then the libraries were amplified using CLM Polymerase along with other three vendors'. For all library preparation and target enrichment process, Celemics Library Preparation Kit and Celemics Target Enrichment Kit were used and sequenced on Illumina platform. The captured data shows that Celemics' CLM Polymerase can outperform other competitors' enzymes by yielding the highest on-target ratio and coverage as well as superior fold-80 base penalty among the comparison group.

CeleMag™ Clean-up Bead

Celemics' Innovative
High Purification Efficiency

Key Features

- Market-leading purification and size selection efficiency
- Unique magnetic bead-based chemistry
- Consistent size selection with flexibility
- Proven performance with significant cost savings
- Compatible with all Celemics' panels as well as other NGS providers



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CeleMag™ Clean-up Bead

The process of DNA clean-up is a mandatory step for Next Generation Sequencing (NGS). In order to streamline the entire NGS workflow without risking the loss of crucial genomic data, CeleMag™ Clean-up Bead has specifically been optimized to meet the stringent requirements for NGS procedure.

CeleMag™ Clean-up Beads utilize unique magnetic bead-based chemistry to enable a simple, flexible, and easily reproducible workflow for the purification and size selection of nucleic acids. It is synthesized to provide market leading purification and size selection efficiency. Not only it is highly optimized to be used with all Celemics' target enrichment kits, but CeleMag™ Clean-up Bead will also demonstrate strong compatibility with NGS kits from other providers due to Celemics' exclusive technology to stabilize the buffer and bead conditions. Our branded CeleMag™ Clean-up Bead will allow flexible size selection options with remarkable consistency, proven to be the most optimized bead for NGS.



Process for Clean-up

Magnetic Bead Purification

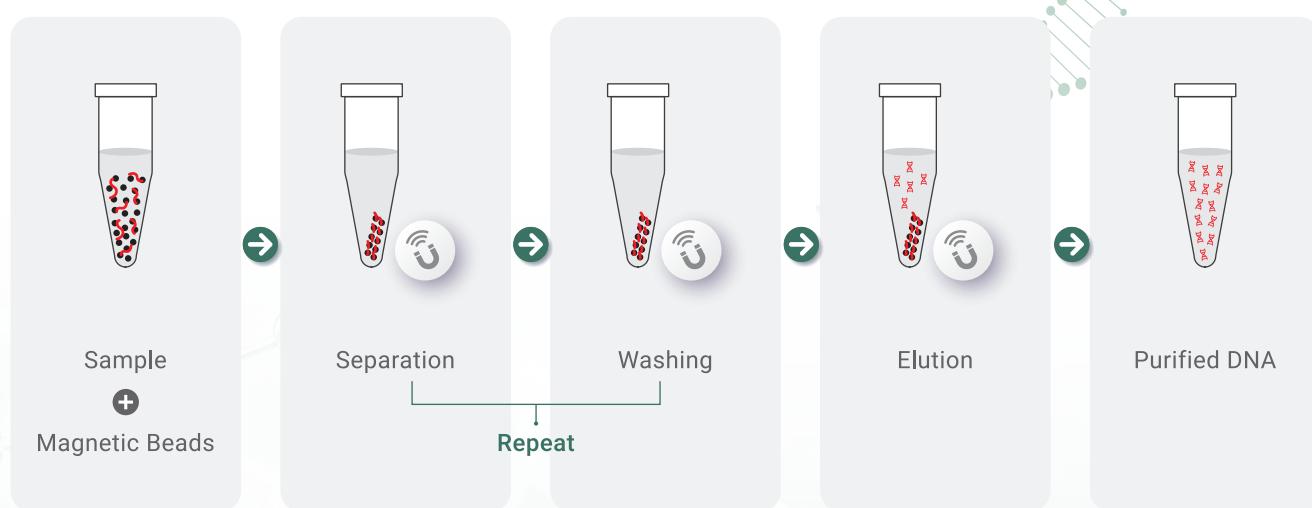


Figure 1. Process for purification using CeleMag™ Clean-up Bead. Sample (fragmented DNA) is mixed and bound to magnetic bead. Fragments bound to magnetic bead will then be washed for repeated times and the final product of selected size will be eluted for the next step.

Performance Data

Total DNA Recovery

Celemics' exclusive magnetic bead and buffer conditioning technologies ensure CeleMag™ Clean-up Bead to maximize the DNA recovery after purification with easy-to-follow protocols.

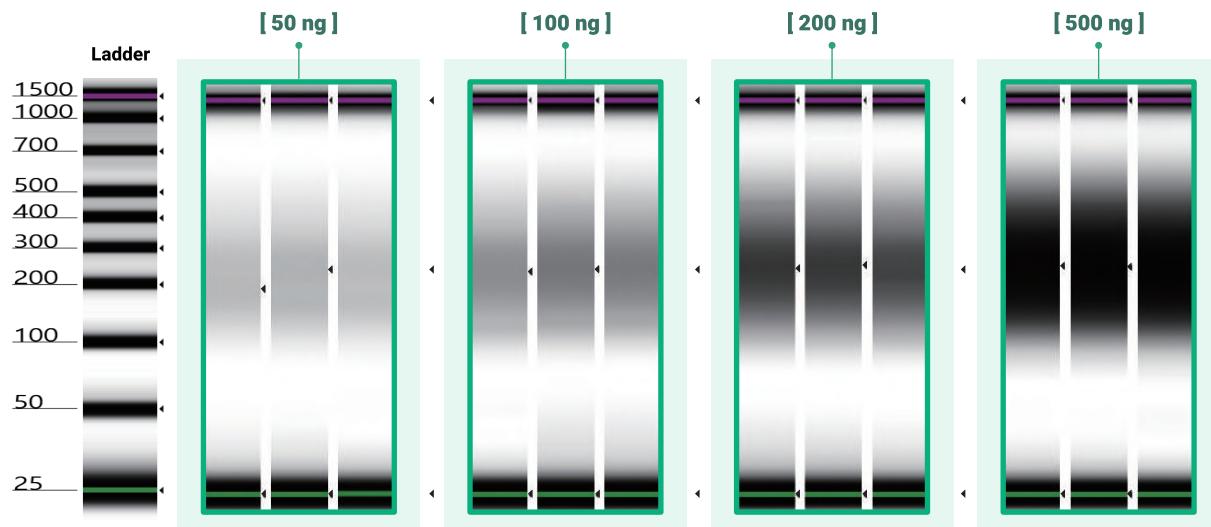


Figure 2: Purification and recovery rate with respect to changes in input DNA amount. The amount of DNA input for each group was loaded with sample amount of 50, 100, 200 and 500 ng, respectively. The sample to bead mixture ratio was set to 50 µL to 90 µL for all groups. For samples loaded with input amount of 100 ng and above, the recovery rates were higher than 99%, maximizing the DNA recovery.

Total DNA Recovery : Celemics vs. Bead AP

DNA recovery rate and reproducibility of CeleMag™ Clean-up Bead were compared with one of our competitors' product.

	Input 500 ng	Total (ng)	Yield(%)	Average Yield
 CELEMICS	Replicate 1	473.6	94.7%	86.5%
	Replicate 2	416.0	83.2%	
	Replicate 3	438.4	87.7%	
	Replicate 4	416.0	83.2%	
	Replicate 5	419.2	83.8%	
Bead AP	Replicate 1	387.2	77.4%	75.8%
	Replicate 2	368.0	73.6%	
	Replicate 3	364.8	73.0%	
	Replicate 4	377.6	75.5%	
	Replicate 5	396.8	79.4%	

Table 1: Comparison of total DNA recovery rate between Celemics' CeleMag™ Clean-up Bead and Competitor's Bead AP. 500 ng of DNA was purified using bead from both parties. Of the replicated 5 samples, the overall average of recovered rate of CeleMag™ Clean-up Bead was higher (average of 86.5%) than those purified with Bead AP (average 75.8%).

DNA Size Selection

CeleMag™ Clean-up Bead allows selective isolation of desired fragments depending on the sample-to-bead ratio. This effective and efficient selection and purification will ensure high recovery rate of both DNA and RNA for your NGS workflow.

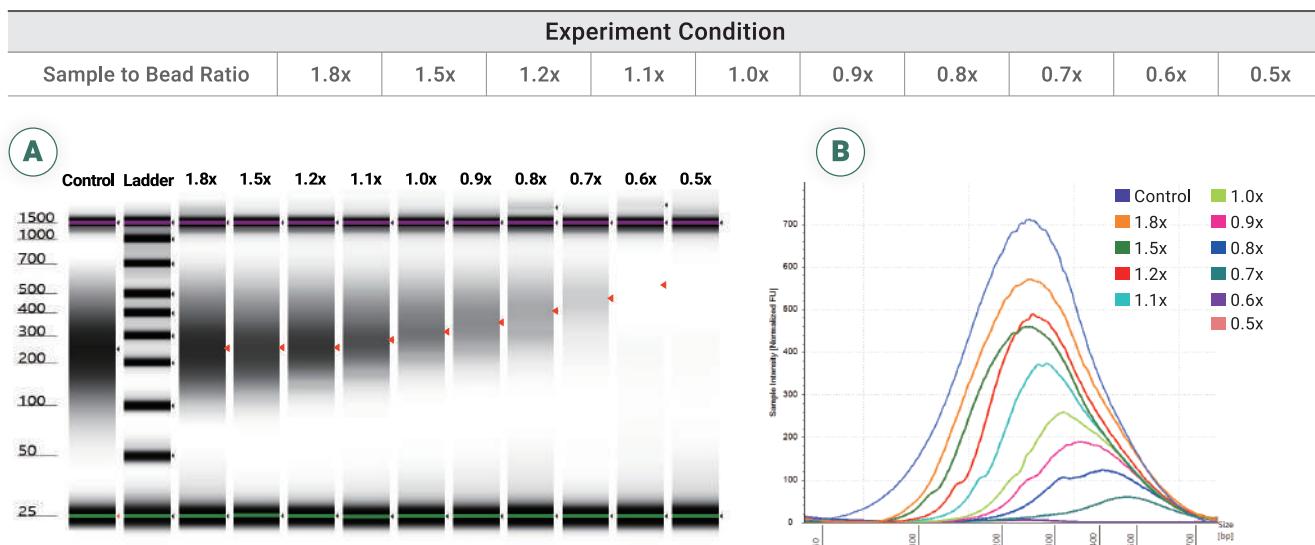


Figure 3. Fragmented DNA size selection with respect to changes in amount of bead. The amount of sample loaded was 50 μ L and was analyzed on Agilent's TapeStation® 4200. The result showed gradual increase in selected band (marked with orange arrow) as the sample to bead ratio decreased.

