Report

# contigs (>= 1000 bp) 10 # contigs (>= 5000 bp) 1 # contigs (>= 5000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 10000 bp) 18699 Total length (>= 5000 bp) 5443 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 71 Largest contig 5443 Total length 56195 Reference length 4641652 GC (%) 51.08 Reference GC (%) 50.79 N50 674 N75 562 L50 22 L75 45 # misassemblies 2 # misassembled contigs 2 Misassembled contigs 2 Misassembled contigs 1 # unaligned contigs 1 # unaligned length 7077 # local misassemblies 1 # unaligned length 795 Genome fraction (%) 1.186 Duplication ratio 1.007 # N's per 100 kbp 676.22 # mismatches per 100 kbp 694.15 # indels per 100 kbp 70.87 Largest alignment 5372 NA50 649 NGA50 NA75 556 LA50 24 LA75 48		
# contigs (>= 5000 bp)	#	scaffolds
# contigs (>= 10000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 1000 bp) 18699 Total length (>= 5000 bp) 5443 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 71 Largest contig 5443 Total length 56195 Reference length 4641652 GC (%) 51.08 Reference GC (%) 50.79 N50 674 N75 562 L50 22 L75 45 # misassemblies 2 # misassembled contigs 2 Misassembled contigs 10 # unaligned contigs 11 # unaligned length 7077 # local misassemblies 1 # unaligned length 795 Genome fraction (%) 1.186 Duplication ratio 1.007 # N's per 100 kbp 676.22 # mismatches per 100 kbp 694.15 # indels per 100 kbp 70.87 Largest alignment 5372 NA50 649 NGA50 - NA75 556 LA50 24	3 \ 17	
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# contigs (>= 50000 bp)		0
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Total length (>= 5000 bp) 5443 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 71 Largest contig 5443 Total length 56195 Reference length 4641652 GC (%) 51.08 Reference GC (%) 50.79 N50 674 N75 562 L50 22 L75 45 # misassembled contigs 2 # misassembled contigs 2 Misassembled contigs 10 + 8 part 10 Unaligned length 795 Genome fraction (%) 1.186 Duplication ratio 1.007 # N's per 100 kbp 676.22 # mismatches per 100 kbp 70.87 Largest alignment 5372 NA50 649 NGA50 - NA75 556 LA50 22		0
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Total length (>= 50000 bp) 0 # contigs 71 Largest contig 5443 Total length 56195 Reference length 4641652 GC (%) 51.08 Reference GC (%) 50.79 N50 674 N75 562 L50 22 L75 45 # misassemblies 2 # misassembled contigs 2 Misassembled contigs 0 + 8 part Unaligned contigs 0 + 8 part Unaligned length 795 Genome fraction (%) 1.186 Duplication ratio 1.007 # N's per 100 kbp 676.22 # mismatches per 100 kbp 694.15 # indels per 100 kbp 70.87 Largest alignment 5372 NA50 649 NA75 556 LA50 24		0
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Largest contig 5443 Total length 56195 Reference length 4641652 GC (%) 51.08 Reference GC (%) 50.79 N50 674 N75 562 L50 22 L75 45 # misassemblies 2 # misassembled contigs 2 Misassembled contigs length 7077 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 795 Genome fraction (%) 1.186 Duplication ratio 1.007 # N's per 100 kbp 676.22 # mismatches per 100 kbp 694.15 # indels per 100 kbp 70.87 Largest alignment 5372 NA50 649 NA75 556 LA50 24	Total length (>= 50000 bp)	0
Total length 56195 Reference length 4641652 GC (%) 51.08 Reference GC (%) 50.79 N50 674 N75 562 L50 22 L75 45 # misassemblies 2 # misassembled contigs 2 Misassembled contigs length 7077 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 795 Genome fraction (%) 1.186 Duplication ratio 1.007 # N's per 100 kbp 676.22 # mismatches per 100 kbp 694.15 # indels per 100 kbp 70.87 Largest alignment 5372 NA50 649 NA75 556 LA50 24	# contigs	71
Reference length 4641652 GC (%) 51.08 Reference GC (%) 50.79 N50 674 N75 562 L50 22 L75 45 # misassemblies 2 # misassembled contigs 2 Misassembled contigs length 7077 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 795 Genome fraction (%) 1.186 Duplication ratio 1.007 # N's per 100 kbp 676.22 # mismatches per 100 kbp 694.15 # indels per 100 kbp 70.87 Largest alignment 5372 NA50 649 NA75 556 LA50 24	Largest contig	5443
GC (%) 51.08 Reference GC (%) 50.79 N50 674 N75 562 L50 22 L75 45 # misassemblies 2 # misassembled contigs 2 Misassembled contigs length 7077 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 795 Genome fraction (%) 1.186 Duplication ratio 1.007 # N's per 100 kbp 676.22 # mismatches per 100 kbp 694.15 # indels per 100 kbp 70.87 Largest alignment 5372 NA50 649 NGA50 - NA75 556 LA50 24	Total length	56195
Reference GC (%) 50.79 N50 674 N75 562 L50 22 L75 45 # misassemblies 2 # misassembled contigs 2 Misassembled contigs length 7077 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 795 Genome fraction (%) 1.186 Duplication ratio 1.007 # N's per 100 kbp 676.22 # mismatches per 100 kbp 694.15 # indels per 100 kbp 70.87 Largest alignment 5372 NA50 649 NGA50 - NA75 556 LA50 24	Reference length	4641652
