Assembly Report

Experiment Details

ExperimentID:	Experiment 67
Sequencing Coverage:	23
Number of Partitions:	2
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	101

Reads Dataset Details

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Total Reads Count:	1212
Total Dataset Size in (Base):	241272
Valid Read Count:	1212
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	419

Assembly Details

Number of Contigs:	26
Contig N50:	937
Contig N90:	892
Number of Scaffold	9
Scaffold N50:	1887
Scaffold N90:	1470
Mis-assembly Count:	0
TotalAssembly Size:	13429

Repeat Details

Total Reads Count(Non-Repeat) :	341
Total Reads Count(Repeat):	47
Retetitve Read Count based on (Partitions Identifier):	40
Retetitve Read Count (Entire Read Frequency Identifier):	4
Retetitve Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	81
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			5600		
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions
1	4348	CGGTCGAAAA ACTGCTGGCA GTGGGGCATT ACCTCGAATCT ACCGTCGATAT TGCTGAGTCC ACCCGCCGTA TTGCGGCAAG TCGTATTCCGG CTGATCACATG GTGCTGATGG CAGGTTTCACC GCCGGTAATG AAAAAGGCGA ACTGGTGGTG CTTGGACGCA ACTGTTCCGA CTACTCTGCTG CGGTGCTGGC TGCCTGTTTAC GCGCCGATTG TTGCGAGATTT GGACGCATTG TTGCGAGATTT GGACGCATTG TTGCGAGATTT GGACGCATTG TTGCGAGATTT GGACGGACGT TGCCTGTTTAC GCGCCGATTG TTGCGAGATTT GGACGGACGT TGACGGGTC TTGCGAGATTT TGCGAGATTT TGCAGGTTCTAC GCGCGTCAG GTGCCCGATG CCGCGTCAG GTGCCCGATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT AGGTCAGGCC	3	350	Start End Position n 1756 2105 3561 3910 3964 4313

GATTCATTCGG GATGGTCTGT GTGGATTAAAA AAAGAGTGTCT GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAACCCTCC AAAACCCTGC GGGTTTTTT TTCGACCAAAAG GTAACGAGGT AACAACATCGC GAGTGTTGAA GTCAAGGAGT ACACAACGC TAGCGCACTT GGCATTAAC CTAAAGCC TGTACCCGTTA CCTAAAGCC TGTACCCGTTA CCTAACGCAC GTATACGGTAC CTAGCCATGA				<u> </u>			1
GTGGATTAAAA AAAGAGTGTCT GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTITATTGAC TTAGGTCACTA AATACTITAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA			GATTCATTCGG				
AAAGAGTGTCT GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTITATTGAC TTAGGTCACTA AATACTITAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTTACAGAGTAC AAAGCCTACC GGTGACAGTG CGGCTTTTT TTCGACCAAAG GTAACGAGT AACAACATCC GATGACAGGT CGGGCTTTTTT TTCGACCAAAG GTAACGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA			GATGGTCTGT				
GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTTACAGAGTAC AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGAT GACACCC GATGACGAGAT AACAACCATCC GATGACGAGAT CCTAAAGGCC TGTACCGGTTA CCTAAAGGCC TGTACCGGTTA CCTAACGCACT CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA			GTGGATTAAAA				
CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTTACAGAGTAC ACAACATCCTC AAAACACTCCTC AAAACACTCTC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGT AACAACACTCC GAGTGACAGT ACAACACTCC GGTGACAGT CCGGGCTTTTT TCGACCAAAG GTAACGAGT AACAACCATGC GAGTGTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA			AAAGAGTGTCT				
ACCTGCCGTG AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGGCTTTTT TTCGACCAAAG GTAACGAGGT AACACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTAC CTAGGCATGAC GTATACGGTAC CTAGGCATGTA CCTAGGCATGTA			GATAGCAGCTT				
AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACATCCTC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGAC CTAGGCATGTA			CTGAACTGGTT				
ATTITATTGAC TTAGGTCACTA AATACTITAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACATCCTC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA			ACCTGCCGTG				
TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACATCCTC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAC GTATACGGTAC CTAGGCATGTA			AGTAAATTAAA				
AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACACTCCTC GGTGACAGTG CGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA			ATTTTATTGAC				
CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACATCCTC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTC GGTATACGGTAC CTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA			TTAGGTCACTA				
TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACATCCTC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA			AATACTTTAAC				
ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA			CAATATAGGCA				
TTACAGAGTAC ACAACATCCTC ACAACATCCTC ACAACATCCTC AAAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA			TAGCGCACAG				
ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA			ACAGATAAAAA			Start	End
1 4348 AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA			TTACAGAGTAC			Positio	Positio
GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGCCATGTA			ACAACATCCTC			n	n
GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA	1	4348	AAAGCCTACC	3	350	409	758
TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA			GGTGACAGTG				
GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA			CGGGCTTTTTT			2228	2577
AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA			TTCGACCAAAG			3182	3531
GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA			GTAACGAGGT				
GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA			AACAACCATGC				
CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA			GAGTGTTGAA				
TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA			GTCAGGAGAT				
CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA			CCTAAAGGCC				
GGCATTAAAC GTATACGGTAC CTAGGCATGTA			TGTACCCGTTA				
GTATACGGTAC CTAGGCATGTA			CCTAGCCAGTT				
CTAGGCATGTA			GGCATTAAAC				
			GTATACGGTAC				
			CTAGGCATGTA				
CGTAATCGTAG			CGTAATCGTAG				
CCTTAGCAATC			CCTTAGCAATC				
TCCAGTCC			TCCAGTCC				

