# Library submission form

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

**Please check the following boxes after reading them carefully:**

* All libraries must be compatible to standard Illumina sequencing primers. In case your libraries are not compatible please contact the TGC to coordinate the sequencing run.
* I understand that custom adapters may cause reduced cluster efficiency resulting in less data.
* I understand that the information on this form is obligatory and the TGC will process the samples according to this information.

**Please fill out the requested information in full:**

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

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Select sequencing run:** | | | | | |
| HiSeq **Rapid mode** 50 bp SR |  | NextSeq **High output** 75 bp SR |  | MiSeq 2X150 bp PE |  |
| HiSeq **Rapid mode** 2 X 100 bp PE |  | NextSeq **High output** 75X2 bp PE |  | MiSeq 50 bp SR |  |
| HiSeq **Rapid mode** Other  (up to 250X2)\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ |  | NextSeq **High output** 150X2 bp PE |  | MiSeq 2X250 bp PE |  |
|  | NextSeq **Mid output** 75X2 bp PE |  | MiSeq 2X75 bp PE **V3** |  |
|  |  | NextSeq **Mid output** 150X2 bp PE |  | MiSeq 2X150 bp PE **Micro** |  |
|  |  | NextSeq CEL-Seq |  | MiSeq 2X150 bp PE **Nano** |  |
|  |  | NextSeq other \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ |  | MiSeq 2X250 bp PE **Nano** |  |
|  |  |  |  | Miseq other \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ |  |

|  |
| --- |
| **Initial bioinformatics analysis**: **Yes/No** If analysis is included please attach the relevant questionnaire from our web site <http://isu.technion.ac.il/tgc>-> Documents & Literature -> Forms  **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

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