

# Assembly Report

## Experiment Details

|                                   |               |
|-----------------------------------|---------------|
| ExperimentID:                     | Experiment 44 |
| Sequencing Coverage:              | 23            |
| Number of Partitions:             | 4             |
| Allowed Mismatch Count in (Base): | 0             |
| Length of Sliding Window:         | 51            |

## 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                    | 376   |

## Assembly Details

|                     |       |
|---------------------|-------|
| Number of Contigs:  | 28    |
| Contig N50:         | 1026  |
| Contig N90:         | 926   |
| Number of Scaffold  | 1     |
| Scaffold N50:       | 10080 |
| Scaffold N90:       | 10080 |
| Mis-assembly Count: | 0     |
| TotalAssembly Size: | 10080 |

## Repeat Details

|  |     |
|--|-----|
| Total Reads Count(Non-Repeat) :                              | 334 |
| Total Reads Count(Repeat):                                   | 67  |
| Retetitive Read Count based on (Partitions Identifier):      | 64  |
| Retetitive Read Count (Entire Read Frequency Identifier):    | 3   |
| Retetitive Read Count (Contained Read Frequency Identifier): | 3   |
| Total Repetitive Sequences Count                             | 382 |
| Total Unique Repetitive Sequences Count                      | 3   |

|                          |        |                      |              |        |           |  |
|--------------------------|--------|----------------------|--------------|--------|-----------|--|
| Total Repeat Size (Base) |        |                      | 3000         |        |           |  |
| Starting                 | Ending | Repetitive Sequences | Repeat Count | Length | Positions |  |
| 1                        | 10080  | CGGTCGAAAA           | 4            | 250    |           |  |
|                          |        | ACTGCTGGCA           |              |        |           |  |
|                          |        | GTGGGGCATT           |              |        |           |  |
|                          |        | ACCTCGAATCT          |              |        |           |  |
|                          |        | ACCGTCGATAT          |              |        |           |  |
|                          |        | TGCTGAGTCC           |              |        |           |  |
|                          |        | ACCCGCCGTA           |              |        |           |  |
|                          |        | TTGCGGCAAG           |              |        |           |  |
|                          |        | TCGTATTCCGG          |              |        |           |  |
|                          |        | CTGATCACATG          |              |        |           |  |
|                          |        | GTGCTGATGG           |              |        |           |  |
|                          |        | CAGGTTTCACC          |              |        |           |  |
|                          |        | GCCGGTAATG           |              |        |           |  |
|                          |        | AAAAAGGCCGA          |              |        |           |  |
|                          |        | ACTGGTGGTG           |              |        |           |  |
|                          |        | CTTGGACGCA           |              |        |           |  |
|                          |        | ACGGTTCCGA           |              |        |           |  |
|                          |        | CTACTCTGCTG          |              |        |           |  |
|                          |        | CGGTGCTGGC           |              |        |           |  |
|                          |        | TGCCTGTTTAC          |              |        |           |  |
|                          |        | GCGCCGATTG           |              |        |           |  |
|                          |        | TTGCGAGATTT          |              |        |           |  |
|                          |        | GGACGGACGT           |              |        |           |  |
|                          |        | TGACGGGGGTC          |              |        |           |  |
|                          |        | TA                   |              |        |           |  |

|                       |                     |              |   |     |  |                       |                     |      |      |      |      |      |      |      |      |
|-----------------------|---------------------|--------------|---|-----|--|-----------------------|---------------------|------|------|------|------|------|------|------|------|
| 1                     | 10080               | 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<br/>Positio<br/>n</td><td>End<br/>Positio<br/>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<br>Positio<br>n | End<br>Positio<br>n | 2885 | 3134 | 4257 | 4506 | 6796 | 7045 | 9434 | 9683 |
| Start<br>Positio<br>n | End<br>Positio<br>n |              |   |     |  |                       |                     |      |      |      |      |      |      |      |      |
| 2885                  | 3134                |              |   |     |  |                       |                     |      |      |      |      |      |      |      |      |
| 4257                  | 4506                |              |   |     |  |                       |                     |      |      |      |      |      |      |      |      |
| 6796                  | 7045                |              |   |     |  |                       |                     |      |      |      |      |      |      |      |      |
| 9434                  | 9683                |              |   |     |  |                       |                     |      |      |      |      |      |      |      |      |

