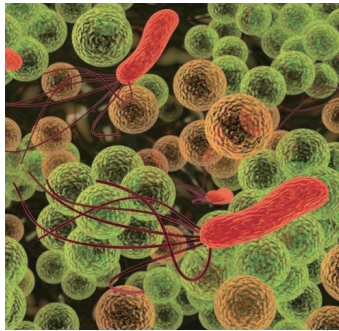


Amplicon-based metagenomic sequencing



Amplicon-based metagenomic sequencing is frequently used to identify and differentiate microbial species. Short (< 500 bp) hypervariable regions of conserved genes or intergenic regions are amplified by PCR, sequenced using NGS technology, and compared against microbial databases for taxonomic identification. Most commonly used targets are 16S rRNA gene of bacteria and archaea, 18S rRNA gene, or two internal transcribed spacers (ITS) of fungi.

At Novogene, we have sequenced over 200,000 microbial samples for our customers. Our standard bioinformatics analyses include OTU analysis, species annotation, alpha-diversity analysis, beta-diversity analysis, and multi-variate statistical analysis. Applications range from identifying a single species in pure culture to characterizing the microbiota of animals or plants to comparing species diversity and population structure in various environmental sources or geographic regions. Our specialists can advise you on the appropriate analyses for your project.



Extensive experience with over 30,000 samples

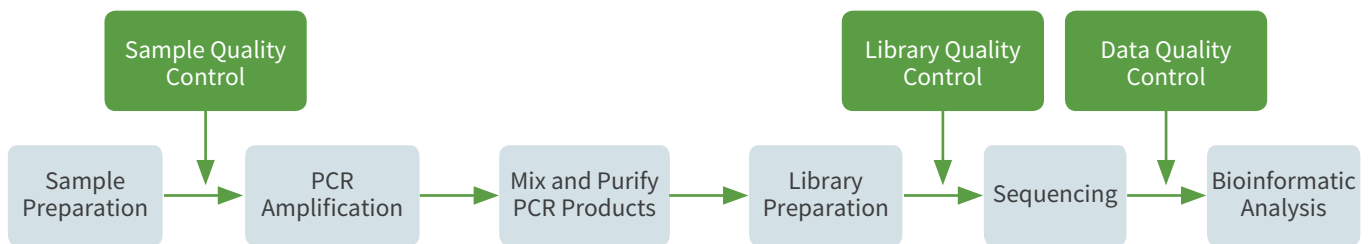


Data quality exceeds Illumina's official guarantee



In house pipeline to meet different analysis requirement

Project workflow



Sequencing parameter

Platform	Illumina NovaSeq 6000 SP
Read length	Pair-end 250
Recommended Sequencing Depth	Recommended: 30K/50K/100K raw tags
Data quality	Guaranteed Q30 \geq 75%
Turnaround time	Within 3 weeks from project verification to data releasing without bioinformatic analysis (<24 samples)

Samples requirement

Library Type	Sample Type	Required	Volume	Concentration	Purity (NanoDrop™)
Amplicon library	Genomic DNA	\geq 200 ng	\geq 12 μ L	\geq 20 ng/ μ L	OD260/280 = 1.8~2.0, no degradation, no contamination
	PCR Products (Fragment size: \leq 470 bp)	\geq 200 ng (pooled samples/library) \geq 1.5 μ g (one sample/library)			

