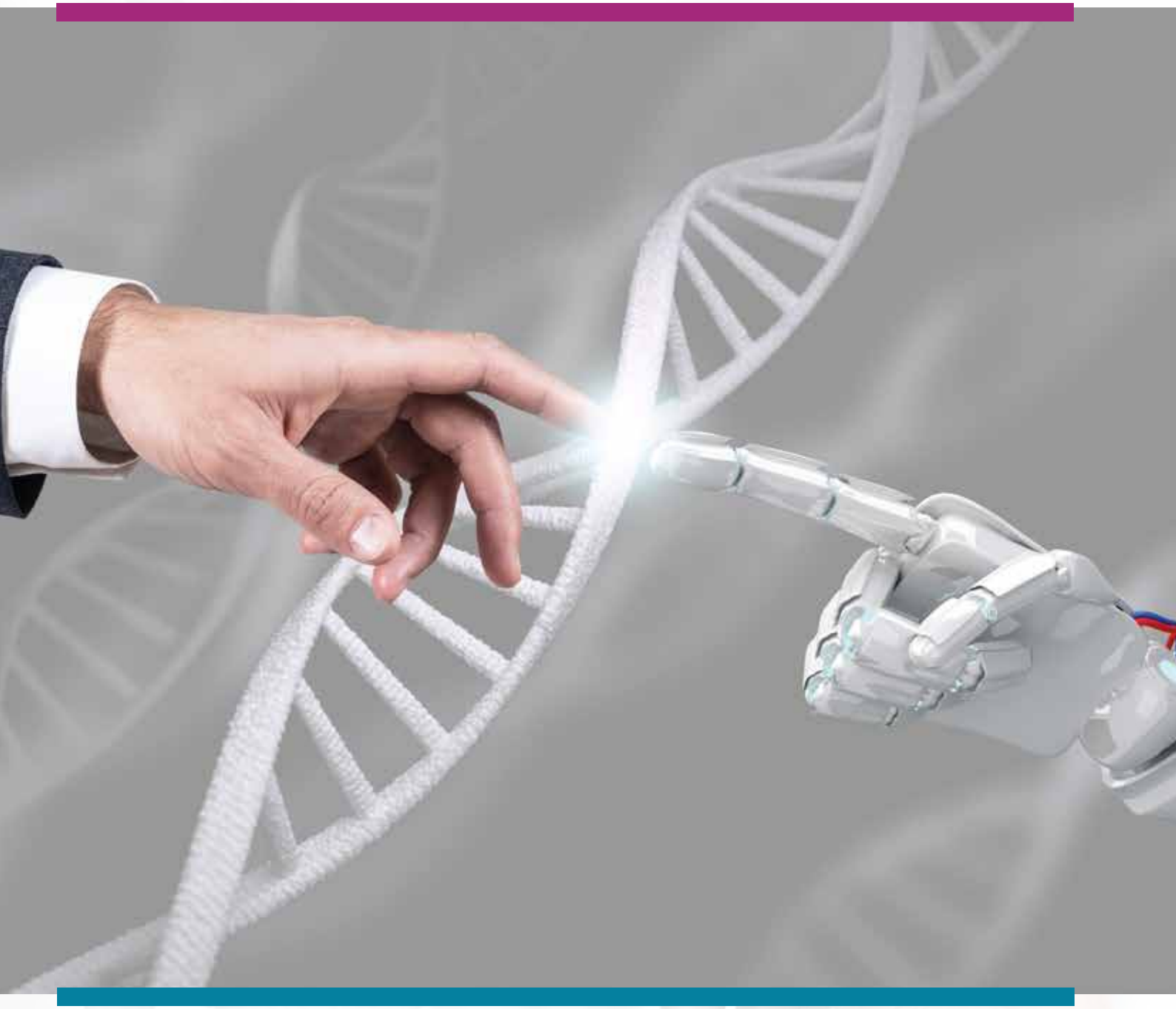
LifeCell® Diagnostics is now mfine /diagnostics



