Assembly Report

Experiment Details

ExperimentID:	Experiment 79
Sequencing Coverage:	35
Number of Partitions:	4
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	76

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	565

Assembly Details

Number of Contigs:	13
Contig N50:	2651
Contig N90:	2101
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

Repeat Details

Total Reads Count(Non-Repeat) :	100
Total Reads Count(Repeat):	292
Retetitve Read Count based on (Partitions Identifier):	291
Retetitve Read Count (Entire Read Frequency Identifier):	3
Retetitve Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	3874
Total Unique Repetitive Sequences Count	4

Total Repea	nt Size (Base)		7357			
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 CGGTGCTGGC TGCCTGTTTAC GCGCCGATTG TGCGAGATTT GGACGCATTG TGCGAGATTT GGACGCATTG TTGCGAGATTT GGACGCATTG TTGCGAGATTT GGACGCATTG TTGCGAGATTT GGACGCATTG TTGCGAGATTT GGACGCATG TTGCGAGTC TTGCCGATG TTGCGAGATTT TGCGAGATTT TGCGAGATTT TGCGAGATTT TGCGAGATTT TGCGAGTTGTT TGCGAGTTGTT TGAGTCCGATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT AGGTCAGGCC	8	350	Start Positio n 1756 3561 3964 5117 5910 7138 8386 9149	End Positio n 2105 3910 4313 5466 6259 7487 8735 9498

ACAACATCCTC AAAAGCCTACC GGTGACAGTG CGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT		_		1			
GTGGATTAAAA AAAGAGTGTCT GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTITATTGAC TTAGGTCACTA AAATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGAT AACAACCATGC GAGTGTTGAA GTCAGGAGAT			GATTCATTCGG				
AAAGAGTGTCT GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGAG GTAACGAGAT ACAGCATGC GAGTGTTGAA GTCAGGAGAT			GATGGTCTGT				
GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACATCCTC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGAT GATAGTAC GAGTGTTGAA GTCAGGAGAT			GTGGATTAAAA				
CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CCAATATAGGCA TAGCGCACAG ACAGATAAAAA TTTACAGAGTAC ACAACATCCTC ACAACATCCTC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT			AAAGAGTGTCT				
ACCTGCCGTG AGTAAATTAAA ATTITATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACATCCTC GGTGACAGTG CGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT			GATAGCAGCTT				
AGTAAATTAAA ATTITATTGAC TTAGGTCACTA AATACTITAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT			CTGAACTGGTT				
ATTITATIGAC TTAGGTCACTA AATACTITAAC CCAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACATCCTC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT			ACCTGCCGTG				
TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACATCCTC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT TTAGGTCACTA CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACATCCTC ACAACATCCTC ACAACATCCTC ACAACATCCTC ACAACATCTC ACAACATTCT ACAACAACATCTC ACAACATCTC			AGTAAATTAAA				
AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACATCCTC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTGAA GTCAGGAGAT ACTACAGAGAT Start End Positio n n 2228 2578 4730 5080 9552 9902			ATTTTATTGAC				
CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CAATATAGGCA TAGCGCACAG ACAGCACAG ACAGCATACC ACAACATCCTC ACAACCATCC ACAACCATCCAT			TTAGGTCACTA				
TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT TAGCGCACAG Start End Positio Positio n n 2228 2578 4730 5080 9552 9902			AATACTTTAAC				
ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAGCCTACC BGTGACAGTG AAAGCCTACC BGTGACAAGG BTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT ACAGGAGAT BTACAGAGT BT			CAATATAGGCA				
TTACAGAGTAC ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT TTACAGAGTAC ACAACATCCTC AAAGCCTACC AAAGCCTACC AAAGCCTACC AAAGCCTACC AAAGCCTACC AAAAGCCTACC AAAAGCCATGC AAAACCATGC GAGTGTTGAA GTCAGGAGAT Positio Positio Positio Positio Positio Positio N Positio N ACACCATGC ATGC AGAGCTTTTTT AGACCAAAG AGTGTTGAA GTCAGGAGAT			TAGCGCACAG				
1 10080 ACAACATCCTC AAAGCCTACC 3 351 CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT			ACAGATAAAAA			Start	End
1 10080 AAAGCCTACC GGTGACAGTG CGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT			TTACAGAGTAC			Positio	Positio
GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT			ACAACATCCTC			n	n
GGTGACAGTG CGGGCTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT	1	10080	AAAGCCTACC	3	351	2228	2578
TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT			GGTGACAGTG				
GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT			CGGGCTTTTTT			4730	5080
AACAACCATGC GAGTGTTGAA GTCAGGAGAT			TTCGACCAAAG			9552	9902
GAGTGTTGAA GTCAGGAGAT			GTAACGAGGT				
GTCAGGAGAT			AACAACCATGC				
			GAGTGTTGAA				
			GTCAGGAGAT				
CCTAAAGGCC			CCTAAAGGCC				
TGTACCCGTTA			TGTACCCGTTA				
CCTAGCCAGTT			CCTAGCCAGTT				
GGCATTAAAC			GGCATTAAAC				
GTATACGGTAC			GTATACGGTAC				
CTAGGCATGTA			CTAGGCATGTA				
CGTAATCGTAG			CGTAATCGTAG				
CCTTAGCAATC			CCTTAGCAATC				
TCCAGTCCC			TCCAGTCCC				

