# contigs (>= 0 bp)	Repoi	UCT50H
# contigs (>= 1000 bp) # contigs (>= 5000 bp) # contigs (>= 5000 bp) # contigs (>= 10000 bp) # contigs (>= 25000 bp) # contigs (>= 25000 bp) # contigs (>= 50000 bp) # contigs (>= 50000 bp) Total length (>= 1000 bp) Total length (>= 1000 bp) Total length (>= 5000 bp) Total length # contigs # co	# contins (>= 0 hn)	
# contigs (>= 5000 bp)		
# contigs (>= 10000 bp) # contigs (>= 25000 bp) # contigs (>= 25000 bp) # contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 1000 bp) Total length (>= 1000 bp) Total length (>= 10000 bp) Total length (>= 5000 bp) Total length (>= 25000 bp) Total length (>= 25000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) Total length (>= 25000 bp) Total length (>= 2500		
# contigs (>= 25000 bp) # contigs (>= 50000 bp) # contigs (>= 50000 bp) Total length (>= 1000 bp) Total length (>= 1000 bp) Total length (>= 5000 bp) Total length (>= 50000 bp) Total length Reference length Total length Reference length Reference GC (%) Reference GC (%) Refo Reference GC (%) Refo Refo Reference GC (%) Refo Refo Reference GC (%) Refo Refo Refo Refo Refo Refo Refo Refo		
# contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 1000 bp) Total length (>= 1000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 10000 bp) Total length (>= 25000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp) Total length Reference length GC (%) Reference length GC (%) Reference GC (%) Rof50 Rof50 Rof50 Rof50 Rof90		
Total length (>= 0 bp)		
Total length (>= 1000 bp)		
Total length (>= 5000 bp)		
Total length (>= 10000 bp)		
Total length (>= 25000 bp)		
# contigs		
# contigs		
Largest contig 902761 Total length 1329478 Reference length 1521208 GC (%) 28.18 N50 902761 N50 902761 N90 24152 N90 24152 NG90 300 auN 624359.2 auNG 545666.2 L50 3 L650 3 L90 5 LG90 5 # misassemblies 16 # misassembled contigs 5 Misassembled contigs 5 Misassembled contigs 6 # scaffold gap loc. mis. 6 # unaligned mis. contigs 5 # unaligned length 118509 Genome fraction (%) 78.509 Duplication ratio 1.014 # N's per 100 kbp 55.42 # genomic features 1232 + 74 part Largest alignment 902581 NA50 902581 NA50 902581		
Total length 1329478 Reference length 1521208 GC (%) 28.33 Reference GC (%) 28.18 N50 902761 NG50 902761 NG90 24152 NG90 34152 auN 624359.2 auNG 545666.2 L50 1 LG50 1 LG90 9 # misassemblies 16 # misassembled contigs 5 Misassembled contigs 5 Misassembled contigs 2 # scaffold gap ext. mis. 6 # scaffold gap ext. mis. 6 # unaligned mis. contigs 6 # unaligned length 118509 Genome fraction (%) 78.509 Duplication ratio 1.014 # N's per 100 kbp 55.42 # genomic features 1232 + 74 part Largest alignment 902581 NA50 902581 NA50 902581 NA90	# contigs	41
Reference length 1521208 GC (%) 28.33 Reference GC (%) 28.18 N50 902761 NG50 902761 NG50 902761 NG90 24152 NG90 301N 624359.2 auN 624359.2 auNG 545666.2 L50 31 LG90 902 # misassembles 16 # misassembled contigs 16 # scaffold gap ext. mis. 16 # scaffold gap ext. mis. 17 # unaligned mis. contigs 17 # unaligned length 118508 Genome fraction (%) 78.508 Duplication ratio 1.014 # N's per 100 kbp 796.43 # indels per 100 kbp 796.43 NA50 902581 NA50 902581 NA90 879 NGA90 auNA 617489.9 auNGA 539662.7 LGA50 13	Largest contig	902761
Reference GC (%) Reference GC (Act of Good and	Total length	1329478
