Assembly Report

Experiment Details

ExperimentID:	Experiment 76
Sequencing Coverage:	35
Number of Partitions:	1
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	301

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	633

Assembly Details

Number of Contigs:	14
Contig N50:	1733
Contig N90:	1673
Number of Scaffold	3
Scaffold N50:	3898
Scaffold N90:	3898
Mis-assembly Count:	0
TotalAssembly Size:	11524

Repeat Details

Total Reads Count(Non-Repeat) :	386
Total Reads Count(Repeat):	6
Retetitve Read Count based on (Partitions Identifier):	0
Retetitve Read Count (Entire Read Frequency Identifier):	3
Retetitve Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	9
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			8050		
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions
1	5608	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	4	350	

Positions subtable:

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

| 1 | 5608 | 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 | Start/End table below |

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

1	5608	GCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGATTAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTGGTTACCTGCCGTGAGTAAATTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGACAGATAAAAATTACAGAGTACACAACATCCATGAAACGCATTAGCACCACCATTACCACCACCATCACCATTACCACAGGTAACGGTGCGGGCTGACGCGTACAGGAAACACAGAAAAAGCCCGCACCTGACAGTGCGGGCTTTTTTTCGACCAAAGGTAACGAGGTAACAACCATGCGAGTGTTGAAGT	5	350	Start Position	End Position
					1	350
					854	1203
					1295	1644
					2705	3054
					4337	4686

| 4779 | 8676 | CGGTCGAAAAACTGCTGGCAGTGGGGCATTACCTCGAATCTACCGTCGATATTGCTGAGTCCACCCGCCGTATTGCGGCAAGTCGTATTCCGGCTGATCACATGGTGCTGATGGCAGGTTTCACCGCCGGTAATGAAAAAGGCGAACTGGTGGTGCTTGGACGCAACGGTTCCGACTACTCTGCTGCGGTGCTGGCTGCCTGTTTACGCGCCGATTGTTGCGAGATTTGGACGGACGTTGACGGGGTCTATACCTGCGACCCGCGTCAGGTGCCCGATGCGAGGTTGTTGAAGTCGATGTCCTACCAGGAAGCGATGGAGCTTTCCTACTTCGGCGCTCTAGGTCAGGCC | 3 | 350 | Start Position / End Position |

| 4779 | 8676 | 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 | 3 | 350 | (see sub-table below) |

Start Position	End Position
5117	5466
5910	6259
7138	7487

4779	8676	GATTCATTCGGGATGGTCTGTGTGGATTAAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTGGTTACCTGCCGTGAGTAAATTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGACAGATAAAAATTACAGAGTACACAACATCCTCAAAGCCTACCGGTGACAGTGCGGGCTTTTTTTTCGACCAAAGGTAACGAGGTAACAACCATGCGAGTGTTGAAGTCAGGAGATCCTAAAGGCCTGTACCCGTTACCTAGCCAGTTGGCATTAAACGTATACGGTACCTAGGCATGTACGTAATCGTAGCCTTAGCAATCTCCAGTCC	3	350	Start Position	End Position
					5529	5878
					6730	7079
					8014	8363

4779	8676	GCTTTTCATTC TGACTGCAAC GGGCAATATG TCTCTGTGTGG ATTAAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG AGTGTTGAAGT	2	350	Start Position	End Position
					6359	6708
					7574	7923

					Start Position	End Position
8063	10080	CGGTCGAAAAACTGCTGGCAGTGGGGCATTACCTCGAATCTACCGTCGATATTGCTGAGTCCACCCGCCGTATTGCGGCAAGTCGTATTCCGGCTGATCACATGGTGCTGATGGCAGGTTTCACCGCCGGTAATGAAAAAGGCGAACTGGTGGTGCTTGGACGCAACGGTTCCGACTACTCTGCTGCGGTGCTGGCTGCCTGTTTACGCGCCGATTGTTGCGAGATTTGGACGGACGTTGACGGGGTCTATACCTGCGACCCGCGTCAGGTGCCCGATGCGAGGTTGTTGAAGTCGATGTCCTACCAGGAAGCGATGGAGCTTTCCTACTTCGGCGCTCTAGGTCAGGCC	2	350	8386	8735
					9149	9498

SRGD Performance Metrics

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

Reads Count after Overlapping:	104
Initial Dataset Size in (Base):	359763
Dataset Sizet after Removing Duplication:	150869
Dataset Size after Overlapping:	41438

Overlapping Metrics

Repeat Identification Time:	00h:00m:05s:000ms
Overlapping Time:	00h:05m:30s:000ms
Reads Alignment Time:	00h:00m:14s:000ms
Total Hybrid Assembly Time:	00h:05m:44s:000ms
Repeat Annotation Time:	00h:00m:02s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
300	148996	216	10	0
299	141376	230	7	0
298	136161	213	6	0
297	131769	197	8	0
296	126025	158	2	0
294	124609	169	3	0
293	122500	126	2	0
291	121104	126	1	0
288	120409	134	1	0
287	119716	163	1	0
286	119025	132	1	0
283	118336	174	1	0

281	117649	142	1	0
280	116964	171	1	0
278	116281	187	1	0
276	115600	431	159	0
274	32761	60	1	0
271	32400	34	1	0
270	32041	28	1	0
269	31684	42	2	0
251	30976	44	5	0
233	29241	40	1	0
227	28900	39	1	0
226	28561	150	65	0
225	10816	18	2	0
222	10404	16	1	0
219	10201	10	2	0
211	9801	11	1	0