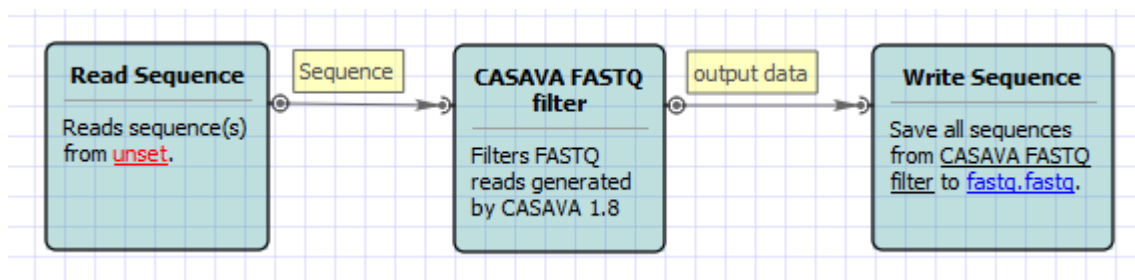


# CASAVA FASTQ Filter

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



## 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.