Size Selection Comparison: Celemics vs. Bead AP

CeleMag™ Clean-up Beads purification capacity was compared with one of our competitors' product by changing the sample to bead ratio.

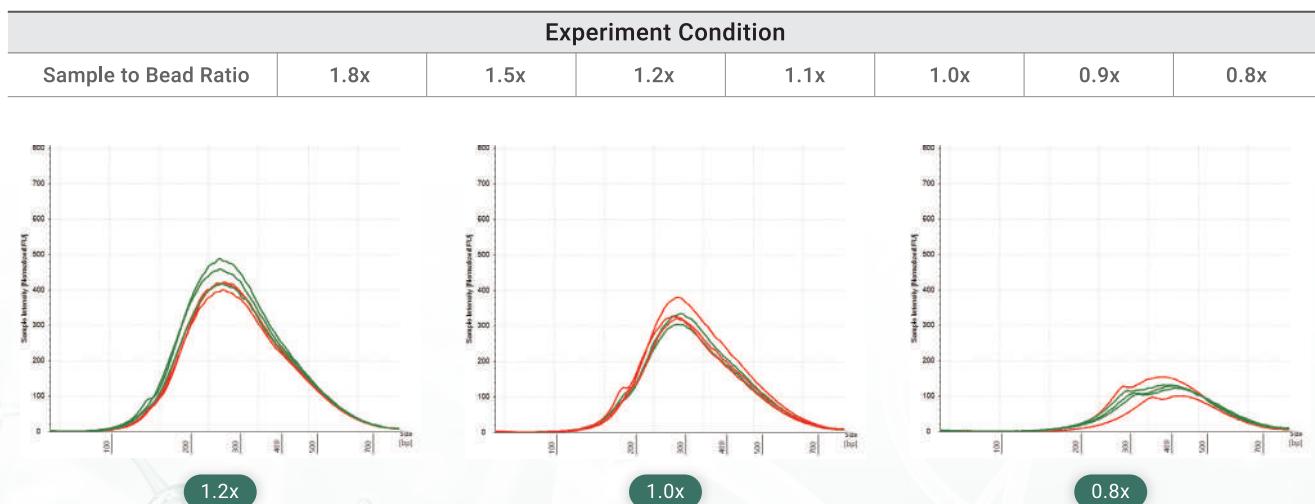


Figure 4: Examples of Size selection comparison between CeleMag™ Clean-up Bead and Bead AP. The size selection result was compared using Celemics' CeleMag™ Clean-up Bead (Green) and Bead AP (Red). The sample (loaded 50 μ L throughout) to bead ratios were altered for thorough comparison and were analyzed on TapeStation® 4200. The selected sizes with CeleMag™ Clean-up Bead were comparable, if not superior, to Bead AP.

DNA Double-sided Bead Clean-up

CeleMag™ Clean-up Bead can also be used for double-sided clean-up to remove both very small and very large fragments for your NGS libraries. The provided data demonstrates effective double-sided selection results using CeleMag™ Clean-up Bead, depending on the library to bead ratio. Celemics' clean-up bead can provide flexibility to choose the desired fragment sizes that you wish to isolate.

	Experiment Condition				
	Range 1	Range 2	Range 3	Range 4	Range 5
1st Selection Sample : Beads (μ L)	100 : 90	100 : 80	100 : 70	100 : 60	100 : 55
2nd Selection Sample : Beads (μ L)	190 : 20	180 : 20	170 : 20	160 : 20	155 : 15

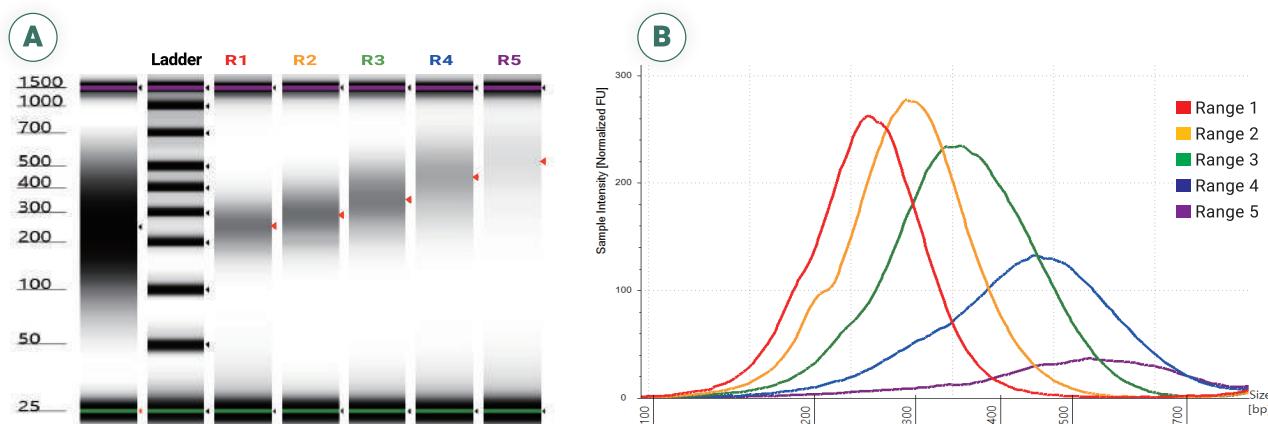


Figure 3: Double-sided bead clean-up using CeleMag™ Clean-up Bead. The double-sided clean-up using CeleMag™ Clean-up Bead by changing the sample to bead ratios for both first and second selection to illustrate robust clean-up and size selection capacity.

DNA Double-sided Clean-up Comparison: Celemics vs. Bead AP

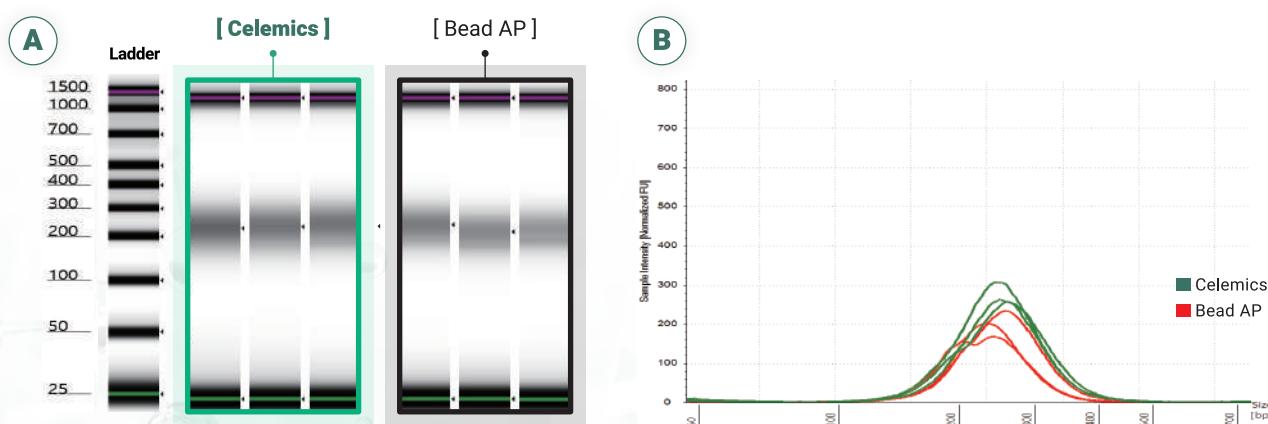


Figure 4: Comparison result of double-sided clean-up between CeleMag™ Clean-up Bead (Green) and Bead AP (Red). First clean-up ratio of sample to beads was 100 μ L : 90 μ L and second clean-up ratio of sample to beads were 190 μ L : 20 μ L for both products. The results were comparable to one another, demonstrating effective and easy purification of CeleMag™ Clean-up Bead for isolating desired fragments.

