

**JGI Sequencing Product List**

| Product  | default platform                            | default run type | estimated seq target (per sample)  | standard analysis  |
|--|---|------------------|--|--|
| Microbial Minimal Draft                        | Illumina NovaSeq                            | 2x150            | 200x coverage  | assembly, annotation                                       |
| Microbial Improved Draft/Methylation           | PacBio Sequel II                            | 900 min          | 100x coverage  | assembly, annotation, methylation analysis                 |
| Microbial Single Cell/Single Particle Sort     | Illumina NovaSeq                            | 2x150            | 2 Gb   | 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                          |
| Microbial smRNA                                | Illumina NovaSeq                            | 2x150            | 1M non-rRNA genome mappable reads (0.3 Gb)   | mapping to reference, miRNA prediction                     |
| Metagenome Cell Enrichments (Mini-Metagenomes) | Illumina NovaSeq                            | 2x150            | 2 Gb   | 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   | combined 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 smRNA                                   | Illumina NovaSeq                            | 1x75             | 10M non-rRNA genome mappable reads (1.8 Gb)  | mapping to reference, miRNA prediction                     |
| 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 smRNA                                    | Illumina NovaSeq                            | 1x75             | 10M non-rRNA genome mappable reads (1.8 Gb)  | mapping to reference, miRNA prediction                     |
| 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 smRNA                                    | Illumina NovaSeq                            | 1x75             | 10M non-rRNA genome mappable reads (1.8 Gb)  | mapping to reference, miRNA prediction                     |
| Plant Resequencing                             | Illumina NovaSeq                            | 2x150            | 50x coverage for standard; 5x for skim   | mapping to reference, variant detection                    |
| Bisulphite-seq (Eukaryotic)                    | Illumina NovaSeq                            | 2x150            | 30x coverage   | methylation analysis                                       |
| ChIP-seq (Eukaryotic)                          | Illumina NovaSeq                            | 2x150            | 50M genome mappable reads (7.5 Gb)   | prediction of protein binding sites                        |
| IsoSeq (Eukaryotic)                            | PacBio Sequel II                            | 1800 min         | 4M reads   | genome annotation  |

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.**