Report

# contigs (>= 0 bp) 2119 # contigs (>= 1000 bp) 1366 # contigs (>= 5000 bp) 180 # contigs (>= 10000 bp) 144 # contigs (>= 25000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 4494570 Total length (>= 1000 bp) 4091008 Total length (>= 10000 bp) 1258082 Total length (>= 50000 bp) 1258082 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 163737 Total length (>= 50000 bp) 0 # contigs 1759 Largest contig 13636 Total length 4383148 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 3404 NG50 3245 N75 2046 NG75 1823 L50 407 LG50 445 L75 821 LG75 921 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 94.325 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # MA50 3404 NGA50 3245 NA75 2046 NGA75 1823 LA50 407 LGA50 445 LA75 2021 LGA75 9221 LGA75 9221 LGA75 9221 LGA75 9221 LGA75 9221 LGA75 9221		
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# contigs (>= 5000 bp)		
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# contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 4494570 Total length (>= 1000 bp) 4091008 Total length (>= 5000 bp) 1258082 Total length (>= 10000 bp) 163737 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 1759 Largest contig 13636 Total length 4383148 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 3404 NG50 3245 N75 2046 NG75 1823 L50 407 LG50 445 L75 821 LG75 921 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 94.325 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # midels per 100 kbp 0.00 Largest alignment 13636 NA50 3245 NA75 2046 NGA75 1823 LA50 407 LGA50 445 LA50 407 LGA50 445		.
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Total length (>= 0 bp)		0
Total length (>= 1000 bp)	# contigs (>= 50000 bp)	0
Total length (>= 5000 bp)	Total length (>= 0 bp)	4494570
Total length (>= 10000 bp)	Total length (>= 1000 bp)	4091008
Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 1759 Largest contig 13636 Total length 4383148 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 3404 NG50 3245 N75 2046 NG75 1823 L50 407 LG50 445 L75 821 LG75 921 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 W unaligned length 0 # unaligned length 0 Genome fraction (%) 94.325 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # anismatches per 100 kbp 0.00 # models per 100 kbp 0.00 Largest alignment 13636 <	Total length (>= 5000 bp)	1258082
Total length (>= 50000 bp) # contigs Largest contig Total length Reference length Reference length NG50 NG50 LT59 LT59 NF5 NF5 NF5 NF5 NF5 NF5 NF5 N	Total length (>= 10000 bp)	163737
# contigs 1759 Largest contig 13636 Total length 4383148 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 3404 NG50 3245 N75 2046 NG75 1823 L50 407 LG50 445 L75 821 LG75 921 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 94.325 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 13636 NA50 3245 NA75 2046 NGA75 1823 LA50 407 LGA50 445 LA75 821	Total length (>= 25000 bp)	0
Largest contig 13636 Total length 4383148 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 3404 NG50 3245 N75 2046 NG75 1823 L50 407 LG50 445 L75 821 LG75 921 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 94.325 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Rod50 3245 NA50 3404 NGA50 3245 NA75 2046 NGA75 1823 <td>Total length (>= 50000 bp)</td> <td>0</td>	Total length (>= 50000 bp)	0
Total length 4383148 Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 3404 NG50 3245 N75 2046 NG75 1823 L50 407 LG50 445 L75 821 LG75 921 # misassembled contigs 0 # misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 94.325 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 13636 NA50 3245 NA75 2046 NGA75 1823 LA50 407 LGA50 445 LA75 821	# contigs	1759
Reference length 4641652 GC (%) 50.78 Reference GC (%) 50.79 N50 3404 NG50 3245 N75 2046 NG75 1823 L50 407 LG50 445 L75 821 LG75 921 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 94.325 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 13636 NA50 3404 NGA50 3245 NA75 2046 NGA75 1823 LA50 407 LGA50 445 LA75 821	Largest contig	13636
GC (%) 50.78 Reference GC (%) 50.79 N50 3404 NG50 3245 N75 2046 NG75 1823 L50 407 LG50 445 L75 821 LG75 921 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 94.325 Duplication ratio 1.001 # N's per 100 kbp 0.00 # indels per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 13636 NA50 3404 NGA50 3245 NA75 2046 NGA75 1823 LA50 407 LGA50 445 LA75 821	Total length	4383148
