Report

# contigs (>= 0 bp)		
# contigs (>= 1000 bp) 72 # contigs (>= 5000 bp) 72 # contigs (>= 10000 bp) 66 # contigs (>= 25000 bp) 52 # contigs (>= 25000 bp) 31 Total length (>= 0 bp) 4572769 Total length (>= 1000 bp) 4554509 Total length (>= 1000 bp) 4507427 Total length (>= 10000 bp) 4507427 Total length (>= 5000 bp) 4246976 Total length (>= 5000 bp) 4246976 Total length (>= 50000 bp) 3540315 # contigs 109 Largest contig 327146 Total length 4562531 Reference length 4641652 N50 105738 N75 54941 L50 14 L75 29 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # unaligned length 51 Genome fraction (%) 98.245 Duplication ratio 1.000 # N's per 100 kbp 9.32 Largest alignment 327146 NA50 105738 NA75 54941 LA50 14		final.contigs
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# contigs (>= 25000 bp)		72
# contigs (>= 50000 bp)		66
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Total length (>= 10000 bp) 4462528 Total length (>= 25000 bp) 4246976 Total length (>= 50000 bp) 3540315 # contigs 109 Largest contig 327146 Total length 4562531 Reference length 4641652 N50 105738 N75 54941 L50 14 L75 29 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 4 # unaligned contigs 0 + 1 part Unaligned length 51 Genome fraction (%) 98.245 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 57.83 # indels per 100 kbp 9.32 Largest alignment 327146 NA50 105738 NA75 54941 LA50 14	Total length (>= 1000 bp)	4554509
Total length (>= 25000 bp) 4246976 Total length (>= 50000 bp) 3540315 # contigs 109 Largest contig 327146 Total length 4562531 Reference length 4641652 N50 105738 N75 54941 L50 14 L75 29 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 4 # unaligned contigs 0 + 1 part Unaligned length 51 Genome fraction (%) 98.245 Duplication ratio 1.000 # N's per 100 kbp 57.83 # indels per 100 kbp 9.32 Largest alignment 327146 NA50 105738 NA75 54941 LA50 14	Total length (>= 5000 bp)	4507427
Total length (>= 50000 bp) 3540315 # contigs 109 Largest contig 327146 Total length 4562531 Reference length 4641652 N50 105738 N75 54941 L50 14 L75 29 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 4 # unaligned contigs 0 + 1 part Unaligned length 51 Genome fraction (%) 98.245 Duplication ratio 1.000 # N's per 100 kbp 57.83 # indels per 100 kbp 9.32 Largest alignment 327146 NA50 105738 NA75 54941 LA50 14	Total length (>= 10000 bp)	4462528
# contigs 109 Largest contig 327146 Total length 4562531 Reference length 4641652 N50 105738 N75 54941 L50 14 L75 29 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 4 # unaligned contigs 0 + 1 part Unaligned length 51 Genome fraction (%) 98.245 Duplication ratio 1.000 # N's per 100 kbp 57.83 # indels per 100 kbp 9.32 Largest alignment 327146 NA50 105738 NA75 54941 LA50	Total length (>= 25000 bp)	4246976
Largest contig 327146 Total length 4562531 Reference length 4641652 N50 105738 N75 54941 L50 14 L75 29 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 4 # unaligned contigs 0 + 1 part Unaligned length 51 Genome fraction (%) 98.245 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 57.83 # indels per 100 kbp 9.32 Largest alignment 327146 NA50 105738 NA75 54941 LA50 14	Total length (>= 50000 bp)	3540315
Total length 4562531 Reference length 4641652 N50 105738 N75 54941 L50 14 L75 29 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 4 # unaligned contigs 0 + 1 part Unaligned length 51 Genome fraction (%) 98.245 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 57.83 # indels per 100 kbp 9.32 Largest alignment 327146 NA50 105738 NA75 54941 LA50 14	# contigs	109
Reference length 4641652 N50 105738 N75 54941 L50 14 L75 29 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 4 # unaligned contigs 0 + 1 part Unaligned length 51 Genome fraction (%) 98.245 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 57.83 # indels per 100 kbp 9.32 Largest alignment 327146 NA50 105738 NA75 54941 LA50 14	Largest contig	327146
