Assembly Report

Experiment Details

ExperimentID:	Experiment 66
Sequencing Coverage:	23
Number of Partitions:	1
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	201

Reads Dataset Details

Iteaus Dataset Details	
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	414

Assembly Details

Number of Contigs:	37
Contig N50:	776
Contig N90:	614
Number of Scaffold	8
Scaffold N50:	2164
Scaffold N90:	1450
Mis-assembly Count:	0
TotalAssembly Size:	12099

Repeat Details

Total Reads Count(Non-Repeat) :	381
Total Reads Count(Repeat):	7
Retetitve Read Count based on (Partitions Identifier):	0
Retetitve Read Count (Entire Read Frequency Identifier):	4
Retetitve Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	12
Total Unique Repetitive Sequences Count	3

Total Repeat	: Size (Base)		6300			
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 ACGGTTCCGA CTACTCTGCTG CGGTGCTGGC TGCCTGTTTAC GCGCCGATTG TTGCGAGATTT GGACGCATTG TTGCGAGATTT GGACGCATTG TTGCGAGATTT GGACGCATTG TTGCGAGATTT GGACGCGTCAG GTGCCCGATTG TTGCGAGTTTT GAAGTCGATG TCCTACCAGG AAGCGATGGA CCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT AGGTCAGGCC	3	350	Positio n 1756 3561	End Positio n 2105 3910 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 CTAGCCAGTT 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 GCATTAAAC 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				

	<u> </u>	1				
		CGGTCGAAAA				
		ACTGCTGGCA				
		GTGGGGCATT				
		ACCTCGAATCT				
		ACCGTCGATAT				
		TGCTGAGTCC				
		ACCCGCCGTA				
		TTGCGGCAAG				
		TCGTATTCCGG				
		CTGATCACATG				
		GTGCTGATGG				
		CAGGTTTCACC				
		GCCGGTAATG				
		AAAAAGGCGA				
		ACTGGTGGTG			Start	End
		CTTGGACGCA			Positio	Positio
4276	6262	ACGGTTCCGA	2	350	n	n
4270	0202	CTACTCTGCTG	2		5117	5466
		CGGTGCTGGC				
		TGCCTGTTTAC			5910	6259
		GCGCCGATTG				
		TTGCGAGATTT				
		GGACGGACGT				
		TGACGGGGTC				
		TATACCTGCGA				
		CCCGCGTCAG				
		GTGCCCGATG				
		CGAGGTTGTT				
		GAAGTCGATG				
		TCCTACCAGG				
		AAGCGATGGA				
		GCTTTCCTACT				
		TCGGCGCTCT				
		AGGTCAGGCC				

GATTCATTCGG GATGGTCTGT GTGGATTAAAA AAAGAGTGTCT GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCATC	
GTGGATTAAAA AAAGAGTGTCT GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTITATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC	
AAAGAGTGTCT GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTTACAGAGTAC	
GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC	
CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC Start Enc	
ACCTGCCGTG AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC Start Enc	
AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC Start Enc	
ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC Start End	
TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC Start End	
AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC AATACTTTAAC Start End	
CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC CAATATAGGCA Start End	
TAGCGCACAG ACAGATAAAAA TTACAGAGTAC Start End	
ACAGATAAAAA TTACAGAGTAC Start End	
TTACAGAGTAC Start End	
	10
4276 6262 AAAGCCTACC 2 350 n n	
GGTGACAGTG 4730 507	'
CGGGCTTTTTT 55529 587	
TTCGACCAAAG	
GTAACGAGGT	
AACAACCATGC	
GAGTGTTGAA	
GTCAGGAGAT	
CCTAAAGGCC	
TGTACCCGTTA	
CCTAGCCAGTT	
GGCATTAAAC	
GTATACGGTAC	
CTAGGCATGTA	
CGTAATCGTAG	
CCTTAGCAATC	
TCCAGTCC	