Proven Leader in

Next-Generation Sequencing Technology

Equipped with a complete portfolio of the most advanced Next-Generation Sequencing (NGS) technology, LifeCell has brought **speed, accuracy, efficiency & cost-effectiveness to genomic testing.**

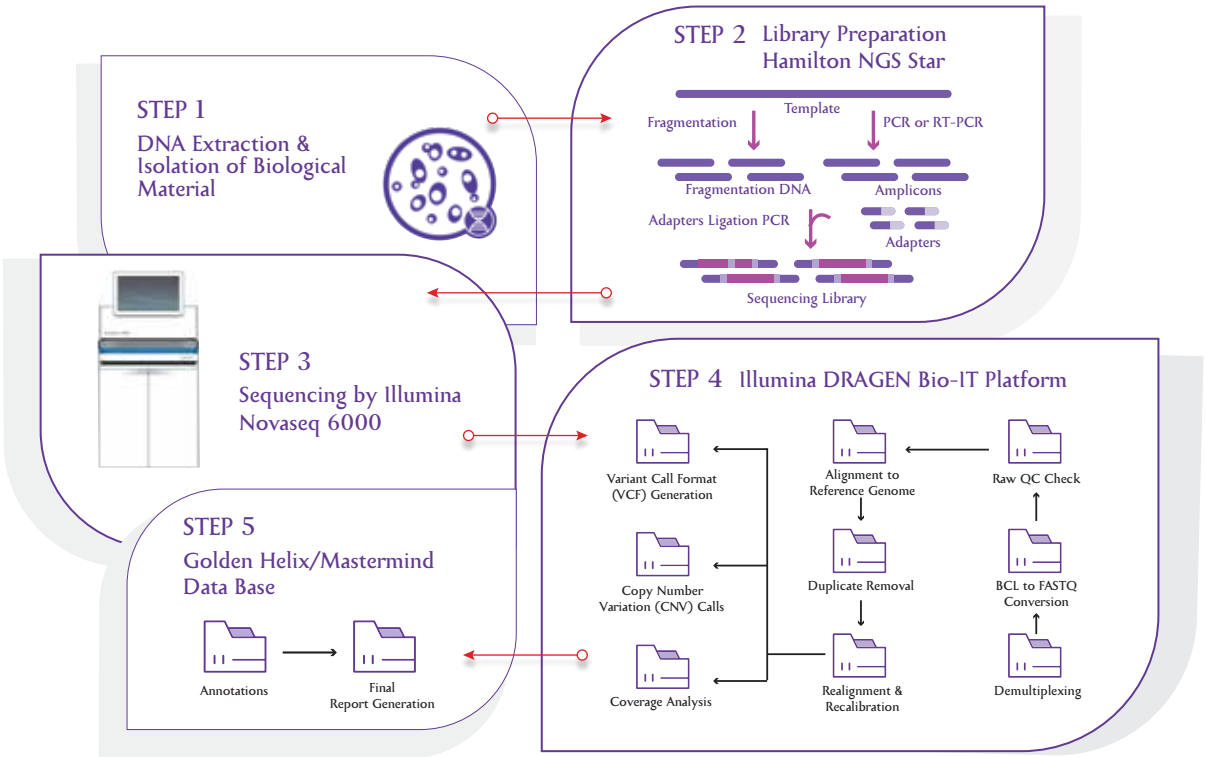
This makes us your trusted partner in every step–from sample preparation to generating insightful data, helping you make the right clinical decisions.

Understanding NGS

The complexity of genomic data and demand for in-depth information has made NGS a preferred choice to address the gaps that traditional DNA sequencing cannot. NGS offers ultra-high throughput, scalability, and speed that support a wide range of applications including rapid whole-genome sequencing, deep target sequencing, and much more.

LifeCell's NGS Workflow

LifeCell has utilised its in-house expertise to create an advanced and sophisticated NGS workflow to empower clinicians with the information they need



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Technology You Can Trust, Results You Need

We have adopted the most advanced systems for the important steps of NGS workflow to provide you with the best results.

