## **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** 

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
Retetitve Read Count based on (Partitions Identifier):	48
Retetitve Read Count (Entire Read Frequency Identifier):	3
Retetitve 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	Position	S
1	4427	CGGTCGAAAA ACTGCTGGCA GTGGGGCATT ACCTCGAATCT ACCGTCGATAT TGCTGAGTCC ACCCGCCGTA TTGCGGCAAG TCGTATTCCGG CTGATCACATG GTGCTGATGG CAGGTTTCACC GCCGGTAATG AAAAAGGCGA ACTGGTGGTG CTGCTGGTGCTGCCGCGTTTAC GCGCCGATTG TGCGAGATTT GGACGCA CTACTCTGCTG CGGTGTTTAC GCGCCGATTG TTGCGAGATTT GGACGCATTT GGACGCATTT GGACGCATTT TGCGAGATTT TGCGAGATTT GGACGCGTCAG CCCGCGTCAG CCCGCTCAG CCCGCTCAG CCCGCTCAG CCCGCTCAG CCCGCGTCAG CCCGCGTCAG CCCGCGTCAG CCCGCGTCAG CCCGCGTCAG CCCGCGTCAG CCCGCGTCAG CCGCGTCAG CCGCGCTCT CGGCGCTCT CGGCGCTCT CGGCCCCT CCGCGCTCT CGGCCCCCT CCGCCCCCT CCGCCCCCT CCGCCCCCT CCGCCCCCT CCGCCCCCT CCGCCCCCT CCGCCCCCT CCGCCCCCT CCGCCCCCCT CCGCCCCCCT CCGCCCCCCT CCGCCCCCCT CCGCCCCCCT CCGCCCCCCCC		350	Start Positio n 1756 3561 3964	End Positio n 2105 3910 4313

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

	1		1			
		GCTTTTCATTC				
		TGACTGCAAC				
		GGGCAATATG				
		TCTCTGTGTGG				
		ATTAAAAAAAAG				
		AGTGTCTGATA				
		GCAGCTTCTG				
		AACTGGTTACC				
		TGCCGTGAGT				
		AAATTAAAATT				
		TTATTGACTTA				
		GGTCACTAAAT				
		ACTTTAACCAA			Start	End
		TATAGGCATAG			Positio	Positio
		CGCACAGACA			n	n
		GATAAAAATTA				
1	4427	CAGAGTACAC	4	350	1	350
		AACATCCATGA			854	1203
		AACGCATTAGC			1295	1644
		ACCACCATTAC				
		CACCACCATCA			2705	3054
		CCATTACCACA				
		GGTAACGGTG				
		CGGGCTGACG				
		CGTACAGGAA				
		ACACAGAAAAA				
		AGCCCGCACC				
		TGACAGTGCG				
		GGCTTTTTTTT				
		CGACCAAAGG				
		TAACGAGGTAA				
		CAACCATGCG				
		AGTGTTGAAGT				

	1	r				
		CGGTCGAAAA ACTGCTGGCA				
	GTGGGGCATT					
	ACCTCGAATCT					
	ACCGTCGATAT					
		TGCTGAGTCC				
		ACCCGCCGTA				
		TTGCGGCAAG				
		TCGTATTCCGG				
		CTGATCACATG				
		GTGCTGATGG				
		CAGGTTTCACC				
		GCCGGTAATG			Start	End
		AAAAAGGCGA			Positio	Positio
		ACTGGTGGTG			n Osilio	n Ositio
		CTTGGACGCA				
3964	7525	ACGGTTCCGA	4		3964	4313
		CTACTCTGCTG			5117	5466
		CGGTGCTGGC			5010	6250
		TGCCTGTTTAC			5910	6259
		GCGCCGATTG			7138	7487
		TTGCGAGATTT				
		GGACGGACGT				
		TGACGGGGTC				
		TATACCTGCGA				
		CCCGCGTCAG				
		GTGCCCGATG				
		CGAGGTTGTT				
		GAAGTCGATG				
		TCCTACCAGG				
		AAGCGATGGA				
		GCTTTCCTACT				
		TCGGCGCTCT				
		AGGTCAGGCC				

