**High-Throughput Sequencing – Exome Sequencing 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/exome-sequencing/>.

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. Please provide details regarding the studied disease (recessive/ dominant, autosomal/ sex linked, penetrance etc.)

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1. For each sample – state the gender, whether it is of an affected or healthy person and family relations. Which sample is the control? Please add a family tree if available.

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1. Please state the reference genome version you prefer for the analysis.

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1. Are there suspected loci in the genome? Please state their coordinates.

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How long are they? How many genes do they contain?

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What methods were used to identify them?

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1. Do you expect to find a certain type of mutations? (SNPs, indels, large deletions, inversions…)

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Do you expect the mutation to be homozygous/ heterozygous?

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Do you expect the mutation to be inherited or de-novo?

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**Thank you!**

**The TGC team**