

Bioinformatic Analysis Report

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Project title: Genome Sequence of Nannochloropsis
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Type of report: RNAseq Read Mapping Report

Date: September 8, 2011
Details: Plus N RNAseq reads mapped to the final unique transcript set

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1. Summary mapping report

1.1 Summary statistics

| | Count | Average length | Total bases |
|---------------------|------------|----------------|-------------|
| Reads | 19,564,728 | 50.87 | 995,348,334 |
| Matched | 12,847,166 | 50.87 | 653,575,202 |
| Not matched | 6,717,562 | 50.88 | 341,773,132 |
| References | 8,921 | 1,186 | 10,583,984 |
| Reads in pairs | 11,373,210 | 160.83 | |
| Broken paired reads | 1,473,956 | 50.76 | |

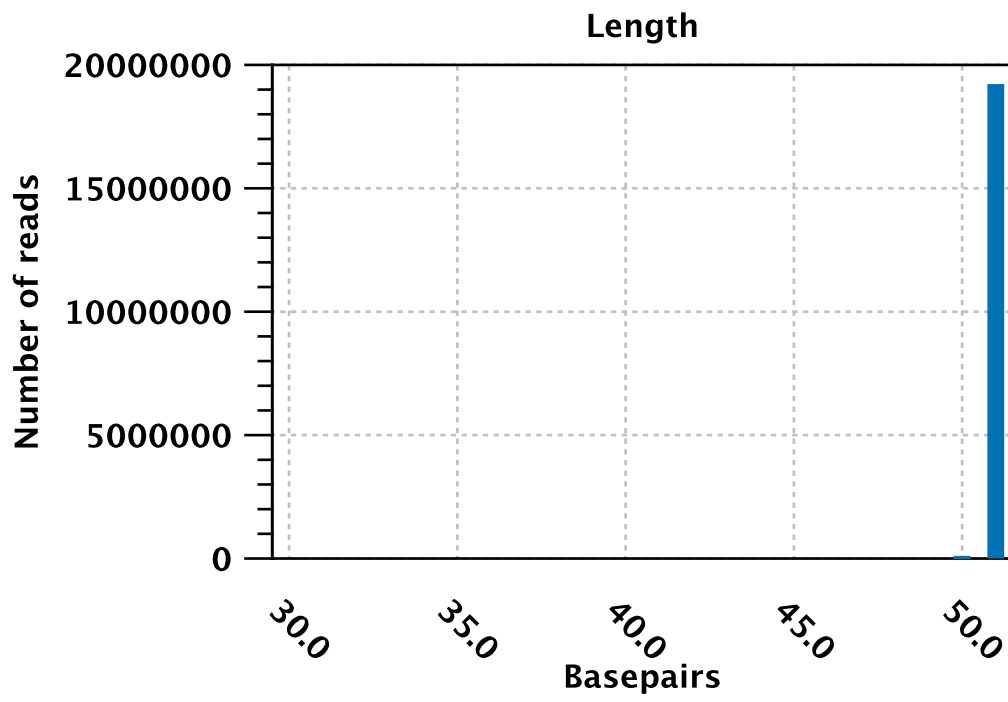
1.2 General algorithm parameters

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

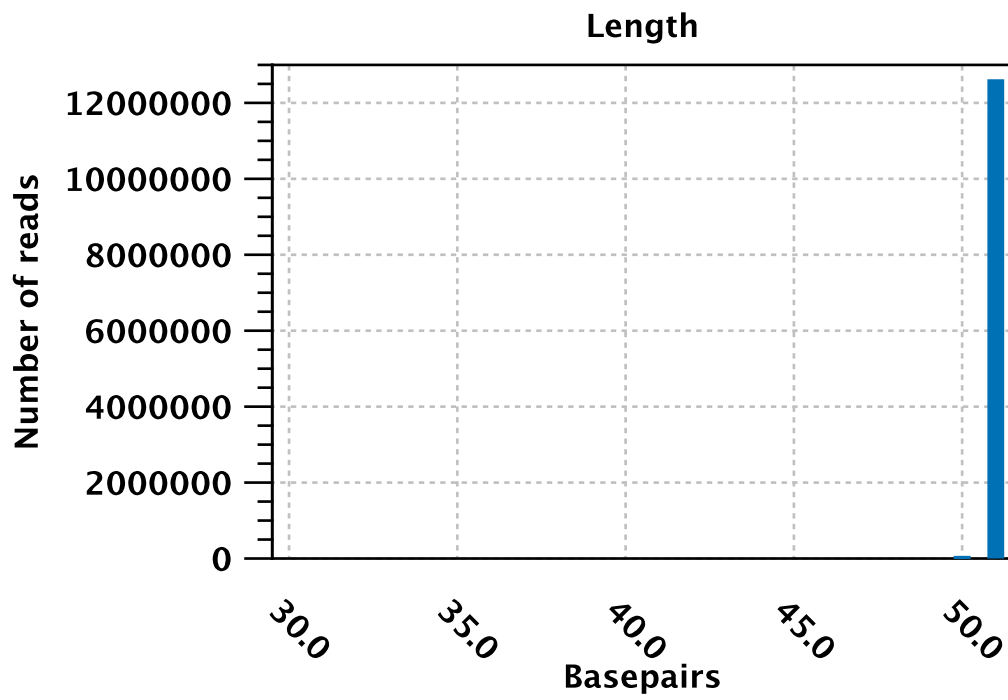
1.3 Reads parameters

| Reads | Length | Type | Parameters |
|---|--------|--------|------------|
| plus_N_NaGa_total_RNA trimmed (paired) | Short | Paired | Default |

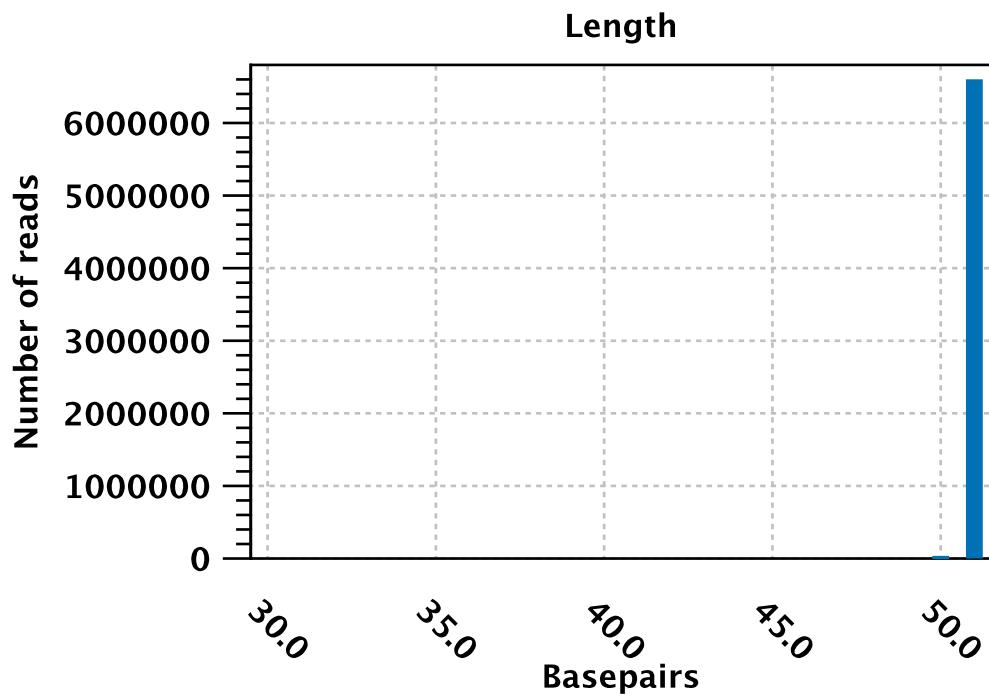
1.4 Distribution of read length



1.5 Distribution of matched read length



1.6 Distribution of non-matched read length



1.7 Paired reads distance distribution

