## Report

# contigs (>= 0 bp)		
# contigs (>= 1000 bp) 90  # contigs (>= 5000 bp) 90  # contigs (>= 10000 bp) 75  # contigs (>= 25000 bp) 54  # contigs (>= 25000 bp) 54  # contigs (>= 50000 bp) 32  Total length (>= 0 bp) 4554872  Total length (>= 1000 bp) 4542294  Total length (>= 5000 bp) 4470400  Total length (>= 10000 bp) 4359028  Total length (>= 25000 bp) 4040495  Total length (>= 50000 bp) 3287630  # contigs 124  Largest contig 233189  Total length 4547231  Reference length 4641652  N50 95475  N75 42936  L50 17  L75 35  # misassemblies 11  # misassembled contigs 7  Misassembled contigs 16  # unaligned contigs 16  # unaligned length 3863  Genome fraction (%) 97.805  Duplication ratio 1.001  # N's per 100 kbp 11.92  # mismatches per 100 kbp 69.94  # indels per 100 kbp 10.00  Largest alignment 202546  NA50 82910  NA75 40166		scaffolds
# contigs (>= 5000 bp) 90  # contigs (>= 10000 bp) 75  # contigs (>= 25000 bp) 54  # contigs (>= 50000 bp) 32  Total length (>= 0 bp) 4554872  Total length (>= 1000 bp) 4542294  Total length (>= 1000 bp) 4470400  Total length (>= 10000 bp) 4359028  Total length (>= 25000 bp) 4040495  Total length (>= 50000 bp) 3287630  # contigs 124  Largest contig 233189  Total length 4547231  Reference length 4641652  N50 95475  N75 42936  L50 17  L75 35  # misassemblies 11  # misassembled contigs 7  Misassembled contigs 16  # unaligned contigs 16  # unaligned length 3863  Genome fraction (%) 97.805  Duplication ratio 1.001  # N's per 100 kbp 11.92  # mismatches per 100 kbp 69.94  # indels per 100 kbp 10.00  Largest alignment 202546  NA50 82910  NA75 40166		156
# contigs (>= 10000 bp) 75 # contigs (>= 25000 bp) 54 # contigs (>= 50000 bp) 32 Total length (>= 0 bp) 4554872 Total length (>= 1000 bp) 4542294 Total length (>= 5000 bp) 4470400 Total length (>= 10000 bp) 4359028 Total length (>= 25000 bp) 4040495 Total length (>= 50000 bp) 3287630 # contigs 124 Largest contig 233189 Total length 4547231 Reference length 4641652 N50 95475 N75 42936 L50 17 L75 35 # misassemblies 11 # misassembled contigs 7 Misassembled contigs 75 Misassembled contigs 16 # unaligned length 3863 Genome fraction (%) 97.805 Duplication ratio 1.001 # N's per 100 kbp 11.92 # mismatches per 100 kbp 69.94 # indels per 100 kbp 10.00 Largest alignment 202546 NA50 82910 NA75 40166	# contigs (>= 1000 bp)	117
# contigs (>= 25000 bp)	• • • • • • • • • • • • • • • • • • • •	90
# contigs (>= 50000 bp) 32  Total length (>= 0 bp) 4554872  Total length (>= 1000 bp) 4542294  Total length (>= 5000 bp) 4470400  Total length (>= 10000 bp) 4359028  Total length (>= 25000 bp) 4040495  Total length (>= 50000 bp) 3287630  # contigs 124  Largest contig 233189  Total length 4547231  Reference length 4641652  N50 95475  N75 42936  L50 17  L75 35  # misassemblies 11  # misassembled contigs 7  Misassembled contigs 124  Wisassembled contigs 164  # unaligned length 569905  # unaligned length 3863  Genome fraction (%) 97.805  Duplication ratio 1.001  # N's per 100 kbp 11.92  # mismatches per 100 kbp 69.94  # indels per 100 kbp 10.00  Largest alignment 202546  NA50 82910  NA75 40166	# contigs (>= 10000 bp)	75
Total length (>= 0 bp)	# contigs (>= 25000 bp)	54
Total length (>= 1000 bp)	# contigs (>= 50000 bp)	32
Total length (>= 5000 bp)	Total length (>= 0 bp)	4554872
Total length (>= 10000 bp) 4359028  Total length (>= 25000 bp) 4040495  Total length (>= 50000 bp) 3287630  # contigs 124  Largest contig 233189  Total length 4547231  Reference length 4641652  N50 95475  N75 42936  L50 17  L75 35  # misassemblies 11  # misassembled contigs 7  Misassembled contigs 7  Misassembled contigs 16  # unaligned length 3863  Genome fraction (%) 97.805  Duplication ratio 1.001  # N's per 100 kbp 11.92  # mismatches per 100 kbp 69.94  NA50 82910  NA75 40166	Total length (>= 1000 bp)	4542294
Total length (>= 25000 bp)         4040495           Total length (>= 50000 bp)         3287630           # contigs         124           Largest contig         233189           Total length         4547231           Reference length         4641652           N50         95475           N75         42936           L50         17           L75         35           # misassemblies         11           # misassembled contigs         7           Misassembled contigs length         569905           # local misassemblies         16           # unaligned contigs         0 + 1 part           Unaligned length         3863           Genome fraction (%)         97.805           Duplication ratio         1.001           # N's per 100 kbp         11.92           # mismatches per 100 kbp         69.94           # indels per 100 kbp         10.00           Largest alignment         202546           NA50         82910           NA75         40166	Total length (>= 5000 bp)	4470400
