Assembly Report

Experiment Details

ExperimentID:	Experiment 27
Sequencing Coverage:	20
Number of Partitions:	2
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	101

Reads Dataset Details

reads Dataset Details	
Total Reads Count:	1054
Total Dataset Size in (Base):	211074
Valid Read Count:	1054
Rejected Read Count:	0
Maximum Read Length:	201
Minimum Read Length:	162

Reference Genome Details

Length of Reference Genome (Base):	10080
Number of K-mers:	9880
Length of K-mer	395

Assembly Details

Number of Contigs:	26
Contig N50:	970
Contig N90:	876
Number of Scaffold	2
Scaffold N50:	4603
Scaffold N90:	4603
Mis-assembly Count:	0
TotalAssembly Size:	10309

Repeat Details

Total Reads Count(Non-Repeat) :	360
Total Reads Count(Repeat):	26
Retetitve Read Count based on (Partitions Identifier):	24
Retetitve Read Count (Entire Read Frequency Identifier):	1
Retetitve Read Count (Contained Read Frequency Identifier):	1
Total Repetitive Sequences Count	56
Total Unique Repetitive Sequences Count	1

Total Repeat Size (Base)		2800				
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Position	s
1	4603	GCTTTTCATTC TGACTGCAAC GGGCAATATG TCTCTGTGTGG ATTAAAAAAAA GAGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA CAGAGTACAC AACATCCATGA AACGCATTAC CACCACCATCA CCACCATCA CGGTAACG CGGCTGACG CGGCTGACG CGGCTGACG CGGCTGACG CGTACAGGAA ACACAGGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG AGTGTTGAAGT	5	350	Start Positio n 1 765 1400 3146 4226	End Positio n 350 1114 1749 3495 4575

