



QIAseq® 16S/ITS panels

Cat. no. 333802, 333805, 333812, 333815, 333822, 333827, 333832

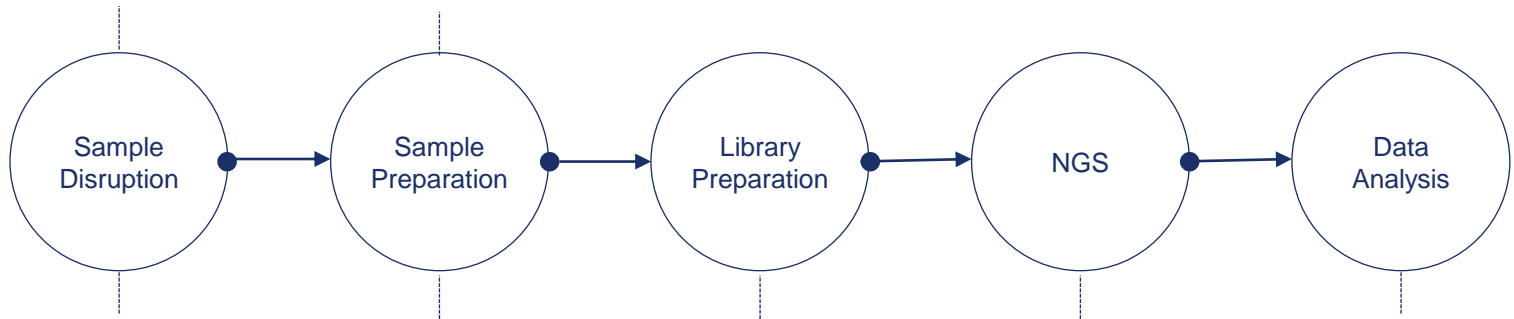
Combining flexibility and quality to give you the results you need

The QIAseq 16S/ITS panels provide several advantages, including:

- The power to interrogate all 16S rRNA gene variable regions and fungal ITS regions
- Phased primers that increase the quality of reads and base calling and eliminate the need for PhiX spike-in
- Low bioburden reagents that decrease background contamination
- The ability to monitor library construction steps and user-introduced contamination
- DNA inputs as low as 1 pg to enable analyses of low biomass samples

