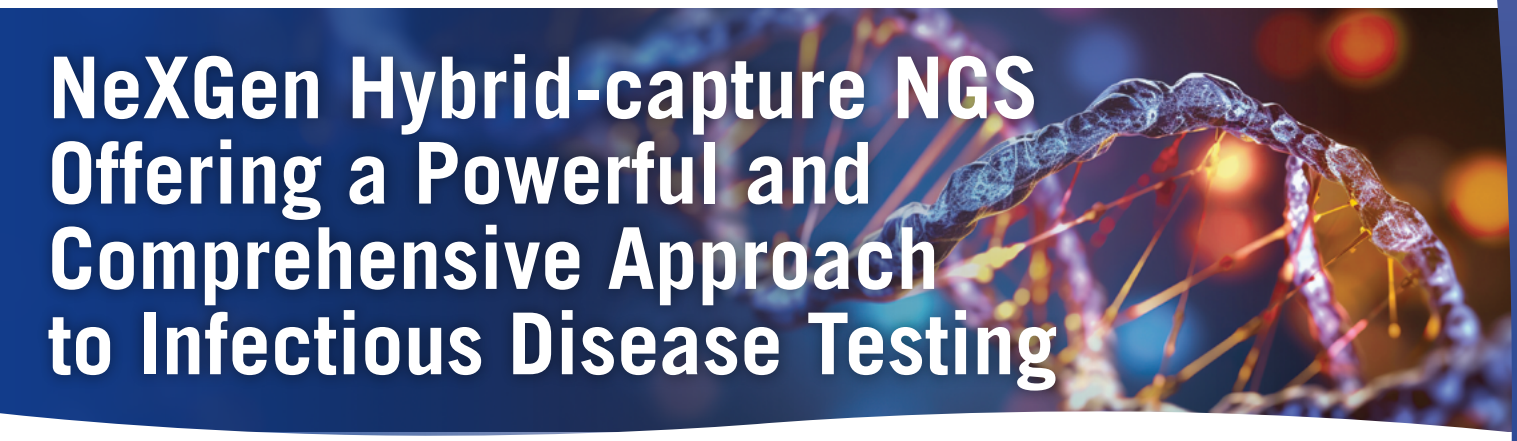
NeXGen
Fungal / AFB NGS

NeXGen Hybrid-capture NGS Offering a Powerful and Comprehensive Approach to Infectious Disease Testing



HYBRID-CAPTURE NGS

Microorganism identification and testing have evolved significantly from early microscopy to Next-Generation Sequencing (NGS) metagenomics. Initially, manual and subjective tests were developed allowing for better specificity, but they have limited in-depth analysis. However, these methods were time-consuming and limited in their ability to identify diverse microbial communities. With the advent of molecular techniques, such as Polymerase Chain Reaction (PCR), specific genes or regions could be targeted for identification. NGS analysis is currently revolutionizing the field by enabling the simultaneous sequencing of multiple microbial genomes, providing a comprehensive understanding of complex microbial communities. This approach allows for high-throughput analysis, species identification, functional profiling, and the discovery of novel microorganisms. This revolutionary testing sequences billions of DNA fragments simultaneously allowing for the unique genomic information of several microorganisms to be detected at once.

> *"With limited time and resources, researchers often have difficult decisions to make, particularly when it comes to sequencing. Hybrid-capture achieves more comprehensive target capture, better uniformity or coverage, and greater analytical sensitivity."*

Hybrid-capture NGS testing is a high-throughput DNA sequencing technology that allows for the analysis of multiple genes. This method offers several advantages over traditional diagnostic techniques, such as culture-based, serological, and PCR methods. NGS can detect a wide range of clinically relevant species, including those that are difficult to culture or identify using conventional methods. It also provides a higher sensitivity and specificity, enabling the detection of low-level infections and the differentiation of closely related species. Invasive fungal disease and Acid-Fast Bacteria testing using hybrid-capture NGS has the potential to improve patient outcomes by enabling early and accurate diagnosis, guiding appropriate (personalized medicine) therapy, and monitoring treatment response.

