Report

# contigs (>= 0 bp)		
# contigs (>= 1000 bp) 136 # contigs (>= 5000 bp) 111 # contigs (>= 10000 bp) 98 # contigs (>= 25000 bp) 59 # contigs (>= 50000 bp) 32 Total length (>= 0 bp) 4659121 Total length (>= 1000 bp) 4547414 Total length (>= 5000 bp) 4379149 Total length (>= 10000 bp) 4379149 Total length (>= 5000 bp) 3733533 Total length (>= 5000 bp) 3733533 Total length (>= 50000 bp) 2766902 # contigs 153 Largest contig 229997 Total length 4559533 Reference length 4641652 N50 58023 N75 31670 L50 24 L75 48 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # local misassemblies 3 # unaligned length 0 Genome fraction (%) 98.353 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.04 # indels per 100 kbp 0.07 Largest alignment 229997 NA50 58023 NA75 31670 LA50 24		final.contigs
# contigs (>= 5000 bp) 111 # contigs (>= 10000 bp) 98 # contigs (>= 25000 bp) 59 # contigs (>= 50000 bp) 32 Total length (>= 0 bp) 4659121 Total length (>= 1000 bp) 4547414 Total length (>= 5000 bp) 4479948 Total length (>= 10000 bp) 4379149 Total length (>= 25000 bp) 3733533 Total length (>= 5000 bp) 2766902 # contigs 153 Largest contig 229997 Total length 4559533 Reference length 4641652 N50 58023 N75 31670 L50 24 L75 48 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # local misassemblies 3 # unaligned contigs 0 Genome fraction (%) 98.353 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.04 # indels per 100 kbp 0.07 Largest alignment 229997 NA50 58023 NA75 31670 LA50 24		464
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# contigs (>= 25000 bp)		111
# contigs (>= 50000 bp) 32 Total length (>= 0 bp) 4659121 Total length (>= 1000 bp) 4547414 Total length (>= 5000 bp) 4479948 Total length (>= 10000 bp) 4379149 Total length (>= 25000 bp) 3733533 Total length (>= 50000 bp) 2766902 # contigs 153 Largest contig 229997 Total length 4559533 Reference length 4641652 N50 58023 N75 31670 L50 24 L75 48 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.353 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.07 Largest alignment 229997 NA50 58023 NA75 31670 L50 244		98
Total length (>= 0 bp) 4659121 Total length (>= 1000 bp) 4547414 Total length (>= 5000 bp) 4479948 Total length (>= 10000 bp) 4379149 Total length (>= 25000 bp) 3733533 Total length (>= 50000 bp) 2766902 # contigs 153 Largest contig 229997 Total length 4559533 Reference length 4641652 N50 58023 N75 31670 L50 24 L75 48 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Unaligned length 0 Genome fraction (%) 98.353 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.07 Largest alignment 229997 NA50 58023 NA75 31670 LA50 24		59
Total length (>= 1000 bp)	# contigs (>= 50000 bp)	32
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Total length (>= 25000 bp) 3733533 Total length (>= 50000 bp) 2766902 # contigs 153 Largest contig 229997 Total length 4559533 Reference length 4641652 N50 58023 N75 31670 L50 24 L75 48 # misassemblies 0 # incal misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.353 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.04 # indels per 100 kbp 0.07 Largest alignment 229997 NA50 58023 NA75 31670 LA50 24	Total length (>= 5000 bp)	4479948
Total length (>= 50000 bp) 2766902 # contigs 153 Largest contig 229997 Total length 4559533 Reference length 4641652 N50 58023 N75 31670 L50 24 L75 48 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.353 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.04 # indels per 100 kbp 0.07 Largest alignment 229997 NA50 58023 NA75 31670 LA50 24	Total length (>= 10000 bp)	4379149
# contigs 153 Largest contig 229997 Total length 4559533 Reference length 4641652 N50 58023 N75 31670 L50 24 L75 48 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.353 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.04 # indels per 100 kbp 0.07 Largest alignment 229997 NA50 58023 NA75 31670 LA50 24	Total length (>= 25000 bp)	3733533
Largest contig 229997 Total length 4559533 Reference length 4641652 N50 58023 N75 31670 L50 24 L75 48 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.353 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.04 # indels per 100 kbp 0.07 Largest alignment 229997 NA50 58023 NA75 31670 LA50 24	Total length (>= 50000 bp)	2766902
