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## IMR Sequencing Services – Current Pricing (January 2017+)

**All prices listed are in Canadian Dollars (CAD). International orders must add a \$25/shipment fee to cover Customs costs.**

*Note: PacBio pricing is currently introductory and could change within 2022 as we perfect the system/depths of coverage.*

### 16S/18S/ITS Short Amplicons (per sample, per amplicon) - MiSeq (2x300 bp PE) – Academic/Govt.

	<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 Short Amplicons (per sample, per amplicon) - MiSeq (2x300 bp PE) - 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>	\$20	\$20	\$20
Standard Bioinformatics Analysis Pipeline <sup>4</sup>	\$750/project	\$1000/project	\$1500/project

### 16S/18S/ITS Full-Length Amplicons (per sample, per amplicon) - PacBio Sequel2 (long reads) – Academic/Govt.

	<50 samples	50-200 samples	>200 samples <sup>1</sup>
Library Preparation + Sequencing (max. 10k CCS reads/sample <sup>2</sup> )	\$35	\$30	\$25
or 2X depth (max. 20k CCS reads/sample <sup>2</sup> )	\$53	\$45	\$38
DNA Extraction <sup>3</sup>	\$15	\$15	\$15
Standard Bioinformatics Analysis Pipeline <sup>4</sup>	\$500/project	\$750/project	\$1000/project

### 16S/18S/ITS Full-Length Amplicons (per sample, per amplicon) - PacBio Sequel2 (long reads) - Commercial

	<50 samples	50-200 samples	>200 samples <sup>1</sup>
Library Preparation + Sequencing (max. 10k CCS reads/sample <sup>2</sup> )	\$50	\$45	\$40
or 2X depth (max. 20k CCS reads/sample <sup>2</sup> )	\$75	\$67	\$60
DNA Extraction <sup>3</sup>	\$20	\$20	\$20
Standard Bioinformatics Analysis Pipeline <sup>4</sup>	\$750/project	\$1000/project	\$1500/project

**Client-Prepared Pool of Amplicons (per whole run) – MiSeq (2x300 bp or 2x150bp PE)**

	Academic/Govt.		Commercial	
	Per run		Per run	
MiSeq Standard Run (~20-25 M PE reads & 12-15 Gb)	\$3000		\$4500	
MiSeq Micro 2x150 bp Run (~4 M PE reads & 1.2 Gb)	\$950		\$1400	
MiSeq Nano 2x150 bp Run (~1 M PE reads & 0.3 Gb)	\$700		\$1000	

Note: For clients wishing to use part of a run with a prepared pool of amplicons, simply divide 380 by your sample # times the above price to determine your pool cost (this is for a 1X depth, simply double the amount for 2X).

**Client-Prepared Pool of Metagenomes (per whole run) – NextSeq (2x150 bp PE)**

	Academic/Govt.		Commercial	
	Per run		Per run	
NextSeq Sequencing Run (~400 M PE reads)	\$8500		\$13000	

Note: For clients wishing to use part of a run with a prepared pool of metagenomes, simply divide 96 by your sample # times the above price to determine your pool cost (this is for a 1X depth).

**Viral/Phage Genomes (1000X typical 150 kb genome) – MiSeq (2x300 bp PE) – De novo Assembly**

	Academic/Govt.		Commercial	
	Per genome		Per genome	
Library Preparation + Sequencing (~0.25 M PE reads = 0.5 M single reads & 150 Mb/gen.)	\$100		\$150	
Bioinformatics Analysis Pipeline Dependent Upon Goal of Analysis	inquire		inquire	

**Small Genomes (>100X typical 5 Mb genome) – MiSeq (2x300 bp PE) – Resequencing**

	Academic/Govt.		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 Sequel2 (long reads) – De novo Assembly**

	Academic/Govt.		Commercial	
	Per run of 48	Per genome	Per run of 48	Per genome
Library Preparation + Sequencing (~2 Gb/genome)	\$10800	\$225	\$16320	\$340
Bioinformatics Analysis Pipeline Dependent Upon Goal of Analysis	inquire		inquire	

