Report

# contigs (>= 0 bp) 801 # contigs (>= 1000 bp) 647 # contigs (>= 5000 bp) 464 # contigs (>= 10000 bp) 320 # contigs (>= 25000 bp) 110 # contigs (>= 25000 bp) 110 # contigs (>= 50000 bp) 15 Total length (>= 0 bp) 9281077 Total length (>= 1000 bp) 9217309 Total length (>= 10000 bp) 7648265 Total length (>= 10000 bp) 7648265 Total length (>= 25000 bp) 7648265 Total length (>= 5000 bp) 7648265 Total length (>= 5000 bp) 966351 # contigs 684 Largest contig 95788 Total length (>= 50000 bp) 9245899 Reference length 9245899 Reference length 9283304 N50 23232 N75 13502 L50 130 L75 259 # misassembled contigs 1 # misassembled contigs 1 Misassembled contigs 0 # unaligned length 0 Genome fraction (%) 99.051 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130 LA75 259		
# contigs (>= 1000 bp)		final.contigs
# contigs (>= 5000 bp)		801
# contigs (>= 10000 bp) 320 # contigs (>= 25000 bp) 110 # contigs (>= 50000 bp) 15 Total length (>= 0 bp) 9281077 Total length (>= 1000 bp) 9217309 Total length (>= 5000 bp) 8680679 Total length (>= 10000 bp) 7648265 Total length (>= 25000 bp) 4157605 Total length (>= 5000 bp) 966351 # contigs 684 Largest contig 95788 Total length 9245899 Reference length 9283304 N50 23232 N75 13502 L50 130 L75 259 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.051 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 1330		647
# contigs (>= 25000 bp) 110 # contigs (>= 50000 bp) 15 Total length (>= 0 bp) 9281077 Total length (>= 1000 bp) 9217309 Total length (>= 5000 bp) 8680679 Total length (>= 10000 bp) 7648265 Total length (>= 25000 bp) 4157605 Total length (>= 50000 bp) 966351 # contigs 684 Largest contig 95788 Total length 9245899 Reference length 9283304 N50 23232 N75 13502 L50 130 L75 259 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.051 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 1330		464
# contigs (>= 50000 bp) 15 Total length (>= 0 bp) 9281077 Total length (>= 1000 bp) 9217309 Total length (>= 5000 bp) 8680679 Total length (>= 10000 bp) 7648265 Total length (>= 25000 bp) 4157605 Total length (>= 50000 bp) 966351 # contigs 684 Largest contig 95788 Total length 9245899 Reference length 9283304 N50 23232 N75 13502 L50 130 L75 259 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.051 Duplication ratio 1.006 # N's per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 1330		320
Total length (>= 0 bp) 9281077 Total length (>= 1000 bp) 9217309 Total length (>= 5000 bp) 8680679 Total length (>= 10000 bp) 7648265 Total length (>= 25000 bp) 4157605 Total length (>= 50000 bp) 966351 # contigs 684 Largest contig 95788 Total length 9245899 Reference length 9283304 N50 23232 N75 13502 L50 130 L75 259 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.051 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130		110
Total length (>= 1000 bp) 9217309 Total length (>= 5000 bp) 8680679 Total length (>= 10000 bp) 7648265 Total length (>= 25000 bp) 4157605 Total length (>= 50000 bp) 966351 # contigs 684 Largest contig 95788 Total length 9245899 Reference length 9283304 N50 23232 N75 13502 L50 130 L75 259 # misassemblies 1 # local misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 99.051 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130	# contigs (>= 50000 bp)	15
Total length (>= 5000 bp) 8680679 Total length (>= 10000 bp) 7648265 Total length (>= 25000 bp) 4157605 Total length (>= 50000 bp) 966351 # contigs 684 Largest contig 95788 Total length 9245899 Reference length 9283304 N50 23232 N75 13502 L50 130 L75 259 # misassemblies 1 # local misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.051 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130		9281077
Total length (>= 10000 bp) 7648265 Total length (>= 25000 bp) 4157605 Total length (>= 50000 bp) 966351 # contigs 684 Largest contig 95788 Total length 9245899 Reference length 9283304 N50 23232 N75 13502 L50 130 L75 259 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.051 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130	Total length (>= 1000 bp)	9217309
Total length (>= 25000 bp) 4157605 Total length (>= 50000 bp) 966351 # contigs 684 Largest contig 95788 Total length 9245899 Reference length 9283304 N50 23232 N75 13502 L50 130 L75 259 # misassemblies 1 # local misassembled contigs 1 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.051 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130	Total length (>= 5000 bp)	8680679
Total length (>= 50000 bp) 966351 # contigs 684 Largest contig 95788 Total length 9245899 Reference length 9283304 N50 23232 N75 13502 L50 130 L75 259 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.051 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130	Total length (>= 10000 bp)	7648265
# contigs 684 Largest contig 95788 Total length 9245899 Reference length 9283304 N50 23232 N75 13502 L50 130 L75 259 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.051 Duplication ratio 1.006 # N's per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130	Total length (>= 25000 bp)	4157605
Largest contig 95788 Total length 9245899 Reference length 9283304 N50 23232 N75 13502 L50 130 L75 259 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (♥) 99.051 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130	Total length (>= 50000 bp)	966351
Total length 9245899 Reference length 9283304 N50 23232 N75 13502 L50 130 L75 259 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.051 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130	# contigs	684
Reference length 9283304 N50 23232 N75 13502 L50 130 L75 259 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.051 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130	Largest contig	95788
N50 23232 N75 13502 L50 130 L75 259 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.051 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130	Total length	9245899
N75 13502 L50 130 L75 259 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.051 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130	Reference length	9283304
L50 130 L75 259 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.051 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130	N50	23232
# misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.051 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130	N75	13502
# misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.051 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130	L50	130
# misassembled contigs 1 Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.051 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130	L75	259
Misassembled contigs length 15109 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.051 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130	# misassemblies	1
# local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.051 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130	# misassembled contigs	1
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.051 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130	Misassembled contigs length	15109
Unaligned length 0 Genome fraction (%) 99.051 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130	# local misassemblies	0
Genome fraction (%) 99.051 Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130	# unaligned contigs	0 + 0 part
Duplication ratio 1.006 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130	Genome fraction (%)	99.051
# mismatches per 100 kbp 0.20 # indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130	Duplication ratio	1.006
# indels per 100 kbp 0.00 Largest alignment 95788 NA50 23232 NA75 13502 LA50 130	# N's per 100 kbp	0.00
Largest alignment 95788 NA50 23232 NA75 13502 LA50 130	# mismatches per 100 kbp	0.20
Largest alignment 95788 NA50 23232 NA75 13502 LA50 130	# indels per 100 kbp	0.00
NA75 13502 LA50 130		95788
LA50 130	NA50	23232
LA50 130	NA75	13502
LA75 259	LA50	1
	LA75	259

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	15109
# local misassemblies	0
# mismatches	18
# 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).









