



Trace settings

Sequence processing

## Consensus settings

Min. confidence score: Consensus algorithm: ☒ Bayesian ☐ SeqTrace 0.8

## Sequence trimming

☐ Automatically trim sequence ends☐ Trim primers if  % of the primer alignment matches.☐ Trim alignment end gap regions☒ Trim until at least  out of  bases are correctly called.

OK



Cancel