

Ion 16S Metagenomics Kit and Ion Reporter metagenomics workflow solution

Culture-free rapid identification of polybacterial research samples using Ion Torrent sequencing systems

Ion 16S Metagenomics Kit

Metagenomics research is made easier with next-generation sequencing. With this culture-free sequencing method, you can get genus- and species-level taxonomic results in less than 3 days. The Ion 16S™ Metagenomics Kit uses two primer pools to amplify seven hypervariable regions (V2, V3, V4, V6, V7, V8, and V9) of bacterial 16S rRNA. The amplified fragments can then be sequenced on either the Ion S5™ or the Ion PGM™ Systems, and analyzed using the Ion 16S metagenomics workflow in Ion Reporter™ Software (Figure 1).

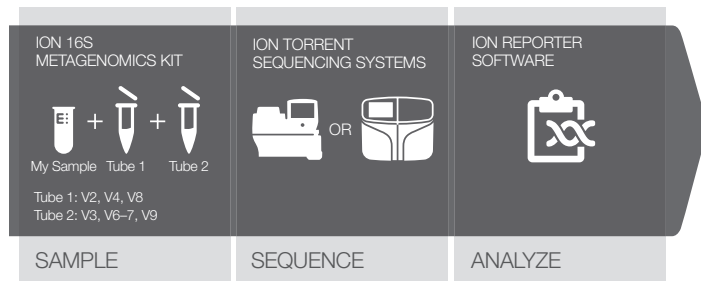


Figure 1. Integrated, cost-effective, scalable 16S rRNA sequencing workflow for the Ion Torrent sequencing systems, with a rapid workflow from library to analyzed results. Following library construction and template preparation, 400 bp sequencing runs are completed in as little as 4 hours. BAM files produced with Torrent Suite™ Software are automatically analyzed, annotated, and taxonomically assigned in the Ion Reporter Software 16S metagenomics workflow.

Benefits of the Ion 16S Metagenomics Solution include:

- Use starting material from direct samples without culture, mixed culture, or pure culture
- Comprehensive primer sets allow for accurate detection and identification of a broad range of bacteria, down to the genus or species level
- Flexibility—primer sets provided as two pools allow for separate analyses using individual pools
- Primers can also be barcoded
- Integrated workflow/end-to-end solution
- Fast analysis with Ion Reporter Software using premium curated Applied Biosystems™ MicroSEQ™ ID 16S rRNA database and curated Greengenes database

The combination of the two primer pools enables broad-range, sequence-based identification of bacteria from complex mixed populations. When applied to ground beef samples, the 16S sequencing results showed high resolution identification of bacterial species. Species diversity was substantially reduced on culture (Figure 2).

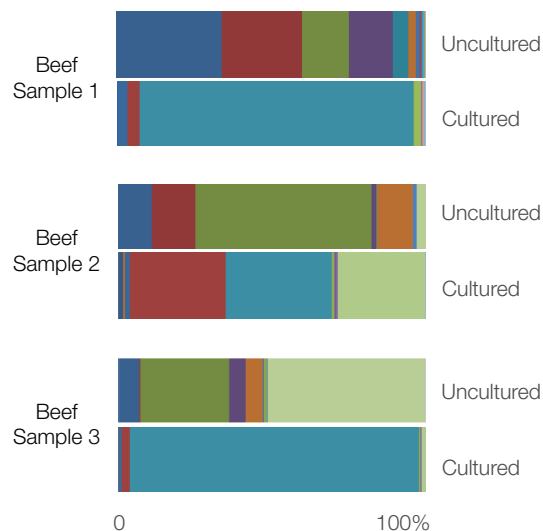


Figure 2. 16S rRNA sequence analysis of ground beef samples. Libraries generated with the Ion 16S Metagenomics Kit were generated from ground beef samples and sequenced on the Ion 530™ Chip. Automated analysis, annotation, and taxonomical assignment were generated using Ion Reporter Software. Uncultured ground beef samples show a greater diversity of genera compared to cultured samples, suggesting that culturing introduces bias. Of note, the number and diversity of bacterial genera differ in ground beef from different sources as shown by color.

Ordering information

Product	Cat. No.
Ion 16S Metagenomics Kit, 100 reactions	A26216
Ion Universal Library Quantitation Kit, 250 reactions	A26217
Ion Plus Fragment Library Kit, 10 reactions	4471252
Ion Xpress Barcode Adapters 1-96 Kit, 1 kit	4474517
Ion 520/530 Kit-Chef, 8 reactions	A27757
Ion 520 Chip Kit, 8 reactions	A27762
Ion 530 Chip Kit, 8 reactions	A27764

Find out more at thermofisher.com/ion16smetagenomics

Ion Reporter Software—metagenomics workflow

Ion Reporter Software enables the rapid identification (at genus or species level) of microbes present in complex polybacterial research samples, using both curated Greengenes and premium curated MicroSEQ ID 16S rRNA reference databases. The Ion Reporter metagenomics workflow also provides primer information, classification information, percent ID, and mapping information. It's easy to interpret population diversity for your research at any taxonomic level with the interactive display (Figure 3).

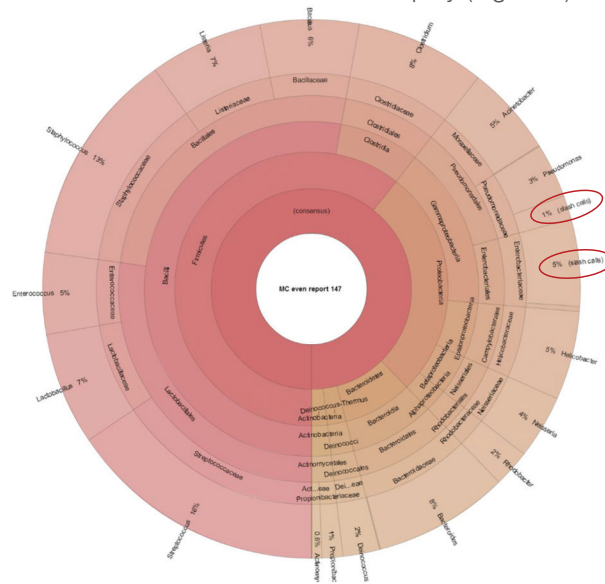


Figure 3. Automated analysis, annotation, and taxonomical assignment implemented in Ion Reporter Software. Consensus view at the genus level of the balanced mock bacterial sample, using more stringent analysis parameters. Slash calls at the genus level are circled in red.