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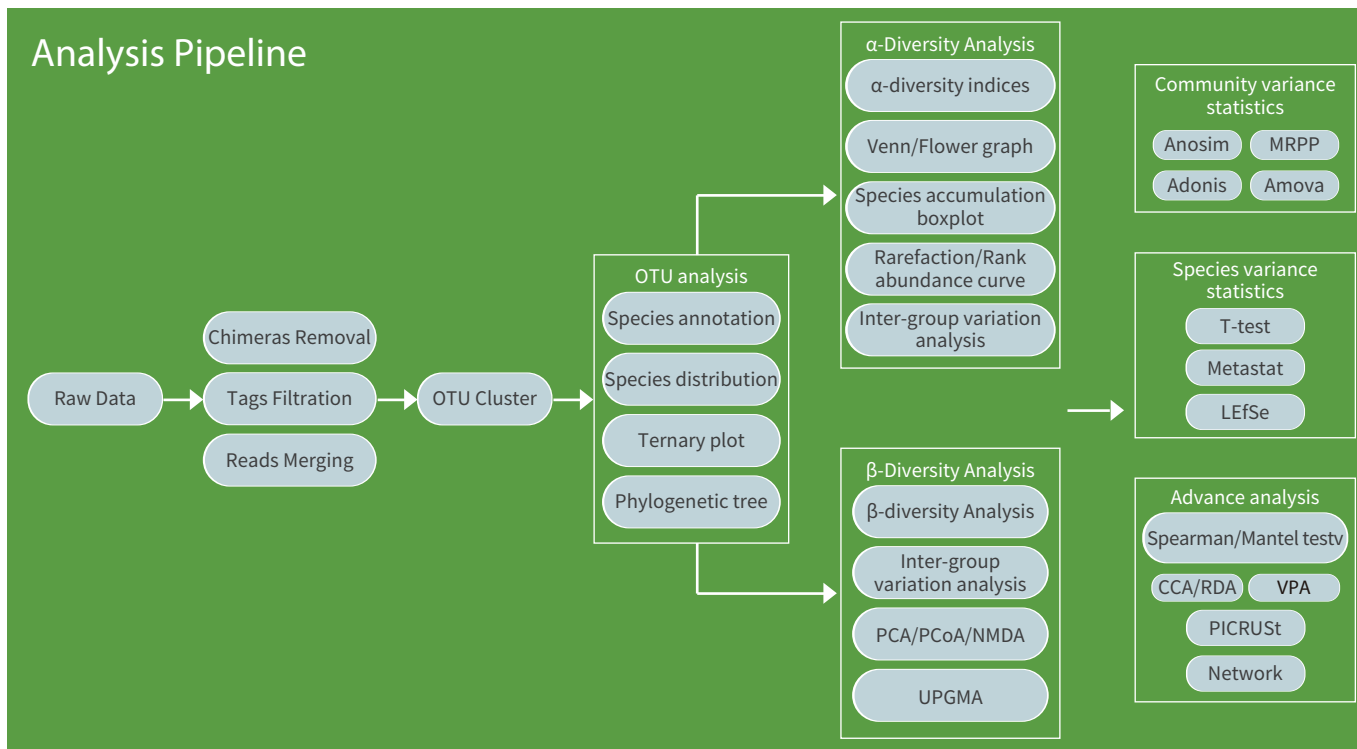
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Analysis Pipeline

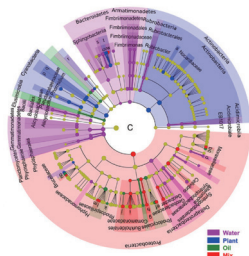
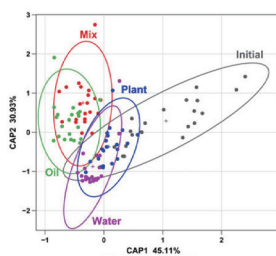


Project Example

The following study utilized Novogene's amplicon-based metagenomic sequencing services.

Plant growth and oil contamination alter the diversity and composition of bacterial communities in agricultural soils across China
Land Degrad Dev, 2018, 29:1660–1671.

The dynamics of microbial diversity in response to biotic and abiotic disturbances provide a sensitive indicator for evaluating the potential stability and degradation of soils in agro-ecosystems. To determine the effect on soil bacterial communities of disturbances by plant (*Robinia pseudoacacia*) growth and oil contamination, 16S rRNA genes were sequenced. Abiotic and biotic disturbances, including treating the soils with sterile water, crude oil, and/or an invasive plant, altered the bacterial community structure in the soils, increased bacterial richness, and reduced bacterial dispersion.



Publications using Novogene's expertise

Year	Journal	Article
2019	Front. Microbiol	Effect of fermented corn-soybean meal on serum immunity, the expression of genes related to gut immunity, gut microbiota, and bacterial metabolites in grower-finisher pigs
2019	The ISME Journal	Wastewater treatment plant resistomes are shaped by bacterial composition, genetic exchange, and upregulated expression in the effluent microbiomes
2019	Nature communications	Pathogen-targeting glycovesicles as a therapy for salmonellosis
2018	Front Microbiol	Metagenomics investigation of agarlytic genes and genomes in mangrove sediments in China: A potential repertory for carbohydrate-active Enzymes
2018	Microbiome	Gut-dependent microbial translocation induces inflammation and cardiovascular events after ST-elevation myocardial infarction
2017	Tumori	Performance comparison of NextSeq and Ion Proton platforms for molecular diagnosis of clinical oncology
2016	J Dairy Sci	Characterization of the indigenous microflora in raw and pasteurized buffalo milk during storage at refrigeration temperature by high-throughput sequencing