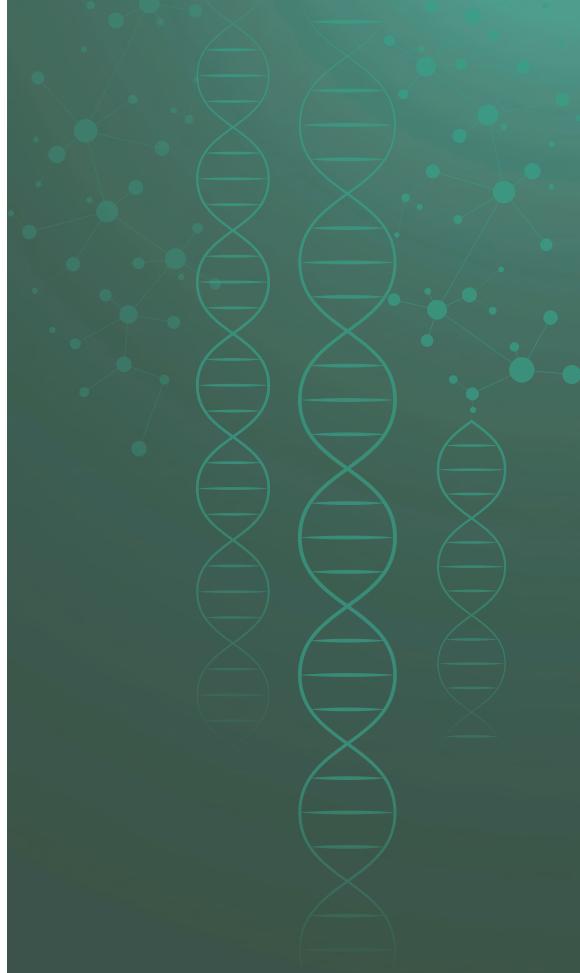


Celemics CeleNM™ Bead

Providing Efficient Method
for Normalizing your Library

Key Features

- Provides robust and reproducible high-quality data
- Time and cost-saving NGS protocol
- Automation friendly
- Ability to replace QC process



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CeleNM™ Bead

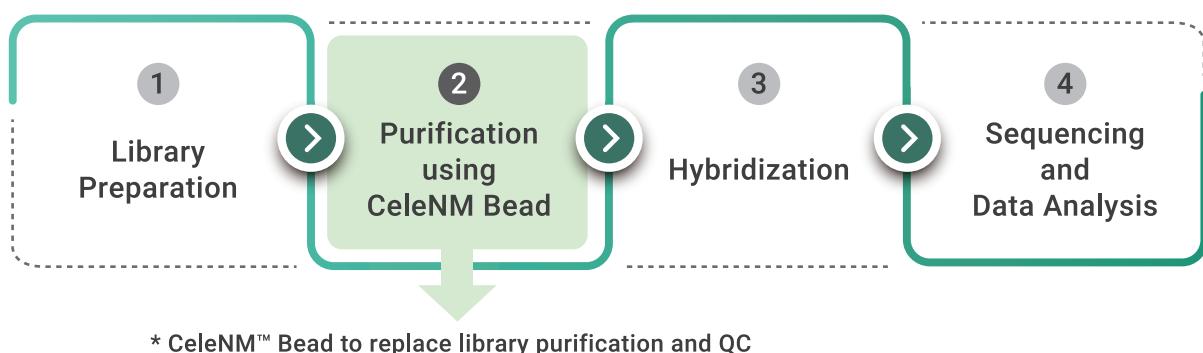
CeleNM™ Bead provides efficient method for normalization and assessment of the library. It can replace QC process after the library preparation, which will allow a time and cost-saving NGS procedure throughout. Also, CeleNM™ Bead can provide robust and reproducible experimental results for quantity assessment compared to fluorescent dyes and electric signals by eliminating errors for detecting the actual fragments of interest.



Process Workflow

Process for CeleNM™ Bead - workflow

Using CeleNM™ Bead can replace the hassle of amplified library purification as well as the quality and quantity assessment steps for your library preparation.



Process for purification using CeleNM™ Bead

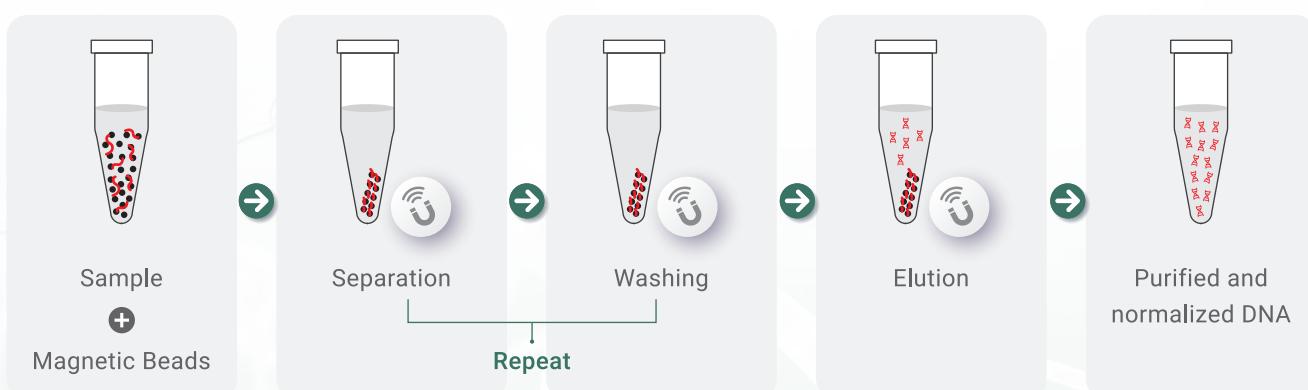


Figure 1. Process of NGS workflow and purification workflow using CeleNM™ Bead.

Performance Data

Uniform sequencing data distribution

CeleNM™ Bead replaces quantification and normalization process of prepared libraries in NGS procedure. In order to show the robustness and capability of normalization using CeleNM™ Bead, the sequencing data amounts were compared with the ones quantified and normalized using TapeStation and Qubit.

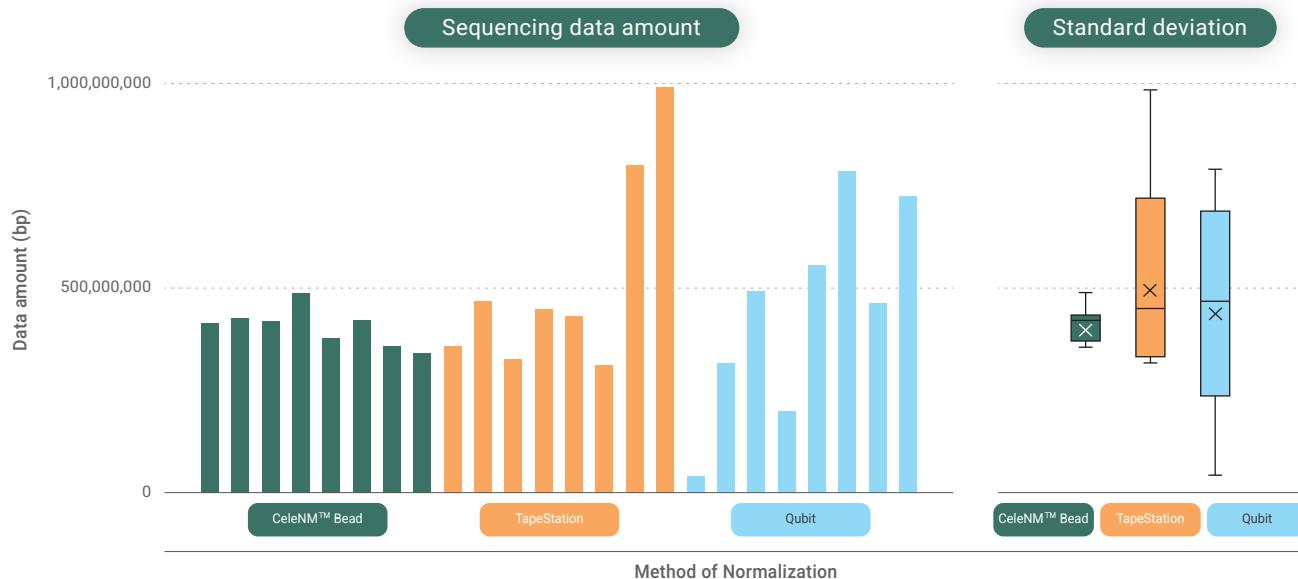


Figure 2. Distribution of sequenced raw base data for libraries quantified and normalized using Qubit, TapeStation and CeleNM™ Bead.

Performance metrics : on-target ratio and fold-80 base penalty

Both single and multiplexed (using CeleNM™ Bead) showed comparable on-target ratio as well as fold-80 base penalty.

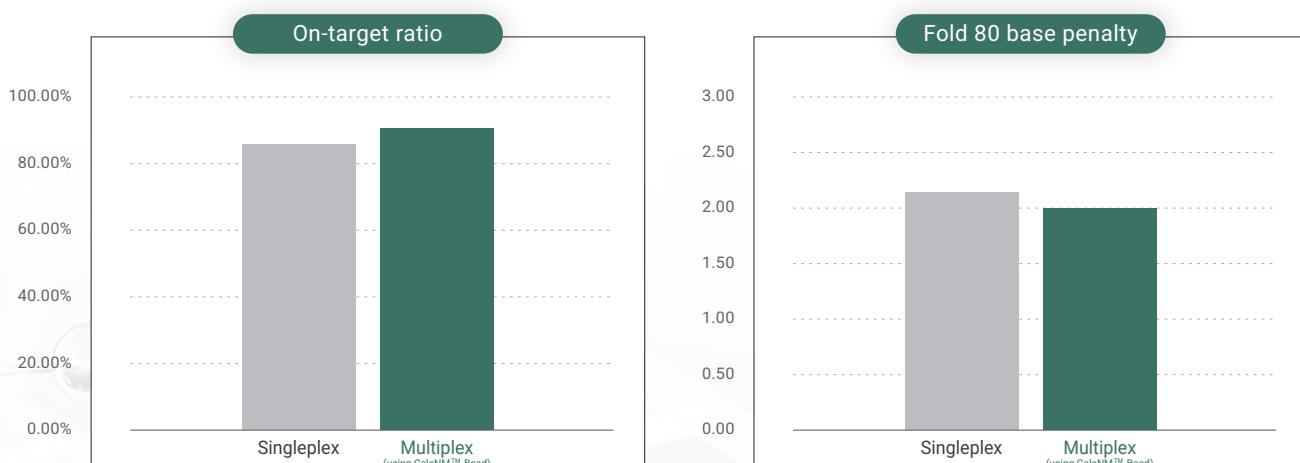


Figure 3. Comparison of on-target ratio and fold-80 base penalty of single reaction versus samples normalized using CeleNM™ Bead.





