Report

# contigs (>= 0 bp) 1003 # contigs (>= 1000 bp) 802 # contigs (>= 5000 bp) 325 # contigs (>= 10000 bp) 102 # contigs (>= 25000 bp) 22 # contigs (>= 25000 bp) 22 # contigs (>= 50000 bp) 00 Total length (>= 0 bp) 4374169 Total length (>= 1000 bp) 4264728 Total length (>= 5000 bp) 2960601 Total length (>= 10000 bp) 1385446 Total length (>= 25000 bp) 66428 Total length (>= 50000 bp) 66428 Total length (>= 50000 bp) 00 # contigs 917 Largest contig 37682 Total length 4348006 Reference length 4641652 N50 7401 N75 4233 L50 195 L75 390 # misassemblies 16 # misassembled contigs 15 Misassembled contigs 15 Misassembled contigs 10 # unaligned contigs 10 # unaligned length 4994 Genome fraction (%) 93.360 Duplication ratio 1.002 # N's per 100 kbp 485.81 # mismatches per 100 kbp 166.82 # indels per 100 kbp 32.63 Largest alignment 37682 NA50 7226 NA75 4109 LA50 196		
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Total length (>= 5000 bp) 2960601 Total length (>= 10000 bp) 1385446 Total length (>= 25000 bp) 66428 Total length (>= 50000 bp) 0 # contigs 917 Largest contig 37682 Total length 4348006 Reference length 4641652 N50 7401 N75 4233 L50 195 L75 390 # misassemblies 16 # misassembled contigs 15 Misassembled contigs length 86787 # local misassemblies 10 # unaligned contigs 4 + 2 part Unaligned length 4994 Genome fraction (♥6) 93.360 Duplication ratio 1.002 # N's per 100 kbp 485.81 # mismatches per 100 kbp 166.82 NA50 7226 NA75 4109 LA50 196	Total length (>= 0 bp)	4374169
Total length (>= 10000 bp) 1385446 Total length (>= 25000 bp) 66428 Total length (>= 50000 bp) 0 # contigs 917 Largest contig 37682 Total length 4348006 Reference length 4641652 N50 7401 N75 4233 L50 195 L75 390 # misassemblies 16 # misassembled contigs 15 Misassembled contigs 15 Misassembled contigs 10 # local misassemblies 10 # unaligned contigs 4 + 2 part Unaligned length 4994 Genome fraction (♥6) 93.360 Duplication ratio 1.002 # N's per 100 kbp 485.81 # mismatches per 100 kbp 166.82 # indels per 100 kbp 32.63 Largest alignment 37682 NA50 7226 NA75 4109 LA50 196	Total length (>= 1000 bp)	4264728
Total length (>= 25000 bp) 66428 Total length (>= 50000 bp) 0 # contigs 917 Largest contig 37682 Total length 4348006 Reference length 4641652 N50 7401 N75 4233 L50 195 L75 390 # misassemblies 16 # misassembled contigs 15 Misassembled contigs length 86787 # local misassemblies 10 # unaligned contigs 4 + 2 part Unaligned length 4994 Genome fraction (%) 93.360 Duplication ratio 1.002 # N's per 100 kbp 485.81 # mismatches per 100 kbp 32.63 Largest alignment 37682 NA50 7226 NA75 4109 LA50 196	Total length (>= 5000 bp)	2960601
Total length (>= 50000 bp) 0 # contigs 917 Largest contig 37682 Total length 4348006 Reference length 4641652 N50 7401 N75 4233 L50 195 L75 390 # misassemblies 16 # misassembled contigs 15 Misassembled contigs length 86787 # local misassemblies 10 # unaligned contigs 4 + 2 part Unaligned length 4994 Genome fraction (%) 93.360 Duplication ratio 1.002 # N's per 100 kbp 485.81 # mismatches per 100 kbp 166.82 # indels per 100 kbp 32.63 Largest alignment 37682 NA50 7226 NA75 4109 LA50 196	Total length (>= 10000 bp)	1385446
