Making the invisible visible

Decode the microbial universe with our workflows for **environmental microbiome research**

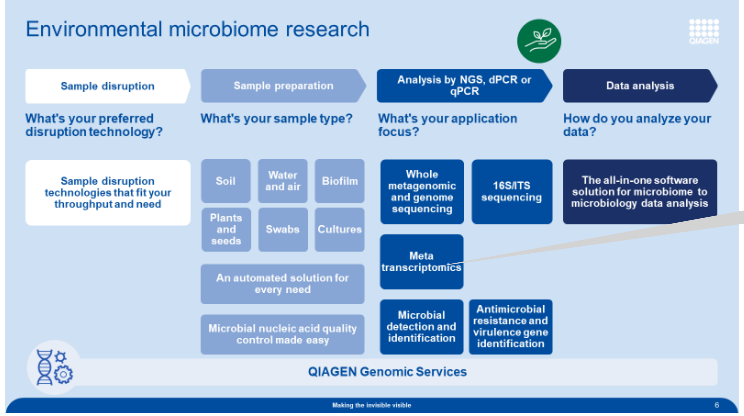
Legal disclaimer

Navigation elements in this booklet

Top navigation:

Environmental microbiome workflow

Workflow navigation:



Environmental microbiome research

Sample disruption
What's your preferred disruption technology?
Sample disruption technologies that fit your throughput and need

Sample preparation
What's your sample type?
Soil
Water and air
Biofilm
Plants and seeds
Swabs
Cultures
An automated solution for every need
Microbial nucleic acid quality control made easy

Analysis by NGS, dPCR or qPCR
What's your application focus?
Whole metagenomic and genome sequencing
16S/ITS sequencing
Meta transcriptomics
Microbial detection and identification
Antimicrobial resistance and virulence gene identification

Data analysis
How do you analyze your data?
The all-in-one software solution for microbiome to microbiology data analysis

QIAGEN Genomic Services

Making the invisible visible 6

Get to the next level

Further navigation:

DNA from stool

RNA and total NA from stool

Digital PCR

Get back to overviews

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Learn more

Decoding the microbial universe from research to routine testing and surveillance

QIAGEN sample technologies and workflow solutions, including dedicated next-generation sequencing (NGS), digital PCR (dPCR) and real-time PCR assays, support various microbiome research applications:

Microbiome research in human applications

Microbiome research in environmental applications

Functional microbiome analysis – metatranscriptomics

Identification of antimicrobial resistance genes

Strain typing and outbreak analysis

Bacterial species identification and detection of virulence genes

Let’s discuss our capabilities based on your focus

Environmental microbiome research

- The environmental microbiome adapts to external changes and is central to the earth’s systems and cycles
- Microbes also play an essential role in agricultural practices and − through applied microbiology − provide solutions to our everyday needs

Want to first get an overview of our complete workflow solutions? Go to the **portfolio overview**

Environmental microbiome research

Sample disruption

What's your preferred disruption technology?

Sample disruption technologies that fit your throughput and need

Sample preparation

What's your sample type?

- Soil
- Water and air
- Biofilm
- Plants and seeds
- Swabs
- Cultures

An automated solution for every need

Microbial nucleic acid quality control made easy

Analysis by NGS, dPCR or qPCR

What's your application focus?

- Whole metagenomic and genome sequencing
- 16S/ITS sequencing
- Meta transcriptomics
- Microbial detection and identification
- Antimicrobial resistance and virulence gene identification

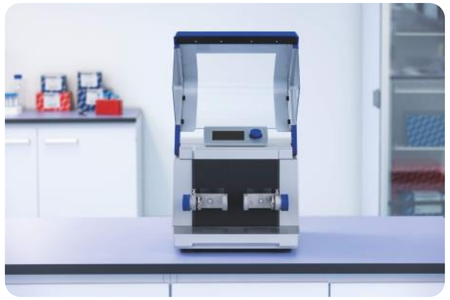
Data analysis

How do you analyze your data?

The all-in-one software solution for microbiome to microbiology data analysis

QIAGEN Genomic Services

Sample disruption – various options to meet your needs



TissueLyser III

Up to 192 samples at the same time

- Throughput of up to 192 samples in 96-well plates
- Tube volumes of 2, 5 mL, 96-well, 50 mL to be added soon
- User-friendly touchscreen and rotary knob
- Seven pre-programmed protocols and five customizable protocols
- Custom program cycles for added convenience

Vortex adapters

Connects directly to the Vortex-Genie 2 Vortex for hands-free disruption

- Maximizes vortexing by shaking multiple tubes at the same time, ideal for bead beating
- Adapters are available for 1.5–2 mL, 5 mL, 15 mL and 50 mL tubes

QIAGEN PowerBead Pro Tubes and Plates

Pre-filled tubes and plates for optimized lysis

- The PowerBead Pro Tubes and Plates use the latest bead-beating technology from QIAGEN
- Filled with zirconia beads
- Combined with the lysis buffer, it allows a better disruption of gram-positive bacteria, archaea and fungi

Soil

Target	Process	Format/ samples per run	Instrument	Recommended kit	Good to know
Microbial DNA	**Manual or automated**	Spin column	Automatable on QIAcube Connect	DNeasy PowerSoil Pro	High purity to achieve amplifiable DNA for unbiased results
		Silica spin filter tubes	N.A.	DNeasy PowerMax Soil	Up to 10 g for low biomass (e.g., sandy and clayey soils)
		96-well plate	N.A.	DNeasy 96 PowerSoil Pro	Manual processing on plates
	Automated	Up to 12	QIAcube Connect	DNeasy PowerSoil Pro QIAcube	For your convenience spin columns and tubes already loaded onto the rotor
		96	QIAcube HT	DNeasy 96 PowerSoil Pro QIAcube HT	High throughput isolation of DNA
		96	KingFisher Flex Eppendorf epMotion	MagAttract PowerSoil Pro DNA	Improved yield, improved inhibitor removal
	Automation compatible	Spin column + seq kit	Extraction automatable QIAcube Connect	DNeasy PowerSoil Pro DNA WGS SeqSet	All-in-one microbial sequencing set
Microbial RNA	**Manual**	Maxi spin column	N.A.	RNeasy PowerMax Soil Pro	Starting amount up to 15 g for all & low biomass soil samples

Soil can contain high amounts of humic substances, which are large water-soluble anionic molecules that interfere with amplification reactions during analysis

The DNeasy and RNeasy Power Pro Kits provide a novel bead tube and optimized chemistry for efficient lysis and the QIAGEN Inhibitor Removal Technology (IRT)* to successfully remove those inhibitors during nucleic acid preparation

***Patent pending**

Water and air

Target	Process	Format/ samples per run	Instrument	Recommended kit	Good to know
Microbial DNA	**Manual or automated**	Spin column	Automatable on QIAcube Connect	DNeasy PowerWater	• Optimized for use with most filter membrane types • Optimized to increase DNA yields from low biomass samples • Easily removes blocks to downstream PCR with IRT
	Manual	Spin column	N.A.	DNeasy PowerWater Sterivex	Optimized for use with Sterivex filter units
RNA	**Manual or automated**	Spin column	Automatable on QIAcube Connect	RNeasy PowerFecal Pro	Recommended for most efficient detection of SARS-CoV-2 in wastewater samples
		Spin column	N.A.	RNeasy PowerWater	For use with most filter membrane types
DNA and RNA	**Manual or automated**	Spin column	Automatable on QIAcube Connect	AllPrep PowerFecal Pro DNA/RNA	Recommended for detection of SARS-CoV-2 in wastewater samples
				AllPrep PowerViral DNA/RNA	Isolate viral or bacterial DNA and RNA from wastewater, stool, biosolids and gut material

Our recommendations for the most efficient detection of SARS-CoV-2 in wastewater samples:

- Centrifuge to create a solid pellet
- Extract nucleic acids with RNeasy PowerFecal Pro (preferred) or AllPrep PowerViral DNA/ RNA
- Elute in 50 µL
- Bead beating is necessary when processing pellets, but not supernatant
- Use of phenol-chloroform-isoamyl (PCI) may be beneficial but is not critical for the detection
- Absolute quantification with nanoplate-based dPCR on the QIAcuity dPCR System

Biofilm

Target	Process	Format	Instrument	Recommended kit	Good to know
Microbial DNA	**Manual or automated**	Spin column	Automatable on QIAcube Connect	DNeasy PowerBiofilm	• Efficient cell lysis by pairing chemical and mechanical lysis techniques • IRT removes concentrated inhibitors such as humic acid, metals, salts and pesticides, typically present in biofilms • High yields of inhibitor-free DNA from all types of biofilms, including microbial mats
RNA	**Manual or automated**	Spin column	N.A.	RNeasy PowerBiofilm	• High-quality RNA isolation from all biofilms, challenging dental plaques and microbial mats • High RNA yields with pre-treatment, mechanical and chemical lysis • Efficient elimination of PCR inhibitors with IRT

Depending on the microbial species producing the biofilm, its structure, chemistry, enzymatic and water compositions and thickness can vary widely

To build biofilms, microbes produce extracellular polymeric substances (EPS), which comprise polysaccharides, proteins, extracellular DNA (eDNA), humic substances and lipids in various amounts

Plants and seeds

Target	Process	Format	Instrument	Recommended kit	Good to know
Microbial DNA	**Manual or automated**	Spin column	Automatable on QIAcube Connect	DNeasy Plant Pro	• Highly efficient lysis and release of DNA from tough plant materials and associated plant pathogens • Superior PCR performance with IRT • Rapid extraction of ready-to-use DNA • No organic extraction or ethanol precipitation
		96-well plate	N.A.	DNeasy 96 Plant	• Uses bead-beating technology, replacing cumbersome DNA isolation procedures such as CTAB, phenol or chloroform extraction • Recovery of high-quality DNA from the toughest sample types • IRT to remove PCR inhibitors, including polysaccharides, polyphenolics and other secondary metabolites
RNA	**Manual or automated**	Spin column	N.A.	RNeasy PowerPlant	• Optimized to isolate RNA from the most difficult plant types • IRT removes 100% of polyphenolics, polysaccharides and other PCR inhibitors • Rapid protocol enables isolation of RNA in 30 minutes without the use of harsh chemicals

Detecting plant pathogens, such as viruses, bacteria, fungi and yeast is essential for monitoring agricultural ecosystems

Plant pathogen detection starts with high-quality nucleic acid extraction from various sample types

Bead-beating technology, IRT and removal of high polyphenolic content ensure efficient and reproducible results for any downstream application, like PCR and NGS

Swabs

DNA from swabs

RNA and total NA from swabs

QIAGEN

Target	Process	Format/ samples per run	Instrument	Recommended kit	Good to know
Microbial DNA	**Manual or automated**	Spin column	Automatable on QIAcube Connect	QIAamp PowerFecal Pro DNA	Yields high alpha diversity in sequencing
		Spin column	Automatable on QIAcube Connect	QIAamp DNA Microbiome	Effective depletion of host DNA
		96-well plate	N.A.	DNeasy 96 PowerSoil Pro	Manual processing on plates
	Automated	Up to 12	QIAcube Connect	QIAamp PowerFecal Pro DNA QIAcube	Spin columns and tubes are already loaded onto the rotor for convenience
		24 or 96	QIAsymphony SP	QIAsymphony PowerFecal Pro DNA	Mid- to high-throughput automated sample preparation
		96	QIAcube HT	DNeasy 96 PowerSoil Pro QIAcube HT	96 well format for scaling up your sample throughput
		96	KingFisher Flex Eppendorf epMotion	MagAttract PowerSoil Pro DNA	Improved yield, improved inhibitor removal
Host gDNA	**Manual or automated**	Spin column	Automatable on QIAcube Connect	QIAamp Fast DNA Stool Mini Kit	Isolate human DNA as well as microbial DNA

In the Power Pro kits, the swabs are put directly in the bead tube or plate

Swabs

DNA from swabs

RNA and total NA from swabs

Target	Process	Format/ samples per run	Instrument	Recommended kit	Good to know
Microbial RNA	**Manual or automated**	Spin column	Automatable on QIAcube Connect	RNeasy PowerFecal Pro	Novel bead tube and optimized chemistry and IRT
Microbial DNA and RNA	**Manual or automated**	Spin column	N.A.	AllPrep PowerFecal Pro DNA/RNA	Metagenomic and metatranscriptomic analysis from the same sample
	Automated	96	KingFisher Flex, Eppendorf epMotion	MagAttract PowerMicrobiome DNA/RNA	Optimized for automated, hands-free purification Improved downstream applications with IRT

The Power Pro kits provide a novel bead tube and optimized chemistry for efficient lysis and QIAGEN IRT to successfully remove those inhibitors during nucleic acid preparation

Cultured bacteria

Target	Process	Format	Instrument	Recommended kit	Good to know
Microbial DNA	**Manual or automated**	Spin column	Automatable on QIAcube Connect	DNeasy PowerSoil Pro	Our latest generation solution for efficient isolation of microbial DNA
		Spin column	Automatable on QIAcube Connect	DNeasy PowerLyzer Microbial	Bead-based isolation of high-quality DNA from microbial culture
		Silica spin filter	Automatable on QIAcube Connect	DNeasy UltraClean Microbial	Fast and easy DNA purification with spin filter extraction
		Spin column	N.A.	QIAamp BiOstic Bacteremia DNA Kit	Isolation of bacterial DNA from cultured blood, fecal and cervical swabs
Microbial RNA	**Manual or automated**	Spin column	Automatable on QIAcube Connect	RNeasy PowerFecal Pro	Our latest generation solution for efficient isolation of microbial RNA
Microbial DNA and RNA	**Manual or automated**	Spin column	N.A.	AllPrep PowerFecal Pro	Our latest generation solution for efficient isolation of microbial DNA and RNA
		Spin column	Automatable on QIAcube Connect	AllPrep Bacterial/Fungal DNA/RNA/Protein Kits	Extraction of protein and nucleic acids from bacterial cell cultures

