NGS Sequencing of Plant Genomes (2025-26)

Specifications and conditions of performance

The subject of performance is the provision of next generation sequencing services (NGS) of plant genomes, consisting of sample quality control, prepartion of DNA/RNA libraries, their subsequent pooling and sequencing to the required coverage.

The Contracting Authority (Client) will order the type and scope of the services according to its actual needs.

The performance includes activities and costs related to the provision of the required services, expert consultations in the design of experiments, as well as all related performance under the terms of the Master Agreement.

The subject of the sequencing will be samples in eppendorf microtubes.

	Type of performance (service)	Period of performance starts from the moment of delivery of materials (samples) for the implementation of the performance to the Provider's premises
Sequencing	Library preparation and genome skimming/re-sequencing (5 Gb/sample) for complex genomes using 10M Illumina PE250 sequencing on Novaseq6000 or comparable sequencing instruments for 1 sample.	30 business days
	Library preparation and high-coverage genome sequencing (90 Gb/sample) using 300 M Illumina PE150 sequencing on Novaseq6000 or comparable sequencing instruments for 1 sample.	30 business days
	Library preparation and RNA-Seq (20 Gb/sample) after poly-A selection using 50M Illumina PE150 sequencing on Novaseq6000 or comparable sequencing instruments for 1 sample.	30 business days
	Library preparation and full-length transcriptome sequencing (20 Gb/sample) using Oxford Nanopore or PacBio sequencing instrument for 1 sample.	30 business days
	Library preparation and Oxford Nanopore sequencing (1 flowcell) using PromethION instrument for 1 sample	30 business days
	Library preparation and Oxford Nanopore sequencing (1 flowcell) using PromethION instrument for 2 samples	30 business days
	Library preparation and PacBio HiFi sequencing (1 flowcell) on the PacBio Revio System for 1 sample	30 business days
	Library preparation and PacBio HiFi sequencing (1 flowcell) on the PacBio Revio System for 2 samples	30 business days

General conditions and requirements	
Sequencing	a) Plant genomes of 150-3200 Mbp will be sequenced.
	b) The Client requires sample QC and library preparation service.
	c) The Client requires output data from the sequencing should at least meet the standard declared by the manufacturer for the respective type of sequencing (e.g. for Illumina PE150 sequencing, Q30>=85%; for Illumina PE250 sequencing Q30>=75%).
	d) The Client requires demultiplexing of individual libraries (if applicable) and quality control (e.g. FastQC/MultiQC) before delivery of the results or sequencing output in *fastq.gz and other formats (e.g. *bam). For Nanopore sequencing, the Client also require fast5 format data for genome methylation calling.
	e) The Client requires the sequencing results to be retained by the Provider for a minimum of 12 weeks from the delivery of the results.
	f) The results of the sequencing will be made available to the Client electronically. The Client requires the Provider to provide the Client with remote access to its repository or database of results by sending a performance report including a service performance protocol. The Provider may also choose to deliver the data by hard drive
	g) The Client requires the samples (libraries) to be kept with the Provider for the duration of the Master Agreement, with the possibility of their release to the Client
	h) The Client requires the samples (libraries) to be kept with the Provider in such a way as to prevent their degradation (e.g. deep-freezer or dry ice).
	i) The Provider is obliged to confirm the order by the second business day to the contact e-mail address of the Client specified in the sub-order.
	j) The Client requires the Provider to arrange free shipping of samples.

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Annex No. 1b – Sample service basket		
	Pricing provisions	
Type of service – Subject of performance		**Unit price (in EUR, excl. VAT) NOTE no. 1**
Sequencing	Low-coverage genome skimming/re-sequencing (6 Gb/sample) for simple genomes using 20M Illumina PE150 sequencing on Novaseq6000 or comparable sequencing instruments	67
	Low-coverage genome skimming/re-sequencing (5 Gb/sample) for complex genomes using 10M Illumina PE250 sequencing on Novaseq6000 or comparable sequencing instruments	168
	Mid-coverage genome re-sequencing (30 Gb/sample) using 100 M Illumina PE150 sequencing on Novaseq6000 or comparable sequencing instruments	190
	High-coverage genome sequencing (90 Gb/sample) using 300 M Illumina PE150 sequencing on Novaseq6000 or comparable sequencing instruments	332
	RNA-Seq (15 Gb/sample) after poly-A selection using 50M Illumina PE150 sequencing on Novaseq6000 or comparable sequencing instruments	123
	Oxford Nanopore sequencing (100 Gb/sample) using PromethION instrument	1550
	PacBio HiFi sequencing (1 flowcell) on the PacBio Revio System for 1 sample	1980
	PacBio HiFi sequencing (1 flowcell) on the PacBio Revio System for 2 samples	2380
Total price		**6790**

Note no. 1 response according to the specification of the type of service (subject of performance) for the specified unit (at X GB/sample or Y samples/flowcell). The Provider expressly confirms that in the case of a different quantity within one requested response, the price increase/decrease per quantity will be linear

Supplier's Name   **Biomarker Technologies (BMK) GmbH**