Report

# contigs (>= 0 bp) 766472 # contigs (>= 1000 bp) 766472 # contigs (>= 5000 bp) 23509 # contigs (>= 10000 bp) 5257 # contigs (>= 25000 bp) 699 # contigs (>= 50000 bp) 146 Total length (>= 0 bp) 1430179911 Total length (>= 1000 bp) 1430179911 Total length (>= 1000 bp) 1430179911 Total length (>= 5000 bp) 214871738 Total length (>= 10000 bp) 29656132 Total length (>= 25000 bp) 29656132 Total length (>= 50000 bp) 11639915 # contigs 766472 Largest contig 387648 Total length 1430179911 Reference length 1430179910 # misassemblies 0 # misassembled contigs 0 # misassembled contigs 0 # misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 4 # unaligned contigs 766433 + 39 part 0 Unaligned length 1430176102 Genome fraction (%) 0.024 Duplication ratio 3.814 # N's per 100 kbp 0.00 # mismatches per 100 kbp 10893.03 # indels per 100 kbp 98.14 Largest alignment 180	·	TARA ASE RAW
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# local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 4 # unaligned contigs 766433 + 39 part Unaligned length 1430176102 Genome fraction (%) 0.024 Duplication ratio 3.814 # N's per 100 kbp 0.00 # mismatches per 100 kbp 10893.03 # indels per 100 kbp 98.14 Largest alignment 180		
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# scaffold gap loc. mis. 0 # unaligned mis. contigs 4 # unaligned contigs 766433 + 39 part Unaligned length 1430176102 Genome fraction (%) 0.024 Duplication ratio 3.814 # N's per 100 kbp 0.00 # mismatches per 100 kbp 10893.03 # indels per 100 kbp 98.14 Largest alignment 180	# local misassemblies	0
# unaligned mis. contigs 4 # unaligned contigs 766433 + 39 part Unaligned length 1430176102 Genome fraction (%) 0.024 Duplication ratio 3.814 # N's per 100 kbp 0.00 # mismatches per 100 kbp 10893.03 # indels per 100 kbp 98.14 Largest alignment 180	# scaffold gap ext. mis.	0
# unaligned contigs 766433 + 39 part Unaligned length 1430176102 Genome fraction (%) 0.024 Duplication ratio 3.814 # N's per 100 kbp 0.00 # mismatches per 100 kbp 10893.03 # indels per 100 kbp 98.14 Largest alignment 180	# scaffold gap loc. mis.	0
Unaligned length 1430176102 Genome fraction (%) 0.024 Duplication ratio 3.814 # N's per 100 kbp 0.00 # mismatches per 100 kbp 10893.03 # indels per 100 kbp 98.14 Largest alignment 180	# unaligned mis. contigs	4
Genome fraction (%) 0.024 Duplication ratio 3.814 # N's per 100 kbp 0.00 # mismatches per 100 kbp 10893.03 # indels per 100 kbp 98.14 Largest alignment 180	# unaligned contigs	766433 + 39 part
Duplication ratio 3.814 # N's per 100 kbp 0.00 # mismatches per 100 kbp 10893.03 # indels per 100 kbp 98.14 Largest alignment 180	Unaligned length	1430176102
# N's per 100 kbp 0.00 # mismatches per 100 kbp 10893.03 # indels per 100 kbp 98.14 Largest alignment 180	Genome fraction (%)	0.024
# mismatches per 100 kbp 10893.03 # indels per 100 kbp 98.14 Largest alignment 180	Duplication ratio	3.814
# indels per 100 kbp 98.14 Largest alignment 180	# N's per 100 kbp	0.00
Largest alignment 180	# mismatches per 100 kbp	10893.03
	# indels per 100 kbp	98.14
Total aligned length 3809	Largest alignment	180
10101 011911	Total aligned length	3809

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

	TARA_ASE_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	35
# possible misassemblies	38
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	111
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	2

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

	TARA_ASE_RAW
# fully unaligned contigs	766433
Fully unaligned length	1430095224
# partially unaligned contigs	39
Partially unaligned length	80878
# 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).















