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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[1]
Library Preparation + Sequencing (~50,000 reads/sample)	$30	$25	$20
or 2X depth (~100,000 reads/sample)	$45	$38	$30
DNA Extraction[2]	$15	$15	$15
Standard Bioinformatics Analysis Pipeline[3]	$500/project	$750/project	$1000/project

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

	<50 samples	50-200 samples	>200 samples[1]
Library Preparation + Sequencing (~50,000 reads/sample)	$40	$35	$30
or 2X depth (~100,000 reads/sample)	$60	$53	$45
DNA Extraction[2]	$16	$16	$16
Standard Bioinformatics Analysis Pipeline[3]	$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 Per run of 24	Academic Per genome	Commercial Per run of 24	Commercial 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	

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[2]	$90	$15	$96	$16
Standard Bioinformatics Analysis Pipeline[4]	$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[2]	variable	$15	variable	$16
Standard Bioinformatics Analysis Pipeline[4]	$750/project		$1500/project	

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

	Academic	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[2]	variable	variable
Standard Bioinformatics Analysis Pipeline[4]	$750/project	$1500/project

Metatranscriptomes – 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)	*$13200*	*$550*	*$19200*	*$800*
RNA Extraction[2]	*$360*	*$15*	*$384*	*$16*
Bioinformatics Analysis Pipeline Under Development	inquire		inquire	

Notes/Details:

1. One control well is required per 96-well PCR library plate, hence a maximum of 4×95 = 380 samples can be done together on one MiSeq run.

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

3. 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)

4. 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 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.