**(Micro)Eukaryote Genomes (100 Gb per cell) – PacBio Sequel2 (long reads) – De novo Assembly**

	Academic/Govt.		Commercial	
	Per run of (X)	Per genome	Per run of (X)	Per genome
Library Preparation + Sequencing (~50 Gb/genome)	\$3200 (2)	\$1600	\$4800 (2)	\$2400
<b>or</b> whole cell (~100 Gb/genome)	\$3000 (1)	\$3000	\$4500 (1)	\$4500
Bioinformatics Analysis Pipeline Dependent Upon Goal of Analysis	inquire		inquire	

**Metagenomes – NextSeq (2x150 bp PE) – Regular Depths**

	Academic/Govt.		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
<b>or</b> 2X depth (~8 M PE = 16 M single & 2.4 Gb/sample)	\$12000 (48)	\$250	\$15360 (48)	\$320
<b>or</b> 3X depth (~12 M PE = 24 M single & 3.6 Gb/sample)	\$11200 (32)	\$350	\$13440 (32)	\$420
<b>or</b> 4X depth (~16 M PE = 32 M single & 4.8 Gb/sample)	\$10800 (24)	\$450	\$12480 (24)	\$520
DNA Extraction <sup>3</sup>	\$15/sample		\$20/sample	
Standard Bioinformatics Analysis Pipeline <sup>5</sup>	\$1000/project		\$1500/project	

**Metagenomes – NextSeq (2x150 bp PE) – High Depths**

	Academic/Govt.	Commercial
	Per run of (X)	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>	\$15/sample	\$20/sample
Standard Bioinformatics Analysis Pipeline <sup>5</sup>	\$1000/project	\$1500/project

**Metagenomes – PacBio Sequel2 (long reads) - MAG Assembly**

	Academic/Govt.		Commercial	
	Per run of (X)	Per sample	Per run of (X)	Per sample
Library Preparation + Sequencing (~50 Gb/sample)	\$3200 (2)	\$1600	\$4800 (2)	\$2400
<b>or</b> whole cell (~100 Gb/sample)	\$3000 (1)	\$3000	\$4500 (1)	\$4500
DNA Extraction <sup>3</sup>	\$15/sample		\$20/sample	
Bioinformatics Analysis Pipeline Dependent Upon Goal of Analysis	inquire		inquire	

### *(Meta)transcriptomes – NextSeq (2x150 bp PE) – Total Stranded RNA w/rRNA Depletion*

	Academic/Govt.		Commercial	
	Per run of 24	Per sample	Per run of 24	Per sample
Library Preparation + Sequencing (~16 M PE reads = 32 M single reads & 4.8 Gb/sample)	\$13200	\$550	\$19200	\$800
RNA Extraction <sup>3</sup>	Not yet available		Not yet available	
Standard Bioinformatics Analysis Pipeline <sup>5</sup>	\$1000/project		\$1500/project	

### *Iso-Seq – PacBio Sequel2 (long reads) – Full-Length Isoform Transcripts*

	Academic/Govt.		Commercial	
	Per run of 8	Per sample	Per run of 8	Per sample
Library Preparation + Sequencing (~12 Gb and ~500k reads/sample)	\$4000	\$500	\$6000	\$750
RNA Extraction <sup>3</sup>	Not yet available		Not yet available	
Standard PacBio Iso-Seq Pipeline	\$1000/project		\$1500/project	

#### 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 (190 for a 2X run) or  $2 \times 95 = 190$  samples on a Sequel 2 run (95 for a 2X run). Any batches  $>380/190$  will need to be spread across multiple MiSeq/Sequel 2 runs.
2. These are generally maximum raw read outputs you will received, but there is inherent variability in runs, meaning averages can be closer to 30k/60k (MiSeq 1X/2X) or 8k/16k (Sequel 2 1X/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 16S/18S/ITS amplicons offered "in-stock", essentially any PCR amplicon (max. size ~550 bp, best ~450-500 bp for MiSeq; no size limit for Sequel2) can be adapted to our systems. Please consult us for primer design/protocol details. Pricing is as follows (one-time extra oligo ordering charge): \$750/1000/1500 for oligos for 1-95/96-190/191-380 samples for MiSeq; \$250/500 for oligos for 1-95/96-190 samples for Sequel2.

**Processing time:** Time to completion may be variable depending upon the amount of other partial projects in the queue – this generally no longer applies to amplicons as we are at capacity, but occurs more when submitting small numbers of samples for metagenomics runs (<<96 for NextSeq) or *de novo* genomes (<<48 for Sequel 2).