	Instrumentation	Features
Library Preparation	Hamilton NGS STAR	It eliminates the tedious, manual process of library preparation and automates the steps to ensure hassle-free and hand-free workflows. Most importantly, it maximizes time efficiency and sample throughput, brings focus on high-value activities, and rules out the risk of manual errors and variations.
Sequencing	Illumina NovaSeq 6000	It is one of the most powerful instruments for high-throughput sequencing and offers deeper and broader coverage. It can sequence whole-genome, whole-exome, and transcriptome more efficiently and in a cost-effective way.
Genomic Analysis	DRAGEN Bio-IT Platform	This platform provides accurate and ultra-rapid genomic analysis of sequencing data. Capable of detecting small variants with sensitivity and specificity, it also enables lossless genomic compression by reducing FASTQ file sizes up to 5 times.
Annotation	Golden Helix VarSeq®	It is a fast and repeatable variant analysis software for whole genomes, gene panels, and exomes. Equipped with a powerful filtering and annotation engine, it can easily sift through large data sets. Plus, it provides two types of coverage metrics to eliminate false-positive/false-negative results, clinical-grade variant annotations, as well as leading annotation sources.
Interpretation	Genomenon® Mastermind Genomic Search Engine	It is one of the most comprehensive AI-driven databases for genomic literature. It helps reduce the turnaround time by quickly identifying the empirical evidence and enabling rapid variant interpretation. It also increases the diagnostic yield by offering 100x more genomic evidence and 20x more variants than other sources.

LifeCell's NGS Capabilities: Advancing Patient Care

Clinical Exome Sequencing

Features

Coverage

- Coding (exonic) and exon-intron boundary (~10bp) of custom exome panel comprising 6016 genes
- Clinically relevant protein-coding genes and intronic pathogenic mutations from ClinVar
- Mean depth around 80-100x; >95% of genes covered at 20x
- Customized capture baits boost coverage of hard-to-sequence areas of the exome and allow detection of intragenic copy number variants
- Results available within 14 days
- Automated re-analysis reduces burden on clinicians and patients
- Annotated supplemental reports are available upon request, which include all rare variants (<1% frequency)

Variants

SNVs and InDels

- (<50 bp) > 95%

Insertions

- 51-99 bp: > 95%
- 100-299 bp: > 95%
- >300 bp: > 95%

Copy number variations

- Single exon deletion/duplication (51-500 bp): >95%
- Multi exon to whole gene(s) deletion/duplication (100 bp-10 kb): >95%
- Whole and partial chromosomal aneuploidies (including sex chromosome aneuploidies): >90%
- Specificity of >99% is guaranteed for all reported variants

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Whole Exome Sequencing

Coverage

Features

- Coding (exonic) and exon-Intron boundary (~10 bp) of Whole exome panel comprising 18000+ genes
- Clinically relevant protein-coding genes and mitochondrial genome
- 33 Mb CCDS coverage, 3 Mb RefSeq Spike-in, Mitochondrial genome Spike-in
- Mean depth around 80-100x, >95% of genes covered at 20x
- Mitochondrial genome coverage depth at 1500-2000x
- Results available within 14 days
- Exon-level deletion duplication coverage included on all tests

  Reliable detection of CNVs >3 exons in size. Single exon CNVs can also be predicted but follow-up confirmation is strongly recommended for any event that reported less than 3 exons.

Variants

SNVs and InDels

- (<50 bp) > 95%

Insertions

- 51-99 bp: > 75%
- 100-299 bp: > 70%
- >300 bp: > 75%

Copy number variations

- Single exon deletion/duplication (51-500 bp): >70%
- Multi exon to whole gene(s) deletion/duplication (100 bp-10 kb): >80%
- Whole and partial chromosomal aneuploidies (Including sex chromosome aneuploidies): >90%
- Specificity of >99% is guaranteed for all reported variants

Enhanced coverage of medically relevant genes

- ~8,000 disease-associated genes
- 99% of ClinVar variants covered
- >90% of all known clinically relevant variants in codingregion from Clinvar, Decipher, Mastermind (Genomenon)