Instruments

- PowerLyzer® 24
- TissueLyser II
- Vortex adaptors
- QIAcube



Kits/Solutions

Microbiome Sample Prep Kits

QIAseq 16S/ITS panels

Microbial Genomics Pro Suite

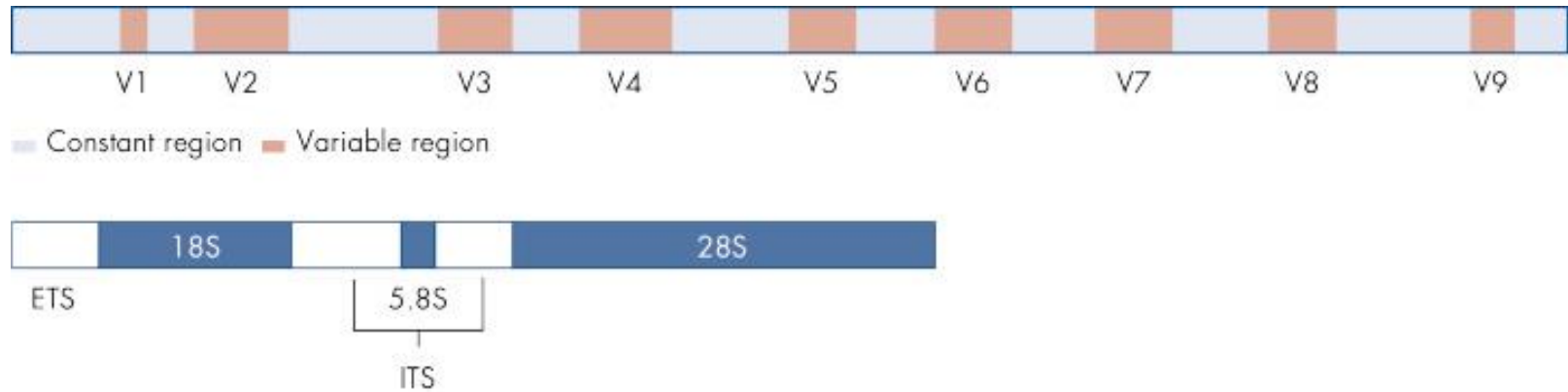
Customer benefits

- Optimized lysis and Inhibitor Removal Technology for pure, high quality DNA

- High-quality libraries for unbiased metagenomic sequencing

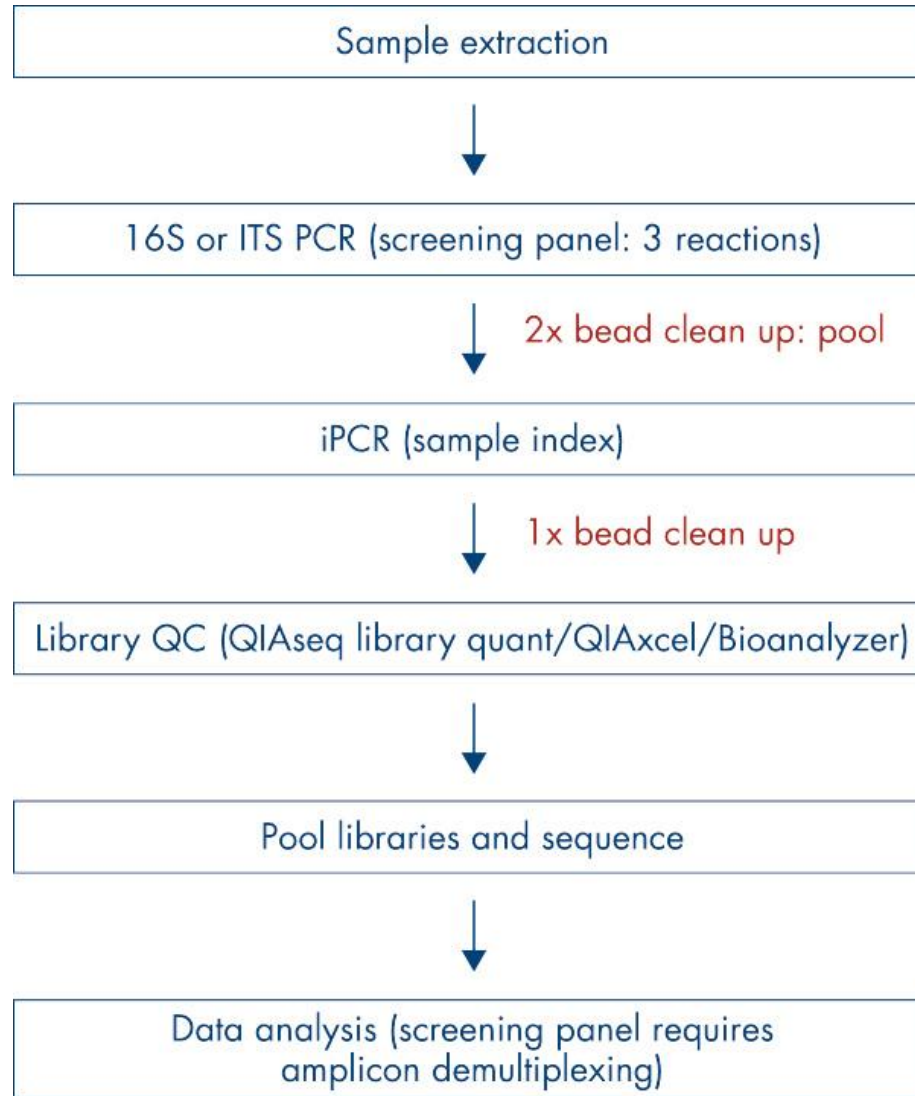
- Seamless integration with Illumina® platforms

- Easy, high-performance analyses spanning taxonomies and biological functions

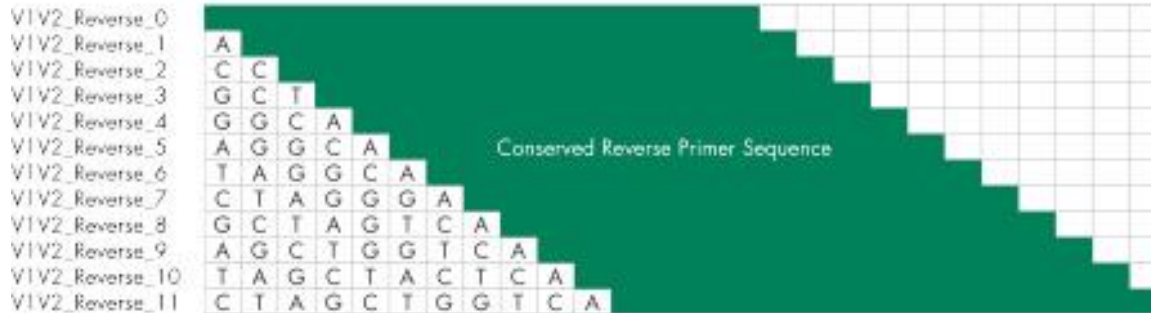


Structure of the bacterial 16S rRNA gene (top) and the fungal ITS region (bottom).

- Poor-quality reads and base calling caused by reduced library complexity
- Inefficient use of flow cell throughput due to the need for considerable amounts of PhiX DNA
- Reduced classification specificity for many bacterial taxa due to incomplete coverage of 16S rRNA variable regions
- High background noise because of contaminated reagents



