Report

# contigs (>= 0 bp) 5179 # contigs (>= 1000 bp) 1106 # contigs (>= 5000 bp) 2 # contigs (>= 10000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 3977249 Total length (>= 1000 bp) 10187 Total length (>= 10000 bp) 10187 Total length (>= 5000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3451 Largest contig 5185 Total length (>= 328682 Reference length 4641652 N50 999 N75 719 L50 1109 L75 2080 # misassembles 11 # misassembled contigs 11 Misassembled contigs 11 Misassembled contigs 12 Unaligned length 1278 Genome fraction (%) 68.984 Duplication ratio 1.030 # N's per 100 kbp 968.05 # indels per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 1112 LA75		
# contigs (>= 1000 bp)		final.contigs
# contigs (>= 5000 bp) 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		5179
# contigs (>= 10000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 3977249 Total length (>= 1000 bp) 1642138 Total length (>= 5000 bp) 10187 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3451 Largest contig 5185 Total length 3288682 Reference length 4641652 N50 999 N75 719 L50 1109 L75 2080 # misassemblies 11 # misassembled contigs 11 Misassembled contigs 11 Misassembled contigs 11 Misassembled contigs 11 Unaligned length 1278 Genome fraction (%) 68.984 Duplication ratio 1.030 # N's per 100 kbp 968.05 # indels per 100 kbp 968.05 # indels per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 1112		1106
# contigs (>= 25000 bp) # contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 1000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 10000 bp) Total length (>= 25000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) # contigs Largest contig Total length # contigs Total length # contigs Total length # 3288682 Reference length # 4641652 N50 # 999 N75 # 719 L50 L75 # misassemblies # misassemblies # misassembled contigs # misassembled contigs # unaligned contigs # unaligned length Genome fraction (%) # N's per 100 kbp # indels per 100 kbp # indels per 100 kbp Largest alignment NA50 998 NA75 718 LA50 1112		2
# contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 1000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 10000 bp) Total length (>= 25000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) Total length (>= 50000 bp) # contigs Largest contig Total length # contigs Total length # contigs Reference length # d641652 N50 999 N75 719 L50 L75 2080 # misassemblies # misassemblies # misassembled contigs # misassembled contigs # local misassemblies # unaligned contigs # unaligned length Genome fraction (%) Genome fraction (%) # N's per 100 kbp # indels per 100 kbp # indels per 100 kbp Largest alignment NA50 998 NA75 718 LA50 1112		0
Total length (>= 0 bp) 3977249 Total length (>= 1000 bp) 1642138 Total length (>= 5000 bp) 10187 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3451 Largest contig 5185 Total length 3288682 Reference length 4641652 N50 999 N75 719 L50 1109 L75 2080 # misassemblies 11 # misassembled contigs 11 Misassembled contigs 11 # local misassemblies 3 # unaligned contigs 1 + 5 part Unaligned length 1278 Genome fraction (%) 68.984 Duplication ratio 1.030 # N's per 100 kbp 0.00 # mismatches per 100 kbp 968.05 # indels per 100 kbp 1.06 Largest alignment 5185 NA50 998	# contigs (>= 25000 bp)	0
Total length (>= 1000 bp) 1642138 Total length (>= 5000 bp) 10187 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3451 Largest contig 5185 Total length 3288682 Reference length 4641652 N50 999 N75 719 L50 1109 L75 2080 # misassemblies 11 # local misassemblies 11 # local misassemblies 3 # unaligned contigs 1 + 5 part Unaligned length 1278 Genome fraction (%) 68.984 Duplication ratio 1.030 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 1112	# contigs (>= 50000 bp)	0
Total length (>= 5000 bp) 10187 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3451 Largest contig 5185 Total length 3288682 Reference length 4641652 N50 999 N75 719 L50 1109 L75 2080 # misassemblies 11 # misassembled contigs 11 Misassembled contigs length 18308 # local misassemblies 3 # unaligned contigs 1 + 5 part Unaligned length 1278 Genome fraction (%) 68.984 Duplication ratio 1.030 # N's per 100 kbp 0.00 # mismatches per 100 kbp 968.05 # indels per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 1112	Total length (>= 0 bp)	3977249
Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3451 Largest contig 5185 Total length 3288682 Reference length 4641652 N50 999 N75 719 L50 1109 L75 2080 # misassemblies 11 # misassembled contigs 11 Misassembled contigs length 18308 # local misassemblies 3 # unaligned contigs 1 + 5 part Unaligned length 1278 Genome fraction (%) 68.984 Duplication ratio 1.030 # N's per 100 kbp 0.00 # mismatches per 100 kbp 968.05 # indels per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 1112	Total length (>= 1000 bp)	1642138
Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 # contigs 3451 Largest contig 5185 Total length 3288682 Reference length 4641652 N50 999 N75 719 L50 1109 L75 2080 # misassemblies 11 # misassembled contigs 11 Misassembled contigs length 18308 # local misassemblies 3 # unaligned contigs 1 + 5 part Unaligned length 1278 Genome fraction (%) 68.984 Duplication ratio 1.030 # N's per 100 kbp 0.00 # mismatches per 100 kbp 968.05 # indels per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 1112	Total length (>= 5000 bp)	10187
Total length (>= 50000 bp) 0 # contigs 3451 Largest contig 5185 Total length 3288682 Reference length 4641652 N50 999 N75 719 L50 1109 L75 2080 # misassemblies 11 # misassembled contigs 11 Misassembled contigs length 18308 # local misassemblies 3 # unaligned contigs 1 + 5 part Unaligned length 1278 Genome fraction (%) 68.984 Duplication ratio 1.030 # N's per 100 kbp 0.00 # mismatches per 100 kbp 968.05 # indels per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 1112	Total length (>= 10000 bp)	0
# contigs 3451 Largest contig 5185 Total length 3288682 Reference length 4641652 N50 999 N75 719 L50 1109 L75 2080 # misassemblies 11 # misassembled contigs 11 Misassembled contigs 12 # unaligned length 18308 # local misassemblies 3 # unaligned length 1278 Genome fraction (%) 68.984 Duplication ratio 1.030 # N's per 100 kbp 968.05 # indels per 100 kbp 968.05 # indels per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 11112	Total length (>= 25000 bp)	0
Largest contig 5185 Total length 3288682 Reference length 4641652 N50 999 N75 719 L50 1109 L75 2080 # misassemblies 11 # misassembled contigs 11 Misassembled contigs length 18308 # local misassemblies 3 # unaligned contigs 1 + 5 part Unaligned length 1278 Genome fraction (%) 68.984 Duplication ratio 1.030 # N's per 100 kbp 0.00 # mismatches per 100 kbp 968.05 # indels per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 1112	Total length (>= 50000 bp)	0
Total length 3288682 Reference length 4641652 N50 999 N75 719 L50 1109 L75 2080 # misassemblies 11 # misassembled contigs 11 Misassembled contigs length 18308 # local misassemblies 3 # unaligned contigs 1 + 5 part Unaligned length 1278 Genome fraction (%) 68.984 Duplication ratio 1.030 # N's per 100 kbp 0.00 # mismatches per 100 kbp 968.05 # indels per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 1112	# contigs	3451
Reference length 4641652 N50 999 N75 719 L50 1109 L75 2080 # misassemblies 11 # misassembled contigs 11 Misassembled contigs length 18308 # local misassemblies 3 # unaligned contigs 1 + 5 part Unaligned length 1278 Genome fraction (%) 68.984 Duplication ratio 1.030 # N's per 100 kbp 0.00 # mismatches per 100 kbp 968.05 # indels per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 1112	Largest contig	5185
N50 999 N75 719 L50 1109 L75 2080 # misassemblies 11 # misassembled contigs 11 Misassembled contigs length 18308 # local misassemblies 3 # unaligned contigs 1 + 5 part Unaligned length 1278 Genome fraction (%) 68.984 Duplication ratio 1.030 # N's per 100 kbp 0.00 # mismatches per 100 kbp 968.05 # indels per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 1112	Total length	3288682
N75 719 L50 1109 L75 2080 # misassemblies 11 # misassembled contigs 11 Misassembled contigs length 18308 # local misassemblies 3 # unaligned contigs 1 + 5 part Unaligned length 1278 Genome fraction (%) 68.984 Duplication ratio 1.030 # N's per 100 kbp 0.00 # mismatches per 100 kbp 968.05 # indels per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 1112	Reference length	4641652