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		GATTCATTCGG				
		GATGGTCTGT				
		GTGGATTAAAA				
		AAAGAGTGTCT				
		GATAGCAGCTT				
		CTGAACTGGTT				
		ACCTGCCGTG				
		AGTAAATTAAA				
		ATTTTATTGAC				
		TTAGGTCACTA				
		AATACTTTAAC				
		CAATATAGGCA				
		TAGCGCACAG				
		ACAGATAAAAA			Start	End
		TTACAGAGTAC			Positio	Positio
		ACAACATCCTC			n	n
3964	7525	AAAGCCTACC	3	350	4730	5079
		GGTGACAGTG			<i>EE</i> 20	5070
		CGGGCTTTTTT			5529	5878
		TTCGACCAAAG			6730	7079
		GTAACGAGGT				
		AACAACCATGC				
		GAGTGTTGAA				
		GTCAGGAGAT				
		CCTAAAGGCC				
		TGTACCCGTTA				
		CCTAGCCAGTT				
		GGCATTAAAC				
		GTATACGGTAC				
		CTAGGCATGTA				
		CGTAATCGTAG				
		CCTTAGCAATC				
		TCCAGTCC				

		GCTTTTCATTC				
		TGACTGCAAC				
		GGGCAATATG				
		TCTCTGTGTGG				
		ATTAAAAAAAAG				
		AGTGTCTGATA				
		GCAGCTTCTG				
		AACTGGTTACC				
		TGCCGTGAGT				
		AAATTAAAATT				
		TTATTGACTTA				
		GGTCACTAAAT				
		ACTTTAACCAA				
		TATAGGCATAG				
		CGCACAGACA			Start	End
		GATAAAAATTA			Positio	Positio
3964	7525	CAGAGTACAC	2	350	n	n
		AACATCCATGA			4337	4686
		AACGCATTAGC			6359	6708
		ACCACCATTAC			0000	0700
		CACCACCATCA				
		CCATTACCACA				
		GGTAACGGTG				
		CGGGCTGACG				
		CGTACAGGAA				
		ACACAGAAAAA				
		AGCCCGCACC				
		TGACAGTGCG				
		GGCTTTTTTTT				
		CGACCAAAGG				
		TAACGAGGTAA				
		CAACCATGCG				
		AGTGTTGAAGT				

		<del>                                     </del>				1
		CGGTCGAAAA				
		ACTGCTGGCA				
		GTGGGGCATT				
		ACCTCGAATCT				
		ACCGTCGATAT				
		TGCTGAGTCC				
		ACCCGCCGTA				
		TTGCGGCAAG				
		TCGTATTCCGG				
		CTGATCACATG				
		GTGCTGATGG				
		CAGGTTTCACC				
		GCCGGTAATG				
		AAAAAGGCGA			Start	End
		ACTGGTGGTG			Positio	Positio
	10080	CTTGGACGCA			n	n
5726		ACGGTTCCGA	4	350	5910	6259
3720		CTACTCTGCTG			7138	7487
		CGGTGCTGGC				
		TGCCTGTTTAC			8386	8735
		GCGCCGATTG			9149	9498
		TTGCGAGATTT				
		GGACGGACGT				
		TGACGGGGTC				
		TATACCTGCGA				
		CCCGCGTCAG				
		GTGCCCGATG				
		CGAGGTTGTT				
		GAAGTCGATG				
		TCCTACCAGG				
		AAGCGATGGA				
		GCTTTCCTACT				
		TCGGCGCTCT				
		AGGTCAGGCC				