Hybridization capture-based target capture sequencing, in which genomic regions of interest are customized into specific probes (single-stranded oligonucleotides) for hybridization with genomic DNA, enriches DNA fragments from the target genomic region and then sequences them using next-generation sequencing technology. Unlike shotgun metagenomics-based methods [aka: Whole Exome Sequencing (WES)], hybrid capture allows the entire genome to be covered by overlapping probes that are used in the hybridization reactions to capture complementary DNA sequences. Hybrid-capture enrichment has led to a large increase in coverage depth, with between 400- and 7,000-fold increases in mean coverage depth achieved with a fraction of the sequencing depth, leading to significant increases in genome coverage for a range of targets.

Whole Exome Sequencing (WES) procedure does not involve enrichment for the targeted microbial sequences. Like hybrid-capture NGS, Shotgun metagenomics is one way to study unculturable microorganisms that are otherwise difficult or impossible to analyze. However, WES contains a large amount of human cfDNAs, much more than those derived from microbes, and is present in sequencing libraries, making the analysis tedious, costly, and error prone.

The advantages of hybrid-capture NGS genomic panel sequencing over WES is the simplicity of testing, as fewer genes will be sequenced with the specific and targeted detection of clinically relevant targets, thereby fewer false positive or false negative results.

About the Assay

Name: NeXGen Fungal / AFB NGS

Panel/Test Code: 33356

Testing Methodology: Hybrid-capture NGS

Turn-around-time: <72 hours after receipt of specimen.

Sample Type: Whole blood collected in a Streck Cell-Free tube.

Sample Volume: 10 mL

Shipping information: Ambient temperature, received within 7 days of collection.

Reporting: Only Detected organisms reported along with their genomic targets used for identification.

This assay has been developed to detect medically relevant and emerging microorganisms known to cause invasive disease.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NeXGen Fungal / AFB NGS

LABORATORY REPORT

PATIENT NAME:
SEX:
DOB:
AGE:
PHYSICIAN:

DATE & TIME
RECEIVED:
REPORT DELIVERED:
COLLECTED:
FINAL APPROVED:

CLIENT MRN:
CLIENT:

NeXGen Fungal / AFB NGS
Client Accession ID:
Eurofins Viracor Accession ID: 2333100326
Performed at: Eurofins Viracor, LLC 18000 W. 99th Street, Ste.#10, Lenexa, KS 66219. Lab Director: Brock Nell PhD, BCLD (ABB), CLIA # 26D-0983643

PATIENT RESULTS

Organism(s) Detected

Organism(s)	Target(s)
Cryptococcus neoformans	81_82

Notes:

Lorem Ipsum is the short-hand term for the most popular placeholder text in history, used for decades by graphic designers, web developers, and the publishing industry. Though lorem ipsum is sometimes referred to as greek copy or greeking, lorem ipsum text is a garbled form of Latin text

This test was developed and its performance characteristics determined by Eurofins Viracor. It has not been cleared or approved by the U.S. Food and Drug Administration. Results should be used in conjunction with clinical findings, and should not form the sole basis for a diagnosis or treatment decision.

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While there are differing versions of Next Generation Sequencing technologies in use, hybrid-capture NGS is the better choice for informative, actionable, and relevant diagnostics.

- Microbial cfDNA provides a broad overview of the microbial community, while hybrid-capture NGS offers higher sensitivity and specificity for identifying individual Fungal and AFB species.
- Hybrid-capture NGS is often preferred over broad-range PCR due to its targeted approach, higher sensitivity and specificity, greater coverage, and depth of sequencing, as well as its flexibility and scalability.
- qPCR plus NGS combines the selective amplification and quantification capabilities of qPCR with the high-throughput sequencing power of NGS. It is suitable for targeted sequencing and quantitative analysis. On the other hand, hybrid-capture NGS utilizes specific probes to selectively capture and enrich DNA regions of interest before sequencing, making it a selective and valuable tool for targeted resequencing and variant discovery.
- While Sanger sequencing is a reliable method for sequencing shorter DNA fragments with high accuracy, hybrid-capture NGS provides higher coverage, throughput, and a more comprehensive view of genetic information.
- Hybrid-capture NGS testing combines the targeted approach of 16s DNA sequencing with the comprehensive nature of NGS, enabling the analysis of specific genomic regions of interest.

