Bioinformatics and Expression analysis core facility
Department of Biosciences and Nutrition, NEO
Karolinska Institutet
SE-141 57 Huddinge, SWEDEN

Bioinformatics and Expression Analysis core facility

Order Form — Updated November 2023

BEA Project Number:		iLabs:		Starting Date:	

Contact Information

Name	Department/Section
Phone	e-mail
Invoice Address (KI customers only) Karolinska Institutet Fakturor Box 23 109, SE-104 35 Stockholm Reference code: ZZ	**Invoice Address (Non-KI customers)**
KI Account in iLabs **Projectnumber:**	**Cost Center:**

Important information regarding iLabs Project Submission

Electronic submission using the iLabs system.

- All projects at BEA are demanded to be handled with the cloud based core facility management system iLabs.
- All BEA users need to be registered and approved by PIs in iLabs to initiate a project request at BEA. https://karolinska.corefacilities.org/account/login
- After delivery of samples, BEA staff will create a project for the customer in iLabs to approve. You should use this BEA order form to specify the desired service for your project.

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- Further information about iLabs and project submission can be found at the KI CFM Web page: https://staff.ki.se/ilab

Core facility platforms and applications.

Indicate desired type of service.

Platform:
- ☐ Affymetrix microarray
- ☐ Illumina Microarray
- ☐ Illumina Miseq
- ☐ Illumina Nextseq 550
- ☐ Illumina Nextseq 2000
- ☐ Illumina Novaseq NGI

Application:
- ☐ Gene/Exon Expression
- ☐ miRNA Expression
- ☐ Genotyping / CNV
- ☐ ChIP seq
- ☐ RNA seq
- ☐ Methylation
- ☐ User provided library

Additional services:
- ☐ RNA isol. and purif.
- ☐ ABI TLDA
- ☐ Agilent Bioanalyzer QC
- ☐ Agilent Tapestation QC
- ☐ Small sample (Pico)
- ☐ Other

Additional Info:
- ☐ Sequencing only
- ☐ Bioinformatic services

Indicate type/species:

Core facility Sequencing sample information

Indicate sequencing specifications and library type (if possible).

Sequencing platform/flowcell:

Sequencing Type:
☐ SR ☐ PE

Single or Dual index:
☐ Single ☐ Dual

Sequencing cycle numbers:
- ☐ Read 1 ____________
- ☐ Read 2 ____________
- ☐ Index 1 ____________
- ☐ Index 2 ____________

Indicate library type:

Library information:
Library has been pooled Yes ☐ No ☐
Library has been QC Yes ☐ No ☐

Indicate:
Library size (bp):

Conc. qubit (ng/ul):

Molar conc. (nM):

Library loading (pM):

Sample sheet submitted:
Yes ☐ No ☐

Data delivery:
- ☐ Fastq only
- ☐ RAW data
- ☐ MFT data delivery
- ☐ Hard drive delivery

Bioinformatic services
- ☐ Multi QC
- ☐ Sequence mapping

Indicate type/species:

Order information and Invoicing:

		No	Cost/Sample	Total Cost
Platform/Type/Array/Assay:				
Labeling/Library/Assay/Protocol:				
Additional Lab Services:				

Service fees charged by BEA :

Additional Information:

Confirmation

I fully agree with the conditions for using the core facility and the different platforms/assays terms and conditions for academic press. The core facility cannot take any responsibilities for damaged or lost samples or data.

It is the responsibility of the customer to secure and pick up remaining samples and data which will otherwise be disposed after 12 months. Although raw data will be stored, the BEA core facility holds no responsibility to store pre-processed data or further analyzed data. It is important that the customer has reflected and responded to all the questions found in this order form. **I fully understand all the conditions and routines applied to the specific project and confirm my agreement by signing below.**

Date	Signature	Signature in block letters

Sample and Project Information

Sample preparation and sample submission checklist

RNA/DNA purification method used:

Column cleanup performed: ☐ Yes ☐ No

DNase treatment: ☐ Yes ☐ No

Concentration measured: ☐ Yes ☐ No

Electronic submission of sample information: ☐ Yes ☐ No

Store remaining RNA/DNA: ☐ Yes ☐ No

Labeling and Description (indicated by the customer)

#	Label	Description	Additional sample information
1			
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Storage (indicated by the core facility)

Bioinformatics

Basic bioinformatics

Basic bioinformatics of microarray data at BEA includes QC of data, normalisations, annotations, experimental group comparisons with fold change and p-value calculations. For sequencing projects we offer bcl conversion and demultiplexing of pooled sequencing reads to fastq files. In the basic service we also include sequencing alignment to sam/bam format if desired.

For annotation and alignment please indicate species and genomic build:

Extended bioinformatics

Depending on the design of the project, bioinformaticians at BEA can assist in further analyses tailored for the specific project. See BEA's homepage (http://apt.bea.ki.se/) for examples and requirements for further applied bioinformatics help.

Indicate type of desired analysis:

Data delivery

BEA will always provide the customer with all raw data as well as pre-processed data with annotations for each assay, including Quality Control plots. The processed data is normalized using the appropriate methods and operating software (depending on assays). This procedure will generate signal values for each measureable point and the document will also include biological annotations for respective platform and assay. If the costumer agreed on bioinformatical help from BEA in forms of Comparative analysis, statistical and bioinformatical lists are generated for the costumer to filter biologically interesting data from. This analysis will also be accompanied by an Analysis report for the specific project.

Important!
The costumer will receive a link by e-mail where the all data and results can be downloaded from the KI MFT server or available alternatives.

It is the responsibility of the customer to download and secure data which will otherwise be disposed after 12 months. Although raw data will be stored, the BEA core facility holds no responsibility to store pre-processed data or further analyzed data.

Please use the field below for special requests regarding data delivery, including additional persons to be contacted, only raw data delivery etc.

Delivery notes

Acknowledgement

Important:

In case of publications, please cite:

"We also would like to thank the core facility at NEO, BEA, Bioinformatics and Expression Analysis, which is supported by the board of research at the Karolinska Institute and the research committee at the Karolinska hospital".