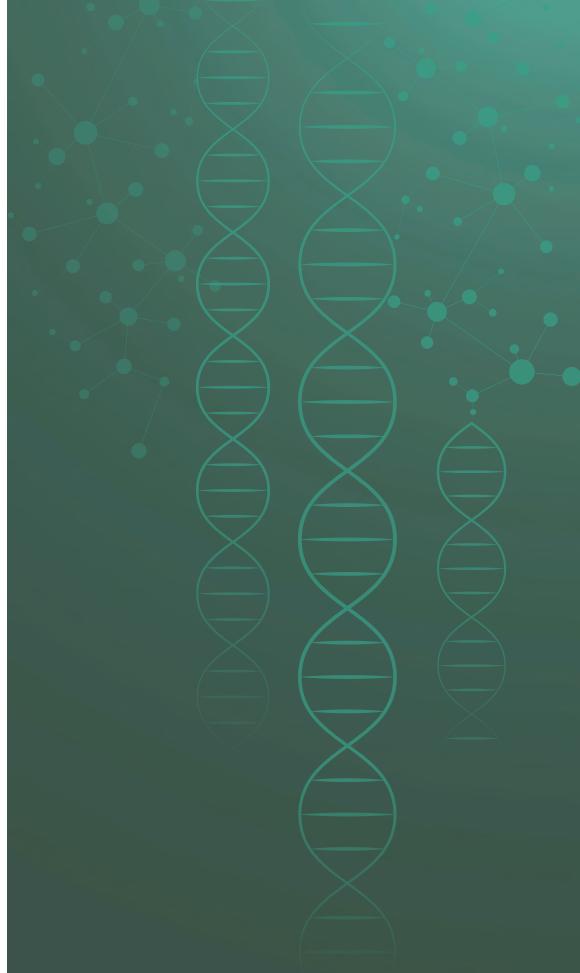
6. BTSeq™

Barcode Tagged Sequencing™ (BTSeq™)

Compact Scale NGS Service

Key Features

- Provides NGS analysis results in various NGS throughput
- Provides digitalized NGS results with a reasonable cost
- NGS data can be received quickly just by providing a sample without any additional experiment



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Not for use in diagnostic procedures

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BTSeq™ Services

BTSeq™ is a small-scale next-generation sequencing (NGS) service that offers various benefits for our customers. Primary goal of the BTSeq™ service is to provide an efficient solution for small-scale NGS projects and research needs. BTSeq™ handles small scale data volumes, making it suitable for projects or research with relatively small sample sizes. It is ideal when large datasets are not required. BTSeq™ specializes in processing small data volumes, minimizing processing time to obtain research results quickly. Fast result delivery allows rapid decision-making. Compared to high-throughput and large-data processing, BTSeq™ offers cost-effective solutions. It allows cost-efficient access to NGS data for small-scale projects or research, helping to save research budgets.

Service Features

BTSeq™ – Raw data service

Low-amount sequencing starting from 50,000 reads. This service dramatically reduces the cost of library preparation, providing NGS results at a reasonable price.

Digitalized NGS data allows analyzing of variations such as SNVs and Indels with low frequency. Customers can conveniently utilize BTSeq™ – Raw data service with just sample submission without the need for additional experiments.

Rapid turnaround time compared to typical NGS, making it beneficial for time-sensitive researchers.

BTSeq™ – Viral analysis service

1 Low sequencing capacity for individuals or projects to analysis virus genome. It offers a cost-effective solution for conducting multiple sequencing runs with accurate detection of low-frequency variations when addressing various mutations is necessary.

2 BTSeq™ – Viral analysis for SARS-CoV-2 provide high-quality results even with clinical samples. This service possesses the technology to selectively amplify SARS-CoV-2 viral RNA by specifically designed primer sets, ensuring high-quality results for viral genome analysis.

3 Digitalized NGS results allows precise analysis for all types of mutations. Accurate sequencing results of BTSeq™ ensures precise analysis of all variants from the Alpha variant to Omicron and the Epsilon variant.

4 BTSeq™ – Viral analysis for SARS-CoV-2 supports both whole genome analysis and individual gene of interest, such as S gene and N gene, analysis within the viral genome.

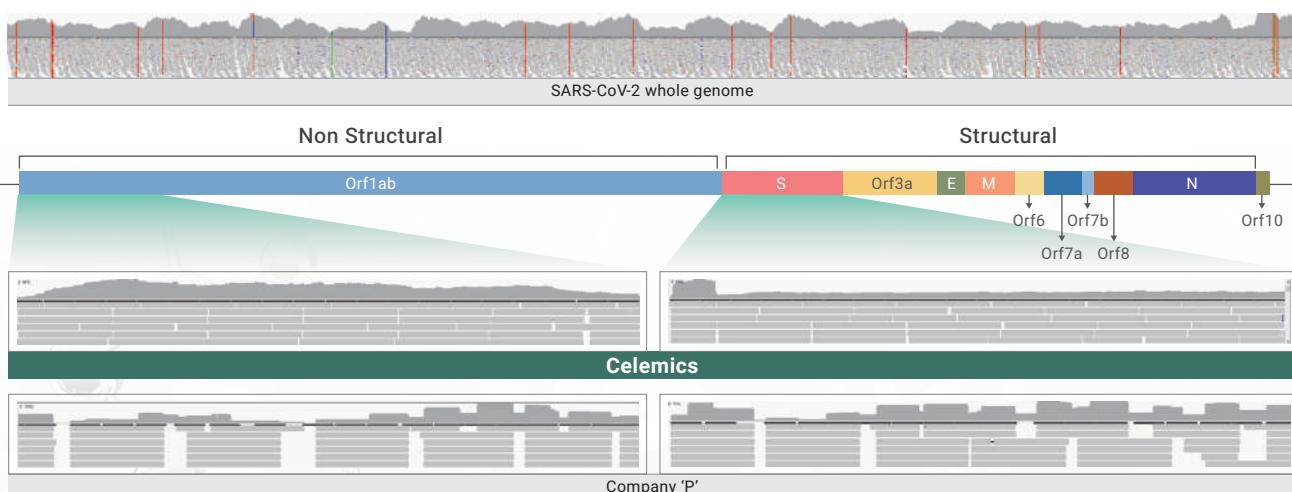


Figure 1. Example of SARS-CoV-2 Whole Genome Sequencing Results. The Celemics BTSeq™ service provides the complete genome information of SARS-CoV-2. Unlike the PCR method, there are no gaps in the genome, allowing for the acquisition of complete genetic information, enabling the analysis of all genetic variations that occur within the genome.

Results for BTSeq™ Service

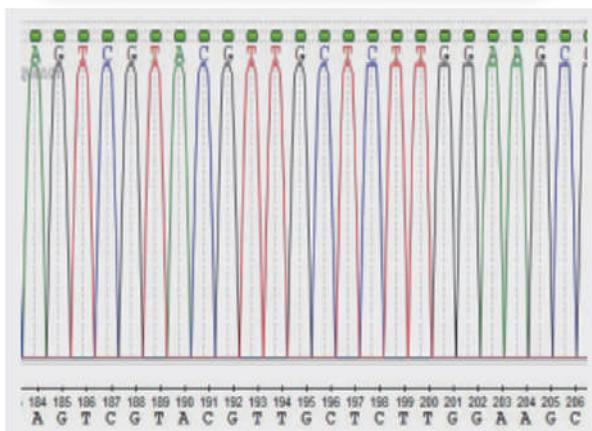
BTSeq™ – Customized service

BTSeq™ is a service that supports sequencing for purified samples such as PCR products and vectors. If the sample requirements are met, custom services can be tailored to the user's preferences in various aspects, including sequencing length, throughput, and result format. Please contact us if you require the desired service.

Digitalized Sequencing Results

BTSeq™ results generate various digital file formats. The type of results provided may vary depending on the customer's request, but three forms of results are generally offered. FASTA and AB1 formats are traditional result types also provided by Sanger Sequencing services, while the Base Frequency Table is a unique result enabled by BTSeq™ as it is an NGS-based service. These results quantitatively analyze information obtained from sequencing reads corresponding to sample base sequence positions, allowing for a detailed examination of base sequence variations. In this way, BTSeq™ can provide a variety of result formats, making it easy for first-time users of the service to obtain base sequence analysis results.

A. AB1



B. FASTA

> Sample_1

```
ACCCCTGAATTGACTCTCTTCCGGGCCTATCATGCCA
```

C. Base Frequency Table

Position	Gene	A	C	T	G
1	A	121	1	1	0
2	C	0	125	0	0
3	C	0	125	0	0
4	C	0	125	0	0
5	T	0	0	125	0
6	G	0	0	0	125
7	A	129	0	0	0
8	A	129	0	0	0
9	T	0	0	129	0
10	T	0	0	124	0
11	G	0	0	1	123
12	A	125	0	0	0
13	C	0	125	0	0
14	T	0	0	125	0
15	C	0	119	0	0
16	T	0	0	115	0
17	C	0	115	0	0

Figure 1. Example of BTSeq™ Results. A. Results in AB1 file format are generated based on base frequency. B. FASTA file is a consensus sequence composed of the most frequently occurring base at each position along the sequence. These results are provided when applying for the raw data service. C. Analyzed base sequences are presented in the form of a base frequency table.