			 			
		GCTTTTCATTC				
		TGACTGCAAC				
		GGGCAATATG				
		TCTCTGTGTGG				
		ATTAAAAAAAAG				
		AGTGTCTGATA				
		GCAGCTTCTG				
		AACTGGTTACC				
		TGCCGTGAGT				
		AAATTAAAATT				
		TTATTGACTTA				
		GGTCACTAAAT				
		ACTTTAACCAA			Start	End
		TATAGGCATAG			Positio	Positio
		CGCACAGACA			n	n
		GATAAAAATTA				
1	4348	CAGAGTACAC	4	350	1	350
		AACATCCATGA			854	1203
		AACGCATTAGC			1295	1644
		ACCACCATTAC				
		CACCACCATCA			2705	3054
		CCATTACCACA				
		GGTAACGGTG				
		CGGGCTGACG				
		CGTACAGGAA				
		ACACAGAAAAA				
		AGCCCGCACC				
		TGACAGTGCG				
		GGCTTTTTTTT				
		CGACCAAAGG				
		TAACGAGGTAA				
		CAACCATGCG				
		AGTGTTGAAGT				

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		CGGTCGAAAA				
		ACTGCTGGCA				
		GTGGGGCATT				
		ACCTCGAATCT				
		ACCGTCGATAT				
		TGCTGAGTCC				
		ACCCGCCGTA				
		TTGCGGCAAG				
		TCGTATTCCGG				
		CTGATCACATG				
		GTGCTGATGG				
		CAGGTTTCACC				
		GCCGGTAATG				
		AAAAAGGCGA				
		ACTGGTGGTG			Start	End
		CTTGGACGCA			Positio	Positio
4376	6262	ACGGTTCCGA	2	350	n	n
4370	0202	CTACTCTGCTG	2		5117	5466
		CGGTGCTGGC			3117	3400
		TGCCTGTTTAC			5910	6259
		GCGCCGATTG				
		TTGCGAGATTT				
		GGACGGACGT				
		TGACGGGGTC				
		TATACCTGCGA				
		CCCGCGTCAG				
		GTGCCCGATG				
		CGAGGTTGTT				
		GAAGTCGATG				
		TCCTACCAGG				
		AAGCGATGGA				
		GCTTTCCTACT				
		TCGGCGCTCT				
		AGGTCAGGCC				