Phased primers include up to 11 additional bases at their 5'-ends



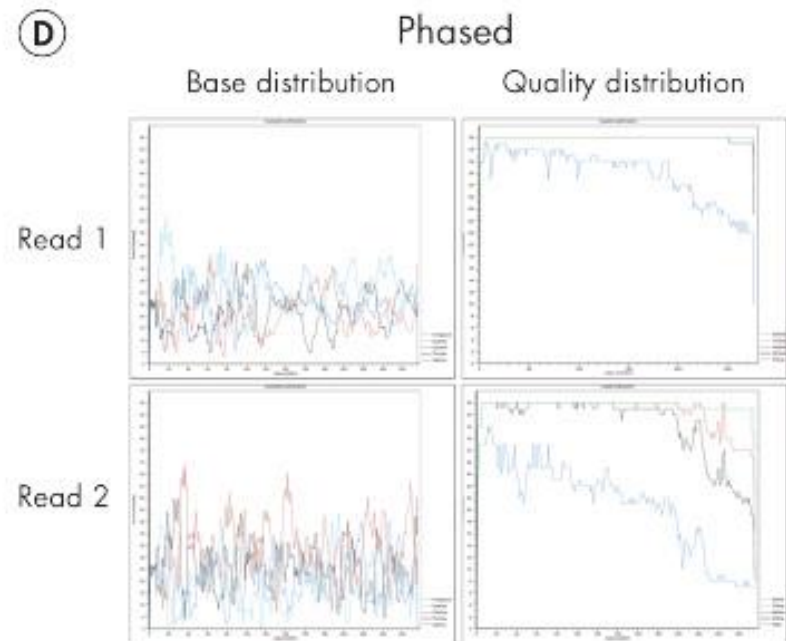
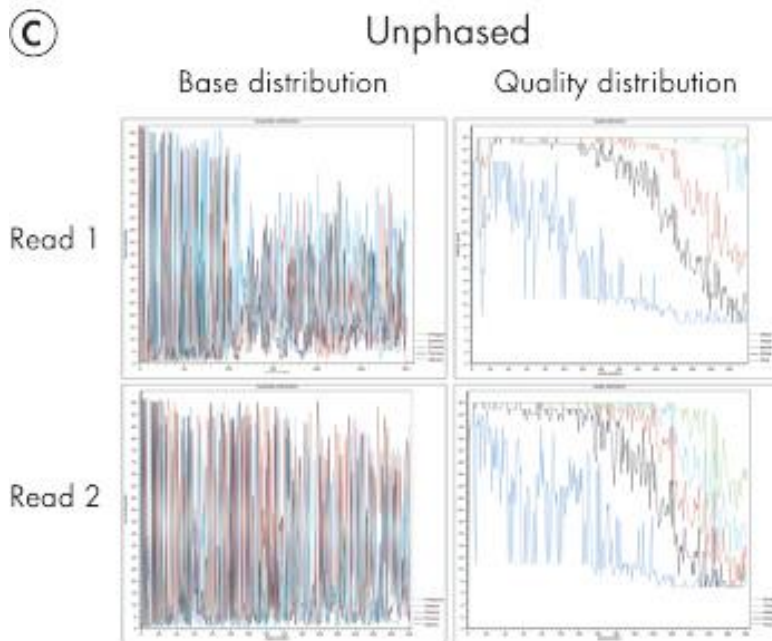
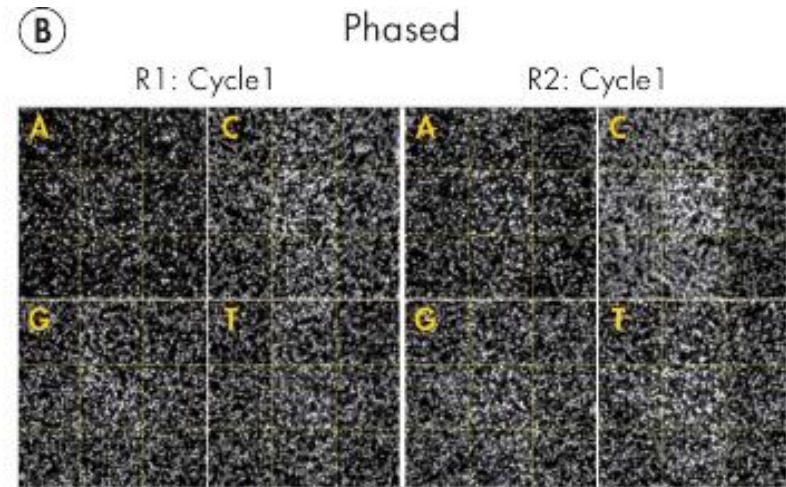
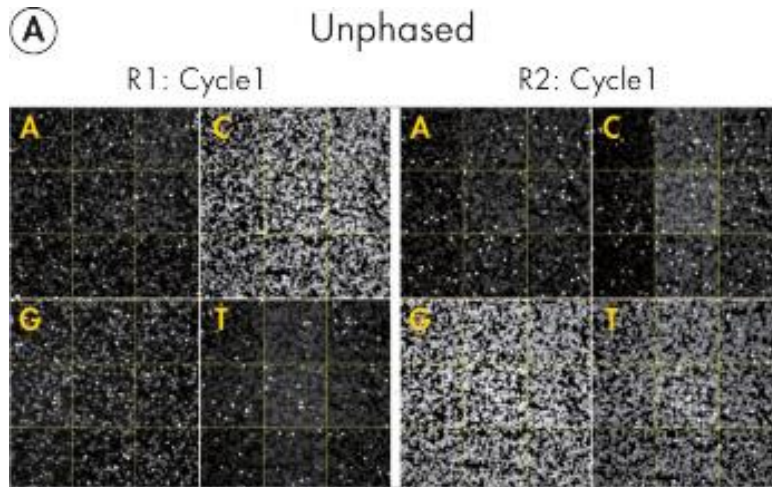
The use of phased primers

