Assembly Report

Experiment Details

ExperimentID:	Experiment 74
Sequencing Coverage:	29
Number of Partitions:	4
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	63

Reads Dataset Details

Total Reads Count:	1209
Total Dataset Size in (Base):	301119
Valid Read Count:	1209
Rejected Read Count:	0
Maximum Read Length:	251
Minimum Read Length:	212

Reference Genome Details

Length of Reference Genome (Base):	10080
Number of K-mers:	9830
Length of K-mer	519

Assembly Details

Number of Contigs:	16
Contig N50:	1694
Contig N90:	1076
Number of Scaffold	2
Scaffold N50:	4605
Scaffold N90:	4605
Mis-assembly Count:	0
TotalAssembly Size:	10999

Repeat Details

Total Reads Count(Non-Repeat) :	111
Total Reads Count(Repeat):	279
Retetitve Read Count based on (Partitions Identifier):	279
Retetitve Read Count (Entire Read Frequency Identifier):	3
Retetitve Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	3921
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			9100			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	6394	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	5	350		

Positions:

Start Position	End Position
1756	2105
3561	3910
3964	4313
5117	5466
5910	6259

| 1 | 6394 | GATTCATTCGGGATGGTCTGTGTGGATTAAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTGGTTACCTGCCGTGAGTAAATTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGACAGATAAAAATTACAGAGTACACAACATCCTCAAAGCCTACCGGTGACAGTGCGGGCTTTTTTTTCGACCAAAGGTAACGAGGTAACAACCATGCGAGTGTTGAAGTCAGGAGATCCTAAAGGCCTGTACCCGTTACCTAGCCAGTTGGCATTAAACGTATACGGTACCTAGGCATGTACGTAATCGTAGCCTTAGCAATCTCCAGTCC | 5 | 350 | Start Position / End Position |

Start Position	End Position
409	758
2228	2577
3182	3531
4730	5079
5529	5878

1	6394	GCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGATTAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTGGTTACCTGCCGTGAGTAAATTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGACAGATAAAAATTACAGAGTACACAACATCCATGAAACGCATTAGCACCACCATTACCACCACCATCACCATTACCACAGGTAACGGTGCGGGCTGACGCGTACAGGAAACACAGAAAAAGCCCGCACCTGACAGTGCGGGCTTTTTTTCGACCAAAGGTAACGAGGTAACAACCATGCGAGTGTTGAAGT	5	350	

Start Position	End Position
1	350
854	1203
1295	1644
2705	3054
4337	4686

| 5476 | 10080 | CGGTCGAAAAACTGCTGGCAGTGGGGCATTACCTCGAATCTACCGTCGATATTGCTGAGTCCACCCGCCGTATTGCGGCAAGTCGTATTCCGGCTGATCACATGGTGCTGATGGCAGGTTTCACCGCCGGTAATGAAAAAGGCGAACTGGTGGTGCTTGGACGCAACGGTTCCGACTACTCTGCTGCGGTGCTGGCTGCCTGTTTACGCGCCGATTGTTGCGAGATTTGGACGGACGTTGACGGGGTCTATACCTGCGACCCGCGTCAGGTGCCCGATGCGAGGTTGTTGAAGTCGATGTCCTACCAGGAAGCGATGGAGCTTTCCTACTTCGGCGCTCTAGGTCAGGCC | 4 | 350 | Start/End |

Start Position	End Position
5910	6259
7138	7487
8386	8735
9149	9498

					Start Position	End Position
5476	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	4	350	5529	5878
					6730	7079
					8014	8363
					9552	9901

5476	10080	GCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGATTAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTGGTTACCTGCCGTGAGTAAATTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGACAGATAAAAATTACAGAGTACACAACATCCATGAAACGCATTAGCACCACCATTACCACCACCATCACCATTACCACAGGTAACGGTGCGGGCTGACGCGTACAGGAAACACAGAAAAAGCCCGCACCTGACAGTGCGGGCTTTTTTTCGACCAAAGGTAACGAGGTAACAACCATGCGAGTGTTGAAGT	3	350	Start Position / End Position

The Start/End position table:

Start Position	End Position
6359	6708
7574	7923
8752	9101

SRGD Performance Metrics

Initial Reads Count:	1209
Reads Count after Removing Duplication:	390

Reads Count after Overlapping:	316
Initial Dataset Size in (Base):	301119
Dataset Sizet after Removing Duplication:	124917
Dataset Size after Overlapping:	81996

Overlapping Metrics

Repeat Identification Time:	00h:00m:06s:000ms
Overlapping Time:	00h:01m:56s:000ms
Reads Alignment Time:	00h:00m:18s:000ms
Total Hybrid Assembly Time:	00h:02m:14s:000ms
Repeat Annotation Time:	00h:04m:26s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
240	12321	16	4	0
237	11449	22	2	0
233	11025	17	1	0
228	10816	14	1	0
226	10609	91	46	0
201	3249	5	2	0
187	3025	8	3	0
176	2704	25	15	0