



ABI Sanger Sequencer



Raw Data



(.ab1) - (.phd.1) - (.seq)



Quality Control (FastQC)



Manual Editing

Inspect chromatogram for
incorrect calls

Remove primer sequences
and poor-quality regions



Sequence Assembly

Pairwise Assembly
(UGENE)

Trim non-overlapping
ends

Merge sequence



Sequence Alignment

BLAST sequence

Visualize output



Phylogenetic
Analysis

Map sequence to a
phylogenetic tree

Visualize output