		GATTCATTCGG			
		GATGGTCTGT			
		GTGGATTAAAA			
		AAAGAGTGTCT			
		GATAGCAGCTT			
		CTGAACTGGTT			
		ACCTGCCGTG			
		AGTAAATTAAA			
		ATTTTATTGAC			
		TTAGGTCACTA			
		AATACTTTAAC			
		CAATATAGGCA			
		TAGCGCACAG			
		ACAGATAAAAA		Start	End
		TTACAGAGTAC		Positio	Positio
		ACAACATCCTC		n	n
5726	10080	AAAGCCTACC 3	350	6730	7079
		GGTGACAGTG			†
		CGGGCTTTTTT		8014	8363
		TTCGACCAAAG		9552	9901
		GTAACGAGGT			
		AACAACCATGC			
		GAGTGTTGAA			
		GTCAGGAGAT			
		CCTAAAGGCC			
		TGTACCCGTTA			
		CCTAGCCAGTT			
		GGCATTAAAC			
		GTATACGGTAC			
		CTAGGCATGTA			
		CGTAATCGTAG			
		CCTTAGCAATC			
		TCCAGTCC			

GCTTTTCATTC TGACTGCAAC GGGCAATATG TCTCTGTGTGG ATTAAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAAATTAAAAATT TTTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 5726  10080  CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATCAC CCACTACAC CACACACACAC GGTAACGGTG CGGCCACAC CCATTACCACA GGTAACGGTG CGGCTGACG CGTACAGGAAA ACACACAGAAAA AGCCCGCACC TGACAGAAAA AGCCCGCACC TGACAGAGAAA AGCCCGCACC TGACAGAGGAA ACACCAATGCG AGTTTTTTTT CGACCAAAAG TAACGAGGTAA CAACCATGCG AGTGTTGAAGT		1	ı		i		1
GGGCAATATG TCTCTGTGGG ATTAAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGCATAG CGCACAGACA GATAAAAATTA ACATCATGA AACATCCATGA AACGCATTACC ACACCACTACA CCATTACCACA CCATTACCACA GGTAACGGTG CGGCTGACG CGGCTTTTTTT CGGACCAAAGG TAACGAGGTAA CAACCATGCG			GCTTTTCATTC				
TCTCTGTGTGG ATTAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA  5726  10080  CAGAGTACC AACATCCATGA AACATCCATGA AACGCATTAGC ACACCATTAC CACACCATCA CCATTACCACA GGTAACGGTG CGGCTGACG CGGCTGACG CGGCTGACG CGGCTGACG CGTACAGCAC CGATTATTTTT CGACCAGACA GGTAACGGTG CGGCTTTTTTT CGACCAGAGG TAACGAGGTAA CAACCATGCG CTACAGAGGAA CAACCATGCG TAACGAGGTAA CAACCATGCG			TGACTGCAAC				
ATTAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA  5726  10080  CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTACAGAA ACACCAGTGC CGGGCTGACG CGTACAGAA ACACAGAAAA ACACCAGGC CGTACAGGAA ACACACACCAC GGTACAGGAA ACACACACCAC GGTACAGGAA ACACACACCAC GGTACAGGAA ACACAGAAAAAA AGCCCGCACC TGACAGTGC GGCTTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG			GGGCAATATG				
AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 5726  10080  CAGAGTACAC AACACCATTAC CACCACTACA CCATTACCACA GGTAACGGTG CGGCTGACG CGTACAGGAA AACGCATTACC CACCACCATCA CCATTACCACA GGTACAGAA ACCACCACC TGACAGGAA ACCACCACC TGACAGGAA ACCACCACC TGACAGGAA ACACCAATGC GGCTTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG			TCTCTGTGTGG				
GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA  5726  10080  CAGAGTACC AACATCCATGA AACGCATTAGC ACCACCATTAC CCACCACCATCA CCATTACCACA GGTAACGGTG CGGCTGACG CGGTACAGGAA ACACCAGGAA ACACCAGCAC GGGCTTTTTTT CGACAGAAAA ACACCAAGG TAACGAGTAA CAACCATCGG			ATTAAAAAAAAG				
AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA  5726  10080  CAGAGTACAC AACATCCATGA AACGCATTAC CACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACCAGCAC GGTAACGCG CCTACAGGAA ACACCAGCAC GGTAACGGTG CGGCTGACG CGTACAGGAA ACACCAGCAC CCATTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG			AGTGTCTGATA				
TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA  5726  10080  CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CCACCACCATAC CCATTACCACA GGTAACGGTG CGGCTGACG CGGCTGACG CGTACAGGAA ACACCGCACC TGACAGGAA ACCCCGCACC TGACAGTAC CACCCACAAAGG TAACGAGTAA CCACCAAAGG TAACGAGTAA CCACCAAAGG TAACGAGTAA CAACCATGCG			GCAGCTTCTG				
AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA  5726  10080  CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CCACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGGCTGACG CGTACAGGAA ACACCAGCAC GGTACAGGAA ACACCAGCAC GGCTTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG			AACTGGTTACC				
TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA  5726  10080  CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CCACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGGCTGACG CGTACAGGAA ACACCACCAC GGTACAGGAA ACACCACCAC GGCTTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG			TGCCGTGAGT				
GGTCACTAAAT ACTTTACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA  5726  10080  CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGGCTGACG CGTACAGAAAA ACGCCGCACC TGACAGTACC TGACAGTGC GGCTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG			AAATTAAAATT				
ACTITAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA 5726  10080  CAGAGTACAC AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGCTGACG CGTACAGGAA ACCCCGCACC TGACAGGAA ACCCCCCC TGACAGTCG GGCTTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATCGC			TTATTGACTTA				
TATAGGCATAG CGCACAGACA GATAAAAATTA 5726  10080  CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CCACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACCAGAAAAA ACACAGAAAAA ACACAGAAAAA AGCCCGCACC TGACAGTGC GGCTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG			GGTCACTAAAT				
CGCACAGACA GATAAAAATTA GATAAAAATTA 5726  10080  CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CCACTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACCAGAAAAA ACACCAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG			ACTTTAACCAA				
GATAAAAATTA CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATCAC CACCACCATCAC CCACTACCACAC GGTAACGGTG CGGGCTGACG CGTACAGGAA ACCCAGCACC TGACAGGACC TGACAGTGCG GGCTTTTTTT CCGACCAAAGG TAACGAGGTAA CAACCATGCG			TATAGGCATAG			Start	End
5726  10080  CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			CGCACAGACA			Positio	Positio
AACATCCATGA AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG			GATAAAAATTA			n	n
AACATCCATGA AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTTT CGACCAAAGG TAACGAGTAA CAACCATGCG	5726	10080	CAGAGTACAC	3	350	6359	6708
ACCACCATTAC  ACCACCATTAC  CACCACCATCA  CCATTACCACA  GGTAACGGTG  CGGCTGACG  CGTACAGGAA  ACACAGAAAAA  ACCCGCACC  TGACAGTGCG  GGCTTTTTTT  CGACCAAAGG  TAACGAGGTAA  CAACCATGCG			AACATCCATGA				
CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			AACGCATTAGC			7574	7923
CCATTACCACA GGTAACGGTG CGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			ACCACCATTAC			8752	9101
GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG			CACCACCATCA				
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			GGCTTTTTTTT				
CAACCATGCG			CGACCAAAGG				
			TAACGAGGTAA				
AGTGTTGAAGT			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 Sizet after Removing Duplication:			150869			
Dataset Size after Overlapping:			49952			
Overlapping Metri	CS					
Repeat Identification	n Time:		00h:00m:08s:000ms			
Overlapping Time:	Overlapping Time:			00h:05m:29s:000ms		
Reads Alignment T	ïme:		00h:00m:16s:000ms			
Total Hybrid Assem	nbly 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