Report

# contigs (>= 1000 bp) 12 # contigs (>= 5000 bp) 1 # contigs (>= 5000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 1000 bp) 32365 Total length (>= 5000 bp) 5625 Total length (>= 5000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 16 Largest contig 5625 Total length 35017 Reference length 3712900 GC (%) 35.95 Reference GC (%) 31.25 N50 4157 N75 1805 L50 4 L75 8 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 10 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 3 + 10 part 1.680 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3809.06 # indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322 NGA50		final.contigs
# contigs (>= 5000 bp)	# contigs (>= 1000 bp)	<u> </u>
# contigs (>= 10000 bp)		
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Total length (>= 5000 bp) 5625 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 16 Largest contig 5625 Total length 35017 Reference length 3712900 GC (%) 35.95 Reference GC (%) 31.25 N50 4157 N75 1805 L50 4 L75 8 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 10 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 3 1 10 part 10 Unaligned length 31533 Genome fraction (%) 0.056 Duplication ratio 1.680 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3809.06 # indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322		32365
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Total length (>= 50000 bp) 0 # contigs 16 Largest contig 5625 Total length 35017 Reference length 3712900 GC (%) 35.95 Reference GC (%) 31.25 N50 4157 N75 1805 L50 4 L75 8 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 1 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 3 + 10 part Unaligned length 31533 Genome fraction (%) 0.056 Duplication ratio 1.680 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3809.06 # indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322	Total length (>= 25000 bp)	0
Largest contig 5625 Total length 35017 Reference length 3712900 GC (%) 35.95 Reference GC (%) 31.25 N50 4157 N75 1805 L50 4 L75 8 # misassemblies 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 3 + 10 part Unaligned length 31533 Genome fraction (%) 0.056 Duplication ratio 1.680 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3809.06 # indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322		0
Total length 35017 Reference length 3712900 GC (%) 35.95 Reference GC (%) 31.25 N50 4157 N75 1805 L50 4 L75 8 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned length 31533 Genome fraction (%) 0.056 Duplication ratio 1.680 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3809.06 # indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322	# contigs	16
Reference length 3712900 GC (%) 35.95 Reference GC (%) 31.25 N50 4157 N75 1805 L50 4 L75 8 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned length 31533 Genome fraction (%) 0.056 Duplication ratio 1.680 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3809.06 # indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322	Largest contig	5625
GC (%) 35.95 Reference GC (%) 31.25 N50 4157 N75 1805 L50 4 L75 8 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 3 + 10 part Unaligned length 31533 Genome fraction (%) 0.056 Duplication ratio 1.680 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3809.06 # indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322	Total length	35017
Reference GC (%) 31.25 N50 4157 N75 1805 L50 4 L75 8 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 3 + 10 part Unaligned length 31533 Genome fraction (%) 0.056 Duplication ratio 1.680 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3809.06 # indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322	Reference length	3712900
N50 4157 N75 1805 L50 4 L75 8 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 3 + 10 part Unaligned length 31533 Genome fraction (%) 0.056 Duplication ratio 1.680 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3809.06 # indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322	GC (%)	35.95
N75 1805 L50 4 L75 8 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 3 + 10 part Unaligned length 31533 Genome fraction (%) 0.056 Duplication ratio 1.680 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3809.06 # indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322	Reference GC (%)	31.25
L50 4 L75 8 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 3 + 10 part Unaligned length 31533 Genome fraction (%) 0.056 Duplication ratio 1.680 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3809.06 # indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322	N50	4157
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 3 + 10 part Unaligned length 31533 Genome fraction (%) 0.056 Duplication ratio 1.680 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3809.06 # indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322	N75	1805
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 3 + 10 part 1 Unaligned length 31533 Genome fraction (%) 0.056 Duplication ratio 1.680 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3809.06 # indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322	L50	4
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 3 + 10 part Unaligned length 31533 Genome fraction (%) 0.056 Duplication ratio 1.680 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3809.06 # indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322	L75	8
Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 3 + 10 part Unaligned length 31533 Genome fraction (%) 0.056 Duplication ratio 1.680 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3809.06 # indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322	# misassemblies	0
# local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 3 + 10 part Unaligned length 31533 Genome fraction (%) 0.056 Duplication ratio 1.680 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3809.06 # indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322	# misassembled contigs	0
# scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 3 + 10 part Unaligned length 31533 Genome fraction (%) 0.056 Duplication ratio 1.680 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3809.06 # indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322	Misassembled contigs length	0
# scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 3 + 10 part Unaligned length 31533 Genome fraction (%) 0.056 Duplication ratio 1.680 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3809.06 # indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322	# local misassemblies	1
# unaligned mis. contigs 1 # unaligned contigs 3 + 10 part Unaligned length 31533 Genome fraction (%) 0.056 Duplication ratio 1.680 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3809.06 # indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322	# scaffold gap ext. mis.	0
# unaligned contigs 3 + 10 part Unaligned length 31533 Genome fraction (%) 0.056 Duplication ratio 1.680 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3809.06 # indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322	# scaffold gap loc. mis.	0
Unaligned length 31533 Genome fraction (%) 0.056 Duplication ratio 1.680 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3809.06 # indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322	# unaligned mis. contigs	1
Genome fraction (%) 0.056 Duplication ratio 1.680 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3809.06 # indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322	# unaligned contigs	3 + 10 part
Duplication ratio 1.680 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3809.06 # indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322	Unaligned length	31533
# N's per 100 kbp 0.00 # mismatches per 100 kbp 3809.06 # indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322	Genome fraction (%)	0.056
# mismatches per 100 kbp 3809.06 # indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322	Duplication ratio	1.680
# indels per 100 kbp 48.22 Largest alignment 619 Total aligned length 2322	# N's per 100 kbp	0.00
Largest alignment 619 Total aligned length 2322	# mismatches per 100 kbp	3809.06
Total aligned length 2322	# indels per 100 kbp	48.22
, , , , , , , , , , , , , , , , , , ,	Largest alignment	619
NGA50 -	Total aligned length	2322
	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	7
# possible misassemblies	11
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	79
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	2

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	3
Fully unaligned length	3965
# partially unaligned contigs	10
Partially unaligned length	27568
# 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).





















