

16S/18S/ITS Amplicon Sequencing library preparation

Metagenomic studies are performed by analyzing the prokaryotic 16S/18S/ITS region to illustrate phylogenetic classifications in diverse microbial populations. CD Genomics provides multiple solutions for 16S/18S/ITS amplicon sequencing corresponding to different library preparation as below:

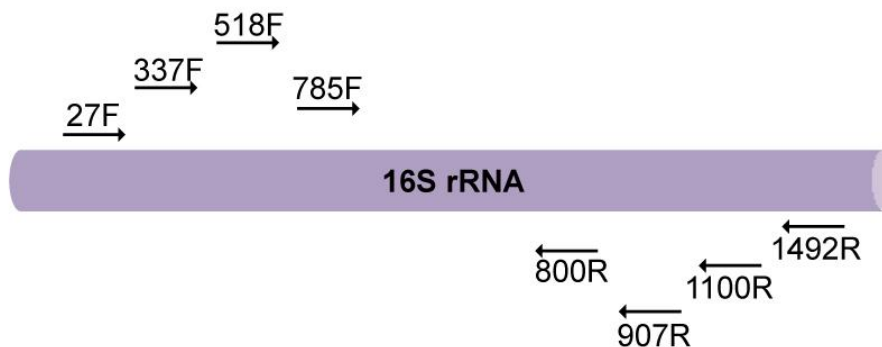
Next-Generation Sequencing

PCR-based Library Preparation Workflow



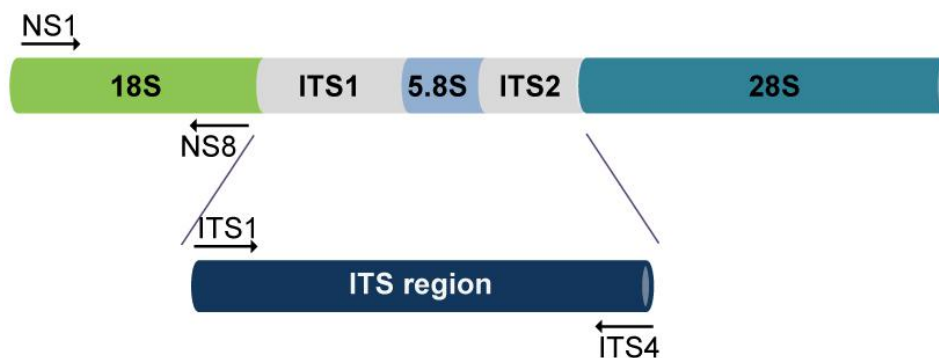
Bacteria

16S rRNA sequencing: several primer sets are optional, and primers 27F and 1492R guarantee length greater than 1,300 bp.



Fungi

- 18S rRNA sequencing: Primers NS1 and NS8 guarantee length greater than 1,600 bp.
- ITS region sequencing: primers ITS1 and ITS2 guarantee length greater than 500 bp.



Library Preparation Workflow



Third generation sequencing

SMRT

With SMRT sequencing, both depth and clarity are enhanced in your sequencing results through long reads, the highest consensus accuracy, uniform coverage, and simultaneous epigenetic detection. And SMRT sequencing technology can analyze large fragment libraries (3-10kb). And the workflow of sequencing libraries is as below:

