Report

# contigs (>= 0 bp) 78 # contigs (>= 1000 bp) 66 # contigs (>= 5000 bp) 66 # contigs (>= 10000 bp) 62 # contigs (>= 25000 bp) 55 # contigs (>= 5000 bp) 55 # contigs (>= 50000 bp) 41 Total length (>= 0 bp) 9157004 Total length (>= 1000 bp) 9135989 Total length (>= 5000 bp) 9112641 Total length (>= 10000 bp) 9079171 Total length (>= 25000 bp) 8963305 Total length (>= 25000 bp) 8497357 # contigs 89 Largest contig 657825 Total length 9144127 Reference length 9283304 N50 315111 N75 131793 L50 11 L75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned length 4507980 Genome fraction (%) 49.893 Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 1.01 Largest alignment 657825 NA50 27820 LA50 16		scaffolds
# contigs (>= 5000 bp) 62 # contigs (>= 10000 bp) 62 # contigs (>= 25000 bp) 55 # contigs (>= 50000 bp) 41 Total length (>= 0 bp) 9157004 Total length (>= 1000 bp) 9135989 Total length (>= 5000 bp) 9112641 Total length (>= 10000 bp) 9079171 Total length (>= 25000 bp) 8963305 Total length (>= 50000 bp) 8497357 # contigs 89 Largest contig 657825 Total length 9144127 Reference length 9283304 N50 315111 N75 131793 L50 11 L75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned length 4507980 Genome fraction (%) 49.893 Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 1.01 Largest alignment 657825 NA50 27820	# contigs (>= 0 bp)	137
# contigs (>= 10000 bp) 62 # contigs (>= 25000 bp) 55 # contigs (>= 50000 bp) 41 Total length (>= 0 bp) 9157004 Total length (>= 1000 bp) 9135989 Total length (>= 5000 bp) 9112641 Total length (>= 10000 bp) 9079171 Total length (>= 25000 bp) 8963305 Total length (>= 50000 bp) 8497357 # contigs 89 Largest contig 657825 Total length 9144127 Reference length 9283304 N50 315111 N75 131793 L50 11 L75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned length 4507980 Genome fraction (%) 49.893 Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 1.01 Largest alignment 657825 NA50 27820	# contigs (>= 1000 bp)	78
# contigs (>= 25000 bp)	# contigs (>= 5000 bp)	66
# contigs (>= 50000 bp) 41 Total length (>= 0 bp) 9157004 Total length (>= 1000 bp) 9135989 Total length (>= 5000 bp) 9112641 Total length (>= 10000 bp) 9079171 Total length (>= 25000 bp) 8963305 Total length (>= 50000 bp) 8497357 # contigs 89 Largest contig 657825 Total length 9144127 Reference length 9283304 N50 315111 N75 131793 L50 11 L75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned length 4507980 Genome fraction (%) 49.893 Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 1.01 Largest alignment 657825 NA50 27820	# contigs (>= 10000 bp)	62
Total length (>= 0 bp) 9157004 Total length (>= 1000 bp) 9135989 Total length (>= 5000 bp) 9112641 Total length (>= 10000 bp) 9079171 Total length (>= 25000 bp) 8963305 Total length (>= 50000 bp) 8497357 # contigs 89 Largest contig 657825 Total length 9144127 Reference length 9283304 N50 315111 N75 131793 L50 11 L75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 48 + 18 part Unaligned length 4507980 Genome fraction (%) 49.893 Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 1.01 Largest alignment 657825 NA50 27820	# contigs (>= 25000 bp)	55
Total length (>= 1000 bp) 9135989 Total length (>= 5000 bp) 9112641 Total length (>= 10000 bp) 9079171 Total length (>= 25000 bp) 8963305 Total length (>= 50000 bp) 8497357 # contigs 89 Largest contig 657825 Total length 9144127 Reference length 9283304 N50 315111 N75 131793 L50 11 L75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned length 4507980 Genome fraction (%) 49.893 Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 1.01 Largest alignment 657825 NA50 27820	# contigs (>= 50000 bp)	41
Total length (>= 5000 bp) 9112641 Total length (>= 10000 bp) 9079171 Total length (>= 25000 bp) 8963305 Total length (>= 50000 bp) 8497357 # contigs 89 Largest contig 657825 Total length 9144127 Reference length 9283304 N50 315111 N75 131793 L50 11 L75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 48 + 18 part Unaligned length 4507980 Genome fraction (%) 49.893 Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 1.01 Largest alignment 657825 NA50 27820	Total length (>= 0 bp)	9157004
Total length (>= 10000 bp) 9079171 Total length (>= 25000 bp) 8963305 Total length (>= 50000 bp) 8497357 # contigs 89 Largest contig 657825 Total length 9144127 Reference length 9283304 N50 315111 N75 131793 L50 11 L75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 48 + 18 part Unaligned length 4507980 Genome fraction (%) 49.893 Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 1.01 Largest alignment 657825 NA50 27820	Total length (>= 1000 bp)	9135989
Total length (>= 25000 bp) 8963305 Total length (>= 50000 bp) 8497357 # contigs 89 Largest contig 657825 Total length 9144127 Reference length 9283304 N50 315111 N75 131793 L50 11 L75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 48 + 18 part Unaligned length 4507980 Genome fraction (%) 49.893 Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 1.01 Largest alignment 657825 NA50 27820	Total length (>= 5000 bp)	9112641
Total length (>= 50000 bp) 8497357 # contigs 89 Largest contig 657825 Total length 9144127 Reference length 9283304 N50 315111 N75 131793 L50 11 L75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 48 + 18 part Unaligned length 4507980 Genome fraction (%) 49.893 Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 248.07 # indels per 100 kbp 1.01 Largest alignment 657825 NA50 27820	Total length (>= 10000 bp)	9079171
