Report

# contigs (>= 1000 bp) 60 # contigs (>= 1000 bp) 10 # contigs (>= 10000 bp) 5 # contigs (>= 25000 bp) 3 # contigs (>= 50000 bp) 1 Total length (>= 50000 bp) 356217 Total length (>= 50000 bp) 322655 Total length (>= 10000 bp) 289201 Total length (>= 50000 bp) 222419 # contigs 60 Largest contig 222419 Total length (>= 50000 bp) 324657 Reference length 448757 Reference length 4234461 GC (%) 50.36 Reference GC (%) 41.03 N50 35322 N75 7257 L50 2 L75 7 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 13 + 46 part 1 Unaligned length 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576 NGA50		TARA_PSW_RAW
# contigs (>= 5000 bp) 10 # contigs (>= 10000 bp) 5 # contigs (>= 25000 bp) 3 # contigs (>= 50000 bp) 1 Total length (>= 1000 bp) 448757 Total length (>= 5000 bp) 356217 Total length (>= 5000 bp) 322655 Total length (>= 25000 bp) 289201 Total length (>= 50000 bp) 222419 # contigs 60 Largest contig 222419 Total length 448757 Reference length 4234461 GC (%) 50.36 Reference GC (%) 41.03 N50 35322 N75 7257 L50 2 L75 7 # misassembled contigs 0 # misassembled contigs 0 # scaffold gap ext. mis. 0 # scaffold gap ext. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 1 Unaligned length 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	# contigs (>= 1000 bp)	
# contigs (>= 25000 bp)		10
# contigs (>= 50000 bp) 1 Total length (>= 1000 bp) 356217 Total length (>= 5000 bp) 356217 Total length (>= 10000 bp) 322655 Total length (>= 25000 bp) 289201 Total length (>= 50000 bp) 222419 # contigs 60 Largest contig 222419 Total length 448757 Reference length 4234461 GC (%) 50.36 Reference GC (%) 41.03 N50 35322 N75 7257 L50 2 L75 7 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned length 443072 Genome fraction (%) 0.027 Duplication ratio 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	# contigs (>= 10000 bp)	5
Total length (>= 1000 bp)	# contigs (>= 25000 bp)	3
Total length (>= 5000 bp) 356217 Total length (>= 10000 bp) 322655 Total length (>= 25000 bp) 289201 Total length (>= 50000 bp) 222419 # contigs 60 Largest contig 222419 Total length 448757 Reference length 4234461 GC (%) 50.36 Reference GC (%) 41.03 N50 35322 N75 7257 L50 2 L75 7 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 13 + 46 part Unaligned length 4987 Unaligned length 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	# contigs (>= 50000 bp)	1
Total length (>= 10000 bp) 322655 Total length (>= 25000 bp) 289201 Total length (>= 50000 bp) 222419 # contigs 60 Largest contig 222419 Total length 448757 Reference length 4234461 GC (%) 50.36 Reference GC (%) 41.03 N50 35322 N75 7257 L50 2 L75 7 # 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 1 # unaligned length 443072 Genome fraction (%) 0.027 Duplication ratio 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1315.79 # indels per 100 kbp 87.72 Largest alignment 201	Total length (>= 1000 bp)	448757
Total length (>= 25000 bp) 289201 Total length (>= 50000 bp) 222419 # contigs 60 Largest contig 222419 Total length 448757 Reference length 4234461 GC (%) 50.36 Reference GC (%) 41.03 N50 35322 N75 7257 L50 2 L75 7 # 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 1 # unaligned length 443072 Genome fraction (%) 0.027 Duplication ratio 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	Total length (>= 5000 bp)	356217
Total length (>= 50000 bp) 222419 # contigs 60 Largest contig 222419 Total length 448757 Reference length 4234461 GC (%) 50.36 Reference GC (%) 41.03 N50 35322 N75 7257 L50 2 L75 7 # 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 1 # unaligned length 443072 Genome fraction (%) 0.027 Duplication ratio 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	Total length (>= 10000 bp)	322655
# contigs 60 Largest contig 222419 Total length 448757 Reference length 4234461 GC (%) 50.36 Reference GC (%) 41.03 N50 35322 N75 7257 L50 2 L75 7 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap ext. mis. 0 # unaligned mis. contigs 1 # unaligned length 443072 Genome fraction (%) 0.027 Duplication ratio 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	Total length (>= 25000 bp)	289201
Largest contig 222419 Total length 448757 Reference length 4234461 GC (%) 50.36 Reference GC (%) 41.03 N50 35322 N75 7257 L50 2 L75 7 # 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 1 # unaligned length 443072 Genome fraction (%) 0.027 Duplication ratio 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	Total length (>= 50000 bp)	222419
Total length 448757 Reference length 4234461 GC (%) 50.36 Reference GC (%) 41.03 N50 35322 N75 7257 L50 2 L75 7 # 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 1 # unaligned length 443072 Genome fraction (%) 0.027 Duplication ratio 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	# contigs	60
