Assembly Report

Experiment Details

ExperimentID:	Experiment 80
Sequencing Coverage:	35
Number of Partitions:	5
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	61

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	476

Assembly Details

Number of Contigs:	13
Contig N50:	2946
Contig N90:	2378
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

Repeat Details

Total Reads Count(Non-Repeat) :	34
Total Reads Count(Repeat):	358
Retetitve Read Count based on (Partitions Identifier):	357
Retetitve Read Count (Entire Read Frequency Identifier):	3
Retetitve Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	10642
Total Unique Repetitive Sequences Count	4

Total Repeat Size (Base)		7706				
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 CTGCTGTTCCGA CTACTCTGCTG CGGCGATTT GCGCGATTT GCGCGATTT GCGCGATTT GCGCGATTT GCGCGATTT GCGCGGTT TGCGAGATT TGCGAGATT TGCGAGATT TGCGAGATT TGCGAGATT TGCGAGTT TGCGAGATT TGCGAGATT TGCGAGATT TGCGAGATT TGCGAGATT TGCGAGATT TGCGAGATT TGCGAGTT TGCGAGT TTGCGAGT TTGCGAGT TTGCGAGT TTGCGAGT TGCCGCTCAG GTGCCCGATG CCGCGTCAG GTGCCCGATG TCGAGGTTGT TGAGGCCCATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT AGGTCAGGCC A	3	351	Start Positio n 3561 8386 9149	End Positio n 3911 8736 9499

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		GATTCATTCGG				
		GATGGTCTGT				
		GTGGATTAAAA				
		AAAGAGTGTCT				
		GATAGCAGCTT				
		CTGAACTGGTT				
		ACCTGCCGTG				
		AGTAAATTAAA				
		ATTTTATTGAC				
		TTAGGTCACTA			C4 = "4	□ al
		AATACTTTAAC			Start	End
		CAATATAGGCA				Positio
		TAGCGCACAG			n	n
		ACAGATAAAAA			409	758
		TTACAGAGTAC			2228	2577
		ACAACATCCTC				
1	10080	AAAGCCTACC	8	350	3182	3531
		GGTGACAGTG			4730	5079
		CGGGCTTTTTT			5529	5878
		TTCGACCAAAG				
		GTAACGAGGT			6730	7079
		AACAACCATGC			8014	8363
		GAGTGTTGAA			9552	9901
		GTCAGGAGAT			9332	19901
		CCTAAAGGCC				
		TGTACCCGTTA				
		CCTAGCCAGTT				
		GGCATTAAAC				
		GTATACGGTAC				
		CTAGGCATGTA				
		CGTAATCGTAG				
		CCTTAGCAATC				
		TCCAGTCC				

