

# Assembly Report

## Experiment Details

ExperimentID:	Experiment 77
Sequencing Coverage:	35
Number of Partitions:	2
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	151

## 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	638

## Assembly Details

Number of Contigs:	13
Contig N50:	1951
Contig N90:	1696
Number of Scaffold	3
Scaffold N50:	4355
Scaffold N90:	3562
Mis-assembly Count:	0
TotalAssembly Size:	12344

## Repeat Details

Total Reads Count(Non-Repeat) :	338
Total Reads Count(Repeat):	54
Retetitive Read Count based on (Partitions Identifier):	48
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	119
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			10150			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	4427	CGGTCGAAAA	3	350		
		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				
		GTGCCCCGATG				
		CGAGGTTGTT				
		GAAGTCGATG				
		TCCTACCAGG				
		AAGCGATGGA				
		GCTTTCCTACT				
		TCGGCGCTCT				
		AGGTCAGGCC				
					1756	2105
					3561	3910
					3964	4313

1	4427	GATTCATTCGG	3	350	<table><tr><th>Start Position</th><th>End Position</th></tr><tr><td>409</td><td>758</td></tr><tr><td>2228</td><td>2577</td></tr><tr><td>3182</td><td>3531</td></tr></table>	Start Position	End Position	409	758	2228	2577	3182	3531
		Start Position				End Position							
		409				758							
		2228				2577							
		3182				3531							
		GATGGTCTGT											
		GTGGATTAAAA											
		AAAGAGTGTCT											
		GATAGCAGCTT											
		CTGAACTGGTT											
		ACCTGCCGTG											
		AGTAAATTAAA											
		ATTTTATTGAC											
		TTAGGTCACTA											
		AATACTTTAAC											
		CAATATAGGCA											
TAGCGCACAG													
ACAGATAAAAA													
TTACAGAGTAC													
ACAACATCCTC													
AAAGCCTACC													
GGTGACAGTG													
CGGGCTTTTTT													
TTCGACCAAAG													
GTAACGAGGT													
AACAACCATGC													
GAGTGTTGAA													
GTCAGGAGAT													
CCTAAAGGCC													
TGTACCCGTTA													
CCTAGCCAGTT													
GGCATTAAAC													
GTATACGGTAC													
CTAGGCATGTA													
CGTAATCGTAG													
CCTTAGCAATC													
TCCAGTCC													

1	4427	GCTTTTCATTC	4	350	<table><tr><th>Start Positio n</th><th>End Positio n</th></tr><tr><td>1</td><td>350</td></tr><tr><td>854</td><td>1203</td></tr><tr><td>1295</td><td>1644</td></tr><tr><td>2705</td><td>3054</td></tr></table>	Start Positio n	End Positio n	1	350	854	1203	1295	1644	2705	3054
		Start Positio n				End Positio n									
		1				350									
		854				1203									
		1295				1644									
		2705				3054									
		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															

3964	7525	CGGTCGAAAA	4	350	<table><tr><th>Start Position</th><th>End Position</th></tr><tr><td>3964</td><td>4313</td></tr><tr><td>5117</td><td>5466</td></tr><tr><td>5910</td><td>6259</td></tr><tr><td>7138</td><td>7487</td></tr></table>	Start Position	End Position	3964	4313	5117	5466	5910	6259	7138	7487
		Start Position				End Position									
		3964				4313									
		5117				5466									
		5910				6259									
		7138			7487										
		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															
GTGCCCCGATG															
CGAGGTTGTT															
GAAGTCGATG															
TCCTACCAGG															
AAGCGATGGA															
GCTTTCCTACT															
TCGGCGCTCT															
AGGTCAGGCC															







5726	10080	CGGTCGAAAA	4	350	<table><tr><th>Start Position</th><th>End Position</th></tr><tr><td>5910</td><td>6259</td></tr><tr><td>7138</td><td>7487</td></tr><tr><td>8386</td><td>8735</td></tr><tr><td>9149</td><td>9498</td></tr></table>	Start Position	End Position	5910	6259	7138	7487	8386	8735	9149	9498
		Start Position				End Position									
		5910				6259									
		7138				7487									
		8386				8735									
		9149				9498									
		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													
		GTGCCCCGATG													
		CGAGGTTGTT													
		GAAGTCGATG													
		TCCTACCAGG													
AAGCGATGGA															
GCTTTCCTACT															
TCGGCGCTCT															
AGGTCAGGCC															



5726	10080	GCTTTTCATTC	3	350	<table><tr><th>Start Positio n</th><th>End Positio n</th></tr><tr><td>6359</td><td>6708</td></tr><tr><td>7574</td><td>7923</td></tr><tr><td>8752</td><td>9101</td></tr></table>	Start Positio n	End Positio n	6359	6708	7574	7923	8752	9101
		Start Positio n				End Positio n							
		6359				6708							
		7574				7923							
		8752				9101							
		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:	392

Reads Count after Overlapping:	136
Initial Dataset Size in (Base):	359763
Dataset Siset after Removing Duplication:	150869
Dataset Size after Overlapping:	49952

Overlapping Metrics

Repeat Identification Time:	00h:00m:08s:000ms
Overlapping Time:	00h:05m:29s:000ms
Reads Alignment Time:	00h:00m:16s:000ms
Total Hybrid Assembly Time:	00h:05m:45s:000ms
Repeat Annotation Time:	00h:00m:17s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
300	114244	169	10	0
299	107584	156	6	0
298	103684	161	6	0
297	99856	147	8	0
296	94864	128	2	0
294	93636	141	3	0
293	91809	95	2	0
291	90601	105	1	0
288	90000	99	1	0
287	89401	120	1	0
286	88804	105	1	0
283	88209	137	1	0

281	87616	117	1	0
280	87025	131	1	0
278	86436	118	1	0
276	85849	349	135	0
274	24964	38	1	0
271	24649	24	1	0
270	24336	24	1	0
269	24025	35	2	0
251	23409	36	5	0
233	21904	35	1	0
227	21609	30	1	0
226	21316	114	58	0
225	7744	12	1	0
223	7569	12	1	0
220	7396	7	1	0
219	7225	9	1	0
214	7056	8	1	0
211	6889	10	1	0