The Power Pro kits provide a novel bead tube and optimized chemistry for efficient lysis and QIAGEN IRT to successfully remove inhibitors during nucleic acid preparation

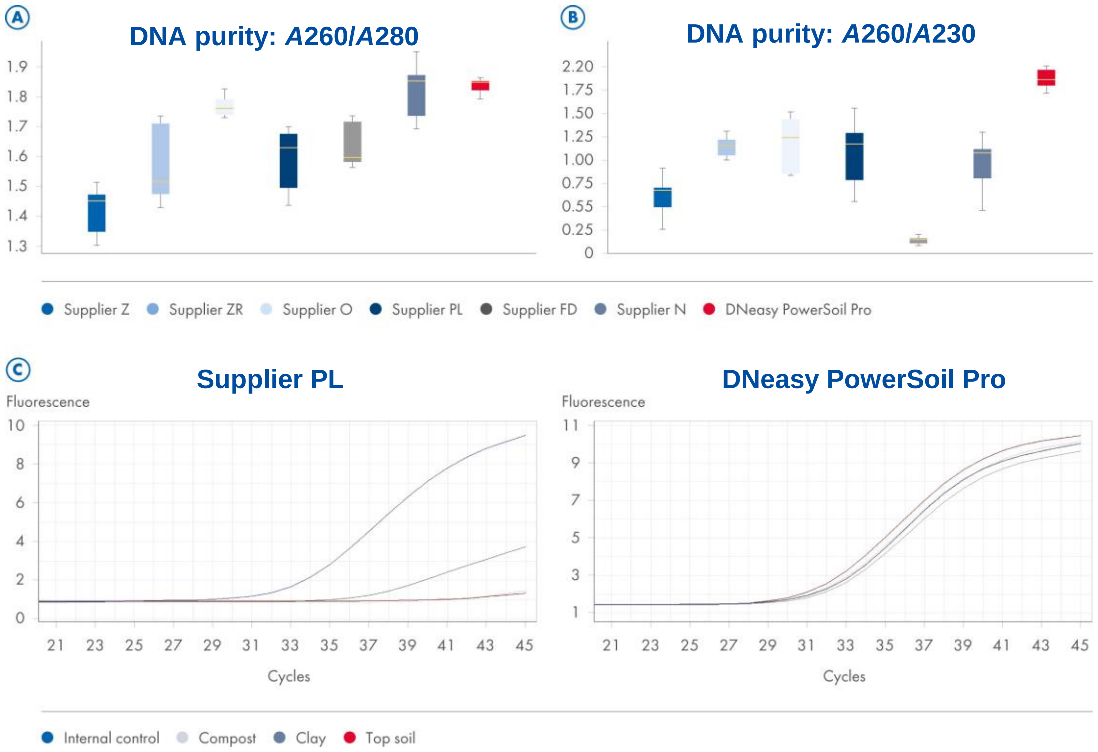
DNeasy PowerSoil Pro Kit
DNeasy PowerSoil Pro QIAcube Kit

Efficient isolation of microbial genomic DNA from all soil types

- Efficient lysis of bacteria and fungi in all soil types
- Up to 8-fold higher DNA yields compared to alternative methods
- Recovery of inhibitor-free DNA for direct use in NGS applications
- Unbiased results accurately represent sample alpha diversity
- Manual processing or automated workflow on the QIAcube Connect

Data obtained using experiments conducted by QIAGEN R&D in Hilden, Germany

DNA extracted with the DNeasy PowerSoil Pro Kit with IRT shows an increased purity with no inhibition of PCR



- Soil samples (250 mg each) were prepared using commercially available sample preparation solutions and compared to the DNeasy PowerSoil Pro Kit and DNA purity depicted via UV measurements
- Inhibitor removal was visualized with an inhibitor-sensitive PCR with an internal control (eluate-free reactions) spiked with eluates from Supplier PL and the DNeasy kit

The kit features a novel bead tube and optimized chemistry for more efficient lysis of soil bacteria and fungi

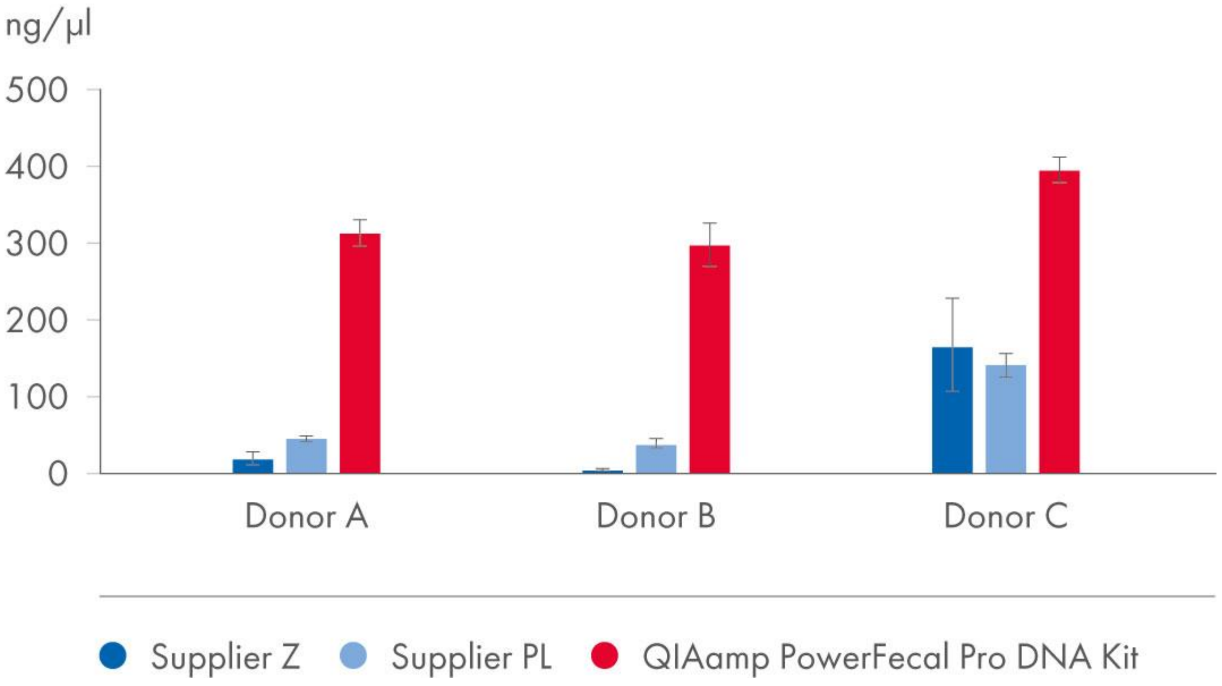
The kit also contains streamlined IRT to rapidly eliminate the challenging inhibitors commonly found in soil and environmental samples

QIAamp PowerFecal Pro DNA Kit
QIAamp PowerFecal Pro DNA QIAcube Kit

Efficient isolation of bacterial and fungal DNA from stool and gut samples

- Up to 20-fold more DNA compared to alternative methods
- Yields higher alpha diversity in sequencing compared to other methods
- Recovers inhibitor-free DNA for direct use in downstream applications
- Manual processing or automated workflow on the QIAcube Connect

Higher yields of DNA with the QIAamp PowerFecal Pro DNA Kit



- DNA was isolated from stool samples (200 mg) from three donors using commercially available sample preparation solutions and the new QIAamp PowerFecal Pro DNA Kit and compared
- Yields were measured by fluorometric quantification (Qubit)

Li S. et al. Salt-Sensitive Ileal Microbiota Plays a Role in Atrial Natriuretic Peptide Deficiency-Induced Cardiac Injury. *Nutrients.* 2022;14(15):3129

Juckel G, Manitz MP, Freund N, Gatermann S. Impact of Poly I:C induced maternal immune activation on offspring's gut microbiome diversity - Implications for schizophrenia. *Prog Neuropsychopharmacol Biol Psychiatry.* 2021;110:110306

Data obtained using experiments conducted by QIAGEN R&D in Hilden, Germany

DNeasy 96 PowerSoil Pro Kit
DNeasy 96 PowerSoil Pro QIAcube HT Kit

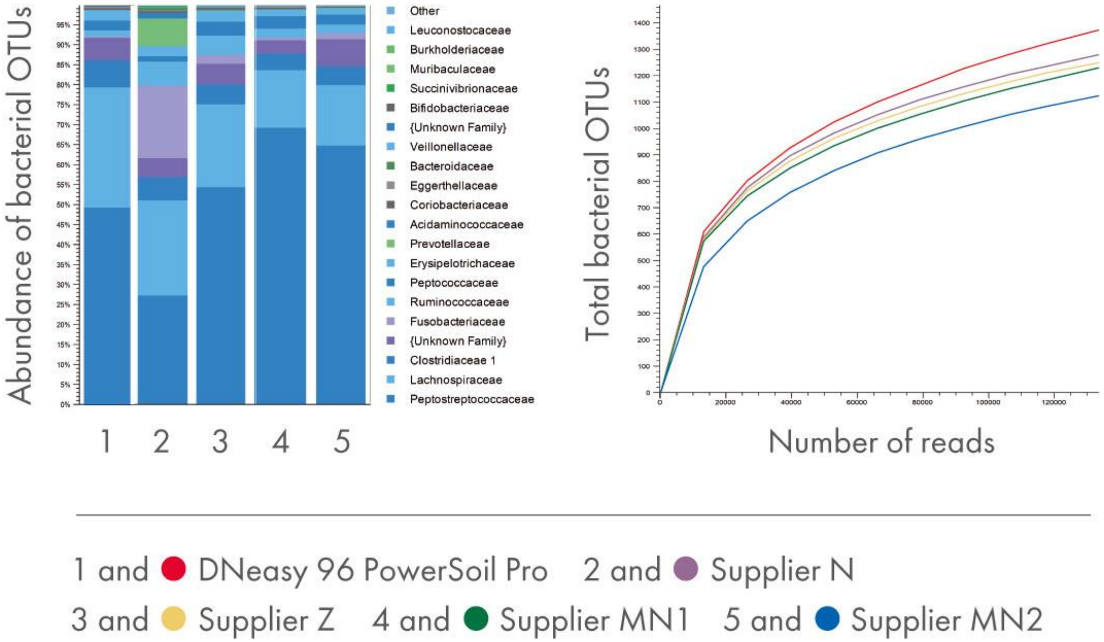
Soil

DNA from swabs

High-throughput isolation (manual or automated on QIAcube HT) of bacterial and fungal DNA from all soil and stool types, including difficult samples such as compost, sediment and manure

- Efficient lysis of bacteria and fungi efficiently from soil, stool and gut samples
- 96-well format for scaling up with the same proven technology of the DNeasy PowerSoil Pro Kit
- Recovers inhibitor-free DNA, ready to use directly in downstream applications

The DNeasy 96 PowerSoil Pro shows increased bacterial representation compared to other technologies



- DNA prepared from dog stool samples was isolated with DNeasy 96 PowerSoil Pro and other technologies
- 16S libraries of the 16S gene (V4 region) were prepared using barcoded 515fB and 806rB primers and the QIAGEN UCP Multiplex PCR Kit
- Data analysis was performed with the QIAGEN CLC Genomics Workbench using the SILVA database, and each result represents an aggregation of two datasets per sample

Antoine D, Singh PK, Tao J, Roy S. Neonatal morphine results in long-lasting alterations to the gut microbiome in adolescence and adulthood in a murine model. *Pharmaceutics.* 2022;14(9):1879

Charles Jacob HK, et al. Identification of novel early pancreatic cancer biomarkers KIF5B and SFRP2 from "first contact" interactions in the tumor microenvironment. *J Exp Clin Cancer Res.* 2022;41(1):258

L.Tian et al. Rhizosphere bacterial community structure of three minor grain crops: A case-study from paired field sites in Northern China. *Land Degrad. Dev.* 2022:33(1),104–116

Data obtained using experiments conducted by QIAGEN R&D in Hilden, Germany

RNeasy PowerMax Soil Pro Kit

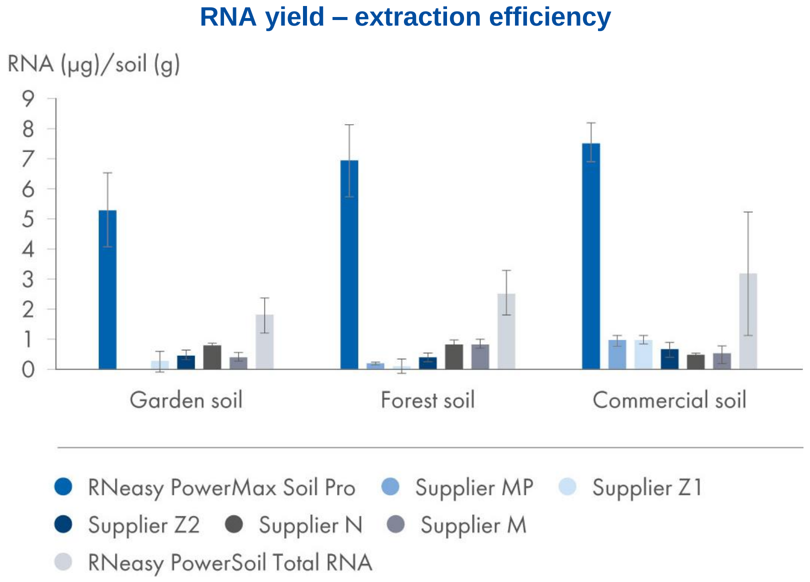
Soil

Maximal isolation of microbial RNA from large volumes of soil samples including compost, sediment, and manure

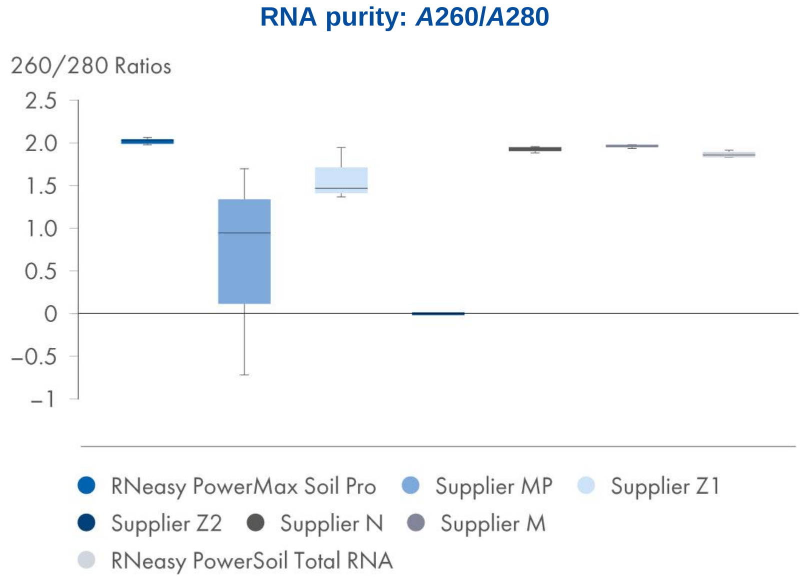
- Uses second-generation IRT
- Efficient bead beating and lysis chemistry ensures high RNA yields from large sample quantities
- Suitable for soil types rich in humic acid, including compost, sediment, and manure
- Ready-to-use RNA suitable for downstream applications such as RT-PCR, digital PCR, qPCR, and next-gen sequencing

Data obtained using experiments conducted by QIAGEN R&D in Hilden, Germany

Extractions using the RNeasy PowerMax Soil Pro Kit result in high RNA yield with excellent purity



RNA yield – extraction efficiency



RNA purity: *A260/A280*

- RNA was isolated from soil of three different sources in triplicate according to the respective manufacturer’s protocol. RNA yield was quantified by a fluorometric measurement and the extraction efficiency was calculated using the soil amount applied for each preparation.
- RNA purity from all sources was determined by a UV-Vis measurement. Error bars represent standard deviation.

