**Finnish Functional Genomics Centre – FFGC**

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https://bioscience.fi/services/functional-genomics

**Sample Submission Form**

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| **Project number** (filled by FFGC) |  |
| **Project title** (with one sentence) |  |

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| **CONTACT INFORMATION** |
| **Contact person(s)*** Name(s)
* Email(s)
* Address
* Phone
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| **Group leader/Principal investigator*** Name
* Email
* Institution
* Department/Laboratory
* Address
* Phone
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| **INVOICING INFORMATION** (the project will be invoiced after the raw data delivery) |
| **Internal invoice** (University of Turku account)* Name
* Department/Laboratory
* Cost pool (kustannuspaikka)
* TY project code: 26xxxxx
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| **External invoice**(other than University of Turku account)* Institution
* Electronic invoicing information (EDI ID, E-invoice operator and Operator ID)
* Customer reference (if applicable)
* VAT number
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| **Project type**- please select one |
| [ ]  Library preparation and sequencing[ ]  Sequencing of ready-made library pool(s) |

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| **INSTRUMENT AND APPLICATION SPECIFICATIONS**Please, ask for help from FFGC if you do not know how to fill this section. |
| **Flow cell type** | **NovaSeq**[ ]  2 x 50 bp [ ]  SP [ ]  S1 [ ]  S2[ ]  2 x 100 bp [ ]  SP [ ]  S1 [ ]  S2 [ ]  S4[ ]  2 x 150 bp [ ]  SP [ ]  S1 [ ]  S2 [ ]  S4[ ]  2 x 250 bp [ ]  SP [ ]  NovaSeq other:[ ]  **Single cell sequencing** 28+10+10+90 bp[ ]  SP [ ]  S1 [ ]  S2 **MiSeq**[ ]  1 x 50 bp v2[ ]  2 x 75 bp v3 [ ]  2 x 150 bp v2 [ ]  std [ ]  micro [ ]  nano[ ]  2 x 250 bp v2 [ ]  std [ ]  nano[ ]  2 x 300 bp v3  |
| **Application type** | [ ] targeted RNA sequencing[ ] stranded mRNA sequencing[ ] stranded total RNA sequencing[ ] miRNA sequencing[ ] reduced representation bisulfite seq. (RRBS)[ ] whole genome bisulfite sequencing (WGBS)[ ] targeted DNA sequencing[ ] whole genome sequencing (WGS) [ ]  PCR-free method [ ]  PCR-based method[ ] whole exome resequencing (WES)[ ] 16S rRNA sequencing[ ] other:  |
| **No of lanes used in sequencing:** |  |
| **No of flow cells used in sequencing:** |  |
| **Library preparation and index kit** **of ready-made libraries:** |  |
| **Desired raw read number or coverage per sample (optional):** |  |
| **Cost of the project:** |  |
| **Additional information (optional):** |  |

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| **SAMPLE INFORMATION** |
| **Total number of samples** (including biological replicates): |  |
| **Organism:** |  |
| **Specify if sequence is expected to be low diversity containing e.g. GC rich areas, sequence repeats or high/low proportion of certain nucleotide:** |  |
| **Origin and type of sample**[ ] Whole blood[ ] Other tissue (specify): [ ] Primary cells (specify): [ ] Cell line (specify): [ ] Other (specify):  | **Storage method**[ ] Fresh [ ] Fresh frozen[ ] FFPE[ ] Lysed (specify): [ ] Other (specify):  |
| **Provided sample material**[ ]  DNA [ ] totalRNA [ ] poly(A) RNA [ ] smallRNA[ ] Other (specify):  | **Other general information for statistics** [ ] the project is linked to human disease research.[ ] the project is linked to clinical diagnostics.[ ] the project is linked to drug development. Please specify the disease:  |
| **DNA / RNA extraction method and used elution buffer:**  |  |
| **Other possible pre-processing done to the samples:**(please specify all applied protocols) |  |
| **Comparison to other results:** (If you are planning to compare these results with another set of results, please indicate the time when the previous samples were processed at FFGC) |  |