7. Immune Repertoire Profiling

Celemics Immunoglobulin Heavy Chain Gene Assay

Accurate and Efficient
Analysis of IGH Population

Key Features

- Detect MRD as low as 10^{-6} with sufficient sample amount
- Up to 24 samples can be tested in single run
- Optimized primers minimize sequencing loss and PCR duplication, enabling accurate and efficient detection
- One-step reaction mix used per sample

For Research Use Only
Not for use in diagnostic procedures

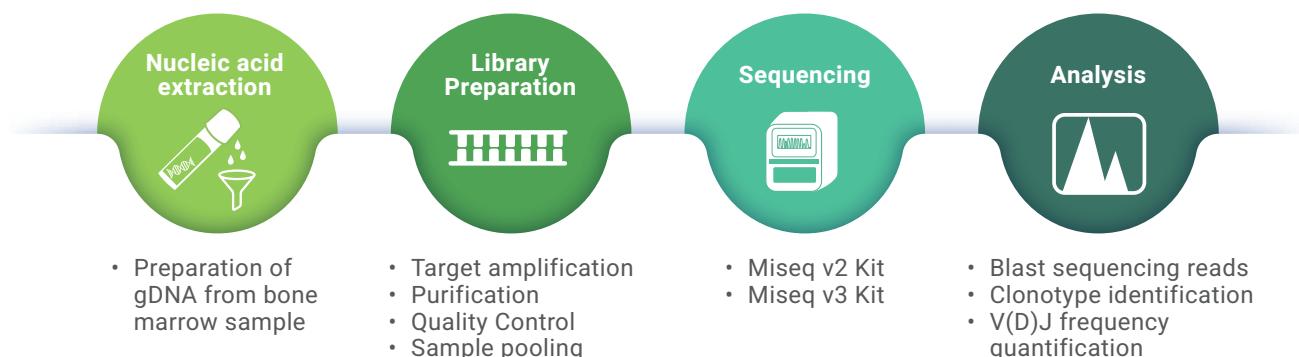
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Celemics Immunoglobulin Heavy Chain (IGH) Gene Assay Service

Antibodies are encoded by immunoglobulin heavy chain (IGH) and light chain (IG Kappa/Lambda) gene and shows dynamic recombination during B-Cell differentiations. Recombination creates unique clonotype in every B-Cell clones, and these B-cell population represents clinical status. Therefore, IGH gene is used as main biomarker for identifying clinical status such as disease onset or progression. Celemics IGH Assay Kit targets IGH gene with V segments domain to J segments domain and identify clonal V(D)J rearrangement combinations in samples. By supporting the analysis bioinformatic software along with the reagent kit, users can identify, track the status of B-cell associated IGH gene rearrangements. These IGH rearrangement tracking can be used to detect MRD (Minimal Residual Disease), enabling clinical follow-up for specific diseases. Celemics IGH Assay Kit provides the clonotype qualitative and quantitative information of IGH rearrangements from DNA samples.



Workflow of Celemics IGH Assay Kit



Specification

Sample type	Genomic DNA (From bone marrow, B-Cell)
Sample amount	> 50 ng
Target gene	IGH gene
Multiplexing	Up to 24
Platform	Illumina MiSeq 500 Cycle V2 reagent Illumina MiSeq 600 Cycle V3 reagent
Bioinformatics pipeline	Linux based sequence blast to IGH region (in-house program)
Analytical method	Quantitative and qualitative analysis of V (Variable), D (Diversity), and J (Joining),

Performance Data

Precision of MRD Detection

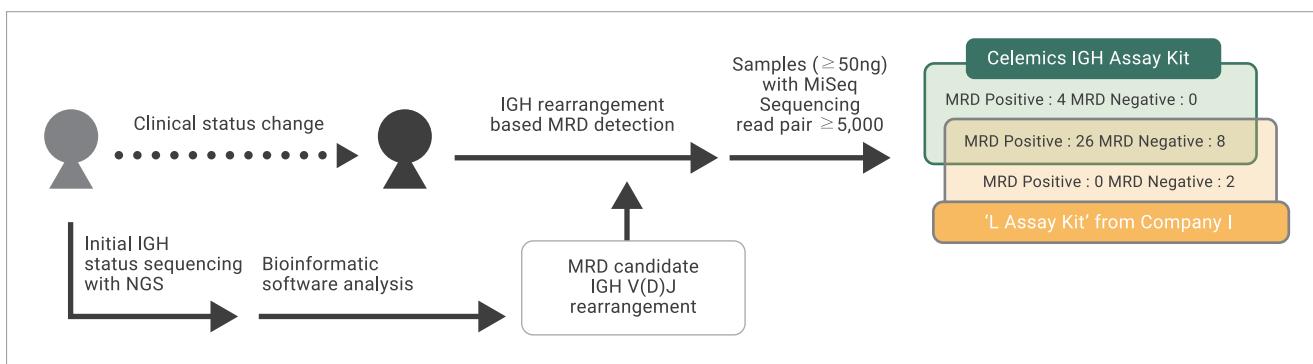


Figure 2. Schematic diagram of MRD analysis. The IGH assay kit shows excellent performance comparing with other commercially available NGS-based IGH gene screening test kits for similar purposes. And by optimizing oligo set, it was possible to increase sensitivity by increasing PCR amplification selectivity for sequences that were poorly amplified in the other commercial kit.

Comparison between Celemics IGH Assay and Other Methods

Assay	MRD Positive (in common)	MRD Negative (in common)	MRD Positive (in partial)	MRD Negative (in partial)
Celemics IGH assay kit			4	0
'L Assay Kit' from Company I	26	8	0	2
Flow cytometry			0	3

Samples ($\geq 50\text{ng}$) with sequencing reads $\geq 5,000$

Table 1. Comparison of IGH assay results among three different methods. Clinical samples were used for a comparison test. Among all the tested samples, 26 were determined as MRD-positive, and 8 were determined as MRD-negative samples in all assays, respectively. Four samples showed positive results only in the Celemics IGH assay kit, and 2 and 3 samples showed MRD-negative results in the 'L Assay Kit' from Company I and flow cytometry, respectively.

Quantification of IGH Rearrangement Population

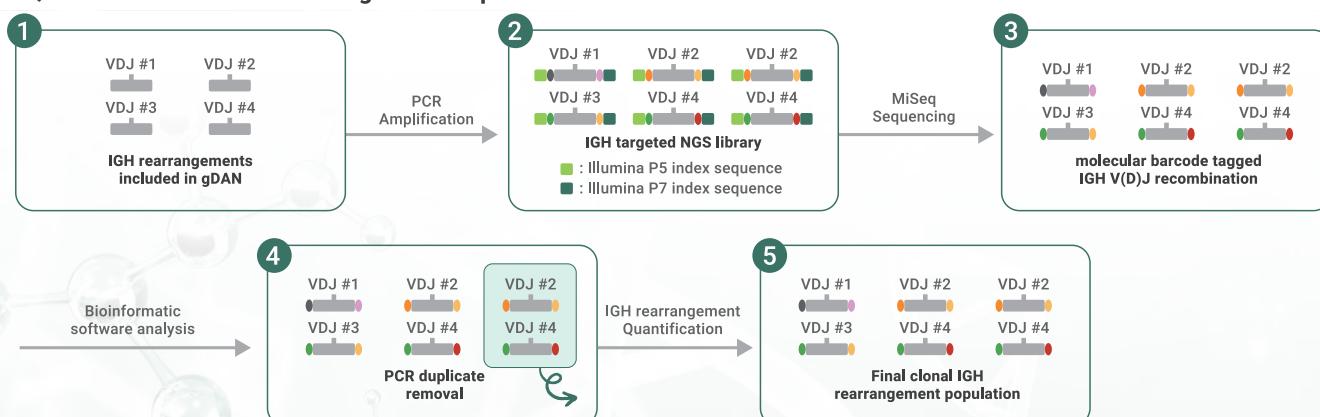


Figure 1. Analysis schematic diagram of IGH rearrangement population. Celemics IGH kit is optimized in removing false-clonal IGH rearrangement due to PCR duplication. Using molecular barcode sequence and bioinformatic pipeline enables quantification of IGH rearrangement population from true B-Cell clones.

Performance Data

Clonotype Analysis Result of IGH Gene Assay

Raw consensus reads	IGH-aligned sequence ratio	IGH-matched consensus reads	V(D)J Clonotype	Clonotype reads	Clonotype population
204,694	98.90%	202,443	IGHV6-1&D3-16&J4	194,214	95.90%
			IGHV3-48D5-18&J5	2,452	1.20%
			IGHV6-1&D1-26&J4	1,194	0.60%
			IGHV6-1&D1-14&J4	608	0.30%

Table 2. Result example for Celemics IGH Assay Kit generated from clinical sample. Celemics IGH Assay Kit is compatible with the Illumina MiSeq Sequencing platform and developed for Research Use Only (RUO) purposes. It includes PCR mix reagents with primer sets incorporating platform specific adapters, and molecular tracking barcode sequences for single step workflow. With this state-of-the-art assay, the IGH gene rearrangement status of each of the several million clones can be identified and characterized.