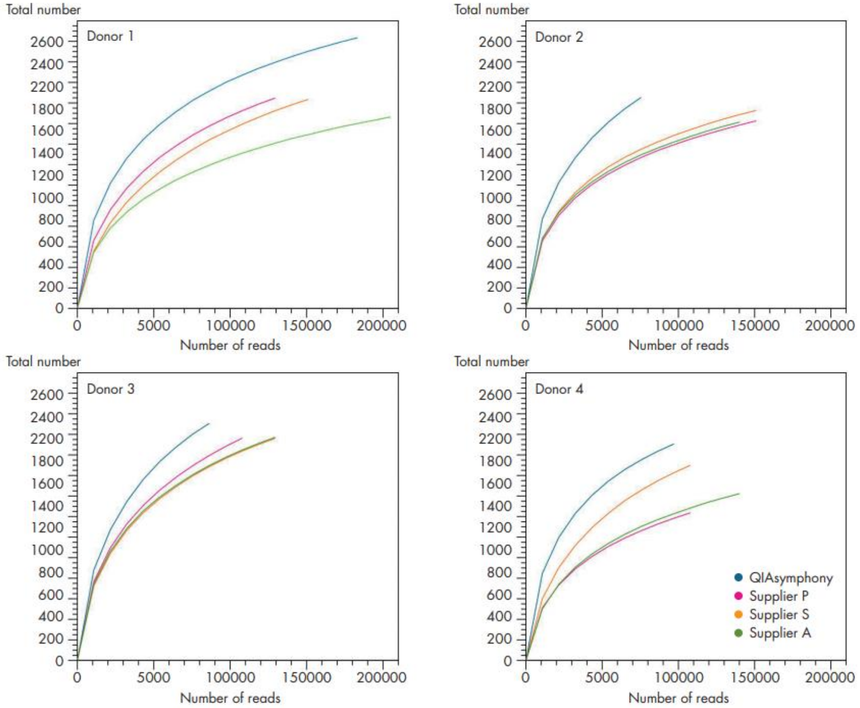
QIAsymphony PowerFecal Pro DNA

DNA from swabs

Efficient lysis of bacteria and fungi in all stool and soil samples

- Automated workflow with medium throughput on QIAsymphony SP
- Standardized DNA extraction
- Unbiased results accurately represent sample alpha diversity
- The kit is designed for 192 samples with continuous loading of 24-sample batches

Highest microbial diversity with QIAsymphony PowerFecal Pro DNA



- DNA from four different stool samples was isolated using the QIAsymphony PowerFecal Pro DNA Kit and three other commercially available kits, with each sample processed in quadruplicate
- DNA was then used for library construction with the QIAGEN UCP Multiplex PCR Kit using adapter-modified 515F-806R 16S primer, sequenced on a MiSeq system and analyzed using QIAGEN CLC Genomics Workbench

Automated viral RNA extraction on QIAsymphony SP – a use case:

Wurtzer. S. et al. Several forms of SARS-CoV-2 RNA can be detected in wastewaters: Implication for wastewater-based epidemiology and risk assessment. *Water Res.* 2021;198:117183

MagAttract PowerSoil Pro DNA

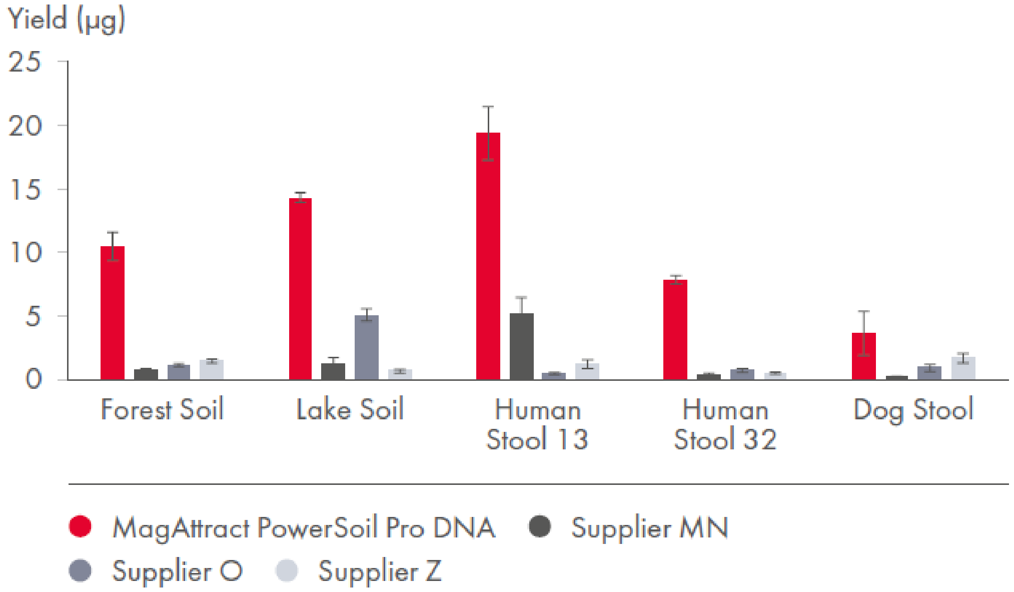
DNA from swabs

Soil

High quality DNA isolation from tough soil, stool and other environmental samples

- Improved yield through more efficient PowerBead Pro Plates and Tubes, and lysis chemistry
- Improved inhibitor removal eliminates more PCR-inhibiting compounds for greater nucleic acid purity

Higher yields were obtained with the MagAttract PowerSoil Pro DNA Kit than all competitor kits



- DNA was isolated from soil (forest, lake) and stool (human and dog) according to the appropriate protocol
- The DNA yields were measured with a Qubit Fluorometer

The MagAttract PowerSoil Pro DNA Kit allows automated high-throughput isolation of DNA from up to 384 soil samples in less than one day and is optimized for use with the ThermoFisher KingFisher Flex platform and Eppendorf epMotion

Data obtained using experiments conducted by QIAGEN R&D in Hilden, Germany

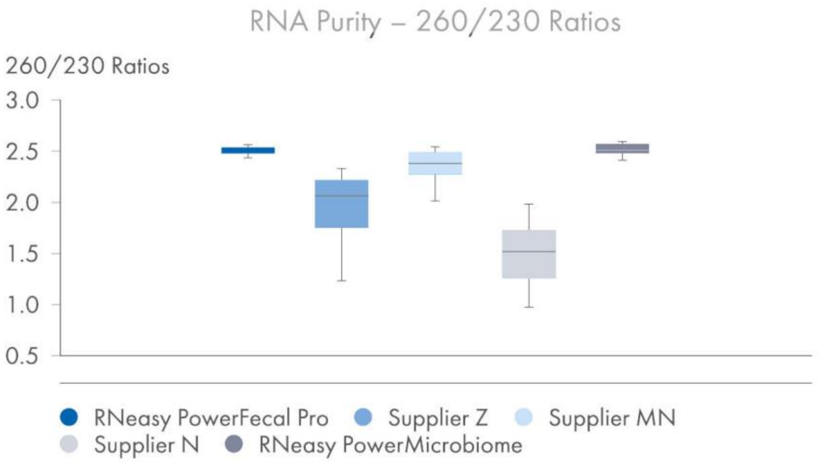
RNeasy PowerFecal Pro

RNA and total NA from swabs

Isolation of microbial RNA from stool and gut samples, sludge, or wastewater or swabs

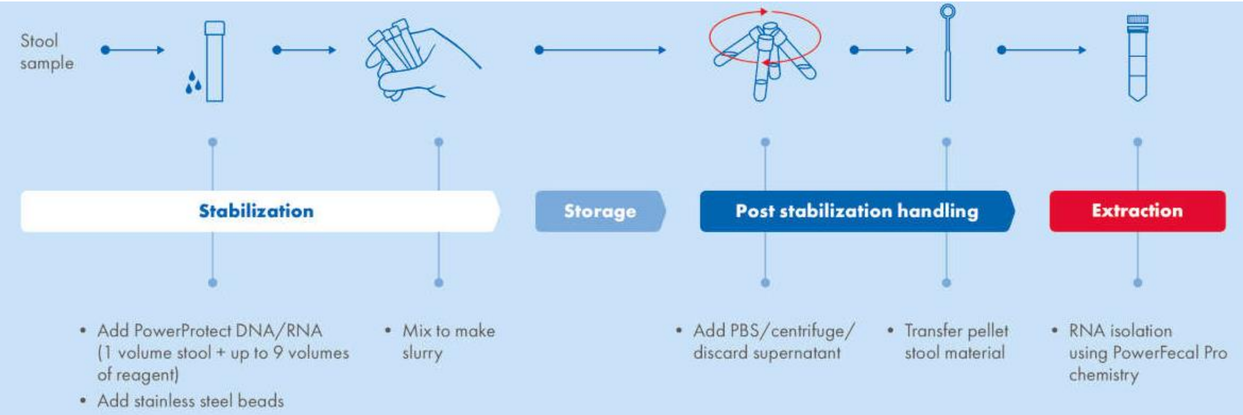
- Efficient isolation of high-quality microbial RNA from difficult microbiome samples
- Easy-to-use protocol
- The kit features a novel bead tube and optimized chemistry for more efficient lysis of stool bacteria and fungi
- The kit also contains streamlined IRT to rapidly eliminate the challenging inhibitors commonly found in stool and gut samples
- Automatable on QIAcube Connect

Pure RNA isolated from stool with RNeasy PowerFecal Pro



- Three commercially available kits and the RNeasy PowerMicrobiome kits were used for the comparison with RNeasy PowerFecal Pro Kit
- Four frozen stool samples in triplicates were tested

Workflow including sample stabilization with PowerProtect DNA/RNA Kit



Data obtained using experiments conducted by QIAGEN R&D in Hilden, Germany

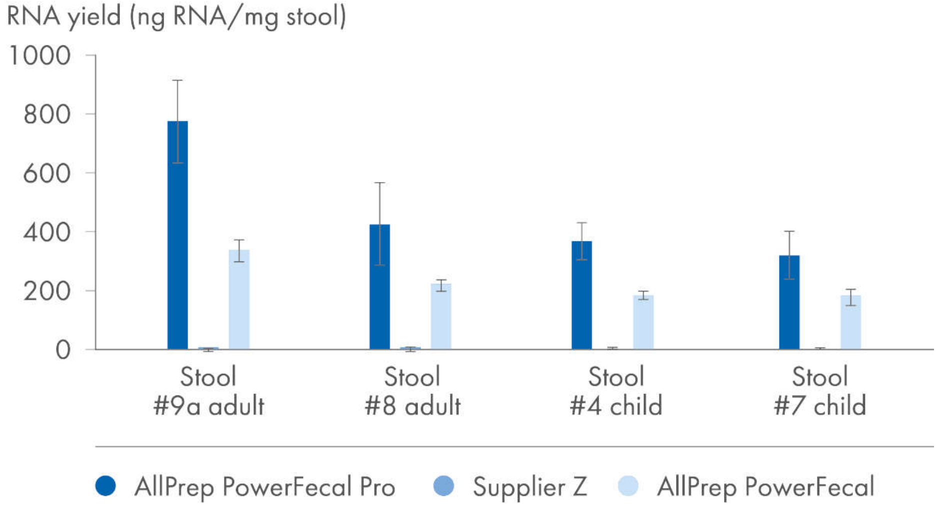
AllPrep PowerFecal Pro DNA/RNA

RNA and total NA from swabs

Simultaneous purification of microbial DNA and total RNA from the same stool sample

- Improved, second generation IRT
- Separates RNA and DNA from the same sample into different eluates in one procedure
- Optimized lysis for increased DNA and RNA yields
- RNA and DNA for metagenomic and metatranscriptomic analysis

AllPrep PowerFecal Pro DNA/RNA Kit shows the highest RNA yields in all four stool samples



- Four frozen stool samples were compares in triplicates; two samples from adults and two from children
- The samples were extracted using one commercially available kit and the legacy AllPrep PowerFecal DNA/RNA Kit
- The RNA yield was quantified by QIAxpert Instrument (high-speed spectrophotometer)

Did you know the “AllPrep” kits come in red QIAGEN boxes?

