Report

# contigs (>= 1000 bp) 52 # contigs (>= 5000 bp) 3 # contigs (>= 10000 bp) 2 # contigs (>= 25000 bp) 1 # contigs (>= 50000 bp) 1 Total length (>= 50000 bp) 120515 Total length (>= 50000 bp) 142551 Total length (>= 50000 bp) 104193 Gold length (>= 50000 bp) 104193 Total length (>= 50000 bp) 104193 Total length (>= 50000 bp) 104193 Total length (>= 10000 bp) 104193 Total length 214615 Reference length 3561038 GC (%) 48.66 Reference GC (%) 41.87 N50 10058 N75 2373 L50 2 L75 17 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 2 # unaligned contigs 0 Duplication ratio 4.650 # N's per 100 kbp 0.00 # mismatches per 100 kbp 13179.07 # indels per 100 kbp 0.00 Largest alignment 200 Total aligned length 4622 NGA50 -		TARA_PSE_RAW
# contigs (>= 5000 bp)	# contigs (>= 1000 bp)	
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# 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 2 # unaligned contigs 4 + 48 part Unaligned length 20993 Genome fraction (%) 0.028 Duplication ratio 4.650 # N's per 100 kbp 0.00 # mismatches per 100 kbp 13179.07 # indels per 100 kbp 0.00 Largest alignment 200 Total aligned length 4622	N75	2373
# 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 2 # unaligned contigs 4 + 48 part 1 Unaligned length 209993 Genome fraction (%) 0.028 Duplication ratio 4.650 # N's per 100 kbp 0.00 # mismatches per 100 kbp 13179.07 # indels per 100 kbp 0.00 Largest alignment 200 Total aligned length 4622	L50	2
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 2 # unaligned contigs 4 + 48 part Unaligned length 209993 Genome fraction (%) 0.028 Duplication ratio 4.650 # N's per 100 kbp 0.00 # mismatches per 100 kbp 13179.07 # indels per 100 kbp 0.00 Largest alignment 200 Total aligned length 4622	L75	17
Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 2 # unaligned contigs 4 + 48 part Unaligned length 209993 Genome fraction (%) 0.028 Duplication ratio 4.650 # N's per 100 kbp 0.00 # mismatches per 100 kbp 13179.07 # indels per 100 kbp 0.00 Largest alignment 200 Total aligned length 4622	# misassemblies	0
# local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 2 # unaligned contigs 4 + 48 part Unaligned length 209993 Genome fraction (%) 0.028 Duplication ratio 4.650 # N's per 100 kbp 0.00 # mismatches per 100 kbp 13179.07 # indels per 100 kbp 0.00 Largest alignment 200 Total aligned length 4622	# misassembled contigs	0
# scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 2 # unaligned contigs 4 + 48 part Unaligned length 209993 Genome fraction (%) 0.028 Duplication ratio 4.650 # N's per 100 kbp 0.00 # mismatches per 100 kbp 13179.07 # indels per 100 kbp 0.00 Largest alignment 200 Total aligned length 4622	Misassembled contigs length	0
# scaffold gap loc. mis. 0 # unaligned mis. contigs 2 # unaligned contigs 4 + 48 part Unaligned length 209993 Genome fraction (%) 0.028 Duplication ratio 4.650 # N's per 100 kbp 0.00 # mismatches per 100 kbp 13179.07 # indels per 100 kbp 0.00 Largest alignment 200 Total aligned length 4622	# local misassemblies	0
# unaligned mis. contigs 2 # unaligned contigs 4 + 48 part Unaligned length 209993 Genome fraction (%) 0.028 Duplication ratio 4.650 # N's per 100 kbp 0.00 # mismatches per 100 kbp 13179.07 # indels per 100 kbp 0.00 Largest alignment 200 Total aligned length 4622	# scaffold gap ext. mis.	0
# unaligned contigs 4 + 48 part Unaligned length 209993 Genome fraction (%) 0.028 Duplication ratio 4.650 # N's per 100 kbp 0.00 # mismatches per 100 kbp 13179.07 # indels per 100 kbp 0.00 Largest alignment 200 Total aligned length 4622	# scaffold gap loc. mis.	0
Unaligned length 209993 Genome fraction (%) 0.028 Duplication ratio 4.650 # N's per 100 kbp 0.00 # mismatches per 100 kbp 13179.07 # indels per 100 kbp 0.00 Largest alignment 200 Total aligned length 4622	# unaligned mis. contigs	2
Genome fraction (%) 0.028 Duplication ratio 4.650 # N's per 100 kbp 0.00 # mismatches per 100 kbp 13179.07 # indels per 100 kbp 0.00 Largest alignment 200 Total aligned length 4622	# unaligned contigs	4 + 48 part
Duplication ratio 4.650 # N's per 100 kbp 0.00 # mismatches per 100 kbp 13179.07 # indels per 100 kbp 0.00 Largest alignment 200 Total aligned length 4622	Unaligned length	209993
# N's per 100 kbp 0.00 # mismatches per 100 kbp 13179.07 # indels per 100 kbp 0.00 Largest alignment 200 Total aligned length 4622	Genome fraction (%)	0.028
# mismatches per 100 kbp 13179.07 # indels per 100 kbp 0.00 Largest alignment 200 Total aligned length 4622	Duplication ratio	4.650
# indels per 100 kbp 0.00 Largest alignment 200 Total aligned length 4622	# N's per 100 kbp	0.00
Largest alignment 200 Total aligned length 4622	# mismatches per 100 kbp	13179.07
Total aligned length 4622	# indels per 100 kbp	0.00
	Largest alignment	200
NGA50 -	Total aligned length	4622
	NGA50	-

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_PSE_RAW
# 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	50
# possible misassemblies	59
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	131
# 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

	TARA_PSE_RAW
# fully unaligned contigs	4
Fully unaligned length	6134
# partially unaligned contigs	48
Partially unaligned length	203859
# 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).



















