**High Throughput Sequencing – ChIP-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/chip-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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1. Was any validation done on the samples with other methods (for example real-time PCR, western)?

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1. Have you measured the fold enrichment of your protein in question in the IP sample? How frequent does the binding expected to be in the genome?

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1. Please provide website address where a genome file (.fasta) and annotation file (.gtf, .gff) can be found. 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. Are the sequenced samples different/significantly different from the relevant reference genome?

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1. Please provide details about your input samples. Does each condition/treatment/antibody has a separate input sample, or do all the samples share a single input?

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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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**Thank you!**

**The TGC team**