- Shifts nucleotide balance
- Increases base diversity

Which leads to increases in quality scores

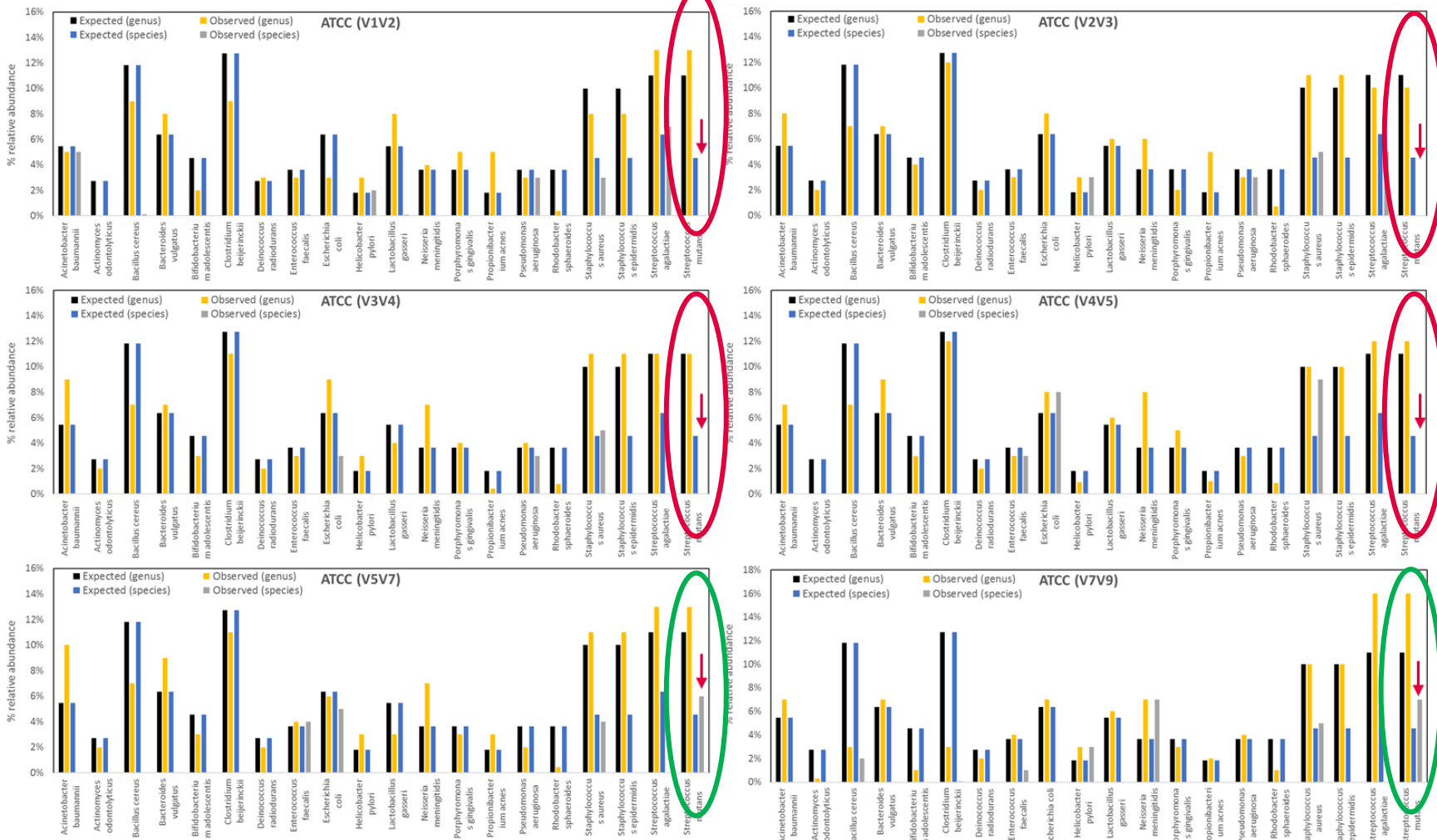
Using phased primers makes libraries produced with the QIAseq 16S/ITS Panels sufficiently complex to eliminate the need for PhiX spike-in, which enables efficient use of flow cell throughput.

