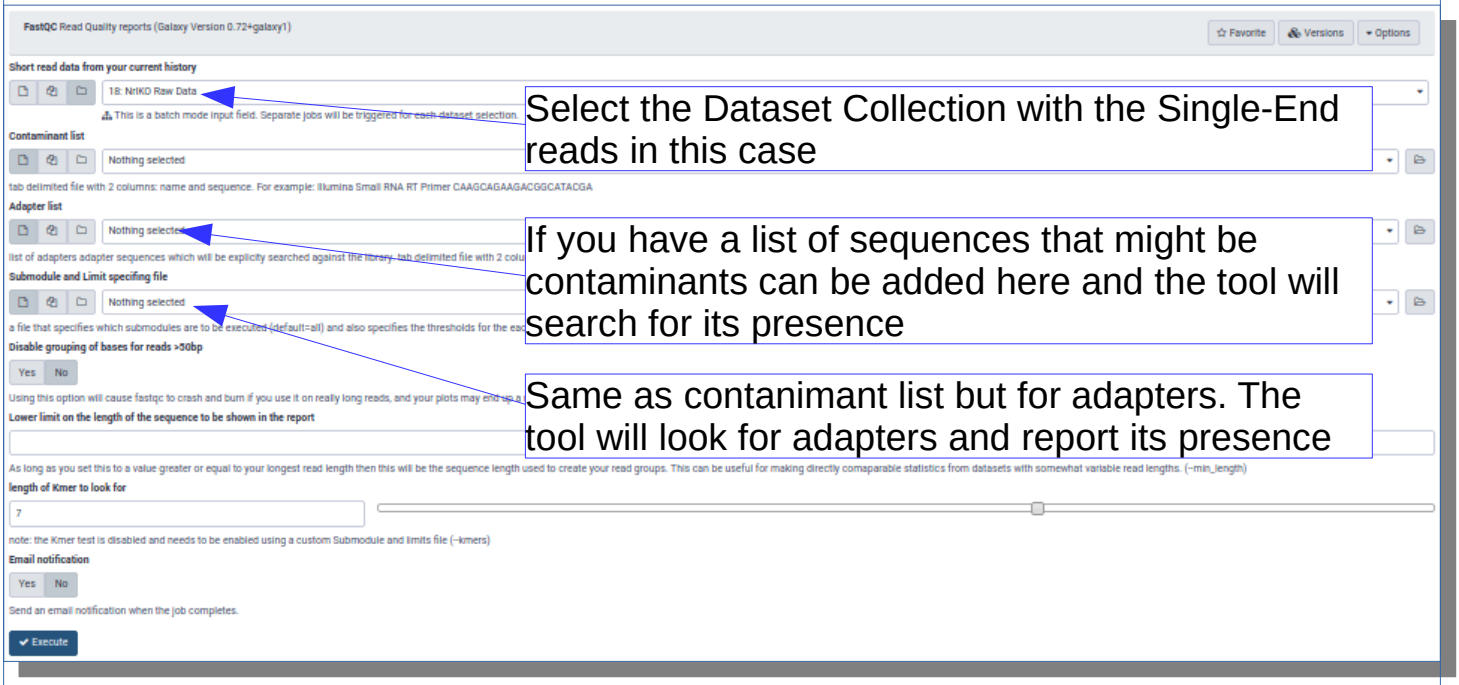
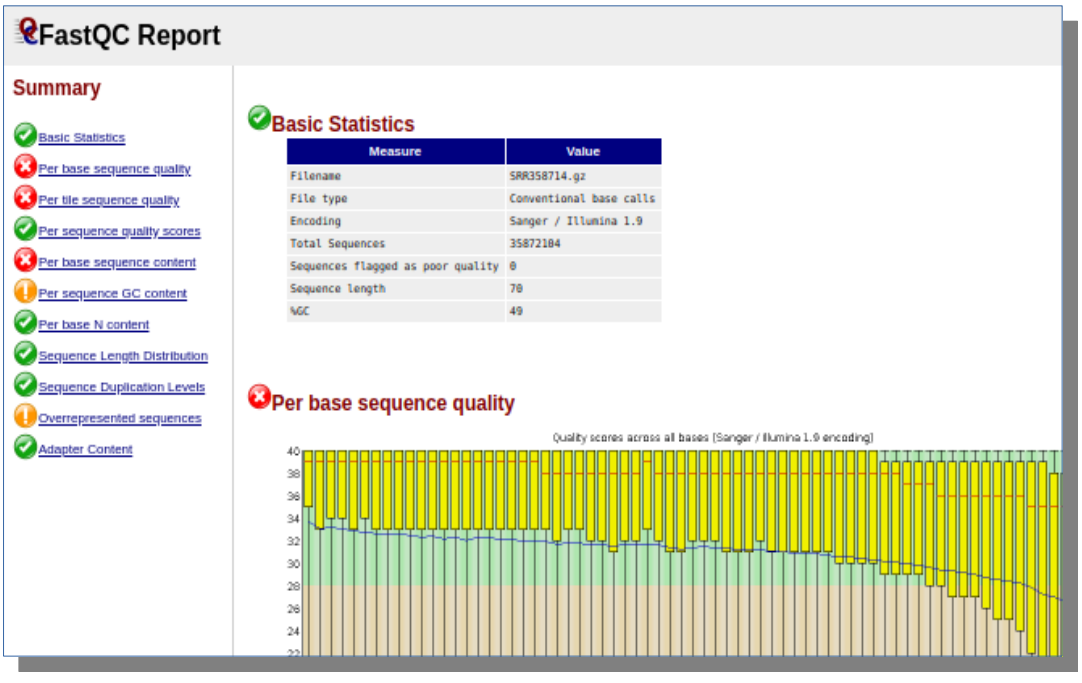
RNA-Seq Analysis: QC

Before the alignment, quantification and farther tests we need to evaluate de quality of the sequencing experiment to see if there is any technical problem that could influence the analysis.