Clinical Status Identification

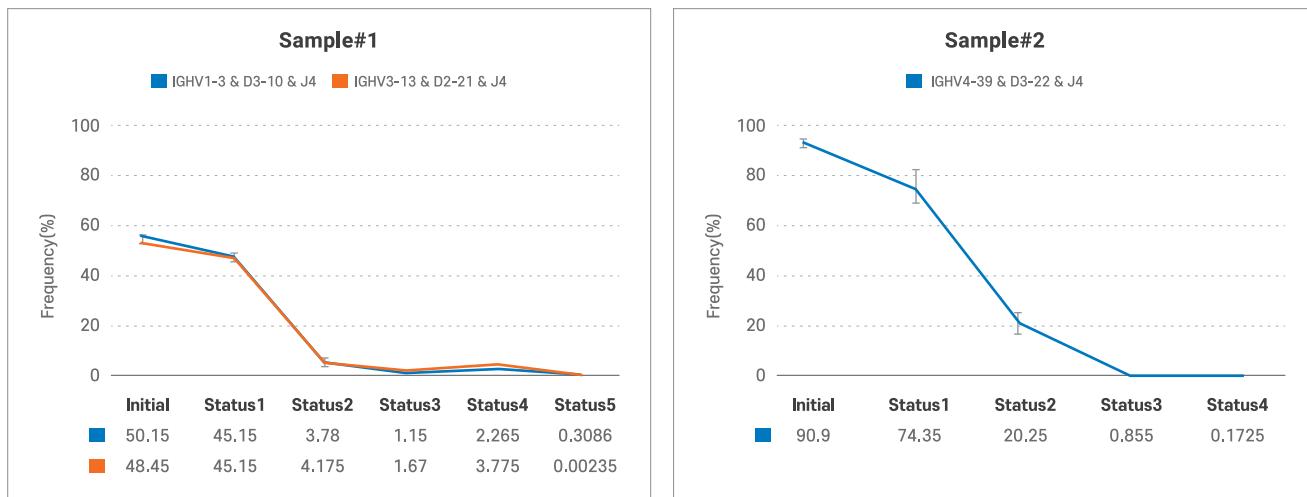


Figure 2. IGH assay results to confirm the MRD status with two samples. IGH assay could achieve clonal IGH rearrangement population result associated with MRD (Minimal Residual Disease) status at sampling point of each sample. The IGH assay kit can be used not only to simply confirm specific clonal expansion of B-Cell, but also to confirm whether MRD remains and whether MRD reoccurs.

Analytical Sensitivity

Sample amount (ng)	50	100	200	500	1,000	2,000	5,000	20,000
Approximate number of clones	7,500	15,000	30,000	75,000	150,000	300,000	750,000	3,000,000
Limit of detection (%)	≥ 0.1	≥ 0.02	≥ 0.01	≥ 0.005	≥ 0.002	≥ 0.001	≥ 0.0005	≥ 0.00001

Table 3. Analytical sensitivity of Celemics IGH Assay Kit. Limit of detection (LOD) is determined by the amount of input genomic DNA. To obtain the IGH rearrangement sequences of numerous B-cell clones, an appropriate amount of DNA is essential along with the number of MiSeq sequencing reads of sample.

Performance Data

Example Analysis Results

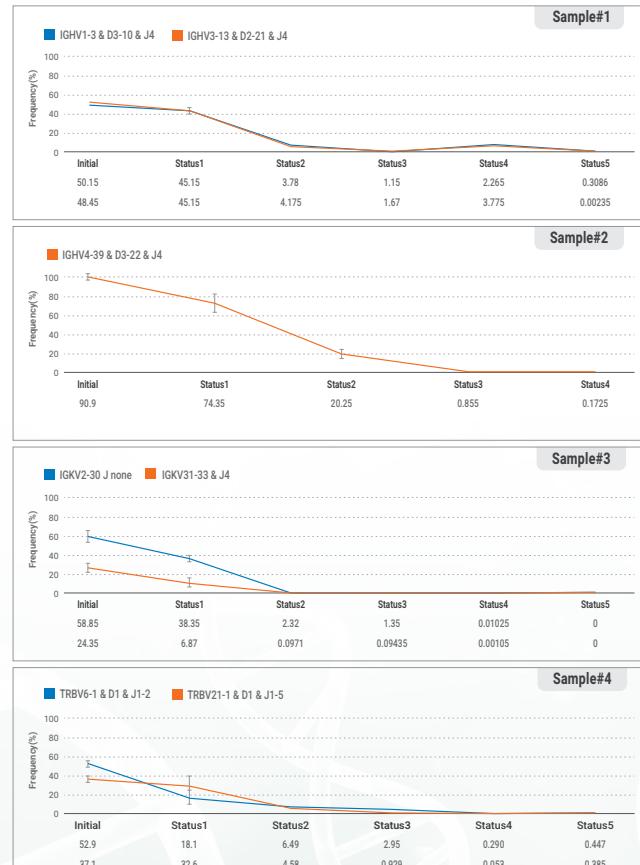
Clonotype Table

junction_aa	v_call	j_call	Epitope	Score	Reference TCRs	Antigen	Species
CAWVGGBTQYF	TRBV30*01	TRBJ2-3*01	PKYVKQNTLKLAT	0.355817	GGGDTQYF*, 10.1038/nature2	Hemagglutinin (HA)	Influenza A virus
CAWVGGBTQYF	TRBV30*01	TRBJ2-3*01	PKYVKQNTLKLAT	0.355817	GGGDTQYF*, 10.1038/nature2	Hemagglutinin (HA)	Influenza A virus
CAWSVLAEEAFF	TRBV30*01	TRBJ1-1*01	GILGFVFTL	0.355817	VSVLPEAFF*, 10.1038/nature22	Matrix protein 1 (M)	Influenza A virus
CAWVGGBTQYF	TRBV30*01	TRBJ2-3*01	PKYVKQNTLKLAT	0.355817	GGGDTQYF*, 10.1038/nature2	Hemagglutinin (HA)	Influenza A virus
CAWVGGBTQYF	TRBV30*01	TRBJ2-3*01	PKYVKQNTLKLAT	0.355817	GGGDTQYF*, 10.1038/nature2	Hemagglutinin (HA)	Influenza A virus
CAWVGGBTQYF	TRBV30*01	TRBJ2-3*01	PKYVKQNTLKLAT	0.355817	GGGDTQYF*, 10.1038/nature2	Hemagglutinin (HA)	Influenza A virus
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CAWVGGBTQYF	TRBV30*01	TRBJ2-3*01	PKYVKQNTLKLAT	0.355817	GGGDTQYF*, 10.1038/nature2	Hemagglutinin (HA)	Influenza A virus
CAWVGGBTQYF	TRBV30*01	TRBJ2-3*01	PKYVKQNTLKLAT	0.355817	GGGDTQYF*, 10.1038/nature2	Hemagglutinin (HA)	Influenza A virus
CAWVGGBTQYF	TRBV30*01	TRBJ2-3*01	PKYVKQNTLKLAT	0.355817	GGGDTQYF*, 10.1038/nature2	Hemagglutinin (HA)	Influenza A virus
CASSLGTGGTEAFF	TRBV11-2*03	TRBJ1-1*01	LLYDANYFL	0.28683	-022-04250-7, (CASSLGS GG	ORF3, ORF3a	SARS-CoV-2
CASSLGTGGTEAFF	TRBV11-2*03	TRBJ1-1*01	LLYDANYFL	0.28683	-022-04250-7, (CASSLGS GG	ORF3, ORF3a	SARS-CoV-2
CASSLGTGGTEAFF	TRBV11-2*03	TRBJ1-1*01	LLYDANYFL	0.28683	-022-04250-7, (CASSLGS GG	ORF3, ORF3a	SARS-CoV-2
CASSLGTGGTEAFF	TRBV11-2*03	TRBJ1-1*01	LLYDANYFL	0.28683	-022-04250-7, (CASSLGS GG	ORF3, ORF3a	SARS-CoV-2

V(D)J Ranking

Group#2	IGH-Sample3	IGH-Sample4	IGH-Sample5	IGH-Sample6	IGH-Sample7	IGH-Sample8
IGHV3-23&D3-10&J4	25.0655	0.3629	0	0.0079	0.4293	0.1057
IGHV3-7&D3-3&J4	9.729	0.151	0	0	0.1237	0
IGHV3-33&D3-3&J5	7.3608	0	0	0	0.0011	0
IGHV2-5&D2-3-3&J4	6.8655	0	1.5414	2.9112	0.0302	9.2446
IGHV2-5&D2-13&J4	2.9716	0.0258	0.0383	0.752	0.2005	0.5283
IGHV6-18&D3-16&J4	2.4707	0.0649	21.7809	1.056	0.4763	2.747
IGHV2-5&D2-21&J4	1.964	0.0641	1.7904	1.5486	0.0295	4.1204
IGHV2-5&D2-2&J4	1.8843	0	17.9986	1.5172	0	2.3948
IGHV2-5&D2-18&J4	1.6168	0.6116	0.0949	0.1467	0.06	0.1057
IGHV2-5&D2-15&J4	1.3663	0.0172	0.4624	2.6701	0.0779	0.3346
IGHV3-23&D5-24&J4	1.1955	0.0798	0	0	0.1052	0
IGHV2-5&D1-26&J4	1.1613	0.0063	0.6758	0.5136	0.08	1.62
IGHV2-5&D2-8&J4	1.0646	0	1.494	0.1651	0.0164	3.9267
IGHV5-51&D4-23&J none	0.9393	0.0336	0	0.7835	0.0182	0.0528
IGHV1-2&D3-10&J6	0.8539	0.0321	0	0	0.1848	0
IGHV1-2&D4-23&J4	0.7685	0.0164	0	0	0.0015	0.1585
IGHV3-13&D none&J6	0.7685	0	0	0	0.0022	0
IGHV2-5&D6-19&J4	0.7458	0.104	0.0593	0.1048	0.0462	0
IGHV2-5&D2-11&J4	0.7116	0	0.1304	0	0.0444	0.1585
IGHV3-9&D2-2&J6	0.6376	0.0673	0	0	0.068	0
IGHV3-11&D5-18&J4	0.5522	0.1517	0	0	0.0651	0
IGHV2-5&D2-2&J none	0.5522	0	0.6403	0.1703	0	1.0037
IGHV4-31&D2-21&J4	0.5237	0.0282	0	0	0	0
IGHV2-5&D4/4R15-4&J4	0.4042	0	0	0	0	0
IGHV2-5&D2-21&J none	0.3814	0	2.9168	0.2044	0	1.1798
IGHV3-69-1&D2-28&J4	0.3643	0.0579	0.1304	0.2751	0	0.3346
IGHV2-5&D2/21-2&J11	0.3643	0	0	0	0	0
IGHV2-5&D3/21-2&J4	0.3188	0	0.3438	0.021	0.0087	0.2289
IGHV4-59&D2-15&J4	0.3017	0.0039	0.1423	0.2961	0.0699	0.3874
IGHV3-69-1&D2-21&J4	0.3017	0	0.2964	0.3118	0.0036	0.405
IGHV6-18&D5-19&J4	0.3017	0	0.0356	0.1415	0.0149	0
IGHV3-64&D5-24&J4	0.2846	0	0	0.0288	0	0
IGHV6-18&D4/4R15-4&J4	0.2846	0	0	0.0262	0	0.0528
IGHV3-7&D2-1-26&J4	0.2846	0	0	0	0	0
IGHV4-59&D6-19&J4	0.2733	0.0289	0.0593	0.1336	0.111	0
IGHV3-69-1&D2-26&J4	0.2676	0	0	0.1887	0.0011	0.2113
IGHV2-5&D4-23&J4	0.2619	0	0	0	0	0
IGHV4-59&D3-10&J4	0.2562	0.1189	0	0.055	0.131	0.2113

