Assembly Report

Experiment Details

ExperimentID:	Experiment 72
Sequencing Coverage:	29
Number of Partitions:	2
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	126

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	522

Assembly Details

Number of Contigs:	15
Contig N50:	1461
Contig N90:	1042
Number of Scaffold	2
Scaffold N50:	2844
Scaffold N90:	2844
Mis-assembly Count:	0
TotalAssembly Size:	10334

Repeat Details

Total Reads Count(Non-Repeat) :	340
Total Reads Count(Repeat):	50
Retetitve Read Count based on (Partitions Identifier):	44
Retetitve Read Count (Entire Read Frequency Identifier):	3
Retetitve Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	114
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			8400		
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions
1	7490	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	6	350	

Start Position	End Position
1756	2105
3561	3910
3964	4313
5117	5466
5910	6259
7138	7487

1	7490	GATTCATTCGGGATGGTCTGTGTGGATTAAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTGGTTACCTGCCGTGAGTAAATTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGACAGATAAAAATTACAGAGTACACAACATCCTCAAAGCCTACCGGTGACAGTGCGGGCTTTTTTTTCGACCAAAGGTAACGAGGTAACAACCATGCGAGTGTTGAAGTCAGGAGATCCTAAAGGCCTGTACCCGTTACCTAGCCAGTTGGCATTAAACGTATACGGTACCTAGGCATGTACGTAATCGTAGCCTTAGCAATCTCCAGTCC	6	350		

Start Position	End Position
409	758
2228	2577
3182	3531
4730	5079
5529	5878
6730	7079

1	7490	GCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGATTAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTGGTTACCTGCCGTGAGTAAATTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGACAGATAAAAATTACAGAGTACACAACATCCATGAAACGCATTAGCACCACCATTACCACCACCATCACCATTACCACAGGTAACGGTGCGGGCTGACGCGTACAGGAAACACAGAAAAAAGCCCGCACCTGACAGTGCGGGCTTTTTTTCGACCAAAGGTAACGAGGTAACAACCATGCGAGTGTTGAAGT	6	350	Start Position	End Position
					1	350
					854	1203
					1295	1644
					2705	3054
					4337	4686
					6359	6708

| 7237 | 10080 | CGGTCGAAAAACTGCTGGCAGTGGGGCATTACCTCGAATCTACCGTCGATATTGCTGAGTCCACCCGCCGTATTGCGGCAAGTCGTATTCCGGCTGATCACATGGTGCTGATGGCAGGTTTCACCGCCGGTAATGAAAAAGGCGAACTGGTGGTGCTTGGACGCAACGGTTCCGACTACTCTGCTGCGGTGCTGGCTGCCTGTTTACGCGCCGATTGTTGCGAGATTTGGACGGACGTTGACGGGGTCTATACCTGCGACCCGCGTCAGGTGCCCGATGCGAGGTTGTTGAAGTCGATGTCCTACCAGGAAGCGATGGAGCTTTCCTACTTCGGCGCTCTAGGTCAGGCC | 2 | 350 | |

| 7237 | 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 | 2 | 350 | |

Position table (rightmost column):

Start Position	End Position
8386	8735
9149	9498

7237	10080	GATTCATTCGGGATGGTCTGTGTGGATTAAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTGGTTACCTGCCGTGAGTAAATTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGACAGATAAAAATTACAGAGTACACAACATCCTCAAAGCCTACCGGTGACAGTGCGGGCTTTTTTTTCGACCAAAGGTAACGAGGTAACAACCATGCGAGTGTTGAAGTCAGGAGATCCTAAAGGCCTGTACCCGTTACCTAGCCAGTTGGCATTAAACGTATACGGTACCTAGGCATGTACGTAATCGTAGCCTTAGCAATCTCCAGTCC	2	350		
					Start Position	End Position
					8014	8363
					9552	9901

7237	10080	GCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGATTAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTGGTTACCTGCCGTGAGTAAATTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGACAGATAAAATTACAGAGTACACAACATCCATGAAACGCATTAGCACCACCATTACCACCACCATCACCATTACCACAGGTAACGGTGCGGGCTGACGCGTACAGGAAACACAGAAAAAGCCCGCACCTGACAGTGCGGGCTTTTTTTCGACCAAAGGTAACGAGGTAACAACCATGCGAGTGTTGAAGT	2	350	

Start Position	End Position
7574	7923
8752	9101

SRGD Performance Metrics

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

Reads Count after Overlapping:	130
Initial Dataset Size in (Base):	301119
Dataset Sizet after Removing Duplication:	124917
Dataset Size after Overlapping:	40030

Overlapping Metrics

Repeat Identification Time:	00h:00m:08s:000ms
Overlapping Time:	00h:04m:26s:000ms
Reads Alignment Time:	00h:00m:14s:000ms
Total Hybrid Assembly Time:	00h:04m:40s:000ms
Repeat Annotation Time:	00h:00m:13s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
250	115600	161	21	0
249	101761	146	13	0
248	93636	141	9	0
247	88209	124	14	0
246	80089	109	4	0
245	77841	77	1	0
244	77284	122	6	0
243	73984	70	3	0
241	72361	79	1	0
240	71824	86	1	0
238	71289	76	3	0
237	69696	96	1	0

236	69169	80	1	0
233	68644	102	1	0
231	68121	85	1	0
230	67600	98	1	0
229	67081	102	1	0
228	66564	91	1	0
227	66049	98	1	0
226	65536	292	117	0
224	19321	38	1	0
221	19044	24	1	0
219	18769	35	2	0
217	18225	13	1	0
216	17956	15	1	0
205	17689	17	1	0
201	17424	26	4	0
176	16384	89	48	0