# contigs 89 Largest contig 657825 Total length 9144127 Reference length 9283304 N50 315111 N75 131793 L50 11 L75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 48 + 18 part Unaligned length 4507980 Genome fraction (%) 49.893 Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 1.01 Largest alignment 657825 NA50 27820	Total length (>= 25000 bp)	8963305
Largest contig 657825 Total length 9144127 Reference length 9283304 N50 315111 N75 131793 L50 11 L75 24 # misassemblies 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 48 + 18 part Unaligned length 4507980 Genome fraction (%) 49.893 Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 248.07 # indels per 100 kbp 1.01 Largest alignment 657825 NA50 27820	Total length (>= 50000 bp)	8497357
Total length 9144127 Reference length 9283304 N50 315111 N75 131793 L50 11 L75 24 # misassemblies 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 48 + 18 part Unaligned length 4507980 Genome fraction (%) 49.893 Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 248.07 # indels per 100 kbp 1.01 Largest alignment 657825 NA50 27820	# contigs	89
Reference length 9283304 N50 315111 N75 131793 L50 11 L75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 48 + 18 part Unaligned length 4507980 Genome fraction (%) 49.893 Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 248.07 # indels per 100 kbp 1.01 Largest alignment 657825 NA50 27820	Largest contig	657825
N50 315111 N75 131793 L50 11 L75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 48 + 18 part Unaligned length 4507980 Genome fraction (%) 49.893 Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 248.07 # indels per 100 kbp 1.01 Largest alignment 657825 NA50 27820	Total length	9144127
N75 131793 L50 11 L75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 48 + 18 part Unaligned length 4507980 Genome fraction (%) 49.893 Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 248.07 # indels per 100 kbp 1.01 Largest alignment 657825 NA50 27820	Reference length	9283304
L50 11 L75 24 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 48 + 18 part Unaligned length 4507980 Genome fraction (%) 49.893 Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 248.07 # indels per 100 kbp 1.01 Largest alignment 657825 NA50 27820	N50	315111
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 48 + 18 part Unaligned length 4507980 Genome fraction (%) 49.893 Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 248.07 # indels per 100 kbp 1.01 Largest alignment 657825 NA50 27820	N75	131793
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 48 + 18 part Unaligned length 4507980 Genome fraction (%) 49.893 Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 248.07 # indels per 100 kbp 1.01 Largest alignment 657825 NA50 27820	L50	11
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 48 + 18 part Unaligned length 4507980 Genome fraction (%) 49.893 Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 248.07 # indels per 100 kbp 1.01 Largest alignment 657825 NA50 27820	L75	24
Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 48 + 18 part Unaligned length 4507980 Genome fraction (%) 49.893 Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 248.07 # indels per 100 kbp 1.01 Largest alignment 657825 NA50 27820	# misassemblies	0
# local misassemblies 0 # unaligned contigs 48 + 18 part Unaligned length 4507980 Genome fraction (%) 49.893 Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 248.07 # indels per 100 kbp 1.01 Largest alignment 657825 NA50 27820	# misassembled contigs	0
# unaligned contigs 48 + 18 part Unaligned length 4507980 Genome fraction (%) 49.893 Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 248.07 # indels per 100 kbp 1.01 Largest alignment 657825 NA50 27820	Misassembled contigs length	0
Unaligned length 4507980 Genome fraction (%) 49.893 Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 248.07 # indels per 100 kbp 1.01 Largest alignment 657825 NA50 27820	# local misassemblies	0
Genome fraction (%) 49.893 Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 248.07 # indels per 100 kbp 1.01 Largest alignment 657825 NA50 27820	# unaligned contigs	48 + 18 part
Duplication ratio 1.001 # N's per 100 kbp 0.84 # mismatches per 100 kbp 248.07 # indels per 100 kbp 1.01 Largest alignment 657825 NA50 27820	Unaligned length	4507980
# N's per 100 kbp 0.84 # mismatches per 100 kbp 248.07 # indels per 100 kbp 1.01 Largest alignment 657825 NA50 27820	Genome fraction (%)	49.893
# mismatches per 100 kbp 248.07 # indels per 100 kbp 1.01 Largest alignment 657825 NA50 27820	Duplication ratio	1.001
# indels per 100 kbp 1.01 Largest alignment 657825 NA50 27820	# N's per 100 kbp	0.84
Largest alignment 657825 NA50 27820	<u> </u>	248.07
NA50 27820	# indels per 100 kbp	
	Largest alignment	657825
LA50 16	NA50	27820
	LA50	16

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	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	8
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	11490
# indels	47
# short indels	46
# long indels	1
Indels length	116

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	48
Fully unaligned length	2812320
# partially unaligned contigs	18
# with misassembly	4
# both parts are significant	8
Partially unaligned length	1695660
# N's	77

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).