Reference GC (%) 28.18 N50 902761 NG50 902761 N90 24152 NG90 34152 auN 624359.2 auNG 545666.2 L50 3 LG50 3 L90 9 LG90 9 # misassemblies 16 # misassembled contigs 5 Misassembled contigs 2 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 5 # unaligned length 118509 Genome fraction (%) 78.509 Duplication ratio 1.014 # N's per 100 kbp 796.43 # genomic features 1232 + 74 part Largest alignment 902581 NA50 902581 NA50 902581 NA50 902581 NA90 879 NA90 879 NA90 879	Reference length	1521208
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N90 24152 N90 24152 NG90 34152 auN 624359.2 auNG 545666.2 L50 1 LG50 1 L90 5 LG90 6 # misassemblies 16 # misassembled contigs 5 Misassembled contigs length 217544 # local misassemblies 4 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 5 # unaligned length 118509 Genome fraction (%) 78.509 Duplication ratio 1.014 # N's per 100 kbp 796.43 # genomic features 1232 + 74 part Largest alignment 902581 NA50 902581 NA50 902583 NA90 879 NGA90 300 auNA 617489.9 auNA 617489.9 auNA 617489.9	Reference GC (%)	28.18
N90 24152 NG90 auN 624359.2 auNG 545666.2 1 L50 1 1 LG50 1 1 L90 5 1 LG90 5 1 # misassemblies 1 1 # misassembled contigs 5 1 Misassembled contigs length 217544 1 # local misassemblies 4 1 # scaffold gap ext. mis. 0 0 # scaffold gap loc. mis. 0 0 # unaligned mis. contigs 6 + 14 part Unaligned length 118509 0 Genome fraction (%) 78.509 Duplication ratio 1.014 # N's per 100 kbp 796.43 # genomic features 1232 + 74 part Largest alignment 902581 NA50 902581 NA50 902583 NA90 879 NGA90 3 auNA 617489.9	N50	902761
NG90 auN 624359.2 auNG 545666.2 L50 1 LG50 1 L90 9 LG90 9 # misassemblies 16 # misassembled contigs 5 Misassembled contigs length 217544 # local misassemblies 4 # scaffold gap ext. mis. 6 # scaffold gap loc. mis. 6 # unaligned mis. contigs 6 + 14 part Unaligned length 118509 Genome fraction (%) 78.509 Duplication ratio 1.014 # N's per 100 kbp 0.00 # mismatches per 100 kbp 796.43 # indels per 100 kbp 55.42 # genomic features 1232 + 74 part Largest alignment 902581 NA50 902581 NA50 902581 NA90 879 NA90 879 NA90 879 NA90 879 NA90 879 NA90 879 NA90	NG50	902761
auN 624359.2 auNG 545666.2 L50 1 LG50 1 LG90 9 LG90 9 # misassemblies 16 # misassembled contigs 16 # local misassemblies 2 # scaffold gap loc. mis. 3 # unaligned mis. contigs 6 + 14 part 11850.5 # unaligned length 11850.5 Genome fraction (%) 78.50.5 Duplication ratio 1.014 # N's per 100 kbp 796.43 # indels per 100 kbp 55.42 # genomic features 1232 + 74 part 1232 +	N90	24152
auNG 545666.2 L50 1 LG50 1 LG90 9 LG90 9 # misassemblies 10 # misassembled contigs 1 # local misassemblies 2 # scaffold gap ext. mis. 1 # scaffold gap loc. mis. 1 # unaligned mis. contigs 1 # unaligned length 1 Unaligned length 1 # N's per 100 kbp 78.50 # indels per 100 kbp 796.43 # genomic features 1 Largest alignment 902581 Total aligned length 1210653 NA50 902581 NA50 902581 NA90 875 NA90 875 NA90 875 NA90 3876 ALA50 1 LA50 1 LA50 1 LGA50 1 LA90 388	NG90	-
L50 LG50 LG90 # misassemblies # misassembled contigs Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length Unaligned length Genome fraction (%) Puplication ratio # N's per 100 kbp # mismatches per 100 kbp # indels per 100 kbp # genomic features Largest alignment Total aligned length NA50 NGA90 auNA auNGA LA50 LGA50 LGA50 LGA50 LGA50 LGA50 LGA50 LGA50 LGA50 LGA50 10 10 10 11 12 12 12 13 14 15 16 17 16 17 17 17 17 18 18 18 18 18 18	auN	624359.2
