Report

# contigs (>= 1000 bp) 106 # contigs (>= 5000 bp) 67 # contigs (>= 10000 bp) 60 # contigs (>= 25000 bp) 46 # contigs (>= 50000 bp) 29 Total length (>= 10000 bp) 4493024 Total length (>= 10000 bp) 4396833 Total length (>= 10000 bp) 4396833 Total length (>= 50000 bp) 417236 Total length (>= 50000 bp) 417236 Total length (>= 50000 bp) 3512590 # contigs 143 Largest contig 317313 Total length 4517317 Reference length 4641652 GC (%) 50.79 Reference GC (%) 50.78 N50 95318 NG50 94928 N75 59591 NG75 58576 L50 13 LG50 14 L75 27 LG75 29 # misassemblies 18 # misassembled contigs 2 Misassembled contigs 2 Misassembled contigs 4 # unaligned length 0 Genome fraction (%) 89.572 Duplication ratio 1.087 # n's per 100 kbp 1.15 # mismatches per 100 kbp 0.91 Largest alignment 317313 NA50 86515 NGA50 14 LGA50 15		scaffolds
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Total length (>= 10000 bp)	Total length (>= 1000 bp)	4493024
Total length (>= 25000 bp)	Total length (>= 5000 bp)	4396833
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Largest contig 317313 Total length 4517317 Reference length 4641652 GC (%) 50.79 Reference GC (%) 50.78 N50 95318 NG50 94928 N75 59591 NG75 58576 L50 13 LG50 14 L75 27 LG75 29 # misassemblies 18 # misassembled contigs 2 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 89.572 Duplication ratio 1.087 # N's per 100 kbp 1.15 # mismatches per 100 kbp 1.91 Largest alignment 317313 NA50 86515 NGA50 84208 NA75 47277 NGA75 40613 LA50 14 LGA50 15 LA75 31	Total length (>= 50000 bp)	3512590
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Reference length 4641652 GC (%) 50.79 Reference GC (%) 50.78 N50 95318 NG50 94928 N75 59591 NG75 58576 L50 13 LG50 14 L75 27 LG75 29 # misassemblies 18 # misassembled contigs 2 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 89.572 Duplication ratio 1.087 # N's per 100 kbp 1.15 # mismatches per 100 kbp 1047.45 # indels per 100 kbp 0.91 Largest alignment 317313 NA50 86515 NGA50 84208 NA75 47277 NGA75 40613 LA50 14 LGA50 15 LA75 31	Largest contig	317313
GC (%) 50.79 Reference GC (%) 50.78 N50 95318 NG50 94928 N75 59591 NG75 58576 L50 13 LG50 14 L75 27 LG75 29 # misassemblies 18 # misassembled contigs 2 Misassembled contigs 302873 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 89.572 Duplication ratio 1.087 # N's per 100 kbp 1.15 # mismatches per 100 kbp 1047.45 # indels per 100 kbp 0.91 Largest alignment 317313 NA50 86515 NGA50 84208 NA75 47277 NGA75 40613 LA50 14 LGA50 15 LA75 31	Total length	4517317
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NG50 94928 N75 59591 NG75 58576 L50 13 LG50 14 L75 27 LG75 29 # misassemblies 18 # misassembled contigs 2 Misassembled contigs length 302873 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 89.572 Duplication ratio 1.087 # N's per 100 kbp 1.15 # mismatches per 100 kbp 1047.45 # indels per 100 kbp 0.91 Largest alignment 317313 NA50 86515 NGA50 84208 NA75 47277 NGA75 40613 LA50 14 LGA50 15 LA75 31	Reference GC (%)	50.78
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NG75 58576 L50 13 LG50 14 L75 27 LG75 29 # misassemblies 18 # misassembled contigs 2 Misassembled contigs length 302873 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 89.572 Duplication ratio 1.087 # N's per 100 kbp 1.15 # mismatches per 100 kbp 1047.45 # indels per 100 kbp 0.91 Largest alignment 317313 NA50 86515 NGA50 84208 NA75 47277 NGA75 40613 LA50 14 LGA50 15 LA75 31	NG50	94928
L50 13 LG50 14 L75 27 LG75 29 # misassemblies 18 # misassembled contigs 2 Misassembled contigs length 302873 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 89.572 Duplication ratio 1.087 # N's per 100 kbp 1.15 # mismatches per 100 kbp 1047.45 # indels per 100 kbp 0.91 Largest alignment 317313 NA50 86515 NGA50 84208 NA75 47277 NGA75 40613 LA50 14 LGA50 15 LA75 31	N75	59591
LG50 14 L75 27 LG75 29 # misassemblies 18 # misassembled contigs 2 Misassembled contigs length 302873 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 89.572 Duplication ratio 1.087 # N's per 100 kbp 1.15 # mismatches per 100 kbp 1047.45 # indels per 100 kbp 0.91 Largest alignment 317313 NA50 86515 NGA50 84208 NA75 47277 NGA75 40613 LA50 14 LGA50 15 LA75 31	NG75	58576