The AllPrep PowerFecal Pro DNA/RNA, launched in May 2022, is the upgraded version of the AllPrep PowerFecal DNA/RNA

Data obtained using experiments conducted by QIAGEN R&D in Hilden, Germany

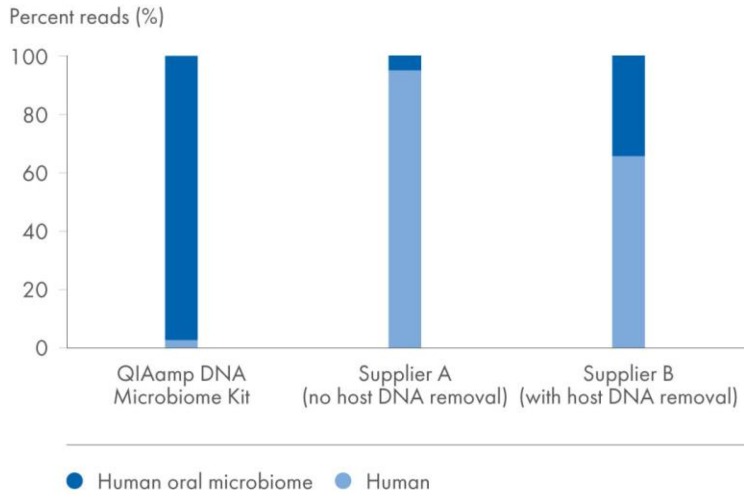
QIAamp DNA Microbiome Kit

DNA from swabs

Isolation of bacterial DNA from swabs and body fluids

- Effective depletion of host DNA
- Optimized mechanical and chemical cell lysis

Effective host DNA removal by the QIAamp DNA Microbiome Kit enhances whole metagenome shotgun sequencing results



DNA isolated from buccal swabs using the QIAamp DNA Microbiome Kit or solutions from alternative suppliers was analyzed by whole metagenome shotgun sequencing on the Illumina MiSeq platform

Removal of host DNA increases the coverage of microbial reads in sequencing experiments

The QIAamp DNA Microbiome Kit efficiently removes host DNA by differential lysis of host cells and subsequent enzymatic digestion of host DNA

Then, using a combination of mechanical and chemical lysis, intact cells are efficiently lysed, and the released bacterial DNA is purified using proven QIAamp chemistry

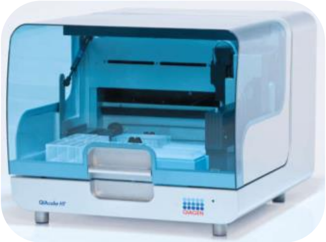
"Human DNA in undepleted CF sputum accounted for 94.3% of the total DNA. Saponin, the NEBNext kit and the QIAamp kit reduced human DNA levels by an average of 38.7%, 61.8% and 94.8%, respectively. None of the depletion methods reduced total bacterial DNA concentrations. QIAamp depletion did not influence taxa richness or alpha diversity however, alterations to the core genera were noted following depletion.

While all methods reduced human DNA in the CF sputum samples, the QIAamp DNA microbiome kit reduced Human DNA levels significantly while leaving bacterial DNA levels unchanged..”

– Klosinka, K. et al. Reducing human DNA bias in cystic fibrosis airway specimens for microbiome analysis, *J Microbiol Methods.* 2022;200:106540.

Data obtained using experiments conducted by QIAGEN R&D in Hilden, Germany

Select your automated solution based on your needs

	Instrument	Technology	Samples per run	Features
 QIAsphere	**QIAcube Connect with QIAsphere**	Spin-column-based	Up to 12	• Automates over 80 QIAGEN kits with over 140 standard protocols for DNA, RNA and protein sample processing • Optional protocol customization expands the use to over 3000 protocols
	**QIAcube HT**	Silica membrane technology	Up to 96	• Mid- to high-throughput solution with dedicated kits for microbial DNA preparation • User-friendly software allows for easy data management and documentation
	**QIAsymphony SP**	QIAGEN magnetic-particles chemistry	1–96 samples in 4 batches	• Flexible loading of new samples during a run • Protocols customizable (protocol steps, labware, etc.) on demand • Traceability and LIMS compatibility

The QIAsphere remote instrument-monitoring app gives full connectivity so you can step out of the lab to ponder on your research while keeping an eye on your instrument run status

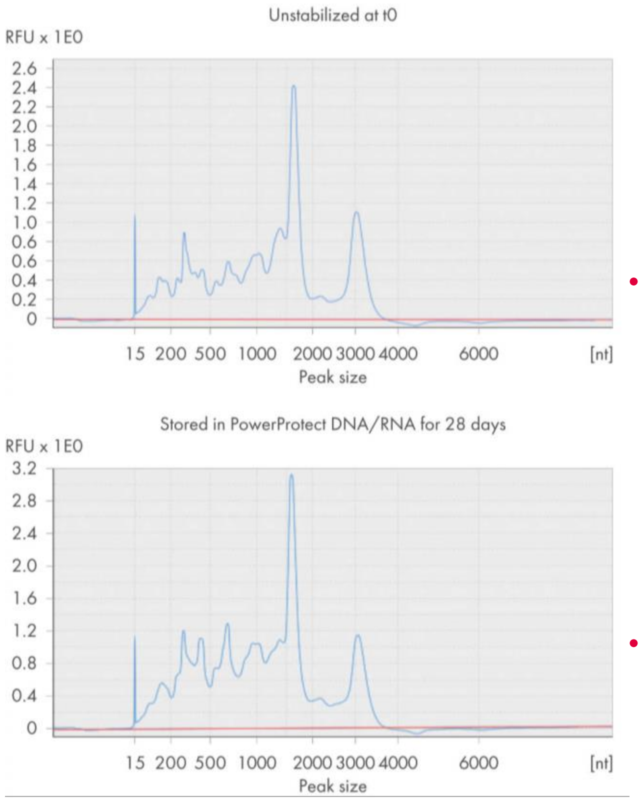
Stay alert to important instrument events with QIAsphere's push notifications or check maintenance status and manage run reports from anywhere or store them locally at any time

Size and integrity assessment made easy

QIAxcel Connect Capillary gel electrophoresis system

- Convenient run setup and cost efficiency with ready-to-use gel cartridges
- Fast turnaround with 12 samples in ~10 minutes and up to 96 samples in a single run
- Sensitive detection of total RNA to 50 pg/µL and DNA fragments down to 5 pg/µL
- User-independent nucleic acid integrity assessment with metrics like RIS (RNA integrity score) or DV200
- NGS library assessment, including the setting of pass/fail criteria based on respective kit specifications

QIAxcel ScreenGel electropherograms confirms RNA quality in terms of the integrity of total RNA samples



- Stool sample (unstabilized at t0 and stored in PowerProtect DNA/RNA for 28 days) and extracted with RNeasy PowerFecal Pro
- The two distinct ribosomal peaks correspond to 16S and 23S

Data obtained using experiments conducted by QIAGEN R&D in Hilden, Germany

Metagenomics or whole genome sequencing

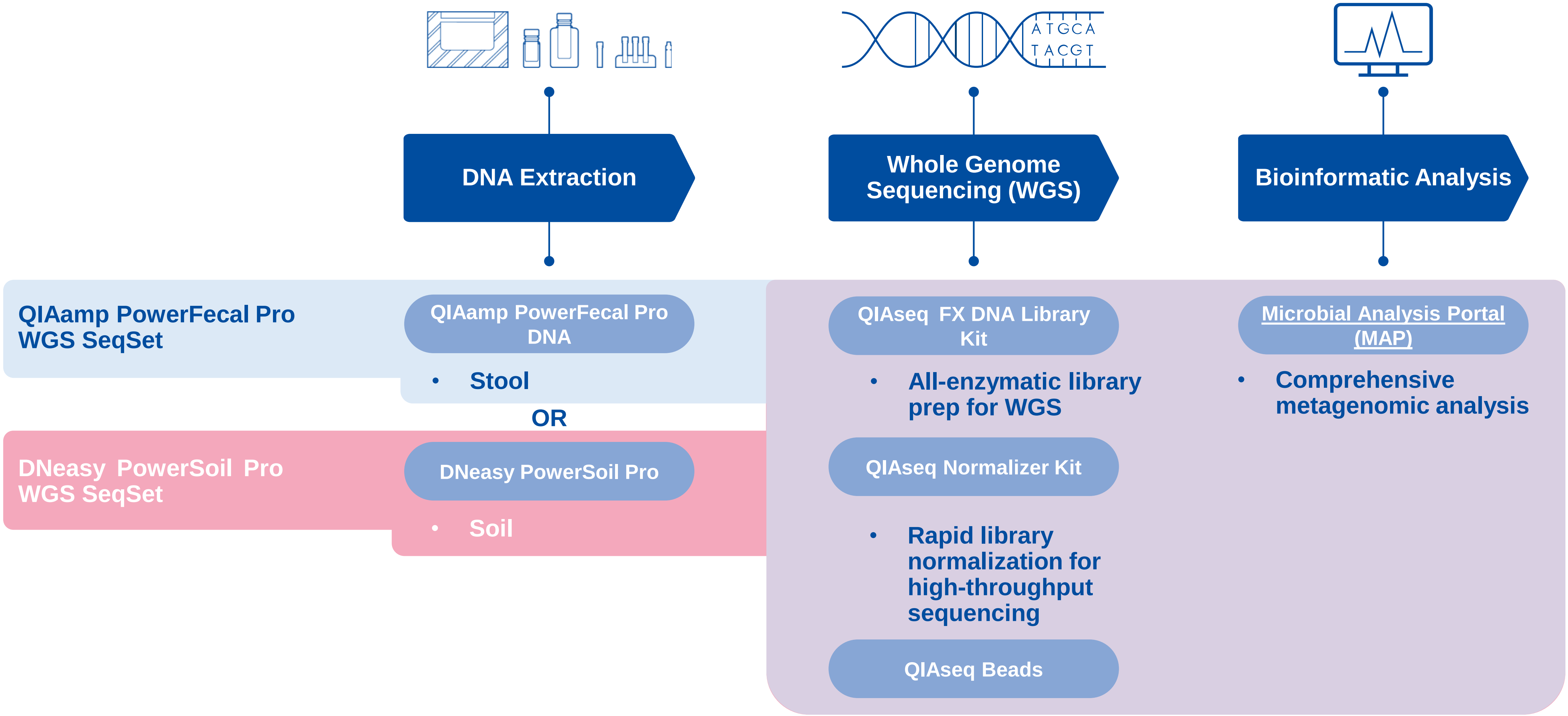
QIAseq FX DNA Library Kit

- All-enzymatic library prep
- Streamlined 2.5-hour workflow from purified DNA to NGS library
- High library complexity and uniform coverage maximizes interpretable data

Microbiome WGS SeqSets

- Sets tailored for microbiome research
- All-in-one sets, including all that you need for DNA extraction, library preparation and Mircobal Analysis Platfrom (MAP) digital analysis
- Available for stool and soil samples

All-in-one sets tailored for microbiome research
Microbiome WGS SeqSets



DNA Extraction

Whole Genome Sequencing (WGS)

Bioinformatic Analysis

QIAamp PowerFecal Pro WGS SeqSet

QIAamp PowerFecal Pro DNA

- Stool

OR

DNeasy PowerSoil Pro WGS SeqSet

DNeasy PowerSoil Pro

- Soil

QIAseq FX DNA Library Kit

- All-enzymatic library prep for WGS

QIAseq Normalizer Kit

- Rapid library normalization for high-throughput sequencing

QIAseq Beads

Microbial Analysis Portal (MAP)

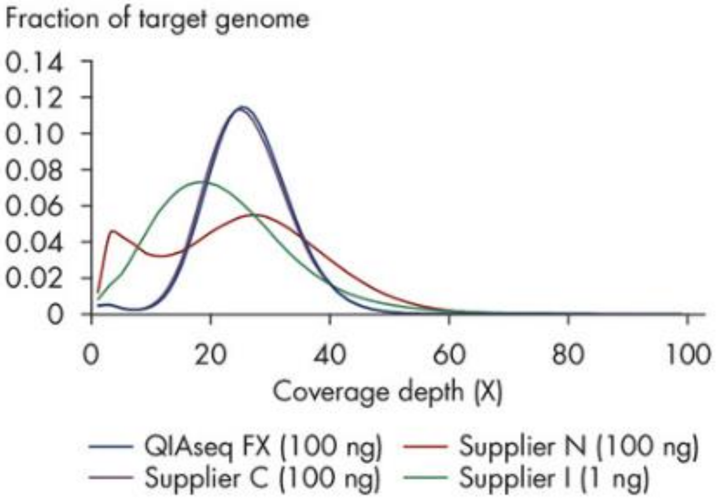
- Comprehensive metagenomic analysis

Metagenomics or whole genome sequencing with an all-enzymatic library prep

QIAseq FX DNA Library Kit

- Streamlined 2.5-hour workflow from purified DNA to NGS library
- High library complexity and uniform coverage maximizes interpretable data
- Unique dual index (UDI) adapters available for multiplexing up to 384 samples
- Fragment size, input amount and batch size customizable to any sequencing experiment
- Flexible DNA inputs of 20 pg –1 µg

Better coverage distribution



- The input was 100 ng samples of an equimolar mixture of gDNA from three bacterial species with vastly different GC contents: *Fusobacterium nucleatum* with 27% GC; *Escherichia coli* with 50% GC; and *Bordetella pertussis* with 67% GC (except the sample undergoing tagmentation, as only specific input amounts are accepted).
- The single, narrow peak for the library created with QIAseq FX DNA Library Kit shows that most genomic targets have very similar total coverage depth, comparable to DNA fragmented by mechanical shearing

"More specifically, we recommend protocol B (QIAseq FX DNA Library Kit) for taxonomic profiling based on its high accuracy of quantification of the DNA mock community, low GC bias, and excellent transferability across laboratories owing to the use of enzymatic DNA fragmentation"

– Tourlousse DM et al. Validation and standardization of DNA extraction and library construction methods for metagenomics-based human fecal microbiome measurements. *Microbiome*; 9 (1):95 2021

Are you dealing with highly fragmented DNA?

