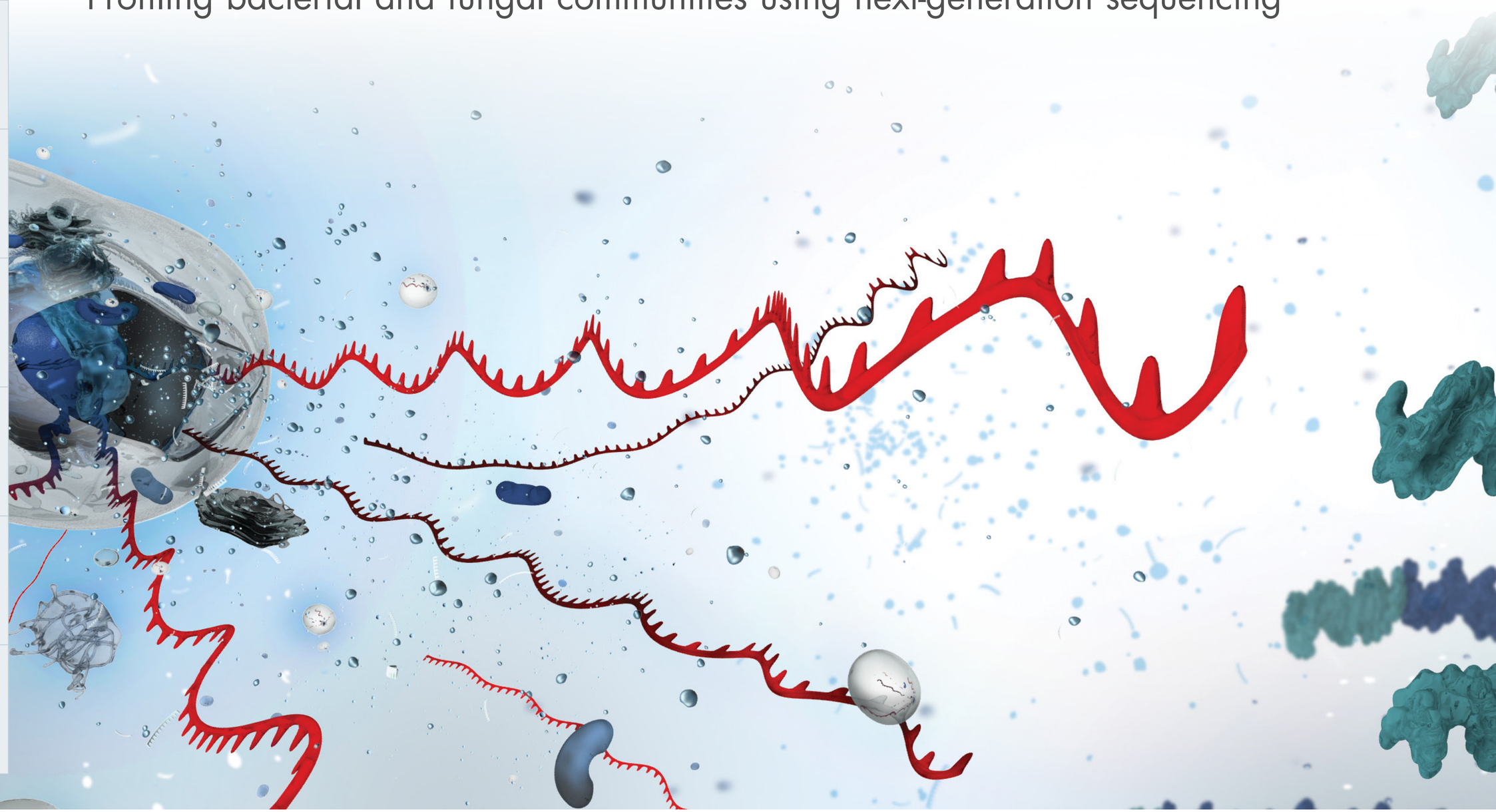
