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IMR Sequencing Services – Current Pricing (2017-2023)

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 (2x300 bp PE) – Academic/Govt.

	<50 samples	50-200 samples	>200 samples ¹
Library Preparation + Sequencing (max. 50k reads/sample ²)	\$30	\$25	\$20
or 2X depth (max. 100k reads/sample ²)	\$45	\$38	\$30
DNA Extraction ³	\$15	\$15	\$15
Standard Bioinformatics Analysis Pipeline ⁴	\$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 ¹
Library Preparation + Sequencing (max. 50k reads/sample ²)	\$40	\$35	\$30
or 2X depth (max. 100k reads/sample ²)	\$60	\$53	\$45
DNA Extraction ³	\$20	\$20	\$20
Standard Bioinformatics Analysis Pipeline ⁴	\$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 ¹
Library Preparation + Sequencing (max. 10k CCS reads/sample ²)	\$35	\$30	\$25
or 2X depth (max. 20k CCS reads/sample ²)	\$53	\$45	\$38
DNA Extraction ³	\$15	\$15	\$15
Standard Bioinformatics Analysis Pipeline ⁴	\$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 ¹
Library Preparation + Sequencing (max. 10k CCS reads/sample ²)	\$50	\$45	\$40
or 2X depth (max. 20k CCS reads/sample ²)	\$75	\$67	\$60
DNA Extraction ³	\$20	\$20	\$20
Standard Bioinformatics Analysis Pipeline ⁴	\$750/project	\$1000/project	\$1500/project

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

	Academic/Govt. Per run	Commercial 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 standard run 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) – NextSeq2000 (2x150 bp PE)

	Academic/Govt. Per run	Commercial Per run
NextSeq2000 P1 cell Run (~100 M PE reads)	\$2400	\$3000
NextSeq2000 P2 cell Run (~400 M PE reads)	\$6500	\$7000
NextSeq2000 P3 cell Run (~1.2 B PE reads)	\$10000	\$10500

Note: For clients wishing to use part of a run with a prepared pool of metagenomes, simply divide 192 by your sample # times the above P3 cell 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. Per genome	Commercial Per genome
Library Preparation + Sequencing (~0.25 M PE reads = 0.5 M single reads & 150 Mb/gen.)	\$100	\$150
Custom Bioinformatics Analysis Pipeline	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
Custom Bioinformatics Analysis Pipeline	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
Custom Bioinformatics Analysis Pipeline	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
or whole cell (~100 Gb/genome)	\$3000 (1)	\$3000	\$4500 (1)	\$4500
Custom Bioinformatics Analysis Pipeline	inquire		inquire	

Metagenomes – NextSeq2000 (2x150 bp PE P3 cell) – Profiling and Contig Assembly

	Academic/Govt.		Commercial	
	Per run of (X)	Per sample	Per run of (X)	Per sample
Library Preparation + Sequencing (~6 M PE reads = 12 M single reads & 1.8 Gb/sample)	\$24960 (192)	\$130	\$38400 (192)	\$200
or 2X depth (~12 M PE = 24 M single & 3.6 Gb/sample)	\$19200 (96)	\$200	\$28800 (96)	\$300
or 4X depth (~24 M PE = 48 M single & 7.2 Gb/sample)	\$14400 (48)	\$300	\$21600 (48)	\$450
or 6X depth (~36 M PE = 72 M single & 11 Gb/sample)	\$13600 (32)	\$425	\$20800 (32)	\$650
or 8X depth (~48 M PE = 96 M single & 14 Gb/sample)	\$13200 (24)	\$550	\$19800 (24)	\$825
or 12X depth (~72 M PE = 144 M single & 22 Gb/sam.)	\$12000 (16)	\$750	\$18000 (16)	\$1125
or 16X depth (~96 M PE = 192 M single & 29 Gb/sam.)	\$11700 (12)	\$975	\$17400 (12)	\$1450
or 24X depth (~144 M PE = 288 M single & 43 Gb/sam.)	\$11400 (8)	\$1425	\$17200 (8)	\$2150
or 32X depth (~192 M PE = 384 M single & 58 Gb/sam.)	\$11400 (6)	\$1900	\$17100 (6)	\$2850
DNA Extraction ³	\$15/sample		\$20/sample	
Standard Bioinformatics Analysis Pipeline ⁵	\$1000/project		\$1500/project	

Metagenomes – PacBio Sequel2 (long reads) – Shallow Profiling

	Academic/Govt.		Commercial	
	Per run of 48	Per sample	Per run of 48	Per sample
Library Preparation + Sequencing (~2 Gb/sample)	\$10800	\$225	\$16320	\$340
DNA Extraction ³	\$15/sample		\$20/sample	
Custom Bioinformatics Analysis Pipeline	inquire		inquire	

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
or whole cell (~100 Gb/sample)	\$3000 (1)	\$3000	\$4500 (1)	\$4500
DNA Extraction ³	\$15/sample		\$20/sample	
Custom Bioinformatics Analysis Pipeline	inquire		inquire	

(Meta)transcriptomes – NextSeq2000 (2x150 bp PE P3 cell) – Total Stranded RNA w/rRNA Depletion

	Academic/Govt.		Commercial	
	Per run of 48	Per sample	Per run of 48	Per sample
Library Preparation + Sequencing (~24 M PE reads = 48 M single reads & 7.2 Gb/sample)	\$26400	\$550	\$38400	\$800
RNA Extraction ³	Not yet available		Not yet available	
Bioinformatics Analysis Pipeline Under Development	\$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 ³	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 4x95=380 samples can be done together on one MiSeq run (190 for a 2X run) or 2x95=190 samples on a Sequel2 run (95 for a 2X run). Any batches >380/190 will need to be spread across multiple MiSeq/Sequel2 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 12k/24k (Sequel2 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, 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, 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 (<<192 for NextSeq2000) or *de novo* genomes (<<48 for Sequel2).