The QIAseq Ultralow Input Library Kit is highly suited for fragmented DNA <1000 bp and/or a DIN of <3

Processes low input quantities of 10 pg – 100 ng while providing similar features and benefits as QIAseq FX DNA Library Kit

Performing multiplexed sequencing?

The **QIAseq Normalizer Kit** quickly normalizes libraries without library quantification

Data obtained using experiments conducted by QIAGEN R&D in Hilden, Germany

16S/ITS sequencing with a phased primer approach

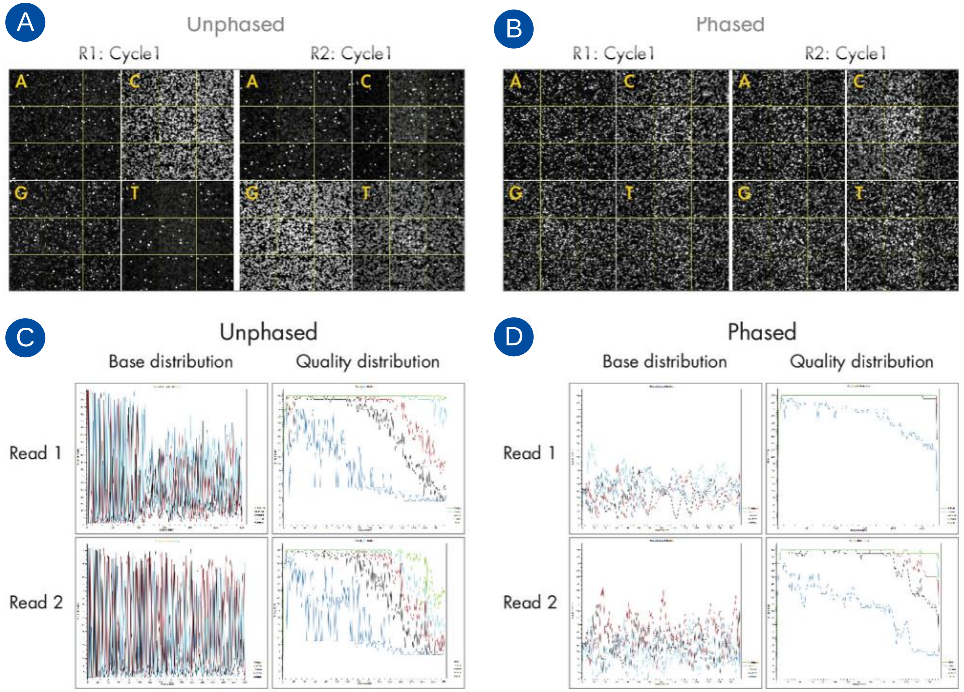
- Interrogate all bacterial 16S rRNA gene variable regions and fungal ITS regions
- The use of "phased primers" increases base diversity, leading to an increase in quality scores
- Low-bioburden reagents minimize background contamination
- DNA input can be as low as 1 pg to profile low-biomass samples

For robust profiling of bacterial and fungal communities:
QIAseq 16S/ITS Region Panels

Select your target regions and configure on: **GeneGlobe Design & Analysis Hub**

For screening a panel of variable regions and more robust bacterial profiling:
QIAseq 16S/ITS Screening Panel

Phased primers increase base diversity and quality scores



- Fluorescent images (top row) taken from the first cycle of read 1 (R1) showing uneven base distribution in an unphased primer run (A) and more even base distribution in a phased primer run (B)
- Low base diversity and read quality scores (bottom row) are apparent in a run using unphased V3V4 primers (C) and significantly improved using phased V3V4 primers (D)

After sequencing, data is analyzed using the **QIAGEN Genomic Workbench Premium**

A custom workflow, which can be further edited as needed, is available for automating FASTQ file import, sample library demultiplexing, quality-controlled filtering and trimming, OUT clustering and secondary bioinformatics analysis

QIAseq 16S/ITS Smart Control is a synthetic DNA that can be used as a positive control for library construction steps

Data obtained using experiments conducted by QIAGEN R&D in Hilden, Germany

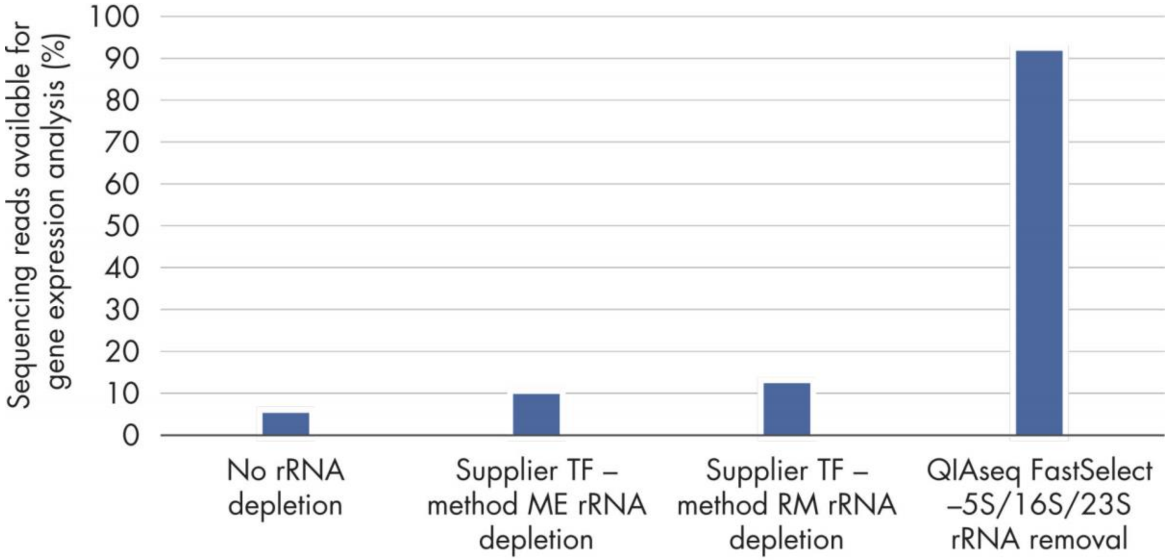
Efficient bacterial rRNA removal for improved read allocation

Library prep methods

QIAseq FastSelect – 5S/16S/23S

- A fast 20-minute workflow for pan-bacterial 5S/16S/23S rRNA removal from fragmented or full-length RNA
- Novel RNA removal mechanism that doesn't involve hybrid capture or enzymatic digestion
- Integrated into **QIAseq FastSelect RNA Library Kit** and **QIAseq UPXome RNA Library Kit** or combine FastSelect with **QIAseq Stranded RNA Library Kit** for whole transcript sequencing
- Compatible with Illumina, NEB and KAPA stranded RNA-seq library preparation kits
- In-silico design predicts blocking of >95% of all 5S, 16S and 23S rRNA database sequences

QIAseq FastSelect method frees up a substantial read budget for gene expression analysis



- Total RNA was isolated from Gut Microbiome Whole cell Mix (ATCC) using the RNeasy PowerMicrobiome Kit (QIAGEN)
- Stranded transcriptome libraries were then prepared from 1 µg aliquots of the RNA using the QIAseq Stranded Total RNA Lib Kit
- For rRNA depletion, three methods were used, as shown
- Sequencing was performed on a NextSeq 550, and data analysis was performed using QIAGEN CLC Genomics Workbench

Working with soil, water, stool or sludge samples?

QIAseq FastSelect – 5S/16S/23S was specifically designed for complex community microbial sample types with numerous and diverse bacterial populations

Want to get rid of Human rRNA for host-microbe studies or analysis of viruses?

Use QIAseq FastSelect Epidemiology Kit for both ribosomal RNA removal from bacteria and human, mouse and rat samples

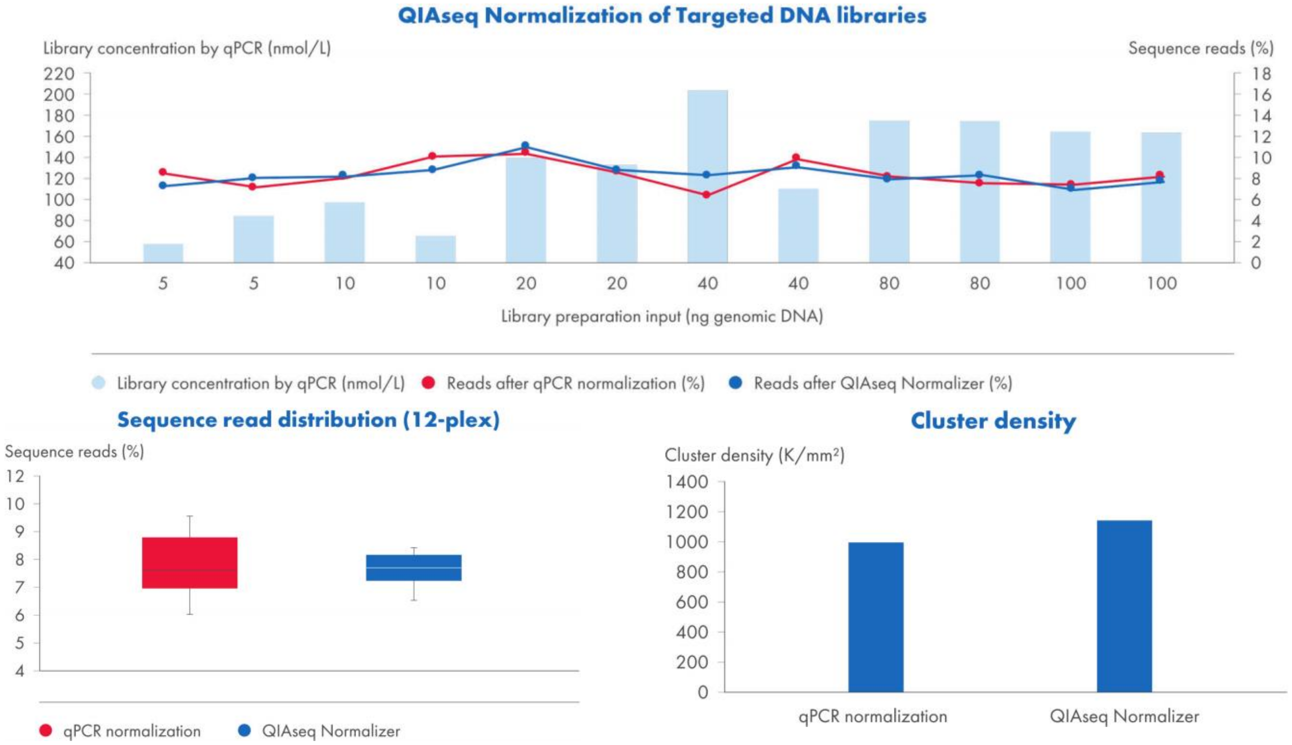
Data obtained using experiments conducted by QIAGEN R&D in Hilden, Germany

Rapid normalization for multiplexed sequencing

QIAseq Normalizer Kit

- Streamlined, 30-min benchtop protocol
- Achieve qPCR-level quality without the long workflow
- Works with a broad range of concentrations from 15 to over 300 nmol/L
- Libraries normalized libraries to 4 nmol/L for optimal clustering on Illumina flow cells
- Compatible with most Illumina libraries
- Automation-friendly workflow

Achieve library normalization without tedious library quantification



- Using 5–100 ng of gDNA, 12 QIAseq Targeted DNA libraries were prepared.
- All libraries were subjected to qPCR and diluted to 4 nmol/L before sequencing on the Ilumina MiSeq (V2 reagents, 2x150 bp paired-end)
- For comparison, the same libraries were normalized using the QIAseq Universal Normalizer Kit and sequenced on the Illumina MiSeq

Compatible QIAseq kits with QIAseq **Library** Normalizer

- QIAseq FX DNA Library kit
- QIAseq 1-Step Amplicon Library Kit
- QIAseq Ultralow Input Kit

Compatible QIAseq kits with QIAseq **Universal** Normalizer

- QIAseq FastSelect RNA Library Kits
- QIAseq UPXome RNA Library Kits
- QIAseq 16S/ITS Screening Panels and Index Kits

Flexible library preparation methods for metatranscriptome sequencing

QIAseq FastSelect rRNA removal

- Efficient bacterial rRNA removal for improved read allocation in metatranscriptomic studies
- Stand-alone kit for bacterial rRNA removal: **QIAseq FastSelect –5S/16S/23S**
- Integrated into QIAseq FastSelect RNA Library Kit and QIAseq UPXome RNA Library Kit or combine FastSelect with QIAseq Stranded RNA Library Kit for whole transcript sequencing

QIAseq FastSelect RNA Lib Bacteria Kit

For meta-transcriptomic studies of bacteria; includes RNA library preparation reagents; QIAseq FastSelect –rRNA Bacteria for removal of ribosomal RNA and QIAseq Beads

- Simple and fast workflow; <5 hours
- Use with QIAseq Normalizer for rapid library normalization
- Up to 768 samples per flow cell lane

QIAseq UPXome RNA Lib Kit Bacteria

For meta-transcriptomic studies of bacteria; includes RNA library preparation reagents; QIAseq FastSelect –rRNA Bacteria for removal of ribosomal RNA and QIAseq Beads.

