

Assembly Report

Experiment Details

| | |
|-----------------------------------|---------------|
| ExperimentID: | Experiment 41 |
| Sequencing Coverage: | 23 |
| Number of Partitions: | 1 |
| Allowed Mismatch Count in (Base): | 0 |
| Length of Sliding Window: | 201 |

Reads Dataset Details

| | |
|-------------------------------|--------|
| Total Reads Count: | 1212 |
| Total Dataset Size in (Base): | 241272 |
| Valid Read Count: | 1212 |
| Rejected Read Count: | 0 |
| Maximum Read Length: | 201 |
| Minimum Read Length: | 162 |

Reference Genome Details

| | |
|------------------------------------|-------|
| Length of Reference Genome (Base): | 10080 |
| Number of K-mers: | 9880 |
| Length of K-mer | 369 |

Assembly Details

| | |
|---------------------|-------|
| Number of Contigs: | 30 |
| Contig N50: | 1026 |
| Contig N90: | 926 |
| Number of Scaffold | 2 |
| Scaffold N50: | 955 |
| Scaffold N90: | 955 |
| Mis-assembly Count: | 0 |
| TotalAssembly Size: | 10655 |

Repeat Details

| | |
|--|-----|
| Total Reads Count(Non-Repeat) : | 395 |
| Total Reads Count(Repeat): | 6 |
| Retetitive Read Count based on (Partitions Identifier): | 0 |
| Retetitive Read Count (Entire Read Frequency Identifier): | 3 |
| Retetitive Read Count (Contained Read Frequency Identifier): | 3 |
| Total Repetitive Sequences Count | 9 |
| Total Unique Repetitive Sequences Count | 3 |

| | | | | | | |
|--------------------------|--------|----------------------|--------------|--------|-----------|--|
| Total Repeat Size (Base) | | | 3000 | | | |
| Starting | Ending | Repetitive Sequences | Repeat Count | Length | Positions | |
| 1 | 9700 | CGGTCGAAAA | 4 | 250 | | |
| | | ACTGCTGGCA | | | | |
| | | GTGGGGCATT | | | | |
| | | ACCTCGAATCT | | | | |
| | | ACCGTCGATAT | | | | |
| | | TGCTGAGTCC | | | | |
| | | ACCCGCCGTA | | | | |
| | | TTGCGGCAAG | | | | |
| | | TCGTATTCCGG | | | | |
| | | CTGATCACATG | | | | |
| | | GTGCTGATGG | | | | |
| | | CAGGTTTCACC | | | | |
| | | GCCGGTAATG | | | | |
| | | AAAAAGGCGA | | | | |
| | | ACTGGTGGTG | | | | |
| | | CTTGGACGCA | | | | |
| | | ACGGTTCCGA | | | | |
| | | CTACTCTGCTG | | | | |
| | | CGGTGCTGGC | | | | |
| | | TGCCTGTTTAC | | | | |
| GCGCCGATTG | | | | | | |
| TTGCGAGATTT | | | | | | |
| GGACGGACGT | | | | | | |
| TGACGGGGTC | | | | | | |
| TA | | | | | | |

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|-----------------------|---------------------|--------------|---|-----|--|-----------------------|---------------------|------|------|------|------|------|------|------|------|
| 1 | 9700 | GATTCATTTCGG | 4 | 250 | | | | | | | | | | | |
| | | GATGGTCTGT | | | | | | | | | | | | | |
| | | GTGGATTAAAA | | | | | | | | | | | | | |
| | | AAAGAGTGTCT | | | | | | | | | | | | | |
| | | GATAGCAGCTT | | | | | | | | | | | | | |
| | | CTGAACTGGTT | | | | | | | | | | | | | |
| | | ACCTGCCGTG | | | | | | | | | | | | | |
| | | AGTAAATTTAAA | | | | | | | | | | | | | |
| | | ATTTTATTGAC | | | | | | | | | | | | | |
| | | TTAGGTCACTA | | | | | | | | | | | | | |
| | | AATACTTTAAC | | | | | | | | | | | | | |
| | | CAATATAGGCA | | | | | | | | | | | | | |
| | | TAGCGCACAG | | | | | | | | | | | | | |
| | | ACAGATAAAAA | | | | | | | | | | | | | |
| | | TTACAGAGTAC | | | | | | | | | | | | | |
| | | ACAACATCCTC | | | | | | | | | | | | | |
| | | AAAGCCTACC | | | | | | | | | | | | | |
| | | GGTGACAGTG | | | | | | | | | | | | | |
| | | CGGGCTTTTTT | | | | | | | | | | | | | |
| | | TTCGACCAAAG | | | | | | | | | | | | | |
| GTAACGAGGT | | | | | | | | | | | | | | | |
| AACAACCATGC | | | | | | | | | | | | | | | |
| GAGTGTTGAA | | | | | | | | | | | | | | | |
| GTCA | | | | | | | | | | | | | | | |
| | | | | | <table><tr><td>Start Positio n</td><td>End Positio n</td></tr><tr><td>2885</td><td>3134</td></tr><tr><td>4257</td><td>4506</td></tr><tr><td>6796</td><td>7045</td></tr><tr><td>9434</td><td>9683</td></tr></table> | Start Positio n | End Positio n | 2885 | 3134 | 4257 | 4506 | 6796 | 7045 | 9434 | 9683 |
| Start Positio n | End Positio n | | | | | | | | | | | | | | |
| 2885 | 3134 | | | | | | | | | | | | | | |
| 4257 | 4506 | | | | | | | | | | | | | | |
| 6796 | 7045 | | | | | | | | | | | | | | |
| 9434 | 9683 | | | | | | | | | | | | | | |

