Report

# contigs (>= 0 bp)		
# contigs (>= 1000 bp) 96 # contigs (>= 5000 bp) 71 # contigs (>= 10000 bp) 65 # contigs (>= 25000 bp) 48 # contigs (>= 50000 bp) 30 Total length (>= 0 bp) 4573911 Total length (>= 1000 bp) 4555364 Total length (>= 5000 bp) 4499789 Total length (>= 10000 bp) 4456499 Total length (>= 25000 bp) 4456499 Total length (>= 5000 bp) 4456499 Total length (>= 50000 bp) 3555196 # contigs 108 Largest contig 327145 Total length 4563479 Reference length 4641652 N50 112493 N75 54947 L50 14 L75 28 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 12 # unaligned length 0 # local misassemblies 12 # unaligned length 0 Genome fraction (%) 98.255 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50		final.contigs
# contigs (>= 5000 bp) 71 # contigs (>= 10000 bp) 65 # contigs (>= 25000 bp) 48 # contigs (>= 50000 bp) 30 Total length (>= 0 bp) 4573911 Total length (>= 1000 bp) 4555364 Total length (>= 5000 bp) 4499789 Total length (>= 10000 bp) 4456499 Total length (>= 25000 bp) 4482272 Total length (>= 5000 bp) 4456499 Total length (>= 50000 bp) 3555196 # contigs 108 Largest contig 327145 Total length 4563479 Reference length 4641652 N50 112493 N75 54947 L50 14 L75 28 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 12 # unaligned length 0 # local misassemblies 12 # unaligned length 0 Genome fraction (%) 98.255 Duplication ratio 1.001 # N's per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50		142
# contigs (>= 10000 bp)		
# contigs (>= 25000 bp)		71
# contigs (>= 50000 bp) 30 Total length (>= 0 bp) 4573911 Total length (>= 1000 bp) 4555364 Total length (>= 5000 bp) 4499789 Total length (>= 10000 bp) 4456499 Total length (>= 25000 bp) 4182272 Total length (>= 50000 bp) 3555196 # contigs 108 Largest contig 327145 Total length 4563479 Reference length 4641652 N50 112493 N75 54947 L50 14 L75 28 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 10 # local misassemblies 12 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.255 Duplication ratio 1.001 # N's per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50 14		65
Total length (>= 0 bp) 4573911 Total length (>= 1000 bp) 4555364 Total length (>= 5000 bp) 4499789 Total length (>= 10000 bp) 4456499 Total length (>= 25000 bp) 4182272 Total length (>= 50000 bp) 3555196 # contigs 108 Largest contig 327145 Total length 4563479 Reference length 4641652 N50 112493 N75 54947 L50 14 L75 28 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Unaligned length 0 Genome fraction (%) 98.255 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 60.06 # indels per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50 14		48
Total length (>= 1000 bp) 4555364 Total length (>= 5000 bp) 4499789 Total length (>= 10000 bp) 4456499 Total length (>= 25000 bp) 4182272 Total length (>= 50000 bp) 3555196 # contigs 108 Largest contig 327145 Total length 4563479 Reference length 4641652 N50 112493 N75 54947 L50 14 L75 28 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 12 # unaligned length 0 Genome fraction (%) 98.255 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 60.06 # indels per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50 14	# contigs (>= 50000 bp)	30
Total length (>= 5000 bp) 4499789 Total length (>= 10000 bp) 4456499 Total length (>= 25000 bp) 4182272 Total length (>= 50000 bp) 3555196 # contigs 108 Largest contig 327145 Total length 4563479 Reference length 4641652 N50 112493 N75 54947 L50 14 L75 28 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.255 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 60.06 # indels per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50 14		4573911
Total length (>= 10000 bp) 4456499 Total length (>= 25000 bp) 4182272 Total length (>= 50000 bp) 3555196 # contigs 108 Largest contig 327145 Total length 4563479 Reference length 4641652 N50 112493 N75 54947 L50 14 L75 28 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 12 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.255 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 60.06 # indels per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50 14	Total length (>= 1000 bp)	4555364
Total length (>= 25000 bp) 4182272 Total length (>= 50000 bp) 3555196 # contigs 108 Largest contig 327145 Total length 4563479 Reference length 4641652 N50 112493 N75 54947 L50 14 L75 28 # misassemblies 0 # insassembled contigs 0 Misassembled contigs length 0 # local misassemblies 12 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.255 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 60.06 # indels per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50 14	Total length (>= 5000 bp)	4499789
Total length (>= 50000 bp) 3555196 # contigs 108 Largest contig 327145 Total length 4563479 Reference length 4641652 N50 112493 N75 54947 L50 14 L75 28 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 12 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.255 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 60.06 # indels per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50 14	Total length (>= 10000 bp)	4456499
