# contigs (>= 1000 bp)	Report	
# contigs (>= 5000 bp)	Пероп	contigs
# contigs (>= 10000 bp)	# contigs (>= 1000 bp)	1
# contigs (>= 25000 bp)	# contigs (>= 5000 bp)	1
# contigs (>= 50000 bp)	# contigs (>= 10000 bp)	1
Total length (>= 1000 bp) 25447 Total length (>= 5000 bp) 25447 Total length (>= 10000 bp) 25447 Total length (>= 25000 bp) 0 # contigs 3 Largest contig 25447 Total length 26910 Reference length 3040590 GC (%) 46.27 Reference GC (%) 0.00 N50 25447 NG50 - N90 25447 NG90 - auN 24103.3 auNG 213.3 L50 1 LG50 - L90 1 LG90 - # misassemblies 0 # misassembled contigs 0 M scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # mismatches per 100 kbp 0.00 Largest alignmen	# contigs (>= 25000 bp)	1
Total length (>= 5000 bp) 25447 Total length (>= 10000 bp) 25447 Total length (>= 50000 bp) 0 # contigs 3 Largest contig 25447 Total length 26910 Reference length 3040590 GC (%) 46.27 Reference GC (%) 0.00 N50 25447 NG50 - N90 25447 NG90 - auN 24103.3 auNG 213.3 L50 1 LG50 - L90 1 LG90 - # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned contigs 0 # unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # mismatches per 100 kbp<	# contigs (>= 50000 bp)	0
Total length (>= 10000 bp) 25447 Total length (>= 25000 bp) 25447 Total length (>= 50000 bp) 3 # contigs 3 Largest contig 25447 Total length 26910 Reference length 3040590 GC (%) 46.27 Reference GC (%) 0.00 N50 25447 NG50 - N90 25447 NG90 - auN 24103.3 auNG 213.3 L50 1 LG50 - L90 1 LG90 - # misassemblies 0 # misassembled contigs 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 0.00 Largest alignment 617 Total aligned length	Total length (>= 1000 bp)	25447
Total length (>= 25000 bp) 25447 Total length (>= 50000 bp) 0 # contigs 3 Largest contig 25447 Total length 26910 Reference length 3040590 GC (%) 46.27 Reference GC (%) 0.00 N50 25447 NG50 - N90 25447 NG90 - auN 24103.3 auNG 213.3 L50 1 LG50 - L90 1 LG90 - # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # nismatches per 100 kbp 0.00 # mismatches per 100 kbp<	Total length (>= 5000 bp)	25447
Total length (>= 50000 bp) 0 # contigs 3 Largest contig 25447 Total length 26910 Reference length 3040590 GC (%) 46.27 Reference GC (%) 0.00 N50 25447 NG50 - N90 25447 NG90 - auN 24103.3 auNG 213.3 L50 1 LG50 - L90 1 LG90 - # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 0.0 # mismatches per 100 kbp 6458.12 # indels per 100 kbp	Total length (>= 10000 bp)	25447
# contigs 3 Largest contig 25447 Total length 26910 Reference length 3040590 GC (%) 46.27 Reference GC (%) 0.00 N50 25447 NG50 - N90 25447 NG90 - auN 24103.3 auNG 213.3 L50 1 LG50 - L90 1 LG90 - # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned contigs 0 # unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 6458.12 # indels per 100 kbp 0.0 Largest alignment 617 T	Total length (>= 25000 bp)	25447
Largest contig 25447 Total length 26910 Reference length 3040590 GC (%) 46.27 Reference GC (%) 0.00 N50 25447 NG50 - N90 25447 NG90 - auN 24103.3 auNG 213.3 L50 1 LG50 - L90 1 LG90 - # misassemblies 0 # misassembled contigs 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 6458.12 # indels per 100 kbp 6458.12 # indels per 100 kbp 6458.12 # indels per 100 kbp 0.0 Largest alignment 617 Total aligned length	Total length (>= 50000 bp)	0
Total length 26910 Reference length 3040590 GC (%) 46.27 Reference GC (%) 0.00 N50 25447 NG50 - N90 25447 NG90 - auN 24103.3 auNG 213.3 L50 1 LG50 - L90 1 LG90 - # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50 - <td># contigs</td> <td>3</td>	# contigs	3
Reference length 3040590 GC (%) 46.27 Reference GC (%) 0.00 N50 25447 NG50 - N90 25447 NG90 - auN 24103.3 auNG 213.3 L50 1 LG50 - L90 1 LG90 - # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50	Largest contig	25447
GC (%) 46.27 Reference GC (%) 0.00 N50 25447 NG50 - N90 25447 NG90 - auN 24103.3 auNG 213.3 L50 1 LG50 - L90 1 LG90 - # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50 - NGA90 - auNA 17.1 auNA 17.1 auNA 17.1	Total length	26910
Reference GC (%) 0.00 N50 25447 NG50 - N90 25447 NG90 - auN 24103.3 auNG 213.3 L50 1 LG50 - L90 1 LG90 - # misassemblies 0 Misassembled contigs 0 Misassembled contigs 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50 - NGA90 - auNA 17.1	Reference length	3040590
N50 25447 NG50 - N90 25447 NG90 - auN 24103.3 auNG 213.3 L50 1 LG50 - L90 1 LG90 - # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50 - NGA90 - auNA 17.1 auNA 17.1 auNGA 0.2 LA50 - LGA50 -	GC (%)	46.27
NG50 25447 NG90 - auN 24103.3 auNG 213.3 L50 1 LG50 - L90 1 LG90 - # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50 - NGA90 - auNA 17.1 auNA 17.1 auNGA 0.2 LA50 - LGA50 -	Reference GC (%)	0.00
N90 25447 NG90 - auN 24103.3 auNG 213.3 L50 1 LG50 - L90 1 LG90 - # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 1 part Unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # mismatches per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50 - NA90 - NGA90 - auNA 17.1 auNGA	N50	25447
