**High Throughput Sequencing –RNA-Seq pre-analysis questionnaire**

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| --- | --- | --- | --- |
| Date: |  | Principal investigator: |  |
| First name: |  | Last name: |  |
| E-mail address: |  | Phone number: |  |

Please note that the details of the analysis we provide are found on our website: <https://tgc.net.technion.ac.il/services/bioinformatics/rna-seq/>

This questionnaire is meant to provide us with more information about your research project to make the bioinformatics analysis more accurate. **Please fill in the following details regarding your experiment.**

1. What questions would you like to answer in this high-throughput sequencing experiment?

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1. Please provide details about each sample: molecular and phenotypic details, what are the relations between the samples? Which of the samples are replicates?

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What pairwise comparisons would you like to make for differential gene-expression? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

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1. What is the organism in this experiment? (If you are interested in specific version of genome or annotation file, please state the specific website where a genome (.fasta) and annotations file (.gff, .gtf) can be found. The annotation file should correspond to the reference genome and be of a GFF/GTF format. In addition, if you know the gender of the samples, please state this).

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1. If you know, please list a few genes that are expected to be differentially expressed, as well as enriched biological pathways and functions expected. For each condition, list the genes that are highly expressed. State if this information was validated.

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Was any of the genes listed above validated using PCR or any other method?

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1. Is there a batch effect expected in the experiment (for example, samples were prepared in different dates, different persons prepared different samples, different batches of medium/serums were used)?

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**Thank you!**

**The TGC team**