Benefits of phased primers

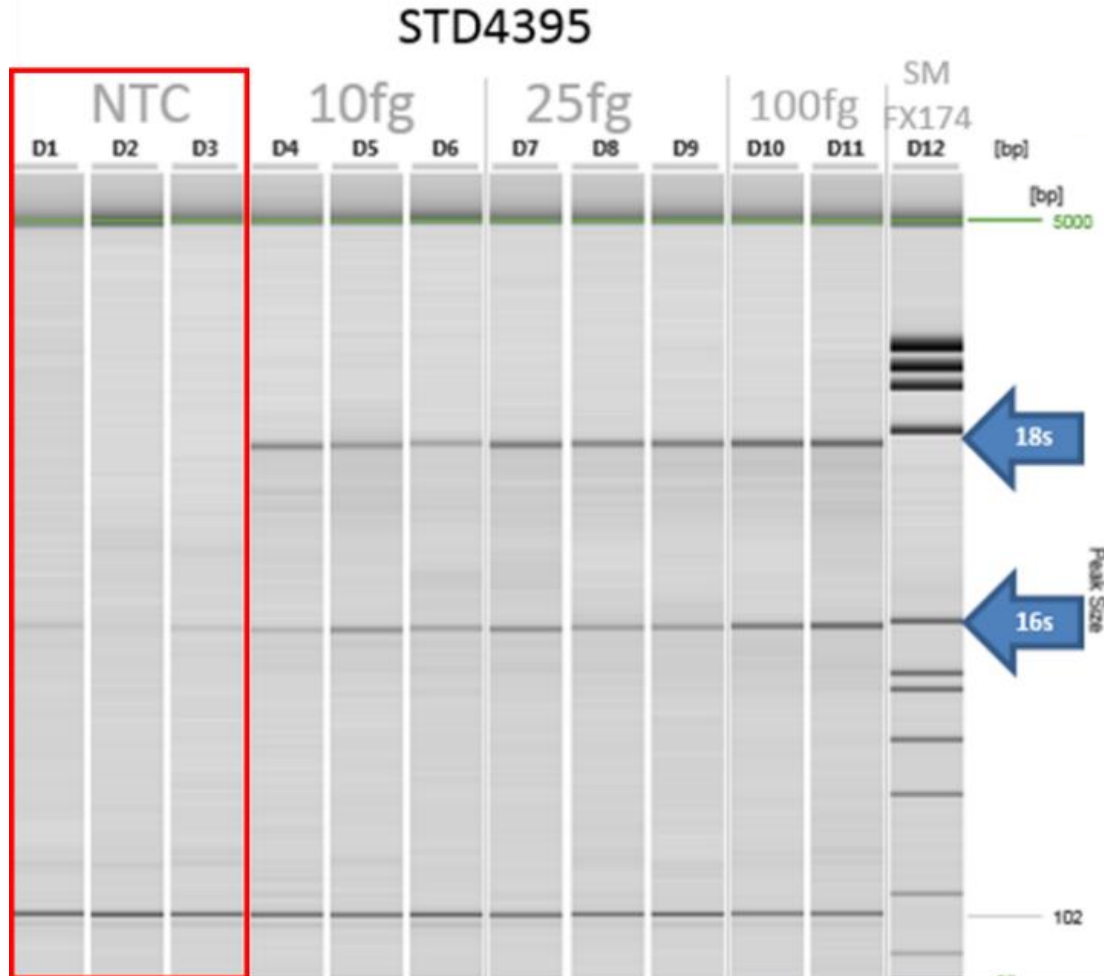


- Each QIAseq 16S/ITS Panel can be used to multiplex up to 96 samples on a MiSeq run using the V3 sequencing chemistry at 2x300
- The appropriate QIAseq 16S/ITS Index Kit (cat no. 33382 or 33387) is necessary to multiplex the required number of samples

