Report

# contigs (>= 1000 bp)		scaffolds
# contigs (>= 5000 bp) 42 # contigs (>= 10000 bp) 35 # contigs (>= 25000 bp) 35 # contigs (>= 50000 bp) 30 Total length (>= 10000 bp) 4597846 Total length (>= 10000 bp) 4574350 Total length (>= 10000 bp) 4567854 Total length (>= 25000 bp) 459002 Total length (>= 50000 bp) 4459002 Total length (>= 50000 bp) 4284789 # contigs 69 Largest contig 527156 Total length 4606111 Reference length 4641652 GC (%) 50.73 Reference GC (%) 50.78 N50 197358 N75 101046 NG75 86132 L50 8 L650 8 L75 18 LG75 19 # misassemblies 6 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 1 # local misassemblies 0 # unaligned length 0 Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.95 Largest alignment 527156 NA50 197358	# contigs (>= 1000 bp)	
# contigs (>= 10000 bp) 41 # contigs (>= 25000 bp) 35 # contigs (>= 50000 bp) 30 Total length (>= 1000 bp) 4597846 Total length (>= 5000 bp) 4574350 Total length (>= 10000 bp) 4567854 Total length (>= 25000 bp) 4459002 Total length (>= 50000 bp) 4459002 Total length (>= 50000 bp) 4284789 # contigs 69 Largest contig 527156 Total length 4606111 Reference length 4641652 GC (%) 50.73 Reference GC (%) 50.78 N50 197358 N75 101046 NG75 86132 L50 8 L75 18 LG75 19 # misassemblies 6 # misassembled contigs 19 # local misassemblies 6 # unaligned length 0 Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NA50 197358		42
# contigs (>= 25000 bp) 35 # contigs (>= 50000 bp) 30 Total length (>= 1000 bp) 4597846 Total length (>= 5000 bp) 4597846 Total length (>= 10000 bp) 4567854 Total length (>= 25000 bp) 4567854 Total length (>= 25000 bp) 4459002 Total length (>= 50000 bp) 4284789 # contigs 69 Largest contig 527156 Total length 4606111 Reference length 4641652 GC (%) 50.73 Reference GC (%) 50.78 N50 197358 NG50 197358 NG50 197358 NG50 197358 L50 86132 L50 8 L75 101046 NG75 86132 L50 8 L75 18 LG75 19 # misassemblies 6 # misassembled contigs 1 Misassembled contigs 10 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 NGA50 197358 NGA50 197358 NGA50 197358 NA75 101046 NGA75 86132 LA50 8 LGA50 8 LA75 18		41
# contigs (>= 50000 bp) 30 Total length (>= 1000 bp) 4597846 Total length (>= 5000 bp) 4574350 Total length (>= 10000 bp) 4567854 Total length (>= 25000 bp) 4459002 Total length (>= 50000 bp) 4459002 Total length (>= 50000 bp) 4284789 # contigs 69 Largest contig 527156 Total length 4606111 Reference length 4641652 GC (%) 50.73 Reference GC (%) 50.78 N50 197358 N75 101046 NG75 86132 L50 8 L75 18 LG75 19 # misassemblies 6 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 NGA50 197358 NA50 197358 NA75 101046 NGA75 86132 LA50 8 LA50 8 LA50 8 LA75 18		35
Total length (>= 1000 bp)		30
Total length (>= 5000 bp)		4597846
Total length (>= 25000 bp)		
Total length (>= 50000 bp) 4284789 # contigs 69 Largest contig 527156 Total length 4606111 Reference length 4641652 GC (%) 50.73 Reference GC (%) 50.78 N50 197358 NG50 197358 N75 101046 NG75 86132 L50 8 L75 18 LG75 19 # misassemblies 6 # misassembled contigs 1 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 # indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NGA50 197358 NGA75 86132 LA50 <	Total length (>= 10000 bp)	4567854
# contigs 69 Largest contig 527156 Total length 4606111 Reference length 4641652 GC (%) 50.73 Reference GC (%) 50.78 N50 197358 NG50 197358 N75 101046 NG75 86132 L50 8 LG50 8 LG50 8 LG75 19 # misassemblies 6 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 # indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NGA75 86132 LA50 8 LGA50 8 LGA50 8 LGA50 8 LGA50 8 LGA50 8	Total length (>= 25000 bp)	4459002
# contigs 69 Largest contig 527156 Total length 4606111 Reference length 4641652 GC (%) 50.73 Reference GC (%) 50.78 N50 197358 NG50 197358 N75 101046 NG75 86132 L50 8 LG50 8 LG50 8 LG75 19 # misassemblies 6 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 # indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NGA75 86132 LA50 8 LGA50 8 LGA50 8 LGA50 8 LGA50 8 LGA50 8	Total length (>= 50000 bp)	4284789
Total length 4606111 Reference length 4641652 GC (%) 50.73 Reference GC (%) 50.78 N50 197358 NG50 197358 N75 101046 NG75 86132 L50 8 L50 8 L75 18 LG75 19 # misassemblies 6 # misassembled contigs 1 Misassembled contigs length 82061 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 # indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NA75 101046 NGA75 86132 LA50 8		69
Reference length 4641652 GC (%) 50.73 Reference GC (%) 50.78 N50 197358 NG50 197358 N75 101046 NG75 86132 L50 8 LG50 8 L75 18 LG75 19 # misassemblies 6 # misassembled contigs 1 Misassembled contigs length 82061 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 # indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NGA50 197358 NA75 101046 NGA75 86132 LA50 8 LGA50 8 LA75 18 <td>Largest contig</td> <td>527156</td>	Largest contig	527156
GC (%) 50.73 Reference GC (%) 50.78 N50 197358 NG50 197358 N75 101046 NG75 86132 L50 8 L75 18 LG75 19 # misassemblies 6 # misassembled contigs 1 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 # indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NA75 101046 NGA75 86132 LA50 8 LGA50 8 LA75 18	Total length	4606111
Reference GC (%) 50.78 N50 197358 NG50 197358 N75 101046 NG75 86132 L50 8 L50 8 L75 18 LG75 19 # misassemblies 6 # misassembled contigs 1 Misassembled contigs length 82061 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 # indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NGA75 86132 LA50 8 LGA50 8 LA75 18	Reference length	4641652
