

## IMR Sequencing Services – Pricing as of June 1, 2025

# All prices listed are in Canadian Dollars (CAD). GST/HST will be added to all Canadian orders. A fee of \$25/shipment to cover Customs costs will be added to all international orders.

16S/18S/ITS Short Amplicons (per sample, per amplicon) – MiSeq i100 (2x300 bp PE)						
	Academic/Govt. Commercial					
	Per sample <sup>1</sup>	Per sample <sup>1</sup>				
Library Preparation + Sequencing (max. 75k reads/sample <sup>2</sup> )	\$30	\$40				
or 2X depth (max. 150k reads/sample <sup>2</sup> )	\$45	\$55				
DNA Extraction <sup>3</sup>	\$35	\$45				
Standard Bioinformatics Analysis Pipeline <sup>4</sup>	\$1000/project	\$1500/project				

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

	Academic/Govt.	Commercial
	Per sample <sup>1</sup>	Per sample <sup>1</sup>
Library Preparation + Sequencing (max. 35k HiFi reads/sample <sup>2</sup> )	\$35	\$45
or 2X depth (max. 70k HiFi reads/sample <sup>2</sup> )	\$65	\$75
DNA Extraction <sup>3</sup>	\$35	\$45
Standard Bioinformatics Analysis Pipeline <sup>4</sup>	\$1000/project	\$1500/project

#### Client-Prepared Pool of Amplicons (per whole run) – MiSeq i100 (150/250/300 PE)

	Academic/Govt.	Commercial
	Per run	Per run
MiSeq Nano 2x250 bp Run (~1 M PE reads & 0.3 Gb) - typically for ~20 samples	\$2400	\$3000
MiSeq Micro 2x150 bp Run (~4 M PE reads & 1.2 Gb) - typically for ~75 samples	\$2600	\$3200
MiSeq Standard 2x300 bp Run (~20-25 M PE reads & 12-15 Gb) - typically for ~380 samples	\$6000	\$7000
MiSeq i100 5M 2x150 bp Run (~5 M PE reads & 1.5 Gb) - typically for ~75 samples	\$1700	\$2000
MiSeq i100 5M 2x300 bp Run (~5 M PE reads & 3 Gb) - typically for ~75 samples	\$2300	\$2500
MiSeq i100 25M 2x150 bp Run (~25 M PE reads & 7 Gb) - typically for ~380 samples	\$2800	\$3200
MiSeq i100 25M 2x300 bp Run (~25 M PE reads & 15 Gb) - typically for ~380 samples	\$3300	\$3600

Note: For clients wishing to use part of a Standard (old MiSeq) or 25M (i100) run with a prepared pool of amplicons, simply divide 380 by your sample # then multiply by 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) – NextSeq2000 (2x150 bp PE)

	Academic/Govt.	Commercial
	Per run	Per run
NextSeq2000 P1 cell Run (~100 M PE reads = 200 M single reads & 30 Gb)	\$4200	\$5200
NextSeq2000 P2 cell Run (~400 M PE reads = 800 M single reads & 120 Gb)	\$9400	\$10400
NextSeq2000 P3 cell Run (~1.2 B PE reads = 2.4 B single reads & 360 Gb)	\$13000	\$14000

Note: For clients wishing to use part of a P3 run with a prepared pool of metagenomes, simply divide 192 by your sample # then multiply by the above price to determine your pool cost (this is for a 1X depth).

Viral/Phage Genomes (~1000X typical 150 kb gen.) – MiSeq i100 (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.)	\$200	\$300			
DNA Extraction <sup>3</sup>	\$35	\$45			
Custom Bioinformatics Analysis Pipeline	inquire	inquire			

Prokaryote Genomes (~100X typical 5 Mb genome) – MiSeq i100 (2x300 bp PE) – Resequencing					
	Academ	ic/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.)	\$12000	\$500	\$14400	\$600	
DNA Extraction <sup>3</sup>	-	\$35	-	\$45	
Custom Bioinformatics Analysis Pipeline	inquire		inquire		

#### Prokaryote Genomes (~100X typical 5 Mb genome) – PacBio Vega (long reads) – De novo Assembly

	Academic/Govt.		Commercial	
	Per run of 48	Per genome	Per run of 48	Per genome
Library Preparation + Sequencing (~500 Mb HiFi/genome) <sup>5</sup>	\$13200	\$275	\$17520	\$365
DNA Extraction <sup>3</sup>	-	\$35	-	\$45
Custom Bioinformatics Analysis Pipeline	inquire		inqu	uire

#### Fungal Genomes (~100X typical 30-40 Mb genome) – NextSeq2000 (2x150 bp PE) – Reseq. or Hybrid

	Academic/Govt.		Commercial	
	Per run of 96	Per genome	Per run of 96	Per genome
Library Preparation + Sequencing (~12 M PE reads = 24 M single reads & 3.6 Gb/genome)	\$24960	\$260	\$32640	\$340
DNA Extraction <sup>3</sup>	-	\$35	-	\$45
Custom Bioinformatics Analysis Pipeline	inquire		inquire	

Fungal Genomes (~100X typical 40 Mb genome) – PacBio Vega (long reads) – De novo Assembly					
	Academ	c/Govt. Commercial		nercial	
	Per run of 5	Per genome	Per run of 5	Per genome	
Library Preparation + Sequencing (~4 Gb HiFi/genome) <sup>5</sup>	\$6000	\$1200	\$8000	\$1600	
DNA Extraction <sup>3</sup>	-	\$35	-	\$45	
Custom Bioinformatics Analysis Pipeline	inquire		inquire		

