## **Assembly Report**

**Experiment Details** 

ExperimentID:	Experiment 65
Sequencing Coverage:	35
Number of Partitions:	5
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	61

**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	633

Assembly Details

Number of Contigs:	15
Contig N50:	1601
Contig N90:	1476
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

Repeat Details

Total Reads Count(Non-Repeat) :	253
Total Reads Count(Repeat):	142
Retetitve Read Count based on (Partitions Identifier):	141
Retetitve Read Count (Entire Read Frequency Identifier):	3
Retetitve Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	1246
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)		4200					
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Position	Positions	
1	10080	CGGTCGAAAA ACTGCTGGCA GTGGGGCATT ACCTCGAATCT ACCGTCGATAT TGCTGAGTCC ACCCGCCGTA TTGCGGCAAG TCGTATTCCGG CTGATCACATG GTGCTGATGG CAGGTTTCACC GCCGGTAATG AAAAAGGCGA ACTGGTGGTG CTTGGACGCA ACTGCTGGTG CTGCTGTTAC GCGCGATTTAC GCGCCGATTT GGACGCA TTGCGAGATTT GGACGCA CTACTCTGCTG CGGTGCTGGC TGCCTGTTTAC GCGCCGATTT GGACGCATTT GGACGCATTT GGACGCATTT GGACGCATTT GGACGCATTT GGACGCATTT TGCGAGATTT TGCGAGATTT TGCGAGATTT TGCGAGATTT TGCGAGTTCTAC TTCCTACTACT TCGAGGTTGTT TCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT AGGTCAGGCC	4	350	Start Positio n 1376 4127 6570 8665	End Positio n 1725 4476 6919 9014	

	1	
GATTCATTCGG		
GATGGTCTGT		
GTGGATTAAAA		
AAAGAGTGTCT		
GATAGCAGCTT		
CTGAACTGGTT		
ACCTGCCGTG		
AGTAAATTAAA		
ATTTATTGAC		
TTAGGTCACTA		
AATACTTTAAC		
CAATATAGGCA		
TAGCGCACAG		Start End
ACAGATAAAAA		Positio Positio
TTACAGAGTAC		n n
ACAACATCCTC		
1 10080 AAAGCCTACC 4	350	3285 3634
GGTGACAGTG		4858 5207
CGGGCTTTTT		7202 7551
TTCGACCAAAG		
GTAACGAGGT		9332 9681
AACAACCATGC		
GAGTGTTGAA		
GTCAGGAGAT		
CCTAAAGGCC		
TGTACCCGTTA		
CCTAGCCAGTT		
GGCATTAAAC		
GTATACGGTAC		
CTAGGCATGTA		
CGTAATCGTAG		
CCTTAGCAATC		
TCCAGTCC		