LG50 L90 LG90 # misassemblies # misassembled contigs Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned length Unaligned len	auNG	545666.2
L90 LG90 # misassemblies	L50	1
# misassembles	LG50	1
# misassemblies 16 # misassembled contigs	L90	9
# misassembled contigs Misassembled contigs length # local misassemblies # scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs One of the part of the	LG90	-
Misassembled contigs length 217544 # local misassemblies 4 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 5 # unaligned contigs 6 + 14 part Unaligned length 118509 Genome fraction (%) 78.509 Duplication ratio 1.014 # N's per 100 kbp 0.00 # mismatches per 100 kbp 796.43 # genomic features 1232 + 74 part Largest alignment 902581 Total aligned length 1210653 NA50 902581 NA50 902581 NA90 875 NA90 875 NA90 875 NA90 875 NA90 875 NA90 875 AuNA 617489.9 auNA 539662.7 LA50 1 LA50 3 LA90 38	# misassemblies	16
Misassembled contigs length 217544 # local misassemblies 4 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 5 # unaligned contigs 6 + 14 part Unaligned length 118509 Genome fraction (%) 78.509 Duplication ratio 1.014 # N's per 100 kbp 0.00 # mismatches per 100 kbp 796.43 # genomic features 1232 + 74 part Largest alignment 902581 Total aligned length 1210653 NA50 902581 NA50 902581 NA90 875 NA90 875 NA90 875 NA90 875 NA90 875 NA90 875 AuNA 617489.9 auNA 539662.7 LA50 1 LA50 3 LA90 38	# misassembled contigs	5
# scaffold gap ext. mis. # scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs # unaligned length Genome fraction (%) Duplication ratio # N's per 100 kbp # mismatches per 100 kbp # genomic features Largest alignment Total aligned length NA50 NGA50 NGA90 auNA auNGA LA50 LA50 LGA50 LA90 S 50 C 70 C	Misassembled contigs length	217544
# scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs 6 + 14 part Unaligned length 118509 Genome fraction (%) Duplication ratio 1.014 # N's per 100 kbp # mismatches per 100 kbp 796.43 # indels per 100 kbp 55.42 # genomic features 1232 + 74 part Largest alignment 902581 Total aligned length 1210653 NA50 902581 NA90 879 NA90 879 NA90 auNA 617489.9 auNA 539662.7 LA50 LA50 LA90 38	# local misassemblies	4
# scaffold gap loc. mis. # unaligned mis. contigs # unaligned contigs 6 + 14 part Unaligned length 118509 Genome fraction (%) Duplication ratio 1.014 # N's per 100 kbp # mismatches per 100 kbp 796.43 # indels per 100 kbp 55.42 # genomic features 1232 + 74 part Largest alignment 902581 Total aligned length 1210653 NA50 902581 NA90 879 NA90 879 NA90 auNA 617489.9 auNA 539662.7 LA50 LA50 LA90 38		0
# unaligned mis. contigs # unaligned contigs 6 + 14 part Unaligned length 118509 Genome fraction (%) 78.509 Duplication ratio 1.014 # N's per 100 kbp 796.43 # indels per 100 kbp 55.42 # genomic features 1232 + 74 part Largest alignment 902581 NA50 902581 NA90 879 NA90 3879 NA90 auNA 617489.9 auNA 539662.7 LA50 LA50 LA50 LA90 38		0
# unaligned contigs 6 + 14 part Unaligned length 118509 Genome fraction (%) 78.509 Duplication ratio 1.014 # N's per 100 kbp 0.00 # mismatches per 100 kbp 796.43 # indels per 100 kbp 1232 + 74 part Largest alignment 902581 Total aligned length 1210653 NA50 902581 NA90 879 NGA90 auNA 617489.9 auNGA 539662.7 LA50 1 LGA50 38		5
Unaligned length 118509 Genome fraction (%) 78.509 Duplication ratio 1.014 # N's per 100 kbp 0.00 # mismatches per 100 kbp 756.42 # indels per 100 kbp 1232 + 74 part Largest alignment 902581 Total aligned length 1210655 NA50 902581 NA90 879 NGA90 400 auNA 617489.9 auNGA 539662.7 LASO 1 LASO 38		
