

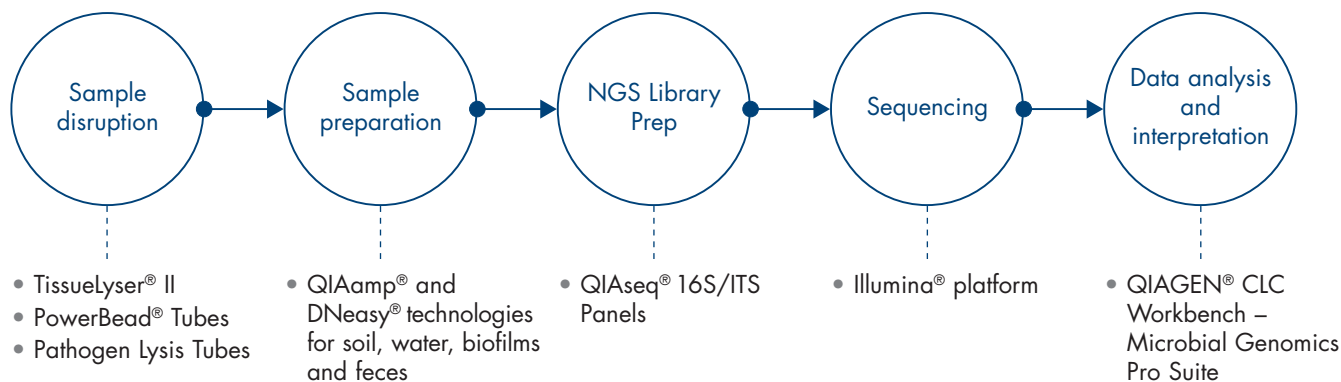
16S/ITS Microbiome Profiling Services

From challenging samples to insight with confidence

Microbiome research encompasses sample types as diverse as the human gut, Antarctic soil, ocean water and acidic hot-spring biofilms. These samples are challenging because they are difficult to lyse, as some microbes have tough extracellular matrices. Incomplete lysis of a microbial community results in an inaccurate representation of the microbial content of the sample. Additionally, PCR inhibitors present in these samples, especially humic acids, polysaccharides, polyphenolics, lipids and heavy metals, result in inaccurate quantification of nucleic acids and may inhibit downstream applications, such as qPCR and next-generation sequencing.

QIAGEN Genomic Services address these challenges with our industry-leading DNA isolation kits, which are based on optimized bead-beating and patented Inhibitor Removal Technology® (IRT), and bioinformatics as well as industry-leading software intelligence for data analysis. Partner with us for expert guidance and comprehensive service — from Sample to Insight — for profiling bacterial and fungal communities.

Sample to Insight microbiome profiling workflow



High-quality metagenomics library preparation

QIAseq 16S/ITS panels are used to prepare high-quality libraries for robust profiling of bacterial and fungal communities on Illumina platforms. Any combination of 16S variable regions and ITS regions can be interrogated (see below). These panels use phased primers to increase the quality of reads and bases and eliminate the need for PhiX spike-in. Low-bioburden reagents decrease background contamination and enable the analysis of low DNA input.

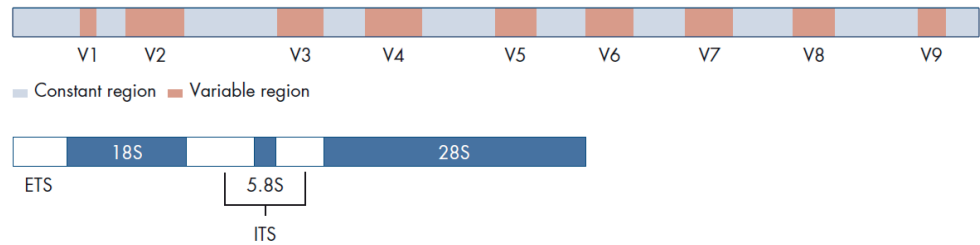


Figure 1. Structure of the bacterial 16S rRNA gene (top) and the fungal ITS region (bottom).

Bioinformatics: a bridge between data and discovery

Novel insights often remain elusive without the right tools for data analysis and interpretation, and specific, optimized tools are needed to meet the challenges microbiologists are facing today. QIAGEN Genomic Services data analysis and interpretation are based on the QIAGEN CLC Genomics Workbench and the Microbial Genomics Pro Suite plugin, which use best-in-class algorithms for metagenome assembly and comparative microbiome profiling.

