Assembly Report

Experiment Details

ExperimentID:	Experiment 78
Sequencing Coverage:	35
Number of Partitions:	3
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	101

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	608

Assembly Details

Number of Contigs:	12
Contig N50:	2046
Contig N90:	1951
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

Repeat Details

Total Reads Count(Non-Repeat) :	201
Total Reads Count(Repeat):	191
Retetitve Read Count based on (Partitions Identifier):	189
Retetitve Read Count (Entire Read Frequency Identifier):	3
Retetitve Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	1190
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			8400		
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	8	350	

Start Position	End Position
1756	2105
3561	3910
3964	4313
5117	5466
5910	6259
7138	7487
8386	8735
9149	9498

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

					Start Position	End Position
1	10080	GCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGATTAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTGGTTACCTGCCGTGAGTAAATTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGACAGATAAAAATTACAGAGTACACAACATCCATGAAACGCATTAGCACCACCATTACCACCACCATCACCATTACCACAGGTAACGGTGCGGGCTGACGCGTACAGGAAACACAGAAAAAGCCCGCACCTGACAGTGCGGGCTTTTTTTCGACCAAAGGTAACGAGGTAACAACCATGCGAGTGTTGAAGT	8	350		
					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:	248
Initial Dataset Size in (Base):	359763
Dataset Sizet after Removing Duplication:	150869
Dataset Size after Overlapping:	80037

Overlapping Metrics

Repeat Identification Time:	00h:00m:10s:000ms
Overlapping Time:	00h:05m:10s:000ms
Reads Alignment Time:	00h:00m:24s:000ms
Total Hybrid Assembly Time:	00h:05m:34s:000ms
Repeat Annotation Time:	00h:04m:30s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
299	40401	47	2	0
298	39601	57	1	0
297	39204	50	2	0
296	38416	47	3	0
294	37249	66	3	0
293	36100	25	1	0
291	35721	37	1	0
290	35344	33	2	0
288	34596	30	1	0
283	34225	55	2	0
280	33489	50	1	0
276	33124	176	79	0

269	10609	15	2	0
258	10201	18	1	0
253	10000	12	1	0
251	9801	10	2	0
237	9409	10	1	0
226	9216	63	37	0
224	3481	3	1	0
219	3364	7	1	0