Assembly Report

Experiment Details

ExperimentID:	Experiment 61
Sequencing Coverage:	35
Number of Partitions:	1
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	301

Reads Dataset Details

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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	637

Assembly Details

Number of Contigs:	16
Contig N50:	1776
Contig N90:	1326
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

Repeat Details

Total Reads Count(Non-Repeat) :	389
Total Reads Count(Repeat):	6
Retetitve Read Count based on (Partitions Identifier):	0
Retetitve Read Count (Entire Read Frequency Identifier):	3
Retetitve Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	9
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)		4200				
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Position	S
1	10080	CGGTCGAAAA ACTGCTGGCA GTGGGGCATT ACCTCGAATCT ACCGTCGATAT TGCTGAGTCC ACCCGCCGTA TTGCGGCAAG TCGTATTCCGG CTGATCACATG GTGCTGATGG CAGGTTTCACC GCCGGTAATG AAAAAGGCGA ACTGGTGGTG CTTGGACGCA ACTGCTGGTG CTGCTGTTAC GCGCGATTTAC GCGCCGATTT GGACGCA TTGCGAGATTT GGACGCA CTACTCTGCTG CGGTGCTGGC TGCCTGTTTAC GCGCCGATTT GGACGCATTT GGACGCATTT GGACGCATTT GGACGCATTT GGACGCATTT GGACGCATTT TGCGAGATTT TGCGAGATTT TGCGAGATTT TGCGAGATTT TGCGAGTTCTAC TTCCTACTACT TCGAGGTTGTT GAAGTCGATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT AGGTCAGGCC	4	350	Start Positio n 1376 4127 6570 8665	End Positio n 1725 4476 6919 9014

	1	
GATTCATTCGG		
GATGGTCTGT		
GTGGATTAAAA		
AAAGAGTGTCT		
GATAGCAGCTT		
CTGAACTGGTT		
ACCTGCCGTG		
AGTAAATTAAA		
ATTTATTGAC		
TTAGGTCACTA		
AATACTTTAAC		
CAATATAGGCA		
TAGCGCACAG		Start End
ACAGATAAAAA		Positio Positio
TTACAGAGTAC		n n
ACAACATCCTC		
1 10080 AAAGCCTACC 4	350	3285 3634
GGTGACAGTG		4858 5207
CGGGCTTTTT		7202 7551
TTCGACCAAAG		
GTAACGAGGT		9332 9681
AACAACCATGC		
GAGTGTTGAA		
GTCAGGAGAT		
CCTAAAGGCC		
TGTACCCGTTA		
CCTAGCCAGTT		
GGCATTAAAC		
GTATACGGTAC		
CTAGGCATGTA		
CGTAATCGTAG		
CCTTAGCAATC		
TCCAGTCC		

