

# Assembly Report

## Experiment Details

ExperimentID:	Experiment 63
Sequencing Coverage:	35
Number of Partitions:	3
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	101

## Reads Dataset Details

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	512

## Assembly Details

Number of Contigs:	12
Contig N50:	1826
Contig N90:	1330
Number of Scaffold	2
Scaffold N50:	2389
Scaffold N90:	2389
Mis-assembly Count:	0
TotalAssembly Size:	10594

## Repeat Details

Total Reads Count(Non-Repeat) :	325
Total Reads Count(Repeat):	70
Retetitive Read Count based on (Partitions Identifier):	68
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	238
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			4200											
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions									
1	2389	GCTTTTCATTC	3	350	<table><tr><td>Start Position</td><td>End Position</td></tr><tr><td>1</td><td>350</td></tr><tr><td>799</td><td>1148</td></tr><tr><td>2039</td><td>2388</td></tr></table>		Start Position	End Position	1	350	799	1148	2039	2388
		Start Position					End Position							
		1					350							
		799					1148							
		2039			2388									
		TGACTGCAAC												
		GGGCAATATG												
		TCTCTGTGTGG												
		ATTAAAAAAG												
		AGTGTCTGATA												
		GCAGCTTCTG												
		AACTGGTTACC												
		TGCCGTGAGT												
		AAATTAAAATT												
		TTATTGACTTA												
		GGTCACTAAAT												
		ACTTTAACCAA												
		TATAGGCATAG												
		CGCACAGACA												
		GATAAAAATTA												
		CAGAGTACAC												
		AACATCCATGA												
		AACGCATTAGC												
		ACCACCATTAC												
		CACCACCATCA												
		CCATTACCACA												
		GGTAACGGTG												
		CGGGCTGACG												
		CGTACAGGAA												
		ACACAGAAAAA												
AGCCCGCACCC														
TGACAGTGCG														
GGCTTTTTTTTT														
CGACCAAAGG														
TAACGAGGTAA														
CAACCATGCG														
AGTGTTGAAGT														

1876	10080	CGGTCGAAAA	3	350	<table><tr><th>Start Positio n</th><th>End Positio n</th></tr><tr><td>4127</td><td>4476</td></tr><tr><td>6570</td><td>6919</td></tr><tr><td>8665</td><td>9014</td></tr></table>	Start Positio n	End Positio n	4127	4476	6570	6919	8665	9014
		Start Positio n				End Positio n							
		4127				4476							
		6570				6919							
		8665				9014							
		ACTGCTGGCA											
		GTGGGGCATT											
		ACCTCGAATCT											
		ACCGTCGATAT											
		TGCTGAGTCC											
		ACCCGCCGTA											
		TTGCGGCAAG											
		TCGTATTCCGG											
		CTGATCACATG											
		GTGCTGATGG											
		CAGGTTTCACC											
		GCCGGTAATG											
		AAAAAGGCGA											
		ACTGGTGGTG											
		CTTGGACGCA											
		ACGGTTCCGA											
		CTACTCTGCTG											
		CGGTGCTGGC											
		TGCCTGTTTAC											
		GCGCCGATTG											
		TTGCGAGATTT											
GGACGGACGT													
TGACGGGGTC													
TATACCTGCGA													
CCCGCGTCAG													
GTGCCCGATG													
CGAGGTTGTT													
GAAGTCGATG													
TCCTACCAGG													
AAGCGATGGA													
GCTTTCCTACT													
TCGGCGCTCT													
AGGTCAGGCC													

1876	10080	GATTCATTTCGG	4	350	<table><tr><th>Start Positio n</th><th>End Positio n</th></tr><tr><td>3285</td><td>3634</td></tr><tr><td>4858</td><td>5207</td></tr><tr><td>7202</td><td>7551</td></tr><tr><td>9332</td><td>9681</td></tr></table>	Start Positio n	End Positio n	3285	3634	4858	5207	7202	7551	9332	9681
		Start Positio n				End Positio n									
		3285				3634									
		4858				5207									
		7202				7551									
		9332				9681									
		GATGGTCTGT													
		GTGGATTAAAA													
		AAAGAGTGTCT													
		GATAGCAGCTT													
		CTGAACTGGTT													
		ACCTGCCGTG													
		AGTAAATTTAA													
		ATTTTATTGAC													
		TTAGGTCACTA													
		AATACTTTAAC													
		CAATATAGGCA													
		TAGCGCACAG													
		ACAGATAAAAA													
		TTACAGAGTAC													
ACAACATCCTC															
AAAGCCTACC															
GGTGACAGTG															
CGGGCTTTTTT															
TTCGACCAAAG															
GTAACGAGGT															
AACAACCATGC															
GAGTGTTGAA															
GTCAGGAGAT															
CCTAAAGGCC															
TGTACCCGTTA															
CCTAGCCAGTT															
GGCATTTAAC															
GTATACGGTAC															
CTAGGCATGTA															
CGTAATCGTAG															
CCTTAGCAATC															
TCCAGTCC															

1876	10080	GCTTTTCATTC	2	350	<table><tr><td>Start Position</td><td>End Position</td></tr><tr><td>2039</td><td>2388</td></tr><tr><td>8043</td><td>8392</td></tr></table>	Start Position	End Position	2039	2388	8043	8392
		Start Position				End Position					
		2039				2388					
		8043				8392					
		TGACTGCAAC									
		GGGCAATATG									
		TCTCTGTGTGG									
		ATTAAAAAAG									
		AGTGTCTGATA									
		GCAGCTTCTG									
		AACTGGTTACC									
		TGCCGTGAGT									
		AAATTAAAATT									
		TTATTGACTTA									
		GGTCACTAAAT									
		ACTTTAACCAA									
		TATAGGCATAG									
		CGCACAGACA									
		GATAAAAATTA									
		CAGAGTACAC									
		AACATCCATGA									
		AACGCATTAGC									
		ACCACCATTAC									
		CACCACCATCA									
		CCATTACCACA									
		GGTAACGGTG									
		CGGGCTGACG									
		CGTACAGGAA									
		ACACAGAAAAA									
		AGCCCGCACCC									
		TGACAGTGCG									
		GGCTTTTTTTTT									
CGACCAAAGG											
TAACGAGGTAA											
CAACCATGCG											
AGTGTTGAAGT											

### SRGD Performance Metrics

Initial Reads Count:	1203
Reads Count after Removing Duplication:	395

Reads Count after Overlapping:	168
Initial Dataset Size in (Base):	359763
Dataset Siset after Removing Duplication:	151772
Dataset Size after Overlapping:	59246

Overlapping Metrics

Repeat Identification Time:	00h:00m:09s:000ms
Overlapping Time:	00h:05m:46s:000ms
Reads Alignment Time:	00h:00m:19s:000ms
Total Hybrid Assembly Time:	00h:06m:05s:000ms
Repeat Annotation Time:	00h:00m:19s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
299	105625	62	1	0
297	104976	45	2	0
296	103684	61	2	0
295	102400	66	1	0
288	101761	62	1	0
286	101124	54	1	0
281	100489	53	1	0
278	99856	47	1	0
276	99225	331	149	0
271	27556	10	1	0
270	27225	21	1	0
251	26896	10	6	0

231	24964	15	1	0
226	24649	140	59	0