GCGGTCGAAA AACTGCTGGC AGTGGGGCAT TACCTCGAATC TACCGTCGATA TTGCTGAGTCC ACCCGCCGTA TTGCGGCAAG TTGCGGCAAG TTGCGGCAAG TTGCGGCAAG TTGCGGCAAG TTGCGGCAAG TTGCGGCAAG TTGCGGCAAG CAGGTTCACC GCCGGTATG AAAAAGGCGA ACTGCTGGTG CTTGGACGCA ACTGCTCGAG CTACTCTCGG CTGCTGTTTAC GCGCCGATTG TTGCAGAGTTT GAGGGAGT TGCAGGGGTC TGACGGGGTC TGACGGGGTC TGACGGGTC TGACGGGGTC TGACGGGTC TGACGGGGTC TGACGGGTC TGACGGGGTC TGACG			<u> </u>	1	<u> </u>	
AGTGGGCAT TACCTCGAATC TACCGCGTAA TTGCTGAGTCC ACCCGCCGTA TTGCGGCAAG TCGTATTCCGG CTGATCACATG GTGCTGATG CAGGTTTCACC GCCGGTAATG AAAAAGCGA ACTGGTGGTG CTTGGACGCA CTACTCTGCTG CGGTCCTGGC CGGCCGATTG TTGCGAGATTT GGACGAATT GGACGAATT GGACGAATT GGACGGACGT TGACGGGTC TGCCGATTTAC GCCCGCGATG TGCCGATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT						
TACCTCGAATC TACCGTCGATA TTGCTGAGTCC ACCCGCCGTA TTGCGGCAAG TCGTATTCCGG CTGATCACATG GTGCTGATGG CAGGTTTCACC GCCGGTAATG AAAAAGGCGA ACTGGTGGTG CTTGGACGCA ACTGGTGGTG CTGATCCGA CTACTCTGCTG CGGTGCTGGC TGCCTGTTTAC GCGCCGATTT GGACGCA TGCCGATTT GGACGCA CCGCGCGTTATC TGCAGATTT TGACGGGGTC TATACCTGCGA CCGCGCTCAG GTGCCCGATG CCGCGCTCAG GTGCCCGATG CCGAGTTGTT GAAGGGGTC TATACCTGCGA CCCGCGTCAG GTGCCCGATG CCAGGTTGTT GAAGGGATG TCCTACCAGG AAGCGATGGT TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT			AACTGCTGGC			
TACCGTCGATA TTGCTGAGTCC ACCCGCCGTA TTGCGGCAAG TCGTATTCCGG CTGATCACATG GTGCTGATGG CAGGTTTCACC GCCGGTAATG AAAAAGGCGA ACTGGTGGTG CTTGGACGCA ACTGTGTGCC CGGTGCTGGC TGCCTGTTAC GCGCCGATTG TTGCGAGATTT GGACGCA CCGCCGATTG TTGCAGATTT GGACGCA CCCGCGTCAG CCGCGTCAG GTGCCCGATG CCAGCTTGTT CGACGTTGTT CGACGTCTT CGACGTTCT TCGACGATG CCAGCTCAT CCACCAGG AAGCGATGGT TCCTACCAGG AAGCGATGGT TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT			AGTGGGGCAT			
TTGCTGAGTCC ACCCGCGTA TTGCGGCAAG TCGTATTCCGG CTGATCACATG GTGCTGATGG CAGGTTTCACC GCCGGTAATG AAAAAGGCGA ACTGGTGGTG CTTGGACGCA ACGGTTCCGA CTACTCTGCTG CGGTGCTGGC TGCCTGTTTAC GCGCCGATTG TTGCGAGATTT GGACGGAGT TGACGGGGTC TGACGGAGT TGACGGGTC TGACGGAGT TGACGGGTC TGACGGAGTT TGACGGGGTC TATACCTGCGA CCGCGTCAG GTGCCCGATG TGACGGATG TGACGGGATG TGACGGATG CGAGGTTGTT GAAGTCGATG CGAGGTTGTT GAAGTCGATG TCCTACCAGG AAGCGATGA GCTTTCCTACT TCGGCGCTCT			TACCTCGAATC			
ACCCGCCGTA TTGCGGCAAG TCGTATTCCGG CTGATCACATG GTGCTGATGG CAGGTTTCACC GCCGGTAATG AAAAAGGCGA ACTGGTGGTG CTTGGACGCA ACGGTTCCGA CTACTCTGCTG CGGCCGATTG TGCCCGATTT GGACGCA TTGCGAGATTT GGACGGAC CTACTCTGCGC TGCCCGATTG TTGCGAGATTT GGACGGACGT TGACGGGGTC TGACCGCATG TGCCCGATG TGACGGGGTC TATACCTGCGA CCGCGTCAG GTGCCCGATG CGAGGTTGTT GAAGTCGATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT			TACCGTCGATA			
TTGCGGCAAG TCGTATTCCGG CTGATCACATG GTGCTGATGG CAGGTTTCACC GCCGGTAATG AAAAAGGCGA ACTGGTGGTG CTTGGACGCA ACGGTTCCGA CTACTCTGCTG CGGTGCTGGC TGCCTGTTTAC GCGCCGATTG TTGCGAGATTT GGACGGAC CCCCGCGTCAG CCCCGCGTCAG CCCCGCGTCAG CCCCGCTCAG CCCCGCGTCAG CCCCGCGTCAG CCCCCGATG CCAGGTTCTAC CCAGCGAAG CCCCCGCTCAG CCCCCGATG CCAGGTTCTT CGAGGTTCT CGAGGTTCT CGAGGTTCT CGAGGTTCT CGAGGTTCT CGAGGTTCT CGAGGTTCT CCACCAGG AAGCGATGA CCCTCTCTCTCT CCGCCCCTT CCACCAGG AAGCGATGA CCTTTCCTACT TCGCCCCTT CCGCCCCTT CCGCCCCTT CCGCCCCTT CCGCCCCTT CCGCCCCCT CCCCCCCT CCCCCCCC			TTGCTGAGTCC			
