Report

# contigs (>= 0 bp)		
# contigs (>= 1000 bp) 1511 # contigs (>= 5000 bp) 108 # contigs (>= 10000 bp) 4 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 4392029 Total length (>= 1000 bp) 3903367 Total length (>= 1000 bp) 709559 Total length (>= 5000 bp) 709559 Total length (>= 25000 bp) 709559 Total length (>= 25000 bp) 709559 Total length (>= 5000 bp) 709559 Total length (>= 50000 bp) 709559 Total length (>= 1000 bp) 709559 Total length (>= 100 bp) 709559 Total length (>= 1000 bp) 709559 Total length (>= 100 bp) 709559 Total length (>= 1000 bp) 709559 Total length (>= 100 bp) 709559 Total length (>= 1		final.contigs
# contigs (>= 5000 bp)		2269
# contigs (>= 10000 bp)		1511
# contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 4392029 Total length (>= 1000 bp) 3903367 Total length (>= 5000 bp) 709559 Total length (>= 10000 bp) 48458 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 2044 Largest contig 14149 Total length 4302638 Reference length 4641652 N50 2830 N75 1666 L50 500 L75 997 # misassemblies 7 # misassembled contigs 7 Misassembled contigs 7 Misassembled contigs 100 # local misassemblies 100 # unaligned length 169 Genome fraction (%) 91.983 Duplication ratio 1.008 # N's per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662 LA50 500		108
# 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 (>= 50000 bp) # contigs 2044 Largest contig Total length 4302638 Reference length 4641652 N50 N75 1666 L50 500 L75 997 # misassemblies 7 # misassemblies 7 # misassembled contigs 7 Misassembled contigs Total length 169 Genome fraction (%) P1.983 Duplication ratio 1.008 # N's per 100 kbp # indels per 100 kbp 9.84 Largest alignment NA50 2825 NA75 1662 LA50	# contigs (>= 10000 bp)	4
Total length (>= 0 bp) 4392029 Total length (>= 1000 bp) 3903367 Total length (>= 5000 bp) 709559 Total length (>= 10000 bp) 48458 Total length (>= 25000 bp) 0 **Total length (>= 50000 bp) 0 # contigs 2044 Largest contig 14149 Total length 4302638 Reference length 4641652 N50 2830 N75 1666 L50 500 L75 997 # misassemblies 7 # misassembled contigs 7 # local misassemblies 10 # unaligned contigs 0 + 4 part Unaligned length 169 Genome fraction (%) 91.983 Duplication ratio 1.008 # N's per 100 kbp 0.00 # mismatches per 100 kbp 207.35 # indels per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662	# contigs (>= 25000 bp)	0
Total length (>= 1000 bp) 3903367 Total length (>= 5000 bp) 709559 Total length (>= 10000 bp) 48458 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 2044 Largest contig 14149 Total length 4302638 Reference length 4641652 N50 2830 N75 1666 L50 500 L75 997 # misassemblies 7 # local misassemblies 7 # local misassemblies 10 # unaligned contigs 0 + 4 part Unaligned length 169 Genome fraction (%) 91.983 Duplication ratio 1.008 # N's per 100 kbp 0.00 # mismatches per 100 kbp 207.35 # indels per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662 LA50 502	# contigs (>= 50000 bp)	0
Total length (>= 5000 bp) 709559 Total length (>= 10000 bp) 48458 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 2044 Largest contig 14149 Total length 4302638 Reference length 4641652 N50 2830 N75 1666 L50 500 L75 997 # misassemblies 7 # misassembled contigs 7 Misassembled contigs length 30951 # local misassemblies 10 # unaligned contigs 0 + 4 part Unaligned length 169 Genome fraction (%) 91.983 Duplication ratio 1.008 # N's per 100 kbp 0.00 # mismatches per 100 kbp 207.35 # indels per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662 LA50 502	Total length (>= 0 bp)	4392029
Total length (>= 10000 bp) 48458 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 2044 Largest contig 14149 Total length 4302638 Reference length 4641652 N50 2830 N75 1666 L50 500 L75 997 # misassemblies 7 # misassembled contigs 7 Misassembled contigs length 30951 # local misassemblies 10 # unaligned contigs 0 + 4 part Unaligned length 169 Genome fraction (%) 91.983 Duplication ratio 1.008 # N's per 100 kbp 0.00 # mismatches per 100 kbp 207.35 # indels per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662 LA50 502	Total length (>= 1000 bp)	3903367
Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 2044 Largest contig 14149 Total length 4302638 Reference length 4641652 N50 2830 N75 1666 L50 500 L75 997 # misassemblies 7 # misassembled contigs 7 Misassembled contigs length 30951 # local misassemblies 10 # unaligned contigs 0 + 4 part Unaligned length 169 Genome fraction (%) 91.983 Duplication ratio 1.008 # N's per 100 kbp 0.00 # mismatches per 100 kbp 207.35 # indels per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662 LA50 502	Total length (>= 5000 bp)	709559
Total length (>= 50000 bp) 0 # contigs 2044 Largest contig 14149 Total length 4302638 Reference length 4641652 N50 2830 N75 1666 L50 500 L75 997 # misassemblies 7 # misassembled contigs 7 Misassembled contigs length 30951 # local misassemblies 10 # unaligned contigs 0 + 4 part Unaligned length 169 Genome fraction (%) 91.983 Duplication ratio 1.008 # N's per 100 kbp 0.00 # mismatches per 100 kbp 207.35 # indels per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662 LA50 502	Total length (>= 10000 bp)	48458
# contigs 2044 Largest contig 14149 Total length 4302638 Reference length 4641652 N50 2830 N75 1666 L50 500 L75 997 # misassemblies 7 # misassembled contigs 7 Misassembled contigs 7 Misassembled contigs 100 # local misassembles 10 # unaligned contigs 0+4 part Unaligned length 169 Genome fraction (%) 91.983 Duplication ratio 1.008 # N's per 100 kbp 0.00 # mismatches per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662 LA50 502	Total length (>= 25000 bp)	0
Largest contig 14149 Total length 4302638 Reference length 4641652 N50 2830 N75 1666 L50 500 L75 997 # misassemblies 7 # misassembled contigs 7 Misassembled contigs length 30951 # local misassemblies 10 # unaligned contigs 0 + 4 part Unaligned length 169 Genome fraction (%) 91.983 Duplication ratio 1.008 # N's per 100 kbp 0.00 # mismatches per 100 kbp 207.35 # indels per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662 LA50 502	Total length (>= 50000 bp)	0
Total length 4302638 Reference length 4641652 N50 2830 N75 1666 L50 500 L75 997 # misassemblies 7 # misassembled contigs 7 Misassembled contigs length 30951 # local misassemblies 10 # unaligned contigs 0 + 4 part Unaligned length 169 Genome fraction (%) 91.983 Duplication ratio 1.008 # N's per 100 kbp 0.00 # mismatches per 100 kbp 207.35 # indels per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662 LA50 502	# contigs	2044
Reference length 4641652 N50 2830 N75 1666 L50 500 L75 997 # misassemblies 7 # misassembled contigs 7 Misassembled contigs length 30951 # local misassemblies 10 # unaligned contigs 0 + 4 part Unaligned length 169 Genome fraction (%) 91.983 Duplication ratio 1.008 # N's per 100 kbp 0.00 # mismatches per 100 kbp 207.35 # indels per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662 LA50 502	Largest contig	14149
N50 2830 N75 1666 L50 500 L75 997 # misassemblies 7 # misassembled contigs 7 Misassembled contigs length 30951 # local misassemblies 10 # unaligned contigs 0 + 4 part Unaligned length 169 Genome fraction (%) 91.983 Duplication ratio 1.008 # N's per 100 kbp 0.00 # mismatches per 100 kbp 207.35 # indels per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662 LA50 502	Total length	4302638
N75 1666 L50 500 L75 997 # misassemblies 7 # misassembled contigs 7 Misassembled contigs length 30951 # local misassemblies 10 # unaligned contigs 0 + 4 part Unaligned length 169 Genome fraction (%) 91.983 Duplication ratio 1.008 # N's per 100 kbp 0.00 # mismatches per 100 kbp 207.35 # indels per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662 LA50 502	Reference length	4641652
