Service name: Transcriptome analysis (RNAseq) of *Ips typographus*

Goal: To facilitate gene annotation and expression analysis for a select number of tissues/life stages in context of the genome sequencing of the bark beetle *Ips typographus*.

Required activities – description, extent (i.e., a number of samples, insect gut, etc.), timing (requirements), etc.:

- RNAseq analysis of supplied samples of *Ips typographus* RNA
- Number of samples: **65**
- Minimum requirements for quality sample: the amount of sample ≥ 1µg, the concentration of RNA c ≥ 20ng/µl, purity OD 260/280≥1.8, OD 260/230 ≥1.8; RNA 28S:18S ≥ 1.0, RIN ≥ 7;

The requirement on the method of preparation:

- Quality control of supplied RNA samples before initiation of analysis.
- Enrichment of mRNA fraction (polyA enrichment) before preparation of cDNA library
- Preparation of cDNA library (type random-primed)
- Use of the latest platform of RNA sequencing (Hiseq 4000)
- 150 bp pair-end reads (both-sided reading in length section 100 bp or 150 bp)
- Min. 30 mil. reads (reading framework) in one single sample
- Data quality requirements: Phred value min. Q30 for a min. 85% reads (reading framework) and simultaneously Phred value min. Q20 for a min. 90% reads (reading Framework)
- Delivery of the data in format fastQ, generally compatible data with databases of reference genome (regardless of sequencing technology used)
- The reads should be multiplexed; adapters should be removed and delivered with full QC reports. Library preparation method should be supplied for the publication purpose.