Report

# contigs (>= 0 bp) 109 # contigs (>= 1000 bp) 72 # contigs (>= 5000 bp) 50 # contigs (>= 10000 bp) 47 # contigs (>= 25000 bp) 47 # contigs (>= 25000 bp) 41 # contigs (>= 50000 bp) 428 Total length (>= 0 bp) 4564265 Total length (>= 1000 bp) 4554625 Total length (>= 5000 bp) 4504386 Total length (>= 10000 bp) 4391325 Total length (>= 25000 bp) 4391325 Total length (>= 50000 bp) 3942965 # contigs 79 Largest contig 327056 Total length 4559734 Reference length 4641652 N50 173981 N75 78600 L50 10 L75 20 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.180 Duplication ratio 1.001 # N's per 100 kbp 9.73 # indels per 100 kbp 59.73 # indels per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10 LA75 20		
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# contigs (>= 25000 bp) 41 # contigs (>= 50000 bp) 28 Total length (>= 0 bp) 4564265 Total length (>= 1000 bp) 4554625 Total length (>= 5000 bp) 4504386 Total length (>= 10000 bp) 4480443 Total length (>= 25000 bp) 4391325 Total length (>= 50000 bp) 3942965 # contigs 79 Largest contig 327056 Total length 4559734 Reference length 4641652 N50 173981 N75 78600 L50 10 L75 20 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 10 # local misassemblies 3 # unaligned length 0 Genome fraction (%) 98.180 Duplication ratio 1.001 # N's per 100 kbp 59.73 # indels per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	# contigs (>= 5000 bp)	50
# contigs (>= 50000 bp) 28 Total length (>= 0 bp) 4564265 Total length (>= 1000 bp) 4554625 Total length (>= 5000 bp) 4504386 Total length (>= 10000 bp) 4480443 Total length (>= 25000 bp) 4391325 Total length (>= 50000 bp) 3942965 # contigs 79 Largest contig 327056 Total length 4559734 Reference length 4641652 N50 173981 N75 78600 L50 10 L75 20 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.180 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	# contigs (>= 10000 bp)	47
Total length (>= 0 bp)	# contigs (>= 25000 bp)	41
Total length (>= 1000 bp) 4554625 Total length (>= 5000 bp) 4504386 Total length (>= 10000 bp) 4480443 Total length (>= 25000 bp) 4391325 Total length (>= 50000 bp) 3942965 # contigs 79 Largest contig 327056 Total length 4559734 Reference length 4641652 N50 173981 N75 78600 L50 10 L75 20 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 10 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (♥) 98.180 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	# contigs (>= 50000 bp)	28
Total length (>= 5000 bp)	Total length ($>= 0 \text{ bp}$)	4564265
Total length (>= 10000 bp) 4480443 Total length (>= 25000 bp) 4391325 Total length (>= 50000 bp) 3942965 # contigs 79 Largest contig 327056 Total length 4559734 Reference length 4641652 N50 173981 N75 78600 L50 10 L75 20 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 10 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (♥6) 98.180 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	Total length (>= 1000 bp)	4554625
Total length (>= 25000 bp) 4391325 Total length (>= 50000 bp) 3942965 # contigs 79 Largest contig 327056 Total length 4559734 Reference length 4641652 N50 173981 N75 78600 L50 10 L75 20 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.180 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	Total length (>= 5000 bp)	4504386
Total length (>= 50000 bp) 3942965 # contigs 79 Largest contig 327056 Total length 4559734 Reference length 4641652 N50 173981 N75 78600 L50 10 L75 20 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.180 Duplication ratio 1.001 # N's per 100 kbp 59.73 # indels per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	Total length (>= 10000 bp)	4480443
# contigs 79 Largest contig 327056 Total length 4559734 Reference length 4641652 N50 173981 N75 78600 L50 10 L75 20 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.180 Duplication ratio 1.001 # N's per 100 kbp 9.73 # indels per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	Total length (>= 25000 bp)	4391325
Largest contig 327056 Total length 4559734 Reference length 4641652 N50 173981 N75 78600 L50 10 L75 20 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.180 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.73 # indels per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	Total length (>= 50000 bp)	3942965
Total length 4559734 Reference length 4641652 N50 173981 N75 78600 L50 10 L75 20 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (♥₀) 98.180 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	# contigs	79
Reference length 4641652 N50 173981 N75 78600 L50 10 L75 20 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.180 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.73 # indels per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	Largest contig	327056
N50 173981 N75 78600 L50 10 L75 20 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.180 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.73 # indels per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	Total length	4559734
N75 78600 L50 10 L75 20 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.180 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.73 # indels per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	Reference length	4641652
L50 10 L75 20 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.180 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.73 # indels per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	N50	173981
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.180 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.73 # indels per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	N75	78600
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.180 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.73 # indels per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	L50	10
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.180 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.73 # indels per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	L75	20
Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.180 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.73 # indels per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	# misassemblies	0
# local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.180 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.73 # indels per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	# misassembled contigs	0
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.180 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.73 # indels per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	Misassembled contigs length	0
Unaligned length 0 Genome fraction (%) 98.180 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.73 # indels per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	# local misassemblies	3
Genome fraction (♥₀) 98.180 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.73 # indels per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	# unaligned contigs	0 + 0 part
Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 59.73 # indels per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 59.73 # indels per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	Genome fraction (%)	98.180
# mismatches per 100 kbp 59.73 # indels per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	Duplication ratio	1.001
# indels per 100 kbp 8.65 Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	# N's per 100 kbp	0.00
Largest alignment 327056 NA50 173981 NA75 78600 LA50 10	# mismatches per 100 kbp	59.73
NA50 173981 NA75 78600 LA50 10	# indels per 100 kbp	8.65
NA50 173981 NA75 78600 LA50 10	Largest alignment	327056
LA50 10	NA50	173981
	NA75	78600
LA75 20	LA50	10
	LA75	20

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

	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	2722
# indels	394
# short indels	394
# long indels	0
Indels length	534

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

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# 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).









