Report

# contigs (>= 1000 bp) 202 # contigs (>= 5000 bp) 155 # contigs (>= 10000 bp) 124 # contigs (>= 25000 bp) 59 # contigs (>= 50000 bp) 12 Total length (>= 10000 bp) 3877089 Total length (>= 10000 bp) 3765485 Total length (>= 10000 bp) 3531953 Total length (>= 25000 bp) 2475094 Total length (>= 50000 bp) 3531953 Total length (>= 50000 bp) 2475094 Total length (>= 50000 bp) 823529 # contigs 222 Largest contig 132022 Total length 3890229 Reference length 4641652 GC (%) 50.79 Reference GC (%) 50.79 N50 32027 NG50 27862 N75 17754 NG75 10818 L50 41 LG50 54 L75 80 LG75 120 # misassemblies 4 # misassembled contigs 4 Misassembled contigs length 152553 # local misassemblies 2 # unaligned length 0 Genome fraction (%) 81.651 Duplication ratio 1.026 # N's per 100 kbp 0.00 # mismatches per 100 kbp 915.16 # indels per 100 kbp 0.37 Largest alignment 132022 NA50 31972 NGA50 27492 NA75 17458 NGA75 10813 LA50 42 LGA50 55 LA75 82 LGA75 122		scaffolds
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N50 32027 NG50 27862 N75 17754 NG75 10818 L50 41 LG50 54 L75 80 LG75 120 # misassemblies 4 # misassembled contigs 4 Misassembled contigs length 152553 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 81.651 Duplication ratio 1.026 # N's per 100 kbp 0.00 # mismatches per 100 kbp 915.16 # indels per 100 kbp 0.37 Largest alignment 132022 NA50 31972 NGA50 27492 NA75 17458 NGA75 10813 LA50 42 LGA50 55 LA75 82		50.79
NG50 27862 N75 17754 NG75 10818 L50 41 LG50 54 L75 80 LG75 120 # misassemblies 4 # misassembled contigs 4 Misassembled contigs length 152553 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 81.651 Duplication ratio 1.026 # N's per 100 kbp 0.00 # mismatches per 100 kbp 915.16 # indels per 100 kbp 0.37 Largest alignment 132022 NA50 31972 NGA50 27492 NA75 17458 NGA75 10813 LA50 42 LGA50 55 LA75 82	Reference GC (%)	50.79
N75 17754 NG75 10818 L50 41 LG50 54 L75 80 LG75 120 # misassemblies 4 # misassembled contigs 4 Misassembled contigs length 152553 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 81.651 Duplication ratio 1.026 # N's per 100 kbp 0.00 # mismatches per 100 kbp 915.16 # indels per 100 kbp 0.37 Largest alignment 132022 NA50 31972 NGA50 27492 NA75 17458 NGA75 10813 LA50 42 LGA50 55 LA75 82	N50	32027
NG75 10818 L50 41 LG50 54 L75 80 LG75 120 # misassemblies 4 # misassembled contigs 4 Misassembled contigs length 152553 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 81.651 Duplication ratio 1.026 # N's per 100 kbp 0.00 # mismatches per 100 kbp 915.16 # indels per 100 kbp 0.37 Largest alignment 132022 NA50 31972 NGA50 27492 NA75 17458 NGA75 10813 LA50 42 LGA50 55 LA75 82	NG50	27862
L50 41 LG50 54 L75 80 LG75 120 # misassemblies 4 # misassembled contigs 4 Misassembled contigs length 152553 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 81.651 Duplication ratio 1.026 # N's per 100 kbp 0.00 # mismatches per 100 kbp 915.16 # indels per 100 kbp 0.37 Largest alignment 132022 NA50 31972 NGA50 27492 NA75 17458 NGA75 10813 LA50 42 LGA50 55 LA75 82	N75	17754
LG50 54 L75 80 LG75 120 # misassemblies 4 # misassembled contigs 4 Misassembled contigs length 152553 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 81.651 Duplication ratio 1.026 # N's per 100 kbp 0.00 # mismatches per 100 kbp 915.16 # indels per 100 kbp 0.37 Largest alignment 132022 NA50 31972 NGA50 27492 NA75 17458 NGA75 10813 LA50 42 LGA50 55 LA75 82	NG75	10818
L75 80 LG75 120 # misassemblies 4 # misassembled contigs 4 Misassembled contigs length 152553 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 81.651 Duplication ratio 1.026 # N's per 100 kbp 0.00 # mismatches per 100 kbp 915.16 # indels per 100 kbp 0.37 Largest alignment 132022 NA50 31972 NGA50 27492 NA75 17458 NGA75 10813 LA50 42 LGA50 55 LA75 82	L50	41
