

# Quality Control by FastQC

FastQC aims to provide a simple way to do some quality control checks on raw sequence data coming from high throughput sequencing pipelines. It provides a molecular set of analyses which you can use to give a quick impression of whether your data has any problems of which you should be aware before doing any further analysis.

## How to Use This Sample

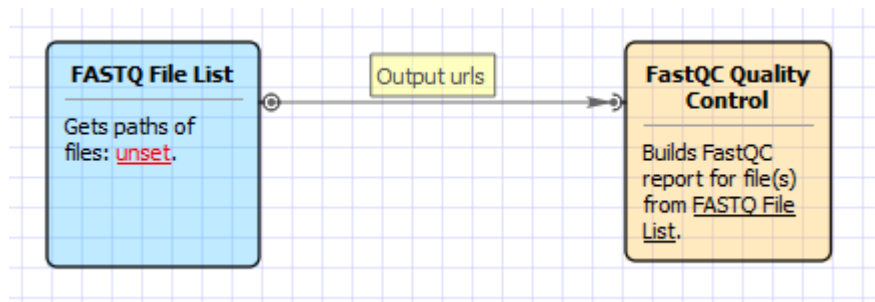
If you haven't used the workflow samples in UGENE before, look at the ["How to Use Sample Workflows"](#) section of the documentation.

## Workflow Sample Location

The workflow sample "Quality Control by FastQC" can be found in the "NGS" section of the Workflow Designer samples.

## Workflow Image

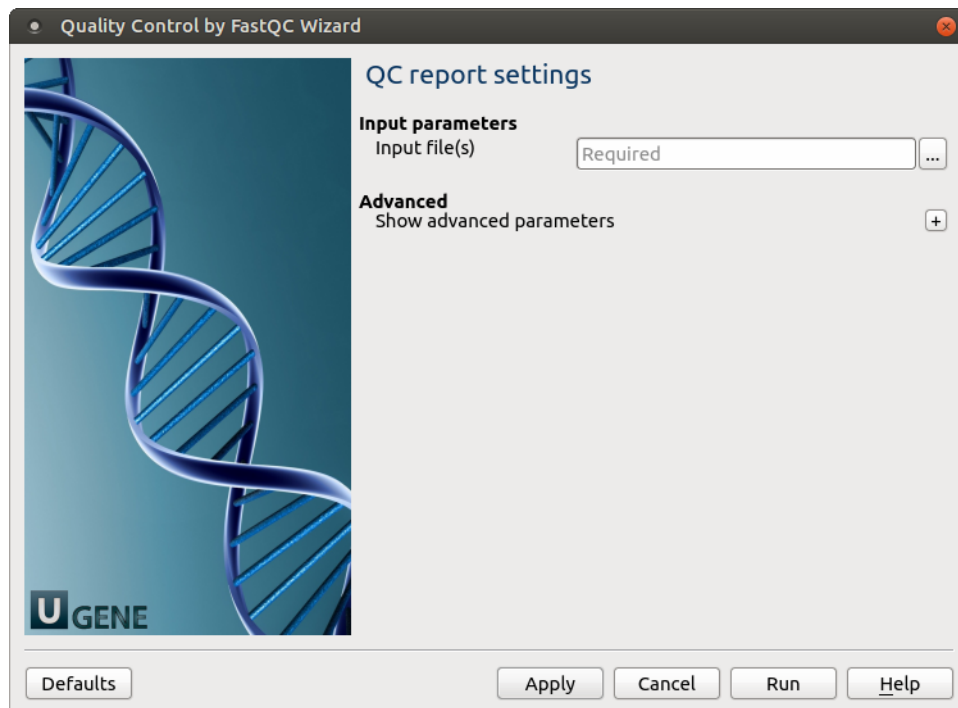
The workflow is the following:



## Workflow Wizard

The wizard has 1 page.

1. [High Throughput Sequence QC Report by FastQC](#): On this page you must input FASTQ file(s) and optionally modify advanced parameters.



The following parameters are available:

FASTQ URL(s)	Semicolon-separated list of paths to the input files.
Output directory	Select an output directory. Custom - specify the output directory in the 'Custom directory' parameter. Workflow - internal workflow directory. Input file - the directory of the input file.
Custom directory	Select the custom output directory.
List of adapters	Specifies a non-default file which contains the list of adapter sequences which will be explicitly searched against the library. The file must contain sets of named adapters in the form name[tab]sequence. Lines prefixed with a hash will be ignored.
List of contaminants	Specifies a non-default file which contains the list of contaminants to screen overrepresented sequences against. The file must contain sets of named contaminants in the form name[tab]sequence. Lines prefixed with a hash will be ignored.