

Bioinformatic Analysis Report

Genome Project Solutions
1024 Promenade Street
Hercules, CA 94547

Informatics@GenomeProjectSolutions.com
<http://www.GenomeProjectSolutions.com>
877-867-0146

Project title: Genome Sequence of Nannochloropsis
Prepared for: Dr. Randor Radakovits and Dr. Matthew Posewitz
Type of report: Sequence Trim Report
Date: May 25, 2011
Details: All Illumina paired mate-pair reads

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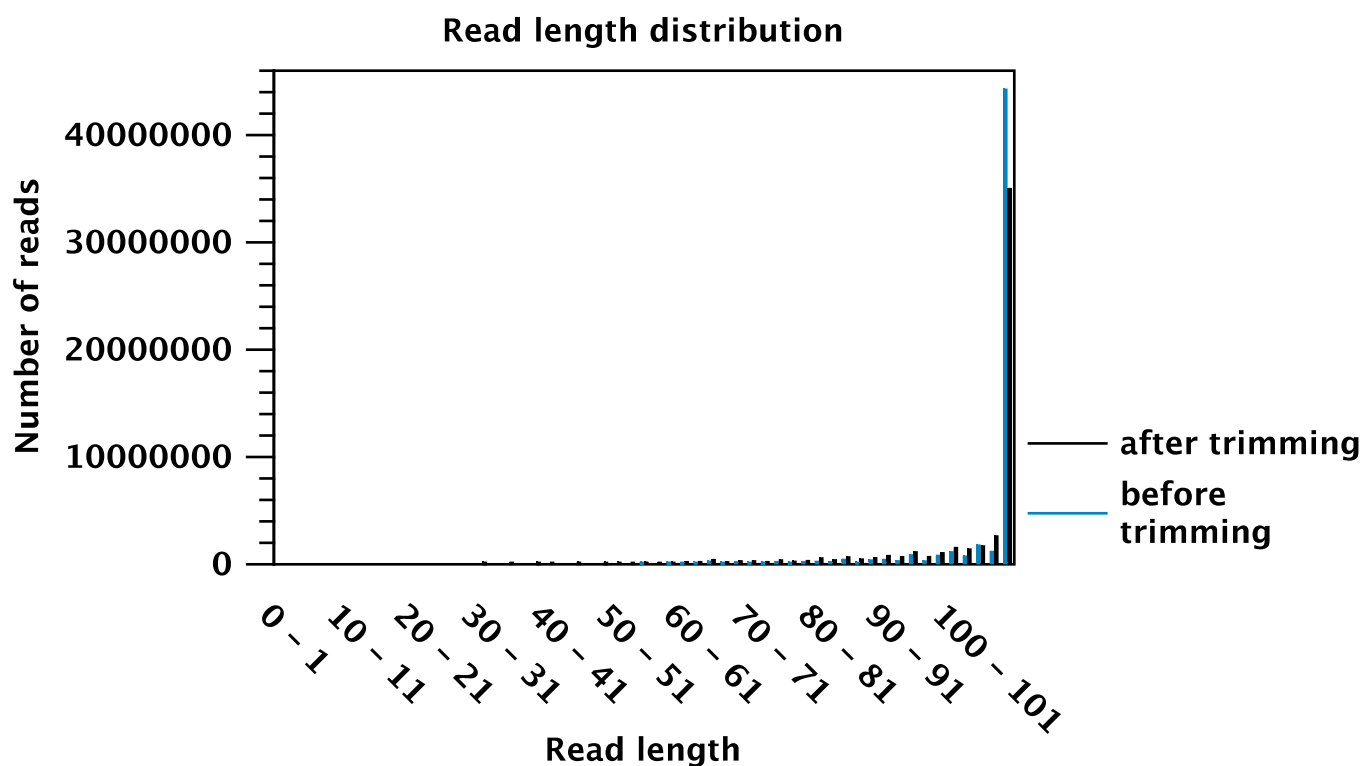
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1. Trim summary

Name	Number of reads	Avg.length	Number of reads after trim	Percentage trimmed
Nano_gDNA_MatePa ir_1.fastq (paired)	57,978,246	103.2	56,644,602	97.7%

Avg.length after trim
100.0

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 30 nucleotides.

4. Detailed trim results

Trim	Input reads	No trim	Trimmed	Nothing left or Discarded
Trim on quality	57,978,246	41,497,483	16,480,761	2
Ambiguity trim	57,978,244	57,617,025	320,013	41,206
Filter on length	57,937,038	56,644,602	0	1,292,436