

16S METAGENOMICS



Metagenomics research is made easier with next-generation sequencing. With this culture-free sequencing method, researcher can get the information about genus and species-level identification of the bacterial diversity in various sources such as a food, environmental and biological samples. 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 to get more insights of the microbial composition in the sample.

Project workflow



DNA extraction

- Test sample
- DNA quantification
- QC analysis



Library preparation and Sequencing

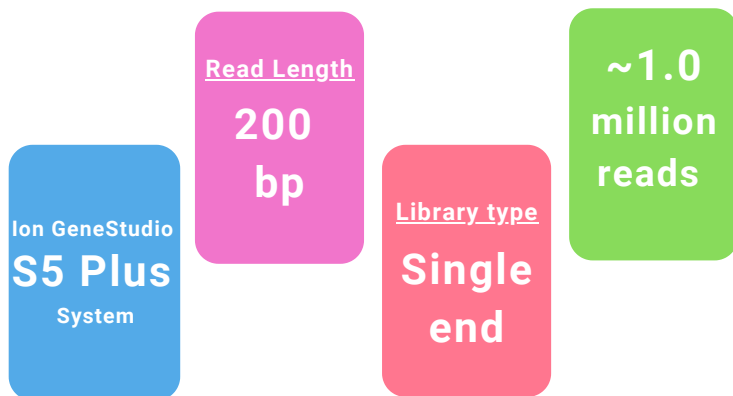
- Ion 16S™ Metagenomics Kit
- Sequencing platform: Ion GeneStudio S5 and S5 Plus



Bioinformatic analysis

- Ion Reporter Software
- Rapid identification (at genus or species level),
- Krona Chart, Alpha & beta diversity, OTUs
- Database: curated Greengenes and premium curated MicroSEQ ID 16S rRNA reference databases

Sequencing parameters



Key information

- Sample type: Environmental (Soil, water & air) and biological (Swabs, body fluid, stool etc.)
- Method: NGS based
- TAT: 15 days

