

Assembly Report

Experiment Details

ExperimentID:	Experiment 92
Sequencing Coverage:	32
Number of Partitions:	2
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	151

Reads Dataset Details

Total Reads Count:	2195
Total Dataset Size in (Base):	658355
Valid Read Count:	2195
Rejected Read Count:	0
Maximum Read Length:	301
Minimum Read Length:	262

Reference Genome Details

Length of Reference Genome (Base):	20160
Number of K-mers:	19860
Length of K-mer	540

Assembly Details

Number of Contigs:	32
Contig N50:	1576
Contig N90:	1276
Number of Scaffold	2
Scaffold N50:	9843
Scaffold N90:	9843
Mis-assembly Count:	0
TotalAssembly Size:	20828

Repeat Details

Total Reads Count(Non-Repeat) :	700
Total Reads Count(Repeat):	93
Retetitive Read Count based on (Partitions Identifier):	87
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	196
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			5250			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	9843	GCTTTTCATTC	5	350		
		TGACTGCAAC				
		GGGCAATATG				
		TCTCTGTGTGG				
		ATTAAAAAAG				
		AGTGTCTGATA				
		GCAGCTTCTG				
		AACTGGTTACC				
		TGCCGTGAGT				
		AAATTAAAATT				
		TTATTGACTTA				
		GGTCACTAAAT				
		ACTTTAACCBA			Start Position	End Position
		TATAGGCATAG			1	350
		CGCACAGACA			1316	1665
		GATAAAAATTA			2021	2370
		CAGAGTACAC			5041	5390
		AACATCCATGA			8441	8790
		AACGCATTAGC				
		ACCACCATTAC				
		CACCACCATCA				
		CCATTACCACA				
		GGTAACGGTG				
		CGGGCTGACG				
		CGTACAGGAA				
		ACACAGAAAAA				
		AGCCCGCACCC				
		TGACAGTGCG				
		GGCTTTTTTTTT				
		CGACCAAAGG				
TAACGAGGTAA						
CAACCATGCG						
AGTGTTGAAGT						

9176	20160	CGGTCGAAAA	5	350	<table><tr><th>Start Position</th><th>End Position</th></tr><tr><td>10761</td><td>11110</td></tr><tr><td>11904</td><td>12253</td></tr><tr><td>14881</td><td>15230</td></tr><tr><td>16995</td><td>17344</td></tr><tr><td>18809</td><td>19158</td></tr></table>	Start Position	End Position	10761	11110	11904	12253	14881	15230	16995	17344	18809	19158
		Start Position				End Position											
		10761				11110											
		11904				12253											
		14881				15230											
		16995				17344											
		18809				19158											
		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															
		GTGCCCCGATG															
		CGAGGTTGTT															
		GAAGTCGATG															
TCCTACCAGG																	
AAGCGATGGA																	
GCTTTCCTACT																	
TCGGCGCTCT																	
AGGTCAGGCC																	

9176	20160	GATTCATTTCGG	5	350	<table><tr><th>Start Position</th><th>End Position</th></tr><tr><td>9464</td><td>9813</td></tr><tr><td>11173</td><td>11522</td></tr><tr><td>13704</td><td>14053</td></tr><tr><td>16623</td><td>16972</td></tr><tr><td>19422</td><td>19771</td></tr></table>	Start Position	End Position	9464	9813	11173	11522	13704	14053	16623	16972	19422	19771
		Start Position				End Position											
		9464				9813											
		11173				11522											
		13704				14053											
		16623				16972											
		19422				19771											
		GATGGTCTGT															
		GTGGATTAAAA															
		AAAGAGTGTCT															
		GATAGCAGCTT															
		CTGAACTGGTT															
		ACCTGCCGTG															
		AGTAAATTTAA															
		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																	

SRGD Performance Metrics

Initial Reads Count:	2195
Reads Count after Removing Duplication:	793

Reads Count after Overlapping:	294
Initial Dataset Size in (Base):	658355
Dataset Siset after Removing Duplication:	271570
Dataset Size after Overlapping:	106910

Overlapping Metrics

Repeat Identification Time:	00h:00m:23s:000ms
Overlapping Time:	00h:05m:37s:000ms
Reads Alignment Time:	00h:00m:12s:000ms
Total Hybrid Assembly Time:	00h:05m:49s:000ms
Repeat Annotation Time:	00h:00m:11s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
300	490000	216	4	0
299	484416	227	11	0
298	469225	219	2	0
297	466489	197	1	0
296	465124	239	2	0
295	462400	182	5	0
294	455625	203	3	0
293	451584	186	1	0
292	450241	224	4	0
291	444889	214	1	0
290	443556	233	2	0
289	440896	165	1	0

278	439569	214	3	0
277	435600	187	1	0
276	434281	794	321	0
274	114244	48	2	0
265	112896	58	1	0
259	112225	42	1	0
251	111556	41	1	0
248	110889	61	1	0
228	110224	54	1	0
226	109561	334	124	0
224	42849	18	1	0
221	42436	16	2	0
213	41616	14	1	0
212	41209	23	1	0
210	40804	21	1	0