N50 105738 N75 54941 L50 14 L75 29 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 4 # unaligned contigs 0 + 1 part Unaligned length 51 Genome fraction (%) 98.245 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 57.83 # indels per 100 kbp 9.32 Largest alignment 327146 NA50 105738 NA75 54941 LA50 14	Total length	4562531
N75 54941 L50 14 L75 29 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 4 # unaligned contigs 0 + 1 part Unaligned length 51 Genome fraction (%) 98.245 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 57.83 # indels per 100 kbp 9.32 Largest alignment 327146 NA50 105738 NA75 54941 LA50 14	Reference length	4641652
L50	N50	105738
L75 29 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 4 # unaligned contigs 0 + 1 part Unaligned length 51 Genome fraction (%) 98.245 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 57.83 # indels per 100 kbp 9.32 Largest alignment 327146 NA50 105738 NA75 54941 LA50 14	N75	54941
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 4 # unaligned contigs 0 + 1 part Unaligned length 51 Genome fraction (%) 98.245 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 57.83 # indels per 100 kbp 9.32 Largest alignment 327146 NA50 105738 NA75 54941 LA50 14	L50	14
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 4 # unaligned contigs 0 + 1 part Unaligned length 51 Genome fraction (%) 98.245 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 57.83 # indels per 100 kbp 9.32 Largest alignment 327146 NA50 105738 NA75 54941 LA50 14	L75	29
Misassembled contigs length0# local misassemblies4# unaligned contigs0 + 1 partUnaligned length51Genome fraction (%)98.245Duplication ratio1.000# N's per 100 kbp0.00# mismatches per 100 kbp57.83# indels per 100 kbp9.32Largest alignment327146NA50105738NA7554941LA5014	# misassemblies	0
# local misassemblies 4 # unaligned contigs 0 + 1 part Unaligned length 51 Genome fraction (%) 98.245 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 57.83 # indels per 100 kbp 9.32 Largest alignment 327146 NA50 105738 NA75 54941 LA50 14		0
# unaligned contigs 0 + 1 part Unaligned length 51 Genome fraction (%) 98.245 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 57.83 # indels per 100 kbp 9.32 Largest alignment 327146 NA50 105738 NA75 54941 LA50 14	Misassembled contigs length	0
Unaligned length 51 Genome fraction (%) 98.245 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 57.83 # indels per 100 kbp 9.32 Largest alignment 327146 NA50 105738 NA75 54941 LA50 14	# local misassemblies	
Genome fraction (%) 98.245 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 57.83 # indels per 100 kbp 9.32 Largest alignment 327146 NA50 105738 NA75 54941 LA50 14	# unaligned contigs	0 + 1 part
Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 57.83 # indels per 100 kbp 9.32 Largest alignment 327146 NA50 105738 NA75 54941 LA50 14	Unaligned length	51
# N's per 100 kbp 0.00 # mismatches per 100 kbp 57.83 # indels per 100 kbp 9.32 Largest alignment 327146 NA50 105738 NA75 54941 LA50 14	Genome fraction (%)	98.245
# mismatches per 100 kbp 57.83 # indels per 100 kbp 9.32 Largest alignment 327146 NA50 105738 NA75 54941 LA50 14	Duplication ratio	1.000
# indels per 100 kbp 9.32 Largest alignment 327146 NA50 105738 NA75 54941 LA50 14	# N's per 100 kbp	0.00
Largest alignment 327146 NA50 105738 NA75 54941 LA50 14	# mismatches per 100 kbp	57.83
NA50 105738 NA75 54941 LA50 14	# indels per 100 kbp	9.32
NA75 54941 LA50 14	Largest alignment	327146
LA50 14	NA50	105738
	NA75	54941
LA75 29	LA50	14
	LA75	29

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	4
# mismatches	2637
# indels	425
# short indels	424
# long indels	1
Indels length	667

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	51
# 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).









