

# FastQC Quality Control Element

Builds quality control reports.

## Parameters in GUI

| Parameter                   | Description  | Default value |
|-----------------------------|--|---------------|
| <b>Output file</b>          | Specify the output file name.  | Input file    |
| <b>List of adapters</b>     | 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. |               |
| <b>List of contaminants</b> | 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.            |               |

## Parameters in Workflow File

**Type:** fastqc

| Parameter           | Parameter in the GUI        | Type          |
|---------------------|-----------------------------|---------------|
| <b>out-file</b>     | <b>Output file</b>          | <i>string</i> |
| <b>adapter</b>      | <b>List of adapters</b>     | <i>string</i> |
| <b>contaminants</b> | <b>List of contaminants</b> | <i>string</i> |

## Input/Output Ports

The element has 1 *input port*.

**Name in GUI:** Short reads

**Name in Workflow File:** in-file

**Slots:**

| Slot In GUI       | Slot in Workflow File | Type          |
|-------------------|-----------------------|---------------|
| <b>Source URL</b> | url                   | <i>string</i> |