N50 197358 NG50 197358 N75 101046 NG75 86132 L50 8 L50 8 L75 18 LG75 19 # misassemblies 6 # misassembled contigs 1 Misassembled contigs length 82061 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 # indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NA75 101046 NGA75 86132 LA50 8 LGA50 8 LA75 18	GC (%)	50.73
NG50 197358 N75 101046 NG75 86132 L50 8 LG50 8 L75 18 LG75 19 # misassemblies 6 # misassembled contigs 1 Misassembled contigs length 82061 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 # indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NA75 101046 NGA75 86132 LA50 8 LA75 18	Reference GC (%)	50.78
N75 101046 NG75 86132 L50 8 L50 8 L75 18 LG75 19 # misassemblies 6 # misassembled contigs 1 Misassembled contigs length 82061 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 # indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NA75 101046 NGA75 86132 LA50 8 LA75 18	N50	197358
NG75 86132 L50 8 LG50 8 L75 18 LG75 19 # misassemblies 6 # misassembled contigs 1 Misassembled contigs length 82061 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 # indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NA75 101046 NGA75 86132 LA50 8 LA75 18	NG50	197358
L50 8 LG50 8 L75 18 LG75 19 # misassemblies 6 # misassembled contigs 1 Misassembled contigs length 82061 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 # indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NA75 101046 NGA75 86132 LA50 8 LGA50 8 LA75 18	N75	101046
LG50 8 L75 18 LG75 19 # misassemblies 6 # misassembled contigs 1 Misassembled contigs length 82061 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 # indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NA75 101046 NGA75 86132 LA50 8 LGA50 8 LA75 18	NG75	86132
L75 18 LG75 19 # misassemblies 6 # misassembled contigs 1 Misassembled contigs length 82061 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 # indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NA75 101046 NGA75 86132 LA50 8 LGA50 8 LA75 18	L50	8
# misassemblies 6 # misassembled contigs 1 Misassembled contigs length 82061 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 # indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NA75 101046 NGA75 86132 LA50 8 LGA50 8 LA75 18	LG50	8
# misassemblies 6 # misassembled contigs 1 Misassembled contigs length 82061 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 # indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NA75 101046 NGA75 86132 LA50 8 LGA50 8 LA75 18	L75	18
# misassembled contigs 1 Misassembled contigs length 82061 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 # indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NA75 101046 NGA75 86132 LA50 8 LGA50 8 LA75 18	LG75	19
Misassembled contigs length 82061 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 # indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NA75 101046 NGA75 86132 LA50 8 LGA50 8 LA75 18	# misassemblies	6
# local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 # indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NA75 101046 NGA75 86132 LA50 8 LGA50 8 LA75 18	# misassembled contigs	1
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 # indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NA75 101046 NGA75 86132 LA50 8 LGA50 8 LA75 18	Misassembled contigs length	82061
Unaligned length 0 Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 # indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NA75 101046 NGA75 86132 LA50 8 LGA50 8 LA75 18	# local misassemblies	0
Genome fraction (%) 97.922 Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 # indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NA75 101046 NGA75 86132 LA50 8 LGA50 8 LA75 18	# unaligned contigs	0 + 0 part
Duplication ratio 1.013 # N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 # indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NA75 101046 NGA75 86132 LA50 8 LGA50 8 LA75 18	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 676.93 # indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NA75 101046 NGA75 86132 LA50 8 LGA50 8 LA75 18	Genome fraction (%)	97.922
# mismatches per 100 kbp 676.93 # indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NA75 101046 NGA75 86132 LA50 8 LGA50 8 LA75 18	Duplication ratio	1.013
# indels per 100 kbp 0.95 Largest alignment 527156 NA50 197358 NGA50 197358 NA75 101046 NGA75 86132 LA50 8 LGA50 8 LA75 18	# N's per 100 kbp	0.00
Largest alignment 527156 NA50 197358 NGA50 197358 NA75 101046 NGA75 86132 LA50 8 LGA50 8 LA75 18		676.93
NA50 197358 NGA50 197358 NA75 101046 NGA75 86132 LA50 8 LGA50 8 LA75 18	· · · · · · · · · · · · · · · · · · ·	
NGA50 197358 NA75 101046 NGA75 86132 LA50 8 LGA50 8 LA75 18	Largest alignment	527156
NA75 101046 NGA75 86132 LA50 8 LGA50 8 LA75 18		
NGA75 86132 LA50 8 LGA50 8 LA75 18		
LA50 8 LGA50 8 LA75 18		
LGA50 8 LA75 18		86132
LA75 18		8
I ICA7E I 10		
LGA75 19	LGA75	19

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	6
# relocations	4
# translocations	0
# inversions	2
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	82061
# local misassemblies	0
# mismatches	30768
# indels	43
# short indels	43
# long indels	0
Indels length	43

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).

