# contigs 917 Largest contig 37682 Total length 4348006 Reference length 4641652 N50 7401 N75 4233 L50 195 L75 390 # misassemblies 16 # misassembled contigs 15 Misassembled contigs length 86787 # local misassemblies 10 # unaligned contigs 4 + 2 part Unaligned length 4994 Genome fraction (%) 93.360 Duplication ratio 1.002 # N's per 100 kbp 485.81 # mismatches per 100 kbp 166.82 # indels per 100 kbp 32.63 Largest alignment 37682 NA50 7226 NA75 4109 LA50 196	Total length (>= 25000 bp)	66428
Largest contig 37682 Total length 4348006 Reference length 4641652 N50 7401 N75 4233 L50 195 L75 390 # misassemblies 16 # misassembled contigs 15 Misassembled contigs length 86787 # local misassemblies 10 # unaligned contigs 4 + 2 part Unaligned length 4994 Genome fraction (%) 93.360 Duplication ratio 1.002 # N's per 100 kbp 485.81 # mismatches per 100 kbp 166.82 # indels per 100 kbp 32.63 Largest alignment 37682 NA50 7226 NA75 4109 LA50 196	Total length (>= 50000 bp)	0
Total length 4348006 Reference length 4641652 N50 7401 N75 4233 L50 195 L75 390 # misassemblies 16 # misassembled contigs 15 Misassembled contigs length 86787 # local misassemblies 10 # unaligned contigs 4 + 2 part Unaligned length 4994 Genome fraction (%) 93.360 Duplication ratio 1.002 # N's per 100 kbp 485.81 # mismatches per 100 kbp 166.82 # indels per 100 kbp 32.63 Largest alignment 37682 NA50 7226 NA75 4109 LA50 196	# contigs	917
Reference length 4641652 N50 7401 N75 4233 L50 195 L75 390 # misassemblies 16 # misassembled contigs 15 Misassembled contigs length 86787 # local misassemblies 10 # unaligned contigs 4 + 2 part Unaligned length 4994 Genome fraction (%) 93.360 Duplication ratio 1.002 # N's per 100 kbp 485.81 # mismatches per 100 kbp 166.82 # indels per 100 kbp 32.63 Largest alignment 37682 NA50 7226 NA75 4109 LA50 196	Largest contig	37682
N50 7401 N75 4233 L50 195 L75 390 # misassemblies 16 # misassembled contigs 15 Misassembled contigs length 86787 # local misassemblies 10 # unaligned contigs 4 + 2 part Unaligned length 4994 Genome fraction (%) 93.360 Duplication ratio 1.002 # N's per 100 kbp 485.81 # mismatches per 100 kbp 166.82 # indels per 100 kbp 32.63 Largest alignment 37682 NA50 7226 NA75 4109 LA50 196	Total length	4348006
N75 4233 L50 195 L75 390 # misassemblies 16 # misassembled contigs 15 Misassembled contigs length 86787 # local misassemblies 10 # unaligned contigs 4 + 2 part Unaligned length 4994 Genome fraction (%) 93.360 Duplication ratio 1.002 # N's per 100 kbp 485.81 # mismatches per 100 kbp 166.82 # indels per 100 kbp 32.63 Largest alignment 37682 NA50 7226 NA75 4109 LA50 196	Reference length	4641652
L50 195 L75 390 # misassemblies 16 # misassembled contigs 15 Misassembled contigs length 86787 # local misassemblies 10 # unaligned contigs 4 + 2 part Unaligned length 4994 Genome fraction (%) 93.360 Duplication ratio 1.002 # N's per 100 kbp 485.81 # mismatches per 100 kbp 166.82 # indels per 100 kbp 32.63 Largest alignment 37682 NA50 7226 NA75 4109 LA50 196	N50	7401
L75 390 # misassemblies 16 # misassembled contigs 15 Misassembled contigs length 86787 # local misassemblies 10 # unaligned contigs 4 + 2 part Unaligned length 4994 Genome fraction (%) 93.360 Duplication ratio 1.002 # N's per 100 kbp 485.81 # mismatches per 100 kbp 166.82 # indels per 100 kbp 32.63 Largest alignment 37682 NA50 7226 NA75 4109 LA50 196	N75	4233
