

Illumina Nextseq 500 Service Request Form

User Information

| | |
|--------------------|----------------------------|
| User name: | User E-mail: |
| Tel no: | Department or School: |
| Supervisor's name: | Account no. to be charged: |
| User's signature: | Date: |

Sequencing Requirement

| | |
|--|--|
| Sequencing Type: <input type="checkbox"/> Small RNA <input type="checkbox"/> RNA-seq (Transcriptome) <input type="checkbox"/> Amplicon <input type="checkbox"/> Exome <input type="checkbox"/> Whole Genome <input type="checkbox"/> Metagenomic sequencing <input type="checkbox"/> Others (Please specify): _____ | |
| Sample Preparation Details: 1. Method of Library Construction: _____ 2. Expected Library Fragment Size: _____ 3. Primer Sequence of Constructing Library: _____ 4. Multiplexing Strategy: <input type="checkbox"/> Single index <input type="checkbox"/> Dual index <input type="checkbox"/> None | |
| Sequencing Kit : <input type="checkbox"/> High Output 300 (2x150) Cycles <input type="checkbox"/> High Output 150 (2x75) Cycles <input type="checkbox"/> High Output 75 (1x75) Cycles <input type="checkbox"/> Mid Output 300 (2x150) Cycles <input type="checkbox"/> Mid Output 150 (2x75) Cycles | |
| Read Types: <input type="checkbox"/> Single Read <input type="checkbox"/> Paired-End | Read Cycles: |
| Custom Primer (If applicable): | <input type="checkbox"/> Read 1 <input type="checkbox"/> Read 2 <input type="checkbox"/> Index (Please give details in Library Submission Form) |
| Spike-in of PhiX: | <input type="checkbox"/> Yes# (spike-in % by volume _____) <input type="checkbox"/> No #Note: 1% of PhiX spike-in by default for quality control purposes if not specify. |
| Data uploaded to BaseSpace: | <input type="checkbox"/> Yes (BaseSpace Account: _____) <input type="checkbox"/> No |
| Supervisor's Signature*: | Date: |

*Supervisor please read and sign for terms and conditions in the next page as well.

For Official Use Only

| | | | |
|---|--|--|--------------------------------------|
| Request Form Submission Date: | | | |
| Sequence Kit Ordered Date: | | Sequence Kit Arrival Date: | |
| Sequence Kit Charge: | Service Charge: | Total Charge: | |
| Library Received Date: | Library Submission Form: <input type="checkbox"/> Print out <input type="checkbox"/> Excel | | |
| Library QC Method | <input type="checkbox"/> qPCR | <input type="checkbox"/> Nanodrop Fluorospectrometer | <input type="checkbox"/> Bioanalyzer |
| Library Quantification (Internal QC) | Date | Method | Concentration of Library |
| | | | |
| Sequencing Result | Start Date: | Complete Date: | Raw Data Delivery Date: |
| | Folder name: | | |
| | Cluster Density (K/mm ²): | Cluster PF(%): | %> Q30 score: |
| | Data Yield: | Reagent ID: | |
| Remarks: _____ | | | |

Terms and Conditions

| <u>General policy</u> | Initial |
|---|----------------|
| 1. BioCRF does not accept any sample with potential biohazard. | |
| 2. This service is for Research Use Only. The reagent has not been approved, cleared, or licensed by the United States Food and Drug Administration or any other regulatory entity whether foreign or domestic for any specific intended use, whether research, commercial, or diagnostic. | |
| 3. BioCRF will order and reserve reagents for this project once the PI has submitted this service request form. PI is responsible for the cost of expired reagents (reagents guaranteed shelf life is 3 months) due to delays in sample submission (i.e. sample quality control issues). | |
| 4. BioCRF does not provide any bioinformatics support for data analysis. | |
| 5. BioCRF makes no representations and extends no warranties of any kind, either express or implied. The results are provided by BioCRF to user "as is". | |
| <u>Sample submission and quality policy</u> | |
| <p>A sample goes into queue only after the reagent cost and sample are received. If a sample does not pass our incoming QC, we will not proceed with the sample until incoming QC is met (or PI can sign a waiver to override this). BioCRF is not responsible for the performance of a library or cDNA sample sequenced on the Nextseq 500 machine. The following items are required for sample submission:</p> <p>Checklist:</p> <ol style="list-style-type: none"> 1) Bioanalyzer or Fragment Analyzer traces of all libraries submitted. 2) Library quantification using KAPA library quantification kit or Fluorescent Nanodrop (ND-3300). | |
| <u>Results and data distribution policy</u> | |
| After checking instrument performance and invoicing the work, a report is sent to the researcher. A run is considered successful if control sequences (i.e. Phi-X control) are within spec. In this report, the researcher will find download instructions. BioCRF is not responsible for backups of customer data after distribution. | |