

History for:

 Trim Reads log

Trim Reads 2.9

29 Jun 2023 15:51:19

Version:

Modified by:

Trim using quality scores

Quality limit

Trim ambiguous nucleotides

Maximum number of ambiguities

Automatic read-through adapter trimming

Trim adapter list

Trim homopolymers from 5'

Trim homopolymers from 3'

polyA

polyC

polyG

polyT

Remove 5' terminal nucleotides

Remove 3' terminal nucleotides

Trim to a fixed length

Discard short reads

Minimum length

Discard long reads

Save discarded sequences

Save broken pairs

Create report

Comments:

Originates from:

CLC Genomics Server 23.0.4

fito

Yes

0.01

Yes

2

Yes

Not set

No

Yes

Yes

No

Yes

Yes

No

No

No

Yes


15

No

No

No

Yes



AM24_1_1 (paired)