- Workflow for ultra-low input samples
- Suitable for high throughput analysis with a large number of samples where 8 to 24 libraries can be pooled
- Up to 18,432 samples possible per flow cell lane

RNA input range per sample	QIAseq products for RNA Library Prep
0.5 to 100 ng	QIAseq UPXome RNA Library Kit
1 to 1000 ng	QIAseq FastSelect RNA Library Kit
More than 1000 ng	QIAseq FastSelect (rRNA removal) QIAseq Stranded Total RNA Lib Kit

Identify species target, AMR or virulence genes for profiling and surveillance

Application		Platform	Recommended assay	Configuration and customization	Data analysis	Good to know
NGS	Targeted sequencing	Illumina sequencer	QIAseq xHYB Viral and Bacterial Panels	N.A.	G	Hybrid capture-based targeted sequencing enables high-sensitivity sequence analysis of focus regions at a low cost and with faster turnaround times
	Whole genome sequencing	Illumina sequencer	QIAseq FX DNA Library Kit & QIAseq Normalizer Kit	N.A.	G CLC	All-enzymatic DNA library kit to go from purified DNA to NGS library in just 2.5 hours and fast normalization with library quantification
dPCR		QIAcuity	dPCR Microbial DNA Detection Assays QIAcuity UCP Probe PCR Kit QIAcuity OneStep Advanced Probe Kit	G	QIAcuity Software Suite	Nanoplate-based dPCR enables highest precision and absolute quantification with a robust workflow
qPCR		QIAquant Rotor-Gene Q	qPCR Microbial DNA Assays & Arrays		N.A.	Application-focused microbial target assays and arrays for detection and quantitation using lab-verified assays and for screening or LDTs in research and surveillance using user-developed assays
			QuantiNova Pathogen +IC Kit	N.A.		Ultrafast, simultaneous detection of viral RNA/DNA and bacterial DNA
PCR		N.A.	UCP Multiplex PCR	N.A.		Ultra-clean produced multiplex hot-start PCR for detection or library amplification.

G **GeneGlobe Design & Analysis Hub**

CLC: QIAGEN CLC Genomics Workbench

Profiling and detection of antimicrobial resistance and virulence genes

Application		Platform	Recommended assay	Configuration and customization	Data analysis	Good to know
NGS	Targeted sequencing	Illumina sequencer	QIAseq xHYB Viral and Bacterial Panels	N.A.	G	Hybrid capture-based targeted sequencing enables high-sensitivity sequence analysis of focus regions at a low cost and faster turnaround times
	Whole genome sequencing	Illumina sequencer	QIAseq FX DNA Library Kit & QIAseq Normalizer Kit	N.A.	CLC, G	An all-enzymatic library preparation kit proven in multiple microbial research studies and fast normalization with library quantification
dPCR		QIAcuity	dPCR Microbial DNA Detection assays: • dPCR AMR Assays • dPCR Virulence Gene Assays	G	QIAcuity Software Suite	Nanoplate-based dPCR enables highest precision and absolute quantification with a robust workflow
qPCR		QIAquant RotorGene Q	qPCR Microbial DNA Assays & Arrays		N.A.	Application-focused microbial target assay and arrays with guaranteed detection and quantitation using lab-verified assays

G **GeneGlobe Design & Analysis Hub**

CLC: QIAGEN CLC Genomics Workbench

Targeted viral and bacterial sequencing

Microbial ID

AMR, VG

QIAseq xHYB Viral and Bacterial Panels

- Target only your genes of interest – no need to “waste” reads on non-relevant genome segments
- Detects low-abundance genes with high-level enrichment – guaranteed to capture your region of interest
- Multiplex up to 384 samples when paired with the QIAseq FX DNA Library Kit

QIAseq xHYB AMR Panel

Detect 2786 antimicrobial resistance genes (6200+ AMR markers) in bacteria and consists of targets pulled from the QIAGEN CLC QMI-AR database

QIAseq xHYB Viral Respiratory Panel

Detect and characterize 89 separate viral targets, including SARS-CoV-2, influenza, rhinovirus, enterovirus and more

QIAseq xHYB Adventitious Agent Panel

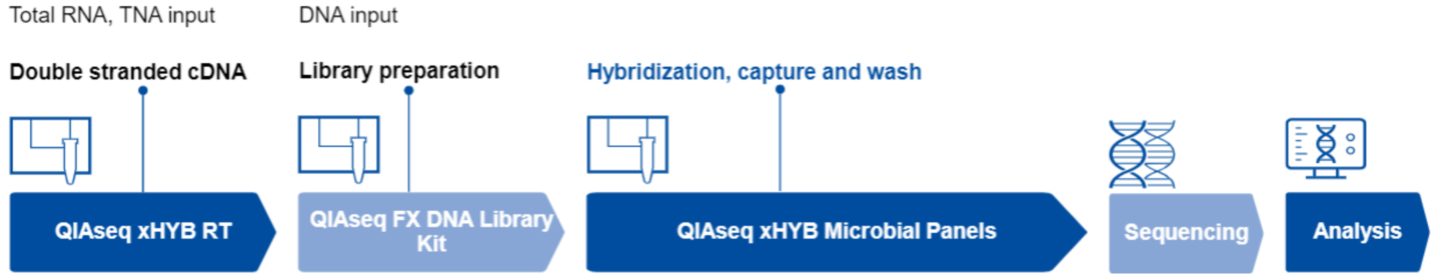
Detect 132 separate viral targets, including human adenovirus, norovirus, rotavirus, influenza, SARS-CoV- 2, HPV, Epstein-Barr, HIV, hepatitis A/B viruses and more

QIAseq xHYB Viral STI Panel

Detect common STI viruses: HBV, HIV-1 and nineteen types of high-risk HPV

QIAseq xHYB Microbial Target List

A flexible sample-to-sequencing workflow:



Resulting FASTQ can be analyzed via the analysis portal on GeneGlobe or via the QIAGEN CLC Genomics Workbench

GeneGlobe Analysis Portal offers a simplified overview of the sequencing results for identifying and quantifying either viral species or antimicrobial resistance genes detected in any samples

QIAGEN CLC Genomic Workbench is also available for deeper analysis for taxonomic identification, variant analysis, phylogenetic trees and viral integration sites

Digital PCR

Microbial ID

AMR, VG

QIAcuity – a nanoplate-based digital PCR system

dPCR Microbial DNA Detection Assays:

1. Accuracy and precision
2. Parallel quantification of RNA and DNA targets
3. Parallel quantification of up to 5 virulence target genes
4. Parallel quantification of up to 5 AMR target genes

QIAcuity – a nanoplate-based digital PCR system

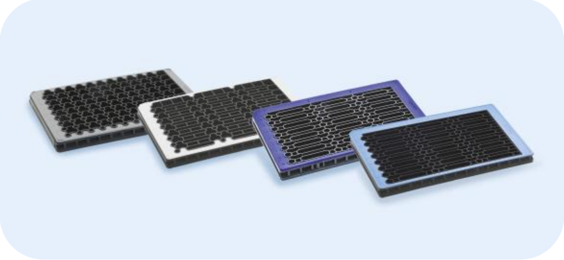
Digital PCR

QIAcuity dPCR Instruments

Fully integrated instrument design; One instrument for partitioning, cycling and imaging

Multiplexing – up to 5 channels

Fast workflow – up to 96 samples in ~2 hours



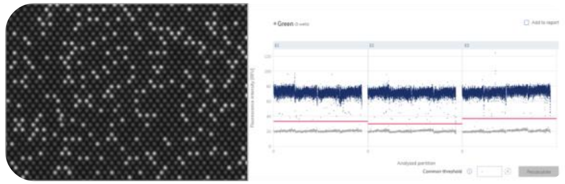
QIAcuity Nanoplates

Nanoplate 26k 8-well/24-well (26,000 partitions)

Nanoplate 8.5k 24-well/ 96-well (8500 partitions)

QIAcuity EvaGreen, Probe PCR, UCP Probe PCR and OneStep Advanced Probe Kits

Nanoplate-optimized chemistry



QIAcuity dPCR Software Suite

Data visualization

Primary and secondary analyses

Top benefits:

Absolute target quantification

- No need for references/standard curves

Higher tolerance to inhibitors

- Due to partitioning and endpoint measurement

High precision

- Detect minute fold changes (<2 fold)

High analytical sensitivity

- Detection of <10 copies/reaction
- Analysis of up to 27 µL template/reaction

High reproducibility

- Eliminate amplification efficiency bias

Large dynamic range

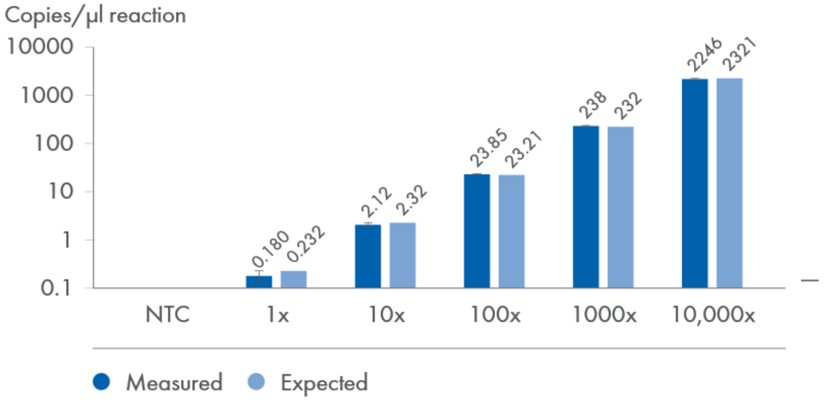
- Quantification of up to 200,000 copies/reaction

Accuracy and precision with dPCR Microbial DNA Detection Assays

Digital PCR

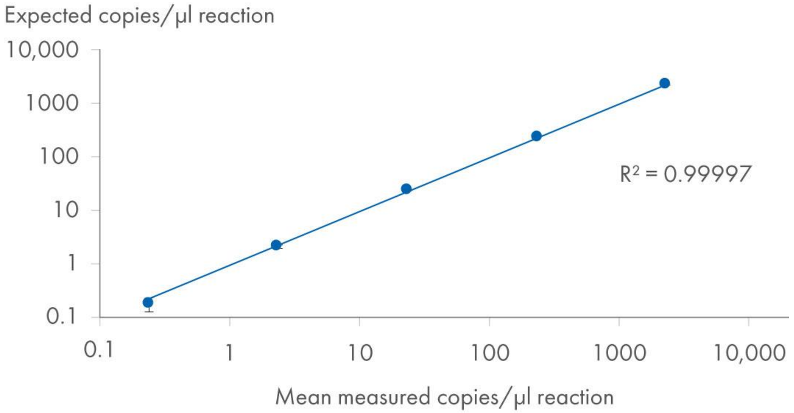
- Detect bacteria, fungi, viruses, parasites, virulence genes or antibiotic-resistance genes
- 685 probe-based assays each premixed and lyophilized in one tube, including over 200 wet-lab tested assays
- Selectable fluorophore (FAM, HEX, ROX, TAMRA, Cy5) enables multiplexing using a mix-and-match approach
- Over 35 wet-lab tested bundles of up to 5 assays combining common targets of interest in multiplex dPCR on the QIAcuity
- Compatible with OneStep Advanced Probe PCR Kit for detection of RNA viruses.
- Select your assays and bundles on [GeneGlobe Design & Analysis Hub]()

Accurate quantification of the NIST gDNA reference standard 8376 from the bacterium *Shigella sonnei* as input



Single-copy gene assay from the dPCR Microbial DNA Detection Assay portfolio to detect one target molecule per genome. Bar chart shows the mean measured concentrations (copies/µL) of three replicates

Precise quantification across a 4-log dynamic range of the NIST gDNA reference standard 8376 from the bacterium *Shigella sonnei*



Individual datapoints represent mean values of 3 replicates each

Data obtained using experiments conducted by QIAGEN R&D in Hilden, Germany

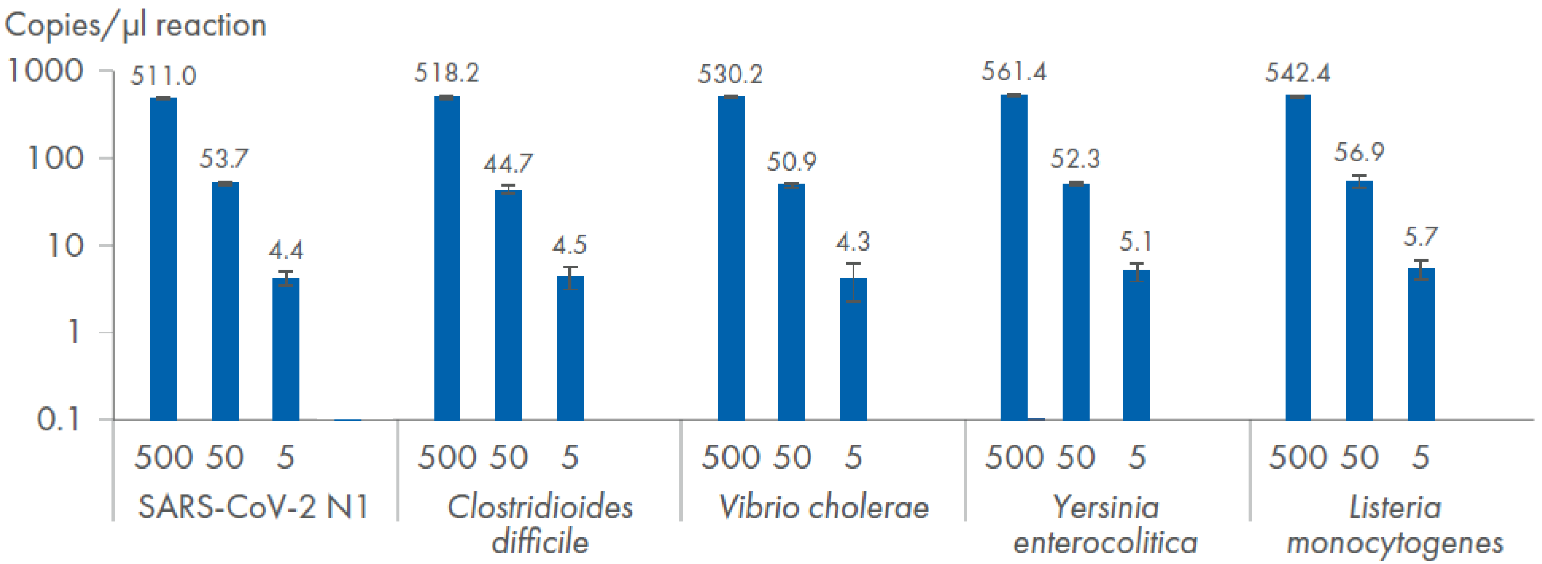
Parallel quantification of RNA and DNA targets

