1. Service Name: Termite Gut Metagenomes Sequencing

1.1. Shotgun sequencing using NovaSeq 6000 technology

Required activities - their description, range (e.g. number of samples, forest area), time perspective (requirements) etc.:

- Samples: Termite gut metagenomes (libraries are provided by the Client)
- 120 dual unique tag indexing libraries will be delivered by the Client
- Number of lanes: 120 lanes for termite gut metagenomes
- 150bp paired-end reads
- Platform: Novaseq, sequencing of 150 bp paired-end reads, (approx. 390 million reads per lane), 120 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)
- Shipping of libraries for sequencing provided by contractor

Methodological requirements

- Sufficient high-quality libraries with the following minimum parameters:

library quantity ≥ 50 ng, volume > 20 μL, clear single band, no noise bands, no contamination