Reference length 4234461 GC (%) 50.36 Reference GC (%) 41.03 N50 35322 N75 7257 L50 2 L75 7 # 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 1 # unaligned length 443072 Genome fraction (%) 0.027 Duplication ratio 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	Largest contig	222419
GC (%) 50.36 Reference GC (%) 41.03 N50 35322 N75 7257 L50 2 L75 7 # 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 1 # unaligned contigs 13 + 46 part 10 Unaligned length 443072 Genome fraction (%) 0.027 Duplication ratio 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	Total length	448757
Reference GC (%) 41.03 N50 35322 N75 7257 L50 2 L75 7 # 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 1 # unaligned length 443072 Genome fraction (%) 0.027 Duplication ratio 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	Reference length	4234461
N50 35322 N75 7257 L50 2 L75 7 # 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 1 # unaligned length 443072 Genome fraction (%) 0.027 Duplication ratio 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	GC (%)	50.36
N75 7257 L50 2 L75 7 # 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 1 # unaligned length 443072 Genome fraction (%) 0.027 Duplication ratio 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	Reference GC (%)	41.03
L50 2 L75 7 # 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 13 + 46 part 1 Unaligned length 443072 Genome fraction (%) 0.027 Duplication ratio 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	N50	35322
# 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 1 # unaligned length 443072 Genome fraction (%) 0.027 Duplication ratio 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	N75	7257
# 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 1 # unaligned contigs 13 + 46 part 13 + 46 part 14 43072 Genome fraction (%) 0.027 Duplication ratio 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	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 1 # unaligned contigs 13 + 46 part Unaligned length 443072 Genome fraction (%) 0.027 Duplication ratio 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	L75	7
Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 13 + 46 part Unaligned length 443072 Genome fraction (%) 0.027 Duplication ratio 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	# misassemblies	0
# local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 13 + 46 part Unaligned length 443072 Genome fraction (%) 0.027 Duplication ratio 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	# misassembled contigs	0
# scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 13 + 46 part Unaligned length 443072 Genome fraction (%) 0.027 Duplication ratio 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	Misassembled contigs length	0
# scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 13 + 46 part Unaligned length 443072 Genome fraction (%) 0.027 Duplication ratio 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	# local misassemblies	0
# unaligned mis. contigs 1 # unaligned contigs 13 + 46 part Unaligned length 443072 Genome fraction (%) 0.027 Duplication ratio 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	# scaffold gap ext. mis.	0
# unaligned contigs 13 + 46 part Unaligned length 443072 Genome fraction (%) 0.027 Duplication ratio 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	# scaffold gap loc. mis.	0
Unaligned length 443072 Genome fraction (%) 0.027 Duplication ratio 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	# unaligned mis. contigs	1
Genome fraction (%) 0.027 Duplication ratio 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	# unaligned contigs	13 + 46 part
Duplication ratio 4.987 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	Unaligned length	443072
# N's per 100 kbp 0.00 # mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	Genome fraction (%)	0.027
# mismatches per 100 kbp 11315.79 # indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	Duplication ratio	4.987
# indels per 100 kbp 87.72 Largest alignment 201 Total aligned length 4576	# N's per 100 kbp	0.00
Largest alignment 201 Total aligned length 4576	# mismatches per 100 kbp	11315.79
Total aligned length 4576	# indels per 100 kbp	87.72
	Largest alignment	201
NGA50 -	Total aligned length	4576
	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_PSW_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	59
# possible misassemblies	70
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	129
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	2

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_PSW_RAW
# fully unaligned contigs	13
Fully unaligned length	252135
# partially unaligned contigs	46
Partially unaligned length	190937
# 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).



















