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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 seq./sample)	$30	$25	$20
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 seq./sample)	$40	$35	$30
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)

	Academic		Commercial	
	Per run of 24	Per genome	Per run of 24	Per genome
Library Preparation + Sequencing (~1 M PE reads = 2 M single reads & 600 Mb/genome)	$6000	$250	$8400	$350
Bioinformatics Analysis Pipeline Under Development	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 (~4 M PE reads = 8 M single reads & 2.4 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)				
	Academic		Commercial	
	Per run of 96	Per sample	Per run of 96	Per sample
Library Preparation + Sequencing (~4 M PE reads = 8 M single reads & 1.2 Gb/sample)	$14400	$150	$21120	$220
DNA Extraction[2]	$1440	$15	$1536	$16
Standard Bioinformatics Analysis Pipeline[4]	$750 / project		$1500 / project	

Metatranscriptomes – NextSeq (150+150 bp PE)				
	Academic		Commercial	
	Per run of 24	Per sample	Per run of 24	Per sample
Library Preparation + Sequencing (~4 M PE reads = 8 M single reads & 1.2 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/mlangill/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):

- Combined FASTA file of the quality-controlled sequences (formatted for use in QIIME)
- Final OTU tables in text, BIOM and STAMP formats (from open-ref. picking at 97%)
- FASTA file of representative sequences (one per OTU)
- Taxonomic assignment files at various levels (ex: phylum, genus, etc.)
- Alpha-diversity rarefaction plots
- Beta-diversity UniFrac plots
- Functional prediction files generated from PICRUSt

4. Details of our metagenomics pipeline are available at https://github.com/mlangill/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
- Taxonomic composition of the samples from MetaPhlAn 2.0 (text and STAMP files)
- Functional prediction files generated from HUMAnN (text and STAMP files) for individual KO numbers, KEGG modules and KEGG 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 amplicon runs when providing less than the full capacity of 380 samples, but may also occur when submitting small numbers of samples for metagenomics runs (<6 for MiSeq or <96 for NextSeq).