**中央研究院 生物多樣性研究中心 新世代基因體定序核心實驗室**

**Illumina Sequencing Application Form　定序服務申請表**

|  |  |  |  |
| --- | --- | --- | --- |
| **Dataset ID**  **(core only)** |  | **Case ID**  **(core only)** |  |

**Please Read NGS Sequencing Service Policy Carefully Before Submitting Your Requisition**

**請詳閱定序服務條款（見第二頁）**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **User Information** | | | | | | | | | | |
| **Principal**  **Investigator** | | Name (中): | | | Institute: | | | | | |
| Name (En): | | | Phone: | | | | E-mail: | |
| **Applicant**  (contact person) | | Name (中): | | | Institute: | | | | | |
| Name (En): | | | Phone: | | | | E-mail: | |
| **Project Name**  (brief description) | |  | | | | | | | **Funding Sources** | |
|  | |
| **Library Construction Services** | | | | | | | | | **Note** | |
| **# of Sample**  Submitted | | **Quality & Quantity Assessment** | | | | | | |  | |
|  | | **Qubit** □ DNA □ RNA  **BioA** □ HS DNA □ RNA Nano □ RNA Pico  **FA** □ DNA 6-Kb □ DNA 50-Kb □ RNA  **qPCR** □ Ready-to-Seq Library only | | | | | | |
| **# of Library**  Construction | | **Application Type (see table below)** | | | | | | |
|  | |  | | | | | | □ Gel-free  □ Gel-plus |
| **Extra Prep**  (at extra cost) | | □ Size Selection　□ Sample Purification | | | | | | |
| **Sequencing Requisition** | | | | | | | | | | |
| **Sequencing Mode (select ONE only)** | | | | **Format**  SR / PE | | | **Read Length** | | **Multiplexing**  # of Lib per Lane | **Total Lane(s)** |
| HiSeq **HT** | HiSeq **Rapid** | | **MiSeq** |
|  |  | |  |  | | |  | |  |  |
| **Signature of Core Manager**  Date (YYYY/MM/DD) | | | | | | **Signature of PI**  Date (YYYY/MM/DD) | | | | |

|  |  |
| --- | --- |
| **請款日期**  **(core only)** | **收款日期**  **(core only)** |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Application Type** | Sample Requirement | | **Application Type** | Sample Requirement | |
| **(S-B)** Methylation DNA | 1-2 ug | in 25 ul | **(S-N)** Synthetic Long-Read DNA | 1-2 ug | in 50 ul |
| **(S-C)** Paired-end DNA | 2-3 ug | in 50 ul | **(S-P)** Indexing PCR (2nd Step PCR) | >300 ng | in 20 ul |
| **(S-D)** Long Insert Paired-end DNA | 2-3 ug | in 50 ul | **(S-R)** Nextera DNA | 5-500 ng | in 20 ul |
| **(S-E)** Small RNA (miRNA) | 8-10 ug | in 10 ul | **(S-S)** Stranded RNA (Poly-A) | 4-6 ug | in 50 ul |
| **(S-G)** Degradome | 100-150 ug | in 100 ul | **(S-T)** Stranded RNA (Ribo-Zero) | 4-6 ug | in 50 ul |
| **(S-H)** Hi-C DNA |  |  | **(S-W)** Low-input Stranded RNA | 5-100 ng | in 25 ul |
| **(S-I)** ChIP DNA | 5-10 ng | in 25 ul | **(S-X)** Human Exome Capture | 1-2 ug | in 50 ul |
| **(S-L)** Ready-to-Seq Library | >10 nM | in 20 ul | **(S-Z)** Customized Prep |  |  |
| **(S-M)** Mate-Pair DNA | 10-20 ug | in 100 ul | **(QC)** QC-only |  |  |

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**NGS Sequencing Service Policy　定序服務條款**

1. **Sample Requirement**
2. Please check on [**NGS Sample Preparation Guide**](http://ngs.biodiv.tw/NGSCore/documentation/) to ensure that your samples meet our requirement and be well-packaged. NGS core facility reserves the right to determine whether the unqualified sample can proceed to the library preparation.
3. Additional fees would be charged if there are any needs to re-prep library or do extra experiments requested by the user due to sample issues. The final service charge will be re-calculated depending on real experiment cost.
4. **Sample Submission**
5. As a part of our standard service procedure ([see Service Flow](http://ngs.biodiv.tw/NGSCore/get-started/)), please email to Dr. Mei-Yeh Lu the NGSApplication Form (Illumina or PacBio) and the Sample Submission Form prior to the actual submission for visual quality inspection. Please kindly include PI in all communicating emails, allowing PI to be updated timely on the project status and information.
6. All sample drop-offs should accompany appropriate forms signed by PI for project approval, and please contact Dr. Lu to make an appointment in advanced before you bring your samples to the NGS core facility. For contact information, please visit our website [Contact & Location](http://ngs.biodiv.tw/NGSCore/contact-location/).
7. **Acknowledgement & Authorship**
8. We appreciate your support if you mention NGS core facility in the acknowledgement section when the data using our sequencing services is published. You may add a sentence like this:

*We thank the High Throughput Sequencing Core hosted in the Biodiversity Research Center at Academia Sinica for performing the NGS experiments. The core facility is funded by Academia Sinica Core Facility and Innovative Instrument Project (AS-CFII-108-114).*

1. If there are substantial contributions from NGS core facility in your research, including intellectual input, data analysis and interpretation, or special experiment design, it might be appropriate to involve core members in the list of authorship.
2. Please kindly share your publications on [here](https://goo.gl/forms/TlyyZtYlrMtPrD1h1) in case we miss it. Thank you.