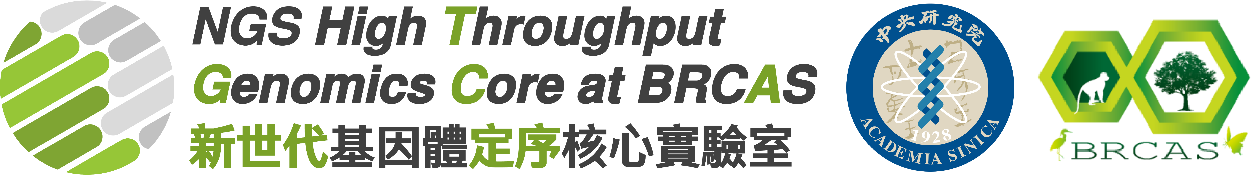
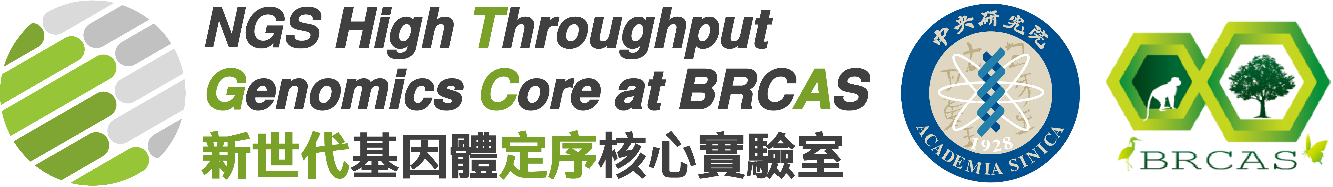
**中央研究院 生物多樣性研究中心**

**新世代基因體定序核心實驗室**

**Illumina Sequencing Application Form　  
Element Bio AVITI24 Sequencing Application Form**

Case ID

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **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 Check & Quantification** | | | | | 1. **Specific Pooling Ratio** Please specify if you require a particular pooling ratio for your libraries. 2. **PhiX Spike-In (%)** *(Ready-to-Seq Library)* Recommended for low-diversity libraries. Please indicate the desired PhiX percentage if applicable. 3. **Special Sample Conditions** Please note any special conditions (e.g., contamination, low purity, FFPE sample, unusual color, etc.). 4. **Custom Library Prep** *(Ready-to-Seq Library)* If using a custom prep, please provide the kit name or a reference protocol. 5. **Demultiplexing** *(Ready-to-Seq Library)* If demultiplexing is needed, please provide the index sequences. | |
|  | **Qubit** □ Qubit DNA □ Qubit RNA  **FA** □ FA DNA 6-Kb □ FA DNA 50-Kb □ FA RNA  **Femto** □ Femto DNA165K □ Femto RNA  **qPCR** □ qPCR (Library QC)  **Sizing** □ BluePippin  **Cleanup** □ AMPure XP □ RNAClean XP □ TURBO DNase  **Sample** □ DMW DNA □ RNA Extraction TRIzol | | | | |
| **# of Library**  Construction | **Application Type** | | | | |
|  |  | | | | |
| **Request Libraries Equal Pooling (Note “A”)**  (Discuss sample pooling ratios) | | | | **Yes**□　**No**□ | |
| **Ready-to-Seq Library with Low Diversity Bases (Note “B”)**  (Discuss PhiX spike-in %) | | | | **Yes**□　**No**□ | |
| **Sequencing Requisition** | | | | | | | |
| **Sequencing Mode** | | **Format**  SR / PE | | | **Read Length** | **Multiplexing**  # of Lib per Lane | **Total Lane(s)** |
|  | |  | | |  |  |  |

**APPROVALS**

Please Read NGS Sequencing Service Policy Carefully Before Submitting Your Requisition

|  |  |
| --- | --- |
| **Signature of Core Manager**  Date (YYYY/MM/DD)  **Signature of Core Manager with Date** | **Signature of PI**  Date (YYYY/MM/DD)  **Signature of PI with Date** |

\*\*\*簽名表示接受上述實驗可能造成的風險；若QC後有其他更動樣本計畫，需要另外簽署**高風險同意書**。\*\*\*

Signing indicates acceptance of the potential risks associated with the above experiment. If the sample plan is modified after QC, an additional **high-risk consent form** must be signed.

**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**

**NGS Sequencing Service Policy**

1. **Sample Requirement**
2. Please check on [**Sample Preparation**](https://ngs.biodiv.tw/NGSCore/sample-preparation/) and [**Sample Requirement**](https://ngs.biodiv.tw/NGSCore/sample-requirement/) 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**](https://ngs.biodiv.tw/NGSCore/service-flow/)), please email to Dr. Mei-Yeh Lu the NGS Sequencing ServiceRequest Form 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://forms.gle/8Q2yzguFRo7CcY4i9) in case we miss it. Thank you.