Report

# contigs (>= 1000 bp)		
# contigs (>= 5000 bp)		final.contigs
# contigs (>= 10000 bp) # contigs (>= 25000 bp) # contigs (>= 50000 bp) Total length (>= 1000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) # contigs Largest contig Geg Total length Total lengt	# contigs (>= 1000 bp)	0
# contigs (>= 25000 bp)		0
# contigs (>= 50000 bp) 0 Total length (>= 1000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3 Largest contig 669 Total length 1793 Reference length 3442017 GC (%) 52.26 Reference GC (%) 58.88 N50 622 N75 502 L50 2 L75 3 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # structural variations 0 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 0.009 Duplication ratio 5.803 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2589.00 # indels per 100 kbp 0.000 Largest alignment 215 Total aligned length 509	# contigs (>= 10000 bp)	0
Total length (>= 1000 bp) Total length (>= 5000 bp) Total length (>= 10000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) # contigs Largest contig Geg Total length Total length 1793 Reference length 3442017 GC (%) 52.26 Reference GC (%) N50 622 N75 502 L50 2 L75 # misassembles # misassembled contigs # misassembled contigs length # local misassemblies # structural variations # unaligned mis. contigs # unaligned length Genome fraction (%) Duplication ratio # nises per 100 kbp # indels per 100 kbp Largest alignment 215 Total aligned length 509		0
Total length (>= 5000 bp) 0 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3 Largest contig 669 Total length 1793 Reference length 3442017 GC (%) 52.26 Reference GC (%) 58.88 N50 622 N75 502 L50 2 L75 3 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # structural variations 0 # unaligned mis. contigs 0 # unaligned contigs 0 Genome fraction (%) 0.009 Duplication ratio 5.803 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 215 Total aligned length 509	# contigs (>= 50000 bp)	0
Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3 Largest contig 669 Total length 1793 Reference length 3442017 GC (%) 52.26 Reference GC (%) 58.88 N50 622 N75 502 L50 2 L75 3 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 10 # local misassemblies 0 # structural variations 0 # unaligned mis. contigs 0 # unaligned contigs 0 # unaligned length 0 Genome fraction (%) 0.009 Duplication ratio 5.803 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2589.00 # indels per 100 kbp 0.000 Largest alignment 215 Total aligned length 509	Total length (>= 1000 bp)	0
Total length (>= 25000 bp) Total length (>= 50000 bp) # contigs Largest contig Fotal length Total length Total length Reference length GC (%) Reference GC (%) N50 622 N75 L50 L50 L75 # misassemblies # misassembled contigs # misassembled contigs # misassembled contigs length # local misassemblies # structural variations # unaligned mis. contigs # unaligned contigs Unaligned length Genome fraction (%) Duplication ratio # N's per 100 kbp # indels per 100 kbp Largest alignment 215 Total aligned length 509		0
Total length (>= 50000 bp) 0 # contigs 3 Largest contig 669 Total length 1793 Reference length 3442017 GC (%) 52.26 Reference GC (%) 58.88 N50 622 N75 502 L50 2 L75 3 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # structural variations 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 0.009 Duplication ratio 5.803 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2589.00 # indels per 100 kbp 0.00 Largest alignment 215 Total aligned length 509	Total length (>= 10000 bp)	0
# contigs 3 Largest contig 669 Total length 1793 Reference length 3442017 GC (%) 52.26 Reference GC (%) 58.88 N50 622 N75 502 L50 2 L75 3 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # structural variations 0 # unaligned mis. contigs 0 # unaligned contigs 0 # unaligned length 0 Genome fraction (%) 0.009 Duplication ratio 5.803 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2589.00 # indels per 100 kbp 0.00 Largest alignment 215 Total aligned length 509	Total length (>= 25000 bp)	0
Largest contig 669 Total length 1793 Reference length 3442017 GC (%) 52.26 Reference GC (%) 58.88 N50 622 N75 502 L50 2 L75 3 # misassemblies 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # structural variations 0 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 0.009 Duplication ratio 5.803 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2589.00 # indels per 100 kbp 0.00 Largest alignment 215 Total aligned length 509	Total length (>= 50000 bp)	0
Total length 1793 Reference length 3442017 GC (%) 52.26 Reference GC (%) 58.88 N50 622 N75 502 L50 2 L75 3 # misassemblies 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # structural variations 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 0.009 Duplication ratio 5.803 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2589.00 # indels per 100 kbp 0.00 Largest alignment 215 Total aligned length 509	# contigs	3
Reference length 3442017 GC (%) 52.26 Reference GC (%) 58.88 N50 622 N75 502 L50 2 L75 3 # misassemblies 0 # misassembled contigs 0 # local misassembles 0 # structural variations 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 0.009 Duplication ratio 5.803 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2589.00 # indels per 100 kbp 0.00 Largest alignment 215 Total aligned length 509	Largest contig	669