Genome fraction (%) 78.508 Duplication ratio 1.014 # N's per 100 kbp 0.00 # mismatches per 100 kbp 796.43 # indels per 100 kbp 55.42 # genomic features 1232 + 74 part Largest alignment 902581 Total aligned length 1210653 NA50 902581 NGA50 902581 NA90 875 NGA90 617489.9 auNA 617489.9 auNGA 539662.7 LA50 3 LA90 38		
Duplication ratio 1.014 # N's per 100 kbp 0.00 # mismatches per 100 kbp 796.43 # indels per 100 kbp 55.42 # genomic features 1232 + 74 part Largest alignment 902581 NA50 902581 NAG50 902581 NA90 879 NGA90 617489.9 auNA 617489.9 auNGA 539662.7 LA50 3 LA90 38		
# N's per 100 kbp		-
# mismatches per 100 kbp 796.43 # indels per 100 kbp 55.42 # genomic features 1232 + 74 part Largest alignment 902581 NA50 902581 NA90 875 NA90 875 NA90 4617489.5 auNA 539662.7 LA50 1 LGA50 38		
# indels per 100 kbp 55.42 # genomic features 1232 + 74 part Largest alignment 902581 Total aligned length 1210653 NA50 902581 NA50 902581 NA90 879 NGA90 401 auNA 617489.9 auNGA 539662.7 LA50 1 LGA50 38		
# genomic features 1232 + 74 part Largest alignment 902581 Total aligned length 1210653 NA50 902581 NA90 902581 NA90 879 NGA90 4017489.5 auNA 539662.7 LA50 1 LGA50 38		
Largest alignment 902581 Total aligned length 1210653 NA50 902581 NGA50 902581 NA90 875 NGA90 auNA 617489.5 auNGA 539662.7 LA50 1 LGA50 38		
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NGA50 902581 NA90 879 NGA90		
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NGA90 auNA 617489.9 auNGA 539662.7 LA50 1 LGA50 38		902581
auNA 617489.9 auNGA 539662.7 LA50 1 LGA50 1 LA90 38	NA90	879
auNGA 539662.7 LA50 1 LGA50 1 LA90 38	NGA90	-
LGA50 1 LGA50 1 LA90 38	auNA	617489.9
LGA50 1	auNGA	539662.7
LA90 38	LA50	1
	LGA50	1
LGA90	LA90	38
	LGA90	-

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

# misassemblies 16 # contig misassemblies 16 # c. relocations 7 # c. translocations 9 # c. inversions 0 # scaffold misassemblies 0 # s. relocations 0 # s. relocations 0 # s. inversions 0 # s. inversions 10 # s. inversions 10 # misassembled contigs 10 # misassembled contigs 10 # misassembled contigs 10 # incal misassemblies 10 # scaffold gap ext. mis. 10 # scaffold gap loc. mis. 10 # unaligned mis. contigs 15 # mismatches 15 # mismatches 16 # indels (<= 5 bp) 602 # indels (<= 5 bp) 69 Indels length 3351		
# contig misassemblies 16 # c. relocations 7 # c. translocations 9 # c. inversions 0 # scaffold misassemblies 0 # s. relocations 0 # s. inversions 0 # misassembled contigs 5 Misassembled contigs 1217544 # local misassemblies 4 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 5 # mismatches 9642 # indels (<= 5 bp) 602 # indels (< 5 bp) 69		UCT50H
# c. relocations 7 # c. translocations 9 # c. inversions 0 # scaffold misassemblies 0 # s. relocations 0 # s. translocations 0 # s. inversions 0 # misassembled contigs 5 Misassembled contigs length 217544 # local misassemblies 4 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 5 # mismatches 9642 # indels (<= 5 bp) 602 # indels (< 5 bp) 69	# misassemblies	16
# c. translocations 9 # c. inversions 0 # scaffold misassemblies 0 # s. relocations 0 # s. translocations 0 # s. inversions 0 # misassembled contigs 5 Misassembled contigs length 217544 # local misassemblies 4 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 5 # mismatches 9642 # indels (<= 5 bp) 602 # indels (> 5 bp) 69	# contig misassemblies	16
# c. inversions 0 # scaffold misassemblies 0 # s. relocations 0 # s. translocations 0 # s. inversions 0 # misassembled contigs 5 Misassembled contigs length 217544 # local misassemblies 4 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 5 # mismatches 9642 # indels (<= 5 bp) 602 # indels (<= 5 bp) 69	# c. relocations	7
# scaffold misassemblies 0 # s. relocations 0 # s. translocations 0 # s. inversions 0 # misassembled contigs 5 Misassembled contigs length 217544 # local misassemblies 4 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 5 # mismatches 9642 # indels (<= 5 bp) 602 # indels (> 5 bp) 69	# c. translocations	9
# s. relocations 0 # s. translocations 0 # s. inversions 0 # misassembled contigs 5 Misassembled contigs length 217544 # local misassemblies 4 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 5 # mismatches 9642 # indels (<= 5 bp) 602 # indels (> 5 bp) 69	# c. inversions	0
# s. translocations 0 # s. inversions 0 # misassembled contigs 5 Misassembled contigs length 217544 # local misassemblies 4 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 5 # mismatches 9642 # indels (<= 5 bp) 602 # indels (> 5 bp) 69	# scaffold misassemblies	0
# s. inversions 0 # misassembled contigs 5 Misassembled contigs length 217544 # local misassemblies 4 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 5 # mismatches 9642 # indels (<= 5 bp) 602 # indels (> 5 bp) 69	# s. relocations	0
# misassembled contigs 5 Misassembled contigs length 217544 # local misassemblies 4 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 5 # mismatches 9642 # indels (<= 5 bp) 602 # indels (> 5 bp) 69	# s. translocations	0
Misassembled contigs length 217544 # local misassemblies 4 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 5 # mismatches 9642 # indels 671 # indels (<= 5 bp)	# s. inversions	0
# local misassemblies 4 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 5 # mismatches 9642 # indels (<= 5 bp) 602 # indels (> 5 bp) 69	# misassembled contigs	5
# scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 5 # mismatches 9642 # indels (<= 5 bp) 602 # indels (> 5 bp) 69	Misassembled contigs length	217544
# scaffold gap loc. mis. 0 # unaligned mis. contigs 5 # mismatches 9642 # indels (<= 5 bp) 602 # indels (> 5 bp) 69	# local misassemblies	4
# unaligned mis. contigs 5 # mismatches 9642 # indels (<= 5 bp) 602 # indels (> 5 bp) 69	# scaffold gap ext. mis.	0
# mismatches 9642 # indels 671 # indels (<= 5 bp) 602 # indels (> 5 bp) 69	# scaffold gap loc. mis.	0
# indels 671 # indels (<= 5 bp) 602 # indels (> 5 bp) 69	# unaligned mis. contigs	5
# indels (<= 5 bp) 602 # indels (> 5 bp) 69	# mismatches	9642
# indels (> 5 bp) 69	# indels	671
	# indels (<= 5 bp)	602
Indels length 3351	# indels (> 5 bp)	69
	Indels length	3351

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

	UCT50H
# fully unaligned contigs	6
Fully unaligned length	37268
# partially unaligned contigs	14
Partially unaligned length	81241
# 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).

























