# Sample information

**Notes**

1. Consult the Methods Guide for filling up Library Prep.
2. If you are combining two different pooling, indicate them in the **pooling group**
3. If you are submitting RNA samples, fill in RIN in ‘other’ column
4. If you use fluorometer for quantification, indicate it in ‘other’ column. No OD ratio is necessary,

## Sample source : Choose an item.

## Genus : Click or tap here to enter text.

## # of samples : Click or tap here to enter text.

# library preparation information

Sample ID column is for the NGS Team to complete. Add new lines when necessary.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **No.** | **Library Prep** | **Sample ID** | **Sample Name** | **Sample Type** | **Sample Conc. (ng/ul)** | **Sample Vol. (ul)** | **OD 260/280** | **OD 260/230** | **Elution Buffer** | **Pooling group (for indexing)** | **other** |
| (e.g ) | Nextera Flex | (blank) | My sample | Genome | 100 | 20 | 1.8 | 2.0 | EB | A | RIN 8 |
| 1 |  |  |  |  |  |  |  |  |  |  |  |
| 2 |  |  |  |  |  |  |  |  |  |  |  |
| 3 |  |  |  |  |  |  |  |  |  |  |  |
| 4 |  |  |  |  |  |  |  |  |  |  |  |
| 5 |  |  |  |  |  |  |  |  |  |  |  |
| 6 |  |  |  |  |  |  |  |  |  |  |  |
| 7 |  |  |  |  |  |  |  |  |  |  |  |
| 8 |  |  |  |  |  |  |  |  |  |  |  |
| 9 |  |  |  |  |  |  |  |  |  |  |  |
| 10 |  |  |  |  |  |  |  |  |  |  |  |
| 11 |  |  |  |  |  |  |  |  |  |  |  |
| 12 |  |  |  |  |  |  |  |  |  |  |  |

I understand that my sample(s) do not meet the minimum quality specification and may result in low quality library or sequencing result. I authorize the sequencing team to proceed in library preparation and sequencing.

# sample qc

Please provide agarose picture with respective samples.



Requestor Name :

Request Date : Click or tap to enter a date.

