# Library submission form

For internal use:

Storage box # \_\_\_\_\_\_\_

Please fill out the requested information in full.

|  |  |  |  |
| --- | --- | --- | --- |
| First name: |  | Last name: |  |
| E-mail address: |  | Phone number: |  |
| Principal investigator: |  | Account number:(Technion only) |  |
| Institution and department\*: |  |

\* Non-Technion investigators, please provide full address.

Submission date \_\_\_\_\_\_\_\_\_\_\_\_

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Check sequencing mode:**

|  |  |  |  |
| --- | --- | --- | --- |
|  | 50 bp Single read |  | 50 bp Single read RAPID mode |
|  | 2 X 50 bp Paired-end reads |  | 2 X 50 bp Paired-end reads RAPID mode |
|  | 100 bp Single read |  | 100 bp Single read RAPID mode |
|  | 2 X 100 bp Paired-end reads |  | 2 X 100 bp Paired-end reads RAPID mode |
|  | MiSeq 50 bp Single read |  | MiSeq 2X150 bp Paired-end reads |
|  | MiSeq 2X250 bp Paired-end reads |  | Other\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ |

 |  |
|  |  |
|  \_\_ Single index \_\_Dual index  |  |
| **Number of tubes submitted per lane**: \_\_\_\_\_\_\_Please fill the following table for each library. |  |

| **Sample** | 1 | 2 | 3 | 4 |
| --- | --- | --- | --- | --- |
| Library Name |  |  |  |  |
| Barcode type (single/dual) |  |  |  |  |
| Barcode name and sequence |  |  |  |  |
| Concentration  |  |  |  |  |
| Method of quantitation(NanoDrop/Qbit etc.) |  |  |  |  |
| Sample prep kit (TruSeq/Nextera/NEBNext etc.) |  |  |  |  |
| Volume |  |  |  |  |
| Mean fragment size  |  |  |  |  |
| Remarks |  |  |  |  |

# If samples are of human source please sign here to confirm you received Helsinki approval for the experiment

All libraries must be compatible to TruSeq sequencing primers. In case your libraries are not compatible please contact the TGC to coordinate the sequencing run.

**PI signature:** \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_