

Bioinformatic Analysis Report

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Project title: Genome Sequence of Nannochloropsis
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Type of report: Sequence Trim Report
Date: May 25, 2011
Details: All Roche reads

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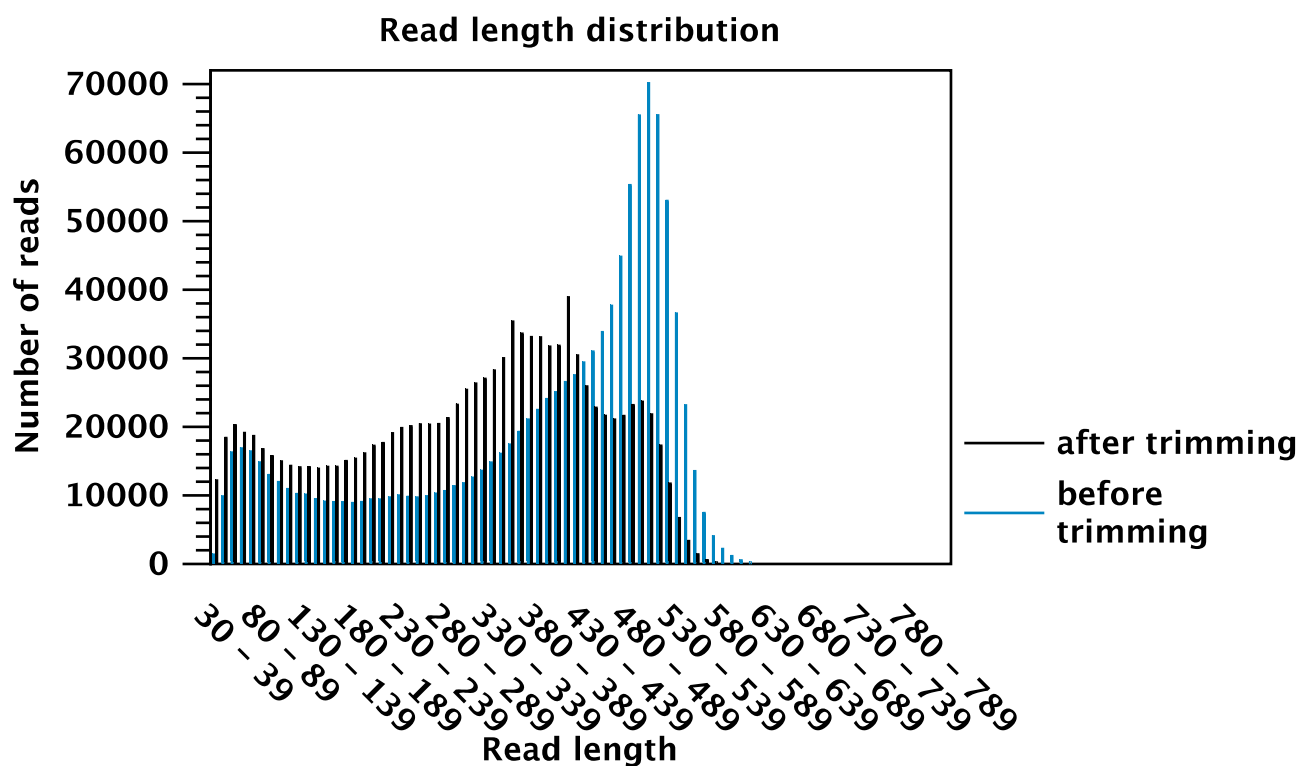
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1. Trim summary

Name	Number of reads	Avg.length	Number of reads after trim	Percentage trimmed
GGFTG2D02	490,547	368.7	481,257	98.11%
GHMDCZM01	632,867	391.7	622,518	98.36%

Avg.length after trim
291.1
318.9

2. Read length before / after trimming



3. Trim settings

- Removal of low quality sequence. (limit = 0.01).
- Removal of ambiguous nucleotides: No ambiguous nucleotides allowed.

- Removal of adapter sequences, using the following adapters :
 - 454 Sequence Primer A (GCCTCCCTCGGCCATCAG), strand = Plus, action = Remove adapter, score = [3, 2, 15, 2]
 - 454 Sequence Primer B (GCCTGCCAGCCCGCTCAG), strand = Minus, action = Remove adapter, score = [3, 2, 15, 2]
- Removal of sequences on length: minimum length 30 nucleotides.

4. Detailed trim results

Trim	Input reads	No trim	Trimmed	Nothing left or Discarded
Trim on quality	1,123,414	95,833	1,027,577	4
Ambiguity trim	1,123,410	1,006,351	111,802	5,257
Adapter trimming	1,118,153	931,996	186,155	2
Filter on length	1,118,151	1,103,775	0	14,376