Total length 4559533 Reference length 4641652 N50 58023 N75 31670 L50 24 L75 48 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.353 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.04 # indels per 100 kbp 0.07 Largest alignment 229997 NA50 58023 NA75 31670 LA50 24	# contigs	153
Reference length 4641652 N50 58023 N75 31670 L50 24 L75 48 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.353 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.04 # indels per 100 kbp 0.07 Largest alignment 229997 NA50 58023 NA75 31670 LA50 24	Largest contig	229997
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N75 31670 L50 24 L75 48 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.353 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.04 # indels per 100 kbp 0.07 Largest alignment 229997 NA50 58023 NA75 31670 LA50 24	Reference length	4641652
L50 24 L75 48 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.353 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.04 # indels per 100 kbp 0.07 Largest alignment 229997 NA50 58023 NA75 31670 LA50 24	N50	58023
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.353 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.04 # indels per 100 kbp 0.07 Largest alignment 229997 NA50 58023 NA75 31670 LA50 24	N75	31670
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.353 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.04 # indels per 100 kbp 0.07 Largest alignment 229997 NA50 58023 NA75 31670 LA50 24	L50	24
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.353 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.04 # indels per 100 kbp 0.07 Largest alignment 229997 NA50 58023 NA75 31670 LA50 24	L75	48
Misassembled contigs length 0 # local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.353 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.04 # indels per 100 kbp 0.07 Largest alignment 229997 NA50 58023 NA75 31670 LA50 24	# misassemblies	0
# local misassemblies 3 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.353 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.04 # indels per 100 kbp 0.07 Largest alignment 229997 NA50 58023 NA75 31670 LA50 24	# misassembled contigs	0
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.353 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.04 # indels per 100 kbp 0.07 Largest alignment 229997 NA50 58023 NA75 31670 LA50 24	Misassembled contigs length	0
Unaligned length 0 Genome fraction (%) 98.353 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.04 # indels per 100 kbp 0.07 Largest alignment 229997 NA50 58023 NA75 31670 LA50 24	# local misassemblies	3
Genome fraction (%) 98.353 Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.04 # indels per 100 kbp 0.07 Largest alignment 229997 NA50 58023 NA75 31670 LA50 24	# unaligned contigs	0 + 0 part
Duplication ratio 1.002 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3.04 # indels per 100 kbp 0.07 Largest alignment 229997 NA50 58023 NA75 31670 LA50 24	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 3.04 # indels per 100 kbp 0.07 Largest alignment 229997 NA50 58023 NA75 31670 LA50 24	Genome fraction (%)	98.353
# mismatches per 100 kbp 3.04 # indels per 100 kbp 0.07 Largest alignment 229997 NA50 58023 NA75 31670 LA50 24	Duplication ratio	1.002
# indels per 100 kbp 0.07 Largest alignment 229997 NA50 58023 NA75 31670 LA50 24	# N's per 100 kbp	0.00
Largest alignment 229997 NA50 58023 NA75 31670 LA50 24	# mismatches per 100 kbp	3.04
NA50 58023 NA75 31670 LA50 24	# indels per 100 kbp	0.07
NA50 58023 NA75 31670 LA50 24	Largest alignment	229997
LA50 24	NA50	
	NA75	31670
LA75 48	LA50	24
	LA75	48

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
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	139
# indels	3
# short indels	3
# long indels	0
Indels length	3

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	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).









