

Aperiomics Xplore-PATHOSM

Not All Next-Generation Sequencing Is Created Equal

Supported by the National Science Foundation, Aperiomics uses a technology called **deep shotgun metagenomic sequencing**, which creates a genetic fingerprint of every known microorganism in clinical samples. Other testing

companies typically use older sequencing techniques that identify just a few pathogens at a time. But **we can test for more than 37,000 microorganisms at once: every bacterium, fungus, parasite and virus known to science.**

DEEP SHOTGUN METAGENOMIC SEQUENCING vs. 16s SEQUENCING

Our next-generation sequencing captures far more information—and identifies many more pathogens, for greater accuracy. We ran identical urine samples through both processes to demonstrate the difference.

Aperiomics: Xplore-PATHOSM

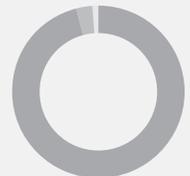
Provider M: 16s sequencing

SAMPLE 1

47% Lactobacillus gasseri	▶ 3% Streptococcus agalactiae
40% Streptococcus sp.	
5% Streptococcus vestibularis	1% Lactobacillus phage phiadh



▶ 96% Streptococcus agalactiae
3% Candida albicans



SAMPLE 2

14% Pseudomonas fulva	5% Alloscardovia omnicolens
11% Actinobaculum massiliense	4% Finegoldia magna
8% Pantoea septica	2% Escherichia vulneris
7% Staphylococcus simulans	



99.9% Escherichia coli
0.01% Prevotella bivia



SAMPLE 3

79% Gardnerella vaginalis	▶ 2% Lactobacillus delbrueckii
▶ 9% Escherichia coli	
5% Lactobacillus gasseri	1% Shigella sonnei
2% Shigella dysenteriae	1% Escherichia sp.



▶ 93% Escherichia coli
▶ 4% Lactobacillus delbrueckii



“Shotgun next generation sequencing metagenomics allows much deeper characterization of the microbiome complexity, allowing **identification of a larger number of species for each sample**, compared to 16s rDNA amplicon sequencing.”¹

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¹ Quantitative Assessment of Shotgun Metagenomics and 16S rDNA Amplicon Sequencing in the Study of Human Gut Microbiome. Laudadio I, Fulci V, Palone F, Stronati L, Cucchiara S, Carissimi C. OMICS. 2018 Apr;22(4):248-254.