Total length (>= 50000 bp)       3287630         # contigs       124         Largest contig       233189         Total length       4547231         Reference length       4641652         N50       95475         N75       42936         L50       17         L75       35         # misassemblies       11         # misassembled contigs       7         Misassembled contigs length       569905         # local misassemblies       16         # unaligned contigs       0 + 1 part         Unaligned length       3863         Genome fraction (%)       97.805         Duplication ratio       1.001         # N's per 100 kbp       11.92         # mismatches per 100 kbp       69.94         # indels per 100 kbp       10.00         Largest alignment       202546         NA50       82910         NA75       40166	Total length (>= 10000 bp)	4359028
# contigs 124 Largest contig 233189 Total length 4547231 Reference length 4641652 N50 95475 N75 42936 L50 17 L75 35 # misassemblies 11 # misassembled contigs 7 Misassembled contigs 16 # unaligned contigs 0 + 1 part Unaligned length 3863 Genome fraction (%) 97.805 Duplication ratio 1.001 # N's per 100 kbp 11.92 # mismatches per 100 kbp 69.94 # indels per 100 kbp 10.00 Largest alignment 202546 NA50 82910 NA75 40166	Total length (>= 25000 bp)	4040495
Largest contig         233189           Total length         4547231           Reference length         4641652           N50         95475           N75         42936           L50         17           L75         35           # misassemblies         11           # misassembled contigs         7           Misassembled contigs length         569905           # local misassemblies         16           # unaligned contigs         0 + 1 part           Unaligned length         3863           Genome fraction (%)         97.805           Duplication ratio         1.001           # N's per 100 kbp         11.92           # mismatches per 100 kbp         69.94           # indels per 100 kbp         10.00           Largest alignment         202546           NA50         82910           NA75         40166	Total length (>= 50000 bp)	3287630
Total length         4547231           Reference length         4641652           N50         95475           N75         42936           L50         17           L75         35           # misassemblies         11           # misassembled contigs         7           Misassembled contigs length         569905           # local misassemblies         16           # unaligned contigs         0 + 1 part           Unaligned length         3863           Genome fraction (%)         97.805           Duplication ratio         1.001           # N's per 100 kbp         11.92           # mismatches per 100 kbp         69.94           # indels per 100 kbp         10.00           Largest alignment         202546           NA50         82910           NA75         40166	# contigs	124
Reference length       4641652         N50       95475         N75       42936         L50       17         L75       35         # misassemblies       11         # misassembled contigs       7         Misassembled contigs length       569905         # local misassemblies       16         # unaligned contigs       0 + 1 part         Unaligned length       3863         Genome fraction (%)       97.805         Duplication ratio       1.001         # N's per 100 kbp       11.92         # mismatches per 100 kbp       69.94         # indels per 100 kbp       10.00         Largest alignment       202546         NA50       82910         NA75       40166	Largest contig	233189
N50       95475         N75       42936         L50       17         L75       35         # misassemblies       11         # misassembled contigs       7         Misassembled contigs length       569905         # local misassemblies       16         # unaligned contigs       0 + 1 part         Unaligned length       3863         Genome fraction (%)       97.805         Duplication ratio       1.001         # N's per 100 kbp       11.92         # mismatches per 100 kbp       69.94         # indels per 100 kbp       10.00         Largest alignment       202546         NA50       82910         NA75       40166	Total length	4547231
N75       42936         L50       17         L75       35         # misassemblies       11         # misassembled contigs       7         Misassembled contigs length       569905         # local misassemblies       16         # unaligned contigs       0 + 1 part         Unaligned length       3863         Genome fraction (%)       97.805         Duplication ratio       1.001         # N's per 100 kbp       11.92         # mismatches per 100 kbp       69.94         # indels per 100 kbp       10.00         Largest alignment       202546         NA50       82910         NA75       40166	Reference length	4641652
