Summary of Celemics Target Enrichment Product & Service

CELEMICS

Category	Products	Gene/Virus Information	Covered Region	Target Size	Mutation Type	Sample Type (amount)	Platform	Bioinformatics Pipeline
ONCOLOGY	BRCA 1/2 Panel	BRCA 1, BRCA 2	Whole CDS (+/- 40 bp), UTR, Promoter	23 kb	SNV, Indel, CNV	FFPE, Blood (> 50 ng of fragmented DNA)	All sequencers from Illumina, Thermo Fisher, MGI, PacBio, and Oxford Nanopore	Primary, Secondary, and Tertiary analysis result (FASTQ to VCF, VCF to Clinical report)
	OncoRisk Panel	31 genes	Whole CDS	96 kb	SNV, Indel, CNV, Rearrangement	FFPE, Blood (> 50 ng of fragmented DNA)		Primary, Secondary, and Tertiary analysis result (FASTQ to VCF, VCF to Clinical report)
	Cancer Screen Panel Core	13 genes	Whole CDS, Rearrangement	61 kb	SNV, Indel, CNV, Rearrangement	FFPE, frozen tissue, cfDNA, RNA		Primary, Secondary, and Tertiary analysis result (FASTQ to VCF, VCF to Clinical report)
	Cancer Screen Panel 50	54 genes	Whole CDS, Rearrangement	197 kb	SNV, Indel, CNV, Rearrangement	FFPE, frozen tissue, cfDNA, RNA		Primary, Secondary, and Tertiary analysis result (FASTQ to VCF, VCF to Clinical report)
	Cancer Screen Panel 100	99 genes	CDS	299 kb	SNV, Indel, CNV, Rearrangement	FFPE, frozen tissue, cfDNA, RNA		Primary, Secondary, and Tertiary analysis result (FASTQ to VCF, VCF to Clinical report)
	Cancer Screen Panel 400	407 genes	CDS	1,123 kb	SNV, Indel, CNV, Rearrangement	FFPE, frozen tissue, cfDNA, RNA		Primary, Secondary, and Tertiary analysis result (FASTQ to VCF, VCF to Clinical report)
	Cancer Master Panel	524 genes	Whole CDS, Custom regions of oncogenes, Immune response genes, and EBV & HPV viruses	2.5 Mb	SNV, Indel, CNV, Rearrangement, TMB, MSI, EBV, HPV	FFPE, frozen tissue (> 50 ng of fragmented DNA)		Primary, Secondary, and Tertiary analysis result (FASTQ to VCF, VCF to Clinical report)
INHERITED DISEASE	G-Mendeliome Clinical Exome Sequencing (CES) Panel Standard	5,508 genes	CDS, Hotspots, Mitochondrial genome	13.8 Mb	SNV, Indel, CNV	Blood (> 50 ng of fragmented DNA)		Primary, Secondary, and Tertiary analysis result (FASTQ to VCF, VCF to Clinical report)
	G-Mendeliome Clinical Exome Sequencing (CES) Panel Expanded	7,515 genes	CDS, Hotspots, Mitochondrial genome	19.7 Mb	SNV, Indel, CNV	Blood (> 50 ng of fragmented DNA)		Primary, Secondary, and Tertiary analysis result (FASTQ to VCF, VCF to Clinical report)
	G-Mendeliome Disease Specific Panel (18 Disease Specific Panels)	25-177 genes	Whole CDS, Hotspots	80-616 kb	SNV, Indel, CNV	Differs by somatic and germline panel		Primary, Secondary, and Tertiary analysis result (FASTQ to VCF, VCF to Clinical report)
PHARMACO-GENOMICS	Pharmaco Screen Panel Standard	122 genes	Whole CDS, UTR (-50 bp, + 10 bp)	534 kb	SNV, Indel, CNV	Blood (> 50 ng of fragmented DNA)		Primary and Secondary results (FASTQ to annotated VCF)
	Pharmaco Screen Panel Epilepsy	91 genes	Whole CDS, UTR (-50 bp, + 10 bp)	575 kb	SNV, Indel, CNV	Blood (> 50 ng of fragmented DNA)		Primary and Secondary results (FASTQ to annotated VCF)
	Pharmaco Screen Panel Anti-tuberculosis	133 genes	Whole CDS, UTR (-50 bp, + 10 bp)	186 kb	SNV, Indel, CNV	Blood (> 50 ng of fragmented DNA)		Primary and Secondary results (FASTQ to annotated VCF)
LIQUID BIOPSY	ctDNA Panel Colorectal	16 genes	Whole CDS	18 kb	SNV, Indel, CNV	Plasma (> 20 ng of cfDNA)	All sequencers from Illumina and MGI	Primary, Secondary, and Tertiary analysis result (FASTQ to VCF, VCF to Clinical report) Linux-based consensus read generation SW provided
	ctDNA Panel Breast	27 genes	Whole CDS	99 kb	SNV, Indel, CNV	Plasma (> 20 ng of cfDNA)	All sequencers from Illumina and MGI	Primary, Secondary, and Tertiary analysis result (FASTQ to VCF, VCF to Clinical report) Linux-based consensus read generation SW provided
	ctDNA Panel Lung	28 genes	Whole CDS, 4 intronic regions	116 kb	SNV, Indel, CNV	Plasma (> 20 ng of cfDNA)	All sequencers from Illumina and MGI	Primary, Secondary, and Tertiary analysis result (FASTQ to VCF, VCF to Clinical report) Linux-based consensus read generation SW provided
MITOCHONDRIAL DNA	Mitochondrial DNA Sequencing Panel	Whole mitochondrial genome	Whole mitochondrial genome	16.6 kb	SNV, Indel	Blood (> 50 ng of fragmented DNA)	All sequencers from Illumina, Thermo Fisher, MGI, PacBio, and Oxford Nanopore	Primary and Secondary results (FASTQ to annotated VCF)
TRANSCRIPTOME	Targeted RNA Sequencing	Selective genes of Interest	Selective regions	-	SNV, Indel, CNV, Rearrangement	FFPE, frozen tissue, cfRNA		Primary, Secondary, and Tertiary analysis result (FASTQ to VCF, VCF to Clinical report)
EPIGENETICS	Targeted Methylation Sequencing	Selective genes of interest	Selective regions	-	SNV, Indel, CNV, Rearrangement	FFPE, frozen tissue, cfRNA		Primary and Secondary results (FASTQ to annotated VCF)
VIRUS RESEARCH	Comprehensive Respiratory Virus Panel	9 types / 39 strains, including SARS-CoV-2	-	706 kb	Viral variants and mutation (SNV, Indel) from generated WGS	URT, NP/OP, and others	All Illumina sequencers	Stand-alone bioinformatics SW and Celemics Virus Verifier (FASTQ to Report)
	African Swine Fever Virus Panel	ASFV 26 strains	-	192 kb	Virus detection, Virus genome asse	Swine blood (50 ng of fragmented DNA)	All Illumina sequencers	elemics ASFV Pipeline (FASTQ to Report)

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