Report

# contigs (>= 1000 bp) 80 # contigs (>= 5000 bp) 61 # contigs (>= 25000 bp) 55 # contigs (>= 25000 bp) 43 # contigs (>= 50000 bp) 28 Total length (>= 10000 bp) 4550585 Total length (>= 5000 bp) 4507705 Total length (>= 10000 bp) 4550585 Total length (>= 10000 bp) 4550585 Total length (>= 50000 bp) 4275525 Total length (>= 25000 bp) 4275525 Total length (>= 50000 bp) 3733992 # contigs 87 Largest contig 326979 Total length 4555927 Reference length 4641652 GC (%) 50.79 N50 132611 N75 60768 NG75 59038 L50 11 LG50 11 L75 23 LG75 24 # misassemblies 2 # misassembled contigs 2 Misassembled contigs 2 Misassembled contigs 14 # unaligned length 0 Genome fraction (%) 98.114 Duplication ratio 1.000 # N's per 100 kbp 62.82 # indels per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11		scaffolds
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# contigs (>= 10000 bp)		61
# contigs (>= 25000 bp)		55
# contigs (>= 50000 bp) 28 Total length (>= 1000 bp) 4550585 Total length (>= 5000 bp) 4507705 Total length (>= 10000 bp) 4463142 Total length (>= 25000 bp) 4275525 Total length (>= 50000 bp) 3733992 # contigs 87 Largest contig 326979 Total length 4555927 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 132611 N75 60768 NG75 59038 L50 11 L75 23 LG75 24 # misassemblies 2 # misassembled contigs 24 # misassembled contigs 24 # unaligned contigs 14 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.114 Duplication ratio 1.000 # N's per 100 kbp 62.82 # indels per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11		43
Total length (>= 5000 bp)		28
Total length (>= 5000 bp)	Total length (>= 1000 bp)	4550585
Total length (>= 25000 bp) 4275525 Total length (>= 50000 bp) 3733992 # contigs 87 Largest contig 326979 Total length 4555927 Reference length 4641652 GC (%) 50.79 N50 132611 NG50 132611 N75 60768 NG75 59038 L50 11 L75 23 LG75 24 # misassembled contigs 2 # misassembled contigs 2 # soassembled contigs 14 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.114 Duplication ratio 1.000 # N's per 100 kbp 6.21 # mismatches per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NA75 60768 NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11		4507705
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# contigs 326979 Largest contig 326979 Total length 4555927 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 132611 NG50 132611 N75 60768 NG75 59038 L50 11 LG50 11 L75 23 LG75 24 # misassemblies 2 # misassembled contigs 2 Misassembled contigs 14 # local misassemblies 14 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.114 Duplication ratio 1.000 # N's per 100 kbp 6.21 # mismatches per 100 kbp 62.82 # indels per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11	Total length (>= 50000 bp)	3733992
Total length 4555927 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 132611 NG50 132611 N75 60768 NG75 59038 L50 11 LG50 11 L75 23 LG75 24 # misassemblies 2 # misassembled contigs 2 Misassembled contigs length 78666 # local misassemblies 14 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.114 Duplication ratio 1.000 # N's per 100 kbp 6.21 # mismatches per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NGA50 132611 NGA50 132611 NGA50 132611 NGA50 132611 NGA75 59037		87
Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 132611 NG50 132611 N75 60768 NG75 59038 L50 11 L75 23 LG75 24 # misassemblies 2 # misassembled contigs 2 Misassembled contigs 14 # local misassemblies 14 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.114 Duplication ratio 1.000 # N's per 100 kbp 62.82 # indels per 100 kbp 62.82 # indels per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11 LA75 23	Largest contig	326979
GC (%) 50.74 Reference GC (%) 50.79 N50 132611 NG50 132611 N75 60768 NG75 59038 L50 11 L75 23 LG75 24 # misassemblies 2 # misassembled contigs 2 Misassembled contigs 14 # local misassemblies 14 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.114 Duplication ratio 1.000 # N's per 100 kbp 6.21 # mismatches per 100 kbp 62.82 # indels per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11 LA75 23	Total length	4555927
Reference GC (%) 50.79 N50 132611 NG50 132611 N75 60768 NG75 59038 L50 11 LG50 11 L75 23 LG75 24 # misassemblies 2 # misassembled contigs 2 Misassembled contigs 0 + 0 part # local misassemblies 14 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.114 Duplication ratio 1.000 # N's per 100 kbp 6.21 # mismatches per 100 kbp 62.82 # indels per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NGA50 132611 NGA75 59037 LA50 11 LGA50 11 LA75 23	Reference length	4641652
N50 132611 NG50 132611 N75 60768 NG75 59038 L50 11 LG50 11 L75 23 LG75 24 # misassemblies 2 # misassembled contigs 2 Misassembled contigs length 78666 # local misassemblies 14 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.114 Duplication ratio 1.000 # N's per 100 kbp 6.21 # mismatches per 100 kbp 62.82 # indels per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11 LA75 23	GC (%)	50.74
NG50 132611 N75 60768 NG75 59038 L50 11 LG50 11 L75 23 LG75 24 # misassemblies 2 # misassembled contigs 2 Misassembled contigs length 78666 # local misassemblies 14 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.114 Duplication ratio 1.000 # N's per 100 kbp 6.21 # mismatches per 100 kbp 62.82 # indels per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LA50 11 LA75 23	Reference GC (%)	50.79
