JGI Sequencing Product List

Product	default platform	default run type	estimated seq target (per sample)	standard analysis
Microbial/Viral Minimal Draft	Illumina NovaSeq	2x150	200x coverage	assembly, annotation
Microbial Improved Draft/Methylation	PacBio Sequel II	900 min	100x coverage	assembly, annotation, methylation analysis
Microbia/Viral Single Cell/Single Particle Sort	Illumina NovaSeq	2x150	1 Gb (viral); 2 Gb (microbial)	assembly, annotation
Microbial Resequencing	Illumina NovaSeq	2x150	15x coverage for isolates, 300x coverage for populations	mapping to reference, variant detection
Microbial Transcriptome (Expression)	Illumina NovaSeq	2x150	5M non-rRNA genome mappable reads (1 Gb)	mapping to reference, gene counts
Metagenome Cell/Viral Enrichments (Mini-Metagenomes)	Illumina NovaSeq	2x150	1 Gb (viral); 2 Gb (microbial)	assembly, annotation
Metagenome Draft (Minimal, Standard)	Illumina NovaSeq	2x150	Coverage depends on sample complexity; typically from 2-10 Gb for viral metagenomes, not less than 5 Gb for engineered or very simple communities, up to 45Gb for complex communities like soil. Requests of <12Gb are considered minimal drafts; >12Gb/sample are standard drafts.	assembly, annotation, binning
Metagenome Draft (Improved)	PacBio Sequel II	1800 min	Coverage depends on sample complexity; typically from 45-200 Gb	assembly, annotation, binning
Metagenome Draft (SIP)	Illumina NovaSeq	2x150	2 Gb	assembly, annotation
Metatranscriptome	Illumina NovaSeq	2x150	Target 100M reads (15 Gb) but will vary based on sample complexity and success of rRNA depletion method.	assembly, annotation, mapping to own assembly, gene counts
Fungal Standard Draft	PacBio Sequel II	1800 min	200x coverage. Request should also include 1 RNA sample for annotation.	assembly, annotation
Fungal Transcriptome (Annotation)	Illumina NovaSeq	2x150	100M non-rRNA genome mappable reads (17 Gb)	assembly
Fungal Transcriptome (Expression)	Illumina NovaSeq	2x150	20M non-rRNA genome mappable reads (3.5 Gb)	mapping to reference, gene counts
Fungal Resequencing	Illumina NovaSeq	2x150	30x coverage	mapping to reference, variant detection
Algal Draft	Illumina NovaSeq, possibly PacBio Sequel II	2x150	Algal Drafts always begin with an evaluation (100x Illumina coverage). Additional sequencing will be recommended based on the genome evaluation. Each algal draft also needs at least 1 RNA sample for annotation.	assembly, annotation
Algal Transcriptome (Annotation)	Illumina NovaSeq	2x150	200M non-rRNA genome mappable reads (35 Gb)	assembly
Algal Transcriptome (Expression)	Illumina NovaSeq	2x150	30M non-rRNA genome mappable reads (5 Gb)	mapping to reference, gene counts
Algal Resequencing	Illumina NovaSeq	2x150	50x coverage for standard; 5x for skim	mapping to reference, variant detection
Plant Draft	Illumina NovaSeq, possibly PacBio Sequel II	2x150	Plant Drafts always begin with an evaluation (100x Illumina coverage, assembly only) to determine genome size and complexity. Additional sequencing will be recommended based on the genome evaluation. Each plant draft that moves beyond the evaluation stage also needs at least 1 RNA sample for annotation.	assembly, annotation
Plant Transcriptome (Annotation)	Illumina NovaSeq	2x150	200M non-rRNA genome mappable reads (35 Gb)	assembly
Plant Transcriptome (Expression)	Illumina NovaSeq	2x150	30M non-rRNA genome mappable reads (5 Gb)	mapping to reference, gene counts
Plant Resequencing	Illumina NovaSeq	2x150	50x coverage for standard; 5x for skim	mapping to reference, variant detection
IsoSeq (Eukaryotic)	PacBio Sequel II	1800 min	4M reads	genome annotation
DAP-seq	Illumina NovaSeq	2x150	Sequence coverage depends on genome size, typically microbe: 2M reads/TF (0.3 Gb); fungi: 10M reads/TF (1.5 Gb); plant: 20-40M reads/TF (3-6 Gb)	prediction of TF-binding sites

The sequencing targets given here are estimates based on JGI's experience with various sample types using our standard analysis pipelines; if you are requesting sequencing using a different coverage target, please provide an explanation within your proposal.

More details on the products that JGI supports can be found here: https://jgi.doe.gov/our-science/product-offerings/
Estimated amounts of DNA or RNA needed can be found here: https://jgi.doe.gov/user-programs/pmo-overview/project-materials-submission-overview/

These estimates will change as new protocols and/or analysis methods are adopted, and in many cases are dependent on experimental design. If your project is approved, JGI staff will work with you individually to determine how best to meet your scientific goals.

Last updated 1/9/23