

# NEXTGENPCR



## APPLICATION NOTE

RESEARCH USE ONLY (RUO)

### NEXTGENPCR™ 16S FULL GENE AMPLIFICATION KIT

#### HIGHLIGHTS

- Single-day laboratory workflow suited for standard microbiological laboratories
  - Ultrafast amplification of full length 16S rDNA sequences in  $\leq 21$  minutes
- Complete PCR kit including all necessary chemistries for target sequence amplification
- High fidelity sequence data generation for V1-V9 regions allowing species-level determination
  - Suitable for complex and difficult to amplify samples, i.e. polymicrobial specimens

THE WORLD'S FASTEST PATENTED PCR THERMAL CYCLER

## BACKGROUND

Sequencing of the 16S ribosomal DNA (16S rDNA) gene is a well-established method to identify bacterial species in biological specimens. Taxonomic identification using 16S sequence is based on exploiting the unique combination of hyper conserved and variable regions (V1 – V9).

The NextGenPCR™ 16S Full Gene Amplification Kit is a complete PCR assay solution intended for ultrafast analysis of bacterial composition in a biological specimen. The kit includes all necessary materials (primer oligonucleotides, ready-to-use polymerase master mix and genomic bacterial DNA control) to amplify the full length 16S rDNA gene in  $\leq 21$  minutes total cycling time.

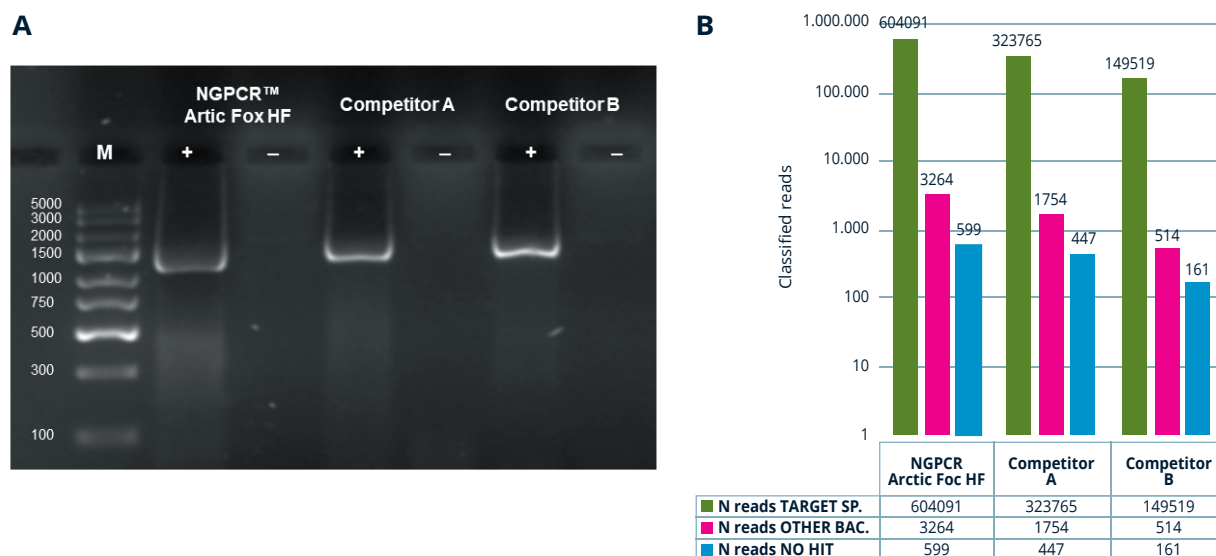
Performance of the NextGenPCR™ 16S Full Gene Amplification Kit was evaluated using DNA template material isolated from the Microbial Community Standard (ZymoBIOMICS) using a MagNA Pure 96 System (Roche). Using 10 ng gDNA template as input and the cycling program listed in Table 1, amplicons were generated on a NextGenPCR™ Thermal Cycler using either NextGenPCR™ Arctic Fox HF Chemistry-2× (Molecular Biology Systems) or a competitor's polymerase mix, of which two were tested. Amplicons were barcoded using a Rapid Barcoding Kit (SQK-RBK114.96) and sequenced using a Flow Cell R9.4.1 on a MinION MK1B sequencer (Oxford Nanopore Technologies). Sequences were analyzed using a custom bioinformatics pipeline (MABA16S, available through GitHub).