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| **SAMPLE LIST FOR LIBRARY PREPARATION AND SEQUENCING**  |
| Avoid spaces and any special characters in the sample names. Please use unique sample names. |
| **Sample** | **Sample name** | **Sample group**  | **c, ng/µl** | **A260/A280** | **Volume, µl** | **Comments** |
| **1** |  |  |  |  |  |  |
| **2** |  |  |  |  |  |  |
| **3** |  |  |  |  |  |  |
| **4** |  |  |  |  |  |  |
| **5** |  |  |  |  |  |  |
| **6** |  |  |  |  |  |  |
| **7** |  |  |  |  |  |  |
| **8** |  |  |  |  |  |  |
| **9** |  |  |  |  |  |  |
| **10** |  |  |  |  |  |  |
| [ ] **Sample sheet provided as a separate file (use same column names as above)** |  |
| **SAMPLE LIST FOR READY-MADE LIBRARY POOL**  |
| Avoid spaces and any special characters in the sample names. Please use unique sample names.  |
| **Sample** | **Sample name** | **index1** **(i7)** | **index1 seq** | **Index2****(i5)** | **Index2 seq** | **Comments** |
| **1** |  |  |  |  |  |  |
| **2** |  |  |  |  |  |  |
| **3** |  |  |  |  |  |  |
| **4** |  |  |  |  |  |  |
| **5** |  |  |  |  |  |  |
| **6** |  |  |  |  |  |  |
| **7** |  |  |  |  |  |  |
| **8** |  |  |  |  |  |  |
| **9** |  |  |  |  |  |  |
| **10** |  |  |  |  |  |  |

[ ] **Sample sheet provided as a separate file (use same column names as above)**

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| **SAMPLE GROUP**Fill this information for library preparation samples. Optional information for ready-made library pools. |
| **Sample group** | **Number of biological replicates** | **Description** |
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| **DATA DELIVERY** |
| [ ] download the raw FASTQ files through an internet link[ ] through Illumina BaseSpace EU-hub, please provide user account (email address): [ ] Other (specify):  |

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| **ADDITIONAL INFORMATION OR COMMENTS** |
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**Sample submission requirements and service work agreement**

The sample requirements and sample preparation instructions are described in the 0017\_FFGC\_Service\_Manual for the different types of samples. FFGC will always check the quality of the samples prior to sequencing and the service user is contacted if there is a concern related to sample quality. Please note that with your consent, samples may be processed even in the case they do not meet the quality requirements but then FFGC will not be able to guarantee the successful sequencing. Please do not hesitate to contact ffgc@utu.fi for any further questions.

**Sequencing run and result delivery**

* Sample quality is carefully controlled during the library preparation and only good quality libraries will be sequenced.
* Sequencing will be rerun without extra costs in case of technical failure during the sequencing if it is not related to the nature or quality of the samples.
* In general, the raw data in Illumina’s default format (fastq) will be downloadable within a week after the sequencing has been finished.

**Sample and data storage**

* FFGC will discard the left-over RNA/DNA sample material after 1 year. Please deliver only the amount of sample needed for the analysis.
* Return of excess amount of starting material back to the service user needs to be agreed separately. The delivery costs are covered by the service users.
* FFGC will store data only for a short time and the service user is responsible for storing the raw data after the project is finished and the data has been delivered to the service user.

Please, fill this form and send it to us before delivery of **your samples and as an e-mail attachment to ffgc@utu.fi.** We will send the form back to you for electronic signature, which is required for processing of the samples.

**As Principal Investigator / contact person on this project, I agree to:**

1. **Acknowledge** the use of the core facility services in the acknowledgements section in any resulting publications with the following sentence: **“We thank Finnish Functional Genomics Centre supported by University of Turku, Åbo Akademi University and Biocenter Finland”**.
2. Inform Finnish Functional Genomics Centre of each resulting publication, innovation disclosure, patent or new commercial product utilizing the infrastructure services.
3. I give my approval for using the Illumina BaseSpace cloud service (EU-hub) for the data transfer and management.
4. I ensure that when required I have an ethical approval for my research and I follow the national legislation and guidelines for good scientific practices.
5. I am familiar with the privacy statement of University of Turku <https://www.utu.fi/en/privacy/notice> and give my approval to be included in the client register of FFGC.