Report

# contigs (>= 0 bp)		
# contigs (>= 1000 bp) 3103 # contigs (>= 5000 bp) 309 # contigs (>= 10000 bp) 10 # contigs (>= 25000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 9554684 Total length (>= 1000 bp) 8513996 Total length (>= 5000 bp) 2021228 Total length (>= 5000 bp) 111271 Total length (>= 25000 bp) 0 Total length (>= 5000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 4144 Largest contig 13353 Total length 9293698 Reference length 9283304 N50 3021 N75 1837 L50 999 L75 1988 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 # unaligned length 55 Genome fraction (%) 97.373 Duplication ratio 1.029 # N's per 100 kbp 0.00 Largest alignment 13353 NA50 3021 NA75 1837		final.contigs
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# contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 9554684 Total length (>= 1000 bp) 8513996 Total length (>= 5000 bp) 2021228 Total length (>= 10000 bp) 111271 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 4144 Largest contig 13353 Total length 9293698 Reference length 9283304 N50 3021 N75 1837 L50 999 L75 1988 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 # unaligned length 55 Genome fraction (%) 97.373 Duplication ratio 1.029 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2.19 # indels per 100 kbp 0.00 Largest alignment 13353 NA50 3021 NA75 1837		309
# contigs (>= 50000 bp)		10
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# contigs	Total length (>= 25000 bp)	0
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L75 1988 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 1 part Unaligned length 55 Genome fraction (%) 97.373 Duplication ratio 1.029 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2.19 # indels per 100 kbp 0.00 Largest alignment 13353 NA50 3021 NA75 1837	N75	1837
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# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 1 part Unaligned length 55 Genome fraction (%) 97.373 Duplication ratio 1.029 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2.19 # indels per 100 kbp 0.00 Largest alignment 13353 NA50 3021 NA75 1837	L75	1988
Misassembled contigs length0# local misassemblies0# unaligned contigs0 + 1 partUnaligned length55Genome fraction (%)97.373Duplication ratio1.029# N's per 100 kbp0.00# mismatches per 100 kbp2.19# indels per 100 kbp0.00Largest alignment13353NA503021NA751837		0
# local misassemblies 0 # unaligned contigs 0 + 1 part Unaligned length 55 Genome fraction (%) 97.373 Duplication ratio 1.029 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2.19 # indels per 100 kbp 0.00 Largest alignment 13353 NA50 3021 NA75 1837		0
# unaligned contigs 0 + 1 part Unaligned length 55 Genome fraction (%) 97.373 Duplication ratio 1.029 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2.19 # indels per 100 kbp 0.00 Largest alignment 13353 NA50 3021 NA75 1837	Misassembled contigs length	0
Unaligned length 55 Genome fraction (%) 97.373 Duplication ratio 1.029 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2.19 # indels per 100 kbp 0.00 Largest alignment 13353 NA50 3021 NA75 1837		·
Genome fraction (%) 97.373 Duplication ratio 1.029 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2.19 # indels per 100 kbp 0.00 Largest alignment 13353 NA50 3021 NA75 1837	# unaligned contigs	0 + 1 part
Duplication ratio 1.029 # N's per 100 kbp 0.00 # mismatches per 100 kbp 2.19 # indels per 100 kbp 0.00 Largest alignment 13353 NA50 3021 NA75 1837	Unaligned length	55
# N's per 100 kbp 0.00 # mismatches per 100 kbp 2.19 # indels per 100 kbp 0.00 Largest alignment 13353 NA50 3021 NA75 1837		97.373
# mismatches per 100 kbp 2.19 # indels per 100 kbp 0.00 Largest alignment 13353 NA50 3021 NA75 1837	Duplication ratio	1.029
# indels per 100 kbp 0.00 Largest alignment 13353 NA50 3021 NA75 1837	# N's per 100 kbp	0.00
Largest alignment 13353 NA50 3021 NA75 1837	# mismatches per 100 kbp	2.19
NA50 3021 NA75 1837	# indels per 100 kbp	0.00
NA75 1837	Largest alignment	13353
	NA50	3021
LA50 999	NA75	1837
	LA50	999
LA75 1988	LA75	1988

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
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	198
# 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	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	55
# 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).









