Report

# contigs (>= 1000 bp) 962 # contigs (>= 5000 bp) 0 # contigs (>= 10000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 1000 bp) 1395402 Total length (>= 10000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3474 Largest contig 4559 Total length 3143916 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.79 N50 929 NG50 969 N75 686 L50 1146 LG50 2080 L75 2134 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 64.212 Duplication ratio 1.055 # N's per 100 kbp 0.00 # mismatches per 100 kbp 258.65 # indels per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081 LA75 2134		final.contigs
# contigs (>= 5000 bp) 0 # contigs (>= 10000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 1000 bp) 1395402 Total length (>= 5000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3474 Largest contig 4559 Total length 3143916 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.79 N50 929 NG50 696 N75 686 L50 1146 LG50 2080 L75 2134 # misassembles 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 64.212 Duplication ratio 1.055 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081	# contigs (>= 1000 bp)	
# contigs (>= 10000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 1000 bp) 1395402 Total length (>= 10000 bp) 0 Total length (>= 10000 bp) 0 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3474 Largest contig 4559 Total length 3143916 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.79 N50 929 NG50 696 N75 686 L50 1146 LG50 2080 L75 2134 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # unaligned length 0 Genome fraction (%) 64.212 Duplication ratio 1.055 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 4559 NA50 929 NG50 696 NA75 686 LA50 1146 LGA50 2081		0
# contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 1000 bp) 1395402 Total length (>= 5000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3474 Largest contig 4559 Total length 3143916 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.79 N50 929 NG50 696 N75 686 L50 1146 LG50 2080 L75 2134 # misassemblies 0 # misassembled contigs 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 64.212 Duplication ratio 1.055 # N's per 100 kbp 0.00 # mismatches per 100 kbp 258.65 # indels per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LASO 1146 LGA50 2081	# contigs (>= 10000 bp)	0
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Total length (>= 1000 bp) 1395402 Total length (>= 5000 bp) 0 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3474 Largest contig 4559 Total length 3143916 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.79 N50 929 NG50 696 N75 686 L50 1146 LG50 2080 L75 2134 # misassemblies 0 Misassembled contigs 0 Misassembled contigs 0 W unaligned length 0 Genome fraction (%) 64.212 Duplication ratio 1.055 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696		0
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Total length (>= 25000 bp) Total length (>= 50000 bp) # contigs 3474 Largest contig Total length Reference length Reference length Reference GC (%) N50 N50 N50 N75 Refo L50 L146 LG50 L75 # misassemblies # misassembled contigs Misassembled contigs length # local misassemblies # unaligned length Genome fraction (%) Genome fraction (%) # N's per 100 kbp Largest alignment NA50 NA50 NA50 NA50 NA50 NA75 Reference GC (%) 50.79 N50.79 N50.79 N50.79 N641652 0 4641652 0 50.79 N6450 N6450 N6450 N6466 N666 N675 Reference GC (%) S0.79 N686 N675 Reference GC (%) S0.79 N686	Total length (>= 5000 bp)	0
Total length (>= 50000 bp) 0 # contigs 3474 Largest contig 4559 Total length 3143916 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.79 N50 929 NG50 696 N75 686 L50 1146 LG50 2080 L75 2134 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 64.212 Duplication ratio 1.055 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081	Total length (>= 10000 bp)	0
# contigs 3474 Largest contig 4559 Total length 3143916 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.79 N50 929 NG50 696 N75 686 L50 1146 LG50 2080 L75 2134 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 64.212 Duplication ratio 1.055 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081	Total length (>= 25000 bp)	0
# contigs 3474 Largest contig 4559 Total length 3143916 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.79 N50 929 NG50 696 N75 686 L50 1146 LG50 2080 L75 2134 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 64.212 Duplication ratio 1.055 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081	Total length (>= 50000 bp)	0
Total length 3143916 Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.79 N50 929 NG50 696 N75 686 L50 1146 LG50 2080 L75 2134 # misassemblies 0 Misassembled contigs 0 Misassembled contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 64.212 Duplication ratio 1.055 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081		3474