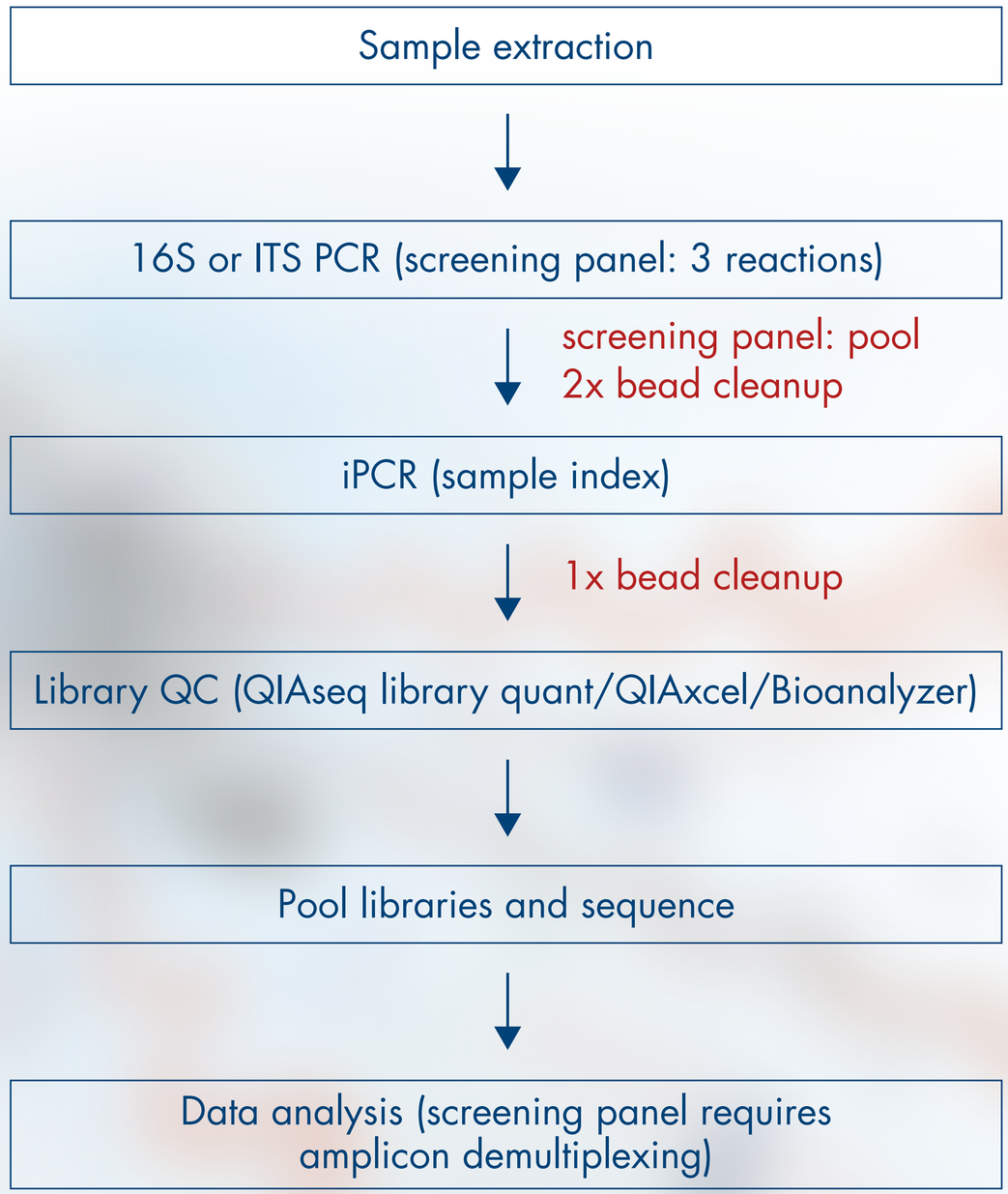
QIAseq® 16S/ITS Panels

