Report

# contigs (>= 0 bp) 47 35 # contigs (>= 1000 bp) 11 7 # contigs (>= 5000 bp) 5 6 # contigs (>= 10000 bp) 5 6 # contigs (>= 25000 bp) 3 3 # contigs (>= 50000 bp) 1 1 Total length (>= 0 bp) 187773 179095 Total length (>= 1000 bp) 173623 169301 Total length (>= 5000 bp) 161370 165854 Total length (>= 10000 bp) 161370 158866 Total length (>= 25000 bp) 132733 132339 Total length (>= 50000 bp) 55106 55421 # contigs 20 12 Largest contig 55106 55421 Total length 180875 173140 Reference length 21154421 21154421 N50 49658 49658 N75 17535 27260 L50 2 2 L75 4 3 # misassemblies 1 1 <th></th> <th></th> <th></th>			
# contigs (>= 1000 bp)		meta_contigs_1	meta_contigs_2
# contigs (>= 5000 bp)	# contigs (>= 0 bp)	47	35
# contigs (>= 10000 bp)	# contigs (>= 1000 bp)	11	7
# contigs (>= 25000 bp) 3 3 3 # contigs (>= 50000 bp) 1 1 1 Total length (>= 0 bp) 187773 179095 Total length (>= 1000 bp) 173623 169301 Total length (>= 5000 bp) 161370 165854 Total length (>= 10000 bp) 161370 158866 Total length (>= 25000 bp) 132733 132339 Total length (>= 50000 bp) 55106 55421 # contigs 20 12 Largest contig 55106 55421 Total length 180875 173140 Reference length 21154421 21154421 N50 49658 49658 N75 17535 27260 L50 2 2 2 L75 4 3 3 # misassemblies 2 2 2 # misassembled contigs 1 1 1 Misassembled contigs 1 1 1 Misassembled contigs 2 + 0 part 1 + 0 part 1 Unaligned length 2730 885 Genome fraction (%) 1.179 0.888 Duplication ratio 1.094 1.004 # N's per 100 kbp 7.74 0.00 # mismatches per 100 kbp 392.45 382.74 # indels per 100 kbp 38.48 31.41 Largest alignment 49639 49639 NA50 20813 20822 NA75 17534 16099 LA50 3 3 3	# contigs (>= 5000 bp)	5	6
# contigs (>= 50000 bp)	# contigs (>= 10000 bp)	5	5
Total length (>= 0 bp) 187773 179095 Total length (>= 1000 bp) 173623 169301 Total length (>= 5000 bp) 161370 165854 Total length (>= 10000 bp) 161370 158866 Total length (>= 25000 bp) 132733 132339 Total length (>= 50000 bp) 55106 55421 # contigs 20 12 Largest contig 55106 55421 Total length 180875 173140 Reference length 21154421 21154421 N50 49658 49658 N75 17535 27260 L50 2 2 L75 4 3 # misassembles 2 2 # misassembled contigs 1 1 Misassembled contigs 1 1 Misassembled contigs 1 1 # unaligned contigs length 55106 55421 # unaligned length 2730 885 Genome fraction (%) 1.179 0.888 Duplication ratio 1.094 1.004 # N's per 100 kbp 7.74 0.00 # mismatches per 100 kbp 392.45 382.74 # indels per 100 kbp 38.48 31.41 Largest alignment 49639 49639 NA50 20813 20822 NA75 17534 16099 LA50 3 3	# contigs (>= 25000 bp)	3	3
Total length (>= 1000 bp) 173623 169301 Total length (>= 5000 bp) 161370 165854 Total length (>= 10000 bp) 161370 158866 Total length (>= 25000 bp) 132733 132339 Total length (>= 50000 bp) 55106 55421 # contigs 20 12 Largest contig 55106 55421 Total length 180875 173140 Reference length 21154421 21154421 N50 49658 49658 N75 17535 27260 L50 2 2 L75 4 3 # misassembles 2 2 # misassembled contigs 1 1 Misassembled contigs 1 1 Misassembled contigs 1 1 # unaligned contigs 2 + 0 part 1 + 0 part Unaligned length 2730 885 Genome fraction (%) 1.179 0.888 Duplication ratio 1.094 1.004 # N's per 100 kbp 7.74 0.00 # mismatches per 100 kbp 392.45 382.74 # indels per 100 kbp 38.48 31.41 Largest alignment 49639 49639 NA50 20813 20822 NA75 17534 16099 LA50 3 3 3	# contigs (>= 50000 bp)	1	1
