1. **Service Name: Termite Genomes**
   1.1. Shotgun sequencing of termite genomes

Required activities - their description, range (e.g. number of samples, forest area), time perspective (requirements) etc.:
- Samples: termite genomes (libraries are provided by the Client)
- Number of lanes: 30 lanes for termite genomes
- Platform: Novaseq, sequencing of 150 bp reads, 2.6 billion read per lane (approx. 2,600 million reads per lane), 800 Gb of data per lane
- Checking the quality of DNA libraries delivered before starting sequencing
- Data quantity for each lane with Q30> 80%
- Quality control of output
- Sequential files, including raw reads, will be delivered in fast or fastq format in another compatible, electronically via server / shared disk
- Professional help on sequencing strategy (depth, pooling)

Methodological requirements
- Sufficient high-quality libraries with the following minimum parameters:
library quantity $\geqslant$ 50 ng, volume > 20 μL, clear single band, no noise bands, no contamination

2. **Service Name: Eukaryotic Genomes and Metagenomes**
   2.1. Library Preparation for Novaseq shotgun sequencing

Required activities - their description, range (e.g. number of samples, forest area), time perspective (requirements) etc.:
- 100 eukaryotic genomes (genomes are expected to have different lengths), 100 metagenomes
- The genomes will be delivered in DNA isolate and it is up to Contractor to do the fragmentation of the DNA prior Library preparation
- Mate pair Library preparation for genome sequencing
- Compatible with degraded samples, including FFPE
- Preservation of species of biological interest
- Compatible with platforms: NovaSeq

Methodological requirements
- Generating Illumina compatible ready-to-sequence libraries from sample DNA
- quantity of prepared library: 200 ng - 1 μg
- size of prepared library: 250 - 350 bp

2.2. Shotgun sequencing through Novaseq

Required activities - their description, range (e.g. number of samples, forest area), time perspective (requirements) etc.:
- Samples: 100 eukaryotic-genome samples, and 100 metagenome samples
- Number of lanes: 10 lanes for eukaryotic genomes, 10 lanes for metagenomes
- Platform: Novaseq, sequencing of 150 bp reads, 2.6 billion read per lane (approx. 2,600 million reads per lane), 800 Gb of data per lane
- Checking the quality of DNA libraries delivered before starting sequencing
- Data quantity for each lane with Q30> 80%
- Quality control of output
- Sequential files, including raw reads, will be delivered in fast or fastq format
in another compatible, electronically via server / shared disk
- Professional help on sequencing strategy (depth, pooling)

Methodological requirements
- Sufficient high libraries with the following minimum parameters: sample quantity $\geqslant$ 250 ng (DNA concentration) $\geqslant$ 10 ng / μL, volume - 20 μL, no degradation, no contamination