Report

# contigs (>= 1000 bp)		
# contigs (>= 5000 bp)		final.contigs
# contigs (>= 10000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 10000 bp) 2420 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 4 Largest contig 2420 Total length 4409 Reference length 4820916 GC (%) 48.47 Reference GC (%) 36.65 N50 2420 N75 672 L50 1 L75 3 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # unaligned mis. contigs 0 # unaligned length 2901 Genome fraction (%) 0.010 Duplication ratio 3.109 # N's per 100 kbp 0.00 # mismatches per 100 kbp 442.37 Largest alignment 248 Total aligned length 483	# contigs (>= 1000 bp)	1
# contigs (>= 25000 bp) # contigs (>= 50000 bp) Total length (>= 1000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 25000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) # contigs 4 Largest contig 2420 Total length 4409 Reference length 4820916 GC (%) A8.47 Reference GC (%) N50 2420 N75 L50 1 L75 3 # misassembled contigs # misassembled contigs Misassembled contigs # unaligned mis. contigs # unaligned mis. contigs # unaligned length Genome fraction (%) Duplication ratio # N's per 100 kbp # indels per 100 kbp 483 Total aligned length 248 Total aligned length 483		0
# contigs (>= 50000 bp)		0
Total length (>= 1000 bp) 2420 Total length (>= 5000 bp) 0 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 4 Largest contig 2420 Total length 4409 Reference length 4820916 GC (%) 36.65 N50 2420 N75 672 L50 1 L75 3 # misassemblies 0 # unaligned contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned length 290 Genome fraction (%) 0.010 Duplication ratio 3.109 # mismatches per 100 kbp 2474.23 # indels per 100 kbp 412.37 Largest alignment 248 Total aligned length 483	# contigs (>= 25000 bp)	0
Total length (>= 5000 bp) Total length (>= 10000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) # contigs 4 Largest contig 2420 Total length Reference length 4820916 GC (%) Reference GC (%) N50 2420 N75 672 L50 1 L75 3 # misassembled contigs # misassembled contigs Misassembled contigs length # local misassemblies # unaligned mis. contigs # unaligned contigs O + 2 part Unaligned length Genome fraction (%) Duplication ratio # N's per 100 kbp # indels per 100 kbp 483 Largest alignment 248 Total aligned length 483	# contigs (>= 50000 bp)	0
Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 4 Largest contig 2420 Total length 4409 Reference length 4820916 GC (%) 48.47 Reference GC (%) 36.65 N50 2420 N75 672 L50 1 L75 3 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned length 2901 Genome fraction (%) 0.010 Duplication ratio 3.109 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2474.23 # indels per 100 kbp 412.37 Largest alignment 248 Total aligned length 483	Total length (>= 1000 bp)	2420
Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 4 Largest contig 2420 Total length 4409 Reference length 4820916 GC (%) 48.47 Reference GC (%) 36.65 N50 2420 N75 672 L50 1 L75 3 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned length 2901 Genome fraction (%) 0.010 Duplication ratio 3.109 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2474.23 # indels per 100 kbp 412.37 Largest alignment 248 Total aligned length 483	Total length (>= 5000 bp)	0
Total length (>= 50000 bp) 0 # contigs 4 Largest contig 2420 Total length 4409 Reference length 4820916 GC (%) 48.47 Reference GC (%) 36.65 N50 2420 N75 672 L50 1 L75 3 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned mis. contigs 0 # unaligned length 2901 Genome fraction (%) 0.010 Duplication ratio 3.109 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2474.23 # indels per 100 kbp 412.37 Largest alignment 248 Total aligned length 483	Total length (>= 10000 bp)	0
# contigs 4 Largest contig 2420 Total length 4409 Reference length 4820916 GC (%) 48.47 Reference GC (%) 36.65 N50 2420 N75 672 L50 1 L75 3 # misassembles 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned contigs 0 # unaligned length 2901 Genome fraction (%) 0.010 Duplication ratio 3.109 # N's per 100 kbp 0.00 # mismatches per 100 kbp 412.37 Largest alignment 248 Total aligned length 483	Total length (>= 25000 bp)	0
Largest contig 2420 Total length 4409 Reference length 4820916 GC (%) 48.47 Reference GC (%) 36.65 N50 2420 N75 672 L50 1 L75 3 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned length 2901 Genome fraction (%) 0.010 Duplication ratio 3.109 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2474.23 # indels per 100 kbp 412.37 Largest alignment 248 Total aligned length 483	Total length (>= 50000 bp)	0
Total length 4409 Reference length 4820916 GC (%) 48.47 Reference GC (%) 36.65 N50 2420 N75 672 L50 1 L75 3 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned length 2901 Genome fraction (%) 0.010 Duplication ratio 3.109 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2474.23 # indels per 100 kbp 412.37 Largest alignment 248 Total aligned length 483	# contigs	4
Reference length 4820916 GC (%) 48.47 Reference GC (%) 36.65 N50 2420 N75 672 L50 1 L75 3 # misassemblies 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 2 part Unaligned length 2901 Genome fraction (%) 0.010 Duplication ratio 3.109 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2474.23 # indels per 100 kbp 412.37 Largest alignment 248 Total aligned length 483	Largest contig	2420