Digital PCR

The combination of the OneStep Advanced Probe PCR Kit with the dPCR Microbial DNA Detection Assays enables:

- Multiplex dPCR quantification of DNA and RNA targets
- Simple and fast one-step RT dPCR workflow on the QIAcuity in less than 3 hours
- Suitability for detection of RNA viruses in e.g., wastewater surveillance approaches
- Improved tolerance towards inhibitors contained in the extracted DNA and/or RNA sample
- Improved performance in multiplex dPCR reactions

Detect viral RNA and microbial DNA together in a multiplex reaction



- A mixture of four bacterial gDNAs (*Clostridioides difficile, Vibrio cholerae, Yersinia enterocolitica, Listeria monocytogenes*) and SARS-CoV-2 RNA was used as input
- dPCR, with three replicates per condition, was run using 8.5k 96-well Nanoplates and the QIAcuity OneStep Advanced Probe Kit on the QIAcuity Digital PCR System
- Three template dilutions with 500, 50 and 5 copies/µL were used
- Bar chart shows the mean measured concentrations (copies/µL) of three replicates for each of the five targets

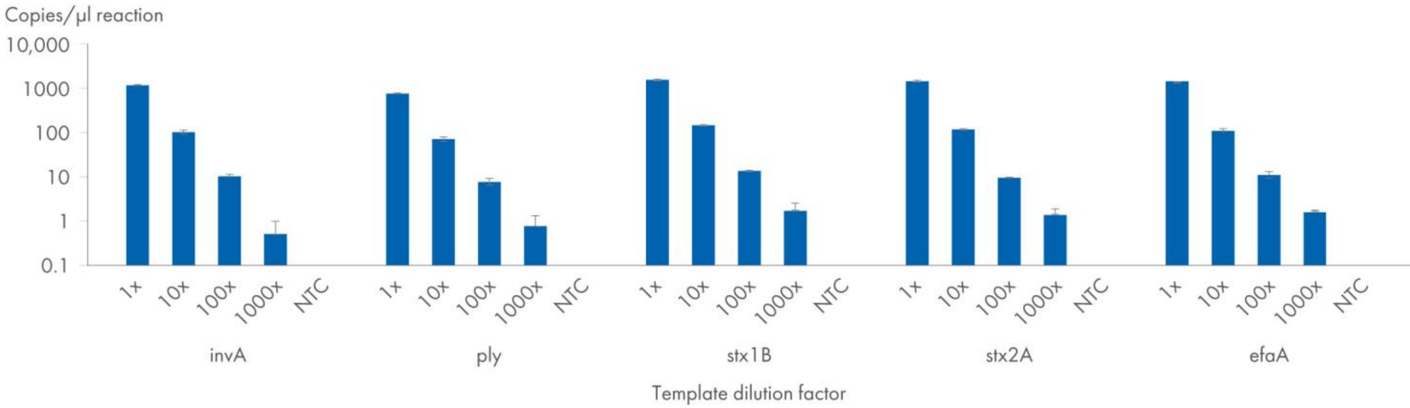
Data obtained using experiments conducted by QIAGEN R&D in Hilden, Germany

Parallel quantification of up to five virulence target genes

Digital PCR

- Six virulence gene assay bundles were wet-lab tested
- Individual bundles can be configured on the GeneGlobe Design & Analysis Hub

Parallel quantification of five virulence target genes – virulence genes 6 bundle



- Four dilutions of positive control input template (PMC) starting with 1 µL input and diluting down to 0.001 µL and no template controls (NTC)
- Three replicates per condition were tested

Bundle name	Assay name
Virulence genes 1	Minor fimbrial subunit (fimH)
	Gamma-hemolysin component B (hlgB)
	Shiga-like toxin 1 subunit B encoded within prophage CP-933V
	Shiga toxin subunit B; receptor binding subunit
	Accessory cholera enterotoxin (ace)
Virulence genes 2	*ply*
	stx1B
	stx2A
	invA
	stxB
Virulence genes 3	*wbkA*
	ptxA
	ace (E. faecalis)
	ace (V. cholerae)
	efaA
Virulence genes 4	glycosyltransferase wbkA
	pertussis toxin subunit 1 precursor
	collagen adhesin protein ace
	accessory cholera enterotoxin ace
	endocarditis specific antigen
Virulence genes 5	Minor fimbrial subunit
	shiga-like toxin 1 subunit B encoded within prophage CP-933V
	gamma-hemolysin component B
	invasion protein invA
	endocarditis specific antigen
Virulence genes 6	*invA*
	ply
	stx1B
	stx2A
	efaA

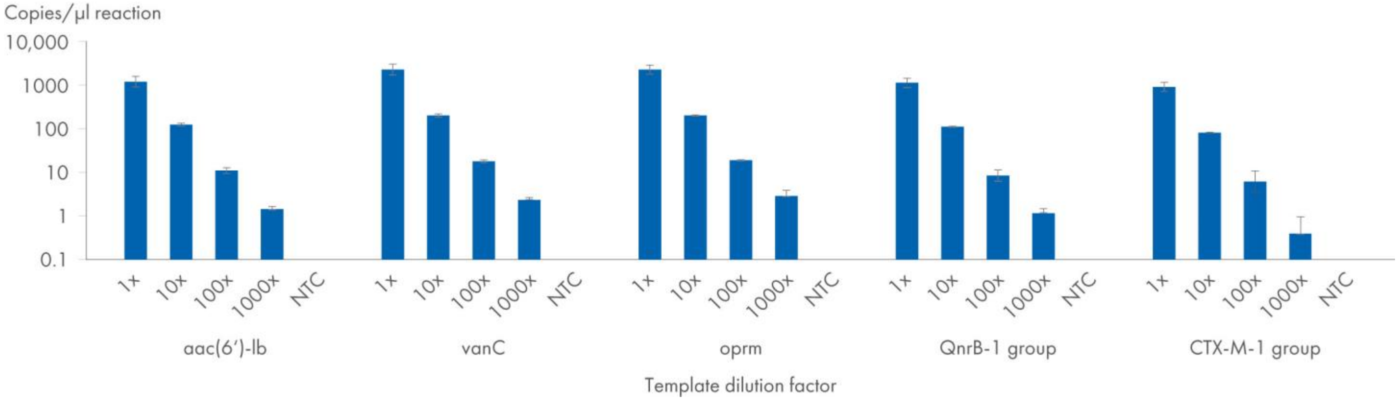
Data obtained using experiments conducted by QIAGEN R&D in Hilden, Germany

Parallel quantification of up to five AMR target genes

Digital PCR

- Five resistance gene assay bundles were wet-lab tested
- Individual bundles can be configured on the GeneGlobe Design & Analysis Hub

Parallel quantification of five AMR target genes – resistance genes 3 bundle



- Four dilutions of positive control input template (PMC) starting with 1 µL input and diluting down to 0.001 µL and no template controls (NTC)
- Three replicates per condition were tested

Bundle name	Assay name
Resistance genes 1	Fluoroquinolone resistance gene QnrS
	Class D beta-lactamase OXA-10 group
	Vancomycin resistance gene vanB
	Tetracycline efflux pump gene tetA
	Tetracycline efflux pump gene tetB
Resistance genes 2	Fluoroquinolone resistance geneQepA
	Class B beta-lactamase blaVIM-1 group
	Class D beta-lactamase OXA-48 group
	Sulfonamide resistance gene sul1
	Class D beta-lactamase OXA-58 group
Resistance genes 3	*aac(6')-Ib*
	vanC
	oprm
	QnrB-1 group
	CTX-M-1 Group
Resistance genes 4	Class C beta-lactamase ACC-1 Group
	Class C beta-lactamase CFE-1
	VanC
	Class C beta-lactamase dha
	Class C beta-lactamase fox
Resistance genes 5	Multidrug efflux pump protein OqxA (*E. coli, Klebsiella sp., Salmonella sp.*)
	fosA (Klebsiella sp.)
	Fluoroquinolone resistance QepA
	Class D beta-lactamase OXA-23 Group
	Class A beta-lactamase Per-1 Group

Data obtained using experiments conducted by QIAGEN R&D in Hilden, Germany

Microbial DNA qPCR assays for characterization of microbes and traits

Microbial ID

AMR, VG

Real-time qPCR for microbial identification and profiling with high sensitivity and specificity

- Uniform qPCR efficiency and amplification conditions
- Experimentally verified microbial DNA qPCR assays with high specificity and sensitivity
- 5′ hydrolysis probe detection for high sensitivity and specificity

A broad range of assays and panels to detect microbial species, virulence genes or antibiotic resistance genes

Microbial DNA qPCR Assays

Experimentally verified assays with high sensitivity and specificity

Microbial DNA qPCR Assay Kits

Complete kit for qPCR-based microbial detection, with assay, controls, and reagents

Microbial DNA qPCR Multi-Assay Kits

Includes 3–6 assay tubes in one box

Microbial DNA qPCR Panels

Collections of assays to identify and profile microbial species, virulence factor genes or antibiotic resistance genes

Each panel includes controls for host DNA to verify the presence of bacterial DNA and the success of the PCR reaction

Configure at GeneGlobe – find or custom design the right target-specific assays and panels to research your biological targets of interest

AMR gene profiling using Microbial DNA qPCR panels – a use case

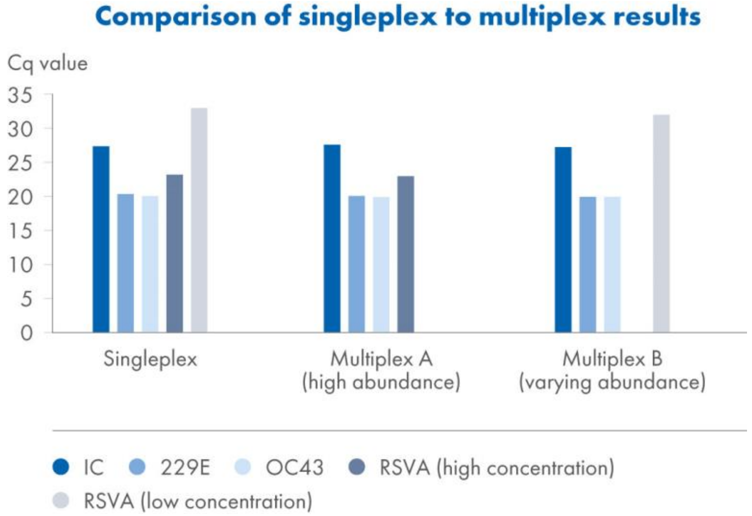
Young, C.C.W. et al (2022) Antibiotic resistance genes of public health importance in livestock and humans in an informal urban community in Nepal, Nature Scientific Reports

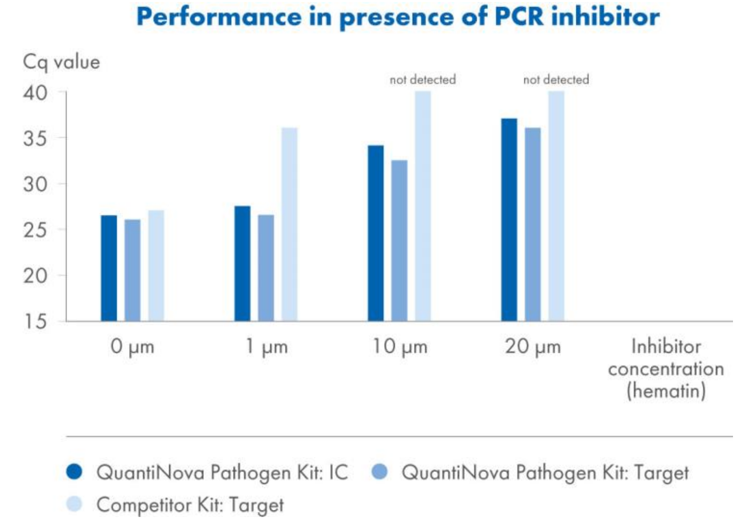
Multiplex qPCR detection – QuantiNova Pathogen kits with Internal Control

Microbial ID

For ultrafast, simultaneous detection of viral RNA/DNA and bacterial DNA, including in-process safety measures

- Pre-optimized internal controls for extraction and amplification at no extra cost
- Four-plex (RT)-PCR for detection of both pathogen targets and internal control
- Unique two-phase hot-start procedure for convenient room-temperature setup (fully automatable)
- Stable RT included in the master mix, providing one easy-to-use protocol
- Visual pipetting control to minimize error





Reliable multiplex detection of low and high abundant targets equivalent to singleplex results

- Coronavirus 229E, OC43, human Respiratory Syncytial Virus A and QuantiNova Internal Control RNA were amplified in singleplex and multiplex PCR showing highly consistent results.
- In multiplex B reactions, no competitive effects or sensitivity loss for low-concentrated RSVA was observed in the presence of various high-abundant targets with Delta Cq of more than 10