Clonotype Tracking



8. Bioinformatics

Celemics Analysis Service (CAS)

Trust CAS with your
Bioinformatics Analysis

Key Features

- Fast, Accurate and Sophisticated Customizing
- Interoperability with Celemics TE Panels
- Cost-Effective and Easy-to-Use
- High Compatibility with other BI Platforms

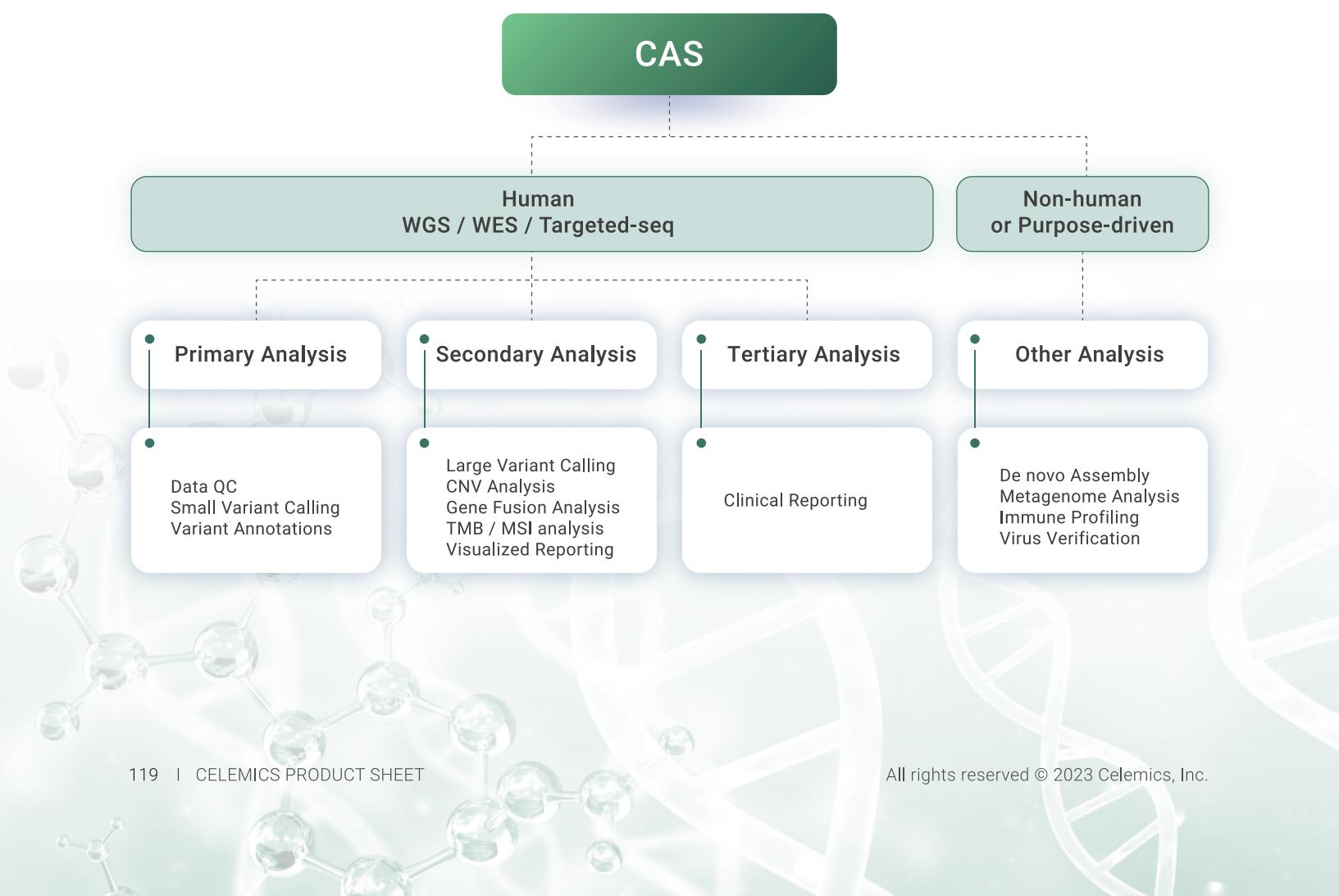
About Celemics Analysis Service (CAS)

Although NGS-based molecular diagnosis technologies have advanced rapidly, existing bioinformatics (BI) analysis platforms have not matched the speed of development. Even as the discovery of various new biomarkers and their applications are becoming more prevalent by the day, there are very few solutions in the market that are able to readily react to client needs. As such, Celemics has developed the Celemics Analysis Service (CAS), a revolutionary BI solution aiming to provide client-specific service for the current convoluted and restrictive market using real-time client interaction, need-based customized analysis, and the expertise of our BI analysts.

Advantages of CAS

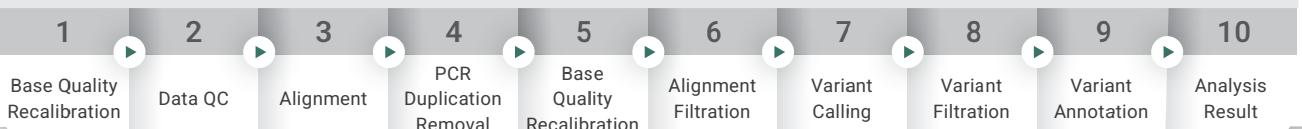
- Fast and Accurate
- Sophisticated Customizing
- Interoperability with Celemics TE Panels
- Cost-Effective
- Easy-to-Use
- High Compatibility with Other BI Platforms

Service Category and Key Outcomes of CAS



CAS - Primary Analysis Service

Workflow of Primary Analysis

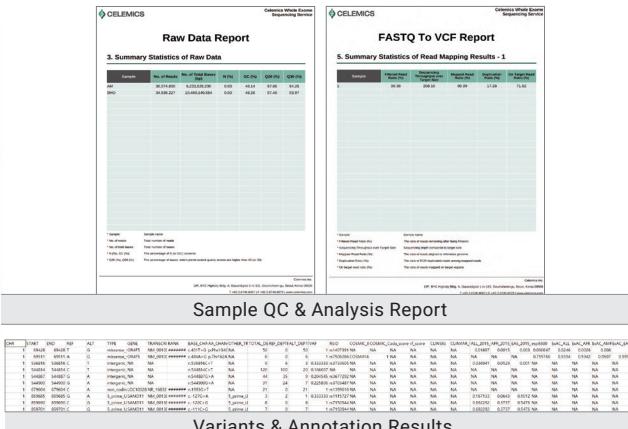


CAS – Primary Analysis Service performs raw data QC, read mapping and SNV/Indel calling.

Celemics also provides the annotations of called variants (SNVs and Indels) using various public database, such as ClinVar, COSMIC, dbSNP, etc.