# misassemblies 16 # misassembled contigs 15 Misassembled contigs length 86787 # local misassemblies 10 # unaligned contigs 4 + 2 part Unaligned length 4994 Genome fraction (%) 93.360 Duplication ratio 1.002 # N's per 100 kbp 485.81 # mismatches per 100 kbp 166.82 # indels per 100 kbp 32.63 Largest alignment 37682 NA50 7226 NA75 4109 LA50 196	L50	195
# misassembled contigs 15 Misassembled contigs length 86787 # local misassemblies 10 # unaligned contigs 4 + 2 part Unaligned length 4994 Genome fraction (%) 93.360 Duplication ratio 1.002 # N's per 100 kbp 485.81 # mismatches per 100 kbp 166.82 # indels per 100 kbp 32.63 Largest alignment 37682 NA50 7226 NA75 4109 LA50 196	L75	390
Misassembled contigs length 86787 # local misassemblies 10 # unaligned contigs 4 + 2 part Unaligned length 4994 Genome fraction (%) 93.360 Duplication ratio 1.002 # N's per 100 kbp 485.81 # mismatches per 100 kbp 166.82 # indels per 100 kbp 32.63 Largest alignment 37682 NA50 7226 NA75 4109 LA50 196	# misassemblies	16
# local misassemblies 10 # unaligned contigs 4 + 2 part Unaligned length 4994 Genome fraction (%) 93.360 Duplication ratio 1.002 # N's per 100 kbp 485.81 # mismatches per 100 kbp 166.82 # indels per 100 kbp 32.63 Largest alignment 37682 NA50 7226 NA75 4109 LA50 196	# misassembled contigs	15
# unaligned contigs 4 + 2 part Unaligned length 4994 Genome fraction (%) 93.360 Duplication ratio 1.002 # N's per 100 kbp 485.81 # mismatches per 100 kbp 166.82 # indels per 100 kbp 32.63 Largest alignment 37682 NA50 7226 NA75 4109 LA50 196	Misassembled contigs length	86787
Unaligned length 4994 Genome fraction (%) 93.360 Duplication ratio 1.002 # N's per 100 kbp 485.81 # mismatches per 100 kbp 166.82 # indels per 100 kbp 32.63 Largest alignment 37682 NA50 7226 NA75 4109 LA50 196	# local misassemblies	10
Genome fraction (%) 93.360 Duplication ratio 1.002 # N's per 100 kbp 485.81 # mismatches per 100 kbp 166.82 # indels per 100 kbp 32.63 Largest alignment 37682 NA50 7226 NA75 4109 LA50 196	# unaligned contigs	4 + 2 part
Duplication ratio 1.002 # N's per 100 kbp 485.81 # mismatches per 100 kbp 166.82 # indels per 100 kbp 32.63 Largest alignment 37682 NA50 7226 NA75 4109 LA50 196	Unaligned length	4994
# N's per 100 kbp 485.81 # mismatches per 100 kbp 166.82 # indels per 100 kbp 32.63 Largest alignment 37682 NA50 7226 NA75 4109 LA50 196	Genome fraction (%)	93.360
# mismatches per 100 kbp 166.82 # indels per 100 kbp 32.63 Largest alignment 37682 NA50 7226 NA75 4109 LA50 196	Duplication ratio	1.002
# indels per 100 kbp 32.63 Largest alignment 37682 NA50 7226 NA75 4109 LA50 196	# N's per 100 kbp	485.81
Largest alignment 37682 NA50 7226 NA75 4109 LA50 196	# mismatches per 100 kbp	166.82
NA50 7226 NA75 4109 LA50 196	# indels per 100 kbp	32.63
NA75 4109 LA50 196	Largest alignment	37682
LA50 196	NA50	7226
	NA75	4109
LA75 396	LA50	196
	LA75	396

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	16
# relocations	16
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	1
# misassembled contigs	15
Misassembled contigs length	86787
# local misassemblies	10
# mismatches	7229
# indels	1414
# short indels	738
# long indels	676
Indels length	11527

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

	scaffolds
# fully unaligned contigs	4
Fully unaligned length	3466
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	1
Partially unaligned length	1528
# N's	21123

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).