N50 674 N75 562 L50 22 L75 45 # misassemblies 2 Misassembled contigs 2 Misassembled contigs length 7077 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 795 Genome fraction (%) 1.186 Duplication ratio 1.007 # N's per 100 kbp 676.22 # mismatches per 100 kbp 694.15 # indels per 100 kbp 70.87 Largest alignment 5372 NA50 649 NA75 556 LA50 24	GC (%)	51.08
N75 562 L50 22 L75 45 # misassemblies 2 # misassembled contigs 2 Misassembled contigs length 7077 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 795 Genome fraction (%) 1.186 Duplication ratio 1.007 # N's per 100 kbp 676.22 # mismatches per 100 kbp 694.15 # indels per 100 kbp 70.87 Largest alignment 5372 NA50 649 NGA50 - NA75 556 LA50 24	Reference GC (%)	50.79
L50 22 L75 45 # misassemblies 2 # misassembled contigs 2 Misassembled contigs length 7077 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 795 Genome fraction (%) 1.186 Duplication ratio 1.007 # N's per 100 kbp 676.22 # mismatches per 100 kbp 694.15 # indels per 100 kbp 70.87 Largest alignment 5372 NA50 649 NGA50 - NA75 556 LA50 24	N50	674
# misassemblies 2 # misassembled contigs 2 Misassembled contigs length 7077 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 795 Genome fraction (%) 1.186 Duplication ratio 1.007 # N's per 100 kbp 676.22 # mismatches per 100 kbp 694.15 # indels per 100 kbp 70.87 Largest alignment 5372 NA50 649 NGA50 - NA75 556 LA50 24	N75	562
# misassemblies 2 # misassembled contigs 2 Misassembled contigs length 7077 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 795 Genome fraction (%) 1.186 Duplication ratio 1.007 # N's per 100 kbp 676.22 # mismatches per 100 kbp 694.15 # indels per 100 kbp 70.87 Largest alignment 5372 NA50 649 NGA50 - NA75 556 LA50 24	L50	22
# misassembled contigs 2 Misassembled contigs length 7077 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 795 Genome fraction (%) 1.186 Duplication ratio 1.007 # N's per 100 kbp 676.22 # mismatches per 100 kbp 694.15 # indels per 100 kbp 70.87 Largest alignment 5372 NA50 649 NGA50 - NA75 556 LA50 24	L75	45
Misassembled contigs length 7077 # local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 795 Genome fraction (%) 1.186 Duplication ratio 1.007 # N's per 100 kbp 676.22 # mismatches per 100 kbp 694.15 # indels per 100 kbp 70.87 Largest alignment 5372 NA50 649 NGA50 - NA75 556 LA50 24	# misassemblies	2
# local misassemblies 1 # unaligned contigs 0 + 8 part Unaligned length 795 Genome fraction (%) 1.186 Duplication ratio 1.007 # N's per 100 kbp 676.22 # mismatches per 100 kbp 694.15 # indels per 100 kbp 70.87 Largest alignment 5372 NA50 649 NGA50 - NA75 556 LA50 24	# misassembled contigs	2
# unaligned contigs 0 + 8 part Unaligned length 795 Genome fraction (%) 1.186 Duplication ratio 1.007 # N's per 100 kbp 676.22 # mismatches per 100 kbp 694.15 # indels per 100 kbp 70.87 Largest alignment 5372 NA50 649 NGA50 - NA75 556 LA50 24	Misassembled contigs length	7077
Unaligned length 795 Genome fraction (%) 1.186 Duplication ratio 1.007 # N's per 100 kbp 676.22 # mismatches per 100 kbp 694.15 # indels per 100 kbp 70.87 Largest alignment 5372 NA50 649 NGA50 - NA75 556 LA50 24	# local misassemblies	1
Genome fraction (%) 1.186 Duplication ratio 1.007 # N's per 100 kbp 676.22 # mismatches per 100 kbp 694.15 # indels per 100 kbp 70.87 Largest alignment 5372 NA50 649 NGA50 - NA75 556 LA50 24	# unaligned contigs	0 + 8 part
Duplication ratio 1.007 # N's per 100 kbp 676.22 # mismatches per 100 kbp 694.15 # indels per 100 kbp 70.87 Largest alignment 5372 NA50 649 NGA50 - NA75 556 LA50 24	Unaligned length	795
# N's per 100 kbp 676.22 # mismatches per 100 kbp 694.15 # indels per 100 kbp 70.87 Largest alignment 5372 NA50 649 NGA50 - NA75 556 LA50 24	Genome fraction (%)	1.186
# mismatches per 100 kbp 694.15 # indels per 100 kbp 70.87 Largest alignment 5372 NA50 649 NGA50 - NA75 556 LA50 24	Duplication ratio	1.007
# indels per 100 kbp 70.87 Largest alignment 5372 NA50 649 NGA50 - NA75 556 LA50 24	# N's per 100 kbp	676.22
Largest alignment 5372 NA50 649 NGA50 - NA75 556 LA50 24	# mismatches per 100 kbp	694.15
NA50 649 NGA50 - NA75 556 LA50 24	# indels per 100 kbp	70.87
NGA50 - NA75 556 LA50 24	Largest alignment	5372
NA75 556 LA50 24	NA50	649
LA50 24	NGA50	-
	NA75	556
LA75 48	LA50	24
	LA75	48

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

	scaffolds
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	7077
# local misassemblies	1
# mismatches	382
# indels	39
# short indels	24
# long indels	15
Indels length	218

All statistics are based on contigs of size \geq 500 bp, unless otherwise noted (e.g., "# contigs (\geq 0 bp)" and "Total length (\geq 0 bp)" include all contigs).

Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	8
# with misassembly	0
# both parts are significant	0
Partially unaligned length	795
# N's	380

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).