NeXGen Fungal / AFB next-generation sequencing (NGS) detects medically relevant and emerging fungal, acid-fast bacteria (AFB) and selected bacterial species which are clinically similar to fungal infections derived from circulating cell free DNA (cfDNA) in the specimen. This test has been validated for human serum isolated from whole blood collected in Streck BCT tubes. If an organism has been detected, the organism and the gene target(s) are reported. A complete list of organisms that can be reported with this test can be found on our website.

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Learn More About NeXGen

About Viracor

With over 35 years of diagnostic expertise in infectious disease, immunology and allergy testing for immunocompromised and critical patients, Eurofins Viracor is passionate about delivering accurate, timely and actionable results, never losing sight of the connection between the testing it performs and the patients it serves.

Eurofins Viracor is a subsidiary of Eurofins Scientific (EUFI.PA), a global leader in bio-analytical testing, and one of the world leaders in genomic services. For more information, please visit eurofins.com and eurofins-viracor.com

NeoGen Fungal / AFB NGS

Organism Dataset

Absidia (26)
Actinomucor (1)
Actinomyces (40)
Aggregatibacter (1)
Alternaria (3)
Apiotrichum (1)
Apophysomyces (3)
Aspergillus (42)
Aureobasidium (4)
Basidiobolus (2)
Blastomyces (3)
Candida (25)
Chaetomium (1)
Chrysosporium (1)
Cladophialophora (5)
Cladosporium (1)
Clavispora (1)
Coccidioides (2)
Cokeromyces (1)
Conidiobolus (1)
Coniosporium (1)
Cryptococcus (2)
Cryptococcus gattii VGI (1)
Cryptococcus gattii VGII (1)
Cryptococcus gattii VGIII (1)
Cunninghamella (11)
Curvularia (2)
Cutaneotrichosporon (1)
Cyberlindnera (2)
Cyphellophora (1)
Debaryomyces (2)
Diutina (1)
Emergomyces (5)
Emmonsia (1)
Enterocytozoon (1)
Exophiala (7)
Filobasidium (1)
Fonsecaea (5)
Fusarium (25)
Geotrichum (1)
Histoplasma (1)
Hyphopichia (1)
Kluyveromyces (2)
Leptosphaeria (1)
Lichtheimia (2)
Lodderomyces (1)
Lomentospora (1)
Madurella (1)
Malassezia (13)
Memnoniella (1)
Metarhizium (7)
Metschnikowia (2)
Meyerozyma (2)
Microsporum (1)
Mortierella (1)
Mucor (5)
Mycobacterium (115)
Mycobacterium avium (1)
Mycobacterium avium subsp. paratuberculosis (1)
Mycobacterium avium subsp. silvaticum (1)
Mycobacterium intracellulare (1)
Mycobacterium intracellulare subsp. chimaera (1)
Mycobacterium intracellulare subsp. yongonense (1)
Mycobacteroides abscessus (1)
Mycobacteroides abscessus subsp. bolletii (1)
Mycobacteroides abscessus subsp. massiliense (1)
Mycobacteroides (1)
Mycolicibacter (2)
Mycolicibacterium (18)
Mycolicibacterium fortuitum (1)
Mycolicibacterium fortuitum subsp. acetamidolyticum (1)
Nakaseomyces (2)
Nannizzia (1)
Nigrograna (1)
Nocardia (98)
Nocardiopsis (1)
Paecilomyces (1)
Paracoccidioides (2)
Pascua (1)
Penicillium (23)
Phaeoacremonium (1)
Phaeotremella (2)
Phialophora (1)
Pichia (1)
Pneumocystis (3)
Podila (1)
Purpureocillium (1)
Rasamsonia (13)
Rhinocladiella (1)
Rhizomucor (2)
Rhizopus (5)
Rhodotorula (3)
Rhytidhysteron (1)
Saccharomyces (1)
Saksenaea (2)
Samsoniella (1)
Scedosporium (4)
Schaalia (3)
Schizophyllum (1)
Sporothrix (4)
Stachybotrys (2)
Starmerella (2)
Suhomyces (1)
Syncephalastrum (2)
Talaromyces (11)
Thermoascus (1)
Thermothelomyces (1)
Trichoderma (9)
Trichophyton (6)
Trichosporon (2)
Ustilago (5)
Verruconis (7)
Wallemia (2)
Wickerhamiella (2)
Wickerhamomyces (2)
Yamadazyma (1)
Yarrowia (1)

View the detailed Organism Dataset PDF

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