## **Assembly Report**

Experiment Details

ExperimentID:	Experiment 90
Sequencing Coverage:	27
Number of Partitions:	5
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	51

Reads Dataset Details

Iteaus Dataset Details	
Total Reads Count:	2200
Total Dataset Size in (Base):	549860
Valid Read Count:	2200
Rejected Read Count:	0
Maximum Read Length:	251
Minimum Read Length:	212

Reference Genome Details

Length of Reference Genome (Base):	20160
Number of K-mers:	19910
Length of K-mer	476

Assembly Details

Number of Contigs:	32
Contig N50:	1426
Contig N90:	1121
Number of Scaffold	2
Scaffold N50:	4085
Scaffold N90:	4085
Mis-assembly Count:	0
TotalAssembly Size:	20481

Repeat Details

Total Reads Count(Non-Repeat) :	422
Total Reads Count(Repeat):	365
Retetitve Read Count based on (Partitions Identifier):	365
Retetitve Read Count (Entire Read Frequency Identifier):	3
Retetitve Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	6683
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)		6650				
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Position	s
1	16396	CGGTCGAAAA ACTGCTGGCA GTGGGGCATT ACCTCGAATCT ACCGTCGATAT TGCTGAGTCC ACCCGCCGTA TTGCGGCAAG TCGTATTCCGG CTGATCACATG GTGCTGATGG CAGGTTTCACC GCCGGTAATG AAAAAGGCGA ACTGGTGGTG CTGCTGTTCCGA CTACTCTGCTG CGGTGCTGGC TGCCTGTTTAC GCGCCGATTG TGCGAGATTT GGACGCATTG TGCGAGATTT GGACGCATTG TTGCGAGATTT GGACGCATTG TTGCGAGATTT GGACGCATTG TTGCGAGATTT GGACGCATTG TTGCGAGATTT GGACGCATG TTGCGAGTC TTGCCGATG TTGCGAGATTT TGCGAGATTT TGCGAGATTT TGCGAGATTT TGCGAGATTT TGCGAGTTGTT TGCGAGTTGTT TGAGTCCGATG CCGCGTCAG GTGCCCGATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT AGGTCAGGCC	6	350	Start Positio n 2832 7245 8068 10761 11904 14881	End Positio n 3181 7594 8417 11110 12253 15230

