Report

# contigs (>= 1000 bp)		scaffolds
# contigs (>= 5000 bp)	# contigs (>= 1000 bp)	
# contigs (>= 10000 bp) 44 # contigs (>= 25000 bp) 38 # contigs (>= 50000 bp) 33 Total length (>= 1000 bp) 4744744 Total length (>= 5000 bp) 4722723 Total length (>= 10000 bp) 4722723 Total length (>= 25000 bp) 4634350 Total length (>= 50000 bp) 47447495 # contigs 71 Largest contig 300358 Total length 4755788 Reference length 4641652 GC (%) 50.85 Reference GC (%) 50.79 N50 167276 N75 92493 NG75 104699 L50 11 LG50 11 L75 20 LG75 19 # misassemblies 20 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.908 Duplication ratio 1.046 # N's per 100 kbp 0.00 # mismatches per 100 kbp 783.29 # indels per 100 kbp 1.10 Largest alignment 300358 NA50 159904 NA75 79751 NGA75 87060 LA50 11 LG50 11 LG50 11 LG50 11 LG50 159904 NA75 79751 NGA75 87060 LA50 11 LG50 11 LG50 11 LG50 11 LG50 11 LG50 11 LG50 11		44
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Total length (>= 50000 bp) 4474495 # contigs 71 Largest contig 300358 Total length 4755788 Reference length 4641652 GC (%) 50.85 Reference GC (%) 50.79 N50 167276 NG50 167276 N75 92493 NG75 104699 L50 11 L75 20 LG75 19 # misassemblies 20 # misassembled contigs 1 Misassembled contigs 1 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.908 Duplication ratio 1.046 # N's per 100 kbp 0.00 # mismatches per 100 kbp 783.29 # indels per 100 kbp 783.29 # indels per 100 kbp 1.59904 NA50 159904 NA75 79751	Total length (>= 10000 bp)	4722723
# contigs 71 Largest contig 300358 Total length 4755788 Reference length 4641652 GC (%) 50.85 Reference GC (%) 50.79 N50 167276 NG50 167276 N75 92493 NG75 104699 L50 11 LG50 11 LG50 11 L75 20 LG75 19 # misassemblies 20 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 21 Unaligned length 0 Genome fraction (%) 97.908 Duplication ratio 1.046 # N's per 100 kbp 0.00 # mismatches per 100 kbp 783.29 # indels per 100 kbp 1.10 Largest alignment 300358 NA50 159904 NA75 79751 NGA75 87060 LA50 11 LGA50 11 LGA50 11 LGA50 11 LGA50 11 LGA50 11 LGA50 11	Total length (>= 25000 bp)	4634350
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Total length 4755788 Reference length 4641652 GC (%) 50.85 Reference GC (%) 50.79 N50 167276 NG50 167276 N75 92493 NG75 104699 L50 11 L75 20 LG75 19 # misassemblies 20 # misassembled contigs 1 Misassembled contigs length 210680 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.908 Duplication ratio 1.046 # N's per 100 kbp 0.00 # mismatches per 100 kbp 783.29 # indels per 100 kbp 1.10 Largest alignment 300358 NA50 159904 NA75 79751 NGA75 87060 LA50 11 LGA50 11 LA75 22 <td># contigs</td> <td>71</td>	# contigs	71
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Reference GC (%) 50.79 N50 167276 NG50 167276 N75 92493 NG75 104699 L50 11 LG50 11 L75 20 LG75 19 # misassemblies 20 # misassembled contigs 1 Misassembled contigs 210680 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.908 Duplication ratio 1.046 # N's per 100 kbp 0.00 # mismatches per 100 kbp 783.29 # indels per 100 kbp 1.10 Largest alignment 300358 NA50 159904 NA75 79751 NGA75 87060 LA50 11 LGA50 11 LA75 22	Reference length	4641652
N50 167276 NG50 167276 N75 92493 NG75 104699 L50 11 LG50 11 L75 20 LG75 19 # misassemblies 20 # misassembled contigs 1 Misassembled contigs length 210680 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.908 Duplication ratio 1.046 # N's per 100 kbp 0.00 # mismatches per 100 kbp 783.29 # indels per 100 kbp 1.10 Largest alignment 300358 NA50 159904 NA75 79751 NGA75 87060 LA50 11 LGA50 11 LA75 22	GC (%)	50.85
NG50 167276 N75 92493 NG75 104699 L50 11 LG50 11 L75 20 LG75 19 # misassemblies 20 # misassembled contigs 1 Misassembled contigs length 210680 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.908 Duplication ratio 1.046 # N's per 100 kbp 0.00 # mismatches per 100 kbp 783.29 # indels per 100 kbp 1.10 Largest alignment 300358 NA50 159904 NA75 79751 NGA75 87060 LA50 11 LA50 11 LA75 22	Reference GC (%)	50.79
N75 92493 NG75 104699 L50 11 LG50 11 L75 20 LG75 19 # misassemblies 20 # misassembled contigs 1 Misassembled contigs length 210680 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.908 Duplication ratio 1.046 # N's per 100 kbp 0.00 # mismatches per 100 kbp 783.29 # indels per 100 kbp 1.10 Largest alignment 300358 NA50 159904 NA75 79751 NGA75 87060 LA50 11 LGA50 11 LA75 22	N50	167276
NG75 104699 L50 11 LG50 11 L75 20 LG75 19 # misassemblies 20 # misassembled contigs 1 Misassembled contigs length 210680 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.908 Duplication ratio 1.046 # N's per 100 kbp 0.00 # mismatches per 100 kbp 783.29 # indels per 100 kbp 1.10 Largest alignment 300358 NA50 159904 NA75 79751 NGA75 87060 LA50 11 LGA50 11 LA75 22	NG50	167276
