Report

# contigs (>= 1000 bp)		scaffolds
# contigs (>= 5000 bp)	# contigs (>= 1000 bp)	
# contigs (>= 10000 bp) 47 # contigs (>= 25000 bp) 41 # contigs (>= 50000 bp) 29 Total length (>= 10000 bp) 4498931 Total length (>= 50000 bp) 4468204 Total length (>= 10000 bp) 4435353 Total length (>= 25000 bp) 4327692 Total length (>= 50000 bp) 3927946 # contigs 90 Largest contig 332248 Total length 4514743 Reference length 4641652 GC (%) 50.77 Reference GC (%) 50.79 N50 131793 NG50 124889 N75 82061 NG75 80259 L50 11 LG50 12 L75 22 LG75 23 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 82061 # local misassemblies 1 # unaligned length 0 Genome fraction (%) 96.796 Duplication ratio 1.005 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12 LA75 22		51
# contigs (>= 25000 bp)		
# contigs (>= 50000 bp) 29 Total length (>= 1000 bp) 4498931 Total length (>= 5000 bp) 4468204 Total length (>= 10000 bp) 4435353 Total length (>= 25000 bp) 4327692 Total length (>= 50000 bp) 3927946 # contigs 90 Largest contig 332248 Total length 4514743 Reference length 4641652 GC (%) 50.77 Reference GC (%) 50.79 N50 131793 NG50 124889 N75 82061 NG75 80259 L50 11 LG50 11 LG50 12 L75 22 LG75 23 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 1 # local misassemblies 1 # unaligned length 0 Genome fraction (%) 96.796 Duplication ratio 1.005 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12 LA75 22		41
Total length (>= 5000 bp)		29
Total length (>= 5000 bp)	Total length (>= 1000 bp)	4498931
Total length (>= 25000 bp)		4468204
Total length (>= 50000 bp) 3927946 # contigs 90 Largest contig 332248 Total length 4514743 Reference length 4641652 GC (%) 50.77 Reference GC (%) 50.79 N50 131793 NG50 124889 N75 80259 L50 11 LG50 12 L75 22 LG75 23 # misassemblies 1 # local misassembled contigs 1 # local misassembles 1 # local misassembles 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.796 Duplication ratio 1.005 # N's per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA50 124889 NA75 80259 <td>Total length (>= 10000 bp)</td> <td>4435353</td>	Total length (>= 10000 bp)	4435353
# contigs 90 Largest contig 332248 Total length 4514743 Reference length 4641652 GC (%) 50.77 Reference GC (%) 50.79 N50 131793 NG50 124889 N75 82061 NG75 80259 L50 11 LG50 11 LG50 12 L75 22 LG75 23 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 1 # local misassemblies 1 # unaligned length 0 Genome fraction (%) 96.796 Duplication ratio 1.005 # N's per 100 kbp 0.00 # mismatches per 100 kbp 617.86 # indels per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12	Total length (>= 25000 bp)	4327692
# contigs 90 Largest contig 332248 Total length 4514743 Reference length 4641652 GC (%) 50.77 Reference GC (%) 50.79 N50 131793 NG50 124889 N75 82061 NG75 80259 L50 11 LG50 11 LG50 12 L75 22 LG75 23 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 1 # local misassemblies 1 # unaligned length 0 Genome fraction (%) 96.796 Duplication ratio 1.005 # N's per 100 kbp 0.00 # mismatches per 100 kbp 617.86 # indels per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12	Total length (>= 50000 bp)	3927946
Total length 4514743 Reference length 4641652 GC (%) 50.77 Reference GC (%) 50.79 N50 131793 NG50 124889 N75 82061 NG75 80259 L50 11 LG50 12 L75 22 LG75 23 # misassemblies 1 # local misassembled contigs 1 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.796 Duplication ratio 1.005 # N's per 100 kbp 0.00 # mismatches per 100 kbp 617.86 # indels per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12 <t< td=""><td></td><td>90</td></t<>		90
Reference length 4641652 GC (%) 50.77 Reference GC (%) 50.79 N50 131793 NG50 124889 N75 82061 NG75 80259 L50 11 LG50 12 L75 22 LG75 23 # misassemblies 1 # local misassembled contigs 1 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.796 Duplication ratio 1.005 # N's per 100 kbp 0.00 # mismatches per 100 kbp 617.86 # indels per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12 LA75 22	Largest contig	332248
GC (%) 50.77 Reference GC (%) 50.79 N50 131793 NG50 124889 N75 82061 NG75 80259 L50 11 LG50 12 L75 22 LG75 23 # misassemblies 1 # local misassembled contigs 1 # local misassembles 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.796 Duplication ratio 1.005 # N's per 100 kbp 0.00 # mismatches per 100 kbp 617.86 # indels per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12 LA75 22	Total length	4514743
Reference GC (%) 50.79 N50 131793 NG50 124889 N75 82061 NG75 80259 L50 11 LG50 12 L75 22 LG75 23 # misassemblies 1 # local misassembled contigs 1 # local misassembles 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.796 Duplication ratio 1.005 # N's per 100 kbp 0.00 # mismatches per 100 kbp 617.86 # indels per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12 LA75 22	Reference length	4641652
N50 131793 NG50 124889 N75 82061 NG75 80259 L50 11 LG50 12 L75 22 LG75 23 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 82061 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.796 Duplication ratio 1.005 # N's per 100 kbp 0.00 # mismatches per 100 kbp 617.86 # indels per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12 LA75 22	GC (%)	50.77