L50 1109 L75 2080 # misassemblies 11 # misassembled contigs 11 Misassembled contigs length 18308 # local misassemblies 3 # unaligned contigs 1 + 5 part Unaligned length 1278 Genome fraction (%) 68.984 Duplication ratio 1.030 # N's per 100 kbp 0.00 # mismatches per 100 kbp 968.05 # indels per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 1112	N50	999
L75 2080 # misassemblies 11 # misassembled contigs 11 Misassembled contigs length 18308 # local misassemblies 3 # unaligned contigs 1 + 5 part Unaligned length 1278 Genome fraction (%) 68.984 Duplication ratio 1.030 # N's per 100 kbp 0.00 # mismatches per 100 kbp 968.05 # indels per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 1112	N75	719
# misassemblies 11 # misassembled contigs 11 Misassembled contigs length 18308 # local misassemblies 3 # unaligned contigs 1 + 5 part Unaligned length 1278 Genome fraction (%) 68.984 Duplication ratio 1.030 # N's per 100 kbp 0.00 # mismatches per 100 kbp 968.05 # indels per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 11112	L50	1109
# misassembled contigs 11 Misassembled contigs length 18308 # local misassemblies 3 # unaligned contigs 1 + 5 part Unaligned length 1278 Genome fraction (%) 68.984 Duplication ratio 1.030 # N's per 100 kbp 0.00 # mismatches per 100 kbp 968.05 # indels per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 11112	L75	2080
Misassembled contigs length 18308 # local misassemblies 3 # unaligned contigs 1 + 5 part Unaligned length 1278 Genome fraction (%) 68.984 Duplication ratio 1.030 # N's per 100 kbp 0.00 # mismatches per 100 kbp 968.05 # indels per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 1112	# misassemblies	11
# local misassemblies 3 # unaligned contigs 1 + 5 part Unaligned length 1278 Genome fraction (%) 68.984 Duplication ratio 1.030 # N's per 100 kbp 0.00 # mismatches per 100 kbp 968.05 # indels per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 11112	# misassembled contigs	11
# unaligned contigs 1 + 5 part Unaligned length 1278 Genome fraction (%) 68.984 Duplication ratio 1.030 # N's per 100 kbp 0.00 # mismatches per 100 kbp 968.05 # indels per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 1112	Misassembled contigs length	18308
Unaligned length 1278 Genome fraction (%) 68.984 Duplication ratio 1.030 # N's per 100 kbp 0.00 # mismatches per 100 kbp 968.05 # indels per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 1112	# local misassemblies	3
Genome fraction (%) 68.984 Duplication ratio 1.030 # N's per 100 kbp 0.00 # mismatches per 100 kbp 968.05 # indels per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 1112	# unaligned contigs	1 + 5 part
Duplication ratio 1.030 # N's per 100 kbp 0.00 # mismatches per 100 kbp 968.05 # indels per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 1112	Unaligned length	1278
# N's per 100 kbp 0.00 # mismatches per 100 kbp 968.05 # indels per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 1112	Genome fraction (%)	68.984
# mismatches per 100 kbp 968.05 # indels per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 1112	Duplication ratio	1.030
# indels per 100 kbp 1.06 Largest alignment 5185 NA50 998 NA75 718 LA50 1112	# N's per 100 kbp	0.00
Largest alignment 5185 NA50 998 NA75 718 LA50 1112	# mismatches per 100 kbp	968.05
NA50 998 NA75 718 LA50 1112	# indels per 100 kbp	1.06
NA75 718 LA50 1112	Largest alignment	5185
LA50 1112	NA50	998
	NA75	718
LA75 2086	LA50	1112
	LA75	2086

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	11
# relocations	11
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	11
Misassembled contigs length	18308
# local misassemblies	3
# mismatches	30997
# indels	34
# short indels	34
# long indels	0
Indels length	45

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	1
Fully unaligned length	963
# partially unaligned contigs	5
# with misassembly	0
# both parts are significant	0
Partially unaligned length	315
# 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).









