Report

# contigs (>= 0 bp) 766472 # contigs (>= 1000 bp) 766472 # contigs (>= 5000 bp) 23509 # contigs (>= 25000 bp) 5257 # contigs (>= 25000 bp) 699 # contigs (>= 50000 bp) 1430179911 Total length (>= 0 bp) 1430179911 Total length (>= 1000 bp) 214871738 Total length (>= 5000 bp) 294359835 Total length (>= 25000 bp) 29656132 Total length (>= 50000 bp) 11639915 # contigs 766472 Largest contig 387648 Total length (>= 50000 bp) 11639915 # contigs 766472 Largest contig 387648 Total length (>= 10000 bp) 129656132 Total length (>= 50000 bp) 129656132 Total length (>= 50000 bp) 129656132 Total length 1430179911 Reference length 5854900 N50 1830 N75 1291 L50 212842 L75 449143 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 766347 + 124 part 1910167553 Genome fraction (%) 0.078 Duplication ratio 3.418 # N's per 100 kbp 0.00 # mismatches per 100 kbp 5830.78 # indels per 100 kbp 0.00 Largest alignment 1116		TARA ASE RAW
# contigs (>= 5000 bp) # contigs (>= 10000 bp) # contigs (>= 25000 bp) # contigs (>= 25000 bp) # contigs (>= 50000 bp) # contigs (>= 10000 bp) # contigs (>= 25000 bp) # contigs (>= 26000 bp) # contigs (>= 26000 bp) # contigs (>= 25000 bp) # contigs (>= 26000 bp) # misassembles (>= 26000 bp) # misassembles (>= 26000 bp) # contigs (>= 26000 b	# contigs (>= 0 bp)	766472
# contigs (>= 10000 bp) 5257 # contigs (>= 25000 bp) 699 # contigs (>= 50000 bp) 146 Total length (>= 0 bp) 1430179911 Total length (>= 10000 bp) 214871738 Total length (>= 10000 bp) 94359835 Total length (>= 25000 bp) 29656132 Total length (>= 50000 bp) 11639915 # contigs 766472 Largest contig 387648 Total length 1430179911 Reference length 5854900 N50 1830 N75 1291 L50 212842 L75 449143 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned length 1430167553 Genome fraction (%) 0.078 Duplication ratio 3.418 # N's per 100 kbp 0.00 Largest alignment 1116	# contigs (>= 1000 bp)	766472
# contigs (>= 25000 bp) 699 # contigs (>= 50000 bp) 146 Total length (>= 0 bp) 1430179911 Total length (>= 1000 bp) 214871738 Total length (>= 5000 bp) 24871738 Total length (>= 10000 bp) 94359835 Total length (>= 25000 bp) 29656132 Total length (>= 50000 bp) 11639915 # contigs 766472 Largest contig 387648 Total length 1430179911 Reference length 5854900 N50 1830 N75 1291 L50 212842 L75 449143 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned length 1430167553 Genome fraction (%) 0.078 Duplication ratio 3.418 # N's per 100 kbp 0.00 Largest alignment 1116	# contigs (>= 5000 bp)	23509
# contigs (>= 50000 bp) 146 Total length (>= 0 bp) 1430179911 Total length (>= 1000 bp) 1430179911 Total length (>= 5000 bp) 214871738 Total length (>= 10000 bp) 94359835 Total length (>= 25000 bp) 29656132 Total length (>= 50000 bp) 11639915 # contigs 766472 Largest contig 387648 Total length 1430179911 Reference length 5854900 N50 1830 N75 1291 L50 212842 L75 449143 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned length 1430167553 Genome fraction (%) 0.078 Duplication ratio 3.418 # N's per 100 kbp 0.00 # mismatches per 100 kbp 5830.78 # indels per 100 kbp 0.00 Largest alignment 1116	# contigs (>= 10000 bp)	5257
Total length (>= 0 bp)	# contigs (>= 25000 bp)	699
Total length (>= 1000 bp)	# contigs (>= 50000 bp)	146
Total length (>= 5000 bp)	Total length (>= 0 bp)	1430179911
Total length (>= 10000 bp) 94359835 Total length (>= 25000 bp) 29656132 Total length (>= 50000 bp) 11639915 # contigs 766472 Largest contig 387648 Total length 1430179911 Reference length 5854900 N50 1830 N75 1291 L50 212842 L75 449143 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # unaligned mis. contigs 3 # unaligned length 1430167553 Genome fraction (%) 0.078 Duplication ratio 3.418 # nisassem length 0.00 # mismatches per 100 kbp 0.00 Largest alignment 1116	Total length (>= 1000 bp)	1430179911