GCTTTTCATTC TGACTGCAAC GGGCAATATG TCTCTGTGTGG ATTAAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 1 10080 CAGAGTACAC AACATCCATGA AACGCCATTAC CACCACCATTAC CACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGCTGACG CGTACAGGAA ACACCAGAAAA ACGCCACCC TGACAGAAAA AACGCCACCC TGACAGCAC GGCTTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG AGTGTTGAAGT			<u> </u>	i		
GGGCAATATG TCTCTGTGTGG ATTAAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA ACATCCATGA AACATCCATGA AACACCATTAC CACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGGCTGACAG GGCTTTTTTT CGACCAAAGG TAACAGGTAA CAACCATGCG CGACCAAGG CGACCAAGGC CGACCAAGGGTAA CAACCATGCG CGACCAAGGGTAA CAACCATGCG CGACCAAAGG CGACCAAGGGTAA CAACCATGCG CGACCAAAGG CAACCATGCG CGACCAAAGG CAACCATGCG CGACCAAAGG CAACCATGCG CGACCAAAGG CAACCATGCG CGACCAAAGG CAACCATGCG CA			GCTTTTCATTC			
TCTCTGTGTGG ATTAAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 1 10080 CAGAGTACAC AACATCCATGA AACACCATTAC CACCACCATCA CCACTACACA CCATTACCACA GGTAACGGTG CGGCTGACG CGGCTGACG CGGCTGACG CGGCTGACG CGTACAGCAC CCATTACCACA GGTAACGGTG CGGCCTGCC CGGCCACC CGGCCACC TGACAGGAA AACACCATGCG GGCTTTTTTT CCGCCCAAAGG TAACGAGGTAA CAACCATGCG			TGACTGCAAC			
ATTAAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 1 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGAAA ACACAGAAAAA ACACCAGTG CGGCTGACG CGTACAGAA ACACAGAAAAA ACACCACC TGACAGGAA ACACCACCC TGACAGTCA CGACTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG			GGGCAATATG			
AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 1 10080 CAGAGTACAC 4 AACATCCATGA AACGCATTAGC ACCACTATAC CACCACTTAC CACCACTACA CCATTACCACA GGTACAGAA ACGCATTACC CACCACCATCA CCATTACCACA GGTACAGAA ACACAGAAAAA ACCCACCAC GGTACAGGAA ACACAGAAAAA ACCCCCCC TGACAGGAC GGCTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG			тстстбтбтбб			
GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 1 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CCACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACCAGGAA ACACCAGCAC GGTAACGGTG CGGCTGACG CGTACAGGAA ACCACGACAC GGTACAGGAA ACACCAGCACC TGACAGGAA ACACCAGCACC TGACAGGAAAA ACACCAGCACC TGACAGGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			ATTAAAAAAAG			
AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 1 10080 CAGAGTACAC AACATCCATGA AACGCATTAC CACCACCATTAC CACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACCAGCAC GGTAACGGTG CGGCTGACG CGTACAGGAA ACACCAGCAC GGTAACGGTG CGGCTGACG CGTACAGGAA ACACCAGCAC GGTACGGAC TGACAGGAA ACACCAGCAC TGACAGGAA ACACCAGCAC TGACAGGTAA CCACCACACC TGACAGGAA ACACCAGGAA ACACCAGGAA ACACCAGGAAAAA ACACAGAAAAA ACACAAGG TAACGAGGTAA CAACCATGCG			AGTGTCTGATA			
TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 1 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCACTAC CCACTACAC CCACTACAC CCATTACCACA GGTAACGATA CCAGTACAC GGTAACGGTG CGGCTGACG CGGCTGACG CGTACAGGAA ACCCCGCACC TGACAGGAA ACCCCGCACC TGACAGGAA ACCCCGACC TGACAGGAA CCACCAAAGG TAACGAGTAA CAACCATGCG			GCAGCTTCTG			
AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 1 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CCACCACCACA CCATTACCACA GGTAACGGTG CGGGCTGACG CGGCTACAGGAA ACACCAGGAA ACACCAGAAAAA AGCCCGCACC TGACAGGTAA CAACCATGCG			AACTGGTTACC			
TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 1 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CCACCACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACCAGGAA ACACCACCC TGACAGGAA ACACCACCAC GGCTTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG			TGCCGTGAGT			
GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 1 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGAC GGTAACGAC GGTACGC GGGCTGACG CGCACCACC TGACAGAAAAA AGCCCGCACC TGACAGTACC GGCTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG			AAATTAAAATT			
ACTITAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 1 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGCTGACG CGGCTGACG CGTACAGGAA ACACAGGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			TTATTGACTTA			
TATAGGCATAG CGCACAGACA GATAAAAATTA 1 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CCACCACCATCA CCATTACCACA GGTAACGGTG CGGCTGACAG ACACCAGAAAAA ACACCAGAAAAA ACACCAGAAAAA ACACCAGACAC GGTACAGGAC CGTACAGGAC CGTACAGGAC CGTACAGGAC CGTACAGGAC CGTACAGGAC CGACCACCAC CGGCTGACG CGGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			GGTCACTAAAT			
TATAGGCATAG CGCACAGACA GATAAAAATTA 1 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CCACCACCATCA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACCAGGAA ACACCACCAC GGTACAGGAA ACACCAGGAA ACACCAGGAA ACACCAGGAA ACACCAGGAA ACACCAGGAA ACACCAGGG CGTACAGGAA ACACCAGGAA ACACCAGGG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			ACTTTAACCAA		Start	End
1			TATAGGCATAG			
1			CGCACAGACA			
AACATCCATGA AACGCATTAGC ACCACCATTAC CCACCACCAC CCACTACCAC GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACCAGCAC GGTACAGGAA ACACCAGCAC GGTACAGGAA ACACCAGCAC GGTACAGGAA ACACCAGCAC TGACAGTGCG GGCTTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			GATAAAAATTA			
AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG	1	10080	CAGAGTACAC 4	350	1	350
ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			AACATCCATGA		799	1148
ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			AACGCATTAGC		2039	2388
CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			ACCACCATTAC			
GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			CACCACCATCA		8043	8392
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			GGCTTTTTTT			
CAACCATGCG			CGACCAAAGG			
			TAACGAGGTAA			
AGTGTTGAAGT			CAACCATGCG			
			AGTGTTGAAGT			

SRGD Performance Metrics

Initial Reads Count:	1203
Reads Count after Removing Duplication:	395

Reads Count after Overlapping:		113			
Initial Dataset Size in (Base):		359763			
Dataset Sizet after	Removing Duplicatio	n:	151772		
Dataset Size after 0	Overlapping:		44555		
Overlapping Metri	CS				
Repeat Identification	n Time:		00h:00r	m:06s:000ms	
Overlapping Time:			00h:05r	m:52s:000ms	
Reads Alignment T	ïme:		00h:00r	m:11s:000ms	
Total Hybrid Assem	nbly Time:		00h:06m:03s:000ms		
Repeat Annotation	Time:		00h:00m:02s:000ms		
Overlapping Length	O(N)2 Time Complexity	Hit Index (Count	Overlapping Matched Count	RI
300	151321	89		3	0
299	148996	85		3	0
297	146689	64		3	0
296	144400	89		3	0
295	142129	106		4	0
294	139129	88		1	0
288	138384	86		2	0
287	136900	79		1	0
286	136161	63		1	0
284	135424	91		1	0
283	134689	71		1	0
279	133956	54		1	0

276	133225	397	175	0
261	36100	10	1	0
259	35721	24	1	0
257	35344	19	1	0
254	34969	11	1	0
251	34596	12	5	0
231	32761	18	1	0
226	32400	176	70	0
223	12100	6	1	0
220	11881	11	1	0
215	11664	5	1	0