Report

# contigs (>= 0 bp) 1740 # contigs (>= 1000 bp) 1386 # contigs (>= 5000 bp) 697 # contigs (>= 10000 bp) 262 # contigs (>= 25000 bp) 277 # contigs (>= 50000 bp) 9352212 Total length (>= 0 bp) 9352212 Total length (>= 1000 bp) 9168181 Total length (>= 1000 bp) 7270597 Total length (>= 5000 bp) 7270597 Total length (>= 5000 bp) 7270597 Total length (>= 5000 bp) 72212 Total length (>= 5000 bp) 72212 Total length (>= 5000 bp) 72212 Total length (>= 50000 bp) 93212 Total length (>= 50000 bp) 93212 Total length 922963 Reference length 9283304 N50 9319 N75 5443 L50 313 L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 1 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.952 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.14 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313		
# contigs (>= 1000 bp) 697 # contigs (>= 5000 bp) 697 # contigs (>= 10000 bp) 262 # contigs (>= 25000 bp) 27 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 9352212 Total length (>= 1000 bp) 9168181 Total length (>= 1000 bp) 7270597 Total length (>= 5000 bp) 7270597 Total length (>= 50000 bp) 72121 Total length (>= 50000 bp) 792121 Total length (>= 50000 bp) 90 # contigs 1555 Largest contig 9292963 Reference length 9283304 N50 9319 N75 5443 L50 313 L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 1 # local misassemblies 0 # unaligned contigs 0 0 + 0 part 1 Unaligned length 0 Genome fraction (%) 98.952 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.14 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313		final.contigs
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# contigs (>= 10000 bp) 262 # contigs (>= 25000 bp) 27 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 9352212 Total length (>= 1000 bp) 7270597 Total length (>= 10000 bp) 7270597 Total length (>= 10000 bp) 7270597 Total length (>= 25000 bp) 7270597 Total length (>= 25000 bp) 792121 Total length (>= 50000 bp) 792121 Total length (>= 50000 bp) 792121 Total length (>= 50000 bp) 90 # contigs 1555 Largest contig 9292963 Reference length 9283304 N50 9319 N75 5443 L50 313 L75 6400 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 # local misassemblies 0 # unaligned contigs 0 0 + 0 part Unaligned length 0 Genome fraction (%) 98.952 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.14 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50		1386
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# contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 1000 bp) Total length (>= 1000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 10000 bp) Total length (>= 25000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) Total length (>= 1000 bp) Total length (>= 10000 bp) Total length (>= 1000 bp) Total length (>= 1	# contigs (>= 10000 bp)	262
Total length (>= 0 bp) 9352212 Total length (>= 1000 bp) 9168181 Total length (>= 5000 bp) 7270597 Total length (>= 10000 bp) 4156298 Total length (>= 25000 bp) 792121 Total length (>= 50000 bp) 0 # contigs 1555 Largest contig 45348 Total length 922963 Reference length 9283304 N50 9319 N75 5443 L50 313 L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 98.952 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	# contigs (>= 25000 bp)	27
Total length (>= 1000 bp) 9168181 Total length (>= 5000 bp) 7270597 Total length (>= 10000 bp) 4156298 Total length (>= 25000 bp) 792121 Total length (>= 50000 bp) 0 # contigs 1555 Largest contig 45348 Total length 9292963 Reference length 9283304 N50 9319 N75 5443 L50 313 L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.952 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	# contigs (>= 50000 bp)	0
Total length (>= 5000 bp) 7270597 Total length (>= 10000 bp) 4156298 Total length (>= 25000 bp) 792121 Total length (>= 50000 bp) 0 # contigs 1555 Largest contig 45348 Total length 9292963 Reference length 9283304 N50 9319 N75 5443 L50 313 L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.952 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Total length (>= 0 bp)	9352212
Total length (>= 10000 bp) 4156298 Total length (>= 25000 bp) 792121 Total length (>= 50000 bp) 0 # contigs 1555 Largest contig 45348 Total length 9292963 Reference length 9283304 N50 9319 N75 5443 L50 313 L75 640 # misassemblies 1 # local misassembled contigs 1 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.952 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Total length (>= 1000 bp)	9168181
Total length (>= 25000 bp) 792121 Total length (>= 50000 bp) 0 # contigs 1555 Largest contig 45348 Total length 9292963 Reference length 9283304 N50 9319 N75 5443 L50 313 L75 640 # misassemblies 1 # local misassembled contigs 1 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.952 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Total length (>= 5000 bp)	7270597
Total length (>= 50000 bp) 0 # contigs 1555 Largest contig 45348 Total length 9292963 Reference length 9283304 N50 9319 N75 5443 L50 313 L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.952 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Total length (>= 10000 bp)	4156298
# contigs 1555 Largest contig 45348 Total length 9292963 Reference length 9283304 N50 9319 N75 5443 L50 313 L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 0 + 0 part 1 Unaligned length 0 Genome fraction (%) 98.952 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.14 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Total length (>= 25000 bp)	792121
Largest contig 45348 Total length 9292963 Reference length 9283304 N50 9319 N75 5443 L50 313 L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.952 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Total length (>= 50000 bp)	0
Total length 9292963 Reference length 9283304 N50 9319 N75 5443 L50 313 L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.952 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.14 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	# contigs	1555
Reference length 9283304 N50 9319 N75 5443 L50 313 L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.952 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Largest contig	45348
N50 9319 N75 5443 L50 313 L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.952 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Total length	9292963
N75 5443 L50 313 L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.952 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.14 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Reference length	9283304
L50 313 L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 1 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.952 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.14 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	N50	9319
L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.952 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.14 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	N75	5443
# misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.952 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.14 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	L50	313
# misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.952 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.14 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	L75	640
Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.952 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.14 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	# misassemblies	1
# local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.952 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.14 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	# misassembled contigs	1
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.952 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.14 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Misassembled contigs length	15101
Unaligned length 0 Genome fraction (%) 98.952 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.14 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	# local misassemblies	0
Genome fraction (%) 98.952 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.14 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	# unaligned contigs	0 + 0 part
Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.14 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 1.14 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Genome fraction (%)	98.952
# mismatches per 100 kbp 1.14 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Duplication ratio	1.013
# indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	# N's per 100 kbp	0.00
Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	# mismatches per 100 kbp	1.14
NA50 9319 NA75 5443 LA50 313	# indels per 100 kbp	0.00
NA75 5443 LA50 313	Largest alignment	45348
LA50 313	NA50	9319
	NA75	5443
ΙΔ75 640	LA50	313
L 040	LA75	640

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	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	15101
# local misassemblies	0
# mismatches	105
# indels	0
# short indels	0
# long indels	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	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).









