Report

# contigs (>= 1000 bp)		final.contigs
# contigs (>= 5000 bp)	# contigs (>= 1000 bp)	
# contigs (>= 10000 bp)		0
# contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 1000 bp) 5355 Total length (>= 5000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 7 Largest contig 1437 Total length 7146 Reference length 4326814 GC (%) 51.79 Reference GC (%) 66.74 N50 1348 N75 679 L50 3 L75 5 # misassembled contigs 0 # misassembled contigs 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned length 5962 Genome fraction (%) 0.014 Duplication ratio 1.993 # N's per 100 kbp 0.00 Largest alignment 156		0
# contigs (>= 50000 bp) 0 Total length (>= 1000 bp) 5355 Total length (>= 5000 bp) 0 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 7 Largest contig 1437 Total length 7146 Reference length 4326814 GC (%) 51.79 Reference GC (%) 66.74 N50 1348 N75 679 L50 3 L75 5 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 1 + 5 part 0 Unaligned length 5962 Genome fraction (%) 0.014 Duplication ratio 1.993 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4040.40 # indels per 100 kbp 0.00 Largest alignment 156		
Total length (>= 1000 bp) 5355 Total length (>= 5000 bp) 0 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 7 Largest contig 1437 Total length 7146 Reference length 4326814 GC (%) 51.79 Reference GC (%) 66.74 N50 1348 N75 679 L50 3 L75 5 # misassemblies 0 Misassembled contigs 0 Misassembled contigs length 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned length 5962 Genome fraction (%) 0.014 Duplication ratio 1.993 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4040.40 # indels per 100 kbp 0.00 <t< td=""><td></td><td>0</td></t<>		0
Total length (>= 5000 bp) Total length (>= 10000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) # contigs Total length I day Eargest contig Largest contig Reference length GC (%) Reference GC (%) Reference GC (%) N50 1348 N75 679 L50 3 L75 # misassembled contigs # misassembled contigs Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs Unaligned length Duplication ratio Pupplication ratio # mismatches per 100 kbp # indels per 100 kbp Outlibread Outlibread # unaligned length Duplication ratio 1.993 # N's per 100 kbp Duplication ratio # unaligned length Duplication ratio Duplication ratio # unaligned length Duplication ratio		5355
Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 7 Largest contig 1437 Total length 7146 Reference length 4326814 GC (%) 51.79 Reference GC (%) 66.74 N50 1348 N75 679 L50 3 L75 5 # misassemblies 0 # misassembled contigs 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned length 5962 Genome fraction (%) 0.014 Duplication ratio 1.993 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 156		
Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 7 Largest contig 1437 Total length 7146 Reference length 4326814 GC (%) 51.79 Reference GC (%) 66.74 N50 1348 N75 679 L50 3 L75 5 # misassemblies 0 # misassembled contigs 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned length 5962 Genome fraction (%) 0.014 Duplication ratio 1.993 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 156		0
Total length (>= 50000 bp) 0 # contigs 7 Largest contig 1437 Total length 7146 Reference length 4326814 GC (%) 51.79 Reference GC (%) 66.74 N50 1348 N75 679 L50 3 L75 5 # misassemblies 0 Misassembled contigs 0 Misassembled contigs length 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned length 5962 Genome fraction (%) 0.014 Duplication ratio 1.993 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 156	Total length (>= 25000 bp)	0
Largest contig		0
Total length 7146 Reference length 4326814 GC (%) 51.79 Reference GC (%) 66.74 N50 1348 N75 679 L50 3 L75 5 # misassemblies 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 1 + 5 part Unaligned length 5962 Genome fraction (%) 0.014 Duplication ratio 1.993 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4040.40 # indels per 100 kbp 0.00 Largest alignment 156	# contigs	7
Reference length 4326814 GC (%) 51.79 Reference GC (%) 66.74 N50 1348 N75 679 L50 3 L75 5 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 1 + 5 part Unaligned length 5962 Genome fraction (%) 0.014 Duplication ratio 1.993 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4040.40 # indels per 100 kbp 0.00 Largest alignment 156	Largest contig	1437
GC (%) 51.79 Reference GC (%) 66.74 N50 1348 N75 679 L50 3 L75 5 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 1 + 5 part Unaligned length 5962 Genome fraction (%) 0.014 Duplication ratio 1.993 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4040.40 # indels per 100 kbp 0.00 Largest alignment 156	Total length	7146