NG90 - auN 24103.3 auNG 213.3 L50 1 LG50 - L90 1 LG90 - # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50 - NA90 - NGA90 - auNA 17.1 auNGA 0.2 LA50 - LGA50 -	NG50	-
auN 24103.3 auNG 213.3 L50 1 LG50 - L90 1 LG90 - # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50 - NGA90 - auNA 17.1 auNA 17.1 auNGA 0.2 LA50 - LGA50 -	N90	25447
auNG 213.3 L50 1 LG50	NG90	-
L50 1 LG50 - L90 1 LG90 - # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50 - NGA90 - auNA 17.1 auNGA 0.2 LA50 - LGA50 -	auN	24103.3
LG50 - L90 1 LG90 - # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 1 part Unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50 - NGA90 - auNA 17.1 auNGA 0.2 LA50 - LGA50 -	auNG	213.3
L90 1 LG90 - # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 1 part Unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50 - NGA90 - auNA 17.1 auNGA 0.2 LA50 - LGA50 -	L50	1
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassembles 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 + 1 part Unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50 NGA50 NGA90 auNA 17.1 auNGA 0.2 LA50 LGA50 LGA50	LG50	-
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 + 1 part Unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50 - NGA50 - NGA90 - auNA 17.1 auNGA 0.2 LGA50 -	L90	1
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50 - NGA50 - NGA90 - auNA 17.1 auNGA 0.2 LGA50 -	LG90	-
Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 # unaligned contigs 0 + 1 part Unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50 - NGA90 - auNA 17.1 auNGA 0.2 LA50 - LGA50 -	# misassemblies	0
# local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 + 1 part Unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50 NGA50 NGA90 auNA 17.1 auNGA 0.2 LA50 LGA50	# misassembled contigs	0
# scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 0 + 1 part Unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50 NGA50 NGA90 auNA 17.1 auNGA 0.2 LA50 LGA50 LGA50 LGA50 **Continuation in the scale of the	Misassembled contigs length	0
# scaffold gap loc. mis. 0 # unaligned mis. contigs 0 + 1 part Unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50 - NGA50 - NA90 - NGA90 auNA 17.1 auNGA 0.2 LA50 - LGA50 - CANAGO - CANA	# local misassemblies	0
# unaligned mis. contigs 0 # unaligned contigs 0 + 1 part Unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50 - NGA50 - NA90 NGA90 auNA 17.1 auNGA 0.2 LGA50 LGA50	# scaffold gap ext. mis.	0
# unaligned mis. contigs 0 # unaligned contigs 0 + 1 part Unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50 - NGA50 - NA90 NGA90 auNA 17.1 auNGA 0.2 LGA50 LGA50	# scaffold gap loc. mis.	0
Unaligned length 25328 Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50 - NGA50 - NGA90 - auNA 17.1 auNGA 0.2 LA50 - LGA50 -		0
Genome fraction (%) 0.033 Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50 - NGA50 - NGA90 - auNA 17.1 auNGA 0.2 LA50 - LGA50 -	# unaligned contigs	0 + 1 part
Duplication ratio 1.000 # N's per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50 - NGA50 - NA90 - auNA 17.1 auNGA 0.2 LA50 - LGA50 -	Unaligned length	25328
# N's per 100 kbp 0.00 # mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50 - NGA50 - NA90 - NGA90 - auNA 17.1 auNGA 0.2 LA50 - LGA50 -	Genome fraction (%)	0.033
# mismatches per 100 kbp 6458.12 # indels per 100 kbp 0.00 Largest alignment 617 Total aligned length 991 NA50	Duplication ratio	1.000
# indels per 100 kbp	# N's per 100 kbp	0.00
# indels per 100 kbp	# mismatches per 100 kbp	6458.12
Largest alignment 617 Total aligned length 991 NA50 - NGA50 - NA90 - NGA90 - auNA 17.1 auNGA 0.2 LA50 - LGA50 -		
Total aligned length 991 NA50 - NGA50 - NA90 - NGA90 - auNA 17.1 auNGA 0.2 LA50 - LGA50 -		
NA50 - NGA50 - NA90 - NA90 - ANA90 - A		
NGA50 - NA90 - NGA90 - auNA 17.1 auNGA 0.2 LA50 - LGA50 -		
NA90 - NGA90 - auNA 17.1 auNGA 0.2 LA50 - LGA50 -		_
NGA90 - auNA 17.1 auNGA 0.2 LA50 - LGA50 -		
auNA 17.1 auNGA 0.2 LA50 - LGA50 -		_
auNGA 0.2 LA50 - LGA50 -		17.1
LA50 - LGA50 -		
LGA50 -		- 0.2
		_
LGA90 -		
Ill statistics are based on contig		n contin

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

	contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	64
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

All statistics are based on contigs of size \geq 500 bp, unless otherwise noted (e.g., "# contigs (\geq 0 bp)" and "Total length (\geq 0 bp)" include all contigs).

Unaligned report

	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	25328
# N's	0

All statistics are based on contigs of size \geq 500 bp, unless otherwise noted (e.g., "# contigs (\geq 0 bp)" and "Total length (\geq 0 bp)" include all contigs).