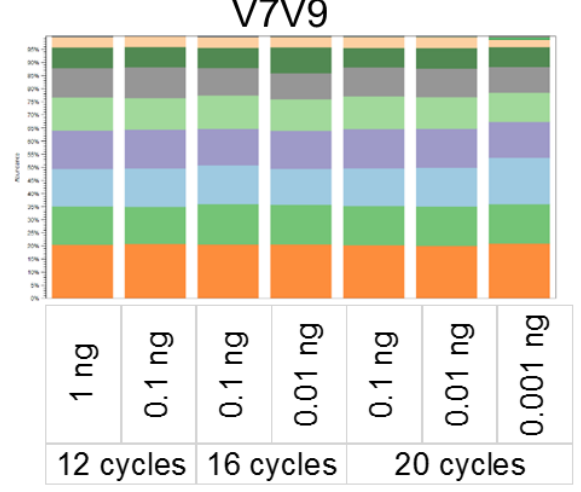
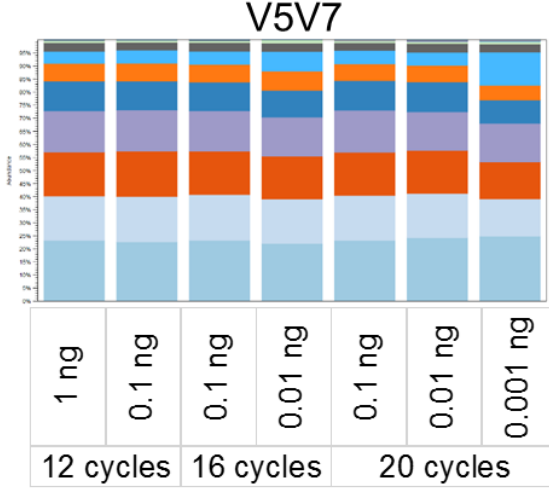
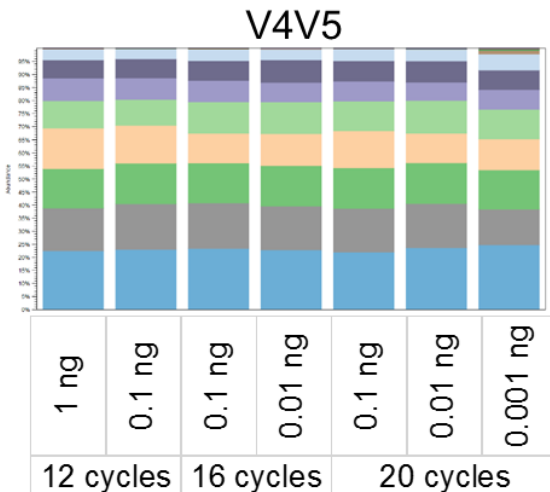
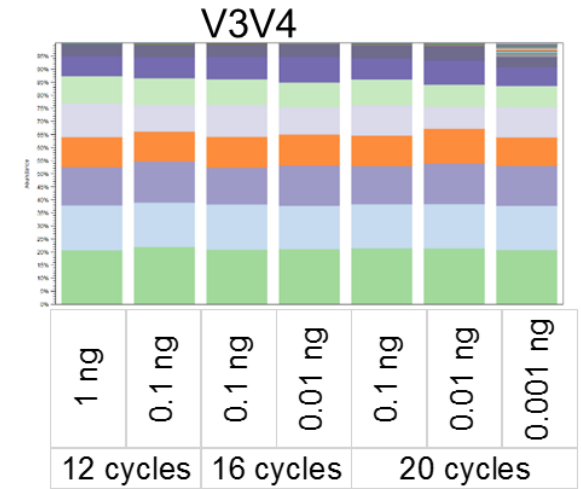
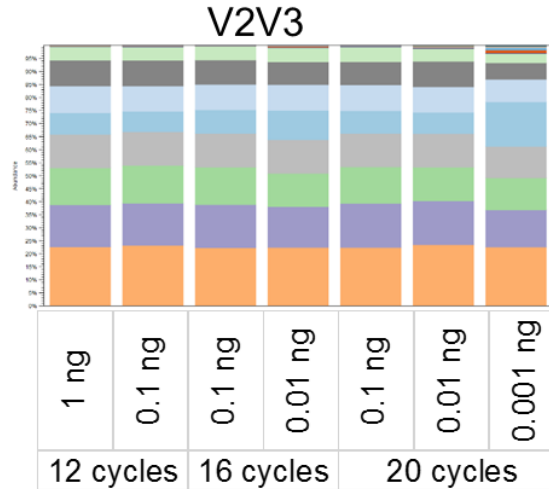
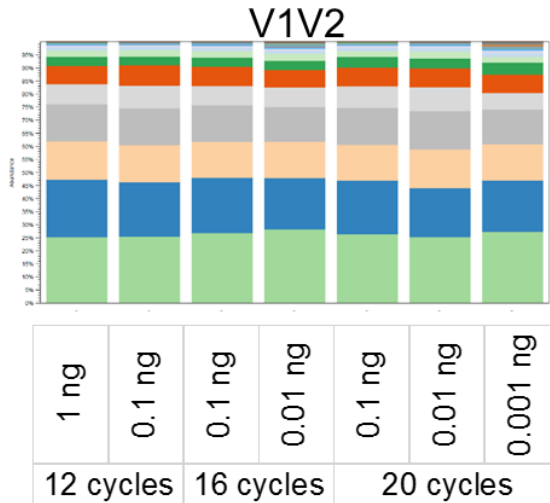
Screening a panel of variable regions provides more robust bacterial profiling compared to screening only individual variable regions.



The QIAseq 16S/ITS Panels have very low levels of background contamination due to the use of reagents with low bioburden.

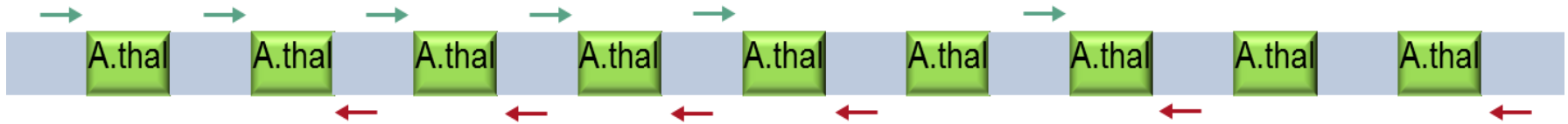


The QIAseq 16S/ITS Panels can be used with as little as 1 pg of input DNA.