Total length (>= 25000 bp)	Total length (>= 5000 bp)	214871738
Total length (>= 50000 bp) 11639915 # contigs 766472 Largest contig 387648 Total length 1430179911 Reference length 5854900 N50 1830 N75 1291 L50 212842 L75 449143 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned length 1430167553 Genome fraction (%) 0.078 Duplication ratio 3.418 # N's per 100 kbp 0.00 # mismatches per 100 kbp 5830.78 # indels per 100 kbp 0.00 Largest alignment 1116	Total length (>= 10000 bp)	94359835
# contigs 766472 Largest contig 387648 Total length 1430179911 Reference length 5854900 N50 1830 N75 1291 L50 212842 L75 449143 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned length 1430167553 Genome fraction (%) 0.078 Duplication ratio 3.418 # N's per 100 kbp 0.00 # mismatches per 100 kbp 5830.78 # indels per 100 kbp 0.00 Largest alignment 1116	Total length (>= 25000 bp)	29656132
Largest contig 387648 Total length 1430179911 Reference length 5854900 N50 1830 N75 1291 L50 212842 L75 449143 # 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 3 # unaligned length 1430167553 Genome fraction (%) 0.078 Duplication ratio 3.418 # N's per 100 kbp 0.00 # mismatches per 100 kbp 5830.78 # indels per 100 kbp 0.00 Largest alignment 1116	Total length (>= 50000 bp)	11639915
Total length 1430179911 Reference length 5854900 N50 1830 N75 1291 L50 212842 L75 449143 # 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 3 # unaligned contigs 766347 + 124 part 124 part 1430167553 Genome fraction (%) 0.078 Duplication ratio 3.418 # N's per 100 kbp 0.00 # mismatches per 100 kbp 5830.78 # indels per 100 kbp 0.00 Largest alignment 1116	# contigs	766472
Reference length 5854900 N50 1830 N75 1291 L50 212842 L75 449143 # 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 3 # unaligned length 1430167553 Genome fraction (%) 0.078 Duplication ratio 3.418 # N's per 100 kbp 0.00 # mismatches per 100 kbp 5830.78 # indels per 100 kbp 0.00 Largest alignment 1116	Largest contig	387648
N50 1830 N75 1291 L50 212842 L75 449143 # 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 3 # unaligned length 1430167553 Genome fraction (%) 0.078 Duplication ratio 3.418 # N's per 100 kbp 0.00 # mismatches per 100 kbp 5830.78 # indels per 100 kbp 0.00 Largest alignment 1116	Total length	1430179911
N75 1291 L50 212842 L75 449143 # 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 3 # unaligned contigs 766347 + 124 part Unaligned length 1430167553 Genome fraction (%) 0.078 Duplication ratio 3.418 # N's per 100 kbp 0.00 # mismatches per 100 kbp 5830.78 # indels per 100 kbp 0.00 Largest alignment 1116	Reference length	5854900
L50 212842 L75 449143 # 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 3 # unaligned length 1430167553 Genome fraction (%) 0.078 Duplication ratio 3.418 # N's per 100 kbp 0.00 # mismatches per 100 kbp 5830.78 # indels per 100 kbp 0.00 Largest alignment 1116	N50	1830
# misassembles 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassembles 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 766347 + 124 part Unaligned length 1430167553 Genome fraction (%) 0.078 Duplication ratio 3.418 # N's per 100 kbp 0.00 # mismatches per 100 kbp 5830.78 # indels per 100 kbp 0.00 Largest alignment 1116	N75	1291
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 766347 + 124 part Unaligned length 1430167553 Genome fraction (%) 0.078 Duplication ratio 3.418 # N's per 100 kbp 0.00 # mismatches per 100 kbp 5830.78 # indels per 100 kbp 0.00 Largest alignment 1116	L50	212842