## (Micro)Eukaryote Genomes (20 Gb HiFi per cell)<sup>5</sup> – PacBio Vega (long reads) – De novo Assembly

	Academic/Govt.		Commercial	
	Per run of (X)	Per genome	Per run of (X)	Per genome
Library Preparation + Sequencing (~10 Gb HiFi) <sup>5</sup>	\$6000 (2)	\$3000	\$8000 (2)	\$4000
or whole cell (~20 Gb HiFi) <sup>5</sup>	\$5500 (1)	\$5500	\$6500 (1)	\$6500
DNA Extraction <sup>3</sup>	-	\$35	-	\$45
Custom Bioinformatics Analysis Pipeline	inquire		inqu	uire

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

	Academic/Govt.		Comm	ercial
	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)	\$34560 (192)	\$180	\$46080 (192)	\$240
or 2X depth (~12 M PE = 24 M single & 3.6 Gb/sample)	\$24960 (96)	\$260	\$32640 (96)	\$340
or 4X depth (~24 M PE = 48 M single & 7.2 Gb/sample)	\$20160 (48)	\$420	\$26880 (48)	\$560
or 6X depth (~36 M PE = 72 M single & 11 Gb/sample)	\$18880 (32)	\$590	\$25280 (32)	\$790
or 8X depth (~48 M PE = 96 M single & 14 Gb/sample)	\$18240 (24)	\$760	\$24000 (24)	\$1000
<b>or</b> 12X depth (~72 M PE = 144 M single & 22 Gb/sam.)	\$17280 (16)	\$1080	\$23200 (16)	\$1450
<b>or</b> 16X depth (~96 M PE = 192 M single & 29 Gb/sam.)	\$16800 (12)	\$1400	\$22800 (12)	\$1900
or 24X depth (~144 M PE = 288 M single & 43 Gb/sam.)	\$16400 (8)	\$2050	\$22400 (8)	\$2800
or 32X depth (~192 M PE = 384 M single & 58 Gb/sam.)	\$16200 (6)	\$2700	\$21600 (6)	\$3600
DNA Extraction <sup>3</sup>	-	\$35	-	\$45
Standard Bioinformatics Analysis Pipeline <sup>4</sup>	\$1000/ <sub> </sub>	project	\$1500/project	

Metagenomes – PacBio Vega (long reads) – Shallow Profiling				
	Academ	Comm	ommercial	
	Per run of 48	Per sample	Per run of 48	Per sample
Library Preparation + Sequencing (~500 Mb HiFi/sample) <sup>5</sup>	\$13200	\$275	\$17520	\$365
DNA Extraction <sup>3</sup>	-	\$35	-	\$45
Custom Bioinformatics Analysis Pipeline	inquire		inquire	

#### Metagenomes – PacBio Vega (long reads) – MAG Assembly

	Academic/Govt.		Commercial	
	Per run of (X)	Per sample	Per run of (X)	Per sample
Library Preparation + Sequencing (~10 Gb HiFi)⁵	\$6000 (2)	\$3000	\$8000 (2)	\$4000
or whole cell (~20 Gb HiFi)⁵	\$5500 (1)	\$5500	\$6500 (1)	\$6500
DNA Extraction <sup>3</sup>	-	\$35	-	\$45
Custom Bioinformatics Analysis Pipeline	inquire		inquire	

(Meta)transcriptomes – NextSeq2000 (2x150 bp PE P3 cell) – Total Stranded w/rRNA Depletion
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	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)	\$26880	\$560	\$34800	\$725
RNA Extraction <sup>3</sup>	Not yet available		Not yet available	
Standard Bioinformatics Analysis Pipeline <sup>4</sup>	\$1000/project		\$1500/project	

Iso-Seq – PacBio Vega (long reads) – Full-Length Isoform Transcripts							
	Academic/Govt.		Commercial				
	Per run of 8	Per sample	Per run of 8	Per sample			
Library Preparation + Sequencing (~2.5 Gb HiFi and ~800k reads/sample) $^{\scriptscriptstyle 5}$	inquire	inquire	inquire	inquire			
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 4x95=380 samples can be done together on one MiSeq run (190 for a 2X run) or 2x95=190 samples on a Vega run (95 for a 2X run). Any batches >380/190 will need to be spread across multiple MiSeq/Vega runs.

2. These are generally maximum raw read outputs you will receive: there is inherent variability in runs and the performance of samples, depending on their quality, so expect a potential range of outputs as there is no way to guarantee the performance of complex DNA samples.

3. Extra costs may be incurred if samples, due to their nature, require more specialized (length, cost, etc.) extraction procedures.

4. Details of our amplicon and metagenomics pipelines are available at

<u>https://github.com/LangilleLab/microbiome\_helper/wiki</u>, but a summary of the major deliverables clients will receive are available on our IMR.bio Protocols page (<u>http://imr.bio/protocols.html</u>). Analyses will require a "mapping file" from the clients containing any relevant metadata for the study.

5. These Gb values are for the estimated HiFi (CCS) reads obtained and are dependent upon the final size of the library inserts, which can vary depending on the quality of the DNA and resulting library success.

**Custom Bioinformatics**: Additional bioinformatic analyses can be requested at a project-based 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 Vega) can be adapted to our systems. Please consults us for primer design/protocol details. Pricing is as follows (one-time extra oligo ordering charge): \$1050/1400/2100 for oligos for 1-95/96-190/191-380 samples for MiSeq; \$350/700 for oligos for 1-95/96-190/191-380 samples for MiSeq; \$350/700 for oligos for 1-95/96-190 samples for Vega.

**Processing time:** Time to completion may be variable depending upon the amount of other partial projects in the queue – amplicons are always full (so not a problem), but occurs more when submitting small numbers of samples for metagenomics runs (<<192 for NextSeq2000) or *de novo* genomes (<<48 for Vega).