

Metagenomics Service Description

Scout & Pioneer

Background/Introduction

Microbiome samples are isolated from myriad sources (everything from human faeces to the bottom of the ocean), this diversity is also reflected in the sample composition itself meaning that a 'one size fits all' service is not possible.

We are excited to launch two entry level metagenomics services that sit between 16S sequencing and very high yield shotgun metagenomics in terms of resolution.

We want the services to be useful to experienced metagenomics customers who want to see the diversity/quality of their sample before embarking on deeper sequencing.

We also want the services to be accessible to customers that are interested in metagenomics but have little experience, where the service is a standalone package in its own right.

Service overview

- Currently we only accept DNA extracted from a microbiome (but if you have unextracted samples please contact us as this is something that we are currently doing R&D to develop).
- We will perform Illumina shotgun metagenomics sequencing 2x250 paired end sequencing:
 - **Scout** - minimum 1 million reads (at least 0.5 Gb)
 - **Pioneer** - minimum 2 million reads (at least 1.0 Gb)
 - **Explorer** (launching soon!) - high yield per sample, with target amount depending on the project requirements
- The outputs will include:
 - Sample level:
 - Raw data:
 - Paired read files (fastq)
 - Taxonomic assignment:
 - Overview report
 - Taxonomic assignment by read
 - Table of taxonomic raw and adjusted taxonomic abundances
 - Derived files:
 - Taxonomic assignment:
 - 2x Filtered tables of taxonomic abundances
 - Specific and sensitive
 - Project level:
 - Derived files:
 - Taxonomic assignment:
 - Combined filtered tables of taxonomic abundances
 - Table with taxon rows and sample columns
 - Visualisation:
 - Stacked barcharts of Genera and Species distributions
 - Principal Component Analysis
- Economically priced
 - **Scout** - £99 (ex VAT) (volume discounts available)
 - **Pioneer**- £149 (ex VAT) (volume discounts available)
 - **Explorer** (launching soon!) - price depending on required yield

Good applications

- Comparing the taxonomic distribution between samples with higher resolution (better species information) than 16S
- Economic metagenomics service for low complexity samples
- Stepping stone into a bigger study to inform questions such as:
 - How diverse is the sample?
 - How much extra sequencing do I need?

Bad applications

- Samples with very high levels of host DNA
- Detection of known target taxa at low abundance (e.g. contaminants, pathogens)

Scout or Pioneer?

Whilst we make every effort to give you support when deciding what service to use, you are best placed to answer this question. The most suitable service option is entirely dependent on what questions you are looking to answer and the nature of your samples (e.g. complexity).

You can also visit our handy Metagenomics Service Guidance to help you make a decision. Once you are happy please visit our quote form [here](#).

Below are our recommendations for the best service by application:

Applications	Scout	Pioneer	Notes
To get higher resolution taxonomy than 16S	Yes (but may not be sufficient)	Yes (recommended)	Some taxa (genus and species) are identical in terms of their 16S sequence. Shotgun metagenomics can resolve some of these taxa giving a higher resolution of taxonomic distribution.
Very low complexity samples	Yes (recommended)	Yes (but may be excessive)	Samples isolated from environments with known low diversity (e.g. gnotobiotic, skin).

			Higher yield is not required.
Medium complexity	Yes (but may not be sufficient)	Yes (recommended)	Samples isolated from faeces or similarly diverse microbiomes. More sequencing with our future Explorer service may be needed if the diversity is higher than expected, or to get enough depth on low abundance genomes.
Very high complexity	Yes (but may not be sufficient)	Yes (recommended)	For very diverse environments like soil, these services could be enough for comparisons of highly abundant taxa between samples. More sequencing with our future Explorer service will usually be required for full characterization of very complex microbiomes.
Discerning sample complexity	Yes (recommended)	Yes (but may be excessive)	For samples of unknown diversity it is more economic to do lower cost preliminary sequencing and then decide whether extra sequencing is required (and how much).
Evaluate extra sequencing requirements	Yes (recommended) This is more economical.	Yes (but may be excessive) For very complex samples the Pioneer won't give much more information than Scout.	For samples known to be skewed or have high levels of diversity. To calculate how much extra sequencing (e.g. with our future Explorer service) is required to recover the genome of a particular taxon present in the sample at a specific coverage.
Metagenomics sample QC	Yes (recommended)	Yes (but may be excessive)	This can be used to: - Evaluate the taxonomic bias of different extraction methods - Assess proportion of host DNA - Evaluate degradation and

			general sample DNA quality
Shotgun sequencing of samples with very high levels of host DNA	No	Maybe	<p>Host DNA in the sample will also be sequenced. The higher the proportion of host DNA, the higher the amount of sequencing required to characterize the taxonomic composition of the microbial portion. Then often more than 2M reads are needed.</p> <p>If it is to determine the level of host DNA, see "Metagenomics sample QC" above.</p>
Detection of target taxa at low abundance (e.g. contaminants, pathogens)	No	Maybe	<p>To detect specific taxa within a metagenomic sample its genome must be abundant enough to generate sufficient reads to distinguish it from false positives. Therefore, to detect low abundance taxa with shotgun metagenomics could require very high sequencing yields (at high cost per sample).</p> <p>Target specific techniques (e.g. target enrichment, target specific qPCR, etc) are usually preferred for these cases.</p>