| 1           | 10080 | GCTTTTCATTC    | 4 | 250 | <table><tr><th>Start Position</th><th>End Position</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 Position | End Position | 1 | 250 | 699 | 948 | 1738 | 1987 | 8344 | 8593 |
|-------------|-------|----------------|---|-----|--|----------------|--------------|---|-----|-----|-----|------|------|------|------|
|             |       | Start Position |   |     |  | End Position   |              |   |     |     |     |      |      |      |      |
|             |       | 1              |   |     |  | 250            |              |   |     |     |     |      |      |      |      |
|             |       | 699            |   |     |  | 948            |              |   |     |     |     |      |      |      |      |
|             |       | 1738           |   |     |  | 1987           |              |   |     |     |     |      |      |      |      |
|             |       | 8344           |   |     |  | 8593           |              |   |     |     |     |      |      |      |      |
|             |       | TGACTGCAAC     |   |     |  |                |              |   |     |     |     |      |      |      |      |
|             |       | GGGCAATATG     |   |     |  |                |              |   |     |     |     |      |      |      |      |
|             |       | TCTCTGTGTGG    |   |     |  |                |              |   |     |     |     |      |      |      |      |
|             |       | ATTAAAAAAG     |   |     |  |                |              |   |     |     |     |      |      |      |      |
|             |       | AGTGTCTGATA    |   |     |  |                |              |   |     |     |     |      |      |      |      |
|             |       | GCAGCTTCTG     |   |     |  |                |              |   |     |     |     |      |      |      |      |
|             |       | AACTGGTTACC    |   |     |  |                |              |   |     |     |     |      |      |      |      |
|             |       | TGCCGTGAGT     |   |     |  |                |              |   |     |     |     |      |      |      |      |
|             |       | AAATTAAAATT    |   |     |  |                |              |   |     |     |     |      |      |      |      |
|             |       | TTATTGACTTA    |   |     |  |                |              |   |     |     |     |      |      |      |      |
|             |       | GGTCACTAAAT    |   |     |  |                |              |   |     |     |     |      |      |      |      |
|             |       | ACTTTAACCBA    |   |     |  |                |              |   |     |     |     |      |      |      |      |
|             |       | 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:            | 229    |
| Initial Dataset Size in (Base):           | 241272 |
| Dataset Sizet after Removing Duplication: | 101778 |
| Dataset Size after Overlapping:           | 50358  |

Overlapping Metrics

|                             |                                   |                   |                           |    |
|-----------------------------|-----------------------------------|-------------------|---------------------------|----|
| Repeat Identification Time: |                                   | 00h:00m:28s:000ms |                           |    |
| Overlapping Time:           |                                   | 00h:03m:30s:000ms |                           |    |
| Reads Alignment Time:       |                                   | 00h:00m:23s:000ms |                           |    |
| Total Hybrid Assembly Time: |                                   | 00h:03m:53s:000ms |                           |    |
| Repeat Annotation Time:     |                                   | 00h:00m:31s:000ms |                           |    |
| Overlapping Length          | O(N) <sup>2</sup> Time Complexity | Hit Index Count   | Overlapping Matched Count | RI |
| 197                         | 111556                            | 45                | 3                         | 0  |
| 196                         | 109561                            | 47                | 1                         | 0  |
| 194                         | 108900                            | 68                | 1                         | 0  |
| 192                         | 108241                            | 50                | 1                         | 0  |
| 190                         | 107584                            | 55                | 2                         | 0  |
| 187                         | 106276                            | 60                | 2                         | 0  |
| 180                         | 104976                            | 39                | 1                         | 0  |
| 176                         | 104329                            | 342               | 153                       | 0  |
| 151                         | 28900                             | 17                | 8                         | 0  |