**High Throughput Sequencing – Resequencing**

**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. What are the relations between the samples?

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1. What are the phenotypes of each? What is the gender, if relevant?

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1. Please state a specific web site and path where a genome file 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 the known gene annotations, please send a path to the annotation file, in a GFF format. Note that the annotation file should correspond to the reference genome build.

If you plan to send the file 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. Are there suspected loci in the genome that you believe the mutation is at? Please state their coordinates.

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

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In what methods were they validated?

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1. Do you expect the genome or the sample to contain contaminates?

If so, please send a fasta file of the sequences or state a specific web site and path where the file can be found \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

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

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 **Thank you! TGC Team**