| 1 | 9700 | GCTTTTCATTC | 4 | 250 | <table><tr><th>Start Positio n</th><th>End Positio n</th></tr><tr><td>1</td><td>250</td></tr><tr><td>699</td><td>948</td></tr><tr><td>1738</td><td>1987</td></tr><tr><td>8344</td><td>8593</td></tr></table> | Start Positio n | End Positio n | 1 | 250 | 699 | 948 | 1738 | 1987 | 8344 | 8593 |
|-------------|------|-----------------------|---|-----|--|-----------------------|---------------------|---|-----|-----|-----|------|------|------|------|
| | | Start Positio n | | | | End Positio n | | | | | | | | | |
| | | 1 | | | | 250 | | | | | | | | | |
| | | 699 | | | | 948 | | | | | | | | | |
| | | 1738 | | | | 1987 | | | | | | | | | |
| | | 8344 | | | | 8593 | | | | | | | | | |
| | | TGACTGCAAC | | | | | | | | | | | | | |
| | | GGGCAATATG | | | | | | | | | | | | | |
| | | TCTCTGTGTGG | | | | | | | | | | | | | |
| | | ATTAAAAAAG | | | | | | | | | | | | | |
| AGTGTCTGATA | | | | | | | | | | | | | | | |
| GCAGCTTCTG | | | | | | | | | | | | | | | |
| AACTGGTTACC | | | | | | | | | | | | | | | |
| TGCCGTGAGT | | | | | | | | | | | | | | | |
| AAATTAAAATT | | | | | | | | | | | | | | | |
| TTATTGACTTA | | | | | | | | | | | | | | | |
| GGTCACTAAAT | | | | | | | | | | | | | | | |
| ACTTTAACC | | | | | | | | | | | | | | | |
| TATAGGCATAG | | | | | | | | | | | | | | | |
| CGCACAGACA | | | | | | | | | | | | | | | |
| GATAAAAATTA | | | | | | | | | | | | | | | |
| CAGAGTACAC | | | | | | | | | | | | | | | |
| AACATCCATGA | | | | | | | | | | | | | | | |
| AACGCATTAGC | | | | | | | | | | | | | | | |
| ACCACCATTAC | | | | | | | | | | | | | | | |
| CACCACCATCA | | | | | | | | | | | | | | | |
| CCATTACCACA | | | | | | | | | | | | | | | |
| GGTAACGGTG | | | | | | | | | | | | | | | |
| CGGG | | | | | | | | | | | | | | | |

SRGD Performance Metrics

| | |
|---|--------|
| Initial Reads Count: | 1212 |
| Reads Count after Removing Duplication: | 401 |
| Reads Count after Overlapping: | 192 |
| Initial Dataset Size in (Base): | 241272 |
| Dataset Sizet after Removing Duplication: | 101778 |
| Dataset Size after Overlapping: | 43558 |

Overlapping Metrics

| | | | | |
|-----------------------------|-----------------------------------|-------------------|---------------------------|----|
| Repeat Identification Time: | | 00h:00m:07s:000ms | | |
| Overlapping Time: | | 00h:04m:15s:000ms | | |
| Reads Alignment Time: | | 00h:00m:13s:000ms | | |
| Total Hybrid Assembly Time: | | 00h:04m:28s:000ms | | |
| Repeat Annotation Time: | | 00h:00m:08s:000ms | | |
| Overlapping Length | O(N) ² Time Complexity | Hit Index Count | Overlapping Matched Count | RI |
| 200 | 156025 | 61 | 2 | 0 |
| 199 | 154449 | 73 | 3 | 0 |
| 197 | 152100 | 64 | 3 | 0 |
| 196 | 149769 | 78 | 4 | 0 |
| 195 | 146689 | 75 | 2 | 0 |
| 194 | 145161 | 90 | 1 | 0 |
| 192 | 144400 | 77 | 1 | 0 |
| 190 | 143641 | 91 | 4 | 0 |
| 189 | 140625 | 81 | 1 | 0 |
| 187 | 139876 | 91 | 1 | 0 |
| 180 | 139129 | 58 | 1 | 0 |
| 177 | 138384 | 47 | 1 | 0 |
| 176 | 137641 | 403 | 176 | 0 |
| 167 | 38025 | 16 | 1 | 0 |
| 165 | 37636 | 25 | 2 | 0 |
| 162 | 36864 | 23 | 1 | 0 |
| 158 | 36481 | 14 | 1 | 0 |
| 156 | 36100 | 18 | 1 | 0 |
| 151 | 35721 | 15 | 3 | 0 |