Assembly Report

Experiment Details

ExperimentID:	Experiment 68
Sequencing Coverage:	23
Number of Partitions:	3
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	67

Reads Dataset Details

IVEAUS DAIASEI DEIAIIS	
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	397

Assembly Details

Number of Contigs:	22
Contig N50:	976
Contig N90:	798
Number of Scaffold	2
Scaffold N50:	4171
Scaffold N90:	4171
Mis-assembly Count:	0
TotalAssembly Size:	10433

Repeat Details

Total Reads Count(Non-Repeat) :	170
Total Reads Count(Repeat):	218
Retetitve Read Count based on (Partitions Identifier):	216
Retetitve Read Count (Entire Read Frequency Identifier):	4
Retetitve Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	2952
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			8750		
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions
1	6262	CGGTCGAAAA ACTGCTGGCA GTGGGGCATT ACCTCGAATCT ACCGTCGATAT TGCTGAGTCC ACCCGCCGTA TTGCGGCAAG TCGTATTCCGG CTGATCACATG GTGCTGATGG CAGGTTTCACC GCCGGTAATG AAAAAGGCGA ACTGGTGGTG CTTGGACGCA ACGGTTCCGA CTACTCTGCTG CGGTGCTGGC TGCCTGTTTAC GCGCCGATTG TGCGAGATTT GGACGGACGT TGCGCGATTT GGACGCATTT GGACGCATTT GGACGCATTT GGACGCATTT GGACGCATTT GGACGCATTT GGACGCATTT GGACGCATTT GGACGCATTT TGCGAGATTT GGACGGATC TTGCGAGATTT TGCGAGATTT TGCGAGTTGTT TGCGAGTTGTT TGCGAGTTGTT TGCGAGTTGTT TGAGTCCCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT AGGTCAGGCC	5	350	Start End Positio n n 1756 2105 3561 3910 3964 4313 5117 5466 5910 6259

			1			1
		GATTCATTCGG				
		GATGGTCTGT				
		GTGGATTAAAA				
		AAAGAGTGTCT				
		GATAGCAGCTT				
		CTGAACTGGTT				
		ACCTGCCGTG				
		AGTAAATTAAA				
		ATTTTATTGAC				
		TTAGGTCACTA				
		AATACTTTAAC				
		CAATATAGGCA			01 - 1	
		TAGCGCACAG			Start	End
		ACAGATAAAAA			Positio	Positio
		TTACAGAGTAC			n	n
		ACAACATCCTC			409	758
1	6262	AAAGCCTACC	5	350	2228	2577
		GGTGACAGTG				
		CGGGCTTTTTT			3182	3531
		TTCGACCAAAG			4730	5079
		GTAACGAGGT			5529	5878
		AACAACCATGC			0029	3070
		GAGTGTTGAA				
		GTCAGGAGAT				
		CCTAAAGGCC				
		TGTACCCGTTA				
		CCTAGCCAGTT				
		GGCATTAAAC				
		GTATACGGTAC				
		CTAGGCATGTA				
		CGTAATCGTAG				
		CCTTAGCAATC				
		TCCAGTCC				

			1	-		
		GCTTTTCATTC				
		TGACTGCAAC				
		GGGCAATATG				
		тстстстстс				
		ATTAAAAAAAAG				
		AGTGTCTGATA				
		GCAGCTTCTG				
		AACTGGTTACC				
		TGCCGTGAGT				
		AAATTAAAATT				
		TTATTGACTTA				
		GGTCACTAAAT			<u> </u>	
		ACTTTAACCAA			Start	End
		TATAGGCATAG			Positio	Positio
		CGCACAGACA			n	n
		GATAAAAATTA			1	350
1	6262	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				

	T	1				
		CGGTCGAAAA				
		ACTGCTGGCA				
		GTGGGGCATT				
		ACCTCGAATCT				
		ACCGTCGATAT				
		TGCTGAGTCC				
		ACCCGCCGTA				
		TTGCGGCAAG				
		TCGTATTCCGG				
		CTGATCACATG				
		GTGCTGATGG				
		CAGGTTTCACC				
		GCCGGTAATG				
		AAAAAGGCGA			Start	End
		ACTGGTGGTG			Positio	Positio
		CTTGGACGCA			n	n
5910	10080	ACGGTTCCGA	1	350	5910	6259
3910	10000	CTACTCTGCTG	- 550	7138	7487	
		СССТССТССС				
		TGCCTGTTTAC			8386	8735
		GCGCCGATTG			9149	9498
		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			Start	End
		TTACAGAGTAC			Positio	Positio
		ACAACATCCTC			n	n
5910	10080	AAAGCCTACC	3	350	6730	7079
		GGTGACAGTG			004.4	
		CGGGCTTTTTT			8014	8363
		TTCGACCAAAG			9552	9901
		GTAACGAGGT				
		AACAACCATGC				
		GAGTGTTGAA				
		GTCAGGAGAT				
		CCTAAAGGCC				
		TGTACCCGTTA				
		CCTAGCCAGTT				
		GGCATTAAAC				
		GTATACGGTAC				
		CTAGGCATGTA				
		CGTAATCGTAG				
		CCTTAGCAATC				
		TCCAGTCC				

			1			ı
		GCTTTTCATTC				
		TGACTGCAAC				
		GGGCAATATG				
		тстстдтдтдд				
		ATTAAAAAAAAG				
		AGTGTCTGATA				
		GCAGCTTCTG				
		AACTGGTTACC				
		TGCCGTGAGT				
		AAATTAAAATT				
		TTATTGACTTA				
		GGTCACTAAAT				
		ACTTTAACCAA				
		TATAGGCATAG			Start	End
		CGCACAGACA			Positio	Positio
		GATAAAAATTA			n	n
5910	10080	CAGAGTACAC	3	350	6359	6708
		AACATCCATGA				
		AACGCATTAGC			7574	7923
		ACCACCATTAC			8752	9101
		CACCACCATCA				
		CCATTACCACA				
		GGTAACGGTG				
		CGGGCTGACG				
		CGTACAGGAA				
		ACACAGAAAAA				
		AGCCCGCACC				
		TGACAGTGCG				
		GGCTTTTTTTT				
		CGACCAAAGG				
		TAACGAGGTAA				
		CAACCATGCG				
		AGTGTTGAAGT				

SRGD Performance Metrics

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

Reads Count after Overlapping:			283				
Initial Dataset Size in (Base):			241272				
Dataset Sizet after Removing Duplication:			99165				
Dataset Size after Overlapping:			58983				
Overlapping Metrics							
Repeat Identification Time:			00h:00m:10s:000ms				
Overlapping Time:			00h:03m:46s:000ms				
Reads Alignment Time:			00h:00m:53s:000ms				
Total Hybrid Assembly Time:			00h:04m:39s:000ms				
Repeat Annotation Time:			00h:12m:21s:000ms				
Overlapping Length	O(N)2 Time Complexity	Hit Index Count		Overlapping Matched Count	RI		
200	28900	63		7	0		
199	26569	61		7	0		
198	24336	58		4	0		
197	23104	46		6	0		
195	21316	33		1	0		
194	21025	51		5	0		
190	19600	40		4	0		
187	18496	29		1	0		
183	18225	41		2	0		
182	17689	28		1	0		
179	17424	45		1	0		
176	17161	133		57	0		

165	5476	12	1	0
162	5329	9	1	0
156	5184	9	1	0
151	5041	10	4	0
140	4489	8	2	0