Assembly Report

Experiment Details

ExperimentID:	Experiment 71
Sequencing Coverage:	29
Number of Partitions:	1
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	251

Reads Dataset Details

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Total Reads Count:	1209
Total Dataset Size in (Base):	301119
Valid Read Count:	1209
Rejected Read Count:	0
Maximum Read Length:	251
Minimum Read Length:	212

Reference Genome Details

Length of Reference Genome (Base):	10080
Number of K-mers:	9830
Length of K-mer	469

Assembly Details

Number of Contigs:	16
Contig N50:	1513
Contig N90:	1413
Number of Scaffold	3
Scaffold N50:	4693
Scaffold N90:	4693
Mis-assembly Count:	0
TotalAssembly Size:	11154

Repeat Details

Total Reads Count(Non-Repeat) :	384
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)			8400		
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions
1	4693	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 GGACGGACGT TGCCTGTTTAC GCGCCGATTG TTGCGAGATTT TGCGAGATTT GGACGGACGT TGACGGGTC TTGCCGATG TTGCCAGG TTGCCCGATG CCGCGTCAG GTGCCCGATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT AGGTCAGGCC		350	Start End Position n 1756 2105 3561 3910 3964 4313

GATTCATTCGG GATGGTCTGT GTGGATTAAAA AAAGAGTGTCT GATAGCAGCTT CCTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC AAAGCCTACC 1 4693 AAAGCCTACC 3 350 409 758 GGTGACAGTG CGGGCTTTTTT TTCGACCAAAAG GTAACGAGGA GAACACATCCCC GAGTGTTGAA GTCAAGGAGT ACACACAGC GAGTGTGAA GTCAAGGAGT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGCCAGTT				<u> </u>	-		1
GTGGATTAAAA AAAGAGTGTCT GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTTACAGACTAC ACAACATCCTC 1 4693 AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATCC GAGTGTTGAA GTCAAGAGAT CCTAAAGGCC TGTACCCGTTA CCTAAAGCC TGTACCCGTTA CCTAAGCCAGTC GGCATTAAAC GTATACGGTAC CTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA CCTAGCCAGTT			GATTCATTCGG				
AAAGAGTGTCT GATAGCAGCTT CTGAACTGGTT ACCTGCGTG AGTAAATTAAA ATTITATTGAC TTAGGTCACTA AATACTITAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTTACAGAGTAC ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA CCTAGGCATGTA			GATGGTCTGT				
GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTTACAGAGTAC ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGGCTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GATGTGAA GTCAGGAGAT CCTAAAGGCC TGTACCGGTTA CCTAAAGGCC TGTACCGGTTA CCTAGCCAGTA CCTAGGCATGA CGTATACGGTAC CTAGGCATGA			GTGGATTAAAA				
CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTTACAGAGTAC ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGCTTTTTT TTCGACCAAAG GTAACGAGTA GTAACGAGTA GCAGAGAT CCTAAAGGCC GAGTGTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA			AAAGAGTGTCT				
ACCTGCCGTG AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAGCCTACC GGTGACAAGG CGGGCTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT CCTAGCCAGTA CCTAGCCATGA CGTATACGGTAC CTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA			GATAGCAGCTT				
AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACATCCTC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTA CCTAGCCATGA CGTATACGGTAC CTAGGCATGTA			CTGAACTGGTT				
ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACATCCTC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA			ACCTGCCGTG				
TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACATCCTC GGTGACAGTG CGGGCTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA			AGTAAATTAAA				
AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACACTCCTC AAAAGCCTACC GGTGACAGTG CGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATCC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA			ATTTTATTGAC				
CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACAGTG CGGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA			TTAGGTCACTA				
TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA			AATACTTTAAC				
ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA			CAATATAGGCA				
TTACAGAGTAC ACAACATCCTC ACAACATCCTC ACAACATCCTC AAAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTGAA 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
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 CTAGGCATGTA			ACAACATCCTC			n	n
GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA	1	4693	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				

