

**1. Service Name:**

DNA library (hwm DNA, PCR products over 1 kb, cDNA) - PacBio (RS II / Sequel)  
1.4.2.2.8; 1.4.2.2.9

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

- 36 samples (6 eukaryotic genomes and 30 bacterial/fungi genomes)
- Library preparation for genome sequencing - PacBio sequencer
- Compatible with degraded samples, including FFPE
- Preservation of species of biological interest
- Compatible with platforms: PacBio (RS II / Sequel)

**Methodological requirements**

- Generating Illumina compatible ready-to-sequence libraries from sample DNA
- quantity of prepared library: 100 ng – 1 µg
- size of prepared library: 30k bp

**2. Service Name:**

Size selection (10-35 kb) and DNA damage repair - PacBio (RS II / Sequel), 1.4.2.2.8; 1.4.2.2.9

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

- 36 samples (6 eukaryotic genomes and 30 bacterial/fungi genomes)
- Genome fragmentation, size selection (30k bp) for PacBio library preparation
- Fragment end repair
- Compatible with degraded samples, including FFPE
- Preservation of species of biological interest
- Compatible with platforms: PacBio (RS II / Sequel)

**Methodological requirements**

- Generating expected size of genome fragments for PacBio library preparation
- quantity of genome: 100 ng – 1 µg
- size of selection: 30k bp

**3. Service Name:**

Pac Bio SEQUEL, single-end, 1-60 kb, 250-300 thousand reads per SMRT cell: 1.4.2.2.8; 1.4.2.2.9

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

- genome sequencing the bacterial/fungal genome libraries
- Number of cells: 36 cells
- Platform: SEQUEL, SMRT cell, sequencing of at least 1 to 60 kb as single reads, minimum of 250,000 reads
- 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 helps on sequencing strategy (depth, pooling)

**Methodological requirements**

- Sufficient high quality libraries with the following minimum parameters: library quantity  $\geq 250$  ng, volume  $> 20$   $\mu$ l, clear single band, no noise bands, no contamination.