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Whole Genome Sequencing

Coverage

Features

- Almost complete and uniform coverage of the genome comprising >20,000 genes
- All non- and protein-coding regions
- Mean depth around 30x, >90% of genes covered at 10x
- Reliable detection of deletions and duplications (≥ 5 exons) in clinically relevant genes that are related to phenotype, as well as large scale CNV events, such as microdeletions and other gene- and chromosomal-level events
  - While smaller CNVs (3-4 exons) may be detected and reported, follow-up testing is recommended if a deletion of smaller than 3 exons is suspected
- Provides a high-resolution, base-by-base view of the genome
- Captures both large and small variants that might bemissed with targeted approaches
- Mean depth around 30x, >90% of genes covered at 10x
- Detects single nucleotide variants, insertions/deletions, copy number changes, and large structural variants.

Variants

SNVs and InDels

- (<50 bp) > 95%

Insertions

- 51-99 bp: > 75%
- 100-299 bp: > 70%
- >300 bp: > 75%

Copy number variations

- Single exon deletion/duplication (51-500 bp): >70%
- Multi exon to whole gene(s) deletion/duplication (100 bp-10 kb): >70%
- Whole and partial chromosomal aneuploidies (Including sex chromosome aneuploidies): >70%
- Specificity of >99% is guaranteed for all reported variants

Who benefits from Exome sequencing ?

- Patient with undiagnosed genetic disease
  (extensive evaluation and multiple genetic tests, without identifying the etiology)
- Patients presenting with Heterogeneous phenotypes:
  - Intellectual disability / developmental delay
  - Cardiomyopathy; Epilepsy; Undiagnosed metabolic disorder; Immunodeficiency
  - Ataxia; Neuropathy; Deafness
  - Bone and connective tissue disorders; Short stature; Complex dysmorphic features
- Whole Exome Analysis can be used to identify variants inherited from the parents causing recessive disease or dominant disease. Additionally, de novo variants that occur in the offspring but are not present in either of the parents can also be detected

Case Study

Case Study: Clinical Exome sequencing detects a Likely Pathogenic CNV in a patient with minimal phenotypes

Although the given phenotypes for this case were very minimal, Clinical exome sequencing (CES) detected a pathogenic Copy number variation (CNV) in a region that is reported in certain families thus providing a molecular diagnosis for patient's mild clinical presentation.

Clinical Indication

Proband is a 7 months old female suspected to be affected with early onset episodic ataxia and paroxysmal head nodding.

Differential Diagnosis

Differential Diagnosis: episodic ataxia, cerebellar disorders, pantocerebellar hypoplasia, essential tremors, hypoglycemia, hypocalcemia, hypomagnesemia, hyperthyroidism, mitochondrial disorders, biotinidase deficiency, ASD, paroxysmal kineginesic dyskinesia

Clinical exome sequencing (CES) results

Gene & Trartati 1p1	Variant	Lociation	Zygosity	Disorder (OMIM)	Inheritance	Classification
16:29802071-30200295	Deletion (298.23 kb)	16p 11.2	Heterozygous	16p 11.2 Microdeletion	Autosomal Dominant	Likely Pathogenic

Variant Interpretation

16:29802071- 30200295del- Likely Pathogenic.
Contiguous regions encompassing cytoband region of 16p 11.2 cytoband region of chromosome 16 could likely have a deletion in this sarnple. This cytoband region of 16p11.2 has previously been reported in ClinVar as Pathogenic, 1 star, criteria provided, singular submitter (variant ID: 58735). The Z-score, Ratio and p-value for this deletion are -2-5, 0.55 and 5.34418876637048e-190 respectively (The Z-score measures the number of' standard deviations from the reference sample mean, while the Ratio is the normalized mean for the sample of interest dvided by the average normalized mean for the reference samples). Microdeletions in 16p11.2 region has previously been reported for Paroxysmal kinesigenic dyskinesia by Termsarasab P, et al.: 2014. Based on the above evidence this variant has been classified as likely pathogenic according to the ACMG guidelines.

Validation of the observed deletion by secondary method is highly recommended

18p11.2 microdeletions are characterized by benign familial infantile epilepsy and infantile convulsions with choreoathetosis, joint laxity, seizures, and balancing issues.

