Report

# contigs (>= 1000 bp)		TARA_ANW_RAW
# contigs (>= 5000 bp)	# contigs (>= 1000 bp)	55
# contigs (>= 25000 bp) 1 # contigs (>= 50000 bp) 207362 Total length (>= 1000 bp) 121401 Total length (>= 5000 bp) 105935 Total length (>= 25000 bp) 105935 Total length (>= 50000 bp) 105935 Total length (>= 50000 bp) 105935 Total length (>= 50000 bp) 105935 # contigs 55 Largest contig 105935 Total length 207362 Reference length 4234461 GC (%) 41.81 Reference GC (%) 41.03 N50 105935 N75 1978 L50 1 L75 166 # misassembled contigs 0 # misassembled contigs 0 # scaffold gap ext. mis. 0 # scaffold gap ext. mis. 0 # unaligned mis. contigs 1 # unaligned length 203124 Genome fraction (%) 0.028 Duplication ratio 3.549 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11139.03 # indels per 100 kbp 1375 Largest alignment 2011		3
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Total length (>= 5000 bp) 121401 Total length (>= 10000 bp) 105935 Total length (>= 25000 bp) 105935 Total length (>= 50000 bp) 105935 # contigs 55 Largest contig 105935 Total length 207362 Reference length 4234461 GC (%) 41.81 Reference GC (%) 41.03 N50 105935 N75 1978 L50 1 L75 16 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 11 + 44 part 1 Unaligned length 203124 Genome fraction (%) 0.028 Duplication ratio 3.549 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11139.03 # indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	# contigs (>= 50000 bp)	1
Total length (>= 10000 bp) 105935 Total length (>= 25000 bp) 105935 Total length (>= 50000 bp) 105935 # contigs 55 Largest contig 105935 Total length 207362 Reference length 4234461 GC (%) 41.81 Reference GC (%) 41.03 N50 105935 N75 1978 L50 1 L75 16 # 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 11 + 44 part 11 yang 144 part 11 yang 154 part	Total length (>= 1000 bp)	207362
Total length (>= 25000 bp) 105935 Total length (>= 50000 bp) 105935 # contigs 55 Largest contig 105935 Total length 207362 Reference length 4234461 GC (%) 41.81 Reference GC (%) 41.03 N50 105935 N75 1978 L50 1 L75 16 # 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 203124 Genome fraction (%) 0.028 Duplication ratio 3.549 # N's per 100 kbp 11139.03 # indels per 100 kbp 11139.03 # indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	Total length (>= 5000 bp)	121401
Total length (>= 50000 bp) 105935 # contigs 55 Largest contig 105935 Total length 207362 Reference length 4234461 GC (%) 41.81 Reference GC (%) 41.03 N50 105935 N75 1978 L50 1 L75 16 # 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 203124 Genome fraction (%) 0.028 Duplication ratio 3.549 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11139.03 # indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	Total length (>= 10000 bp)	105935
# contigs 55 Largest contig 105935 Total length 207362 Reference length 4234461 GC (%) 41.81 Reference GC (%) 41.03 N50 105935 N75 1978 L50 1 L75 16 # 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 203124 Genome fraction (%) 0.028 Duplication ratio 3.549 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11139.03 # indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	Total length (>= 25000 bp)	105935
Largest contig 105935 Total length 207362 Reference length 4234461 GC (%) 41.81 Reference GC (%) 41.03 N50 105935 N75 1978 L50 1 L75 16 # 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 203124 Genome fraction (%) 0.028 Duplication ratio 3.549 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11139.03 # indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	Total length (>= 50000 bp)	105935
Total length 207362 Reference length 4234461 GC (%) 41.81 Reference GC (%) 41.03 N50 105935 N75 1978 L50 1 L75 16 # 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 203124 Genome fraction (%) 0.028 Duplication ratio 3.549 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11139.03 # indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	# contigs	55
Reference length 4234461 GC (%) 41.81 Reference GC (%) 41.03 N50 105935 N75 1978 L50 1 L75 16 # 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 203124 Genome fraction (%) 0.028 Duplication ratio 3.549 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11139.03 # indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	Largest contig	105935
GC (%) 41.81 Reference GC (%) 41.03 N50 105935 N75 1978 L50 1 L75 16 # 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 11 + 44 part 11 Unaligned length 203124 Genome fraction (%) 0.028 Duplication ratio 3.549 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11139.03 # indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	Total length	207362
Reference GC (%) 41.03 N50 105935 N75 1978 L50 1 L75 16 # 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 203124 Genome fraction (%) 0.028 Duplication ratio 3.549 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11139.03 # indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	Reference length	4234461
