#  Sample submission form

For internal use:

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

 Ready libraries # \_\_\_\_\_\_\_

Sample submission date \_\_\_\_\_\_\_\_\_\_\_\_

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.

|  |  |
| --- | --- |
| **Check sequencing application:** | **Check sequencing mode and lane/run quantity:** |
| Resequencing |  | 50 bp SR rapid mode |  | 50 bp SR |  |
| Exome sequencing |  | 2 X 50 bp PE reads rapid mode |  | 2 X 50 bp PE  |  |
| mRNA-Seq |  | 100 bp SR rapid mode |  | 100 bp SR |  |
| ChIP-Seq |  | 2 X 100 bp PE reads rapid mode |  | 2 X 100 bp PE  |  |
| CEL-Seq |  | MiSeq 2X150 bp PE |  | MiSeq 50 bp SR |  |
| Other\_\_\_\_\_\_\_\_\_\_ |  | Other\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ |  | MiSeq 2X250 bp PE  |  |

|  |  |
| --- | --- |
| **Number of samples per lane**: \_\_\_\_\_\_\_**Initial bioinformatics analysis**: Yes/No If analysis is included please attach the relevant questionnaire from our web site [http://isu.technion.ac.il/tgc](http://isu.technion.ac.il/tgc-)-> services->forms |  |

| **Sample** | 1 | 2 | 3 | 4 |
| --- | --- | --- | --- | --- |
| Sample Name |  |  |  |  |
| Sample Type (total RNA/gDNA etc.) |  |  |  |  |
| Concentration and method of quantitation (NanoDrop/Qbit etc.) |  |  |  |  |
| Volume |  |  |  |  |
| DNA quality (260/280 ratio) |  |  |  |  |
| 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** | 1 | 2 | 3 | 4 |
| --- | --- | --- | --- | --- |
| Sample Name |  |  |  |  |
| Sample Type (total RNA/gDNA etc.) |  |  |  |  |
| Concentration and method of quantitation (NanoDrop/Qbit etc.) |  |  |  |  |
| Volume |  |  |  |  |
| DNA quality (260/280 ratio) |  |  |  |  |
| Species and reference genome\*# |  |  |  |  |

| **Sample** | 1 | 2 | 3 | 4 |
| --- | --- | --- | --- | --- |
| Sample Name |  |  |  |  |
| Sample Type (total RNA/gDNA etc.) |  |  |  |  |
| Concentration and method of quantitation (NanoDrop/Qbit etc.) |  |  |  |  |
| Volume |  |  |  |  |
| DNA quality (260/280 ratio) |  |  |  |  |
| Species and reference genome\*# |  |  |  |  |

| **Sample** | 1 | 2 | 3 | 4 |
| --- | --- | --- | --- | --- |
| Sample Name |  |  |  |  |
| Sample Type (total RNA/gDNA etc.) |  |  |  |  |
| Concentration and method of quantitation (NanoDrop/Qbit etc.) |  |  |  |  |
| Volume |  |  |  |  |
| DNA quality (260/280 ratio) |  |  |  |  |
| Species and reference genome\*# |  |  |  |  |