Profiling bacterial and fungal communities using next-generation sequencing



Workflow

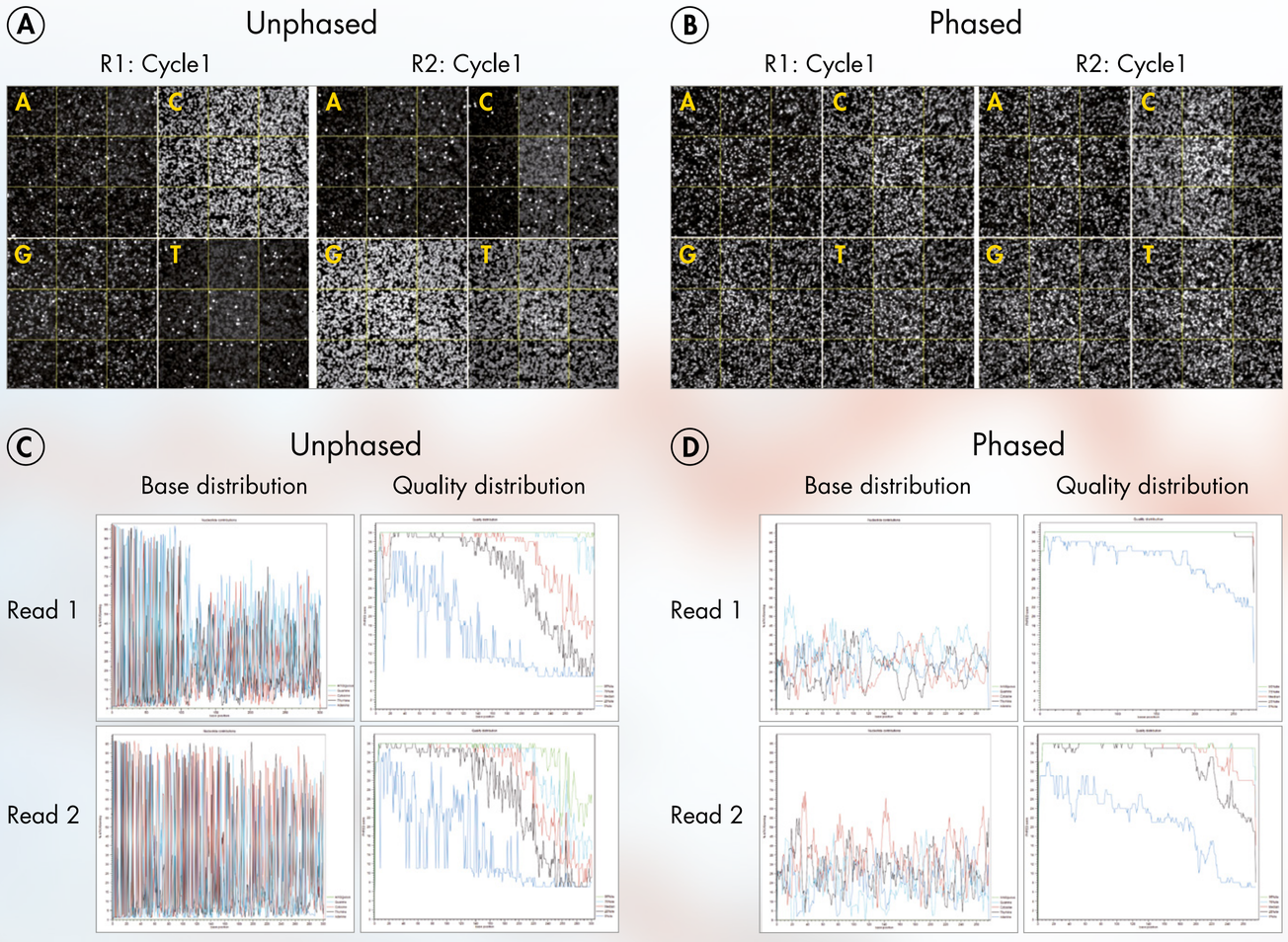


2-stage PCR workflow for targeted enrichment of bacterial 16S rRNA gene and fungal ITS region

