Report

# contigs (>= 1000 bp) 711 # contigs (>= 5000 bp) 343 # contigs (>= 10000 bp) 126 # contigs (>= 25000 bp) 100 # contigs (>= 50000 bp) 100 # contigs (>= 50000 bp) 100 Total length (>= 10000 bp) 3521706 Total length (>= 10000 bp) 1959553 Total length (>= 25000 bp) 295277 Total length (>= 25000 bp) 295277 Total length (>= 50000 bp) 295277 Total length (>= 50000 bp) 295277 Total length (>= 50000 bp) 3521706 Reference length 4602596 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 9051 NG50 8818 N75 5232 NG75 5109 L50 162 LG50 165 L75 330 LG75		
# contigs (>= 5000 bp) 343 # contigs (>= 10000 bp) 126 # contigs (>= 25000 bp) 0 Total length (>= 1000 bp) 4532792 Total length (>= 50000 bp) 3521706 Total length (>= 10000 bp) 1959553 Total length (>= 25000 bp) 295277 Total length (>= 50000 bp) 3521706 # contigs 805 Largest contig 45348 Total length 4602596 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 9051 N650 8818 N75 5232 NG75 5109 L50 162 LG50 165 L75 330 LG75 330 LG75 330 LG75 330 LG75 336 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.931 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LGA50 163 LGA50 165 LA75 330		final.contigs
# contigs (>= 10000 bp)		711
# contigs (>= 25000 bp)	# contigs (>= 5000 bp)	343
# contigs (>= 50000 bp)	•	126
Total length (>= 1000 bp)	# contigs (>= 25000 bp)	10
Total length (>= 5000 bp) 3521706 Total length (>= 10000 bp) 1959553 Total length (>= 25000 bp) 295277 Total length (>= 50000 bp) 0 # contigs 805 Largest contig 45348 Total length 4602596 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 9051 NG50 8818 N75 5232 NG75 5109 L50 162 LG50 165 L75 330 LG75 336 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 97.931 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 </td <td></td> <td>0</td>		0
Total length (>= 10000 bp) 1959553 Total length (>= 25000 bp) 295277 Total length (>= 50000 bp) 0 # contigs 805 Largest contig 45348 Total length 4602596 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 9051 NG50 8818 N75 5232 NG75 5109 L50 162 LG50 165 L75 330 LG75 336 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 97.931 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 </td <td></td> <td>4532792</td>		4532792
Total length (>= 25000 bp) 295277 Total length (>= 50000 bp) 0 # contigs 805 Largest contig 45348 Total length 4602596 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 9051 NG50 8818 N75 5232 NG75 5109 L50 162 LG50 165 L75 330 LG75 336 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 97.931 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912		3521706
Total length (>= 50000 bp) 0 # contigs 805 Largest contig 45348 Total length 4602596 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 9051 NG50 8818 N75 5232 NG75 5109 L50 162 LG50 165 L75 330 LG75 336 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.931 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232		
# contigs 805 Largest contig 45348 Total length 4602596 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 9051 NG50 8818 N75 5232 NG75 5109 L50 162 LG50 165 L75 330 LG75 336 # misassemblies 1 # local misassembled contigs 1 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.931 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LA50 165		295277
Largest contig 45348 Total length 4602596 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 9051 NG50 8818 N75 5232 NG75 5109 L50 162 L650 165 L75 330 LG75 336 # misassemblies 1 # local misassembled contigs 1 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.931 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LA50 165 LA75 330	Total length (>= 50000 bp)	0
Total length 4602596 Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 9051 NG50 8818 N75 5232 NG75 5109 L50 162 LG50 165 L75 330 LG75 336 # misassemblies 1 # local misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.931 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163	# contigs	805
Reference length 4641652 GC (%) 50.74 Reference GC (%) 50.79 N50 9051 NG50 8818 N75 5232 NG75 5109 L50 162 LG50 165 L75 330 LG75 336 # misassemblies 1 # local misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.931 Duplication ratio 1.013 # Ni's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LA50 165 LA75 330		45348
GC (%) 50.74 Reference GC (%) 50.79 N50 9051 NG50 8818 N75 5232 NG75 5109 L50 162 LG50 165 L75 330 LG75 336 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.931 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LA50 165 LA75 330	Total length	4602596
Reference GC (%) 50.79 N50 9051 NG50 8818 N75 5232 NG75 5109 L50 162 LG50 165 L75 330 LG75 336 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.931 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LA50 165 LA75 330	Reference length	4641652
N50 9051 NG50 8818 N75 5232 NG75 5109 L50 162 LG50 165 L75 330 LG75 336 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.931 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LA50 165 LA75 330		50.74
NG50 8818 N75 5232 NG75 5109 L50 162 LG50 165 L75 330 LG75 336 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.931 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LA50 165 LA75 330	Reference GC (%)	50.79
N75 5232 NG75 5109 L50 162 LG50 165 L75 330 LG75 336 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.931 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LGA50 165 LA75 330	N50	9051
NG75 5109 L50 162 LG50 165 L75 330 LG75 336 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.931 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LGA50 165 LA75 330	NG50	8818
L50 162 LG50 165 L75 330 LG75 336 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.931 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LGA50 165 LA75 330	N75	5232
LG50 165 L75 330 LG75 336 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.931 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LGA50 165 LA75 330	NG75	5109
L75 330 LG75 336 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.931 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LGA50 165 LA75 330	L50	162
LG75 336 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.931 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LGA50 165 LA75 330		165
# misassemblies 1 # misassembled contigs 1 Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.931 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LGA50 165 LA75 330	L75	330
# misassembled contigs	LG75	336
Misassembled contigs length 15101 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.931 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LGA50 165 LA75 330		1
# local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.931 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LGA50 165 LA75 330		1
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.931 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LGA50 165 LA75 330	Misassembled contigs length	15101
Unaligned length 0 Genome fraction (%) 97.931 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LGA50 165 LA75 330	# local misassemblies	0
Genome fraction (%) 97.931 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LGA50 165 LA75 330	# unaligned contigs	0 + 0 part
Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LGA50 165 LA75 330		0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LGA50 165 LA75 330		97.931
# mismatches per 100 kbp 0.64 # indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LGA50 165 LA75 330	Duplication ratio	1.013
# indels per 100 kbp 0.00 Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LGA50 165 LA75 330		0.00
Largest alignment 45348 NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LGA50 165 LA75 330		0.64
NA50 8912 NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LGA50 165 LA75 330		
NGA50 8818 NA75 5232 NGA75 5109 LA50 163 LGA50 165 LA75 330	Largest alignment	45348
NA75 5232 NGA75 5109 LA50 163 LGA50 165 LA75 330	NA50	
NGA75 5109 LA50 163 LGA50 165 LA75 330	NGA50	8818
LA50 163 LGA50 165 LA75 330	NA75	5232
LGA50 165 LA75 330	NGA75	5109
LA75 330	LA50	163
	LGA50	
LGA75 336		330
	LGA75	336

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
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	15101
# local misassemblies	0
# mismatches	29
# 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).