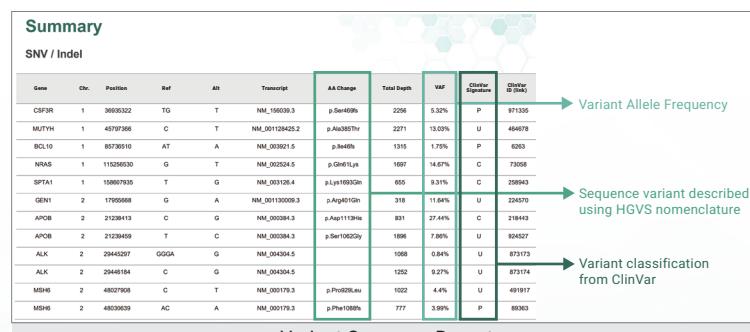
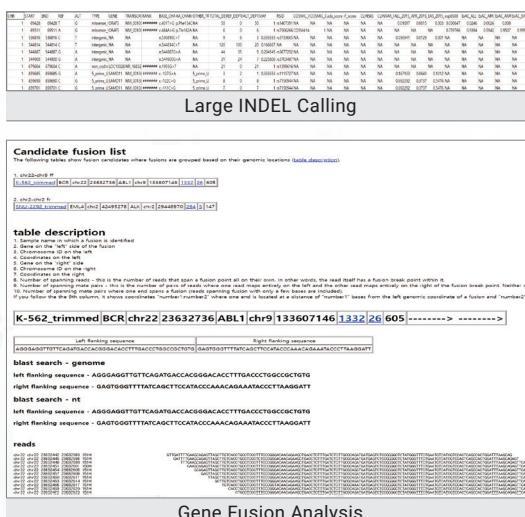
Final Outcomes for Clients

- Summary Report (PDF)
- Read alignment (BAM & BAI)
- Target Regions (BED)
- Summary of Statistics (XLSX)
- All Variants & Annotations (TSV)



CAS - Secondary Analysis

- **CAS - Secondary Analysis Service** provides large indel calling, copy number variation analysis, gene fusion analysis and MSI/TMB analysis.
- Moreover, each analysis can be chosen and applied selectively based on the specific analysis objectives, panel types, and more.

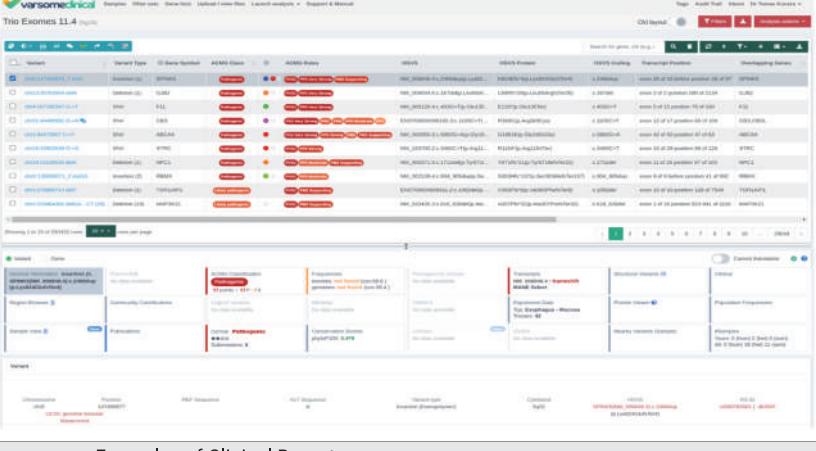


CAS - Tertiary Analysis

CAS - Tertiary Analysis offers clinical reports through our affiliated partners.



This screenshot shows a clinical report from Strand Whole Exome Test. It includes sections for Patient Information, Test Details, Indications for Test, Results (noting a heterozygous variant in exon 12 of the ACVR2A gene), and Key Findings. A detailed table of variants is provided, along with a summary of findings and interpretation.

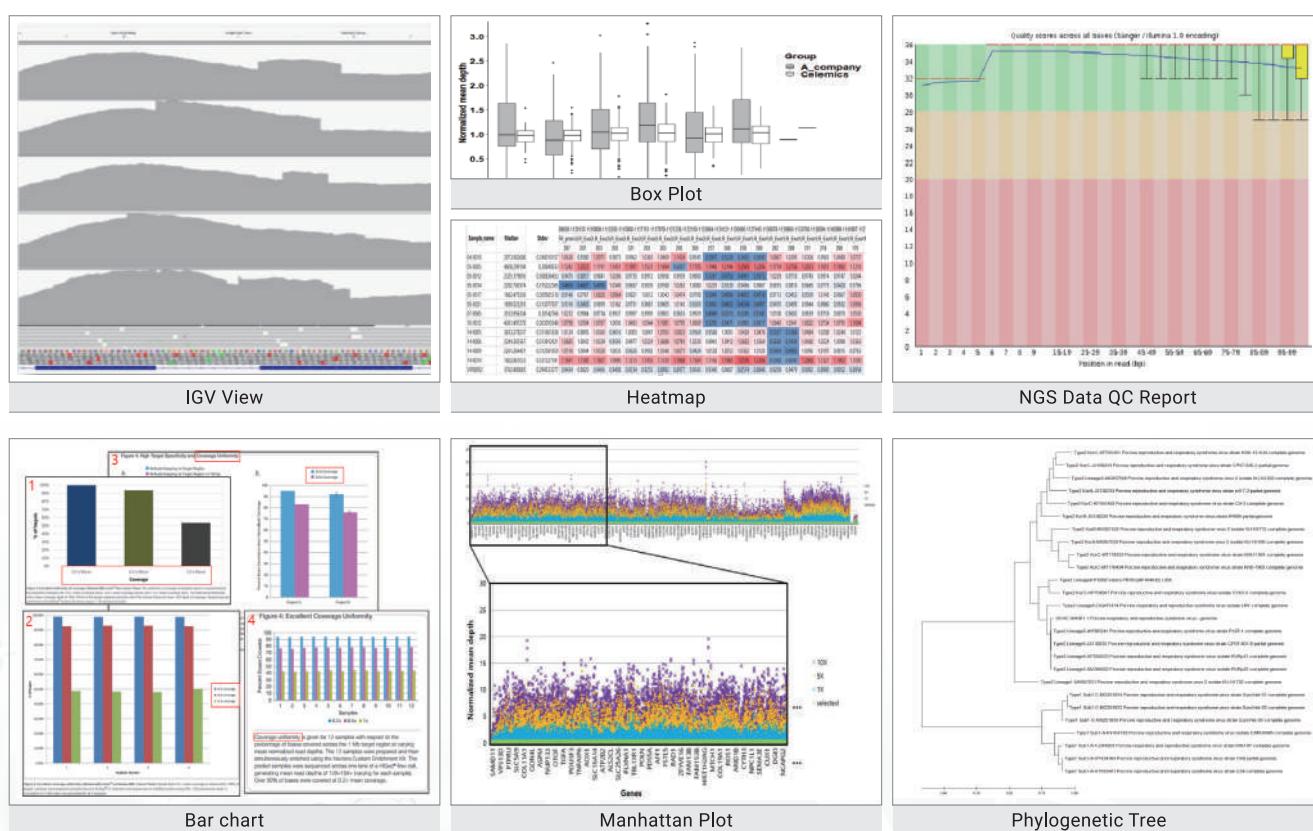


This screenshot shows a clinical report from Varseomedical. It features a main dashboard with various tabs like Variant, Allele, and Genotype. A large central area displays a grid of variants with columns for ID, Gene, Position, Effect, and other annotations. Below the grid, there are sections for Summary, Disease Associations, and Clinical Interpretation.

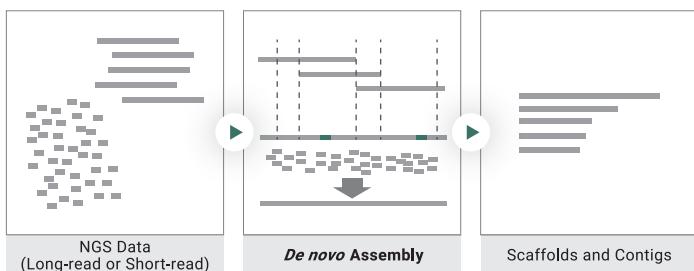
Examples of Clinical Reports

CAS - Customized Analysis

CAS - Customized Analysis can provide a variety of analytical results to meet customer requirements.



CAS - Other analysis



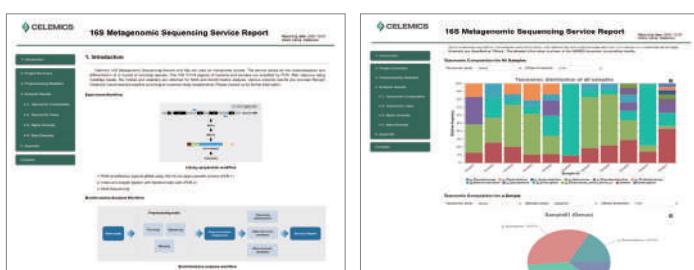
CAS - *de novo* Assembly Service

Scaffolds or contigs built by optimized *de novo* assembly pipelines for the input long-read or short-read NGS data. Furthermore, there are evaluations and annotations available.

[De novo assembly](#)

[WGS](#)

[BTSeq](#)



CAS - 16S Metagenome Analysis Service

Provides taxonomic classification, taxonomic abundance estimation, alpha diversity and beta diversity.

All results are presented in the form of interactive HTML reports.

[Metagenomics](#)

[Microbiome](#)

[16S rRNA](#)



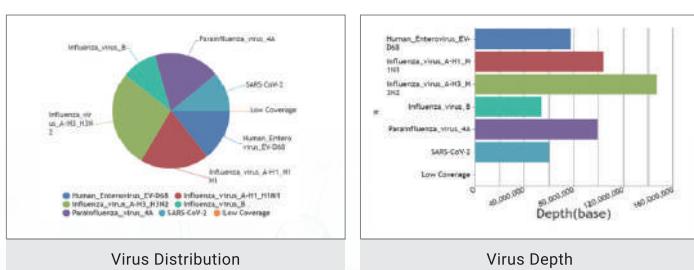
CAS - Immune Profiling Analysis Service

Provides amino acid sequences for annotated immune genes from the input DNA sequence.

Additionally, it offers post-translational modification estimation results in a visually enhanced format with color highlights.

[Immune Profiling](#)

[PTM](#)



CAS - Virus Verification

Provides virus verification information for Celemics' virus panels, such as CRVP.

All results are presented in the form of interactive HTML reports.

[CRV Panel](#)

[Virus Verification](#)





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