

Assembly Report

Experiment Details

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|-----------------------------------|---------------|
| ExperimentID: | Experiment 10 |
| Sequencing Coverage: | 20 |
| Number of Partitions: | 5 |
| Allowed Mismatch Count in (Base): | 0 |
| Length of Sliding Window: | 41 |

Reads Dataset Details

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|-------------------------------|--------|
| Total Reads Count: | 1054 |
| Total Dataset Size in (Base): | 211074 |
| Valid Read Count: | 1054 |
| Rejected Read Count: | 0 |
| Maximum Read Length: | 201 |
| Minimum Read Length: | 162 |

Reference Genome Details

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|------------------------------------|-------|
| Length of Reference Genome (Base): | 10080 |
| Number of K-mers: | 9880 |
| Length of K-mer | 305 |

Assembly Details

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|---------------------|-------|
| Number of Contigs: | 20 |
| Contig N50: | 1176 |
| Contig N90: | 951 |
| Number of Scaffold | 1 |
| Scaffold N50: | 10080 |
| Scaffold N90: | 10080 |
| Mis-assembly Count: | 0 |
| TotalAssembly Size: | 10080 |

Repeat Details

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|--|-----|
| Total Reads Count(Non-Repeat) : | 309 |
| Total Reads Count(Repeat): | 85 |
| Retetitive Read Count based on (Partitions Identifier): | 84 |
| Retetitive Read Count (Entire Read Frequency Identifier): | 1 |
| Retetitive Read Count (Contained Read Frequency Identifier): | 1 |
| Total Repetitive Sequences Count | 759 |
| Total Unique Repetitive Sequences Count | 2 |

| | | | | | | |
|--------------------------|--------|--|--------------|--------|----------------|--------------|
| Total Repeat Size (Base) | | | 2082 | | | |
| Starting | Ending | Repetitive Sequences | Repeat Count | Length | Positions | |
| 1 | 10080 | GAAACCACGC AACAGACAATG CGTGAGTTAAA AGAACTGGG | 2 | 41 | Start Position | End Position |
| | | | | | 2501 | 2541 |
| | | | | | 9724 | 9764 |
| 1 | 10080 | GCTTTTCATTC TGA CTGCAAC GGGCAATATG TCTCTGTGTGG ATTAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTA AAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCBA TATAGGCATAG CGCACAGACA GATAAAAATTA CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGG | 8 | 250 | Start Position | End Position |
| | | | | | 1 | 250 |
| | | | | | 665 | 914 |
| | | | | | 1200 | 1449 |
| | | | | | 2846 | 3095 |
| | | | | | 3826 | 4075 |
| | | | | | 6163 | 6412 |
| | | | | | 7273 | 7522 |
| | | | | | 8425 | 8674 |
| | | | | | | |

SRGD Performance Metrics

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|----------------------|------|
| Initial Reads Count: | 1054 |
|----------------------|------|

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|---|--------|
| Reads Count after Removing Duplication: | 394 |
| Reads Count after Overlapping: | 241 |
| Initial Dataset Size in (Base): | 211074 |
| Dataset Siset after Removing Duplication: | 86253 |
| Dataset Size after Overlapping: | 52334 |

Overlapping Metrics

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|-----------------------------|-------------------|
| Repeat Identification Time: | 00h:00m:56s:000ms |
| Overlapping Time: | 00h:06m:27s:000ms |
| Reads Alignment Time: | 00h:00m:11s:000ms |
| Total Hybrid Assembly Time: | 00h:06m:38s:000ms |
| Repeat Annotation Time: | 00h:00m:32s:000ms |

| Overlapping Length | O(N) ² Time Complexity | Hit Index Count | Overlapping Matched Count | RI |
|--------------------|-----------------------------------|-----------------|---------------------------|----|
| 197 | 95481 | 35 | 1 | 0 |
| 176 | 94864 | 334 | 148 | 0 |
| 162 | 25600 | 7 | 1 | 0 |
| 151 | 25281 | 13 | 3 | 0 |