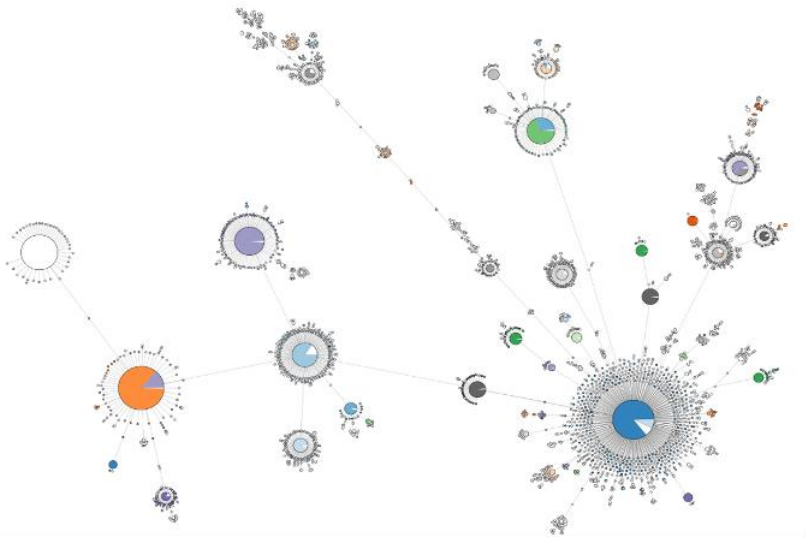
Robust performance and IC alert in presence of PCR inhibitors

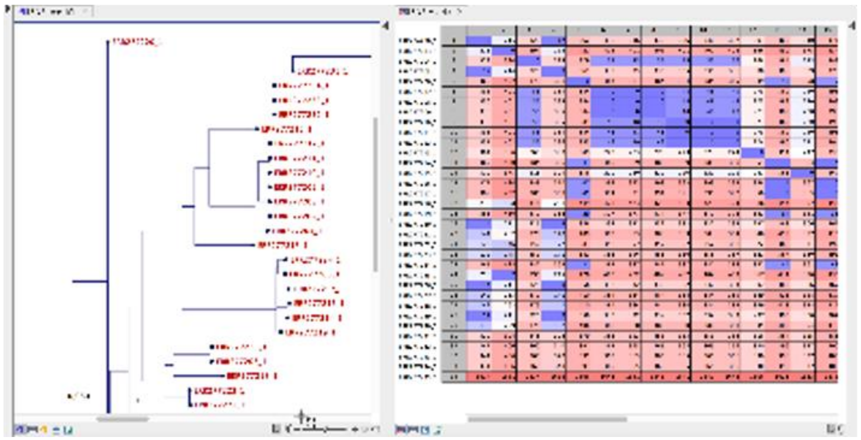
- Increasing concentrations of a common inhibitor (hematin) were spiked into PCR reactions using QuantiNova Pathogen Kit and a commonly used Competitor Kit
- While QuantiNova chemistry showed excellent inhibitor robustness, the QuantiNova Internal Control clearly indicated the presence of inhibitors by Cq shifts of more than 2 Cq's, providing additional process safety

Data obtained using experiments conducted by QIAGEN R&D in Hilden, Germany

QIAGEN CLC Genomics Workbench Premium – a platform for microbial bioinformatic analysis

- NGS analysis of virus and bacterial outbreak
- Antimicrobial resistance analysis
- Easy access to relevant reference data
- Workflows for the analysis of data from targeted panels, WGS and whole metagenome samples
- Supports QIAseq and other panels with workflows bundled with reference data
- Tools for sequence alignment and phylogenetic analysis
- Tools for wg/cgMLST and k-mer and SNP-trees
- Rich, interactive visualizations





Graphical user interface

Easy onboarding with tutorials

"CLC Genomics Workbench […] does not require previous knowledge of Unix-based tools; it is arguably the most user-friendly [of the tools tested] and delivers reliable results for microbial identification and antimicrobial resistance gene detection."

– Couto N. et al. Critical steps in clinical shotgun metagenomics for the concomitant detection and typing of microbial pathogens [published correction appears in Sci Rep. 2019 Apr 17;9(1):6406]. Sci Rep. 2018;8(1):13767

GeneGlobe Design and Analysis Hub

The GeneGlobe Design and Analysis Hub streamlines the complete research cycle of target exploration, product configuration, data analysis and follow-up experiment planning – with just one tool: https://geneglobe.qiagen.com

GeneGlobe Design

- Supports customization and configuration of real-time PCR and NGS-based products
- Assays and panels can be configured to contain different fluorophores and chemical modifications or to fit specific instruments
- PCR customization tools can be used to design assays and panels that interrogate specific targets of interest
- NGS customization tools can be used to create panels that contain the specific targets most pertinent to the researcher

Visit: https://geneglobe.qiagen.com/customize

GeneGlobe Data Analysis Center

- Includes various web-based tools to streamline and simplify your data analysis
- Access is complimentary when analyzing data acquired with QIAGEN kits
- The real-time PCR modules transform threshold cycle (Cq) values to calculated results for gene and miRNA expression, somatic mutation detection and copy number measurements from QIAGEN PCR assays and panels
- The NGS modules support primary and secondary analysis of QIAseq NGS library prep kits and target enrichment panels.
- The new RNA-seq Analysis Portal takes your NGS analyses further and provides a fully integrated analysis and biomarker discovery workflow

Visit: https://geneglobe.qiagen.com/analyze

Microbial Analysis Portal (MAP)

Comprehensive

- **Advanced taxonomic and antimicrobial resistance**
- **Powered by QIAGEN CLC Genomics workbench**

Easy

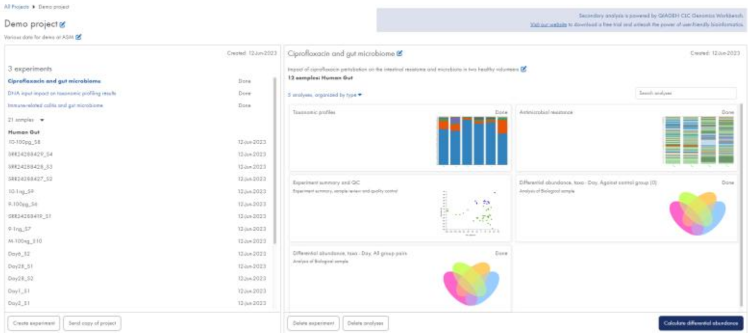
- **Standardized analysis accessible to non-bioinformaticians**
- **Quickly get the breakdown of the microbial species in a sample**

Online

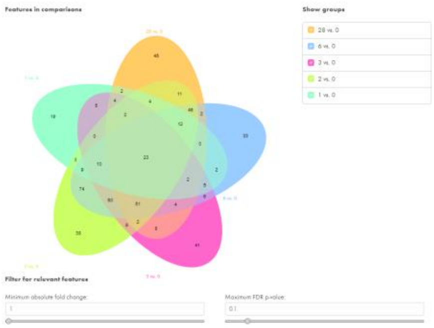
- **Web-based platform**
- **Access is included as standard with QIAamp PowerFecal Pro WGS Seqset or DNeasy PowerSoil Pro WGS SeqSet**

Features include:

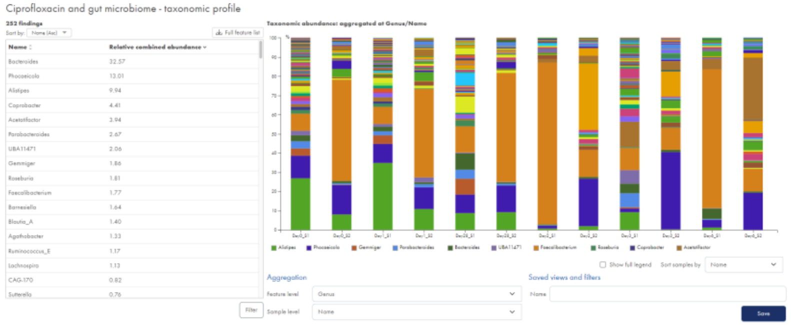
CLC genomics workbench



Differential abundance calculation



Taxonomic ID and abundance



AMR abundance and profiling

RNA-seq Analysis Portal – easy data analysis

Comprehensive

- Analyzes data from 18 different species using proven published algorithms
- Analyzes data from QIAseq and other major RNA Library Kits

Easy

- Takes the stress out of data analysis
- Fast-tracks path to gene expression insights
- Integrates results with dPCR and qPCR verification

Fast

- Goes from FASTQ files to pathway analysis insights in hours instead of days

Online

- Performs analyses anytime, anywhere

Demo version

- Allows software evaluation using demo data without registering or logging in

Free trial

- Allows software evaluation using real data

Graphics tell your story

All Projects › Demo project v2.5 › QIAseq miRNA on tissue types › Kidney vs. Liver

Kidney vs. Liver

Features: 431 of 2632

Sort by: Name (Asc)

Name	Fold change	FDR p-value	P-value
hsa-let-7a-2-3p	3.11	0.03	0.01
hsa-let-7a-3p	1.23	1.35e-3	4.13e-4
hsa-let-7c-5p	-1.37	7.30e-11	1.29e-11
hsa-let-7d-5p	1.22	1.24e-4	3.36e-5
hsa-let-7e-5p	-1.19	7.56e-4	2.24e-4
hsa-let-7f-1-3p	1.51	0.05	0.02
hsa-let-7g-5p	1.13	0.02	7.70e-3

Biological insights: Diseases and f

Diseases and functions	-log10 of pvalue	z-score
Nonobstructive azoospermia	70.554	-
Sporadic amyotrophic lateral sclerosis	58.550	-
Sporadic psychological disorder	55.029	-
Early stage invasive cervical squamous cell car...	52.747	-
Sporadic neurological disorder	49.719	-
Early stage squamous-cell carcinoma	48.857	-
Amyotrophic lateral sclerosis	48.139	-

View details

Filter
FDR p-value ≤ 0.1
Fold change < -1.1
Fold change > 1.1
Filter not saved
Biological insights filter: None selected

What's next?
Design follow-up experiments in GeneGlobe.

Powered by QIAGEN CLC Genomics Workbench and QIAGEN Ingenuity Pathway Analysis

RNA-seq Analysis Portal 3.0 George Quellhorst

1. Features table listing differentially expressed targets
2. Volcano plot graphs fold-change versus p-value
3. Heatmap clusters targets and samples
4. Biological insights lists related biological information
5. Filter narrow down the target list
6. What’s next helps design follow-up experiments

Access is included as standard with QIAseq RNA and miRNA library kits

Analysis credits can be purchased separately for analyzing data from the commonly used third-party kits

Genomic Services

Sample disruption → **Sample preparation** → **Analysis by NGS, dPCR or qPCR** → **Data analysis**

Genomic Services bacterial and fungal communities profiling:

- **DNA isolation** based on optimized bead-beating and IRT

- **End-to-end service:** We take care of every step, from sample preparation to data analysis
- **Improved sequencing output:** We help increase read and base quality
- **Guidance and flexibility:** We aid in designing your project and help you make the right decisions
- **Ready-to-publish data:** We deliver comprehensive reports and data packages and provide guidance on the next steps

Microbial profiling

- Microbiome analysis 16S/ITS
- Metagenomic sequencing

Viral genotyping

- SARS-CoV-2 whole genome sequencing

NGS

- Whole transcriptome-seq
- Targeted 3′-mRNA
- Targeted RNA-seq panels
- miRNA-seq
- Whole genome sequencing

Digital PCR services

Visit:
www.qiagen.com/applications/genomic-services

A comprehensive portfolio for microbiome and microbial identification applications

Back to intro slide

- TissueLyser III
- Vortex adapters

Sample disruption

- PowerBead Pro Tubes
- PowerBead Pro Plates

Stabilization (stool)

- PowerProtect DNA/RNA

- QIAcube Connect
- QIAcube HT
- QIAsymphony SP
- QIAxcel Connect for QC

Nucleic acid isolation

DNA

- QIAamp PowerFecal Pro DNA; QIAsymphony PowerFecal Pro DNA Kit; QIAamp DNA Microbiome
- DNeasy PowerSoil Pro DNeasy PowerMax Soil; MagAttract PowerSoil Pro
- DNeasy PowerWater; DNeasy PowerWater Sterivex; DNeasy PowerBiofilm

RNA

- RNeasy PowerFecal Pro
- RNeasy PowerSoil Total RNA; RNeasy PowerMax Soil Pro
- RNeasy PowerWater; RNeasy PowerBiofilm

DNA and RNA

- AllPrep PowerFecal Pro DNA/RNA; AllPrep PowerViral DNA/RNA; MagAttract PowerMicrobiome DNA/RNA

… and more

NGS

Microbial detection

- QIAseq xHYB Viral and Bacterial Panels

16S rRNA and ITS profiling

- QIAseq 16S/ITS Panels

Metagenomic shotgun sequencing

- QIAseq FX DNA Library Prep

Metatranscriptomics

- QIAseq FastSelect -5S/16S/23S; QIAseq FastSelect RNA Lib Bacteria Kit; QIAseq UPXome RNA Lib Kit Bacteria

Host gene expression analysis

- QIAseq FastSelect RNA Library Kit; QIAseq UPXome RNA Library Kit; … and more

Microbial-host interaction

- QIAseq FastSelect RNA Lib Epidemiology Kit; QIAseq UPXome Dual-seq RNA Lib Kit

Normalization

- QIAseq Normalizer Kits

- QIAcuity
- QIAquant
- Rotor-Gene Q
- QIAgility

dPCR, qPCR and PCR

dPCR

- dPCR Microbial DNA Detection Assays
- QIAcuity UCP Probe PCR Kit
- QIAcuity OneStep Advanced Probe Kit

qPCR/PCR

- Microbial DNA qPCR Assays and Arrays
- UCP Multiplex PCR
- QuantiNova Pathogen +IC Kit

Data analysis

- QIAGEN CLC Workbench Premium
- GeneGlobe Design & Analysis Hub
- RNA-seq Analysis Portal
- Microbial Analysis Portal
- QIAcuity Software Suite

Nucleic acid isolation, NGS & data analysis

- QIAamp PowerFecal Pro WGS SeqSet; DNeasy PowerSoil Pro WGS SeqSet

QIAGEN Genomic Services

Discover more at www.qiagen.com/applications/microbiome