

Bioinformatics and Expression Analysis core facility

NEWSLETTER JUNE -22

BEA located in the NEO building in Huddinge

BEA –the core facility for Bioinformatics and Expression Analysis is a core facility providing access to a broad repertoire of genomic technologies located in the NEO building under the authority of the department of Biosciences and Nutrition at the Karolinska Institute in Huddinge.

BEA has extensive experience of implementing and maintaining microarray and sequencing technologies as core facility services which are highly requested by researchers at KI and researchers from other Swedish universities. BEA operates as a core facility offering services with a strict "fee-for-service" principle. The overall principle is that customer fees cover costs for reagents, operating investments and service agreements.

Sequencing at BEA

BEA is offering services for different sequencing applications on the Illumina Nextseq platforms in Huddinge. The service can be adapted for your needs and we provide different library construction and sequencing methods together with complete bioinformatics service for your research project. We have an established collaboration with NGI for larger sequencing projects on the Illumina Novaseq platform. Please inquire for details about different library protocols, sequencing workflows and prices.

10X Genomics Single Cell sequencing

BEA will provide single cell gene expression analysis with the 10X genomics platform which provides solutions for cell characterization and gene expression of thousands of cells simultaneously. BEA will help users to design experiments, provide reagents and service starting from the initial cell separation step. The 10x chromium controller device, has been jointly bought by several departments and groups at KI south campus and is placed at ANA Futura.

RRBS

BEA provides service for Reduced representation bisulfite sequencing (RRBS). This technique combines a methylation independent restriction enzyme digest and bisulfite sequencing in order to enrich for the areas of the genome that have a high CpG content. The fragments that comprise the reduced genome include the majority of promoters, as well as regions such as repeat sequences that are difficult to profile using conventional bisulfite sequencing approaches.

Bioinformatic support

Bioinformatic support is crucial to many of the different projects at the core facility. BEA offers help with different types of analyses with the latest software for advanced variation analysis and visualization. This service is free of charge and included in the project processing cost. The core facility aims to improve NGS analysis services in terms of customer options for mapping methods, reference genomes and downstream analysis, together with more extensive quality control summaries.

Request to our customers

We would like to request our customers to inform BEA about publications that have resulted from projects at the core facility. BEA provides a [reference list](#) on our webpage which continuously needs to be updated. We would also like to urge our customers to collect their samples after completed analysis since we have limited space in our freezers.

Summer vacation

BEA will be partly open during the whole summer but the staff will be reduced and the service will be limited. We strongly recommend visitors to [contact](#) the core facility before visiting and to make sure that we are present before visiting or delivering samples.

BEA will have limited opening hours during the summer. Please contact before visiting!

We wish you all a nice summer!



Bioinformatics and Expression Analysis core facility (BEA)

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