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

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

### 16S/18S/ITS Short Amplicons (per sample, per amplicon) - MiSeq (300+300 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 (300+300 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 Sequel (long reads)

	Academic/Govt. Per sample	Commercial Per sample
Library Preparation + Sequencing (max. 5k CCS reads/sample <sup>2</sup> )	<del>\$50</del> \$45	<del>\$75</del> \$67
or 2X depth (max. 10k reads/sample <sup>2</sup> )	<del>\$75</del> \$67	<del>\$115</del> \$100
or 0.5X depth (max. 2k reads/sample <sup>2</sup> ) < Sanger alternative	<del>\$30</del> \$25	<del>\$45</del> \$40
DNA Extraction <sup>3</sup>	\$15	\$20
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.**

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

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

### ***Viral/Phage Genomes (1000X typical 150 kb genome) – MiSeq (300+300 bp PE) – De novo Assembly***

	<b>Academic/Govt. Per genome</b>	<b>Commercial Per genome</b>
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 (300+300 bp PE) – Resequencing***

	<b>Academic/Govt.</b>		<b>Commercial</b>	
	<b>Per run of 24</b>	<b>Per genome</b>	<b>Per run of 24</b>	<b>Per genome</b>
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***

	<b>Academic/Govt.</b>		<b>Commercial</b>	
	<b>Per run of 6</b>	<b>Per genome</b>	<b>Per run of 6</b>	<b>Per genome</b>
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***

	<b>Academic/Govt. Per cell</b>	<b>Commercial Per cell</b>
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 – NextSeq (150+150 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
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	\$20
Standard Bioinformatics Analysis Pipeline <sup>5</sup>	\$750/project		\$1500/project	

### Metagenomes – NextSeq (150+150 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>	variable	variable
Standard Bioinformatics Analysis Pipeline <sup>5</sup>	\$750/project	\$1500/project

### Metagenomes – MiSeq (300+300 bp PE)

	Academic/Govt.		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	\$120	\$20
Standard Bioinformatics Analysis Pipeline <sup>5</sup>	\$750/project		\$1500/project	

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

	Academic/Govt.		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)	\$13200	\$550	\$19200	\$800
RNA Extraction <sup>3</sup>	\$360	\$15	\$480	\$20
Bioinformatics Analysis Pipeline Under Development	inquire		inquire	

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

	Academic/Govt. 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 runs, meaning averages can be closer to 30k (MiSeq 1X), 60k (MiSeq 2X) or TBA (Sequel).
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.