Report

# contigs (>= 1000 bp)		scaffolds
# contigs (>= 5000 bp) 117 # contigs (>= 10000 bp) 93 # contigs (>= 25000 bp) 58 # contigs (>= 50000 bp) 26 Total length (>= 10000 bp) 3925106 Total length (>= 10000 bp) 3850531 Total length (>= 10000 bp) 3681144 Total length (>= 25000 bp) 3130123 Total length (>= 50000 bp) 1957319 # contigs 157 Largest contig 148188 Total length 3932767 Reference length 4641652 GC (%) 50.69 Reference GC (%) 50.78 N50 49952 N75 32043 NG75 13768 L50 27 LG50 35 L75 52 LG75 77 # misassemblies 5 # misassembled contigs 5 Misassembled contigs 55 Misassembled contigs 10 + 0 part Unaligned length 0 Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA75 13365 LA50 29 LA50 29 LA50 3920 NA75 13365	# contigs (>= 1000 bp)	
# contigs (>= 10000 bp)		117
# contigs (>= 25000 bp)		93
# contigs (>= 50000 bp)		58
Total length (>= 1000 bp) 3925106 Total length (>= 5000 bp) 3850531 Total length (>= 10000 bp) 3681144 Total length (>= 25000 bp) 3130123 Total length (>= 50000 bp) 1957319 # contigs 157 Largest contig 148188 Total length 3932767 Reference length 4641652 GC (%) 50.69 Reference GC (%) 50.78 N50 49952 NG50 40252 N75 32043 NG75 13768 L50 27 LG50 35 L75 52 LG75 77 # misassembled contigs 5 # misassembled contigs 5 # soas misassembles 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56		26
Total length (>= 10000 bp) 3681144 Total length (>= 25000 bp) 3130123 Total length (>= 50000 bp) 1957319 # contigs 157 Largest contig 148188 Total length 3932767 Reference length 4641652 GC (%) 50.69 Reference GC (%) 50.78 N50 49952 NG50 40252 N75 32043 NG75 13768 L50 27 LG50 35 L75 52 LG75 77 # misassemblies 5 # misassembled contigs 5 Misassembled contigs 5 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LA50 29 LA50 38 LA75 56	Total length (>= 1000 bp)	3925106
Total length (>= 25000 bp) 3130123 Total length (>= 50000 bp) 1957319 # contigs 157 Largest contig 148188 Total length 3932767 Reference length 4641652 GC (%) 50.69 Reference GC (%) 50.78 N50 49952 NG50 40252 N75 32043 NG75 13768 L50 27 LG50 35 L75 52 LG75 77 # misassemblies 5 # misassembled contigs 5 Misassembled contigs 475557 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	Total length (>= 5000 bp)	3850531
# contigs 157 Largest contig 148188 Total length 3932767 Reference length 4641652 GC (%) 50.69 Reference GC (%) 50.78 N50 49952 NG50 40252 N75 32043 NG75 13768 L50 27 LG50 35 L75 52 LG75 77 # misassemblies 5 # misassembled contigs 5 Misassembled contigs 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	Total length (>= 10000 bp)	3681144
# contigs 157 Largest contig 148188 Total length 3932767 Reference length 4641652 GC (%) 50.69 Reference GC (%) 50.78 N50 49952 NG50 40252 N75 32043 NG75 13768 L50 27 LG50 35 L75 52 LG75 77 # misassemblies 5 # misassembled contigs 5 Misassembled contigs 475557 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	Total length (>= 25000 bp)	3130123
Largest contig 148188 Total length 3932767 Reference length 4641652 GC (%) 50.69 Reference GC (%) 50.78 N50 49952 NG50 40252 N75 32043 NG75 13768 L50 27 LG50 35 L75 52 LG75 77 # misassemblies 5 # misassembled contigs 5 Misassembled contigs length 475557 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75	Total length (>= 50000 bp)	1957319
Total length 3932767 Reference length 4641652 GC (%) 50.69 Reference GC (%) 50.78 N50 49952 NG50 40252 N75 32043 NG75 13768 L50 27 LG50 35 L75 52 LG75 77 # misassemblies 5 # local misassembled contigs 475557 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	# contigs	157
Reference length 4641652 GC (%) 50.69 Reference GC (%) 50.78 N50 49952 NG50 40252 N75 32043 NG75 13768 L50 27 LG50 35 L75 52 LG75 77 # misassemblies 5 # local misassembled contigs 475557 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	Largest contig	148188
GC (%) 50.69 Reference GC (%) 50.78 N50 49952 NG50 40252 N75 32043 NG75 13768 L50 27 LG50 35 L75 52 LG75 77 # misassemblies 5 # misassembled contigs 5 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	Total length	3932767