Total length (>= 5000 bp) 161370 165854 Total length (>= 10000 bp) 161370 158866 Total length (>= 25000 bp) 132733 132339 Total length (>= 50000 bp) 55106 55421 # contigs 20 12 Largest contig 55106 55421 Total length 180875 173140 Reference length 21154421 21154421 N50 49658 49658 N75 17535 27260 L50 2 2 L75 4 3 # misassemblies 2 2 # misassembled contigs 1 1 Misassembled contigs length 55106 55421 # local misassemblies 1 1 # unaligned contigs 2 + 0 part 1 + 0 part Unaligned length 2730 885 Genome fraction (%) 1.179 0.888 Duplication ratio 1.094 1.004 # nismatches per 100 kbp 38.48 3	Total length (>= 0 bp)	187773	179095
Total length (>= 10000 bp) 161370 158866 Total length (>= 25000 bp) 132733 132339 Total length (>= 50000 bp) 55106 55421 # contigs 20 12 Largest contig 55106 55421 Total length 180875 173140 Reference length 21154421 21154421 N50 49658 49658 N75 17535 27260 L50 2 2 L75 4 3 # misassemblies 2 2 # misassembled contigs 1 1 Misassembled contigs length 55106 55421 # local misassemblies 1 1 # unaligned contigs 2 + 0 part 1 + 0 part Unaligned length 2730 885 Genome fraction (%) 1.179 0.888 Duplication ratio 1.094 1.004 # N's per 100 kbp 7.74 0.00 # mismatches per 100 kbp 38.48 31.41	Total length (>= 1000 bp)	173623	169301
Total length (>= 25000 bp) 132733 132339 Total length (>= 50000 bp) 55106 55421 # contigs 20 12 Largest contig 55106 55421 Total length 180875 173140 Reference length 21154421 21154421 N50 49658 49658 N75 17535 27260 L50 2 2 L75 4 3 # misassemblies 2 2 # misassembled contigs 1 1 Misassembled contigs 1 1 Misassembled contigs 1 1 # unaligned length 2730 885 Genome fraction (%) 1.179 0.888 Duplication ratio 1.094 1.004 # N's per 100 kbp 392.45 382.74 # indels per 100 kbp 392.45 382.74 Largest alignment 49639 49639 NA50 20813 20822 NA75 17534 16099 LA50 3 3 3	Total length (>= 5000 bp)	161370	165854
Total length (>= 50000 bp) 55106 55421 # contigs 20 12 Largest contig 55106 55421 Total length 180875 173140 Reference length 21154421 21154421 N50 49658 49658 N75 17535 27260 L50 2 2 L75 4 3 # misassemblies 2 2 # misassembled contigs 1 1 # local misassemblies 1 1 # unaligned contigs 2 + 0 part 1 + 0 part Unaligned length 2730 885 Genome fraction (%) 1.179 0.888 Duplication ratio 1.094 1.004 # N's per 100 kbp 7.74 0.00 # mismatches per 100 kbp 38.48 31.41 Largest alignment 49639 49639 NA50 20813 20822 NA75 17534 16099 LA50 3	Total length (>= 10000 bp)	161370	158866
# contigs 20 12 Largest contig 55106 55421 Total length 180875 173140 Reference length 21154421 21154421 N50 49658 49658 N75 17535 27260 L50 2 2 L75 4 3 # misassemblies 2 2 # misassembled contigs 1 1 Misassembled contigs 1 1 Misassembled contigs 1 1 # local misassemblies 1 1 # unaligned contigs 2 + 0 part 1 + 0 part Unaligned length 2730 885 Genome fraction (%) 1.179 0.888 Duplication ratio 1.094 1.004 # N's per 100 kbp 7.74 0.00 # mismatches per 100 kbp 392.45 382.74 # indels per 100 kbp 38.48 31.41 Largest alignment 49639 49639 NA50 20813 20822 NA75 17534 16099 LA50 3 3 3	Total length (>= 25000 bp)	132733	132339
Largest contig 55106 55421 Total length 180875 173140 Reference length 21154421 21154421 N50 49658 49658 N75 17535 27260 L50 2 2 L75 4 3 # misassemblies 1 1 Misassembled contigs 1 1 # local misassemblies 1 1 # unaligned contigs 2 + 0 part 1 + 0 part Unaligned length 2730 885 Genome fraction (%) 1.179 0.888 Duplication ratio 1.094 1.004 # N's per 100 kbp 7.74 0.00 # mismatches per 100 kbp 392.45 382.74 # indels per 100 kbp 38.48 31.41 Largest alignment 49639 49639 NA50 20813 20822 NA75 17534 16099 LA50 3 3	Total length (>= 50000 bp)	55106	55421