TCGTATTCCGG CTGATCACATG GTGCTGATGG CAGGTTTCACC GCCGGTAATG AAAAAGGCGA ACTGGTGGTG CTTGGACGCA ACGGTTCCGA CTACTCTGCTG CGGTGCTGCC TGCCTGTTTAC GCGCCGATTG TTGCAGACTT TTGCAGACGT TGACGGGGTC TGACCGACGA CTACTCTGCTG CGGTGCTGC TGCCTGTTTAC GCGCCGATTG TTGCAGACTT TTGCAGACTT TGACGGGGTC TATACCTGCGA CCCGCGTCAG GTGCCCGATG CGAGGTTGTT GAAGTCGATG CCAGCGTCAG GTGCCCGATG CCAGCGTCAG GTGCCCGATG CCAGCGTCAG GTCCCACAGG AAGCGATGA CCCGCGTCAC CGAGGTTGTT GAAGTCGATG TCCTACCAGG AAGCGATGA GCTTTCCTACT TCGGCGCTCT			ACCCGCCGTA			
CTGATCACATG GTGCTGATGG CAGGTTTCACC GCCGGTAATG AAAAAGGCGA ACTGGTGGTG CTTGGACGCA ACGGTTCCGA CTACTCTGCTG CGGTGCTGGC TGCCTGTTTAC GCGCCGATTG TTGCAGGGATT TGACGGGGTC TATACCTGCGA CCGCGGTCAG GTGCCCGATG CCGAGTTCT TGACGGGGTC TATACCTGCGA CCCCGCGTCAG GTGCCCGATG CCGAGTTGT TGACGGGGTC TATACCTGCGA CCCGCGTCAG GTGCCCGATG CCGAGTTGT GAAGCCGATG CCGAGGTTGT GAAGTCGATG CCGAGGTTGT CGACGATG CCGAGGTTGT CGACGATG CCCGCGTCAG GTGCCCGATG CCGAGGTTGT CGACGATG CCCGCGTCAC CCGCGTCAC CCGCGCTCAC CCGCGCTCCT CCGCGCTCCT CCGCGCTCCT CCGCGCTCCT CCGCGCTCCT CCGCGCTCCT CCGCGCTCCT CCGCGCTCCT CCGCCCCAC CCGCGCTCCC CCGCGCTCCCCCCCC			TTGCGGCAAG			
GTGCTGATGG CAGGTTTCACC GCCGGTAATG AAAAAGGCGA ACTGGTGGTG CTTGGACGCA ACGGTTCCGA CTACTCTGCTG CGGTGCTGGC TGCCTGTTTAC GCGCCGATTG TTGCGAGATTT GGACGGACCT TGACGGGGTC TATACCTGCGA CCCGCGTCAG GTGCCCGATG CCGCGTCAG CTGCTGTTT GGAGTCGT TGACGGGGTC TATACCTGCGA CCCGCGTCAG GTGCCCGATG CCAGGTTGTT GAAGTCGATG TCCTACCAGG AAGCGATGG CCAGGTTGTT GAAGTCGATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT TCGGCGCTCT			TCGTATTCCGG			
CAGGTTTCACC GCCGGTAATG AAAAAGGCGA ACTGGTGGTG CTTGGACGCA ACGGTTCCGA CTACTCTGCTG CGGTGCTGCC TGCCTGTTTAC GCGCCGATTG TTGCGAGATTT GGACGGACCT TGACGGGGTC TATACCTGCGA CCGCGTCAG GTGCCCGATG CCGCGTCAG GTGCCCGATG CCAGGTTGTT GAAGTCGAG CCCGCGTCAG GTGCCCGATG CCAGGTTGTT GAAGTCGATG CCAGGTTGTT GAAGTCGATG CCAGGTTGTT GAAGTCGATG CCAGGTTGT TGCAGGATG CCAGGTTGTT CGAGGTTGTT CGAGGTTGTT CGAGGTTGTT CGAGGTTGTT CGAGGTGGA CCTTCCTACT TCGGCGCTCT			CTGATCACATG			
GCCGGTAATG AAAAAGGCGA ACTGGTGGTG CTTGGACGCA ACGGTTCCGA CTACTCTGCTG CGGTGCTGGC TGCCTGTTAC GCGCGATTG TTGCGAGATTT GGACGGACT TGACGGGGTC TATACCTGCGA CCCGCGTCAG GTGCCCGATG TTGCCAGTC TGCCGGTCCT TGACGGGTC TATACCTGCGA CCCGCGTCAG GTGCCCGATG TCCACCAGG AAGCGATGGT TGACGGGGTC TATACCTGCGA CCCGCGTCAG GTGCCCGATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT			GTGCTGATGG			
AAAAAGGCGA ACTGGTGGTG CTTGGACGCA ACGGTTCCGA CTACTCTGCTG CGGTGCTGGC TGCCTGTTTAC GCGCCGATTG TTGCGAGACTT TGACGGGGTC TATACCTGCGA CCGCGTCAG GTGCCCGATG CCGAGTTGTT TGACGGGGTC TATACCTGCGA CCGCGTCAG GTGCCCGATG CGAGGTTGTT GAAGTCGATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT TCGGCGCTCT			CAGGTTTCACC			
