Next Generation Sequencing Service

Please return this completed form by
fax to +49(0)8161-18516-12
or email to info@vertis-biotech.com

vertis Biotechnologie AG
Lise-Meitner Straße 30
D-85354 Freising
Germany

Tel. +49 (0) 8161/18516-11
Fax: +49 (0) 8161/18516-12

www.vertis-biotech.com
info@vertis-biotech.com

Name (first/last):

Company/Institution:

Address:

Phone: Fax:

email:

Material Supplied

Organism	Specification (tissue, cells, total RNA, small RNA, gDNA, etc.)	Amount	Number of samples

Additional Sample Description (solvent, nucleic acid isolation method, etc.)

Any known hazard associated with the sample must be reported. We cannot accept infectious material!

Customer Services Details

1. Nucleic acid isolation

☐ Genomic DNA (gDNA)	☐ Total RNA	☐ small RNA (< 200 nt)

2. VERTIS RNA-seq Applications

2.1. Removal of rRNA molecules from total RNA preparations

☐ In case of eukaryotic RNA, enrichment of poly(A)+ RNA by oligo-dT chromatography
☐ By hybridization using hybrid subtraction-based kits (Ribo-Zero from Illumina/Epicentre)

2.2. RNA-seq library preparation

Analysis of eukaryotic and prokaryotic transcriptomes

☐ Whole Transcriptome	Strand specific sequencing from poly(A)+ or rRNA depleted RNA
☐ FL-cDNA	Full-lenght cDNA for sequencing with the PacBio system
☐ DGE	Digital Gene Expression analysis (sequencing of 3' ends of transcripts)
☐ PARE	Identification of miRNA targets
☐ MicroRNA	Professional miRNA sequencing services
☐ Small RNA	Identification of bacterial regulatory sRNAs (sRNome)

Identification of the structure of bacterial transcriptomes

☐ dRNA-seq	Differential RNA-seq for annotation of transcriptional start sites (TSS)
☐ Cappable-seq	Most sensitive and robust method for the identification of bacterial TSS
☐ tagRNA-seq	Method to discriminate primary from processed 5' RNA ends

Special applications

☐ Dual RNA-seq	Quantifying mixed transcriptomes (eukaryotic and prokaryotic)
☐ Metatranscriptomics	Analysis of environmental samples and complete communities
☐ Quantitative RNA-seq	Elimination of amplification noise
☐ cDNA Normalisation	For equalization of gene representation in NGS libraries

3. Genomic libraries

☐ Genomic shotgun library
☐ Genomic mate-pair library (4, 8 or 20 kb span – please indicate)
☐ Chip-seq Library (from ChIP-enriched DNA fragments)

4. Illumina NextSeq 500 Sequencing Service

130 or 400 million reads per run

☐ single-end	☐ paired-end	☐ 75 bp read length	☐ 150 bp read length

In case of multiplexing, minimum number of reads per sample required:

_____ million reads

For further details about our NGS services, please visit our homepage **(**www.vertis-biotech.com**)**

5. Bioinformatics

Basic service
☐ Cleaning of reads, poly(A) and adaptor clipping
RNA-seq service
☐ mRNA: de-novo clustering or mapping of reads to reference genome and calculation of expression value for each contig (derived from de-novo clustering) or gene in the reference sequence
☐ microRNA: mapping of reads to miRBase database and calculation of expression value for each miR in the database
Genomic service
☐ De novo assembly
☐ Resequencing analysis (identification of SNPs, InDels)
☐ Chip-seq analysis of reads

For further details about our NGS services, please visit our homepage **(**www.vertis-biotech.com**)**

Remarks and Additional Project Information **(Please indicate the number of samples to be analyzed and the number of sequence runs to be performed)**

Confidentiality Statement

VERTIS will only use the material from the customer for the creation of the NGS library. It will not transfer or sell the material to third parties, and it will turn over and transfer ownership of the material created to the customer. VERTIS shall have no rights of utilization of results that stem exclusively from the use of the material and data created for the customer. All information will be treated in confidence and no details will be passed on to third parties.