Report

# contigs (>= 1000 bp) 102 # contigs (>= 5000 bp) 75 # contigs (>= 10000 bp) 69 # contigs (>= 25000 bp) 50 # contigs (>= 50000 bp) 50 # contigs (>= 50000 bp) 31 Total length (>= 10000 bp) 44553482 Total length (>= 10000 bp) 4497911 Total length (>= 10000 bp) 4454422 Total length (>= 25000 bp) 4452419 Total length (>= 50000 bp) 4452419 Total length (>= 50000 bp) 3508368 # contigs 122 Largest contig 327151 Total length (>= 50000 bp) 4566723 Reference length 4566723 Reference length 4641652 GC (%) 50.75 Reference GC (%) 50.79 N50 105736 NG50 105683 N75 53827 NG75 53820 L50 14 LG50 15 L75 30 LG75 31 # misassemblies 0 # misassembled contigs 0 Misassembled 0 Misas		
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# contigs (>= 25000 bp)		75
# contigs (>= 50000 bp)	•	69
Total length (>= 1000 bp)	# contigs (>= 25000 bp)	50
Total length (>= 5000 bp) 4497911 Total length (>= 10000 bp) 4454422 Total length (>= 25000 bp) 4152419 Total length (>= 50000 bp) 3508368 # contigs 122 Largest contig 327151 Total length 4566723 Reference length 4641652 GC (%) 50.75 Reference GC (%) 50.79 N50 105736 NG50 105683 N75 53827 NG75 53820 L50 14 LG50 15 L75 30 LG75 31 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # unaligned length 53 Genome fraction (%) 98.303 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.07 Largest alignment 327151 NA50 105736		31
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Total length (>= 50000 bp) 3508368 # contigs 122 Largest contig 327151 Total length 4566723 Reference length 4641652 GC (%) 50.75 Reference GC (%) 50.79 N50 105736 NG50 105683 N75 53827 NG75 53820 L50 14 LG50 15 L75 30 LG75 31 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 7 # unaligned length 53 Genome fraction (%) 98.303 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.07 Largest alignment 327151 NA50 105683 NA75 53827 NGA75 53820 LA50 14 <td></td> <td>4454422</td>		4454422
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N50 105736 NG50 105683 N75 53827 NG75 53820 L50 14 LG50 15 L75 30 LG75 31 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 7 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.303 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.07 Largest alignment 327151 NA50 105736 NGA50 105683 NA75 53827 NGA75 53820 LA50 14 LGA50 15 LA75 30		50.75
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NG75 53820 L50 14 LG50 15 L75 30 LG75 31 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 7 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.303 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.07 Largest alignment 327151 NA50 105736 NGA50 105683 NA75 53827 NGA75 53820 LA50 14 LGA50 15 LA75 30	NG50	105683
L50 14 LG50 15 L75 30 LG75 31 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 7 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.303 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.07 Largest alignment 327151 NA50 105736 NGA50 105683 NA75 53827 NGA75 53820 LA50 14 LGA50 15 LA75 30	N75	53827
LG50 15 L75 30 LG75 31 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 7 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.303 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.07 Largest alignment 327151 NA50 105736 NGA50 105683 NA75 53827 NGA75 53820 LA50 14 LGA50 15 LA75 30	NG75	53820
L75 30 LG75 31 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 7 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.303 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.07 Largest alignment 327151 NA50 105736 NGA50 105683 NA75 53827 NGA75 53820 LA50 14 LGA50 15 LA75 30	L50	14
LG75 31 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 7 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.303 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.16 # indels per 100 kbp 0.07 Largest alignment 327151 NA50 105736 NGA50 105683 NA75 53827 NGA75 53820 LA50 14 LGA50 15 LA75 30		15
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 7 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.303 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.16 # indels per 100 kbp 0.07 Largest alignment 327151 NA50 105736 NGA50 105683 NA75 53827 NGA75 53820 LA50 14 LGA50 15 LA75 30	L75	30
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 7 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.303 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.07 Largest alignment 327151 NA50 105736 NGA50 105683 NA75 53827 NGA75 53820 LA50 14 LGA50 15 LA75 30	LG75	31
Misassembled contigs length 0 # local misassemblies 7 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.303 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.16 # indels per 100 kbp 0.07 Largest alignment 327151 NA50 105736 NGA50 105683 NA75 53827 NGA75 53820 LA50 14 LGA50 15 LA75 30		0
# local misassemblies 7 # unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.303 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.16 # indels per 100 kbp 0.07 Largest alignment 327151 NA50 105736 NGA50 105683 NA75 53827 NGA75 53820 LA50 14 LGA50 155 LA75 30		0
# unaligned contigs 0 + 1 part Unaligned length 53 Genome fraction (%) 98.303 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.16 # indels per 100 kbp 0.07 Largest alignment 327151 NA50 105736 NGA50 105683 NA75 53827 NGA75 53827 NGA75 53820 LA50 14 LGA50 155 LA75 30	Misassembled contigs length	0
Unaligned length 53 Genome fraction (%) 98.303 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.16 # indels per 100 kbp 0.07 Largest alignment 327151 NA50 105736 NGA50 105683 NA75 53827 NGA75 53820 LA50 14 LGA50 15 LA75 30	# local misassemblies	7
Genome fraction (%) 98.303 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.16 # indels per 100 kbp 0.07 Largest alignment 327151 NA50 105736 NGA50 105683 NA75 53827 NGA75 53820 LA50 14 LGA50 15 LA75 30	# unaligned contigs	0 + 1 part
Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.16 # indels per 100 kbp 0.07 Largest alignment 327151 NA50 105736 NGA50 105683 NA75 53827 NGA75 53820 LA50 14 LGA50 15 LA75 30		53
# N's per 100 kbp 0.00 # mismatches per 100 kbp 1.16 # indels per 100 kbp 0.07 Largest alignment 327151 NA50 105736 NGA50 105683 NA75 53827 NGA75 53820 LA50 14 LGA50 155 LA75 30		98.303
# mismatches per 100 kbp 1.16 # indels per 100 kbp 0.07 Largest alignment 327151 NA50 105736 NGA50 105683 NA75 53827 NGA75 53820 LA50 14 LGA50 155 LA75 30	Duplication ratio	1.001
# indels per 100 kbp 0.07 Largest alignment 327151 NA50 105736 NGA50 105683 NA75 53827 NGA75 53820 LA50 14 LGA50 155 LA75 30	# N's per 100 kbp	0.00
Largest alignment 327151 NA50 105736 NGA50 105683 NA75 53827 NGA75 53820 LA50 14 LGA50 15 LA75 30		1.16
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NGA75 53820 LA50 14 LGA50 15 LA75 30	NGA50	
LA50 14 LGA50 15 LA75 30	NA75	53827
LGA50 15 LA75 30	NGA75	53820
LA75 30	LA50	14
	LGA50	15
LGA75 31		30
	LGA75	31

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

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	7
# mismatches	53
# indels	3
# short indels	3
# long indels	0
Indels length	3

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

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	53
# 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).