Reference GC (%) 50.78 N50 49952 NG50 40252 N75 32043 NG75 13768 L50 27 LG50 35 L75 52 LG75 77 # misassemblies 5 # misassembled contigs 5 Misassembled contigs length 475557 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 12264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	Reference length	4641652
N50 49952 NG50 40252 N75 32043 NG75 13768 L50 27 LG50 35 L75 52 LG75 77 # misassemblies 5 # misassembled contigs 5 Misassembled contigs length 475557 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 12264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	GC (%)	50.69
NG50 40252 N75 32043 NG75 13768 L50 27 LG50 35 L75 52 LG75 77 # misassemblies 5 # misassembled contigs 5 Misassembled contigs length 475557 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	Reference GC (%)	50.78
N75 32043 NG75 13768 L50 27 LG50 35 L75 52 LG75 77 # misassemblies 5 # misassembled contigs 475557 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	N50	49952
NG75 13768 L50 27 LG50 35 L75 52 LG75 77 # misassemblies 5 # misassembled contigs 5 Misassembled contigs length 475557 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	NG50	40252
L50 27 LG50 35 L75 52 LG75 77 # misassemblies 5 # misassembled contigs 5 Misassembled contigs length 475557 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	N75	32043
LG50 35 L75 52 LG75 77 # misassemblies 5 # misassembled contigs 5 Misassembled contigs length 475557 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	NG75	13768
L75 52 LG75 77 # misassemblies 5 # misassembled contigs 5 Misassembled contigs length 475557 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	L50	27
LG75 77 # misassemblies 5 # misassembled contigs 5 Misassembled contigs length 475557 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	LG50	35
# misassemblies 5 # misassembled contigs 5 Misassembled contigs length 475557 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	L75	52
# misassembled contigs 5 Misassembled contigs length 475557 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	LG75	77
Misassembled contigs length 475557 # local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	# misassemblies	5
# local misassemblies 4 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	# misassembled contigs	5
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	Misassembled contigs length	475557
Unaligned length 0 Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	# local misassemblies	4
Genome fraction (%) 83.212 Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	# unaligned contigs	0 + 0 part
Duplication ratio 1.018 # N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	Unaligned length	0
# N's per 100 kbp 93.80 # mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	Genome fraction (%)	
# mismatches per 100 kbp 746.56 # indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56		1.018
# indels per 100 kbp 0.80 Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56		<u> </u>
Largest alignment 122264 NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	' '	
NA50 48914 NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	# indels per 100 kbp	!
NGA50 39220 NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56	Largest alignment	122264
NA75 29421 NGA75 13365 LA50 29 LGA50 38 LA75 56		
NGA75 13365 LA50 29 LGA50 38 LA75 56		
LA50 29 LGA50 38 LA75 56		
LGA50 38 LA75 56		
LA75 56		
LGA75 81		
	LGA75	81

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	5
# relocations	4
# translocations	0
# inversions	1
# possibly misassembled contigs	2
# misassembled contigs	5
Misassembled contigs length	475557
# local misassemblies	4
# mismatches	28835
# indels	31
# short indels	20
# long indels	11
Indels length	631

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	3689

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).

















