# Assembly Report

## Experiment Details

| | |
|---|---|
| ExperimentID: | Experiment 80 |
| Sequencing Coverage: | 35 |
| Number of Partitions: | 5 |
| Allowed Mismatch Count in (Base): | 0 |
| Length of Sliding Window: | 61 |

## Reads Dataset Details

| | |
|---|---|
| Total Reads Count: | 1203 |
| Total Dataset Size in (Base): | 359763 |
| Valid Read Count: | 1203 |
| Rejected Read Count: | 0 |
| Maximum Read Length: | 301 |
| Minimum Read Length: | 262 |

## Reference Genome Details

| | |
|---|---|
| Length of Reference Genome (Base): | 10080 |
| Number of K-mers: | 9780 |
| Length of K-mer | 476 |

## Assembly Details

| | |
|---|---|
| Number of Contigs: | 13 |
| Contig N50: | 2946 |
| Contig N90: | 2378 |
| Number of Scaffold | 1 |
| Scaffold N50: | 10080 |
| Scaffold N90: | 10080 |
| Mis-assembly Count: | 0 |
| TotalAssembly Size: | 10080 |

## Repeat Details

| | |
|---|---|
| Total Reads Count(Non-Repeat) : | 34 |
| Total Reads Count(Repeat): | 358 |
| Retetitve Read Count based on (Partitions Identifier): | 357 |
| Retetitve Read Count (Entire Read Frequency Identifier): | 3 |
| Retetitve Read Count (Contained Read Frequency Identifier): | 3 |
| Total Repetitive Sequences Count | 10642 |
| Total Unique Repetitive Sequences Count | 4 |

| Total Repeat Size (Base) | | | 7706 | | |
|---|---|---|---|---|---|
| Starting | Ending | Repetitive Sequences | Repeat Count | Length | Positions |
| 1 | 10080 | CGGTCGAAAA ACTGCTGGCA GTGGGGCATT ACCTCGAATCT ACCGTCGATAT TGCTGAGTCC ACCCGCCGTA TTGCGGCAAG TCGTATTCCGG CTGATCACATG GTGCTGATGG CAGGTTTCACC GCCGGTAATG AAAAAGGCGA ACTGGTGGTG CTTGGACGCA ACGGTTCCGA CTACTCTGCTG CGGTGCTGGC TGCCTGTTTAC GCGCCGATTG TTGCGAGATTT GGACGGACGT TGACGGGGTC TATACCTGCGA CCCGCGTCAG GTGCCCGATG CGAGGTTGTT GAAGTCGATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT AGGTCAGGCC A | 3 | 351 | <table>Start Position / End Position</table> |

| Start Position | End Position |
|---|---|
| 3561 | 3911 |
| 8386 | 8736 |
| 9149 | 9499 |

| 1 | 10080 | GATTCATTCGG GATGGTCTGT GTGGATTAAAA AAAGAGTGTCT GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA CGTAATCGTAG CCTTAGCAATC TCCAGTCC | 8 | 350 | Start Position | End Position |
|---|---|---|---|---|---|---|
| | | | | | 409 | 758 |
| | | | | | 2228 | 2577 |
| | | | | | 3182 | 3531 |
| | | | | | 4730 | 5079 |
| | | | | | 5529 | 5878 |
| | | | | | 6730 | 7079 |
| | | | | | 8014 | 8363 |
| | | | | | 9552 | 9901 |

| 1 | 10080 | GCGGTCGAAAAACTGCTGGCAGTGGGGCATTACCTCGAATCTACCGTCGATATTGCTGAGTCCACCCGCCGTATTGCGGCAAGTCGTATTCCGGCTGATCACATGGTGCTGATGGCAGGTTTCACCGCCGGTAATGAAAAAGGCGAACTGGTGGTGCTTGGACGCAACGGTTCCGACTACTCTGCTGCGGTGCTGGCTGCCTGTTTACGCGCCGATTGTTGCGAGATTTGGACGGACGTTGACGGGGTCTATACCTGCGACCCGCGTCAGGTGCCCGATGCGAGGTTGTTGAAGTCGATGTCCTACCAGGAAGCGATGGAGCTTTCCTACTTCGGCGCTCTAGGTCAGGCC | 3 | 351 | Start Position | End Position |
| | | | | | 3560 | 3910 |
| | | | | | 5909 | 6259 |
| | | | | | 9148 | 9498 |

| 1 | 10080 | GCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGATTAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTGGTTACCTGCCGTGAGTAAATTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGACAGATAAAAATTACAGAGTACACAACATCCATGAAACGCATTAGCACCACCATTACCACCACCATCACCATTACCACAGGTAACGGTGCGGGCTGACGCGTACAGGAAACACAGAAAAAGCCCGCACCTGACAGTGCGGGCTTTTTTTCGACCAAAGGTAACGAGGTAACAACCATGCGAGTGTTGAAGT | 8 | 350 | | |
| --- | --- | --- | --- | --- | --- | --- |

| Start Position | End Position |
| --- | --- |
| 1 | 350 |
| 854 | 1203 |
| 1295 | 1644 |
| 2705 | 3054 |
| 4337 | 4686 |
| 6359 | 6708 |
| 7574 | 7923 |
| 8752 | 9101 |

## SRGD Performance Metrics

| | |
| --- | --- |
| Initial Reads Count: | 1203 |
| Reads Count after Removing Duplication: | 392 |

| Reads Count after Overlapping: | 374 |
|---|---|
| Initial Dataset Size in (Base): | 359763 |
| Dataset Sizet after Removing Duplication: | 150869 |
| Dataset Size after Overlapping: | 113299 |

## Overlapping Metrics

| Repeat Identification Time: | 00h:00m:08s:000ms |
|---|---|
| Overlapping Time: | 00h:02m:21s:000ms |
| Reads Alignment Time: | 00h:00m:16s:000ms |
| Total Hybrid Assembly Time: | 00h:02m:37s:000ms |
| Repeat Annotation Time: | 00h:18m:33s:000ms |

| Overlapping Length | O(N)2 Time Complexity | Hit Index Count | Overlapping Matched Count | RI |
|---|---|---|---|---|
| 276 | 1156 | 24 | 12 | 0 |
| 251 | 484 | 1 | 1 | 0 |
| 226 | 441 | 6 | 5 | 0 |