

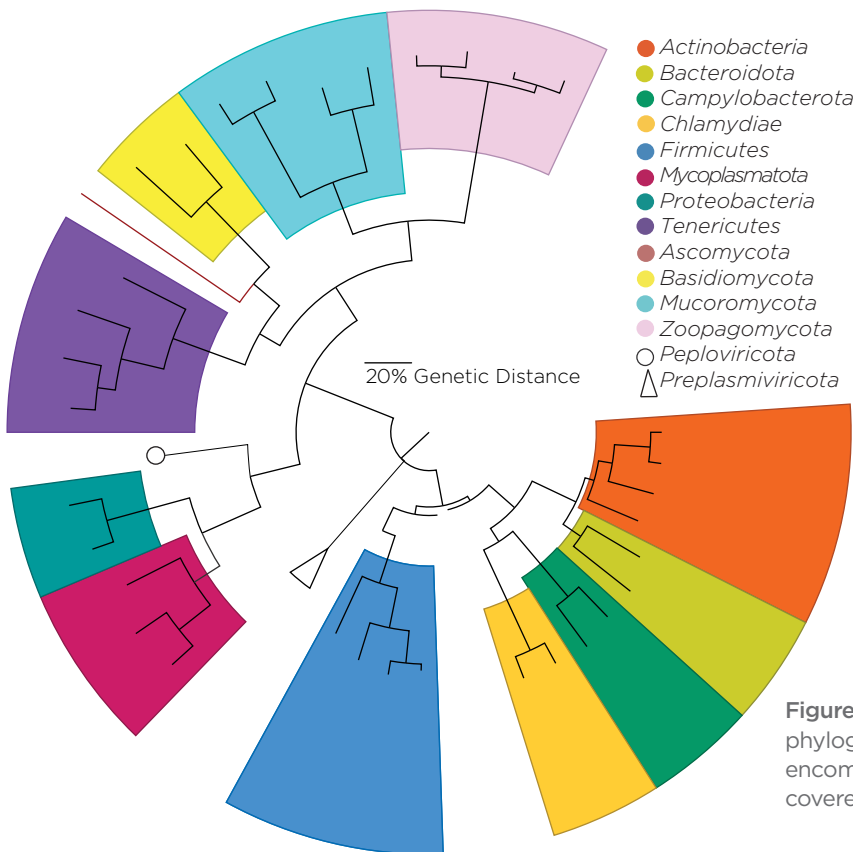
ONETest™ PathoGenome

Core-Genome Enrichment for Comprehensive Microbial Profiling

The **ONETest™ PathoGenome** is metagenomic assay that uses proprietary QuantumProbes™ to enrich core-genome loci across a broad spectrum of microbial families—including bacteria, fungi, and DNA viruses. It covers 254 microbial species across 50 microbial families.

Unlike assays relying on predefined panels or short amplicons, ONETest™ PG can capture entire microbial lineages, positioning it as a **new class of targeted metagenomics assay**.

- 1 Lineage-Wide Coverage:** Engineered to accommodate up to ~20% sequence divergence, allowing the assay to enrich both well-characterized pathogens and their known and novel phylogenetically related, counterparts
- 2 Species-Level Resolution:** Achieve high signal-to-noise detection that supports confident taxonomic placement, even in commensal-rich matrices such as BAL or tracheal aspirates.
- 3 Actionable Intelligence (AI) with FusionCloud™ bioinformatics platform:** Delivers secure, end-to-end data processing. From raw sequence files to taxonomic classification, genome reconstruction, and signal strength categorization



Category	Recognizable Etiologic Taxa
Bacteria	173
DNA Viruses	15
Fungi	67
Total	255

Table 1: Breakdown of bacteria, viruses and fungi covered.

Figure 1: Graphical representation of an un-rooted phylogenetic tree showing the 10 phylum which encompass the >250 etiologic causes of infection covered by the **ONETest™ PathoGenome**.

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Species	960K CFU/ml	96K CFU/ml	9.6k CFU/ml	960 CFU/ml	96 CFU/ml	10 CFU/ml	1 CFU/ml
<i>Aspergillus flavus</i>	+	+	+	+	+	-	-
<i>Escherichia coli</i>	+	+	+	+	+	-	-
<i>Mycobacterium kansasii</i>	+	+	+	+	+	+	-
<i>Nocardia brasiliensis</i>	+	+	+	+	+	-	-
<i>Pseudomonas aeruginosa</i>	+	+	+	+	+	-	-
<i>Staphylococcus aureus</i>	+	+	+	+	-	-	-

Table 2: Limit of detection of the ONETest™ for a diverse set of microorganisms. Unpublished Alamouti *et al*, 2025

Species Name	Culture (+)	ONETest (-)	ONETest (+)	Sensitivity %	Specificity %	PPV %	NPV %	Strong / Moderate	Background
<i>Escherichia coli</i>	5	—	5	100	97.3	35.7	100	3	2
<i>Haemophilus influenzae</i>	6	—	6	100	92.8	19.4	100	6	—
<i>Klebsiella pneumoniae</i>	5	—	5	100	97.4	45.5	100	5	—
<i>Pseudomonas aeruginosa</i>	33	—	33	100	93.7	62.3	99.4	30	3
<i>Staphylococcus aureus</i>	18	2	16	90	97.2	66.7	99.4	15	1
<i>Stenotrophomonas maltophilia</i>	10	—	10	100	97.9	58.8	100	9	1

Table 3: Key performance metrics of the ONETest™ in 328 BAL samples compared to Culture for the most frequently detected pathogens. Unpublished Alamouti *et al*, 2025

Species Name	Culture (+)	ONETest (-)	ONETest (+)	Sensitivity %	Specificity %	PPV %	NPV %	Strong / Moderate	Background
<i>Achromobacter xylosoxidans</i>	16	0	16	100%	87.98%	28.1%	100%	11	5
<i>Burkholderia cepacia</i>									
<i>Enterobacter</i>									
<i>Moraxella catarrhalis</i>									
<i>Proteus mirabilis</i>									
<i>Pseudomonas fluorescens</i>									
<i>Serratia marcescens</i>									
<i>Streptococcus pneumoniae</i>									
<i>Streptococcus pyogenes</i>									

Table 4: Key performance metrics of the ONETest™ in 328 BAL samples compared to Culture for all other detected pathogens. Unpublished Alamouti *et al*, 2025

Sample ID	Organism	Categorization	FPKM	Length (BoC)	Relative Abundance
103	<i>Klebsiella pneumoniae</i>	Strong	0.3	31,9309 (0.007)	11.9
	<i>Enterobacter hormaechei</i>	Strong	0.18	327,898 (0.0002)	12.9
	<i>Prevotella denticola</i>	Moderate	0.11	129,600 (0.1)	7.85
	<i>Prevotella oris</i>	Moderate	0.14	161,690 (0.2)	9.89
	<i>Streptococcus oralis</i>	Background	0.07	51,343 (0.0001)	5.19

Table 5: Taxonomic classification and signal strength categorization as reported by the ONE-Test™ from a BAL sample.

Learn more

For more information about the ONETest™ PathoGenome assay and the ONETest™ system, please visit: WWW.FUSIONGENOMICS.COM

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