Total length 180875 173140 Reference length 21154421 21154421 N50 49658 49658 N75 17535 27260 L50 2 2 L75 4 3 # misassemblies 2 2 # misassembled contigs 1 1 Misassembled contigs length 55106 55421 # local misassemblies 1 1 # unaligned contigs 2 + 0 part 1 + 0 part Unaligned length 2730 885 Genome fraction (%) 1.179 0.888 Duplication ratio 1.094 1.004 # N's per 100 kbp 7.74 0.00 # mismatches per 100 kbp 392.45 382.74 # indels per 100 kbp 38.48 31.41 Largest alignment 49639 49639 NA50 20813 20822 NA75 17534 16099 LA50 3 3	# contigs	20	12
Reference length 21154421 21154421 N50 49658 49658 N75 17535 27260 L50 2 2 L75 4 3 # misassemblies 2 2 # misassembled contigs 1 1 Misassembled contigs length 55106 55421 # local misassemblies 1 1 # unaligned contigs 2 + 0 part 1 + 0 part Unaligned length 2730 885 Genome fraction (%) 1.179 0.888 Duplication ratio 1.094 1.004 # N's per 100 kbp 7.74 0.00 # mismatches per 100 kbp 392.45 382.74 # indels per 100 kbp 38.48 31.41 Largest alignment 49639 49639 NA50 20813 20822 NA75 17534 16099 LA50 3 3	Largest contig	55106	55421
N50 49658 49658 N75 17535 27260 L50 2 2 L75 4 3 # misassemblies 2 2 # misassembled contigs 1 1 Misassembled contigs length 55106 55421 # local misassemblies 1 1 # unaligned contigs 2 + 0 part 1 + 0 part Unaligned length 2730 885 Genome fraction (%) 1.179 0.888 Duplication ratio 1.094 1.004 # N's per 100 kbp 7.74 0.00 # mismatches per 100 kbp 392.45 382.74 # indels per 100 kbp 38.48 31.41 Largest alignment 49639 49639 NA50 20813 20822 NA75 17534 16099 LA50 3 3	Total length	180875	173140
N75 17535 27260 L50 2 2 L75 4 3 # misassemblies 2 2 # misassembled contigs 1 1 Misassembled contigs length 55106 55421 # local misassemblies 1 1 # unaligned contigs 2 + 0 part 1 + 0 part Unaligned length 2730 885 Genome fraction (%) 1.179 0.888 Duplication ratio 1.094 1.004 # N's per 100 kbp 7.74 0.00 # mismatches per 100 kbp 392.45 382.74 # indels per 100 kbp 38.48 31.41 Largest alignment 49639 49639 NA50 20813 20822 NA75 17534 16099 LA50 3 3	Reference length	21154421	21154421
L50 2 2 L75 4 3 # misassemblies 2 2 # misassembled contigs 1 1 Misassembled contigs length 55106 55421 # local misassemblies 1 1 # unaligned contigs 2 + 0 part 1 + 0 part Unaligned length 2730 885 Genome fraction (%) 1.179 0.888 Duplication ratio 1.094 1.004 # N's per 100 kbp 7.74 0.00 # mismatches per 100 kbp 392.45 382.74 # indels per 100 kbp 38.48 31.41 Largest alignment 49639 49639 NA50 20813 20822 NA75 17534 16099 LA50 3 3	N50	49658	49658
L75 4 3 # misassemblies 2 2 # misassembled contigs 1 1 Misassembled contigs length 55106 55421 # local misassemblies 1 1 # unaligned contigs 2 + 0 part 1 + 0 part Unaligned length 2730 885 Genome fraction (%) 1.179 0.888 Duplication ratio 1.094 1.004 # N's per 100 kbp 7.74 0.00 # mismatches per 100 kbp 392.45 382.74 # indels per 100 kbp 38.48 31.41 Largest alignment 49639 49639 NA50 20813 20822 NA75 17534 16099 LA50 3 3	N75	17535	27260
# misassemblies 2 2 2 # misassembled contigs 1 1 1 Misassembled contigs length 55106 55421 # local misassemblies 1 1 1 # unaligned contigs 2 + 0 part 1 + 0 part Unaligned length 2730 885 Genome fraction (%) 1.179 0.888 Duplication ratio 1.094 1.004 # N's per 100 kbp 7.74 0.00 # mismatches per 100 kbp 392.45 382.74 # indels per 100 kbp 38.48 31.41 Largest alignment 49639 49639 NA50 20813 20822 NA75 17534 16099 LA50 3 3	L50	2	2
# misassembled contigs 1 1 1 1 1	L75	4	3
Misassembled contigs length 55106 55421 # local misassemblies 1 1 # unaligned contigs 2 + 0 part 1 + 0 part Unaligned length 2730 885 Genome fraction (%) 1.179 0.888 Duplication ratio 1.094 1.004 # N's per 100 kbp 7.74 0.00 # mismatches per 100 kbp 392.45 382.74 # indels per 100 kbp 38.48 31.41 Largest alignment 49639 49639 NA50 20813 20822 NA75 17534 16099 LA50 3 3	# misassemblies	2	2
