

Assembly Report

Experiment Details

ExperimentID:	Experiment 37
Sequencing Coverage:	31
Number of Partitions:	2
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	151

Reads Dataset Details

Total Reads Count:	1045
Total Dataset Size in (Base):	313765
Valid Read Count:	1045
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	569

Assembly Details

Number of Contigs:	15
Contig N50:	2169
Contig N90:	1126
Number of Scaffold	3
Scaffold N50:	3755
Scaffold N90:	3755
Mis-assembly Count:	0
TotalAssembly Size:	11544

Repeat Details

Total Reads Count(Non-Repeat) :	352
Total Reads Count(Repeat):	38
Retetitive Read Count based on (Partitions Identifier):	36
Retetitive Read Count (Entire Read Frequency Identifier):	1
Retetitive Read Count (Contained Read Frequency Identifier):	1
Total Repetitive Sequences Count	139
Total Unique Repetitive Sequences Count	1

Total Repeat Size (Base)			3500			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	1120	GCTTTTCATTC	2	350		
		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				
		AGCCCGCACCC				
		TGACAGTGCG				
		GGCTTTTTTTT				
		CGACCAAAGG				
		TAACGAGGTAA				
		CAACCATGCG				
		AGTGTTGAAGT				

526	7194	GCTTTTCATTC TGA CTGCAAC GGGCAATATG TCTCTGTGTGG ATTAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACCC TGACAGTGCG GGCTTTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG AGTGTTGAAGT	5	350		
					Start Positio n	End Positio n
					765	1114
					1400	1749
					3146	3495
					4226	4575
					6742	7091

6326	10080	GCTTTTCATTC	3	350	<table><tr><th>Start Positio n</th><th>End Positio n</th></tr><tr><td>6742</td><td>7091</td></tr><tr><td>7650</td><td>7999</td></tr><tr><td>8549</td><td>8898</td></tr></table>	Start Positio n	End Positio n	6742	7091	7650	7999	8549	8898
		Start Positio n				End Positio n							
		6742				7091							
		7650				7999							
		8549				8898							
		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													
AGCCCGCACCC													
TGACAGTGCG													
GGCTTTTTTTTT													
CGACCAAAGG													
TAACGAGGTAA													
CAACCATGCG													
AGTGTTGAAGT													

SRGD Performance Metrics

Initial Reads Count:	1045
Reads Count after Removing Duplication:	390

Reads Count after Overlapping:	147
Initial Dataset Size in (Base):	313765
Dataset Siset after Removing Duplication:	128349
Dataset Size after Overlapping:	53301

Overlapping Metrics

Repeat Identification Time:	00h:00m:04s:000ms
Overlapping Time:	00h:04m:58s:000ms
Reads Alignment Time:	00h:00m:25s:000ms
Total Hybrid Assembly Time:	00h:05m:23s:000ms
Repeat Annotation Time:	00h:00m:33s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
300	123904	93	2	0
299	122500	78	2	0
298	121104	49	2	0
297	119716	65	3	0
287	117649	53	1	0
286	116964	58	1	0
285	116281	76	1	0
276	115600	422	164	0
272	30976	21	1	0
258	30625	9	1	0
251	30276	25	3	0
226	29241	173	60	0

222	12321	8	1	0
217	12100	9	1	0