Report

# contigs (>= 0 bp)		
# contigs (>= 1000 bp) 697 # contigs (>= 5000 bp) 697 # contigs (>= 10000 bp) 262 # contigs (>= 25000 bp) 27 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 9352212 Total length (>= 1000 bp) 9168181 Total length (>= 5000 bp) 7270597 Total length (>= 10000 bp) 7270597 Total length (>= 5000 bp) 7270597 Total length (>= 5000 bp) 7270597 Total length (>= 50000 bp) 7270597 Total length (>= 50000 bp) 72121 Total length (>= 50000 bp) 792121 Total length (>= 50000 bp) 9168181 Total length 9292963 Reference length 9283304 N50 9319 M75 5443 L50 313 L75 640 # misassemblies 1 # misassembled contigs 1 # local misassembles 1 # local misassembles 0 # unaligned contigs length 15101 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 98.866 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.34 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313		final.contigs
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Total length (>= 1000 bp) 9168181 Total length (>= 5000 bp) 7270597 Total length (>= 10000 bp) 4156298 Total length (>= 25000 bp) 792121 Total length (>= 50000 bp) 0 # contigs 1555 Largest contig 45348 Total length 9292963 Reference length 9283304 N50 9319 N75 5443 L50 313 L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 98.866 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.34 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313		0
Total length (>= 5000 bp) 7270597 Total length (>= 10000 bp) 4156298 Total length (>= 25000 bp) 792121 Total length (>= 50000 bp) 0 # contigs 1555 Largest contig 45348 Total length 9292963 Reference length 9283304 N50 9319 N75 5443 L50 313 L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.866 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.34 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Total length (>= 0 bp)	9352212
Total length (>= 10000 bp) 4156298 Total length (>= 25000 bp) 792121 Total length (>= 50000 bp) 0 # contigs 1555 Largest contig 45348 Total length 9292963 Reference length 9283304 N50 9319 N75 5443 L50 313 L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.866 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.34 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Total length (>= 1000 bp)	9168181
Total length (>= 25000 bp) 792121 Total length (>= 50000 bp) 0 # contigs 1555 Largest contig 45348 Total length 9292963 Reference length 9283304 N50 9319 N75 5443 L50 313 L75 640 # misassemblies 1 # local misassembled contigs 1 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.866 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.34 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Total length (>= 5000 bp)	7270597
Total length (>= 50000 bp) 0 # contigs 1555 Largest contig 45348 Total length 9292963 Reference length 9283304 N50 9319 N75 5443 L50 313 L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.866 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.34 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Total length (>= 10000 bp)	4156298
# contigs 1555 Largest contig 45348 Total length 9292963 Reference length 9283304 N50 9319 N75 5443 L50 313 L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 0 + 0 part 1 Unaligned length 0 Genome fraction (%) 98.866 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Total length (>= 25000 bp)	792121
Largest contig 45348 Total length 9292963 Reference length 9283304 N50 9319 N75 5443 L50 313 L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.866 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.34 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Total length (>= 50000 bp)	0
Total length 9292963 Reference length 9283304 N50 9319 N75 5443 L50 313 L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.866 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.34 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	# contigs	1555
Reference length 9283304 N50 9319 N75 5443 L50 313 L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.866 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.34 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Largest contig	45348
N50 9319 N75 5443 L50 313 L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.866 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.34 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Total length	9292963
N75 5443 L50 313 L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.866 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.34 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Reference length	9283304
L50 313 L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.866 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.34 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	N50	9319
L75 640 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.866 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.34 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	N75	5443
# misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.866 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.34 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	L50	313
# misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.866 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.34 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	L75	640
Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.866 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.34 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	# misassemblies	1
# local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.866 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.34 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	# misassembled contigs	1
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.866 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.34 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Misassembled contigs length	15101
Unaligned length 0 Genome fraction (%) 98.866 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.34 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	# local misassemblies	0
Genome fraction (%) 98.866 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.34 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	# unaligned contigs	0 + 0 part
Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.34 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 0.34 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Genome fraction (%)	98.866
# mismatches per 100 kbp 0.34 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	Duplication ratio	1.013
# indels per 100 kbp 0.00 Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	# N's per 100 kbp	0.00
Largest alignment 45348 NA50 9319 NA75 5443 LA50 313	# mismatches per 100 kbp	0.34
NA50 9319 NA75 5443 LA50 313	# indels per 100 kbp	0.00
NA75 5443 LA50 313	Largest alignment	45348
LA50 313	NA50	9319
	NA75	5443
LA75 640	LA50	313
	LA75	640

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	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	15101
# local misassemblies	0
# mismatches	31
# 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).