GCTTTTCATTC TGACTGCAAC GGGCAATATG TCTCTGTGTGG ATTAAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAAATTAAAAATT TTTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 4375 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACACAGCA GGTAACGGAA ACACAGAAAAA AGCCCGCACC TGACAGAAA AACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATCCG AGTCTTCAAGT		i			i		1
GGGCAATATG TCTCTGTGGG ATTAAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTITAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 4375 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACACCATTAC CACCACCATCA CCATTACCACA GGTAACGGG CGGCTGACG CGGCTACAC CCATTACCACA GGTAACGGTG CGGCCGACC TGACAGGAA ACCCCGCACC TGACAGGCG GGCTTTTTTT CCGCCCAAAGG TAACGAGGTAA CAACCATGCG			GCTTTTCATTC				
TCTCTGTGTGG ATTAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 4375 10080 CAGAGTACCA AACATCCATGA AACATCCATGA AACGCATTACC CCACTACAC CCATTACCACA CCATTACCACA GGTAACGTG CGGCCTGACG CGGCTGACG CGGCTGACG CGGCTGACG CGGCTGACG CGGCTGACG CGGCTCACG CGACAGACA ACACCATTTTTTT CGACCAGAGC GGCTTTTTTT CGACCAGAGC TAACGAGGTAA CAACCATGCG			TGACTGCAAC				
ATTAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 4375 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CCACCACCATCA CCATTACCACA GGTACAGGAA ACACCAGTGC CGGCTGACG CGTACAGGAA ACACCACTCA CCATTACCACA GGTACAGAAA ACACCAGGAA ACACCAGCAC GGTACAGGAA ACACAGAAAAAA AGCCCGCACC TGACAGGAA ACACCACTGC GGCTTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG			GGGCAATATG				
AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 4375 10080 CAGAGTACAC AACACCATTAC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACCAGACA GGTACAGAA ACACCAGCAC GGTACAGGAA ACACCACC CGGCCTGACG CGTACAGGAA ACACCACCAC GGTACAGGAA ACACCAGCAC GGCTTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			тстстдтдтдд				
GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 4375 10080 CAGAGTACC AACATCCATGA AACGCATTAGC ACCACCATTAC CCACCACCATCA CCATTACCACA GGTAACGGTG CGGCTGACG CGTACAGGAA ACACCAGGAA ACACCAGCAC GGGCTTTTTTT CGACAGAAAA ACACCAGACA GGTAACGGTA CCACACACCAC GGGCTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG			ATTAAAAAAAAG				
AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 4375 10080 CAGAGTACAC AACATCCATGA AACGCATTAC CACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACCAGCAC GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACCAGCAC GGTAACGGTG CGGCTGACG CGTACAGGAA ACACCAGCAC GGTACGGCG CGTACAGGAA ACACCAGCAC TGACAGTACC			AGTGTCTGATA				
TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 4375 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCACTACA CCACTACACA CCATTACC CACCACCACA GGTAACGGTG CGGCTGACG CGGCTGACG CGTACAGGAA ACACCGCACC TGACAGGAA ACCCGCACC TGACAGTAC CACCCACAAAGG TAACGAGTAA CCACCAAAGG TAACGAGTAA CCACCAAGG TAACGAGTAA CAACCATGCG			GCAGCTTCTG				
AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 4375 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CCACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACCAGGAA ACACCAGCAC GGTACAGGAA ACACCAGCAC GGTACAGGAA ACACCAGCAC CGTACAGGAA ACACCAGCAC CGGCTTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG			AACTGGTTACC				
TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 4375 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CCACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGGCTGACG CGTACAGGAA ACACCAGCAC GGTACAGGAA ACACCAGCAC GGCTTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			TGCCGTGAGT				
GGTCACTAAAT ACTTTACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 4375 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGAAAA ACCCCGCACC TGACAGGAA ACCCCGCACC TGACAGTGC GGCTTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG			AAATTAAAATT				
ACTITAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 4375 10080 CAGAGTACAC AACGCATTAGC ACCACCATTAC CACCACCATCAA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACCCCGCACC TGACAGGAA ACCCCGCACC TGACAGGTAA CAACCATGCG TAACGAGGTAA CAACCATGCG CGACCAAAGG TAACGAGGTAA CAACCATGCG			TTATTGACTTA				
TATAGGCATAG CGCACAGACA GATAAAAATTA 4375 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CCACTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACCAGAAAAA ACACCAGAAAAA ACACCAGAAAAA ACACCAGACAC CGTACAGGAA ACACCACCAC CGGCTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG			GGTCACTAAAT				
CGCACAGACA GATAAAAATTA 4375 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CCACTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACCAGAAAAA ACACCAGAAAAA ACACCAGACAC GGCTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG			ACTTTAACCAA				
GATAAAAATTA 4375 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATCAC CACCACCATCAC CCACTACCACAC GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			TATAGGCATAG			Start	End
4375 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			CGCACAGACA			Positio	Positio
AACATCCATGA AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG			GATAAAAATTA			n	n
AACATCCATGA AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG	4375	10080	CAGAGTACAC	3	350	6742	7091
ACCACCATTAC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGCTGACG CGTACAGGAA ACACAGAAAAA ACACAGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			AACATCCATGA				
CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			AACGCATTAGC			7650	7999
CCATTACCACA GGTAACGGTG CGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			ACCACCATTAC			8549	8898
GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			CACCACCATCA				
CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			CCATTACCACA				
CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			GGTAACGGTG				
ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			CGGGCTGACG				
AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			CGTACAGGAA				
TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			ACACAGAAAAA				
GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			AGCCCGCACC				
CGACCAAAGG TAACGAGGTAA CAACCATGCG			TGACAGTGCG				
TAACGAGGTAA CAACCATGCG			GGCTTTTTTTT				
CAACCATGCG			CGACCAAAGG				
			TAACGAGGTAA				
			CAACCATGCG				
MOTOTTOMOT			AGTGTTGAAGT				

SRGD Performance Metrics

Initial Reads Count:	1054
Reads Count after Removing Duplication:	386

Reads Count after Overlapping:		190			
Initial Dataset Size in (Base):		211074			
Dataset Sizet after	Removing Duplication	n:	84645		
Dataset Size after 0	Overlapping:		42564		
Overlapping Metri	CS				
Repeat Identificatio	n Time:		00h:00m	n:08s:000ms	
Overlapping Time:			00h:03m	n:21s:000ms	
Reads Alignment T	ime:		00h:00m	n:15s:000ms	
Total Hybrid Assem	nbly Time:		00h:03m:36s:000ms		
Repeat Annotation	Repeat Annotation Time:		00h:00m:05s:000ms		
Overlapping Length	O(N)2 Time Complexity	Hit Index (Count	Overlapping Matched Count	RI
200	129600	88		6	0
199	125316	72		6	0
198	121104	49		6	0
197	116964	58		7	0
187	112225	53		5	0
186	108900	56		1	0
185	108241	65		1	0
176	107584	393		157	0
175	29241	15		1	0
174	28900	14		1	0
171	28561	12		1	0
158	28224	9		1	0

151	27889	19	2	0
143	27225	8	1	0