JGI sequencing product list with estimated sequencing output

Last updated 1/8/25

Detailed Product Descriptions: https://jgi.doe.gov/work-with-us/offerings-capabilities/product-offerings
Sample Requirements: https://jgi.doe.gov//work-with-us/offerings-capabilities/sequencing-technologies/sample-overview

Product	sequencing platform*	estimated sequencing target (per sample)**	standard analysis
Algal			
Draft Genome	Illumina, possibly PacBio	Algal Drafts begin with an evaluation (100x Illumina coverage). Additional sequencing will be recommended based on the eval.	assembly, annotation
Resequencing	Illumina	50x coverage for standard; 5x for skim	mapping to reference, variant detection
Transcriptome (Annotation)	Illumina	200M non-rRNA genome mappable reads (35 Gb)	assembly
Transcriptome (IsoSeq)	PacBio	4M reads	assembly
Transcriptome (Expression)	Illumina	30M non-rRNA genome mappable reads (5 Gb)	mapping to reference, gene counts, DGE analysis
DAP-Seq	Illumina	Sequence coverage depends on genome size. For a 5Mb genome: 2M reads/TF (0.3 Gb). For a 30 Mb genome: 10M reads/TF (1.5 Gb). For a 200 Mb genome: 20-40M reads/TF (3-6 Gb).	prediction of TF-binding sites
Fungal			
Draft Genome	PacBio	200x coverage. Request should also include 1 RNA sample for annotation.	assembly, annotation
Resequencing	Illumina	30x coverage	mapping to reference, variant detection
Transcriptome (Annotation)	Illumina	100M non-rRNA genome mappable reads (17 Gb)	assembly
Transcriptome (IsoSeq)	PacBio	4M reads	assembly
Transcriptome (Expression)	Illumina	20M non-rRNA genome mappable reads (3.5 Gb)	mapping to reference, gene counts, DGE analysis
DAP-seq	Illumina	Sequence coverage depends on genome size. For a 30 Mb genome: 10M reads/TF (1.5 Gb). For a 200 Mb genome: 20-40M reads/TF (3-6 Gb).	prediction of TF-binding sites
Metagenome			
Metagenome Draft	Illumina	Coverage depends on sample complexity; typically from 2-10 Gb for viral samples, >5 Gb for very simple communities, up to 45Gb for complex communities like soil.	assembly, annotation, binning
Metagenome Improved Draft	PacBio	Coverage depends on sample complexity; typically 4 Gb HiFi CCS reads.	assembly, annotation, binning
Enrichments (mini-metagenomes)	Illumina	1 Gb (viral); 2 Gb (microbial)	assembly, annotation
SIP Metagenome	Illumina	2 Gb	combined assembly, annotation
Metatranscriptome	Illumina	Target 100M reads (15 Gb) but will vary based on sample complexity and success of rRNA depletion/polyA enrichment method.	assembly, annotation, mapping to own assembly, gene counts
Microbial, Viral (single organism)			
Improved Draft Genome	PacBio	100x coverage (microbial)	assembly, annotation, methylation analysis
Draft Genome	Illumina	200x coverage (microbial or viral)	assembly, annotation
Single Cell/ Single Particle Sort	Illumina	1 Gb (viral); 2 Gb (microbial)	assembly, annotation
Resequencing	Illumina	15x coverage for isolates, 300x coverage for populations	mapping to reference, variant detection
Transcriptome (Expression)	Illumina	5M non-rRNA genome mappable reads (1 Gb)	mapping to reference, gene counts, DGE analysis
DAP-seq	Illumina	Sequence coverage depends on genome size. For a 5Mb genome: 2M reads/TF (0.3 Gb).	prediction of TF-binding sites
Plant			
Draft Genome	Illumina, possibly PacBio	Plant Drafts begin with an evaluation (100x Illumina coverage, assembly only) to determine genome size and complexity. Additional sequencing will be recommended based on the eval.	assembly, annotation
Resequencing	Illumina	50x coverage for standard; 5x for skim	mapping to reference, variant detection
Transcriptome (Annotation)	Illumina	200M non-rRNA genome mappable reads (35 Gb)	assembly
Transcriptome (IsoSeq)	PacBio	4M reads	assembly
Transcriptome (Expression)	Illumina	30M non-rRNA genome mappable reads (5 Gb)	mapping to reference, gene counts, DGE analysis
DAP-seq	Illumina	Sequence coverage depends on genome size. For a 200 Mb genome: 20-40M reads/TF (3-6 Gb).	prediction of TF-binding sites

* Illumina sequencing uses 2x150 nt runs on the NovaseqX platform. PacBio sequencing uses 1440 min runs on the Revio platform.

**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.

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