		1				
		GATTCATTCGG				
		GATGGTCTGT				
		GTGGATTAAAA				
		AAAGAGTGTCT				
		GATAGCAGCTT				
		CTGAACTGGTT				
		ACCTGCCGTG				
		AGTAAATTAAA				
		ATTTTATTGAC				
		TTAGGTCACTA				
		AATACTTTAAC				
		CAATATAGGCA				
		TAGCGCACAG				
		ACAGATAAAAA				
		TTACAGAGTAC			Start	End
		ACAACATCCTC			Positio	Positio
4376	6262	AAAGCCTACC	2	350	n	n
		GGTGACAGTG			4730	5079
		CGGGCTTTTTT			5529	5878
		TTCGACCAAAG			0020	0070
		GTAACGAGGT				
		AACAACCATGC				
		GAGTGTTGAA				
		GTCAGGAGAT				
		CCTAAAGGCC				
		TGTACCCGTTA				
		CCTAGCCAGTT				
		GGCATTAAAC				
		GTATACGGTAC				
		CTAGGCATGTA				
		CGTAATCGTAG				
		CCTTAGCAATC				
		TCCAGTCC				

	1	<u> </u>	1		
		CGGTCGAAAA			
		ACTGCTGGCA			
		GTGGGGCATT			
		ACCTCGAATCT			
		ACCGTCGATAT			
		TGCTGAGTCC			
		ACCCGCCGTA			
		TTGCGGCAAG			
		TCGTATTCCGG			
		CTGATCACATG			
		GTGCTGATGG			
		CAGGTTTCACC			
		GCCGGTAATG			
		AAAAAGGCGA			
		ACTGGTGGTG		Start	End
		CTTGGACGCA		Positio	Positio
8276	9944	ACGGTTCCGA	350	n	n
0276	9944	CTACTCTGCTG 2	350	8386	8735
		СССТССТССС		8386	0733
		TGCCTGTTTAC		9149	9498
		GCGCCGATTG			
		TTGCGAGATTT			
		GGACGGACGT			
		TGACGGGGTC			
		TATACCTGCGA			
		CCCGCGTCAG			
		GTGCCCGATG			
		CGAGGTTGTT			
		GAAGTCGATG			
		TCCTACCAGG			
		AAGCGATGGA			
		GCTTTCCTACT			
		TCGGCGCTCT			
		AGGTCAGGCC			
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SRGD Performance Metrics

Initial Reads Count:	1212
Reads Count after Removing Duplication:	388

Reads Count after Overlapping:			158		
Initial Dataset Size in (Base):			241272		
Dataset Sizet after Removing Duplication:			99165		
Dataset Size after Overlapping:			35306		
Overlapping Metri					
Repeat Identification Time:			00h:00m:05s:000ms		
Overlapping Time:			00h:01m:35s:000ms		
Reads Alignment Time:			00h:00m:10s:000ms		
Total Hybrid Assembly Time:			00h:01m:45s:000ms		
Repeat Annotation Time:			00h:00m:07s:000ms		
Overlapping Length	O(N)2 Time Complexity	Hit Index Count		Overlapping Matched Count	RI
200	116281	158		31	0
199	96100	140		20	0
198	84100	124		13	0
197	76729	109		20	0
196	66049	88		6	0
195	63001	64		1	0
194	62500	107		8	0
193	58564	56		4	0
191	56644	56		1	0
190	56169	68		2	0
188	55225	64		5	0
187	52900	73		1	0

186	52441	53	1	0
183	51984	82	1	0
181	51529	66	1	0
180	51076	81	1	0
179	50625	80	2	0
178	49729	68	1	0
177	49284	77	1	0
176	48841	242	96	0
174	15625	30	2	0
172	15129	26	1	0
171	14884	17	1	0
170	14641	13	1	0
169	14400	27	3	0
155	13689	18	1	0
151	13456	16	2	0
146	12996	26	1	0
144	12769	19	1	0
141	12544	19	1	0
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