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		GCTTTTCATTC				
		TGACTGCAAC				
		GGGCAATATG				
		TCTCTGTGTGG				
		ATTAAAAAAAAG				
		AGTGTCTGATA				
		GCAGCTTCTG				
		AACTGGTTACC				
		TGCCGTGAGT				
		AAATTAAAATT				
		TTATTGACTTA				
		GGTCACTAAAT			<u> </u>	
		ACTTTAACCAA			Start	End
		TATAGGCATAG			Positio	Positio
		CGCACAGACA			n	n
		GATAAAAATTA			1	350
1	4693	CAGAGTACAC	5	350	854	1203
		AACATCCATGA				
		AACGCATTAGC			1295	1644
		ACCACCATTAC			2705	3054
		CACCACCATCA			4337	4686
		CCATTACCACA			-1331	4000
		GGTAACGGTG				
		CGGGCTGACG				
		CGTACAGGAA				
		ACACAGAAAAA				
		AGCCCGCACC				
		TGACAGTGCG				
		GGCTTTTTTTT				
		CGACCAAAGG				
		TAACGAGGTAA				
		CAACCATGCG				
		AGTGTTGAAGT				

		 				
		CGGTCGAAAA				
		ACTGCTGGCA				
		GTGGGGCATT				
		ACCTCGAATCT				
		ACCGTCGATAT				
		TGCTGAGTCC				
		ACCCGCCGTA				
		TTGCGGCAAG				
		TCGTATTCCGG				
		CTGATCACATG				
		GTGCTGATGG				
		CAGGTTTCACC				
		GCCGGTAATG			Start	End
		AAAAAGGCGA			Positio	Positio
		ACTGGTGGTG			n	n
		CTTGGACGCA			5117	5466
4451	10080	ACGGTTCCGA	5	350	3117	3400
4431	10080	CTACTCTGCTG	5	330	5910	6259
		CGGTGCTGGC			7138	7487
		TGCCTGTTTAC			8386	8735
		GCGCCGATTG			0300	6733
		TTGCGAGATTT			9149	9498
		GGACGGACGT				
		TGACGGGGTC				
		TATACCTGCGA				
		CCCGCGTCAG				
		GTGCCCGATG				
		CGAGGTTGTT				
		GAAGTCGATG				
		TCCTACCAGG				
		AAGCGATGGA				
		GCTTTCCTACT				
		TCGGCGCTCT				
		AGGTCAGGCC				

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		GATTCATTCGG				
		GATGGTCTGT				
		GTGGATTAAAA				
		AAAGAGTGTCT				
		GATAGCAGCTT				
		CTGAACTGGTT				
		ACCTGCCGTG				
		AGTAAATTAAA				
		ATTTTATTGAC				
		TTAGGTCACTA				
		AATACTTTAAC				
		CAATATAGGCA			G	
		TAGCGCACAG			Start	End
		ACAGATAAAAA			Positio	Positio
		TTACAGAGTAC			n	n
		ACAACATCCTC			4730	5079
4451	10080	AAAGCCTACC	5	350	5529	5878
		GGTGACAGTG				
		CGGGCTTTTTT			6730	7079
		TTCGACCAAAG			8014	8363
		GTAACGAGGT			9552	9901
		AACAACCATGC			0002	3301
		GAGTGTTGAA				
		GTCAGGAGAT				
		CCTAAAGGCC				
		TGTACCCGTTA				
		CCTAGCCAGTT				
		GGCATTAAAC				
		GTATACGGTAC				
		CTAGGCATGTA				
		CGTAATCGTAG				
		CCTTAGCAATC				
		TCCAGTCC				

