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COMPARING METAGENOMIC SEQUENCING APPROACHES

	Metagenomic Amplicon Sequencing	Metagenomic Shotgun Sequencing	Metatranscriptome Sequencing	Long-Read Metagenomic Sequencing
Purpose	Taxonomic profiling of 16S/ITS/18S genes. *"Who is present?"*	Functional potential *"What can they do?"*	Active gene expression *"What are they doing?"*	Genome assembly (MAGs), full genome structure
Targeted Organisms	Target organisms (Bacteria, archaea, fungi)	All organisms (Bacteria, archaea, fungi, viruses, etc.)	All active (RNA-transcribing) organisms (Bacteria, archaea, fungi, viruses)	All organisms (optimized for bacteria and archaea)
Sample Type	gDNA	gDNA	Total RNA	HMW DNA
Platform	Illumina MiSeq i100/NextSeq	Illumina NovaSeq X Plus	Illumina NovaSeq X Plus	PacBio Revio
Basic Output	FASTQ Taxonomy abundance matrix Diversity (alpha, beta)	FASTQ Taxonomy abundance matrix Diversity (alpha, beta)	FASTQ Gene expression table Taxonomy abundance matrix	FASTQ / BAM HIgh-quality MAGs Assembly statistics
Advanced Analysis Options	LEfSe (biomarkers) PICRUSt2 (inferred function)	Functional analysis (UniRef, MetaCyc, KEGG) ARGs, VFs	Differential gene expression (DEGs) Functional analysis (KEGG, COG)	MAG annotation Strain phasing Comparative genomics
Report Available?	Yes	Yes	No (custom analysis only)	Yes
Clean Data Output*	50k, 100k reads	1Gb, 5Gb, and 10Gb options	100M reads	3Gb
Key Benefits	Affordable, rapid profiling for large cohorts.	Comprehensive analysis of all genes, including ARGs and metabolic pathways.	Quantifiy gene expression to link genetic potential to phenotypic reality.	Full genomic resolution and accurate strain phasing across complex regions.
Cost	$	$$	$$$	$$$

*Additional data output (higher Gb/read) available upon request.

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