

Task	Suggested Minimal Read Depth per Sample	Notes:
Taxonomic Profiling (Reference-Based)	0.5-30 Million Reads*	*Suggested Minimum Shallow Sequencing Depth: 500,000 Reads/Sample *Suggested Minimum Normal Sequencing Depth: 5 Million Reads/Sample *Suggested Minimum Deep Sequencing Depth: 30 Million Reads/Sample Relies on existing databases; cannot detect novel or uncharacterized taxa
Taxonomic Profiling (Assembly-Based)	30 Million	Requires deep sequencing to enable reliable metagenome assembly
Functional Profiling (Metabolic Pathways)	6 Million	Dependent on well-annotated gene catalogs
Functional Profiling (Full Proteomic Coverage)	30 Million	Targeting gene-level resolution; best for gene-centric studies or pathway completeness analyses
Antimicrobial Resistance Gene Profiling	80 Million	AMR genes are often in low abundance or on mobile elements; high depth and curated databases needed

	Shallow Sequencing	Normal Sequencing	Deep Sequencing
Reads/sample	~0.5–5M	~5–30M	30M+ (up to 100M+)
Taxonomic resolution	Genus level reliable; species level possible for dominant taxa with good reference database	Species level reliable; some strain-level with good databases	Strain-level good; better resolution of low-abundance and novel taxa
Detect rare taxa	Not Possible	Some	Yes
Functional profiling	Limited	Good	Excellent
Metagenome assembly	Not Possible	Partial/limited	Yes

Sources:

1. <https://www.biorxiv.org/content/10.1101/2025.03.27.645659v1>
2. <https://environmentalmicrobiome.biomedcentral.com/articles/10.1186/s40793-019-0347-1>
3. <https://cdnsiencepub.com/doi/full/10.1139/gen-2021-0120>