# local misassemblies 1 1 1 # unaligned contigs 2 + 0 part 1 + 0 part Unaligned length 2730 885 Genome fraction (%) 1.179 0.888 Duplication ratio 1.094 1.004 # N's per 100 kbp 7.74 0.00 # mismatches per 100 kbp 392.45 382.74 # indels per 100 kbp 38.48 31.41 Largest alignment 49639 49639 NA50 20813 20822 NA75 17534 16099 LA50 3 3	# misassembled contigs	1	1
# unaligned contigs 2 + 0 part 1 + 0 part Unaligned length 2730 885 Genome fraction (%) 1.179 0.888 Duplication ratio 1.094 1.004 # N's per 100 kbp 7.74 0.00 # mismatches per 100 kbp 392.45 382.74 # indels per 100 kbp 38.48 31.41 Largest alignment 49639 49639 NA50 20813 20822 NA75 17534 16099 LA50 3 3	Misassembled contigs length	55106	55421
Unaligned length 2730 885 Genome fraction (%) 1.179 0.888 Duplication ratio 1.094 1.004 # N's per 100 kbp 7.74 0.00 # mismatches per 100 kbp 392.45 382.74 # indels per 100 kbp 38.48 31.41 Largest alignment 49639 49639 NA50 20813 20822 NA75 17534 16099 LA50 3 3	# local misassemblies	1	1
Genome fraction (%) 1.179 0.888 Duplication ratio 1.094 1.004 # N's per 100 kbp 7.74 0.00 # mismatches per 100 kbp 392.45 382.74 # indels per 100 kbp 38.48 31.41 Largest alignment 49639 49639 NA50 20813 20822 NA75 17534 16099 LA50 3 3	# unaligned contigs	2 + 0 part	1 + 0 part
Duplication ratio 1.094 1.004 # N's per 100 kbp 7.74 0.00 # mismatches per 100 kbp 392.45 382.74 # indels per 100 kbp 38.48 31.41 Largest alignment 49639 49639 NA50 20813 20822 NA75 17534 16099 LA50 3 3	Unaligned length	2730	885
# N's per 100 kbp 7.74 0.00 # mismatches per 100 kbp 392.45 382.74 # indels per 100 kbp 38.48 31.41 Largest alignment 49639 49639 NA50 20813 20822 NA75 17534 16099 LA50 3 3	Genome fraction (%)	1.179	0.888
# mismatches per 100 kbp 392.45 382.74 # indels per 100 kbp 38.48 31.41 Largest alignment 49639 49639 NA50 20813 20822 NA75 17534 16099 LA50 3 3	Duplication ratio	1.094	1.004
# indels per 100 kbp 38.48 31.41 Largest alignment 49639 49639 NA50 20813 20822 NA75 17534 16099 LA50 3 3	# N's per 100 kbp	7.74	0.00
Largest alignment 49639 49639 NA50 20813 20822 NA75 17534 16099 LA50 3 3	# mismatches per 100 kbp	392.45	382.74
NA50 20813 20822 NA75 17534 16099 LA50 3 3	# indels per 100 kbp	38.48	31.41
NA75 17534 16099 LA50 3 3	Largest alignment	49639	49639
LA50 3 3	NA50	20813	20822
	NA75	17534	16099
LA75 5 5	LA50	3	3
	LA75	5	5

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

	meta_contigs_1	meta_contigs_2
# misassemblies	2	2
# relocations	1	1
# translocations	0	0
# inversions	0	0
# interspecies translocations	1	1
# possibly misassembled contigs	0	0
# misassembled contigs	1	1
Misassembled contigs length	55106	55421
# local misassemblies	1	1
# mismatches	979	719
# indels	96	59
# short indels	92	55
# long indels	4	4
Indels length	171	119

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

	meta_contigs_1	meta_contigs_2
# fully unaligned contigs	2	1
Fully unaligned length	2730	885
# partially unaligned contigs	0	0
# with misassembly	0	0
# both parts are significant	0	0
Partially unaligned length	0	0
# N's	14	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).