GCTTTTCATTC TGACTGCAAC GGGCAATATG TCTCTGTGTGG ATTAAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 4451 10080 CAGAGTACAC AACATCCATGA GGGCAATATC AACTGGTTACC AACATCCATGA Start Enc Positio Pos n n n 6359 670	 -
GGGCAATATG TCTCTGTGTGG ATTAAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 4451 10080 GGGCAATATG TCTCTGTGTGA AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA ACGAGTACAC 3 350 6359 670	
TCTCTGTGTGG ATTAAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 4451 10080 TCTCTGTGTGG ATTAAAAAAAAAAAAAAAAAAAAAAA	
ATTAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 4451 10080 ATTAAAAAAG ACTGGTTACC TGCCGTGAGT AAATTAAAATT ACTTAACCTTA ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA ACTTAACCAA TATAGGCATAG ACGACACA ACGACACACA ACTTAACCAA ACTTAACCAAA ACTTAACCAAA ACTTAACCAAAAAAAA	
AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 4451 10080 AGTGTCTGATA GCACTGATA AACTTAAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 4451 6359 670	
GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 4451 10080 GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT ACTTTAACCTAA Start Enc Positio Pos n n	
AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 4451 10080 AACTGGTTACC TGCCGTGAGT AAATTAAAAATT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA AGGCATACAC AGAGTACAC AGAGTACACC AGAGTACCACC AGAGTACCACC AGAGTACCACC AGAGTACCACC AGAGTACCACC AGAGTACCACC AGAGTACCACCACCACC AGAGTACCACCACCACCACCACCACCACCACCA	
TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 4451 10080 TGCCGTGAGT AAATTAAAATT ACTTAAAAATT ACTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAAATTA ACAGGAGTACAC TATAGGCATAG ACAGGAGTACAC ACAGGAGTACACC ACAGGAGTACACCACCACCACCACCACCACCACCACCACCACCACCA	
AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA CAGAGTACAC 3 350 6359 670	
TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA CAGAGTACAC 3 TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA Positio n n 6359 670	
GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAAATTA 4451 10080 CAGAGTACAC 3 350 6359 670	
ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA CAGAGTACAC 3 ACTTTAACCAA Start End Positio Pos n n 6359 670	
TATAGGCATAG CGCACAGACA GATAAAAATTA CAGAGTACAC 3 Start End Positio Pos n n 6359 670	
CGCACAGACA Positio Pos	
GATAAAAATTA n n n n n n n n n n	
4451 10080 CAGAGTACAC 3 350 6359 670	itio
	8
AACGCATTAGC 7574 792	3
ACCACCATTAC 8752 910	1
CACCACCATCA	
CCATTACCACA	
GGTAACGGTG	
CGGGCTGACG	
CGTACAGGAA	
ACACAGAAAAA	
AGCCCGCACC	
TGACAGTGCG	
GGCTTTTTTT	
CGACCAAAGG	
TAACGAGGTAA	
CAACCATGCG	
AGTGTTGAAGT	

SRGD Performance Metrics

Initial Reads Count:	1209
Reads Count after Removing Duplication:	390

Reads Count after Overlapping:			102				
Initial Dataset Size in (Base):			301119				
Dataset Sizet after Removing Duplication:			124917				
Dataset Size after Overlapping:			33904				
Overlapping Metrics							
Repeat Identification Time:			00h:00m:09s:000ms				
Overlapping Time:			00h:04m:07s:000ms				
Reads Alignment Time:			00h:00m:12s:000ms				
Total Hybrid Assembly Time:			00h:04m:19s:000ms				
Repeat Annotation Time:			00h:00m:02s:000ms				
Overlapping Length	O(N)2 Time Complexity	Hit Index Count		Overlapping Matched Count	RI		
250	147456	212		22	0		
249	131044	212		13	0		
248	121801	192		10	0		
247	114921	170		15	0		
246	104976	132		4	0		
245	102400	98		1	0		
244	101761	143		6	0		
243	97969	98		4	0		
241	95481	97		1	0		
238	94864	107		2	0		
237	93636	126		1	0		
236	93025	110		2	0		

233	91809	140	1	0	
231	91204	111	2	0	
230	90000	143	1	0	
229	89401	141	1	0	
228	88804	152	1	0	
227	88209	139	1	0	
226	87616	363	135	0	
224	25921	52	1	0	
221	25600	25	1	0	
219	25281	39	2	0	
217	24649	22	1	0	
216	24336	18	1	0	
205	24025	26	1	0	
201	23716	38	5	0	
176	22201	119	53	0	