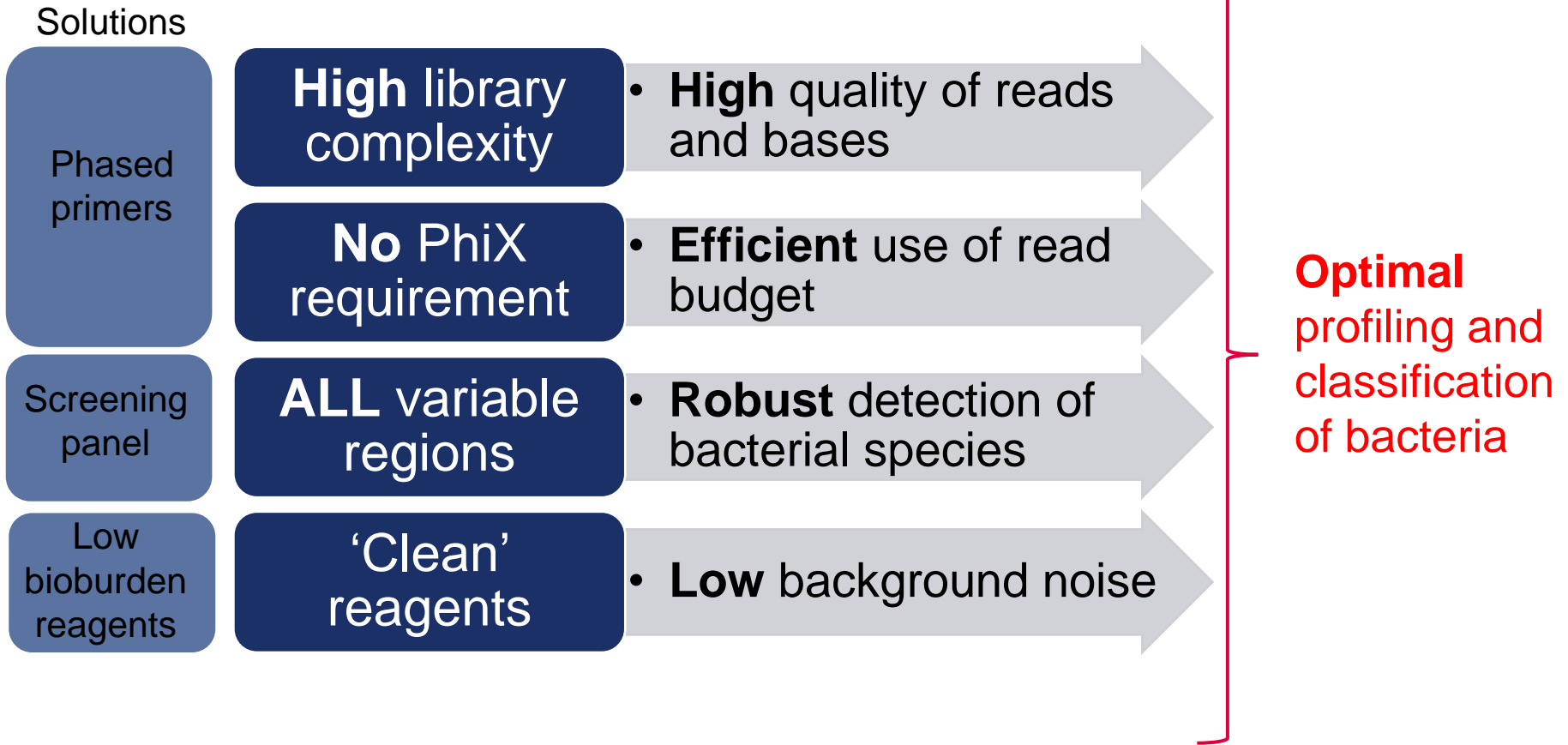
- Post sequencing, data are analyzed using QIAGEN Bioinformatics CLC Genomic Workbench (CLC GWB) and Microbial Genomics Pro Suite Module
- A custom workflow, which can be further edited as needed, is available to automate FASTQ file import, sample library demultiplexing, quality-controlled filtering and trimming, OUT clustering and secondary bioinformatics analysis
- QIAGEN Bioinformatics CLC Genomics Workbench with Microbial Genomics Pro Suite Module enables researchers to output standardized reports on sample library quality metrics and organism abundance tables and provide numerous options for downstream interactive analyses of microbiome profiles and reporting experimental results
- The Microbial Genomics Pro Suite Module also includes tools for calculating diversity metrics and for comparing the microbial profiles of different samples
- The CLC Genomics Workbench also produces publication-quality figures in formats that are readily useable for researchers to present their results