N50 105935 N75 1978 L50 1 L75 16 # 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 203124 Genome fraction (%) 0.028 Duplication ratio 3.549 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11139.03 # indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	GC (%)	41.81
N75 1978 L50 1 L75 16 # 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 11 + 44 part Unaligned length 203124 Genome fraction (%) 0.028 Duplication ratio 3.549 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11139.03 # indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	Reference GC (%)	41.03
L50 1 L75 16 # 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 11 + 44 part 1 Unaligned length 203124 Genome fraction (%) 0.028 Duplication ratio 3.549 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11139.03 # indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	N50	105935
# 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 203124 Genome fraction (%) 0.028 Duplication ratio 3.549 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11139.03 # indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	N75	1978
# 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 11 + 44 part 11 + 44 part 12 13 14 14 14 14 15 14 14 15 15 15 15 15 15 15 15 15 15 15 15 15	L50	1
# 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 11 + 44 part Unaligned length 203124 Genome fraction (%) 0.028 Duplication ratio 3.549 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11139.03 # indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	L75	16
Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 11 + 44 part Unaligned length 203124 Genome fraction (%) 0.028 Duplication ratio 3.549 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11139.03 # indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	# misassemblies	0
# local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 11 + 44 part Unaligned length 203124 Genome fraction (%) 0.028 Duplication ratio 3.549 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11139.03 # indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	# misassembled contigs	0
# scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 11 + 44 part Unaligned length 203124 Genome fraction (%) 0.028 Duplication ratio 3.549 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11139.03 # indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	Misassembled contigs length	0
# scaffold gap loc. mis. 0 # unaligned mis. contigs 1 # unaligned contigs 11 + 44 part Unaligned length 203124 Genome fraction (%) 0.028 Duplication ratio 3.549 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11139.03 # indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	# local misassemblies	0
# unaligned mis. contigs 1 # unaligned contigs 11 + 44 part Unaligned length 203124 Genome fraction (%) 0.028 Duplication ratio 3.549 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11139.03 # indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	# scaffold gap ext. mis.	0
# unaligned contigs 11 + 44 part Unaligned length 203124 Genome fraction (%) 0.028 Duplication ratio 3.549 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11139.03 # indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	# scaffold gap loc. mis.	0
Unaligned length 203124 Genome fraction (%) 0.028 Duplication ratio 3.549 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11139.03 # indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	# unaligned mis. contigs	1
Genome fraction (%) 0.028 Duplication ratio 3.549 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11139.03 # indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	# unaligned contigs	11 + 44 part
Duplication ratio 3.549 # N's per 100 kbp 0.00 # mismatches per 100 kbp 11139.03 # indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	Unaligned length	203124
# N's per 100 kbp 0.00 # mismatches per 100 kbp 11139.03 # indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	Genome fraction (%)	0.028
# mismatches per 100 kbp 11139.03 # indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	Duplication ratio	3.549
# indels per 100 kbp 83.75 Largest alignment 201 Total aligned length 4238	# N's per 100 kbp	0.00
Largest alignment 201 Total aligned length 4238	# mismatches per 100 kbp	11139.03
Total aligned length 4238	# indels per 100 kbp	83.75
	Largest alignment	201
NGA50 -	Total aligned length	4238
	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_ANW_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	52
# possible misassemblies	59
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	133
# 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_ANW_RAW
# fully unaligned contigs	11
Fully unaligned length	23368
# partially unaligned contigs	44
Partially unaligned length	179756
# 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).



