### CYCLING CONDITIONS FOR THE SEQUENCED SAMPLES

	Cycle Nº	Time	Temp	Total cycling
NextGenPCR™ Arctic Fox HF	1	30 sec	98 °C	21 min
	30	10 sec	98 °C	
		15 sec	54 °C	
		15 sec	68 °C	
Competitor A	1	30 sec	98 °C	43 min
	30	10 sec	98 °C	
		15 sec	54 °C	
		60 sec	68 °C	
Competitor B	1	30 sec	98 °C	36 min
	30	10 sec	98 °C	
		15 sec	54 °C	
		30 sec	68 °C	

Analysis of the microbial community standard sample mix revealed excellent amplification results for all three tested chemistries, with clear bands at the ~1,500 bp range corresponding to the full length 16S ribosomal DNA gene sequence (Figure 1A). Sequencing amplicons for 26 hours on a MinION flow cell yielded the highest number of classified reads for the NextGenPCR™ Arctic Fox HF Chemistry library (604,091 reads) as compared to competitor A (323,765 reads) and competitor B (149,519 reads) libraries while also having the shortest total amplification time of 21 minutes. In all three cases, the number of reads mapping to other bacterial species was  $\leq 0.5\%$  and the number of unmappable reads was  $\leq 0.1\%$  (Figure 1B), demonstrating that the NextGenPCR™ Thermal Cycler is compatible with multiple polymerase mixes and generates excellent quality sequence data.