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		GCTTTTCATTC				
		TGACTGCAAC				
		GGGCAATATG				
		тстствтвтв				
		ATTAAAAAAAAG				
		AGTGTCTGATA				
		GCAGCTTCTG				
		AACTGGTTACC				
		TGCCGTGAGT				
		AAATTAAAATT			C4 = "4	□ al
		TTATTGACTTA			Start	End
1		GGTCACTAAAT				Positio
		ACTTTAACCAA			n	n
		TATAGGCATAG			1	350
	10080	CGCACAGACA		350 <u>2</u>	854	1203
		GATAAAAATTA				
		CAGAGTACAC			1295	1644
		AACATCCATGA			2705	3054
		AACGCATTAGC			4337	4686
		ACCACCATTAC				
		CACCACCATCA			6359	6708
		CCATTACCACA			7574	7923
		GGTAACGGTG			8752	9101
		CGGGCTGACG			0732	9101
		CGTACAGGAA				
		ACACAGAAAAA				
		AGCCCGCACC				
		TGACAGTGCG				
		GGCTTTTTTTT				
		CGACCAAAGG				
		TAACGAGGTAA				
		CAACCATGCG				
		AGTGTTGAAGT				

		GTGATTCATTC				
		GGGATGGTCT				
		GTGTGGATTAA				
		AAAAAGAGTGT				
		CTGATAGCAG				
		CTTCTGAACTG				
		GTTACCTGCC				
		GTGAGTAAATT				
		AAAATTTTATT				
		GACTTAGGTCA				
		CTAAATACTTT				
		AACCAATATAG				
		GCATAGCGCA				
		CAGACAGATAA				
		AAATTACAGAG			Start	End
		TACACAACATC			Positio	Positio
1	10080	CTCAAAGCCTA	2	352	n	n
		CCGGTGACAG			2226	2577
		TGCGGGCTTTT			4728	5079
		TTTTCGACCAA			1720	0070
		AGGTAACGAG				
		GTAACAACCAT				
		GCGAGTGTTG				
		AAGTCAGGAG				
		ATCCTAAAGGC				
		CTGTACCCGTT				
		ACCTAGCCAG				
		TTGGCATTAAA				
		CGTATACGGTA				
		CCTAGGCATG				
		TACGTAATCGT				
		AGCCTTAGCAA				
		TCTCCAGTCC				

SRGD Performance Metrics

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

Reads Count after Overlapping:			326		
Initial Dataset Size in (Base):			359763		
Dataset Sizet after Removing Duplication:			150869		
Dataset Size after Overlapping:		100358			
Overlapping Metri	cs				
Repeat Identification Time:			00h:00m	n:19s:000ms	
Overlapping Time:		00h:05m	n:12s:000ms		
Reads Alignment Time:		00h:00m:28s:000ms			
Total Hybrid Assembly Time:		00h:05m:40s:000ms			
Repeat Annotation Time:		00h:22m:03s:000ms			
Overlapping Length	O(N)2 Time Complexity	Hit Index Count		Overlapping Matched Count	RI
297	10000	14		2	0
294	9604	27		3	0
290	9025	16		2	0
280	8649	16		2	0
276	8281	72		40	0
269	2601	8		2	0
251	2401	4		2	0
237	2209	4		1	0
226	2116	15		11	0
215	1225	4		1	0