Reference GC (%) 50.79 N50 3404 NG50 3245 N75 2046 NG75 1823 L50 407 LG50 445 L75 821 LG75 921 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 94.325 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 # argest alignment 13636 NA50 3404 NGA50 3245 NA75 2046 NGA75 1823 LA50 407 LGA50 445 LA75 821	Reference length	4641652
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NG50 3245 N75 2046 NG75 1823 L50 407 LG50 445 L75 821 LG75 921 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 94.325 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 13636 NA50 3404 NGA50 3245 NA75 2046 NGA75 1823 LA50 407 LGA50 445 LA75 821	Reference GC (%)	50.79
N75 2046 NG75 1823 L50 407 LG50 445 L75 821 LG75 921 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 94.325 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 13636 NA50 3404 NGA50 3245 NA75 2046 NGA75 1823 LA50 407 LGA50 445 LA75 821	N50	3404
NG75 1823 L50 407 LG50 445 L75 821 LG75 921 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 94.325 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 13636 NA50 3404 NGA50 3245 NA75 2046 NGA75 1823 LA50 407 LGA50 445 LA75 821	NG50	3245
L50 407 LG50 445 L75 821 LG75 921 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 94.325 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 13636 NA50 3404 NGA50 3245 NA75 2046 NGA75 1823 LA50 407 LGA50 445 LA75 821	N75	2046
L50 407 LG50 445 L75 821 LG75 921 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 94.325 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 13636 NA50 3404 NGA50 3245 NA75 2046 NGA75 1823 LA50 407 LGA50 445 LA75 821	NG75	1823
LG50 445 L75 821 LG75 921 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 94.325 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 13636 NA50 3404 NGA50 3245 NA75 2046 NGA75 1823 LA50 407 LGA50 445 LA75 821		
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# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 94.325 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 13636 NA50 3404 NGA50 3245 NA75 2046 NGA75 1823 LA50 407 LGA50 445 LA75 821		
Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 94.325 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 13636 NA50 3404 NGA50 3245 NA75 2046 NGA75 1823 LA50 407 LGA50 445 LA75 821		
# local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 94.325 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 13636 NA50 3404 NGA50 3245 NA75 2046 NGA75 1823 LA50 407 LGA50 445 LA75 821		
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 94.325 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 13636 NA50 3404 NGA50 3245 NA75 2046 NGA75 1823 LA50 407 LGA50 445 LA75 821		
Unaligned length 0 Genome fraction (%) 94.325 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 13636 NA50 3404 NGA50 3245 NA75 2046 NGA75 1823 LA50 407 LGA50 445 LA75 821		
Genome fraction (%) 94.325 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 13636 NA50 3404 NGA50 3245 NA75 2046 NGA75 1823 LA50 407 LGA50 445 LA75 821		
Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 13636 NA50 3404 NGA50 3245 NA75 2046 NGA75 1823 LA50 407 LGA50 445 LA75 821		
# N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 13636 NA50 3404 NGA50 3245 NA75 2046 NGA75 1823 LA50 407 LGA50 445 LA75 821		
# mismatches per 100 kbp 0.00 # indels per 100 kbp 0.00 Largest alignment 13636 NA50 3404 NGA50 3245 NA75 2046 NGA75 1823 LA50 407 LGA50 445 LA75 821		
# indels per 100 kbp 0.00 Largest alignment 13636 NA50 3404 NGA50 3245 NA75 2046 NGA75 1823 LA50 407 LGA50 445 LA75 821		
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NA75 2046 NGA75 1823 LA50 407 LGA50 445 LA75 821		
NGA75 1823 LA50 407 LGA50 445 LA75 821		
LA50 407 LGA50 445 LA75 821		
LGA50 445 LA75 821		
LA75 821	LA50	407
		445
LGA75 921	LA75	821
	LGA75	921

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

	anonymous_gsa
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	0
# 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

	anonymous_gsa
# 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).