GATTCATTCGG GATGGTCTGT GTGGATTAAAA AAAAGAGTGTCT GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATITITATIGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAACCTCTC GGTGACAGTG CGGGCTTTTT TTCGACCAAAG GTAACGAGGT AACACACTCGC GAGTGTTGAA GTCAGCAGGT CCGAGTTTGAA GTCAGCAGTT CCTAAAAGCC TTACCCGTTA CCTAAACGCTTA CCTAGCACATC CTAGCACATC GTATACGGTAC CTAGCACTTA CCTAGCACATC CTAGCACATC CTAGCACATC CTAGCACATC CTAGCCAGTT CCTAGCAATC CTAGCACATC CTAGCCAGTT CCTAGCAATC CTAGCAATCTAC CTAGCCAGTT CCTAGCCAGTT CCTAGCAATC CTAGCAATCTAC CCTAGCCAGTT CCTAGCAATC CCTAGCAATC CCTAGCAATC CCTAGCAATC CCTAGCAATC CCTAGCAATC CCTAGCAATC CCTAGCAATC CCTTAGCAATC TCCAGTTC TCCAGCTCC		1			-		
GTGGATTAAAA   AAAGAGTGTCT   GATAGCAGCTT   CTGAACTGGTT   ACCTGCCGTG   AGTAAATTAAA   ATTTTATTGAC   TTAGGTCACTA   AATACTTTAAC   CAATATAGGCA   TAGCGCACAG   ACAGATAAAAA   TTACAGAGTAC   ACAACATCCTC   GGTGACAGTG   CGGGCTTTTTT   TTCGACCAAAG   GTAACGAGT   AACAACATGC   GAGTGTTGAA   GTCAGGAGAT   GCCAGAGAG   GTAACGAGT   GGCATTAAC   GTATACGGTAC   GGTATACGGTAC   GGTATACGGTAC   GGTATACGGTAC   GGTATACGGTAC   GGTATACGGTAC   GGCATTAAAC   GTATACGGTAC   GTATACGGTAC   GCTAATCGGTAC   GCTAATCGTAG   GCTAATCGTAG   CCTAGCCAATC   GCTAATCGTAG   CCTTAGCAATC   CCTAGCAATC			GATTCATTCGG				
AAAGAGTGTCT GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AAATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAACCATCCC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGTA AACACCATGC GAGTGTTGAA GTCAGGAGAT GCAGAGAAC GTAACCATGC GAGTATTGAA GTCAGGAGAT CCTAAGGCC TGTACCCGTTA CCTAAGCACTT GGCATTAAC GTATACGGTAC CTAGCCATTA CCTAGCCAGTC CTAGCCAGTC CTAGCACATC CTAGCCATCA CCTAGCCATCA CCTAGCCATCA CCTAGCCATCA CCTAGCCACTC CTAGCCATCA CCTAGCCATCA CCTAGCCACTC CCTAGCACC CCTAGCCACTC CCTAGCACACC CCTAGCCACTC CCTAGCACACC CCTAGCCACTC CCTAGCCACTC CCTAGCCACTC CCTAGCCACTC CCTAGCCACTC CCTAGCACC CCTAGCACC CCTAGCCACTC CCTAGCACC CCTAGCCACTC CCTAGCACC CCTAGCCACTC CCTAGCACC CCTAGCCACTC CCTAGCACC CCTAGCCACTC CCTAGCACC CCTACCC CCTACC CCTACCC CCTACC CCTACC CCTACCC CCTACC CCTA			GATGGTCTGT				
GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTITATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACATCCTC GGTGACAGTG CGGCTTTTT TTCGACCAAAG GTAACGAGGT AACACCATGC GATGACGAGT GAGGGTT AACAACCATGC GAGTGTTGAA GTCACGAGTT GCACTAAAC GTAACCGTTA CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAC GTAATCGTAC CTAGGCATCT CTAGCCATC CTAGCCATC CTAGCCATC CTAGCCATC CTAGCATC			GTGGATTAAAA				
CTGAACTGGTT   ACCTGCCGTG   AGTAAATTAAA   ATTITTATTGAC   TTAGGTCACTA   AATACTTTAAC   CAATATAGGCA   TAGCGCACAG   ACAGATAAAAA   TTACAGAGTAC   ACAGACATCCTC   ACAGACCATGC   ACAGACCATT   ACCTAGCCAGTT   ACCTAGCCAGTT   ACCTAGCCAGTT   ACCTAGCCAGTT   ACCTAGCCAGTA   ACAGACCATGC   ACAGACATGC   ACAGACCATGC   ACAGACCATGC   ACAGACCATGC   ACAGACCATGC   ACAGACCATGC   ACAGACCATGC   ACAGACCATGC   ACAGACCATGC   ACAGACCATG			AAAGAGTGTCT				
ACCTGCCGTG AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTITTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAAGCCC CTAGCCAGTA CCTAGCCAGTC CTAGCCATCA  ACCTGCCAGTC AATACTTCAC ACAACTTCCT AACACCATGC GATGTTGAA GTCAGGAGAT CCTAAAGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGCCAGTC CTAGCCAGTC CTAGCCAGTC CCTAGCCAGTC CCTAGCCAGTC CCTAGCCAGTC CCTAGCCAGTC CCTAGCCAGTC CCTAGCCAGTC CCTAGCAATC CCTAGCAATC			GATAGCAGCTT				
AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC GGTGACAGTG CGGGCTTTTT TTCGACCAAAG GTAACGAGT AACAACATGC GAGTGTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAACGCTAC GGTATACGGTAC CTAGCCATGA GTATACGGTAC CTAGCCATTA CCTAGCCATTA CCTAGCCATTA CCTAGCCATTA CCTAGCCATTA CCTAGCATTA CGTAATCGTAG CCTTAGCAATC			CTGAACTGGTT				
ATTITATIGAC TTAGGTCACTA AATACTITAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACAGGGT AACAACCATGC GAGTGTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT CCTAGCCAGTC CTAGCCATCA CTAGCAATC CTAGCCATCA CTAGCAATC CTAGCCATC CTAGCATC CTAGCCATC CTAGCCATC CTAGCCATC CTAGCCATC CTAGCCATC CTAGCCATC CTAGCCATC CTTAGCAATC			ACCTGCCGTG				
TTAGGTCACTA   AATACTITAAC   CAATATAGGCA   TAGCGCACAG   ACAGATAAAAA   TTACAGAGTAC   ACAACATCCTC   ACAACATCCTC   GGTGACAGAG   GTAACCAGAG   GTAACCGTTA   CCTAAGAGGC   GGTAACGAGTC   GGCATTAAAC   GTATACGGTAC   GCTAATCGTAG   GCTATACCAATC   GCTAATCGTAG   GCTAATCGTAG   GCTATACCAATC   GCTAGCAATC   GCTAATCGTAG   GCTATACCAATC   GCTAGCAATC   GCTATACCAATC   GCTAATCGTAG   GCTATACCAATC   GCTAATCAATC   GCTAATCAATC   GCTAATCAATCAATCAATC   GCTAATCAATCAATCAATCAATCAATCAATCAATCAATCA			AGTAAATTAAA				
AATACTITAAC CAATATAGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGA CGTAATCGTAG CCTTAGCAATC			ATTTTATTGAC				
CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACATCCTC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAC GTATACGGTAC CTAGGCATGT CGTAATCGTAG CCTAGCAATC CCTAGGCATGT CCTAGCAGTC CTAGCCATC CCTAGCCATC CCTAGCCATC CCTAGCCATC			TTAGGTCACTA				
TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACACTCCTC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGCCATC CCTAGCCATC CCTAGCAATC CCTAGCAATC			AATACTTTAAC				
ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACATCCTC ACAACATCCTC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATCAGGTAC CTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGCAATC CTAGGCATGTA CCTAGCAATC			CAATATAGGCA			Start	End
TTACAGAGTAC ACAACATCCTC ACAACATCCTC ACAACATCCTC ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGCATGA CCTAGCATGA CCTAGCAATC			TAGCGCACAG			Positio	Positio
ACAACATCCTC  AAAGCCTACC  GGTGACAGTG  CGGGCTTTTTT  TTCGACCAAAG  GTAACGAGGT  AACAACCATGC  GAGTGTTGAA  GTCAGGAGAT  CCTAAAGGCC  TGTACCCGTTA  CCTAGCCAGTT  GGCATTAAAC  GTAATCGTAG  CTTAGCATTC  CTAGCATGTA  CCTAGCATGTA  CCTAGCAATCCTAG  CCTTAGCAATC			ACAGATAAAAA			n	n
ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCGGTTA CCTAGCCAGTT GGCATTAAAC GTATCGGTAC CTAGGCATGT GGCATTACGGTAC CTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGCAGTA CCTAGCAGTA CCTAGCAGTA CCTAGCAATC CTAGCAATC CTAGCAATC			TTACAGAGTAC			871	1220
Telegraphic   Section			ACAACATCCTC				
CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGCAATC CTAGGCATGTA CCTAGCAATC	1	16396	AAAGCCTACC	6	350	4144	4493
TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA CCTAGGCATGTA CCTAGCATGTA CCTAGCATGTA CCTAGCATGTA CCTAGCATGTA CCTAGCATGTA CCTAGCATGTA CCTAGCAATC			GGTGACAGTG			6008	6357
TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGCAATC			CGGGCTTTTTT			9464	0813
AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGCCAGTC CTAGGCATGTA CCTAGCATC			TTCGACCAAAG				
GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA CCTAGGCATGTA			GTAACGAGGT			11173	11522
GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA CGTAATCGTAG CCTTAGCAATC			AACAACCATGC			13704	14053
CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA CGTAATCGTAG CCTTAGCAATC			GAGTGTTGAA				
TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA CGTAATCGTAG CCTTAGCAATC			GTCAGGAGAT				
CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA CGTAATCGTAG CCTTAGCAATC			CCTAAAGGCC				
GGCATTAAAC GTATACGGTAC CTAGGCATGTA CGTAATCGTAG CCTTAGCAATC			TGTACCCGTTA				
GTATACGGTAC CTAGGCATGTA CGTAATCGTAG CCTTAGCAATC			CCTAGCCAGTT				
CTAGGCATGTA CGTAATCGTAG CCTTAGCAATC			GGCATTAAAC				
CGTAATCGTAG CCTTAGCAATC			GTATACGGTAC				
CCTTAGCAATC			CTAGGCATGTA				
			CGTAATCGTAG				
TCCAGTCC			CCTTAGCAATC				
			TCCAGTCC				