L75 27 LG75 29 # misassemblies 18 # misassembled contigs 2 Misassembled contigs length 302873 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 89.572 Duplication ratio 1.087 # N's per 100 kbp 1.15 # mismatches per 100 kbp 1047.45 # indels per 100 kbp 0.91 Largest alignment 317313 NA50 86515 NGA50 84208 NA75 47277 NGA75 40613 LA50 14 LGA50 15 LA75 31	L50	13
# misassemblies 18 # misassembled contigs 2 Misassembled contigs length 302873 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 89.572 Duplication ratio 1.087 # N's per 100 kbp 1.15 # mismatches per 100 kbp 1047.45 # indels per 100 kbp 0.91 Largest alignment 317313 NA50 86515 NGA50 84208 NA75 47277 NGA75 40613 LA50 14 LGA50 15 LA75 31	LG50	14
# misassemblies	L75	27
# misassembled contigs 2 Misassembled contigs length 302873 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 89.572 Duplication ratio 1.087 # N's per 100 kbp 1.15 # mismatches per 100 kbp 1047.45 # indels per 100 kbp 0.91 Largest alignment 317313 NA50 86515 NGA50 84208 NA75 47277 NGA75 40613 LA50 14 LGA50 15 LA75 31	LG75	29
Misassembled contigs length 302873 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 89.572 Duplication ratio 1.087 # N's per 100 kbp 1.15 # mismatches per 100 kbp 1047.45 # indels per 100 kbp 0.91 Largest alignment 317313 NA50 86515 NGA50 84208 NA75 47277 NGA75 40613 LA50 14 LGA50 15 LA75 31	# misassemblies	18
# local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 89.572 Duplication ratio 1.087 # N's per 100 kbp 1.15 # mismatches per 100 kbp 0.91 Largest alignment 317313 NA50 86515 NGA50 84208 NA75 47277 NGA75 40613 LA50 14 LGA50 15 LA75 31	# misassembled contigs	2
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 89.572 Duplication ratio 1.087 # N's per 100 kbp 1.15 # mismatches per 100 kbp 1047.45 # indels per 100 kbp 0.91 Largest alignment 317313 NA50 86515 NGA50 84208 NA75 47277 NGA75 40613 LA50 14 LGA50 15 LA75 31	Misassembled contigs length	302873
Unaligned length 0 Genome fraction (%) 89.572 Duplication ratio 1.087 # N's per 100 kbp 1.15 # mismatches per 100 kbp 1047.45 # indels per 100 kbp 0.91 Largest alignment 317313 NA50 86515 NGA50 84208 NA75 47277 NGA75 40613 LA50 14 LGA50 15 LA75 31	# local misassemblies	4
Genome fraction (%) 89.572 Duplication ratio 1.087 # N's per 100 kbp 1.15 # mismatches per 100 kbp 1047.45 # indels per 100 kbp 0.91 Largest alignment 317313 NA50 86515 NGA50 84208 NA75 47277 NGA75 40613 LA50 14 LGA50 15 LA75 31		0 + 0 part
Duplication ratio 1.087 # N's per 100 kbp 1.15 # mismatches per 100 kbp 1047.45 # indels per 100 kbp 0.91 Largest alignment 317313 NA50 86515 NGA50 84208 NA75 47277 NGA75 40613 LA50 14 LGA50 15 LA75 31	Unaligned length	0
# N's per 100 kbp 1.15 # mismatches per 100 kbp 1047.45 # indels per 100 kbp 0.91 Largest alignment 317313 NA50 86515 NGA50 84208 NA75 47277 NGA75 40613 LA50 14 LGA50 15 LA75 31	Genome fraction (%)	89.572
# mismatches per 100 kbp 1047.45 # indels per 100 kbp 0.91 Largest alignment 317313 NA50 86515 NGA50 84208 NA75 47277 NGA75 40613 LA50 14 LGA50 15 LA75 31		1.087
# indels per 100 kbp 0.91 Largest alignment 317313 NA50 86515 NGA50 84208 NA75 47277 NGA75 40613 LA50 14 LGA50 15 LA75 31		
Largest alignment 317313 NA50 86515 NGA50 84208 NA75 47277 NGA75 40613 LA50 14 LGA50 15 LA75 31	# mismatches per 100 kbp	1047.45
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LGA50 15 LA75 31		
LA75 31		
LGA75 33		
	LGA75	33

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	18
# relocations	15
# translocations	0
# inversions	3
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	302873
# local misassemblies	4
# mismatches	43549
# indels	38
# short indels	38
# long indels	0
Indels length	45

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	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	52

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).

