L50 11 LG50 11 L75 20 LG75 19 # misassemblies 20 # misassembled contigs 1 Misassembled contigs length 210680 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.908 Duplication ratio 1.046 # N's per 100 kbp 0.00 # mismatches per 100 kbp 783.29 # indels per 100 kbp 1.10 Largest alignment 300358 NA50 159904 NA75 79751 NGA75 87060 LA50 11 LGA50 11 LA75 22	N75	92493
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L75 20 LG75 19 # misassemblies 20 # misassembled contigs 1 Misassembled contigs length 210680 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.908 Duplication ratio 1.046 # N's per 100 kbp 0.00 # mismatches per 100 kbp 783.29 # indels per 100 kbp 1.10 Largest alignment 300358 NA50 159904 NA75 79751 NGA75 87060 LA50 11 LGA50 11 LA75 22	L50	11
# misassemblies 20 # misassembled contigs 1 Misassembled contigs length 210680 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.908 Duplication ratio 1.046 # N's per 100 kbp 0.00 # mismatches per 100 kbp 783.29 # indels per 100 kbp 1.10 Largest alignment 300358 NA50 159904 NGA50 159904 NA75 79751 NGA75 87060 LA50 11 LGA50 11 LGA50 11	LG50	11
# misassemblies 20 # misassembled contigs 1 Misassembled contigs length 210680 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.908 Duplication ratio 1.046 # N's per 100 kbp 0.00 # mismatches per 100 kbp 783.29 # indels per 100 kbp 1.10 Largest alignment 300358 NA50 159904 NGA50 159904 NA75 79751 NGA75 87060 LA50 11 LGA50 11 LGA50 11	L75	20
# misassembled contigs 1 Misassembled contigs length 210680 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.908 Duplication ratio 1.046 # N's per 100 kbp 0.00 # mismatches per 100 kbp 783.29 # indels per 100 kbp 1.10 Largest alignment 300358 NA50 159904 NGA50 159904 NA75 79751 NGA75 87060 LA50 11 LGA50 11 LGA50 12	LG75	19
Misassembled contigs length 210680 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.908 Duplication ratio 1.046 # N's per 100 kbp 0.00 # mismatches per 100 kbp 783.29 # indels per 100 kbp 1.10 Largest alignment 300358 NA50 159904 NGA50 159904 NA75 79751 NGA75 87060 LA50 11 LGA50 11 LA75 22	# misassemblies	20
# local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.908 Duplication ratio 1.046 # N's per 100 kbp 0.00 # mismatches per 100 kbp 783.29 # indels per 100 kbp 1.10 Largest alignment 300358 NA50 159904 NGA50 159904 NA75 79751 NGA75 87060 LA50 11 LGA50 11 LGA50 11	# misassembled contigs	1
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.908 Duplication ratio 1.046 # N's per 100 kbp 0.00 # mismatches per 100 kbp 783.29 # indels per 100 kbp 1.10 Largest alignment 300358 NA50 159904 NGA50 159904 NA75 79751 NGA75 87060 LA50 11 LGA50 11 LGA50 12	Misassembled contigs length	210680
Unaligned length 0 Genome fraction (%) 97.908 Duplication ratio 1.046 # N's per 100 kbp 0.00 # mismatches per 100 kbp 783.29 # indels per 100 kbp 1.10 Largest alignment 300358 NA50 159904 NGA50 159904 NA75 79751 NGA75 87060 LA50 11 LGA50 11 LA75 22	# local misassemblies	2
Genome fraction (%) 97.908 Duplication ratio 1.046 # N's per 100 kbp 0.00 # mismatches per 100 kbp 783.29 # indels per 100 kbp 1.10 Largest alignment 300358 NA50 159904 NGA50 159904 NA75 79751 NGA75 87060 LA50 11 LGA50 11 LA75 22	# unaligned contigs	0 + 0 part
Duplication ratio 1.046 # N's per 100 kbp 0.00 # mismatches per 100 kbp 783.29 # indels per 100 kbp 1.10 Largest alignment 300358 NA50 159904 NGA50 159904 NA75 79751 NGA75 87060 LA50 11 LGA50 11 LA75 22	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 783.29 # indels per 100 kbp 1.10 Largest alignment 300358 NA50 159904 NGA50 159904 NA75 79751 NGA75 87060 LA50 11 LGA50 11 LGA50 22	Genome fraction (%)	97.908
# mismatches per 100 kbp 783.29 # indels per 100 kbp 1.10 Largest alignment 300358 NA50 159904 NGA50 159904 NA75 79751 NGA75 87060 LA50 11 LGA50 11 LA75 22	Duplication ratio	1.046
# indels per 100 kbp 1.10 Largest alignment 300358 NA50 159904 NGA50 159904 NA75 79751 NGA75 87060 LA50 11 LGA50 11 LA75 22	# N's per 100 kbp	0.00
Largest alignment 300358 NA50 159904 NGA50 159904 NA75 79751 NGA75 87060 LA50 11 LGA50 11 LA75 22		783.29
NA50 159904 NGA50 159904 NA75 79751 NGA75 87060 LA50 11 LGA50 11 LA75 22	# indels per 100 kbp	1.10
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LA75 22		
LGA75 21		
	LGA75	21

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	20
# relocations	18
# translocations	0
# inversions	2
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	210680
# local misassemblies	2
# mismatches	35597
# indels	50
# short indels	49
# long indels	1
Indels length	58

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	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).

















