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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 <sup>1</sup>
Library Preparation + Sequencing (max. 50k reads/sample <sup>2</sup> )	\$30	\$25	\$20
or 2X depth (max. 100k reads/sample <sup>2</sup> )	\$45	\$38	\$30
DNA Extraction <sup>3</sup>	\$15	\$15	\$15
Standard Bioinformatics Analysis Pipeline <sup>4</sup>	\$500/project	\$750/project	\$1000/project

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

	<50 samples	50-200 samples	>200 samples <sup>1</sup>
Library Preparation + Sequencing (max. 50k reads/sample <sup>2</sup> )	\$40	\$35	\$30
or 2X depth (max. 100k reads/sample <sup>2</sup> )	\$60	\$53	\$45
DNA Extraction <sup>3</sup>	\$16	\$16	\$16
Standard Bioinformatics Analysis Pipeline <sup>4</sup>	\$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) – Resequencing

	Academic		Commercial	
	Per run of 24	Per genome	Per run of 24	Per genome
Library Preparation + Sequencing (~0.9 M PE reads = 1.8 M single reads & 540 Mb/gen.)	\$6000	\$250	\$8400	\$350
Bioinformatics Analysis Pipeline Dependent Upon Goal of Analysis	inquire		inquire	

### *Small Genomes (>400X typical 5 Mb genome) – PacBio Sequel (long reads) – De novo Assembly*

	Academic		Commercial	
	Per run of 6	Per genome	Per run of 6	Per genome
Library Preparation + Sequencing (~2 Gb/genome)	\$3900	\$650	\$5700	\$950
Bioinformatics Analysis Pipeline Dependent Upon Goal of Analysis	inquire		inquire	

*Note: PacBio pricing is currently introductory and could change within 2019 as we perfect the system/depths of coverage.*

### *Mid-Sized Genomes (>400X typical 15-30 Mb genome) – PacBio Sequel (long reads) – De novo Assembly*

	Academic		Commercial	
	Per cell		Per cell	
Library Preparation + Sequencing (~12 Gb and ~425k reads/cell)	\$2500		\$3700	
Bioinformatics Analysis Pipeline Dependent Upon Goal of Analysis	inquire		inquire	

*Note: PacBio pricing is currently introductory and could change within 2019 as we perfect the system/depths of coverage.*

### *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 & 2.1 Gb/sample)	\$4500	\$750	\$6300	\$1050
DNA Extraction <sup>3</sup>	\$90	\$15	\$96	\$16
Standard Bioinformatics Analysis Pipeline <sup>5</sup>	\$750/project		\$1500/project	

### *Metagenomes – NextSeq (150+150 bp PE) – Regular Depths*

	Academic		Commercial	
	Per run of (X)	Per sample	Per run of (X)	Per sample
Library Preparation + Sequencing (~4 M PE reads = 8 M single reads & 1.2 Gb/sample)	\$14400 (96)	\$150	\$21120 (96)	\$220
or 2X depth (~8 M PE = 16 M single & 2.4 Gb/sample)	\$12000 (48)	\$250	\$15360 (48)	\$320
or 3X depth (~12 M PE = 24 M single & 3.6 Gb/sample)	\$11200 (32)	\$350	\$13440 (32)	\$420
or 4X depth (~16 M PE = 32 M single & 4.8 Gb/sample)	\$10800 (24)	\$450	\$12480 (24)	\$520
DNA Extraction <sup>3</sup>	variable	\$15	variable	\$16
Standard Bioinformatics Analysis Pipeline <sup>5</sup>	\$750/project		\$1500/project	

### Metagenomes – NextSeq (150+150 bp PE) – High Depths

	Academic Per run of (X)	Commercial Per run of (X)
Library Preparation + Sequencing (Whole run = ~400 M PE reads = 800 M single & 120 Gb)	-	-
<6 samples (80+ M PE reads = 160+ M single)	\$7000 (<6)	\$10500 (<6)
6-8 samples (~50-67 M PE reads = 100-133 M single)	\$8000 (6-8)	\$12000 (6-8)
9-10 samples (~40-44 M PE reads = 80-88 M single)	\$9000 (9-10)	\$13500 (9-10)
11-12 samples (~33-36 M PE reads = 66-73 M single)	\$10000 (11-12)	\$15000 (11-12)
DNA Extraction <sup>3</sup>	variable	variable
Standard Bioinformatics Analysis Pipeline <sup>5</sup>	\$750/project	\$1500/project

### (Meta)transcriptomes – NextSeq (150+150 bp PE) – under development

	Academic		Commercial	
	Per run of 24	Per sample	Per run of 24	Per sample
Library Preparation + Sequencing (~17 M PE reads = 33 M single reads & 5 Gb/sample)	<b>\$13200</b>	<b>\$550</b>	<b>\$19200</b>	<b>\$800</b>
RNA Extraction <sup>3</sup>	<b>\$360</b>	<b>\$15</b>	<b>\$384</b>	<b>\$16</b>
Bioinformatics Analysis Pipeline Under Development	inquire		inquire	

### Iso-Seq – PacBio Sequel (long reads) – Full-Length Isoform Transcripts

	Academic Per cell	Commercial Per cell
Library Preparation + Sequencing (~12 Gb and ~425k reads/cell)	\$2500	\$3700
Standard PacBio Iso-Seq Pipeline <sup>5</sup>	inquire	inquire

*Note: PacBio pricing is currently introductory and could change within 2019 as we perfect the system/depths of coverage.*

### 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. These are generally maximum raw read outputs you will received, but there is inherent variability in MiSeq runs, meaning averages can be closer to 30k (1X) & 60k (2X).
3. Extra costs may be incurred if samples, due to their nature, require more specialized (length, cost, etc.) extraction procedures.

4. Details of our 16S pipeline are available at [https://github.com/LangilleLab/microbiome\\_helper/wiki](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 ASV/OTU tables in text, BIOM and STAMP formats
- Accompanying QIIME-formatted mapping/metadata file
- FASTA file of representative sequences (one per ASV/OTU)
- Phylogenetic tree of ASVs/OTUs placed within reference sequences
- Taxonomic assignment files at various levels (ex: phylum, genus, etc.)
- Alpha-diversity rarefaction plots + statistics
- Beta-diversity UniFrac plots
- Logfiles from the various major steps in the QC process
- Functional prediction files generated from PICRUSt2.0 (if requested)

5. Details of our metagenomics pipeline are available at [https://github.com/LangilleLab/microbiome\\_helper/wiki](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 (available upon request)
- Taxonomic composition of the samples from MetaPhlAn 2.0 (text and STAMP files)
- Stratified (by taxa) and unstratified functional prediction files generated from HUMAnN 2.0 (text and STAMP files) for individual UniRef90 gene families and MetaCyc 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 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 small numbers of samples for metagenomics runs (<6 for MiSeq or <96 for NextSeq) or PacBio SMRT cells.