# Sample submission form

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

**Please check the following box after reading it carefully:**

* 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 library preparation:** | | | | | | |
| TruSeq RNA |  | TruSeq DNA nano |  | CEL-Seq2 | |  |
| NEBNext-RNA **non**-**directional** |  | ChIP |  | Amplicons | |  |
| NEBNext-RNA **directional** |  | Exome |  | 16S | |  |
| Ribosomal depletion |  |  |  |  | |  |
| SMARTer stranded RNA-seq **pico** |  |  |  | Other \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ | | |
| **Select sequencing mode and run quantity:** | | | | | | |
| 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 \_\_\_\_\_\_\_\_\_\_\_\_\_ |  | |

**Number of samples per run**: \_\_\_\_\_\_\_ **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

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| | **Sample** | 1 | 2 | 3 | 4 | | --- | --- | --- | --- | --- | | Sample Name |  |  |  |  | | Sample Type (total RNA/gDNA etc.) |  |  |  |  | | Concentration and method of quantitation (NanoDrop/Qbit etc.) |  |  |  |  | | Volume |  |  |  |  | | Species and reference genome\*# |  |  |  |  | |

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

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

| **Sample** | 5 | 6 | 7 | 8 |
| --- | --- | --- | --- | --- |
| Sample Name |  |  |  |  |
| Sample Type (total RNA/gDNA etc.) |  |  |  |  |
| Concentration and method of quantitation (NanoDrop/Qbit etc.) |  |  |  |  |
| Volume |  |  |  |  |
| Species and reference genome\*# |  |  |  |  |
|  |  |  |  |  |
| **Sample** | 9 | 10 | 11 | 12 |
| Sample Name |  |  |  |  |
| Sample Type (total RNA/gDNA etc.) |  |  |  |  |
| Concentration and method of quantitation (NanoDrop/Qbit etc.) |  |  |  |  |
| Volume |  |  |  |  |
| Species and reference genome\*# |  |  |  |  |
|  |  |  |  |  |
| **Sample** | 13 | 14 | 15 | 16 |
| Sample Name |  |  |  |  |
| Sample Type (total RNA/gDNA etc.) |  |  |  |  |
| Concentration and method of quantitation (NanoDrop/Qbit etc.) |  |  |  |  |
| Volume |  |  |  |  |
| Species and reference genome\*# |  |  |  |  |