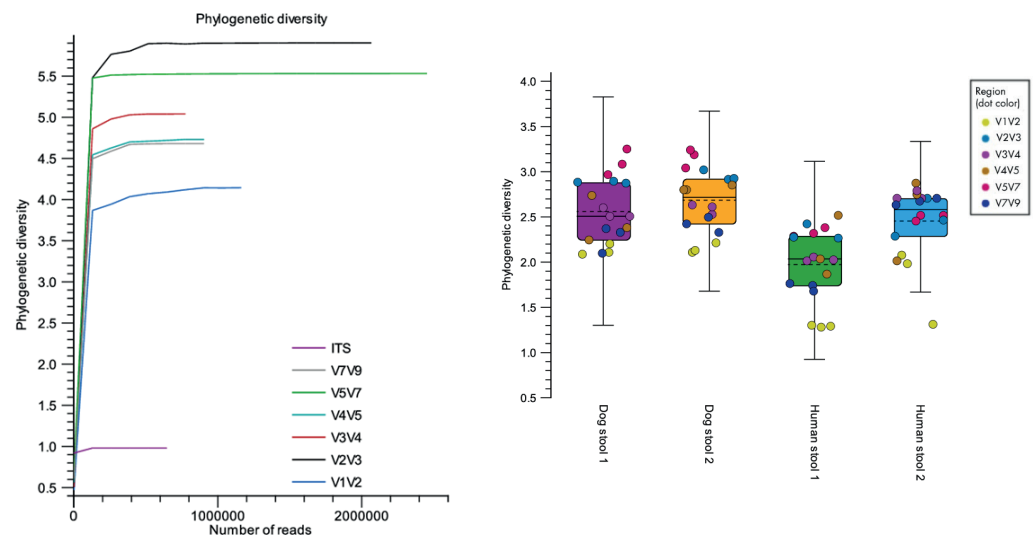










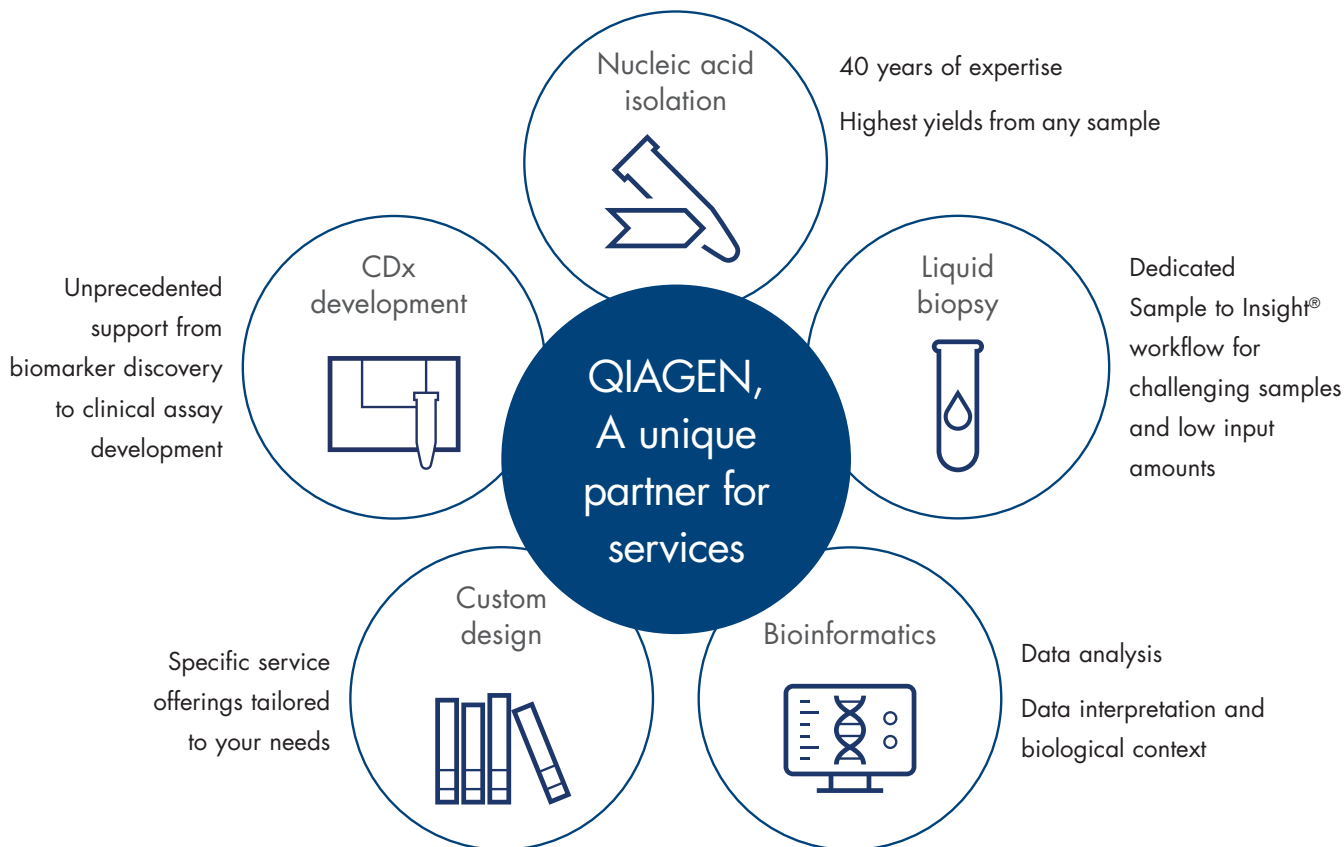
Figure 2. Rarefaction curve (left), alpha diversity (right).