GC (%) 52.26 Reference GC (%) 58.88 N50 622 N75 502 L50 2 L75 3 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # structural variations 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 0.009 Duplication ratio 5.803 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2589.00 # indels per 100 kbp 0.00 Largest alignment 215 Total aligned length 509	Total length	1793
Reference GC (%) 58.88 N50 622 N75 502 L50 2 L75 3 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # structural variations 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 0.009 Duplication ratio 5.803 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2589.00 # indels per 100 kbp 0.00 Largest alignment 215 Total aligned length 509	Reference length	3442017
N50 622 N75 502 L50 2 L75 3 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # structural variations 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 0.009 Duplication ratio 5.803 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2589.00 # indels per 100 kbp 0.00 Largest alignment 215 Total aligned length 509	GC (%)	52.26
N75 502 L50 2 L75 3 # misassemblies 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # structural variations 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 0.009 Duplication ratio 5.803 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2589.00 # indels per 100 kbp 0.00 Largest alignment 215 Total aligned length 509	Reference GC (%)	58.88
L50 2 L75 3 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # structural variations 0 # unaligned mis. contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 0.009 Duplication ratio 5.803 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2589.00 # indels per 100 kbp 0.00 Largest alignment 215 Total aligned length 509	N50	622
L75 3 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # structural variations 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 0.009 Duplication ratio 5.803 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2589.00 # indels per 100 kbp 0.00 Largest alignment 215 Total aligned length 509	N75	502
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # structural variations 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 0.009 Duplication ratio 5.803 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2589.00 # indels per 100 kbp 0.00 Largest alignment 215 Total aligned length 509	L50	2
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # structural variations 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 0.009 Duplication ratio 5.803 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2589.00 # indels per 100 kbp 0.00 Largest alignment 215 Total aligned length 509	L75	3
Misassembled contigs length 0 # local misassemblies 0 # structural variations 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 0.009 Duplication ratio 5.803 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2589.00 # indels per 100 kbp 0.00 Largest alignment 215 Total aligned length 509	# misassemblies	0
# local misassemblies 0 # structural variations 0 # unaligned mis. contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 0.009 Duplication ratio 5.803 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2589.00 # indels per 100 kbp 0.00 Largest alignment 215 Total aligned length 509	# misassembled contigs	0
# structural variations 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 0.009 Duplication ratio 5.803 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2589.00 # indels per 100 kbp 0.00 Largest alignment 215 Total aligned length 509	Misassembled contigs length	0
# unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 0.009 Duplication ratio 5.803 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2589.00 # indels per 100 kbp 0.00 Largest alignment 215 Total aligned length 509	# local misassemblies	0
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 0.009 Duplication ratio 5.803 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2589.00 # indels per 100 kbp 0.00 Largest alignment 215 Total aligned length 509	# structural variations	0
Unaligned length 0 Genome fraction (%) 0.009 Duplication ratio 5.803 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2589.00 # indels per 100 kbp 0.00 Largest alignment 215 Total aligned length 509	# unaligned mis. contigs	0
Genome fraction (%) 0.009 Duplication ratio 5.803 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2589.00 # indels per 100 kbp 0.00 Largest alignment 215 Total aligned length 509	# unaligned contigs	0 + 0 part
Duplication ratio 5.803 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2589.00 # indels per 100 kbp 0.00 Largest alignment 215 Total aligned length 509	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 2589.00 # indels per 100 kbp 0.00 Largest alignment 215 Total aligned length 509	Genome fraction (%)	0.009
# mismatches per 100 kbp 2589.00 # indels per 100 kbp 0.00 Largest alignment 215 Total aligned length 509	Duplication ratio	5.803
# indels per 100 kbp 0.00 Largest alignment 215 Total aligned length 509	# N's per 100 kbp	0.00
Largest alignment 215 Total aligned length 509	# mismatches per 100 kbp	2589.00
Total aligned length 509	# indels per 100 kbp	0.00
	Largest alignment	215
NGA50 -	Total aligned length	509
	NGA50	-

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
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# mismatches	8
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	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
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).



















