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IMR Sequencing Services – Current Pricing (January 2016)

16S/18S Amplicon Pricing (per sample) – Academic

| | <50 samples | 50-200 samples | >200 samples ¹ |
|--|-----------------|-----------------|---------------------------|
| Library Preparation + Sequencing (~50,000 seq./sample) | \$23 | \$18 | \$15 |
| DNA/RNA Extraction ² | \$14 | \$14 | \$14 |
| Standard Bioinformatics Analysis Pipeline ³ | \$500 / project | \$750 / project | \$1000 / project |

16S/18S Amplicon Pricing (per sample) – Commercial

| | <50 samples | 50-200 samples | >200 samples ¹ |
|--|-----------------|------------------|---------------------------|
| Library Preparation + Sequencing (~50,000 seq./sample) | \$40 | \$30 | \$25 |
| DNA/RNA Extraction ² | \$16 | \$16 | \$16 |
| Standard Bioinformatics Analysis Pipeline ³ | \$750 / project | \$1000 / project | \$1500 / project |

Metagenome Pricing – MiSeq

| | Academic | | Commercial | |
|--|-----------------|------------|------------------|------------|
| | Per run of 6 | Per sample | Per run of 6 | Per sample |
| Extraction + Library Preparation + Sequencing (~3-4 M seq./sample) | \$3960 | \$660 | \$5400 | \$900 |
| Standard Bioinformatics Analysis Pipeline ⁴ | \$750 / project | | \$1500 / project | |

Metagenome Pricing – NextSeq (coming Spring 2016)

| | Academic | | Commercial | |
|--|-----------------|------------|------------------|------------|
| | Per run of 96 | Per sample | Per run of 96 | Per sample |
| Extraction + Library Preparation + Sequencing (~3-4 M seq./sample) | \$13440 | \$140 | \$19200 | \$200 |
| Standard Bioinformatics Analysis Pipeline ⁴ | \$750 / project | | \$1500 / project | |

Metatranscriptome Pricing – NextSeq (coming Spring 2016)

Contact us – pricing is currently being developed and is dependent upon multiple experimental choices.

Notes/Details:

1. One control well is required per 96-well PCR library plate, hence a maximum of $4 \times 95 = 380$ samples can be done together on one MiSeq run.

2. Extra costs may be incurred if samples, due to their nature, require more specialized (length, cost, etc.) extraction procedures.

3. Details of our 16S pipeline are available at https://github.com/mlangill/microbiome_helper, but the following is a summary of the major deliverables clients will receive (analyses will require a “mapping file” from the clients containing any relevant metadata for the study):

- Combined FASTA file of the quality-controlled sequences (formatted for use in QIIME)
- Final OTU tables in text, BIOM and STAMP formats (from open-ref. picking at 97%)
- FASTA file of representative sequences (one per OTU)
- Taxonomic assignment files at various levels (ex: phylum, genus, etc.)
- Alpha-diversity rarefaction plots
- Beta-diversity UniFrac plots
- Functional prediction files generated from PICRUSt

4. Details of our metagenomics pipeline are available at https://github.com/mlangill/microbiome_helper, but the following is a summary of the major deliverables clients will receive (analyses will require a “mapping file” from the clients containing any relevant metadata for the study):

- FASTA files of the final sequences screened to remove human (or other) contaminants
- Taxonomic composition of the samples from MetaPhlAn 2.0 (text and STAMP files)
- Functional prediction files generated from HUMAnN (text and STAMP files) for individual KO numbers, KEGG modules and KEGG pathways

Custom Bioinformatics: Additional bioinformatic analyses can be requested at an hourly rate or through research collaboration. Please contact us for more details.

Customs primers/amplicons: Beyond the 16/18S amplicons offered “in-stock”, essentially any PCR amplicon (max. size ~550 bp) can be adapted to our MiSeq system. Please consults us for primer design/protocol details.

Processing time: Time to completion may be variable depending the amount of other partial projects in the queue – this applies primarily to amplicon runs when providing less than the full capacity of 380 samples, but may also occur when submitting small numbers of samples for metagenomics runs (<6 for MiSeq or <96 for NextSeq).