## AMPLIFICATION OF ~1500BP FRAGMENT OF THE 16S FULL GENE SEGMENT

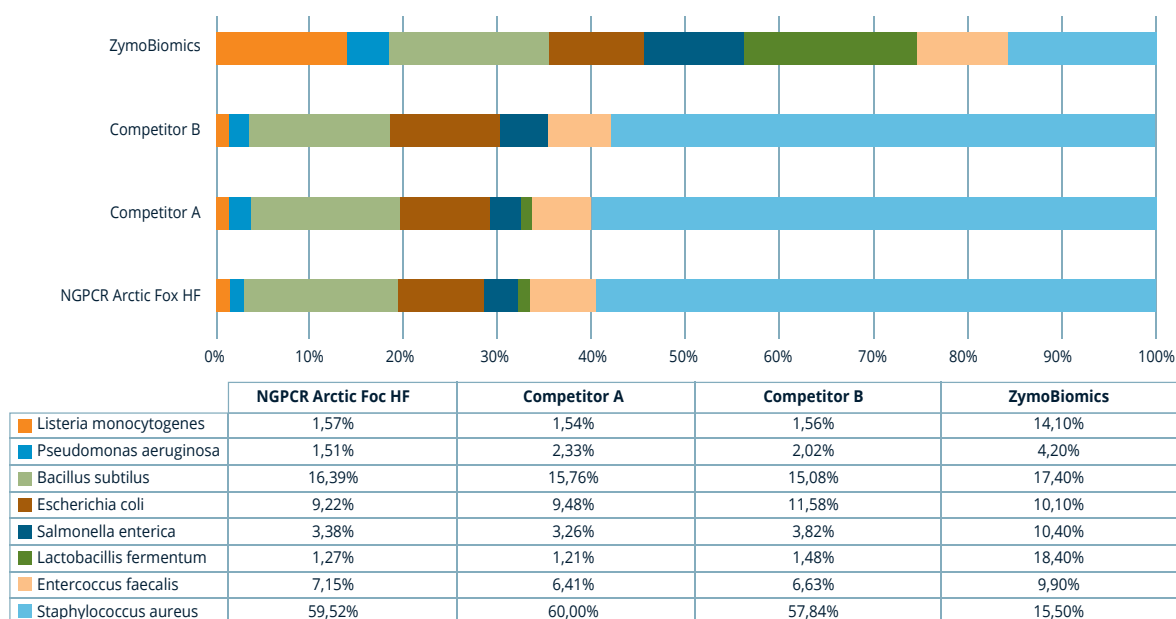


**Figure 1.**

**(A)** Amplification of ~1500bp fragment of the 16S full gene segment using different polymerases and cycling programs on the NextGenPCR™ Thermal Cycler. The starting template was ~10 ng input Microbial Community Standard (+), with a non-template control (-) for each condition.

**(B)** Number of classified reads was highest using the NextGenPCR Arctic Fox HF Chemistry as compared to competitors.

## DISTRIBUTION OF CLASSIFIED SPECIES IN EXPERIMENTAL CONDITIONS



**Figure 2.** Distribution of classified species in experimental conditions as compared to the theoretical composition of the ZymoBIOMICS Microbial Community Standard.



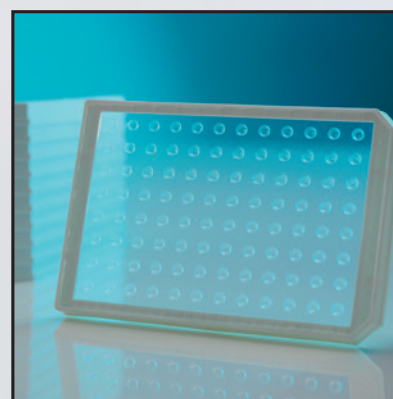
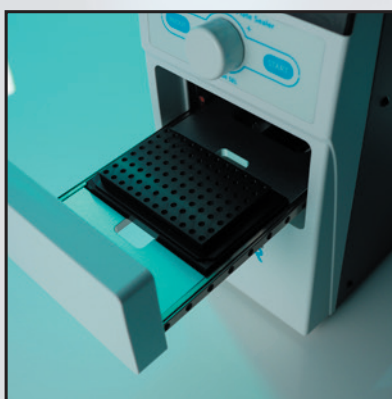
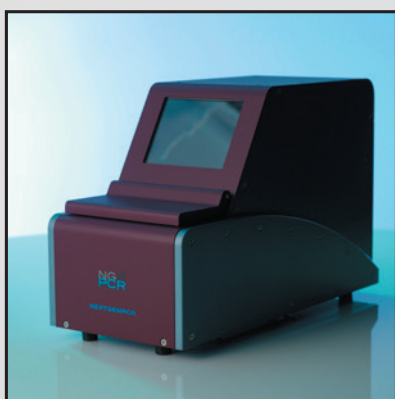
## CONCLUSION

Integration of ultrafast amplification of the 16S gene using NextGenPCR™ products and rapid sequencing provides a promising new avenue for bacterial identification in a biological sample within a single working day. The NextGenPCR™ 16S Full Gene Amplification Kit offers several pronounced advantages over existing bacterial identification methods such as Sanger sequencing and MALDI-TOF, including the capability to simultaneously detect multiple organisms in a sample and the ability to confidently determine negative results if no reads are obtained.

Find out more about NextGenPCR™ ultrafast PCR products and applications on our website over at: [www.nextgenpcr.com](http://www.nextgenpcr.com)

## RELATED PRODUCTS

P/N	Product name	Packaging size
#10001	NextGenPCR™ Thermal Cycler	1 unit
#10101/10102	NextGenPCR™ Semiautomatic Heat Sealer	1 unit
#20102	NextGenPCR™ Sealing Anvil 96×20 µL	1 unit
#20301/20305	NextGenPCR™ Pipetting Anvil 96×20 µL	1 unit in white/black color
#33602/33603	EZtrieve™ Microplates 96×20 µL	50/500 microplates per pack
#30110/30111	EZtrieve™ Aluminum Heat Seals	50/500 sheets per pack
#50034	NextGenPCR™ 16S rDNA Full Gene Amplification Kit	100×20 µL reactions per pack



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