Reference length 4641652 GC (%) 50.76 Reference GC (%) 50.79 N50 929 NG50 696 N75 686 L50 1146 LG50 2080 L75 2134 # misassemblies 0 Misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 64.212 Duplication ratio 1.055 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081	Largest contig	4559
GC (%) 50.76 Reference GC (%) 50.79 N50 929 NG50 696 N75 686 L50 1146 LG50 2080 L75 2134 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 64.212 Duplication ratio 1.055 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081	Total length	3143916
Reference GC (%) 50.79 N50 929 NG50 696 N75 686 L50 1146 LG50 2080 L75 2134 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 64.212 Duplication ratio 1.055 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081	Reference length	4641652
N50 929 NG50 696 N75 686 L50 1146 LG50 2080 L75 2134 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 64.212 Duplication ratio 1.055 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081	GC (%)	50.76
NG50 696 N75 686 L50 1146 LG50 2080 L75 2134 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 64.212 Duplication ratio 1.055 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081	Reference GC (%)	50.79
N75 686 L50 1146 LG50 2080 L75 2134 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 64.212 Duplication ratio 1.055 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081	N50	929
L50 1146 LG50 2080 L75 2134 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 64.212 Duplication ratio 1.055 # N's per 100 kbp 0.00 # mismatches per 100 kbp 258.65 # indels per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081	NG50	696
LG50 2080 L75 2134 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 64.212 Duplication ratio 1.055 # N's per 100 kbp 0.00 # mismatches per 100 kbp 258.65 # indels per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081	N75	686
L75 2134 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 64.212 Duplication ratio 1.055 # N's per 100 kbp 0.00 # mismatches per 100 kbp 258.65 # indels per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081	L50	1146
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 64.212 Duplication ratio 1.055 # N's per 100 kbp 0.00 # mismatches per 100 kbp 258.65 # indels per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081	LG50	2080
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 64.212 Duplication ratio 1.055 # N's per 100 kbp 0.00 # mismatches per 100 kbp 258.65 # indels per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081	L75	2134
Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 64.212 Duplication ratio 1.055 # N's per 100 kbp 0.00 # mismatches per 100 kbp 258.65 # indels per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081	# misassemblies	0
# local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 64.212 Duplication ratio 1.055 # N's per 100 kbp 0.00 # mismatches per 100 kbp 258.65 # indels per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081	# misassembled contigs	0
# unaligned contigs	Misassembled contigs length	0
Unaligned length 0 Genome fraction (%) 64.212 Duplication ratio 1.055 # N's per 100 kbp 0.00 # mismatches per 100 kbp 258.65 # indels per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081	# local misassemblies	0
Genome fraction (%) 64.212 Duplication ratio 1.055 # N's per 100 kbp 0.00 # mismatches per 100 kbp 258.65 # indels per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081	# unaligned contigs	0 + 0 part
Duplication ratio 1.055 # N's per 100 kbp 0.00 # mismatches per 100 kbp 258.65 # indels per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 258.65 # indels per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081	Genome fraction (%)	64.212
# mismatches per 100 kbp 258.65 # indels per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081	Duplication ratio	1.055
# indels per 100 kbp 0.00 Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081	# N's per 100 kbp	0.00
Largest alignment 4559 NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081	# mismatches per 100 kbp	258.65
NA50 929 NGA50 696 NA75 686 LA50 1146 LGA50 2081		0.00
NGA50 696 NA75 686 LA50 1146 LGA50 2081		4559
NA75 686 LA50 1146 LGA50 2081		929
LA50 1146 LGA50 2081	NGA50	696
LGA50 2081		686
		1146
LA75 2134	LGA50	2081
	LA75	2134

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	0
# mismatches	7709
# indels	0
# short indels	0
# long indels	0
Indels length	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).

Unaligned report

	final.contigs
# 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).