GCTTTTCATTC TGACTGCAAC GGGCAATATG TCTCTGTGTGG ATTAAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA  1 10080 CAGAGTACAC AACATCCATGA AACGCCATTAC CACCACCATTAC CACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGCTGACG CGTACAGGAA ACACCAGAAAA ACGCCACCC TGACAGAAAA AACGCCACCC TGACAGCAC GGCTTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG AGTGTTGAAGT			<u> </u>	i		
GGGCAATATG   TCTCTGTGTGG   ATTAAAAAAAG   AGTGTCTGATA   GCAGCTTCTG   AACTGGTTACC   TGCCGTGAGT   AAATTAAAATT   TTATTGACTTA   GGTCACTAAAT   ACTTTAACCAA   TATAGGCATAG   CGCACAGACA   GATAAAAATTA   ACTTTAACCAA   TATAGGCATAG   CGCACAGACA   GATAAAAATTA   ACATCCATGA   AACATCCATGA   AACACCATTAC   CACCACCATTAC   CACCACCATCA   CCATTACCACA   GGTAACGGTG   CGGGCTGACG   CGGCTGACAG   GGCTTTTTTT   CGACCAAAGG   TAACAGGTAA   CAACCATGCG   CGACCAAGG   CGACCAAGGC   CGACCAAGGGTAA   CAACCATGCG   CGACCAAGGGTAA   CAACCATGCG   CGACCAAAGG   CGACCAAGGGTAA   CAACCATGCG   CGACCAAAGG   CAACCATGCG   CGACCAAAGG   CAACCATGCG   CGACCAAAGG   CAACCATGCG   CGACCAAAGG   CAACCATGCG   CGACCAAAGG   CAACCATGCG   CA			GCTTTTCATTC			
TCTCTGTGTGG ATTAAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA  1 10080 CAGAGTACAC AACATCCATGA AACACCATTAC CACCACCATCA CCACTACACA CCATTACCACA GGTAACGGTG CGGCTGACG CGGCTGACG CGGCTGACG CGGCTGACG CGTACAGCAC CCATTACCACA GGTAACGGTG CGGCCTGCC CGGCCACC CGGCCACC TGACAGGAA AACACCATGCG GGCTTTTTTT CCGCCCAAAGG TAACGAGGTAA CAACCATGCG			TGACTGCAAC			
ATTAAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA  1 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGAAA ACACAGAAAAA ACACCAGTG CGGCTGACG CGTACAGAA ACACAGAAAAA ACACCACC TGACAGGAA ACACCACCC TGACAGTCA CGACTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG			GGGCAATATG			
AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA  1 10080 CAGAGTACAC 4 AACATCCATGA AACGCATTAGC ACCACTATAC CACCACTTAC CACCACTACA CCATTACCACA GGTACAGAA ACGCATTACC CACCACCATCA CCATTACCACA GGTACAGAA ACACAGAAAAA ACCCACCAC GGTACAGGAA ACACAGAAAAA ACCCCCCC TGACAGGAC GGCTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG			тстстбтбтбб			
GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA  1 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CCACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACCAGGAA ACACCAGCAC GGTAACGGTG CGGCTGACG CGTACAGGAA ACCACGACAC GGTACAGGAA ACACCAGCACC TGACAGGAA ACACCAGCACC TGACAGGAAAA ACCCGCACC TGACAGGAAAA CAACCATGCG TAACGAGGTAA CAACCATGCG			ATTAAAAAAAG			
AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA  1 10080 CAGAGTACAC AACATCCATGA AACGCATTAC CACCACCATTAC CACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACCAGCAC GGTAACGGTG CGGCTGACG CGTACAGGAA ACACCAGCAC GGTACGGAC GGTACGGAC CCATTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			AGTGTCTGATA			
TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA  1 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCACTAC CCACTACAC CCACTACAC CCATTACCACA GGTAACGATA CCAGTACAC CCATTACCACA GGTAACGGTG CGGCTGACG CGGCTGACG CGTACAGGAA ACCCCGCACC TGACAGGAA ACCCCGCACC TGACAGGAA ACCCCGCACC TGACAGGAA CACCCAAAAGG TAACGAGTAA CAACCATGCG			GCAGCTTCTG			
AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA  1 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CCACCACCACA CCATTACCACA GGTAACGGTG CGGGCTGACG CGGCTACAGGAA ACACCAGGAA ACACCAGAAAAA AGCCCGCACC TGACAGGTAA CAACCATGCG			AACTGGTTACC			
TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA  1 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CCACCACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACCAGGAA ACACCACCC TGACAGGAA ACACCACCAC GGCTTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG			TGCCGTGAGT			
GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA  1 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGAC GGTAACGAC GGTACGC GGGCTGACG CGCACCACC TGACAGAAAAA AGCCCGCACC TGACAGTACC GGCTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG			AAATTAAAATT			
ACTITAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 1 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGCTGACG CGGCTGACG CGTACAGGAA ACACAGGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			TTATTGACTTA			
TATAGGCATAG CGCACAGACA GATAAAAATTA 1 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CCACCACCATCA CCATTACCACA GGTAACGGTG CGGCTGACAG ACACCAGAAAAA ACACCAGAAAAA ACACCAGAAAAA ACACCAGACAC GGTACAGGAC CGTACAGGAC CGTACAGGAC CGTACAGGAC CGTACAGGAC CGTACAGGAC CGACCACCAC CGGCTGACG CGGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			GGTCACTAAAT			
TATAGGCATAG CGCACAGACA GATAAAAATTA 1 10080 CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CCACCACCATCA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACCAGGAA ACACCACCAC GGTACAGGAA ACACCAGGAA ACACCAGGAA ACACCAGGAA ACACCAGGAA ACACCAGGAA ACACCAGGG CGTACAGGAA ACACCAGGAA ACACCAGGG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			ACTTTAACCAA		Start	End
1			TATAGGCATAG			
1			CGCACAGACA			
AACATCCATGA AACGCATTAGC ACCACCATTAC CCACCACCAC CCACTACCAC GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACCAGCAC GGTACAGGAA ACACCAGCAC GGTACAGGAA ACACCAGCAC GGTACAGGAA ACACCAGCAC TGACAGTGCG GGCTTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			GATAAAAATTA			
AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG	1	10080	CAGAGTACAC 4	350	1	350
ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			AACATCCATGA		799	1148
ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			AACGCATTAGC		2039	2388
CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			ACCACCATTAC			
GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			CACCACCATCA		8043	8392
CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			CCATTACCACA			
CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			GGTAACGGTG			
ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			CGGGCTGACG			
AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			CGTACAGGAA			
TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			ACACAGAAAAA			
GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			AGCCCGCACC			
CGACCAAAGG TAACGAGGTAA CAACCATGCG			TGACAGTGCG			
TAACGAGGTAA CAACCATGCG			GGCTTTTTTT			
CAACCATGCG			CGACCAAAGG			
			TAACGAGGTAA			
AGTGTTGAAGT			CAACCATGCG			
			AGTGTTGAAGT			

## SRGD Performance Metrics

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

Reads Count after Overlapping:			218		
Initial Dataset Size	in (Base):		359763		
Dataset Sizet after	Removing Duplication	n:	151772		
Dataset Size after 0	Overlapping:		72704		
Overlapping Metric	CS				
Repeat Identificatio			00h:00m	n:14s:000ms	
Overlapping Time:			00h:05m:36s:000ms		
Reads Alignment T	ime:		00h:00m:26s:000ms		
Total Hybrid Assembly Time:		00h:06m:02s:000ms			
Repeat Annotation	Time:		00h:01m:40s:000ms		
Overlapping Length	O(N)2 Time Complexity	Hit Index Count		Overlapping Matched Count	RI
297	64009	23		1	0
294	63504			1	0
283	63001 34			1	0
276	62500	255		118	0
251 17424 5			4	0	
226 16384 112			51	0	
219	5929	5		1	0