ACTGGTGGTG CTTGGACGCA ACGGTTCCGA CTACTCTGCTG CGGTGCTGGC TGCCTGTTTAC GCGCCGATTG TTGCGAGACT TGACGGGGTC TGACGGGGTC TGACGGAGTT TGACGGGGTC TGACGGGGTC TGACGGGGTC TGACGGGGTC TGACGGGGTC TGACGGGGTC TGACGGGGTC TATACCTGCGA CCCGCGTCAG GTGCCCGATG TGAAGTCGATG TCCTACCAGG AAGCGATGGT TGAAGTCGATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT			GCCGGTAATG			
1 10080 ACTGGTGGTG CTTGGACGCA ACGGTTCCGA CTACTCTGCTG CGGTGCTGGC TGCCTGTTTAC GCGCCGATTG TTGCGAGACTT GGACGGACGT TGACGGGGTC TTGCGAGACTT TGACGGGGTC TATACCTGCGA CCCGCGTCAG GTGCCCGATG TGACGGAGTC TATACCTGCGA CCCGCGTCAG GTGCCCGATG TGAAGTCGATG TCCTACCAGG AAGCGATGG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT			AAAAAGGCGA		Ctort	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			ACTGGTGGTG			
1 10080 ACGGTTCCGA CTACTCTGCTG CGGTGCTGGC TGCCTGTTTAC GCGCCGATTG TTGCGAGATTT GGACGGACGT TGACGGGGTC TATACCTGCGA CCCGCGTCAG GTGCCCGATG CGAGGTTGTT GAAGTCGATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT			CTTGGACGCA			
CTACTCTGCTG CGGTGCTGGC TGCCTGTTTAC GCGCCGATTG TTGCGAGATTT GGACGGACGT TGACCGGGGTC TATACCTGCGA CCCGCGTCAG GTGCCCGATG CGAGGTTGTT GAAGTCGATG CGAGGTTGTT GAAGTCGATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT TCGGCGCTCT		40000	ACGGTTCCGA	054	ln l	n
TGCCTGTTTAC GCGCCGATTG TTGCGAGATTT GGACGGACGT TGACGGGGTC TATACCTGCGA CCCGCGTCAG GTGCCCGATG CGAGGTTGTT GAAGTCGATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT	1	10080	CTACTCTGCTG 3	351	3560	3910
TGCCTGTTTAC GCGCCGATTG TTGCGAGATTT GGACGGACGT TGACGGGGTC TATACCTGCGA CCCGCGTCAG GTGCCCGATG CGAGGTTGTT GAAGTCGATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT			сдетдет		5909	6259
TTGCGAGATTT GGACGGACGT TGACGGGGTC TATACCTGCGA CCCGCGTCAG GTGCCCGATG CGAGGTTGTT GAAGTCGATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT			TGCCTGTTTAC			
GGACGGACGT TGACGGGGTC TATACCTGCGA CCCGCGTCAG GTGCCCGATG CGAGGTTGTT GAAGTCGATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT			GCGCCGATTG		9148	9498
TGACGGGGTC TATACCTGCGA CCCGCGTCAG GTGCCCGATG CGAGGTTGTT GAAGTCGATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT			TTGCGAGATTT			
TATACCTGCGA CCCGCGTCAG GTGCCCGATG CGAGGTTGTT GAAGTCGATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT			GGACGGACGT			
CCCGCGTCAG GTGCCCGATG CGAGGTTGTT GAAGTCGATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT			TGACGGGGTC			
GTGCCCGATG CGAGGTTGTT GAAGTCGATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT			TATACCTGCGA			
CGAGGTTGTT GAAGTCGATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT			CCCGCGTCAG			
GAAGTCGATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT			GTGCCCGATG			
TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT			CGAGGTTGTT			
AAGCGATGGA GCTTTCCTACT TCGGCGCTCT			GAAGTCGATG			
GCTTTCCTACT TCGGCGCTCT			TCCTACCAGG			
TCGGCGCTCT			AAGCGATGGA			
			GCTTTCCTACT			
AGGTCAGGCC			TCGGCGCTCT			
			AGGTCAGGCC			