GC (%) 48.47 Reference GC (%) 36.65 N50 2420 N75 672 L50 1 L75 3 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 2 part Unaligned length 2901 Genome fraction (%) 0.010 Duplication ratio 3.109 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2474.23 # indels per 100 kbp 412.37 Largest alignment 248 Total aligned length 483	Total length	4409
Reference GC (%) 36.65 N50 2420 N75 672 L50 1 L75 3 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 2 part Unaligned length 2901 Genome fraction (%) 0.010 Duplication ratio 3.109 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2474.23 # indels per 100 kbp 412.37 Largest alignment 248 Total aligned length 483	Reference length	4820916
N50 2420 N75 672 L50 1 L75 3 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 + 2 part Unaligned length 2901 Genome fraction (%) 0.010 Duplication ratio 3.109 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2474.23 # indels per 100 kbp 412.37 Largest alignment 248 Total aligned length 483	GC (%)	48.47
N75 672 L50 1 L75 3 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 + 2 part Unaligned length 2901 Genome fraction (%) 0.010 Duplication ratio 3.109 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2474.23 # indels per 100 kbp 412.37 Largest alignment 248 Total aligned length 483	Reference GC (%)	36.65
L50 1 L75 3 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 2 part Unaligned length 2901 Genome fraction (%) 0.010 Duplication ratio 3.109 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2474.23 # indels per 100 kbp 412.37 Largest alignment 248 Total aligned length 483	N50	2420
L75 3 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 2 part Unaligned length 2901 Genome fraction (%) 0.010 Duplication ratio 3.109 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2474.23 # indels per 100 kbp 412.37 Largest alignment 248 Total aligned length 483	N75	672
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 2 part Unaligned length 2901 Genome fraction (%) 0.010 Duplication ratio 3.109 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2474.23 # indels per 100 kbp 412.37 Largest alignment 248 Total aligned length 483	L50	1
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 2 part Unaligned length 2901 Genome fraction (%) 0.010 Duplication ratio 3.109 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2474.23 # indels per 100 kbp 412.37 Largest alignment 248 Total aligned length 483	L75	3
Misassembled contigs length # local misassemblies # unaligned mis. contigs # unaligned contigs # unaligned length Genome fraction (%) Duplication ratio # N's per 100 kbp # mismatches per 100 kbp 412.37 Largest alignment 248 Total aligned length 0 # N's seminoration 483	# misassemblies	0
# local misassemblies 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 2 part Unaligned length 2901 Genome fraction (%) 0.010 Duplication ratio 3.109 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2474.23 # indels per 100 kbp 412.37 Largest alignment 248 Total aligned length 483	# misassembled contigs	0
# unaligned mis. contigs 0 # unaligned contigs 0 + 2 part Unaligned length 2901 Genome fraction (%) 0.010 Duplication ratio 3.109 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2474.23 # indels per 100 kbp 412.37 Largest alignment 248 Total aligned length 483	Misassembled contigs length	0
# unaligned contigs 0 + 2 part Unaligned length 2901 Genome fraction (%) 0.010 Duplication ratio 3.109 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2474.23 # indels per 100 kbp 412.37 Largest alignment 248 Total aligned length 483	# local misassemblies	0
Unaligned length 2901 Genome fraction (%) 0.010 Duplication ratio 3.109 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2474.23 # indels per 100 kbp 412.37 Largest alignment 248 Total aligned length 483	# unaligned mis. contigs	0
Genome fraction (%) 0.010 Duplication ratio 3.109 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2474.23 # indels per 100 kbp 412.37 Largest alignment 248 Total aligned length 483	# unaligned contigs	0 + 2 part
Duplication ratio 3.109 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2474.23 # indels per 100 kbp 412.37 Largest alignment 248 Total aligned length 483	Unaligned length	2901
# N's per 100 kbp 0.00 # mismatches per 100 kbp 2474.23 # indels per 100 kbp 412.37 Largest alignment 248 Total aligned length 483	Genome fraction (%)	0.010
# mismatches per 100 kbp 2474.23 # indels per 100 kbp 412.37 Largest alignment 248 Total aligned length 483	Duplication ratio	3.109
# indels per 100 kbp 412.37 Largest alignment 248 Total aligned length 483	# N's per 100 kbp	0.00
Largest alignment 248 Total aligned length 483	# mismatches per 100 kbp	2474.23
Total aligned length 483	# indels per 100 kbp	412.37
	Largest alignment	248
NGA50 -	Total aligned length	483
	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
# unaligned mis. contigs	0
# mismatches	12
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	2

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	2
Partially unaligned length	2901
# 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).



