Reference GC (%) 66.74 N50 1348 N75 679 L50 3 L75 5 # misassemblies 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 1 + 5 part Unaligned length 5962 Genome fraction (%) 0.014 Duplication ratio 1.993 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4040.40 # indels per 100 kbp 0.00 Largest alignment 156	Reference length	4326814
N50 1348 N75 679 L50 3 L75 5 # misassemblies 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 1 + 5 part Unaligned length 5962 Genome fraction (%) 0.014 Duplication ratio 1.993 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4040.40 # indels per 100 kbp 0.00 Largest alignment 156	GC (%)	51.79
N75 679 L50 3 L75 5 # misassemblies 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 1 + 5 part Unaligned length 5962 Genome fraction (%) 0.014 Duplication ratio 1.993 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4040.40 # indels per 100 kbp 0.00 Largest alignment 156	Reference GC (%)	66.74
L50 3 L75 5 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 1 + 5 part Unaligned length 5962 Genome fraction (%) 0.014 Duplication ratio 1.993 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4040.40 # indels per 100 kbp 0.00 Largest alignment 156	N50	1348
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 1 + 5 part 1 Unaligned length 5962 Genome fraction (%) 0.014 Duplication ratio 1.993 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4040.40 # indels per 100 kbp 0.00 Largest alignment 156	N75	679
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 1 + 5 part 1 Unaligned length 5962 Genome fraction (%) 0.014 Duplication ratio 1.993 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4040.40 # indels per 100 kbp 0.00 Largest alignment 156	L50	3
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 1 + 5 part Unaligned length 5962 Genome fraction (%) 0.014 Duplication ratio 1.993 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4040.40 # indels per 100 kbp 0.00 Largest alignment 156	L75	5
Misassembled contigs length # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 1 + 5 part Unaligned length 5962 Genome fraction (%) 0.014 Duplication ratio 1.993 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4040.40 # indels per 100 kbp 0.00 Largest alignment 156	# misassemblies	0
# local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 1 + 5 part Unaligned length 5962 Genome fraction (%) 0.014 Duplication ratio 1.993 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4040.40 # indels per 100 kbp 0.00 Largest alignment 156	# misassembled contigs	0
# scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 1 + 5 part Unaligned length 5962 Genome fraction (%) 0.014 Duplication ratio 1.993 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4040.40 # indels per 100 kbp 0.00 Largest alignment 156	Misassembled contigs length	0
# scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 1 + 5 part Unaligned length 5962 Genome fraction (%) 0.014 Duplication ratio 1.993 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4040.40 # indels per 100 kbp 0.00 Largest alignment 156	# local misassemblies	0
# unaligned mis. contigs 1 # unaligned contigs 1 + 5 part Unaligned length 5962 Genome fraction (%) 0.014 Duplication ratio 1.993 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4040.40 # indels per 100 kbp 0.00 Largest alignment 156	# scaffold gap ext. mis.	0
# unaligned contigs	# scaffold gap loc. mis.	0
Unaligned length 5962 Genome fraction (%) 0.014 Duplication ratio 1.993 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4040.40 # indels per 100 kbp 0.00 Largest alignment 156	# unaligned mis. contigs	1
Genome fraction (%) 0.014 Duplication ratio 1.993 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4040.40 # indels per 100 kbp 0.00 Largest alignment 156	# unaligned contigs	1 + 5 part
Duplication ratio 1.993 # N's per 100 kbp 0.00 # mismatches per 100 kbp 4040.40 # indels per 100 kbp 0.00 Largest alignment 156	Unaligned length	5962
# N's per 100 kbp 0.00 # mismatches per 100 kbp 4040.40 # indels per 100 kbp 0.00 Largest alignment 156	Genome fraction (%)	0.014
# mismatches per 100 kbp 4040.40 # indels per 100 kbp 0.00 Largest alignment 156	Duplication ratio	1.993
# indels per 100 kbp 0.00 Largest alignment 156	# N's per 100 kbp	0.00
Largest alignment 156	# mismatches per 100 kbp	4040.40
	# indels per 100 kbp	0.00
Total aligned length 690	Largest alignment	156
Total aligned leligeri 050	Total aligned length	690
NGA50 -	NGA50	-

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	final.contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	2
# possible misassemblies	2
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	24
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	1
Fully unaligned length	519
# partially unaligned contigs	5
Partially unaligned length	5443
# N's	0

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).





