First PCR step incorporates a phased primer pool to enrich for conserved regions of the 16S gene and ITS regions

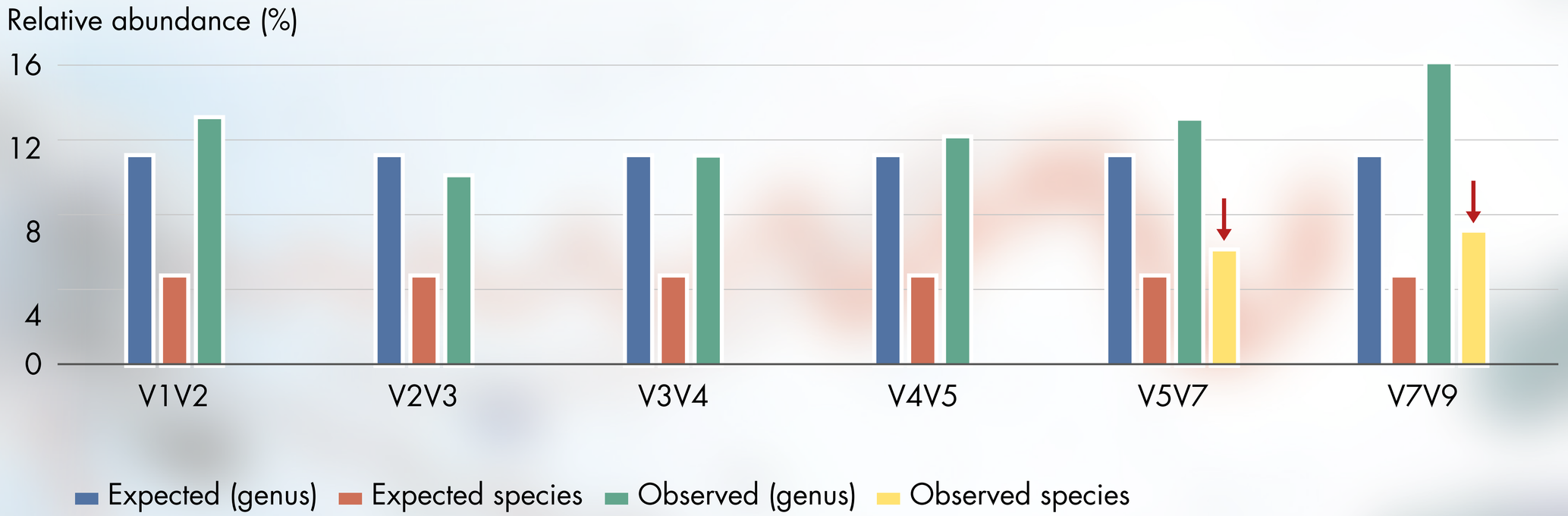
Second library amplification step introduces sample indices and ensures sufficient target is present for NGS

Phased primers increase base diversity and quality scores



Fluorescent images (top row) taken from the first cycle of read 1 (R1) and read 2 (R2) 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).