		GCTTTTCATTC				
		TGACTGCAAC				
		GGGCAATATG				
		TCTCTGTGTGG				
		ATTAAAAAAAAG				
		AGTGTCTGATA				
		GCAGCTTCTG				
		AACTGGTTACC				
		TGCCGTGAGT				
		AAATTAAAATT			_	
		TTATTGACTTA			Start	End
		GGTCACTAAAT			Positio	Positio
		ACTTTAACCAA			n	n
		TATAGGCATAG				
		CGCACAGACA			1	350
		GATAAAAATTA			1316	1665
1	16396	CAGAGTACAC	7	350	2021	2370
		AACATCCATGA				
		AACGCATTAGC			5041	5390
		ACCACCATTAC			8441	8790
		CACCACCATCA			13123	13472
		CCATTACCACA				
		GGTAACGGTG			15543	15892
		CGGGCTGACG				
		CGTACAGGAA				
		ACACAGAAAAA				
		AGCCCGCACC				
		TGACAGTGCG				
		GGCTTTTTTTT				
		CGACCAAAGG				
		TAACGAGGTAA				
		CAACCATGCG				
		AGTGTTGAAGT				

## SRGD Performance Metrics

Initial Reads Count:	2200
Reads Count after Removing Duplication:	787

Reads Count after Overlapping:			496			
Initial Dataset Size	in (Base):		549860			
Dataset Sizet after Removing Duplication:			224564			
Dataset Size after Overlapping:			136065			
Overlapping Metri	CS					
Repeat Identificatio			00h:00m	n:16s:000ms		
Overlapping Time:		00h:02m:54s:000ms				
Reads Alignment Time:		00h:00m:39s:000ms				
Total Hybrid Assembly Time:		00h:03m:33s:000ms				
Repeat Annotation	Time:		00h:12m:42s:000ms			
Overlapping Length	O(N)2 Time Complexity	Hit Index Count		Overlapping Matched Count	RI	
242	178084	80		1	0	
226	177241	444		199	0	
211	49284	16		1	0	
201	48841	19		8	0	
181	45369	17		1	0	
176	44944	181		81	0	