# contigs 108 Largest contig 327145 Total length 4563479 Reference length 4641652 N50 112493 N75 54947 L50 14 L75 28 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 12 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.255 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50 144	Total length (>= 25000 bp)	4182272
Largest contig 327145 Total length 4563479 Reference length 4641652 N50 112493 N75 54947 L50 14 L75 28 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 12 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.255 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 60.06 # indels per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50 14	Total length (>= 50000 bp)	3555196
Total length 4563479 Reference length 4641652 N50 112493 N75 54947 L50 14 L75 28 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 12 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.255 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 60.06 # indels per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50 14	# contigs	108
Reference length 4641652 N50 112493 N75 54947 L50 14 L75 28 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 12 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.255 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 60.06 # indels per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50 14	Largest contig	327145
N50 112493 N75 54947 L50 14 L75 28 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 12 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.255 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 60.06 # indels per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50 14	Total length	4563479
N75 54947 L50 14 L75 28 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 12 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.255 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 60.06 # indels per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50 14	Reference length	4641652
L50 14 L75 28 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 12 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.255 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 60.06 # indels per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50 14	N50	112493
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 12 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.255 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 60.06 # indels per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50 14	N75	54947
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 12 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.255 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 60.06 # indels per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50 14	L50	14
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 12 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.255 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 60.06 # indels per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50 14	L75	28
Misassembled contigs length0# local misassemblies12# unaligned contigs0 + 0 partUnaligned length0Genome fraction (%)98.255Duplication ratio1.001# N's per 100 kbp0.00# mismatches per 100 kbp60.06# indels per 100 kbp9.93Largest alignment327145NA50112493NA7554947LA5014	# misassemblies	0
# local misassemblies 12 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.255 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 60.06 # indels per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50 14	# misassembled contigs	0
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.255 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 60.06 # indels per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50 14	Misassembled contigs length	0
Unaligned length 0 Genome fraction (%) 98.255 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 60.06 # indels per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50 14	# local misassemblies	12
Genome fraction (%) 98.255 Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 60.06 # indels per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50 14	# unaligned contigs	0 + 0 part
Duplication ratio 1.001 # N's per 100 kbp 0.00 # mismatches per 100 kbp 60.06 # indels per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50 14	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 60.06 # indels per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50 14	Genome fraction (%)	98.255
# mismatches per 100 kbp 60.06 # indels per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50 14	Duplication ratio	1.001
# indels per 100 kbp 9.93 Largest alignment 327145 NA50 112493 NA75 54947 LA50 14	# N's per 100 kbp	0.00
Largest alignment 327145 NA50 112493 NA75 54947 LA50 14	# mismatches per 100 kbp	60.06
NA50 112493 NA75 54947 LA50 14	# indels per 100 kbp	9.93
NA50 112493 NA75 54947 LA50 14	Largest alignment	327145
LA50 14	NA50	
	NA75	54947
LA75 28	LA50	14
	LA75	28

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	12
# mismatches	2739
# indels	453
# short indels	447
# long indels	6
Indels length	804

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).