					 1
7776	9939	CGGTCGAAAA ACTGCTGGCA GTGGGGCATT ACCTCGAATCT ACCGTCGATAT TGCTGAGTCC ACCCGCCGTA TTGCGGCAAG TCGTATTCCGG CTGATCACATG GTGCTGATGG CAGGTTTCACC GCCGGTAATG AAAAAGGCGA ACTGGTGGTG CTTGGACGCA ACGGTTCCGA CTACTCTGCTG CGGTGCTGGC TGCCTGTTTAC GCGCCGATTG TTGCGAGATTT GGACGCATTG TTGCGAGATTT GGACGCATTG TTGCGAGATTT GGACGCGTCAG CCCGCGTCAG CCCGCGTCAG GTGCCCGATG CCGAGGTTGTT	350	Start Positio n 8386 9149	End Positio n 8735 9498
		TGACGGGGTC TATACCTGCGA			
		AAGCGATGGA GCTTTCCTACT TCGGCGCTCT AGGTCAGGCC			

		i i	<u> </u>		1
		GATTCATTCGG			
		GATGGTCTGT			
		GTGGATTAAAA			
		AAAGAGTGTCT			
		GATAGCAGCTT			
		CTGAACTGGTT			
		ACCTGCCGTG			
		AGTAAATTAAA			
		ATTTTATTGAC			
		TTAGGTCACTA			
		AATACTTTAAC			
		CAATATAGGCA			
		TAGCGCACAG			
		ACAGATAAAAA			<u> </u>
		TTACAGAGTAC		Start	End
		ACAACATCCTC		Positio	Positio
7776	9939	AAAGCCTACC 2	350	n	n
		GGTGACAGTG		8014	8363
		CGGGCTTTTTT		9552	9901
		TTCGACCAAAG		[3002	10001
		GTAACGAGGT			
		AACAACCATGC			
		GAGTGTTGAA			
		GTCAGGAGAT			
		CCTAAAGGCC			
		TGTACCCGTTA			
		CCTAGCCAGTT			
		GGCATTAAAC			
		GTATACGGTAC			
		CTAGGCATGTA			
		CGTAATCGTAG			
		CCTTAGCAATC			
		TCCAGTCC			
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SRGD Performance Metrics

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

Reads Count after Overlapping:		134			
Initial Dataset Size in (Base):		241272			
Dataset Sizet after Removing Duplication:		99165			
Dataset Size after Overlapping:		30984			
Overlapping Metrics					
Repeat Identification Time:		00h:00m:04s:000ms			
Overlapping Time:		00h:01m:39s:000ms			
Reads Alignment Time:		00h:00m:09s:000ms			
Total Hybrid Assembly Time:		00h:01m:48s:000ms			
Repeat Annotation Time:		00h:00m:01s:000ms			
Overlapping Length	O(N)2 Time Complexity	Hit Index Count		Overlapping Matched Count	RI
200	145161	207		33	0
199	121104	201		19	0
198	108241	172		15	0
197	98596	150		21	0
196	85849	114		6	0
195	82369	79		2	0
194	81225	119		8	0
193	76729	78		6	0
191	73441	70		1	0
188	72900	83		4	0
187	70756	87		1	0
186	70225	84		2	0

69169	108	1	0
68644	88	2	0
67600	116	1	0
67081	116	2	0
66049	121	1	0
65536	111	1	0
65025	302	114	0
19881	33	1	0
19600	45	1	0
19321	23	1	0
19044	14	1	0
18769	27	3	0
17956	21	1	0
17689	25	3	0
16900	23	1	0
16641	22	1	0
16384	21	1	0
	68644 67600 67081 66049 65536 65025 19881 19600 19321 19044 18769 17956 17689 16900 16641	68644 88 67600 116 67081 116 66049 121 65536 111 65025 302 19881 33 19600 45 19321 23 19044 14 18769 27 17956 21 17689 25 16900 23 16641 22	68644 88 2 67600 116 1 67081 116 2 66049 121 1 65536 111 1 65025 302 114 19881 33 1 19600 45 1 19321 23 1 19044 14 1 18769 27 3 17956 21 1 17689 25 3 16900 23 1 16641 22 1