

Bioinformatic Analysis Report

Genome Project Solutions
1024 Promenade Street
Hercules, CA 94547

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

Project title: Chlorella Genome Sequence

Prepared for: Dr. Micheal Guarnieri

Type of report: RNAseq mapping summary

Date: May 25, 2012

Details: Summary report on mapping all RNAseq raw reads to the transcript contigs of the transcriptome assembly

Table of contents

1. Summary mapping report	3
1.1 Summary statistics	3
1.2 General algorithm parameters	3
1.3 Reads parameters	3
1.4 Distribution of read length	4
1.5 Distribution of matched read length	5
1.6 Distribution of non-matched read length	6

1. Summary mapping report

1.1 Summary statistics

	Count	Average length	Total bases
Reads	412,236,998	35.48	14,627,995,026
Matched	345,520,531	35.56	12,285,158,508
Not matched	66,716,467	35.12	2,342,836,518
References	27,303	761	20,780,790

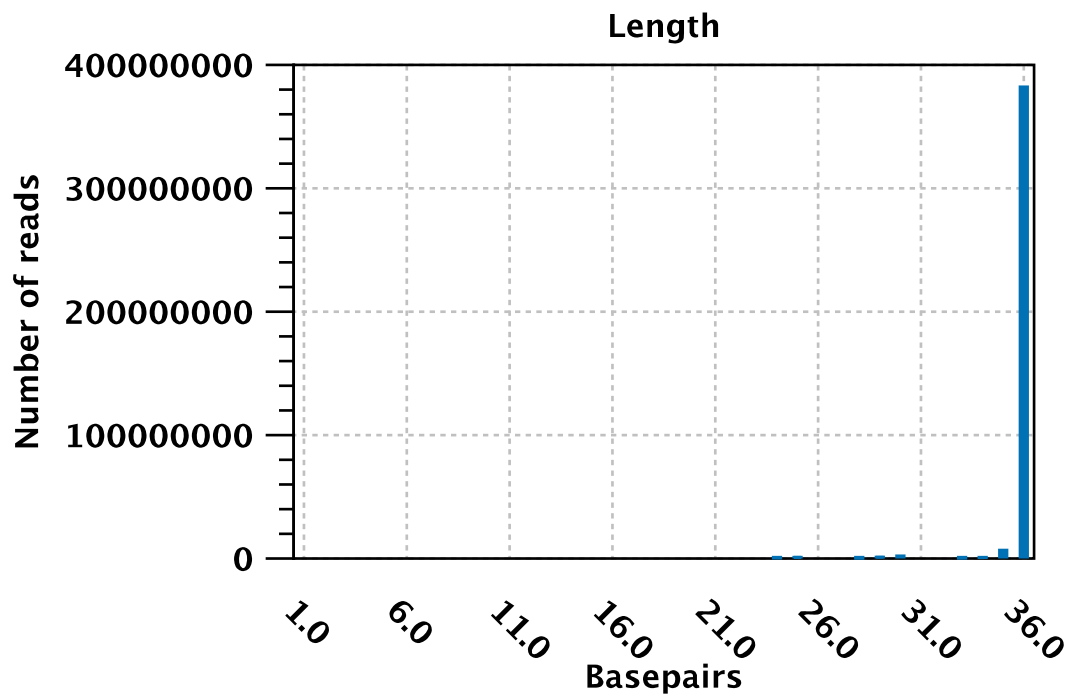
1.2 General algorithm parameters

Parameter	Value
Conflict resolution	Vote (A, C, G, T)
Non specific matches	random
Masking of references	none

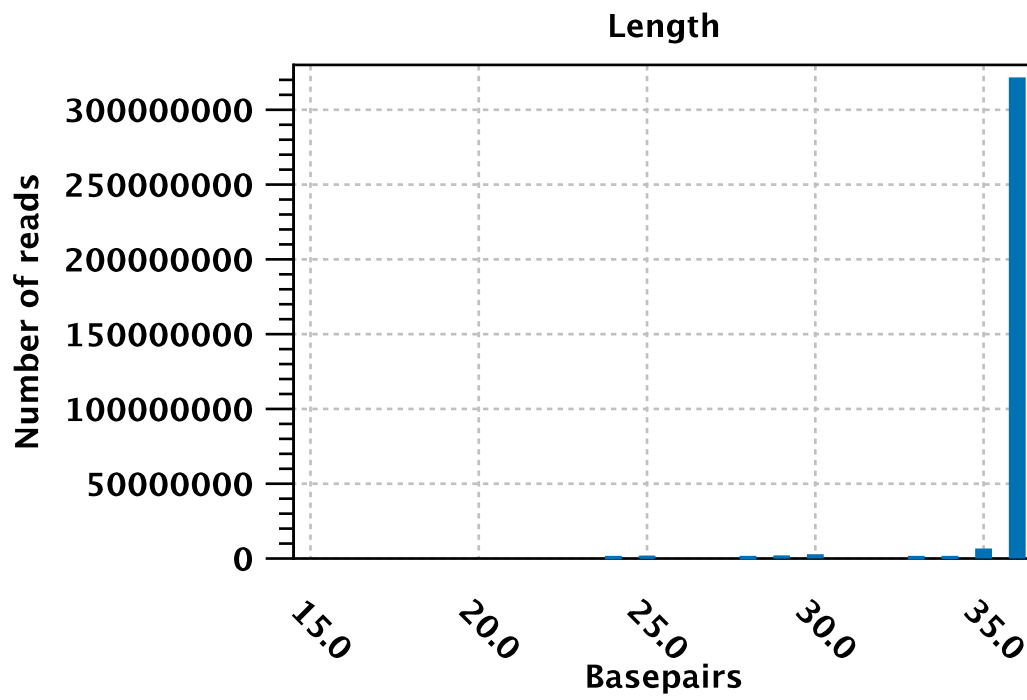
1.3 Reads parameters

Reads	Length	Type	Parameters
Hetero	Short	Single	Default
OD2a	Short	Single	Default
OD2b	Short	Single	Default
OD2c	Short	Single	Default
OD4A	Short	Single	Default
OD4B	Short	Single	Default
OD6A	Short	Single	Default
OD6B	Short	Single	Default
OD7Ra	Short	Single	Default
OD7Ra2	Short	Single	Default
OD7Rb	Short	Single	Default
OD8a	Short	Single	Default
OD8b	Short	Single	Default
OD8c	Short	Single	Default

1.4 Distribution of read length



1.5 Distribution of matched read length



1.6 Distribution of non-matched read length

