Report

# contigs (>= 0 bp)		
# contigs (>= 1000 bp) 749 # contigs (>= 5000 bp) 749 # contigs (>= 10000 bp) 221 # contigs (>= 25000 bp) 5 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 9840987 Total length (>= 1000 bp) 9601076 Total length (>= 1000 bp) 9601076 Total length (>= 5000 bp) 6834637 Total length (>= 10000 bp) 3175832 Total length (>= 25000 bp) 133677 Total length (>= 50000 bp) 0 # contigs 2023 Largest contig 31188 Total length 9769814 Reference length 9714864 N50 7229 N75 4304 L50 424 L75 855 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # unaligned contigs 0 # unaligned length 0 Genome fraction (%) 99.196 Duplication ratio 1.015 # N's per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424		
# contigs (>= 5000 bp) 749 # contigs (>= 10000 bp) 221 # contigs (>= 25000 bp) 5 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 9840987 Total length (>= 1000 bp) 9601076 Total length (>= 10000 bp) 9601076 Total length (>= 5000 bp) 6834637 Total length (>= 10000 bp) 3175832 Total length (>= 25000 bp) 133677 Total length (>= 50000 bp) 0 # contigs 2023 Largest contig 31188 Total length 9769814 Reference length 9714864 N50 7229 N75 4304 L50 424 L75 855 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 99.196 Duplication ratio 1.015 # N's per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424		2240
# contigs (>= 10000 bp)		1794
# contigs (>= 25000 bp) # contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 1000 bp) Total length (>= 5000 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 (>= 50000 bp) Total length (>= 50000 bp) # contigs Largest contig Total length Reference length N50 Total length Reference length N50 Total length Soon Total length Pofestate Total length Soon Total length Soon Total length Pofestate Soon Total length Soon Soon Total length Soon Soon Total length Soon Soon Total length Soon So		749
# contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 1000 bp) Total length (>= 1000 bp) Fotal length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 25000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) Fotal length (>= 50000 bp) # contigs Largest contig Total length Reference length Reference length Reference length Reference length Roso Roso Roso Roso Roso Roso Roso Ros	# contigs (>= 10000 bp)	221
Total length (>= 0 bp) 9840987 Total length (>= 1000 bp) 9601076 Total length (>= 5000 bp) 6834637 Total length (>= 10000 bp) 3175832 Total length (>= 25000 bp) 133677 Total length (>= 50000 bp) 0 # contigs 2023 Largest contig 31188 Total length 9769814 Reference length 9714864 N50 7229 N75 4304 L50 424 L75 855 # misassemblies 0 # incal misassemblies 0 # unaligned contigs length 0 # unaligned length 0 Genome fraction (%) 99.196 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	# contigs (>= 25000 bp)	5
Total length (>= 1000 bp) 9601076 Total length (>= 5000 bp) 6834637 Total length (>= 10000 bp) 3175832 Total length (>= 25000 bp) 133677 Total length (>= 50000 bp) 0 # contigs 2023 Largest contig 31188 Total length 9769814 Reference length 9714864 N50 7229 N75 4304 L50 424 L75 855 # misassemblies 0 # local misassemblies 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.196 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	# contigs (>= 50000 bp)	0
Total length (>= 5000 bp) 6834637 Total length (>= 10000 bp) 3175832 Total length (>= 25000 bp) 133677 Total length (>= 50000 bp) 0 # contigs 2023 Largest contig 31188 Total length 9769814 Reference length 9714864 N50 7229 N75 4304 L50 424 L75 855 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.196 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	Total length (>= 0 bp)	9840987
Total length (>= 10000 bp) 3175832 Total length (>= 25000 bp) 133677 Total length (>= 50000 bp) 0 # contigs 2023 Largest contig 31188 Total length 9769814 Reference length 9714864 N50 7229 N75 4304 L50 424 L75 855 # misassemblies 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.196 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	Total length (>= 1000 bp)	9601076
Total length (>= 25000 bp) 133677 Total length (>= 50000 bp) 0 # contigs 2023 Largest contig 31188 Total length 9769814 Reference length 9714864 N50 7229 N75 4304 L50 424 L75 855 # misassemblies 0 # incal misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.196 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.67 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	Total length (>= 5000 bp)	6834637
Total length (>= 50000 bp) 0 # contigs 2023 Largest contig 31188 Total length 9769814 Reference length 9714864 N50 7229 N75 4304 L50 424 L75 855 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.196 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	Total length (>= 10000 bp)	3175832
# contigs 2023 Largest contig 31188 Total length 9769814 Reference length 9714864 N50 7229 N75 4304 L50 424 L75 855 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.196 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.67 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	Total length (>= 25000 bp)	133677
Largest contig 31188 Total length 9769814 Reference length 9714864 N50 7229 N75 4304 L50 424 L75 855 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.196 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	Total length (>= 50000 bp)	0
Total length 9769814 Reference length 9714864 N50 7229 N75 4304 L50 424 L75 855 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.196 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.67 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	# contigs	2023
Reference length 9714864 N50 7229 N75 4304 L50 424 L75 855 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.196 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	Largest contig	31188
N50 7229 N75 4304 L50 424 L75 855 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.196 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.67 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	Total length	9769814
N75 4304 L50 424 L75 855 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.196 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.67 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	Reference length	9714864
L50 424 L75 855 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.196 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.67 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	N50	7229
L75 855 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.196 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.67 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	N75	4304
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.196 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.67 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	L50	424
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.196 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.67 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	L75	855
Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.196 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.67 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	# misassemblies	0
# local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.196 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.67 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	# misassembled contigs	0
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.196 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.67 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	Misassembled contigs length	0
Unaligned length 0 Genome fraction (%) 99.196 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.67 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	# local misassemblies	0
Genome fraction (%) 99.196 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.67 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	# unaligned contigs	0 + 0 part
Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.67 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 1.67 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	Genome fraction (%)	99.196
# mismatches per 100 kbp 1.67 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	Duplication ratio	1.015
# indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	# N's per 100 kbp	0.00
Largest alignment 31188 NA50 7229 NA75 4304 LA50 424	# mismatches per 100 kbp	1.67
NA50 7229 NA75 4304 LA50 424	# indels per 100 kbp	0.00
NA75 4304 LA50 424	Largest alignment	31188
NA75 4304 LA50 424	NA50	7229
	NA75	
1.475	LA50	424
LA/5 855	LA75	855

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	0
# mismatches	161
# 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).









