## **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)				Save all sequences
from <u>unset</u> .		Filters FASTQ		from CASAVA FAST
		reads generated		filter to fastq.fastq.
		by CASAVA 1.8		



## 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.