CASAVA FASTQ Filter

Reads in FASTQ file produced by CASAVA 1.8 contain 'N' or 'Y' as a part of an idetifier. 'Y' if a read if filtered, 'N' if the read if the read is not filtered. The workflow cleans up the filtered reads.

| Read Sequence | Sequence | CASAVA FASTQ filter | output data | Write Sequence |
|-------------------|----------|------------------------|-------------|------------------------|
| Reads sequence(s) | Ŭ, | | · | Save all sequences |
| from <u>unset</u> | | Filters FASTQ | | from CASAVA FASTO |
| | | reads generated | | filter to fastq.fastq. |
| | | by CASAVA 1.8 | | |

Also, if required, you can change parameters. Use the workflow wizard to guide you through the parameters setup process. The first wizard page will appear when you click on the Show wizard button on the Workflow Designer toolbar:

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