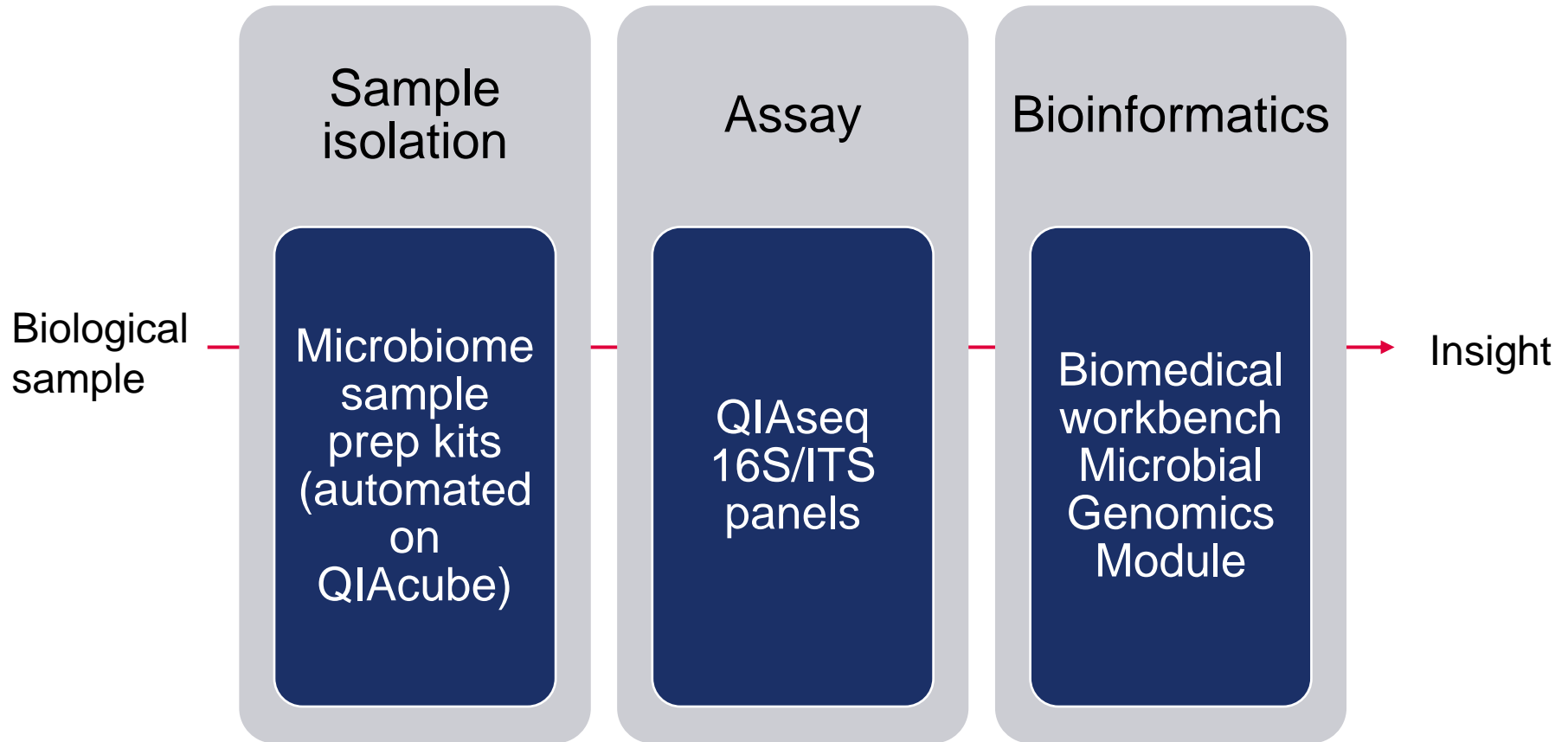
Structure of the QIAseq 16S/ITS Smart Control synthetic DNA



- Contains synthetic DNA to assess library construction steps and user-introduced contamination while using QIAseq 16S/ITS Panels
- Includes primer binding sites from *E. coli*
- Artificial sequences from *Arabidopsis thaliana* replace the hypervariable 16S rRNA region between the primer binding sites
- The artificial sequence cannot be classified as bacterial or fungal
- Therefore, any sequences that are classified as bacterial or fungal will be due to environmental contamination introduced during library construction

QIAseq 16S ITS Library Kit





Individual region kit

1. Primers to interrogate different variable regions, separately:

V1V2

V2V3

V3V4

V4V5

V5V7

V7V9

V4

ITS

2. Low-bioburden mastermix and water

3. QIAseq beads

Screening kit

1. Primers to interrogate all variable regions (in 3 reactions):

V1V2

V2V3

V3V4

V4V5

V5V7

V7V9

V4

ITS

2. Low-bioburden mastermix and water

3. QIAseq beads

Index kits

(24-, 96-, and 384-index)

1. Indexes
2. Custom sequencing primer

16S/ITS process control kit

Synthetic template
(Serves as positive control for library construction and NTC)

Biomedical workbench microbial module

1. Demultiplexing
2. Profiling

Product	Contents	Cat. no.
QIAseq 16S/ITS Regional Panel (24)	For 24 samples: Contains all reagents (except indexes) for sequencing either specific variable regions of the 16S bacterial gene or the fungal ITS gene	333802
QIAseq 16S/ITS Regional Panel (96)	For 96 samples: Contains all reagents (except indexes) for sequencing either specific variable regions of the 16S bacterial gene or the fungal ITS gene	333805
QIAseq 16S/ITS Screening Panel (24)	For 24 samples: Contains all reagents (except indexes) for sequencing all variable regions of the 16S bacterial gene and the fungal ITS gene	333812
QIAseq 16S/ITS Screening Panel (96)	For 96 samples: Contains all reagents (except indexes) for sequencing all variable regions of the 16S bacterial gene and the fungal ITS gene	333815
Related Products		
QIAseq 16S/ITS 24-Index I (96)	For indexing up to 24 samples for 16S/ITS sequencing using Illumina platforms: contains library adapters for 96 samples	333822
QIAseq 16S/ITS 384-Index I (1536)	For indexing up to 384 samples for 16S/ITS sequencing using Illumina platforms: contains library adapters for 1536 samples	333827
QIAseq 16S/ITS Smart Control	For 10 samples: Contains synthetic template that can be as positive control with QIAseq16S/ITS Panels	333832



For up-to-date licensing information and product-specific disclaimers, see the respective QIAGEN kit handbook or user manual. QIAGEN kit handbooks and user manuals are available at www.qiagen.com or can be requested from QIAGEN Technical Services or your local distributor.

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