TECHNICAL DATA SHEET

QuantumProbes™

Probe-Based Hybrid Capture Technology for Core-Genome Metagenomic Sequencing

QuantumProbes™ are a patented library of oligonucleotide capture probes engineered by Fusion Genomics Corporation to enrich microbial core-genome loci from complex clinical specimens for next-generation sequencing (NGS). Unlike conventional probe-based targeted sequencing assays limited to a narrow panel of predefined targets, QuantumProbes™ are designed to tolerate up to ~20%.

KEY SPECIFICATIONS AT A GLANCE

~20%	35–75%	6.5× FPKM
Sequence divergence tolerance from reference sequence	GC content capture range validated across all target organisms	Enrichment vs. whole metagenome sequencing (WmGS)

TARGET SCOPE: 50 MICROBIAL FAMILIES

173	67	15
Bacterial Species	**Fungal Species**	**DNA Viruses**
Gram-positive, Gram-negative, Mycobacteria, Nocardia & more	Aspergillus, Coccidioides, Paecilomyces & more	Adenoviridae & other DNA viral families relevant to LRTI

DESIGN PRINCIPLES

Core-Genome Targeting

Core genes are vertically inherited, conserved within a taxonomic lineage, and often carry species-specific polymorphisms. Targeting these loci provides a high signal-to-noise framework for accurate phylogenetic inference — without the limitations of amplicon-based genus-level methods or the cost of whole metagenome sequencing.

Divergence-Tolerant Hybridization

QuantumProbes™ are engineered to hybridize with target sequences that carry up to ~20% nucleotide divergence from the probe reference. This enables lineage-wide capture — enriching sequences at the species, genus, family, or phylum level depending on sequence homology. This is critical for detecting novel, divergent, or rare strains not anticipated by rigid probe panels.

HYBRIDIZATION CAPTURE WORKFLOW (IN ONETEST™)

1. **Library Prep** — Frag End-repair A-tail Ligation
2. **Blocking** — Blocking Mix (BM) suppresses adapters
3. **Hybridization (65°C)** — Probe (PRP) + Enhancer (ENH) + HYB Buffer
4. **Bead Capture + Wash** — CB + CBB; WS1–WS4; NaOH elution
5. **Enriched Library** — NGS-ready · stored at 10°C (ODTC)

>6.2 M	>703,000	254
Individual QuantumProbes™ in the full probe library	Core & orthologous gene targets across 50 microbial families	Detectable pathogenic organisms 173 bacteria · 67 fungi · 15 DNA viruses

Fully automated on Hamilton STAR Liquid Handling System. Total run time ~18 hours.

VALIDATION STRATEGY: REPRESENTATIVE-PROBE-PATHOGEN APPROACH

Because QuantumProbes™ target conserved core-genome loci shared across taxonomic lineages, exhaustive validation of all 254 reportable species is scientifically unnecessary. Once probe capture is demonstrated for a core locus in a representative organism, the same probe set is expected to enrich that locus in all species that share it — a principle rooted in DNA-DNA hybridization, vertical inheritance and conservation of core genes.

6 LoD Organisms	55 BAL Cohort Organisms	115 Total Organisms to Date
Full limit-of-detection validation	510 clinical BAL samples; culture + PCR	~80% probe set validated; 147 confirmed in silico

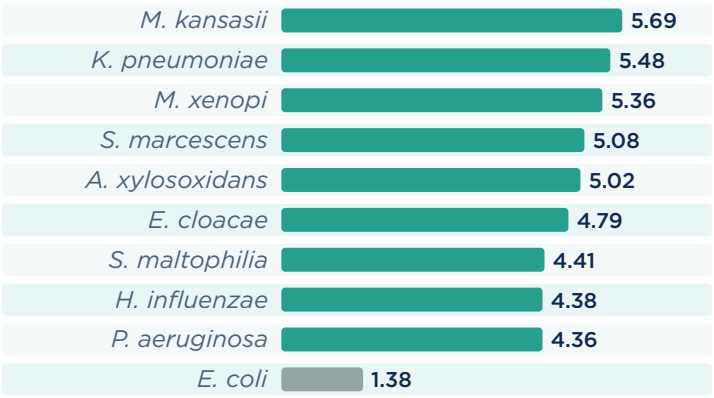
ANALYTICAL PERFORMANCE DATA

Limit of Detection (LoD) — Six Representative Organisms

Organism	LoD (CFU/sample)	Detected
Mycobacterium kansasii	96	√
Escherichia coli	96	√
Aspergillus flavus	96	√
Nocardia brasiliensis	96	√
Pseudomonas aeruginosa	96	√
Staphylococcus aureus	960	√

Organisms standardised to 1.5 McFarland;
LoD = concentration detected in 3/3 replicates.

FPKM Enrichment vs. WmGS (Log_2 Fold-Change)



Source: Rand et al.,Preprint. Values expressed as Log_2 fold-change FPKM vs. WmGS.

ADVANTAGES OVER CONVENTIONAL APPROACHES

Attribute	Amplicon (16S rRNA)	Whole Metagenome (WmGS)	QuantumProbes™ (ONETest™)
Taxonomic Resolution	Genus-level only	Species-level	**Species-level**
Pathogen Scope	Bacteria only	All organisms	**254 (bacteria+fungi+DNA viruses)**
Host Read Burden	Moderate	Very high (90–99%)	**Substantially reduced**
Signal Enrichment	Low (amplicon)	None	**Up to 6.5× FPKM vs. WmGS**
Novel / Divergent Strains	None	Detected (no enrichment)	**Detected (up to ~20% divergence)**
Compute Burden	Low	Very high	**Low (targeted; FusionCloud™)**

STORAGE & HANDLING

QuantumProbes™ Component

Storage temperature: −20°C
Supplied as part of ONETest™ Assay Kit (Cat. OTPG-24)
Kit includes: Probes, Enzymes, HYB Buffer, Blocking Mix, Capture Beads (4°C), Capture Bead Buffer, Cleanup Beads (4°C), Wash Buffers WS1–WS4, and all other library prep reagents.

ORDERING & CONTACT

Fusion Genomics Corporation
Richmond, British Columbia, Canada
www.fusiongenomics.com

Product: ONETest™ PathoGenome Assay Kit
Cat. No.: OTPG-24
For ordering & technical support: info@fusiongenomics.com

Learn more

For more information about the **ONE**Test™ system, please visit: www.fusiongenomics.com

For research use only. Not intended for any animal or human therapeutic or diagnostic use.

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