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IMR Sequencing Services – Current Pricing (January 2017)

16S/18S/ITS Amplicons (per sample) – Academic

	<50 samples	50-200 samples	>200 samples ¹
Library Preparation + Sequencing (~50,000 reads/sample)	\$30	\$25	\$20
DNA Extraction ²	\$15	\$15	\$15
Standard Bioinformatics Analysis Pipeline ³	\$500 / project	\$750 / project	\$1000 / project

16S/18S/ITS Amplicons (per sample) – Commercial

	<50 samples	50-200 samples	>200 samples ¹
Library Preparation + Sequencing (~50,000 reads/sample)	\$40	\$35	\$30
DNA Extraction ²	\$16	\$16	\$16
Standard Bioinformatics Analysis Pipeline ³	\$750 / project	\$1000 / project	\$1500 / project

Client-Prepared Pool of Amplicons (per whole run) – MiSeq (300+300 bp PE)

	Academic Per run	Commercial Per run
MiSeq Sequencing Run (~20-25 M PE reads)	\$3200	\$4700

Small Genomes (>100X typical 5 Mb genome) – MiSeq (300+300 bp PE)

	Academic		Commercial	
	Per run of 24	Per genome	Per run of 24	Per genome
Library Preparation + Sequencing (~1 M PE reads = 2 M single reads & 600 Mb/genome)	\$6000	\$250	\$8400	\$350
Bioinformatics Analysis Pipeline Dependent Upon Goal of Analysis	inquire		inquire	

Metagenomes – MiSeq (300+300 bp PE)

	Academic		Commercial	
	Per run of 6	Per sample	Per run of 6	Per sample
Library Preparation + Sequencing (~3.5 M PE reads = 7 M single reads & 2.2 Gb/sample)	\$4500	\$750	\$6300	\$1050
DNA Extraction ²	\$90	\$15	\$96	\$16
Standard Bioinformatics Analysis Pipeline ⁴	\$750 / project		\$1500 / project	

Metagenomes – NextSeq (150+150 bp PE)

	Academic		Commercial	
	Per run of (X)	Per sample	Per run of (X)	Per sample
Library Preparation + Sequencing (~3.5 M PE reads = 7 M single reads & 1 Gb/sample)	\$14400 (96)	\$150	\$21120 (96)	\$220
or 2X depth (~7 M PE = 14 M single & 2 Gb/sample)	\$12000 (48)	\$250	\$15360 (48)	\$320
or 3X depth (~10.5 M PE = 21 M single & 3 Gb/sample)	\$11200 (32)	\$350	\$13440 (32)	\$420
or 4X depth (~14 M PE = 28 M single & 4 Gb/sample)	\$10800 (24)	\$450	\$12480 (24)	\$520
DNA Extraction ²	variable	\$15	variable	\$16
Standard Bioinformatics Analysis Pipeline ⁴	\$750 / project		\$1500 / project	

Metatranscriptomes – NextSeq (150+150 bp PE)

	Academic		Commercial	
	Per run of 24	Per sample	Per run of 24	Per sample
Library Preparation + Sequencing (~4 M PE reads = 8 M single reads & 1.2 Gb/sample)	\$13200	\$550	\$19200	\$800
RNA Extraction ²	\$360	\$15	\$384	\$16
Bioinformatics Analysis Pipeline Under Development	inquire		inquire	

Notes/Details:

- 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.
- Extra costs may be incurred if samples, due to their nature, require more specialized (length, cost, etc.) extraction procedures.
- Details of our 16S pipeline are available at https://github.com/LangilleLab/microbiome_helper/wiki, 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):
 - Final OTU tables in text, BIOM and STAMP formats (from open-reference picking at 97% [Bacteria+Archaea+ITS] or 98% [Eukarya])
 - Accompanying QIIME-formatted mapping file
 - FASTA file of representative sequences (one per OTU)
 - Phylogenetic tree of OTUs placed within reference sequences
 - Taxonomic assignment files at various levels (ex: phylum, genus, etc.)
 - Alpha-diversity rarefaction plots
 - Beta-diversity UniFrac plots
 - Logfiles from the various major steps in the QC process
 - Functional prediction files generated from PICRUSt (if requested)

4. Details of our metagenomics pipeline are available at https://github.com/LangilleLab/microbiome_helper/wiki, 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/ITS amplicons offered “in-stock”, essentially any PCR amplicon (max. size ~550 bp) can be adapted to our MiSeq system. Please consult 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).