N75 60768 NG75 59038 L50 11 LG50 11 L75 23 LG75 24 # misassemblies 2 # misassembled contigs 2 Misassembled contigs length 78666 # local misassemblies 14 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.114 Duplication ratio 1.000 # N's per 100 kbp 6.21 # mismatches per 100 kbp 62.82 # indels per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11 LA75 23	N50	132611
NG75 59038 L50 11 LG50 11 L75 23 LG75 24 # misassemblies 2 # misassembled contigs 2 Misassembled contigs length 78666 # local misassemblies 14 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.114 Duplication ratio 1.000 # N's per 100 kbp 6.21 # mismatches per 100 kbp 62.82 # indels per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11 LA75 23	NG50	132611
L50 11 LG50 11 L75 23 LG75 24 # misassemblies 2 # misassembled contigs 2 Misassembled contigs length 78666 # local misassemblies 14 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.114 Duplication ratio 1.000 # N's per 100 kbp 6.21 # mismatches per 100 kbp 62.82 # indels per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11 LA75 23	N75	60768
LG50 11 L75 23 LG75 24 # misassemblies 2 # misassembled contigs 2 Misassembled contigs length 78666 # local misassemblies 14 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.114 Duplication ratio 1.000 # N's per 100 kbp 6.21 # mismatches per 100 kbp 62.82 # indels per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11 LA75 23	NG75	59038
L75 23 LG75 24 # misassemblies 2 # misassembled contigs 2 Misassembled contigs length 78666 # local misassemblies 14 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.114 Duplication ratio 1.000 # N's per 100 kbp 6.21 # mismatches per 100 kbp 62.82 # indels per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11 LA75 23	L50	11
LG75 24 # misassemblies 2 # misassembled contigs 2 Misassembled contigs length 78666 # local misassemblies 14 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.114 Duplication ratio 1.000 # N's per 100 kbp 6.21 # mismatches per 100 kbp 62.82 # indels per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11 LA75 23	LG50	11
# misassemblies 2 # misassembled contigs 2 Misassembled contigs length 78666 # local misassemblies 14 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.114 Duplication ratio 1.000 # N's per 100 kbp 6.21 # mismatches per 100 kbp 62.82 # indels per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11 LGA50 11 LGA50 12	L75	23
# misassembled contigs 2 Misassembled contigs length 78666 # local misassemblies 14 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.114 Duplication ratio 1.000 # N's per 100 kbp 6.21 # mismatches per 100 kbp 62.82 # indels per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11 LGA50 11 LGA50 12	LG75	24
Misassembled contigs length 78666 # local misassemblies 14 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.114 Duplication ratio 1.000 # N's per 100 kbp 6.21 # mismatches per 100 kbp 62.82 # indels per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11 LA75 23	# misassemblies	2
# local misassemblies 14 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.114 Duplication ratio 1.000 # N's per 100 kbp 6.21 # mismatches per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11 LGA50 11 LA75 23	# misassembled contigs	2
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.114 Duplication ratio 1.000 # N's per 100 kbp 6.21 # mismatches per 100 kbp 62.82 # indels per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11 LGA50 11 LA75 23	Misassembled contigs length	78666
Unaligned length 0 Genome fraction (%) 98.114 Duplication ratio 1.000 # N's per 100 kbp 6.21 # mismatches per 100 kbp 62.82 # indels per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11 LA75 23	# local misassemblies	14
Genome fraction (%) 98.114 Duplication ratio 1.000 # N's per 100 kbp 6.21 # mismatches per 100 kbp 62.82 # indels per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11 LA75 23	# unaligned contigs	0 + 0 part
Duplication ratio 1.000 # N's per 100 kbp 6.21 # mismatches per 100 kbp 62.82 # indels per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11 LA75 23	Unaligned length	0
# N's per 100 kbp 6.21 # mismatches per 100 kbp 62.82 # indels per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11 LGA50 23	Genome fraction (%)	98.114
# mismatches per 100 kbp 62.82 # indels per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11 LGA50 23	Duplication ratio	1.000
# indels per 100 kbp 8.08 Largest alignment 326979 NA50 132611 NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11 LA75 23	· '	
Largest alignment 326979 NA50 132611 NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11 LA75 23		
NA50 132611 NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11 LA75 23	# indels per 100 kbp	
NGA50 132611 NA75 60768 NGA75 59037 LA50 11 LGA50 11 LA75 23	Largest alignment	326979
NA75 60768 NGA75 59037 LA50 11 LGA50 11 LA75 23		
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LGA50 11 LA75 23		
LA75 23		
LGA75 24		
	LGA75	24

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	78666
# local misassemblies	14
# mismatches	2861
# indels	368
# short indels	364
# long indels	4
Indels length	686

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	283

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).

