L50 500 L75 997 # misassemblies 7 # misassembled contigs 7 Misassembled contigs length 30951 # local misassemblies 10 # unaligned contigs 0 + 4 part Unaligned length 169 Genome fraction (%) 91.983 Duplication ratio 1.008 # N's per 100 kbp 0.00 # mismatches per 100 kbp 207.35 # indels per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662 LA50 502	N50	2830
L75 997 # misassemblies 7 # misassembled contigs 7 Misassembled contigs length 30951 # local misassemblies 10 # unaligned contigs 0 + 4 part Unaligned length 169 Genome fraction (%) 91.983 Duplication ratio 1.008 # N's per 100 kbp 0.00 # mismatches per 100 kbp 207.35 # indels per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662 LA50 502	N75	1666
# misassemblies 7 # misassembled contigs 7 Misassembled contigs length 30951 # local misassemblies 10 # unaligned contigs 0 + 4 part Unaligned length 169 Genome fraction (%) 91.983 Duplication ratio 1.008 # N's per 100 kbp 0.00 # mismatches per 100 kbp 207.35 # indels per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662 LA50 502	L50	500
# misassembled contigs 7 Misassembled contigs length 30951 # local misassemblies 10 # unaligned contigs 0 + 4 part Unaligned length 169 Genome fraction (%) 91.983 Duplication ratio 1.008 # N's per 100 kbp 0.00 # mismatches per 100 kbp 207.35 # indels per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662 LA50 502	L75	997
Misassembled contigs length 30951 # local misassemblies 10 # unaligned contigs 0 + 4 part Unaligned length 169 Genome fraction (%) 91.983 Duplication ratio 1.008 # N's per 100 kbp 0.00 # mismatches per 100 kbp 207.35 # indels per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662 LA50 502	# misassemblies	7
# local misassemblies 10 # unaligned contigs 0 + 4 part Unaligned length 169 Genome fraction (%) 91.983 Duplication ratio 1.008 # N's per 100 kbp 0.00 # mismatches per 100 kbp 207.35 # indels per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662 LA50 502	# misassembled contigs	7
# unaligned contigs 0 + 4 part Unaligned length 169 Genome fraction (%) 91.983 Duplication ratio 1.008 # N's per 100 kbp 0.00 # mismatches per 100 kbp 207.35 # indels per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662 LA50 502	Misassembled contigs length	30951
Unaligned length 169 Genome fraction (%) 91.983 Duplication ratio 1.008 # N's per 100 kbp 0.00 # mismatches per 100 kbp 207.35 # indels per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662 LA50 502	# local misassemblies	10
Genome fraction (%) 91.983 Duplication ratio 1.008 # N's per 100 kbp 0.00 # mismatches per 100 kbp 207.35 # indels per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662 LA50 502	# unaligned contigs	0 + 4 part
Duplication ratio 1.008 # N's per 100 kbp 0.00 # mismatches per 100 kbp 207.35 # indels per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662 LA50 502	Unaligned length	169
# N's per 100 kbp 0.00 # mismatches per 100 kbp 207.35 # indels per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662 LA50 502	Genome fraction (%)	91.983
# mismatches per 100 kbp 207.35 # indels per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662 LA50 502	Duplication ratio	1.008
# indels per 100 kbp 9.84 Largest alignment 14149 NA50 2825 NA75 1662 LA50 502	# N's per 100 kbp	0.00
Largest alignment 14149 NA50 2825 NA75 1662 LA50 502	# mismatches per 100 kbp	207.35
NA50 2825 NA75 1662 LA50 502	# indels per 100 kbp	9.84
NA75 1662 LA50 502	Largest alignment	14149
LA50 502	NA50	2825
	NA75	1662
LA75 1000	LA50	502
	LA75	1000

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	7
# relocations	7
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	7
Misassembled contigs length	30951
# local misassemblies	10
# mismatches	8853
# indels	420
# short indels	416
# long indels	4
Indels length	714

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	4
# with misassembly	0
# both parts are significant	0
Partially unaligned length	169
# 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).