NG50 124889 N75 82061 NG75 80259 L50 11 LG50 12 L75 22 LG75 23 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 82061 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.796 Duplication ratio 1.005 # N's per 100 kbp 0.00 # mismatches per 100 kbp 617.86 # indels per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12 LA75 22	Reference GC (%)	50.79
N75 82061 NG75 80259 L50 11 LG50 12 L75 22 LG75 23 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 82061 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.796 Duplication ratio 1.005 # N's per 100 kbp 0.00 # mismatches per 100 kbp 617.86 # indels per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12 LA75 22	N50	131793
NG75 80259 L50 11 LG50 12 L75 22 LG75 23 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 82061 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.796 Duplication ratio 1.005 # N's per 100 kbp 0.00 # mismatches per 100 kbp 617.86 # indels per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12 LA75 22	NG50	124889
L50 11 LG50 12 L75 22 LG75 23 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 82061 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.796 Duplication ratio 1.005 # N's per 100 kbp 0.00 # mismatches per 100 kbp 617.86 # indels per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12 LA75 22	N75	82061
LG50 12 L75 22 LG75 23 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 82061 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.796 Duplication ratio 1.005 # N's per 100 kbp 0.00 # mismatches per 100 kbp 617.86 # indels per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12 LA75 22	NG75	80259
L75 22 LG75 23 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 82061 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.796 Duplication ratio 1.005 # N's per 100 kbp 0.00 # mismatches per 100 kbp 617.86 # indels per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12 LA75 22	L50	11
LG75 23 # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 82061 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.796 Duplication ratio 1.005 # N's per 100 kbp 0.00 # mismatches per 100 kbp 617.86 # indels per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12 LA75 22	LG50	12
# misassemblies 1 # misassembled contigs 1 Misassembled contigs length 82061 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.796 Duplication ratio 1.005 # N's per 100 kbp 0.00 # mismatches per 100 kbp 617.86 # indels per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12	L75	22
# misassembled contigs 1 Misassembled contigs length 82061 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.796 Duplication ratio 1.005 # N's per 100 kbp 0.00 # mismatches per 100 kbp 617.86 # indels per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12	LG75	23
Misassembled contigs length 82061 # local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.796 Duplication ratio 1.005 # N's per 100 kbp 0.00 # mismatches per 100 kbp 617.86 # indels per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12 LA75 22	# misassemblies	1
# local misassemblies 1 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.796 Duplication ratio 1.005 # N's per 100 kbp 0.00 # mismatches per 100 kbp 617.86 # indels per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12	# misassembled contigs	1
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 96.796 Duplication ratio 1.005 # N's per 100 kbp 0.00 # mismatches per 100 kbp 617.86 # indels per 100 kbp 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12 LA75 22	Misassembled contigs length	82061
Unaligned length 0 Genome fraction (%) 96.796 Duplication ratio 1.005 # N's per 100 kbp 0.00 # mismatches per 100 kbp 617.86 # indels per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12 LA75 22	# local misassemblies	1
Genome fraction (%) 96.796 Duplication ratio 1.005 # N's per 100 kbp 0.00 # mismatches per 100 kbp 617.86 # indels per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12 LA75 22	# unaligned contigs	0 + 0 part
Duplication ratio 1.005 # N's per 100 kbp 0.00 # mismatches per 100 kbp 617.86 # indels per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12 LA75 22	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 617.86 # indels per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12	Genome fraction (%)	96.796
# mismatches per 100 kbp 617.86 # indels per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12 LA75 22	Duplication ratio	1.005
# indels per 100 kbp 0.76 Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12 LA75 22		0.00
Largest alignment 332248 NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12 LA75 22	# mismatches per 100 kbp	617.86
NA50 131793 NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12 LA75 22	# indels per 100 kbp	
NGA50 124889 NA75 80259 NGA75 79547 LA50 11 LGA50 12 LA75 22	Largest alignment	332248
NA75 80259 NGA75 79547 LA50 11 LGA50 12 LA75 22		
NGA75 79547 LA50 11 LGA50 12 LA75 22		124889
LA50 11 LGA50 12 LA75 22		
LGA50 12 LA75 22		
LA75 22		
LGA75 23		
	LGA75	23

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

	scaffolds
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	82061
# local misassemblies	1
# mismatches	27760
# indels	34
# short indels	34
# long indels	0
Indels length	41

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

	scaffolds
# 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).















