

## **Bioinformatic Analysis Report**

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Project title: Chlorella Genome Sequence  
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Type of report: Sequence Trim Report  
Date: October 22, 2011  
Details: Trimming of all Illumina paired-end reads

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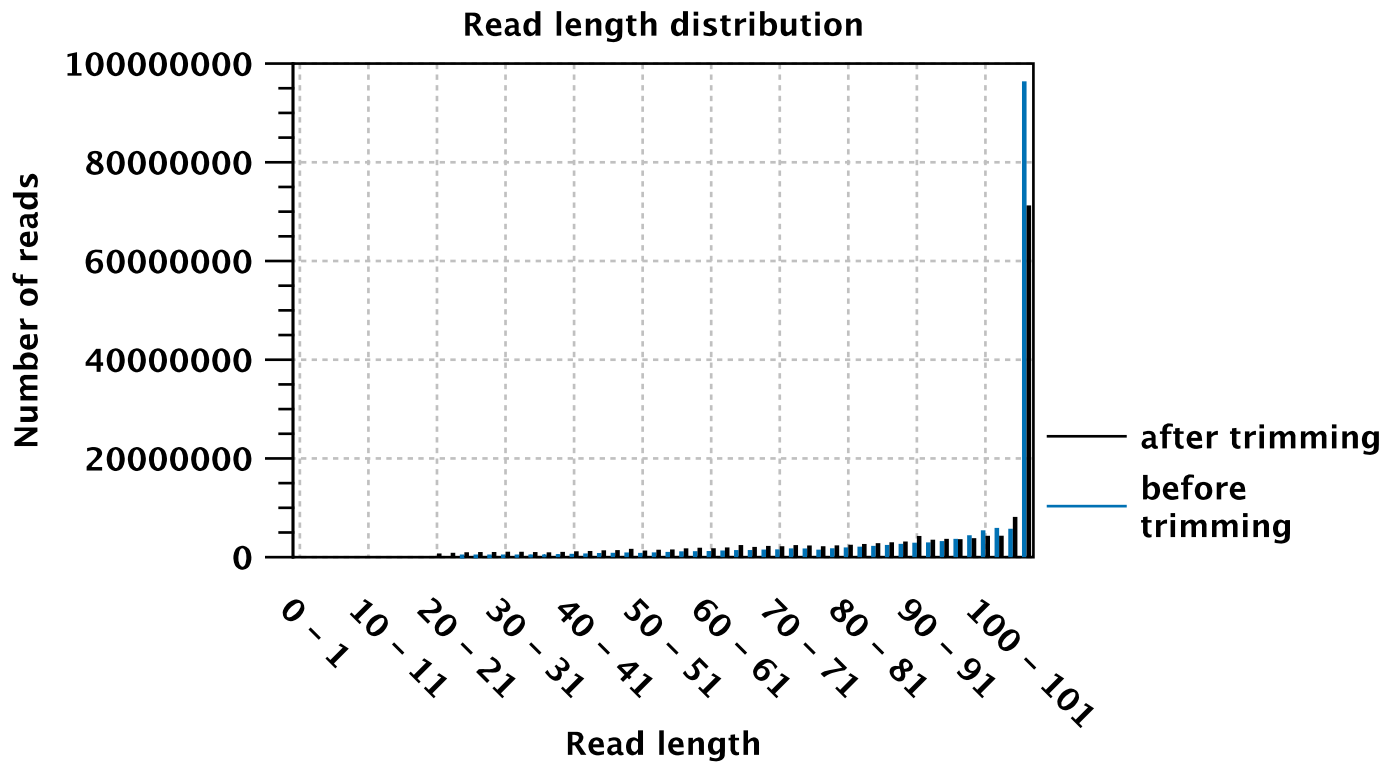
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# 1. Trim summary

Name	Number of reads	Avg.length	Number of reads after trim	Percentage trimmed
s_7_1_sequence (paired)	171,758,456	94.8	168,611,711	98.17%
s_7_1_sequence	82,020	82.5	74,680	91.05%

Avg.length after trim
88.3
74.4

# 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 sequences on length: minimum length 20 nucleotides.

## 4. Detailed trim results

Trim	Input reads	No trim	Trimmed	Nothing left or Discarded
Trim on quality	171,840,476	106,843,983	64,996,202	291
Ambiguity trim	171,840,185	171,641,520	193,448	5,217
Filter on length	171,834,968	168,686,391	0	3,148,577