Service specifications

 <p>Consultation</p>	<p>Free consultation with an expert to design an experimental setup that best meets your needs and budget.</p>		
 <p>DNA extraction</p>	<p>Input sample</p>	<p>Isolation kit</p>	<p>Input requirements</p>
	<p>Customer-isolated DNA</p>	<p>Not applicable</p>	<p>Minimum of 3 ng/μl in 5 μl; $A_{260}/A_{280} > 1.7$ Host DNA depleted.</p>
	<p>Soil</p>	<p>DNeasy PowerSoil® Pro Kit</p>	<p>Preferred sample aliquoting: 200 mg in PowerBead Pro Tubes</p>
	<p>Stool</p>	<p>DNeasy PowerSoil Pro Kit, QIAamp PowerFecal® Pro DNA Kit</p>	<p>Preferred sample aliquoting: 200 mg in PowerBead Pro Tubes</p>
	<p>other</p>	<p>Inquire</p>	
 <p>DNA quality control</p>	<p>Quality assessment by fluorometric measurement for determination of sample concentration. We will notify you about the QC results. This is a STOP/GO point where it is possible to omit samples, replace samples before proceeding or terminate the project.</p>		
 <p>Library preparation</p>	<p>Library preparation is performed using the QIAseq 16S/ITS Screening Panel (full 16S and ITS1 sequencing) or QIAseq 16S/ITS1 Region Panels (V1V2, V2V3, V3V4, V4V5, V5V7, V7V9 or ITS1).</p>		
 <p>Library quality control</p>	<p>Library quality control is assessed by gel electrophoresis to check for the fragment size and concentration. We will notify you about the QC results. This is a STOP/GO point where it is possible to terminate or adjust before proceeding to the sequencing.</p>		
 <p>DNA sequencing parameters</p>	<p>Sequencing primers are chosen /designed using the MiSeq®, system, v3, for paired-end reads, with a read length of 2 x 300 bp. Recommended minimum read depth is 50,000 reads per region (read depth depends on the number of samples and regions). The recommended minimum read depth is 10,000 reads per region for screening only (screening panel).</p>		
 <p>Complete data analysis</p>	<p>After analysis is complete, you received a comprehensive report with all the relevant data from your project. The table below lists some of the types of data that could be included in your report, depending on the services requested.</p>		
	<p>Type of data</p>	<p>Data delivered as</p>	
	<p>Raw data</p>	<p>De-multiplexed FASTQ files</p>	
	<p>Raw quality-control data</p>	<p>CLC Graphical QC report (per sample) CLC Supplementary QC report (per sample)</p>	
	<p>16S region demultiplex</p>	<p>16S demultiplex report (Reads per different 16S/ITS regions (e.g. V1V2, V3V4, and ITS)</p>	
	<p>Data trimming</p>	<p>CLC trim report (per sample, removal of adapters, low-quality sequences, short sequences and ambiguous nucleotides)</p>	
	<p>Operational taxonomic unit (OTU) clustering</p>	<p>OTU table (per region) Based on our in-house reference databases for 16S environmental samples, 16S human and microbiome samples and ITS data</p>	
	<p>Estimated alpha + beta diversity</p>	<p>Alpha diversity (diversity within a particular ecosystem): rarefaction table (per region) rarefaction curve (per region) and Combined alpha diversity box plot. Beta diversity (diversity between ecosystems): distance matrix and beta diversity PCoA plot (both per region)</p>	
	<p>Data merge</p>	<p>Data can be merged with data from previous projects upon request</p>	
	<p>Data delivery</p>	<p>Encrypted universal serial bus (USB) hard-disk drive or cloud delivery</p>	
 <p>Final report and consultation</p>	<p>The final data analysis package contains an overview of data analysis and algorithms used, the files and tables listed above and publication-ready figures. A teleconference is scheduled with QIAGEN scientists to discuss analysis and validation of results. Consultation and support are provided for 90 days following delivery or analysis. Extended support is available on request.</p>		

How can we accelerate your research?

Our expert team is looking forward to learning about your research project and designing your customized service with QIAGEN.



Tell us about your project

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