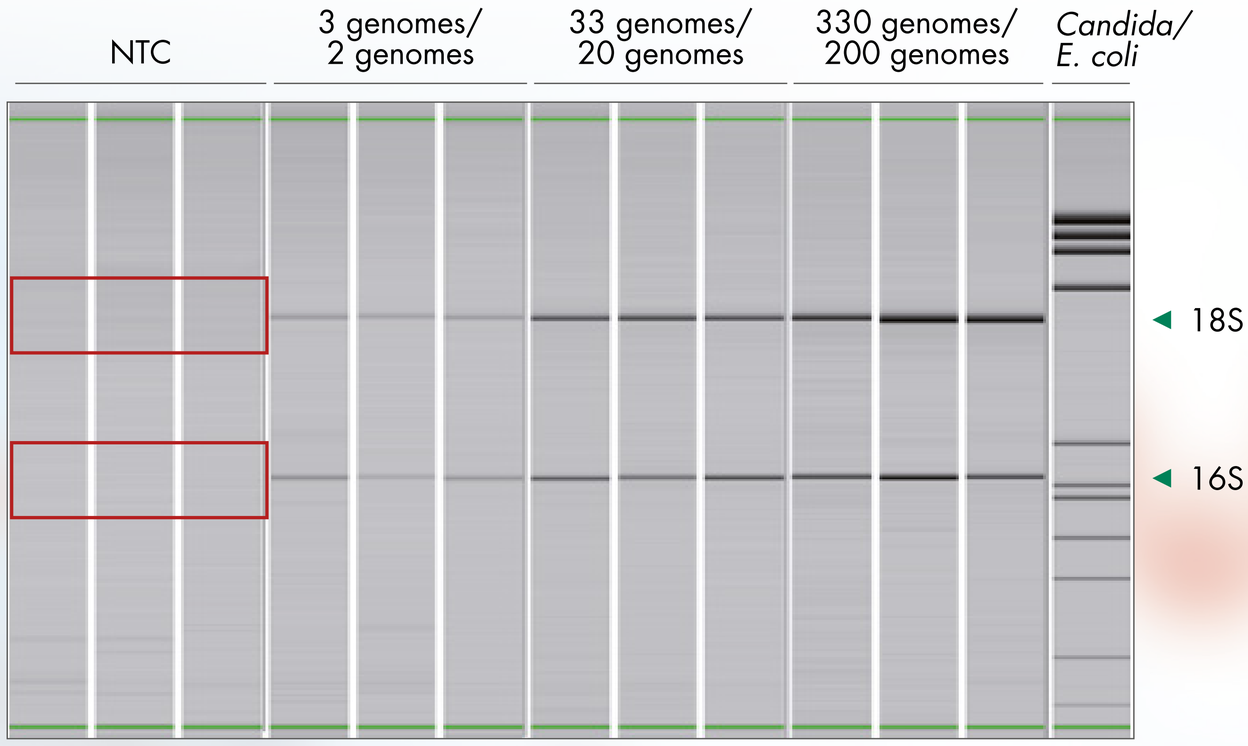
Screen a panel of variable regions to achieve more robust bacterial profiling compared to screening only individual variable regions



QIAseq 16S/ITS Panels were used to generate libraries from the ATCC® 20 Strain Even Mock Community. Demultiplexing of the variable regions was performed using the CLC Microbial Genomics Module and the QIAseq 16S/ITS Demultiplexer tool. Classification was performed for each of the variable regions at the species level using the SILVA database. Results are shown only for *Streptococcus mutans*. Only a subset of the variable regions (red arrows) can be used to classify *S. mutans*.

