Assembly Report

Experiment Details

ExperimentID:	Experiment 97
Sequencing Coverage:	21
Number of Partitions:	2
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	101

Reads Dataset Details

Total Reads Count:	2205
Total Dataset Size in (Base):	440864
Valid Read Count:	2205
Rejected Read Count:	0
Maximum Read Length:	201
Minimum Read Length:	162

Reference Genome Details

Length of Reference Genome (Base):	20160
Number of K-mers:	19960
Length of K-mer	476

Assembly Details

Number of Contigs:	56
Contig N50:	976
Contig N90:	876
Number of Scaffold	1
Scaffold N50:	20160
Scaffold N90:	20160
Mis-assembly Count:	0
TotalAssembly Size:	20160

Repeat Details

Total Reads Count(Non-Repeat) :	751
Total Reads Count(Repeat):	41
Retetitve Read Count based on (Partitions Identifier):	34
Retetitve Read Count (Entire Read Frequency Identifier):	4
Retetitve Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	77
Total Unique Repetitive Sequences Count	4

Total Repeat Size (Base)			6800		
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions
1	20160	ATTACAGAGTA CACAACATCCT CAAAGCCTAC CGGTGACAGT GCGGGCTTTTT TTTCGACCAAA GGTAACGAGG TAACAACTCAT GGCATGCGAG TGTTGAAGTTT TCAGGAGATC CTAAAGGCAG GCTGTACCCG TTACCTAGCCA GTTGGCATTAA ACGTATCCTAG ACGGTACCTA GGCATGCCCT ACGTAATCGTA GCCTTAGCAAT CTCCAGTCC	8	220	(positions table below)

Start Position	End Position
1378	1597
4583	4802
6820	7039
10076	10295
12215	12434
14561	14780
17100	17319
19552	19771

| 1 | 20160 | CGGTCGAAAAACTGCTGGCAGTGGGGCATTACCTCGAATCTACCGTCGATATTGCTGAGTCCACCCGCCGTATTGCGGCAAGTCGTATTCCGGCTGATCACATGGTGCTGATGGCAGGTTTCACCGCCGGTAATGAAAAAGGCGAACTGGTGGTGCTTGGACGCAACGGTTCCGACTACTCTGCTGCGGTGCTGGCTGCCTGTTTACGCGCCGATTGTTGCGAGATTTGGACGGACGTTGACGGGGTCTATACCTGCGACCCGCGTCAGGTGCCCGATGCGAGGTTGTTGAAGTCGATGTCCTACCAGGAAGCGATGGAGCTTTCCTACTTCGGCGCTCTAGGTCAGGCC | 8 | 350 | |

Start Position	End Position
3271	3620
7927	8276
8750	9099
11803	12152
13026	13375
15428	15777
17342	17691
18939	19288

| 1 | 20160 | GCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGATTAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTGGTTACCTGCCGTGAGTAAATTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGACAGATAAAAATTACAGAGTACACAACATCCATGAAACGCATTAGCACCACCATTACCACCACCATCACCATTACCACAGGTAACGGTGCGGGCTGACGCGTACAGGAAACACAGAAAAAGC | 8 | 280 | |

| 1 | 20160 | GCTTTTCATTC TGACTGCAAC GGGCAATATG TCTCTGTGTGG ATTAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGC | 8 | 280 |

Start Position	End Position
1	280
1693	1972
2328	2607
5350	5629
9123	9402
14050	14329
16090	16369
18332	18611

SRGD Performance Metrics

Initial Reads Count:	2205
Reads Count after Removing Duplication:	792
Reads Count after Overlapping:	379
Initial Dataset Size in (Base):	440864
Dataset Sizet after Removing Duplication:	180168

Dataset Size after Overlapping:		85362		

Overlapping Metrics

Repeat Identification Time:		00h:00m:13s:000ms		
Overlapping Time:		00h:04m:03s:000ms		
Reads Alignment Time:		00h:00m:34s:000ms		
Total Hybrid Assembly Time:		00h:04m:37s:000ms		
Repeat Annotation Time:		00h:00m:08s:000ms		

Overlapping Length	$O(N)^2$ Time Complexity	Hit Index Count	Overlapping Matched Count	RI
200	564001	233	8	0
199	552049	256	7	0
198	541696	232	16	0
197	518400	215	10	0
196	504100	220	9	0
195	491401	168	1	0
193	490000	207	3	0
192	485809	173	3	0
190	481636	183	5	0
189	474721	185	3	0
188	470596	168	2	0
187	467856	209	1	0
184	466489	195	1	0
183	465124	186	1	0
182	463761	169	1	0
180	462400	174	1	0
179	461041	179	1	0

178	459684	182	2	0
177	456976	177	1	0
176	455625	786	324	0
172	123201	47	1	0
170	122500	36	1	0
169	121801	42	1	0
165	121104	57	1	0
156	120409	60	1	0
155	119716	51	1	0
151	119025	30	6	0
146	114921	41	1	0