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		GCTTTTCATTC				
		TGACTGCAAC				
		GGGCAATATG				
		TCTCTGTGTGG				
		ATTAAAAAAAAG				
		AGTGTCTGATA				
		GCAGCTTCTG				
		AACTGGTTACC				
		TGCCGTGAGT				
		AAATTAAAATT			G	<u>. </u>
		TTATTGACTTA			Start	End
		GGTCACTAAAT			Positio	Positio
		ACTTTAACCAA			n	n
		TATAGGCATAG			1	350
		CGCACAGACA			854	1203
		GATAAAAATTA				
1	10080	CAGAGTACAC	8	350	1295	1644
		AACATCCATGA			2705	3054
		AACGCATTAGC			4337	4686
		ACCACCATTAC				
		CACCACCATCA			6359	6708
		CCATTACCACA			7574	7923
		GGTAACGGTG			9750	0101
		CGGGCTGACG			8752	9101
		CGTACAGGAA				
		ACACAGAAAAA				
		AGCCCGCACC				
		TGACAGTGCG				
		GGCTTTTTTTT				
		CGACCAAAGG				
		TAACGAGGTAA				
		CAACCATGCG				
		AGTGTTGAAGT				
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SRGD Performance Metrics

Initial Reads Count:	1203
Reads Count after Removing Duplication:	392

Reads Count after Overlapping:			374		
Initial Dataset Size in (Base):			359763		
Dataset Sizet after Removing Duplication:			150869		
Dataset Size after (Overlapping:		113299		
Overlapping Metric	cs				
Repeat Identification Time:			00h:00m	n:08s:000ms	
Overlapping Time:			00h:02m:21s:000ms		
Reads Alignment T	ime:		00h:00m:16s:000ms		
Total Hybrid Assem	ably Time:		00h:02m:37s:000ms		
Repeat Annotation	Time:		00h:18m:33s:000ms		
Overlapping Length	Overlapping Length Complexity Hit Index C		Count	Overlapping Matched Count	RI
276	1156	24		12	0
251	484	1		1	0
226	441	6		5	0