FastQC: tool to explore the quality of sequencing experiments.



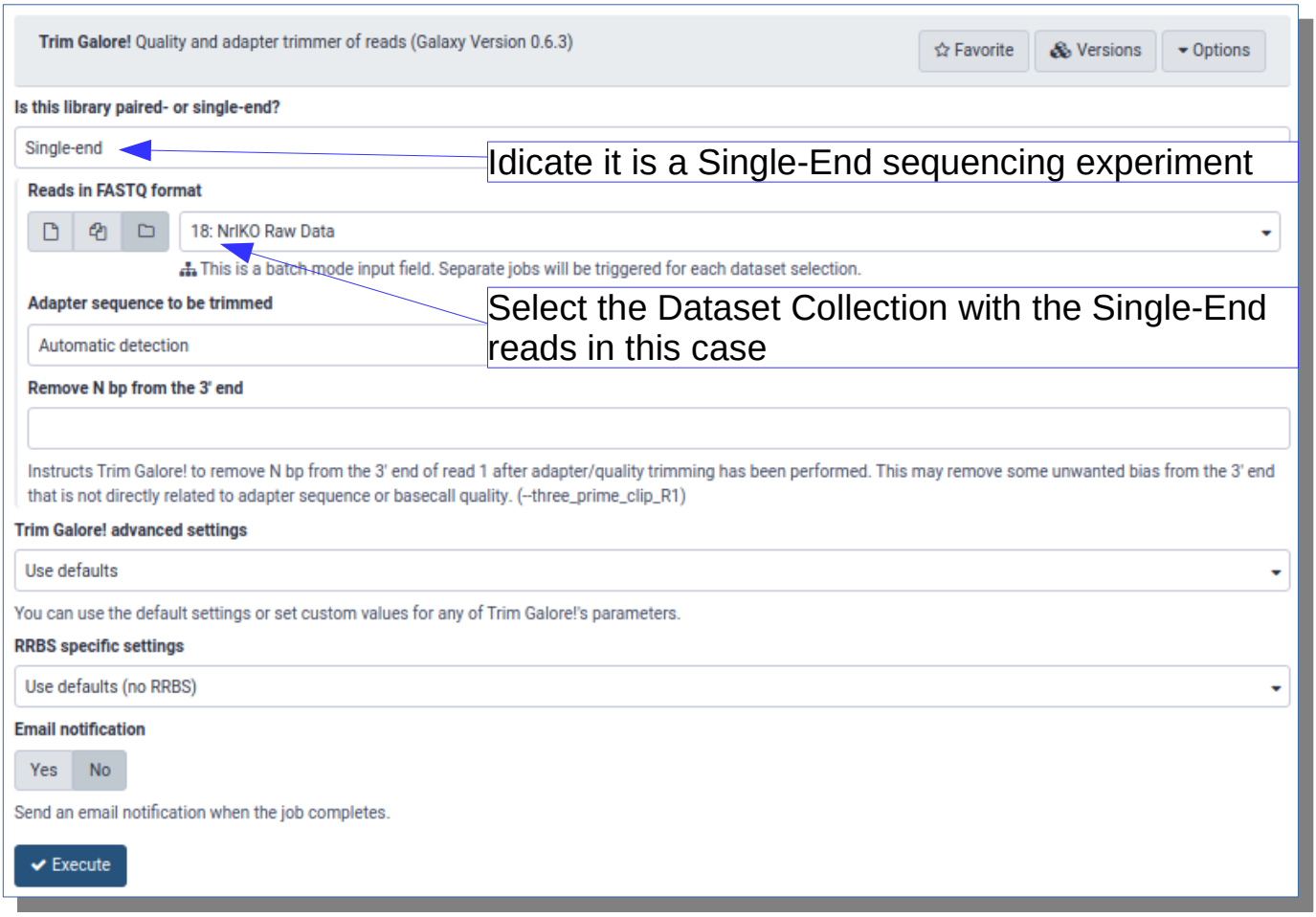
- We can leave all the options as default
- Repeat the step for both collections of Singe-End reads, the WT and the KO
- The tool produces an html report with all the metrics.
- Explore the output and compare it with the FastQC we will do after processing the raw reads



RNA-Seq Analysis: Preprocess Reads

This step will help to remove low quality reads and remove adapter contaminations. This will improve the later alignments and quantification.

Trim-Galore: Will preprocess the reads



- The rest of the options will be OK to leave them as default.
- Repeat the step for both, the WT collection and the KO collection.
- Proceed later with another round of FastQC steps on the processed reads and compare it with the QCs made before. Notice how the quality plots are improved