**High Throughput Sequencing –Experiment Plan Questionnaire**

**Please fill in the following details regarding your experiment.**

**Note** that we provide an initial bioinformatic analysis, as was presented to you in the first meeting, and as detailed in our site. This questionnaire is meant to provide us more details about your research to make the initial analysis more accurate.

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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1. What pairs of samples would you like to compare for differential gene-expression? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

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1. Are you specifically interested in lowly-expressed genes?

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1. Please state a specific web site where a genome and annotations file can be found. The annotation file should corresponds to the reference genome and be of a GFF format. If you plan to send the files via mail, please state it here.

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1. Do you know whether the samples you sent for sequencing are closely related to the reference genome or not?

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1. Please list a few genes that are expected to be differentially expressed and genes that are highly expressed. State if this information was validated.

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1. If you know the percentage of gene duplication in the genome please provide it here. When mapping the reads to the reference genome, if the percentage of multi mapped reads (reads mapped to more than one location) is low we remove these reads from the analysis. If you wish to include multi mapped reads (probably reads mapped to gene duplication regions) state it here. \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_
2. Do you expect the sample to contain contaminates?\_\_\_\_\_\_\_\_\_\_\_\_\_\_

If so, please send it via email in fasta/fastq format.

1. Do you expect the sample to contain rRNA? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_
2. Are you interested alternative splicing? Are there annotations for alternative splicing in the annotation file given above?

Note: for alternative splicing paired-end sequencing is recommended.

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**Thank you! Technion Genome Center Team**