

# Assembly Report

## Experiment Details

ExperimentID:	Experiment 42
Sequencing Coverage:	23
Number of Partitions:	2
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	101

## Reads 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	369

## Assembly Details

Number of Contigs:	28
Contig N50:	1015
Contig N90:	876
Number of Scaffold	3
Scaffold N50:	1990
Scaffold N90:	1990
Mis-assembly Count:	0
TotalAssembly Size:	10870

## Repeat Details

Total Reads Count(Non-Repeat) :	395
Total Reads Count(Repeat):	6
Retetitive Read Count based on (Partitions Identifier):	0
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	9
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			3000			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	1990	GCTTTTCATTC	3	250		
		TGACTGCAAC				
		GGGCAATATG				
		TCTCTGTGTGG				
		ATTAAAAAAG				
		AGTGTCTGATA				
		GCAGCTTCTG				
		AACTGGTTACC				
		TGCCGTGAGT				
		AAATTAAAATT				
		TTATTGACTTA				
		GGTCACTAAAT				
		ACTTTAACCBA				
		TATAGGCATAG				
		CGCACAGACA				
		GATAAAAATTA				
		CAGAGTACAC				
		AACATCCATGA				
		AACGCATTAGC				
		ACCACCATTAC				
CACCACCATCA						
CCATTACCACA						
GGTAACGGTG						
CGGG						

1576	9700	CGGTCGAAAA ACTGCTGGCA GTGGGGCATT ACCTCGAATCT ACCGTCGATAT TGCTGAGTCC ACCCGCCGTA TTGCGGCAAG TCGTATTCCGG CTGATCACATG GTGCTGATGG CAGGTTTCACC GCCGGTAATG AAAAAGGCGA ACTGGTGGTG CTTGGACGCA ACGGTTCCGA CTACTCTGCTG CGGTGCTGGC TGCCTGTTTAC GCGCCGATTG TTGCGAGATTT GGACGGACGT TGACGGGGTC TA	3	250		
					Start Positio n	End Positio n
					3630	3879
					5894	6143
					8864	9113

1576	9700	GATTCATTTCGG	4	250											
		GATGGTCTGT													
		GTGGATTAAAA													
		AAAGAGTGTCT													
		GATAGCAGCTT													
		CTGAACTGGTT													
		ACCTGCCGTG													
		AGTAAATTA													
		ATTTTATTGAC													
		TTAGGTCAC													
		AATACTTTAAC													
		CAATATAGGCA													
		TAGCGCACAG													
		ACAGATAAAAA													
		TTACAGAGTAC													
		ACAACATCCTC													
		AAAGCCTACC													
		GGTGACAGTG													
		CGGGCTTTTTT													
		TTCGACCAAAG													
GTAACGAGGT															
AACAACCATGC															
GAGTGTTGAA															
GTCA															
					<table><tr><td>Start Positio n</td><td>End Positio n</td></tr><tr><td>2885</td><td>3134</td></tr><tr><td>4257</td><td>4506</td></tr><tr><td>6796</td><td>7045</td></tr><tr><td>9434</td><td>9683</td></tr></table>	Start Positio n	End Positio n	2885	3134	4257	4506	6796	7045	9434	9683
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2885	3134														
4257	4506														
6796	7045														
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1576	9700	GCTTTTCATTC	2	250							
		TGACTGCAAC									
		GGGCAATATG									
		TCTCTGTGTGG									
		ATTAAAAAAG									
		AGTGTCTGATA									
		GCAGCTTCTG									
		AACTGGTTACC									
		TGCCGTGAGT									
		AAATTAAAATT									
		TTATTGACTTA									
		GGTCACTAAAT									
		ACTTTAACCAA									
		TATAGGCATAG									
		CGCACAGACA									
		GATAAAAATTA									
		CAGAGTACAC									
		AACATCCATGA									
		AACGCATTAGC									
		ACCACCATTAC									
CACCACCATCA											
CCATTACCACA											
GGTAACGGTG											
CGGG											
					<table><tr><td>Start Positio n</td><td>End Positio n</td></tr><tr><td>1738</td><td>1987</td></tr><tr><td>8344</td><td>8593</td></tr></table>	Start Positio n	End Positio n	1738	1987	8344	8593
Start Positio n	End Positio n										
1738	1987										
8344	8593										

SRGD Performance Metrics

Initial Reads Count:	1212
Reads Count after Removing Duplication:	401
Reads Count after Overlapping:	192
Initial Dataset Size in (Base):	241272
Dataset Siset after Removing Duplication:	101778
Dataset Size after Overlapping:	43558

Overlapping Metrics

Repeat Identification Time:		00h:00m:07s:000ms		
Overlapping Time:		00h:02m:52s:000ms		
Reads Alignment Time:		00h:00m:14s:000ms		
Total Hybrid Assembly Time:		00h:03m:06s:000ms		
Repeat Annotation Time:		00h:00m:01s:000ms		
Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
200	156025	61	2	0
199	154449	73	3	0
197	152100	64	3	0
196	149769	78	4	0
195	146689	75	2	0
194	145161	90	1	0
192	144400	77	1	0
190	143641	91	4	0
189	140625	81	1	0
187	139876	91	1	0
180	139129	58	1	0
177	138384	47	1	0
176	137641	403	176	0
167	38025	16	1	0
165	37636	25	2	0
162	36864	23	1	0
158	36481	14	1	0
156	36100	18	1	0
151	35721	15	3	0