**High Throughput Sequencing – Resequencing 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/resequencing/>

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? What is the gender, if relevant? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_
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1. Please provide website address where a genome file (.fasta) can be found. If you plan to send the file via mail, please state it here.

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1. If you wish the variants table to contain attributes of known gene annotations, please send a path to the annotation file, in a GFF/GTF format. Note that the annotation file should correspond to the reference genome.

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1. Are the sequenced samples different/significantly different from the relevant reference genome?

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1. Do you expect the genome or any of the samples to contain contaminates? If so, please provide the contaminates’ sequence (fasta/fastq format) in advance via email.

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1. If known, what kind of mutations do you expect to find in your samples (point mutations/ big deletions/ inversion etc.)?

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**Thank you!**

**The TGC team**