Expanded screening yields more robust microbial profiles

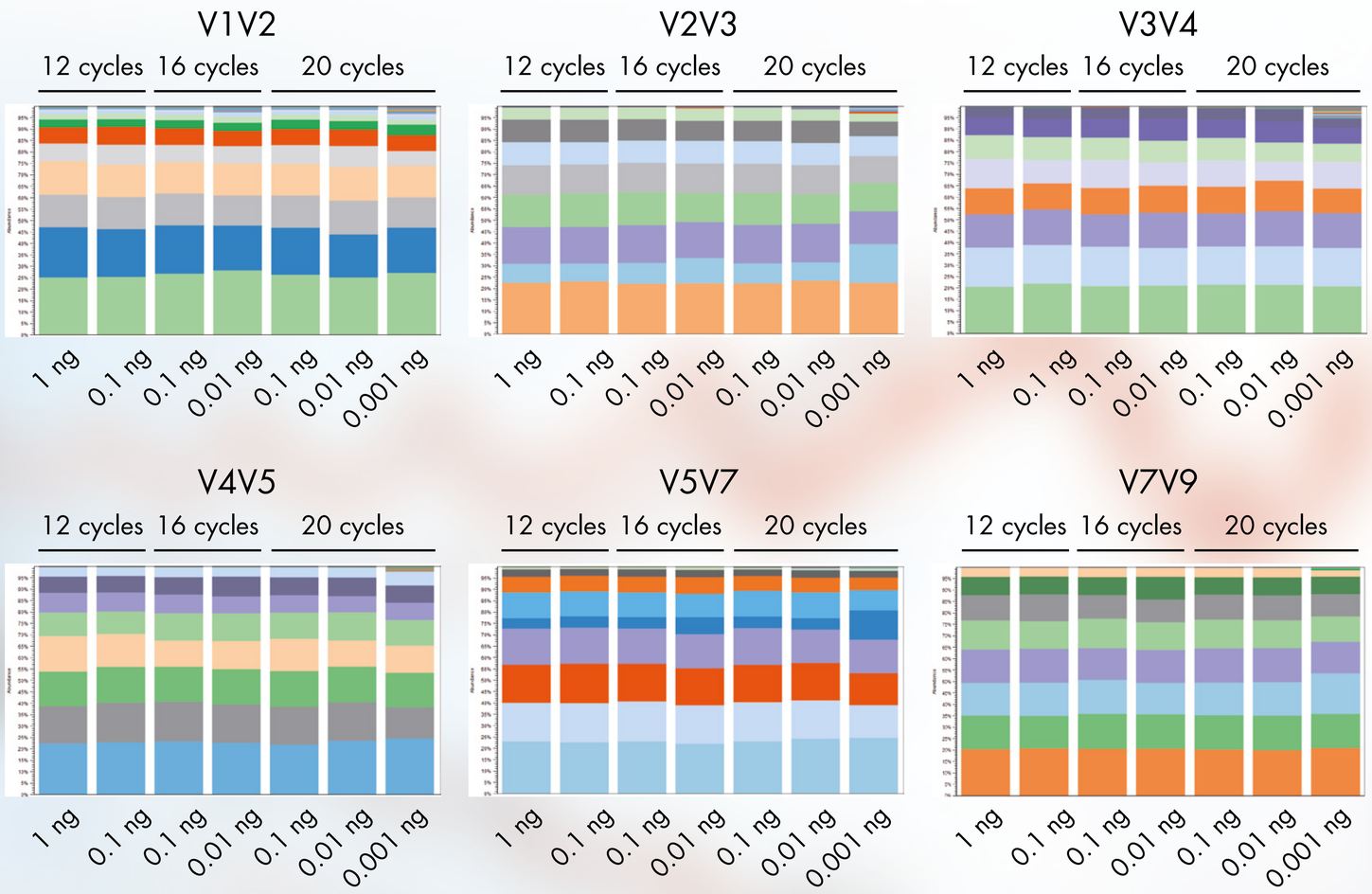
Achieve very low levels of background contamination due to the use of reagents with low bioburden



Contamination levels were monitored by amplifying with PCR primers targeting 16S (bacteria) and 18S (fungal) rRNA genes with UCP Multiplex Mastermix and UCP PCR Water. Thirty eight cycles of PCR were performed and the reaction was run on a QIAxcel to detect the 16S and 18S amplicons.

Low background contamination can increase the robustness of microbial profiling

Start with as little as 1 pg of DNA to profile microbial communities in samples with low biomass



Serial dilutions of a mixed bacterial DNA sample were used to generate libraries using the QIAseq 16S/ITS Region Panel. PCR for 12, 16 or 20 cycles was carried out followed by index PCR. The CLC Microbial Genomics Module and SILVA database were used to perform classification.

Ordering Information

Product	Description	Cat. no.
QIAseq 16S/ITS Region 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	333842
QIAseq 16S/ITS Region 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	333845
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 96-Index I (384)	For indexing up to 96 samples for 16S/ITS sequencing using Illumina platforms: contains library adapters for 384 samples	333825
QIAseq 16S/ITS Smart Control	For 10 samples: contains synthetic template that can be as positive control with QIAseq16S/ITS Panels	333832

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