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 766347 + 124 part Unaligned length 1430167553 Genome fraction (%) 0.078 Duplication ratio 3.418 # N's per 100 kbp 0.00 # mismatches per 100 kbp 5830.78 # indels per 100 kbp 0.00 Largest alignment 1116	L75	449143
Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 766347 + 124 part Unaligned length 1430167553 Genome fraction (%) 0.078 Duplication ratio 3.418 # N's per 100 kbp 0.00 # mismatches per 100 kbp 5830.78 # indels per 100 kbp 0.00 Largest alignment 1116	# misassemblies	0
# local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 766347 + 124 part Unaligned length 1430167553 Genome fraction (%) 0.078 Duplication ratio 3.418 # N's per 100 kbp 0.00 # mismatches per 100 kbp 5830.78 # indels per 100 kbp 0.00 Largest alignment 1116	# misassembled contigs	0
# scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 766347 + 124 part Unaligned length 1430167553 Genome fraction (%) 0.078 Duplication ratio 3.418 # N's per 100 kbp 0.00 # mismatches per 100 kbp 5830.78 # indels per 100 kbp 0.00 Largest alignment 1116	Misassembled contigs length	0
# scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 766347 + 124 part Unaligned length 1430167553 Genome fraction (%) 0.078 Duplication ratio 3.418 # N's per 100 kbp 0.00 # mismatches per 100 kbp 5830.78 # indels per 100 kbp 0.00 Largest alignment 1116	# local misassemblies	0
# unaligned mis. contigs 3 # unaligned contigs 766347 + 124 part Unaligned length 1430167553 Genome fraction (%) 0.078 Duplication ratio 3.418 # N's per 100 kbp 0.00 # mismatches per 100 kbp 5830.78 # indels per 100 kbp 0.00 Largest alignment 1116	# scaffold gap ext. mis.	0
# unaligned contigs 766347 + 124 part Unaligned length 1430167553 Genome fraction (%) 0.078 Duplication ratio 3.418 # N's per 100 kbp 0.00 # mismatches per 100 kbp 5830.78 # indels per 100 kbp 0.00 Largest alignment 1116	# scaffold gap loc. mis.	0
Unaligned length 1430167553 Genome fraction (%) 0.078 Duplication ratio 3.418 # N's per 100 kbp 0.00 # mismatches per 100 kbp 5830.78 # indels per 100 kbp 0.00 Largest alignment 1116	# unaligned mis. contigs	3
Genome fraction (%) 0.078 Duplication ratio 3.418 # N's per 100 kbp 0.00 # mismatches per 100 kbp 5830.78 # indels per 100 kbp 0.00 Largest alignment 1116	# unaligned contigs	766347 + 124 part
Duplication ratio 3.418 # N's per 100 kbp 0.00 # mismatches per 100 kbp 5830.78 # indels per 100 kbp 0.00 Largest alignment 1116	Unaligned length	1430167553
# N's per 100 kbp 0.00 # mismatches per 100 kbp 5830.78 # indels per 100 kbp 0.00 Largest alignment 1116	Genome fraction (%)	0.078
# mismatches per 100 kbp 5830.78 # indels per 100 kbp 0.00 Largest alignment 1116	Duplication ratio	3.418
# indels per 100 kbp 0.00 Largest alignment 1116	# N's per 100 kbp	0.00
Largest alignment 1116	# mismatches per 100 kbp	5830.78
	# indels per 100 kbp	0.00
Total aligned length 11671	Largest alignment	1116
	Total aligned length	11671

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	122
# possible misassemblies	140
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	266
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	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).

Unaligned report

	TARA_ASE_RAW
# fully unaligned contigs	766347
Fully unaligned length	1429891681
# partially unaligned contigs	124
Partially unaligned length	275872
# 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).