[Genes covered: PRRT2, KIF22, MAZ, PAGR1, MVP, CDIPT, CDIPTOSP. SEZ6L2, ASPHD1, KCTD13,. TMEM219, TA0K2, HIRIP3, INO80E, DOC2A, C16orf92, TLCD3B, LOC112694756, ALDOA, PPP4C, TBX6, YPEL3, LOC101928595, GDPD3, MAPK3, and COR01A]

Test Ordering Information

Test Code	Test Name	Components	Specimen Type	Method	TAT
GEN0245O	Clinical Exome Sequencing(CES)	CES	Whole blood - EDTA vacutainer, DBS - DBS card AF - Sterile 15 ml Falcon tube CVS - Steril 15 ml Falcon tube with nutrient medium (provided by LifeCell) DNA - 1.5ml sterile cryotube	NGS	21 Days
GEN0226O	Whole Exome Sequencing(WES)	WGS			
GEN0055O	Microdeletion and Duplication Analysis by MLPA_ONCO	Cri-du-Chat syndrome,Sotos syndrome, Saethre-Chotzen syndrome, Williams-Beuren syndrome, Williams-Beuren duplication syndrome, Langer-Giedion syndrome, WAGR syndrome, Prader-Willi/ Angelman syndrome, Rubinstein-Taybi syndrome, Miller-Dieker syndrome, Lissencephaly-1, Smith-Magenis syndrome, Potocki-Lupski syndrome, Alagille syndrome, DiGeorge syndrome, 22q11.2 microduplication syndrome, Phelan-McDermid syndrome		MLPA	10 Days
GEN0173O	Sanger Sequencing Confirmation_ONCO	Sanger confirmation of reported mutation		Sanger sequencing	15 Days
GEN0034O	Chromosomal Microarray(CMA 750 K) - Affymetrix Cytoscan 750K	CMA		Affymetrix-CNV based analysis	8 Days
GEN0632O	Clinical Exome Sequencing(CES) + Mitochondrial Genome Sequencing	CES+ Mitochondrial Genome Sequencing		NGS	21 Days
GEN0228O	Whole Exome Sequencing(WES) + Mitochondrial Genome Sequencing	Whole Exome Sequencing(WES) + Mitochondrial genome		NGS	21 Days
GEN0487O	Hereditary cancer gene panel_ONCO	AIP, ALK, APC, AR, ATM, BAP1, BARD1, BLM, BMPR1A, BRCA1, BRCA2, BRIP1, BUB1B, CD82, CDC73, CDH1, CDK4, CDKN1C, CDKN2A, CEBPA, CEP57, CHEK2, CYLD, DDB2, DICER1, DIS3L2, EGFR, ELAC2, ENG, EPCAM, ERCC2, ERCC3, ERCC4, ERCC5, EXT1, EXT2, EZH2, FANCA, FANCB, FANCC, FANCD2, FANCE, FANCF, FANCG, FANCI, FANCL, FANCM, FH, FLCN, GATA2, GPC3, HRAS, KIT, MAX, MEN1, MET, MLH1, MLH3, MRE11A, MSH2, MSH3, MSH6, MSR1, MUTYH, MXI1, NBN, NF1, NF2, NSD1, PALB2, PHOX2B, PMS1, PMS2, PRF1, PRKAR1A, PTCH1, PTEN, RAD5, RAD51C, RAD51D, RB1, RECQL4, RET, RHBDF2, RNASEL, RUNX1, SBDS, SDHAF2, SDHB, SDHC, SDHD, SLX4, SMAD4, SMARCB1, STK11, SUFU, TGFBR2, TMEM127, TP53, TSC1, TSC2, VHL, WRN, WT1, XPA, XPC	Whole blood - EDTA vacutainer Dry - DBS card Amniotic Fluid - Sterile 15 ml Falcon tube Corionic Villus Sample - Sterile 15 ml Falcon tube with nutrient medium (provided by LifeCell) DNA - 1.5ml sterile cryotube	NGS	21 days

Name of Salesperson: ..... Contact: .....