L50       17         L75       35         # misassemblies       11         # misassembled contigs       7         Misassembled contigs length       569905         # local misassemblies       16         # unaligned contigs       0 + 1 part         Unaligned length       3863         Genome fraction (%)       97.805         Duplication ratio       1.001         # N's per 100 kbp       11.92         # mismatches per 100 kbp       69.94         # indels per 100 kbp       10.00         Largest alignment       202546         NA50       82910         NA75       40166	N50	95475
# misassemblies 11  # misassembled contigs 7  Misassembled contigs length 569905  # local misassemblies 16  # unaligned contigs 0 + 1 part  Unaligned length 3863  Genome fraction (%) 97.805  Duplication ratio 1.001  # N's per 100 kbp 11.92  # mismatches per 100 kbp 69.94  # indels per 100 kbp 10.00  Largest alignment 202546  NA50 82910  NA75 40166	N75	42936
# misassemblies 11  # misassembled contigs 7  Misassembled contigs length 569905  # local misassemblies 16  # unaligned contigs 0 + 1 part  Unaligned length 3863  Genome fraction (%) 97.805  Duplication ratio 1.001  # N's per 100 kbp 11.92  # mismatches per 100 kbp 69.94  # indels per 100 kbp 10.00  Largest alignment 202546  NA50 82910  NA75 40166	L50	17
# misassembled contigs 7 Misassembled contigs length 569905 # local misassemblies 16 # unaligned contigs 0 + 1 part Unaligned length 3863 Genome fraction (%) 97.805 Duplication ratio 1.001 # N's per 100 kbp 11.92 # mismatches per 100 kbp 69.94 # indels per 100 kbp 10.00 Largest alignment 202546 NA50 82910 NA75 40166	L75	35
Misassembled contigs length         569905           # local misassemblies         16           # unaligned contigs         0 + 1 part           Unaligned length         3863           Genome fraction (%)         97.805           Duplication ratio         1.001           # N's per 100 kbp         11.92           # mismatches per 100 kbp         69.94           # indels per 100 kbp         10.00           Largest alignment         202546           NA50         82910           NA75         40166	# misassemblies	11
# local misassemblies 16 # unaligned contigs 0 + 1 part Unaligned length 3863 Genome fraction (%) 97.805 Duplication ratio 1.001 # N's per 100 kbp 11.92 # mismatches per 100 kbp 69.94 # indels per 100 kbp 10.00 Largest alignment 202546 NA50 82910 NA75 40166	# misassembled contigs	7
# unaligned contigs 0 + 1 part Unaligned length 3863 Genome fraction (%) 97.805 Duplication ratio 1.001 # N's per 100 kbp 11.92 # mismatches per 100 kbp 69.94 # indels per 100 kbp 10.00 Largest alignment 202546 NA50 82910 NA75 40166	Misassembled contigs length	569905
Unaligned length 3863 Genome fraction (%) 97.805 Duplication ratio 1.001 # N's per 100 kbp 11.92 # mismatches per 100 kbp 69.94 # indels per 100 kbp 10.00 Largest alignment 202546 NA50 82910 NA75 40166	# local misassemblies	16
Genome fraction (%)       97.805         Duplication ratio       1.001         # N's per 100 kbp       11.92         # mismatches per 100 kbp       69.94         # indels per 100 kbp       10.00         Largest alignment       202546         NA50       82910         NA75       40166	# unaligned contigs	0 + 1 part
Duplication ratio       1.001         # N's per 100 kbp       11.92         # mismatches per 100 kbp       69.94         # indels per 100 kbp       10.00         Largest alignment       202546         NA50       82910         NA75       40166	Unaligned length	3863
# N's per 100 kbp 11.92 # mismatches per 100 kbp 69.94 # indels per 100 kbp 10.00 Largest alignment 202546 NA50 82910 NA75 40166	Genome fraction (%)	97.805
# mismatches per 100 kbp 69.94 # indels per 100 kbp 10.00 Largest alignment 202546 NA50 82910 NA75 40166	Duplication ratio	1.001
# indels per 100 kbp 10.00 Largest alignment 202546 NA50 82910 NA75 40166	# N's per 100 kbp	11.92
Largest alignment         202546           NA50         82910           NA75         40166	# mismatches per 100 kbp	69.94
NA50         82910           NA75         40166	# indels per 100 kbp	10.00
NA75 40166	Largest alignment	202546
	NA50	82910
1450	NA75	40166
LA50   19	LA50	19
LA75 39	LA75	39

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	11
# relocations	11
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	1
# misassembled contigs	7
Misassembled contigs length	569905
# local misassemblies	16
# mismatches	3175
# indels	454
# short indels	440
# long indels	14
Indels length	878

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	1
# with misassembly	0
# both parts are significant	1
Partially unaligned length	3863
# N's	542

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).