LG75 120 # misassemblies 4 # misassembled contigs 4 Misassembled contigs length 152553 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 81.651 Duplication ratio 1.026 # N's per 100 kbp 0.00 # mismatches per 100 kbp 915.16 # indels per 100 kbp 0.37 Largest alignment 132022 NA50 31972 NGA50 27492 NA75 17458 NGA75 10813 LA50 42 LGA50 55 LA75 82	LG50	54
# misassemblies 4 # misassembled contigs 4 Misassembled contigs length 152553 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 81.651 Duplication ratio 1.026 # N's per 100 kbp 0.00 # mismatches per 100 kbp 915.16 # indels per 100 kbp 132022 NA50 31972 NGA50 27492 NA75 17458 NGA75 10813 LA50 42 LGA50 55 LA75 82	L75	80
# misassembled contigs 4 Misassembled contigs length 152553 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 81.651 Duplication ratio 1.026 # N's per 100 kbp 0.00 # mismatches per 100 kbp 915.16 # indels per 100 kbp 0.37 Largest alignment 132022 NA50 31972 NGA50 27492 NA75 17458 NGA75 10813 LA50 42 LGA50 55 LA75 82	LG75	120
Misassembled contigs length 152553 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 81.651 Duplication ratio 1.026 # N's per 100 kbp 0.00 # mismatches per 100 kbp 915.16 # indels per 100 kbp 0.37 Largest alignment 132022 NA50 31972 NGA50 27492 NA75 17458 NGA75 10813 LA50 42 LGA50 55 LA75 82	# misassemblies	4
# local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 81.651 Duplication ratio 1.026 # N's per 100 kbp 0.00 # mismatches per 100 kbp 915.16 # indels per 100 kbp 0.37 Largest alignment 132022 NA50 31972 NGA50 27492 NA75 17458 NGA75 10813 LA50 42 LGA50 55 LA75 82	# misassembled contigs	4
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 81.651 Duplication ratio 1.026 # N's per 100 kbp 0.00 # mismatches per 100 kbp 915.16 # indels per 100 kbp 0.37 Largest alignment 132022 NA50 31972 NGA50 27492 NA75 17458 NGA75 10813 LA50 42 LGA50 55 LA75 82	Misassembled contigs length	152553
Unaligned length 0 Genome fraction (%) 81.651 Duplication ratio 1.026 # N's per 100 kbp 0.00 # mismatches per 100 kbp 915.16 # indels per 100 kbp 0.37 Largest alignment 132022 NA50 31972 NGA50 27492 NA75 17458 NGA75 10813 LA50 42 LGA50 55 LA75 82	# local misassemblies	2
Genome fraction (%) 81.651 Duplication ratio 1.026 # N's per 100 kbp 0.00 # mismatches per 100 kbp 915.16 # indels per 100 kbp 0.37 Largest alignment 132022 NA50 31972 NGA50 27492 NA75 17458 NGA75 10813 LA50 42 LGA50 55 LA75 82	# unaligned contigs	0 + 0 part
Duplication ratio 1.026 # N's per 100 kbp 0.00 # mismatches per 100 kbp 915.16 # indels per 100 kbp 0.37 Largest alignment 132022 NA50 31972 NGA50 27492 NA75 17458 NGA75 10813 LA50 42 LGA50 55 LA75 82	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 915.16 # indels per 100 kbp 0.37 Largest alignment 132022 NA50 31972 NGA50 27492 NA75 17458 NGA75 10813 LA50 42 LGA50 55 LA75 82	Genome fraction (%)	81.651
# mismatches per 100 kbp 915.16 # indels per 100 kbp 0.37 Largest alignment 132022 NA50 31972 NGA50 27492 NA75 17458 NGA75 10813 LA50 42 LGA50 55 LA75 82	Duplication ratio	1.026
# indels per 100 kbp 0.37 Largest alignment 132022 NA50 31972 NGA50 27492 NA75 17458 NGA75 10813 LA50 42 LGA50 55 LA75 82	# N's per 100 kbp	0.00
Largest alignment 132022 NA50 31972 NGA50 27492 NA75 17458 NGA75 10813 LA50 42 LGA50 55 LA75 82	# mismatches per 100 kbp	915.16
NA50 31972 NGA50 27492 NA75 17458 NGA75 10813 LA50 42 LGA50 55 LA75 82	# indels per 100 kbp	0.37
NGA50 27492 NA75 17458 NGA75 10813 LA50 42 LGA50 55 LA75 82	Largest alignment	132022
NA75 17458 NGA75 10813 LA50 42 LGA50 55 LA75 82	NA50	31972
NGA75 10813 LA50 42 LGA50 55 LA75 82	NGA50	
LA50 42 LGA50 55 LA75 82	NA75	17458
LGA50 55 LA75 82	NGA75	10813
LA75 82	LA50	42
	LGA50	55
LGA75 122		
	LGA75	122

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	4
# relocations	4
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	152553
# local misassemblies	2
# mismatches	34684
# indels	14
# short indels	14
# long indels	0
Indels length	22

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).

















