## Report

# contigs (>= 1000 bp)		TARA_ANW_RAW
# contigs (>= 5000 bp)	# contigs (>= 1000 bp)	51
# contigs (>= 25000 bp) 1  # contigs (>= 50000 bp) 200221  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 51  Largest contig 105935  Total length 200221  Reference length 3561038  GC (%) 41.62  Reference GC (%) 41.87  N50 105935  N75 2041  L50 1  L75 14  # misassembled contigs 0  # misassembled contigs 0  # scaffold gap ext. mis. 0  # scaffold gap ext. mis. 0  # unaligned mis. contigs 1  # unaligned length 196465  Genome fraction (%) 0.022  Duplication ratio 4.719  # N's per 100 kbp 0.00  Largest alignment 145  Total aligned length 3756		3
# contigs (>= 50000 bp) 1 Total length (>= 1000 bp) 200221 Total length (>= 5000 bp) 121401 Total length (>= 10000 bp) 105935 Total length (>= 25000 bp) 105935 Total length (>= 50000 bp) 105935 # contigs 51 Largest contig 105935 Total length 200221 Reference length 3561038 GC (%) 41.62 Reference GC (%) 41.87 N50 105935 N75 2041 L50 1 L75 14 # misassembled contigs 0 # misassembled contigs 0 # scaffold gap ext. mis. 0 # scaffold gap ext. mis. 0 # unaligned length 196465 Genome fraction (%) 0.022 Duplication ratio 4.719 # N's per 100 kbp 0.00 Largest alignment 145 Total aligned length 0.05935 Total length 0.00 105935 Total length 105935 Total length 0.00 105935 Total length 0.000 105935 1059	# contigs (>= 10000 bp)	1
Total length (>= 1000 bp)         200221           Total length (>= 5000 bp)         121401           Total length (>= 10000 bp)         105935           Total length (>= 50000 bp)         105935           Total length (>= 50000 bp)         105935           # contigs         51           Largest contig         105935           Total length         200221           Reference length         3561038           GC (%)         41.62           Reference GC (%)         41.87           N50         105935           N75         2041           L50         1           L75         14           # 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         196465           Genome fraction (%)         0.022           Duplication ratio         4.719           # N's per 100 kbp         0.00           # mismatches per 100 kbp         14698.49<	# contigs (>= 25000 bp)	1
Total length (>= 5000 bp) 121401  Total length (>= 10000 bp) 105935  Total length (>= 25000 bp) 105935  Total length (>= 50000 bp) 105935  # contigs 51  Largest contig 105935  Total length 200221  Reference length 3561038  GC (%) 41.62  Reference GC (%) 41.87  N50 105935  N75 2041  L50 1  L75 14  # misassemblies 0  # misassembled contigs 0  Misassembled contigs 0  # local misassemblies 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 10 + 41 part 196465  Genome fraction (%) 0.022  Duplication ratio 4.719  # N's per 100 kbp 0.00  Largest alignment 145  Total aligned length 145935	# contigs (>= 50000 bp)	1
Total length (>= 10000 bp) 105935  Total length (>= 25000 bp) 105935  # contigs 51  Largest contig 105935  Total length (>= 50000 bp) 105935  # contigs 51  Largest contig 105935  Total length 200221  Reference length 3561038  GC (%) 41.62  Reference GC (%) 41.87  N50 105935  N75 2041  L50 1  L75 14  # misassemblies 0  # misassembled contigs 0  Misassembled contigs 0  # local misassemblies 0  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 1  # unaligned contigs 10 + 41 part 196465  Genome fraction (%) 0.022  Duplication ratio 4.719  # N's per 100 kbp 0.00  # mismatches per 100 kbp 14698.49  # indels per 100 kbp 0.00  Largest alignment 145  Total aligned length 3756	Total length (>= 1000 bp)	200221
Total length (>= 25000 bp)         105935           Total length (>= 50000 bp)         105935           # contigs         51           Largest contig         105935           Total length         200221           Reference length         3561038           GC (%)         41.62           Reference GC (%)         41.87           N50         105935           N75         2041           L50         1           L75         14           # misassemblies         0           # sassembled 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         10 + 41 part           Unaligned length         196465           Genome fraction (%)         0.022           Duplication ratio         4.719           # N's per 100 kbp         0.00           # mismatches per 100 kbp         14698.49           # indels per 100 kbp         0.00           Largest alignment         145	Total length (>= 5000 bp)	121401
Total length (>= 50000 bp)         105935           # contigs         51           Largest contig         105935           Total length         200221           Reference length         3561038           GC (%)         41.62           Reference GC (%)         41.87           N50         105935           N75         2041           L50         1           L75         14           # 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         196465           Genome fraction (%)         0.022           Duplication ratio         4.719           # N's per 100 kbp         0.00           # mismatches per 100 kbp         14698.49           # indels per 100 kbp         0.00           Largest alignment         145           Total aligned length         3756	Total length (>= 10000 bp)	105935
# contigs 51 Largest contig 105935 Total length 200221 Reference length 3561038 GC (%) 41.62 Reference GC (%) 41.87 N50 105935 N75 2041 L50 1 L75 14 # 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 196465 Genome fraction (%) 0.022 Duplication ratio 4.719 # N's per 100 kbp 0.00 # mismatches per 100 kbp 14698.49 # indels per 100 kbp 0.00 Largest alignment 145 Total aligned length 3756	Total length (>= 25000 bp)	105935
Largest contig         105935           Total length         200221           Reference length         3561038           GC (%)         41.62           Reference GC (%)         41.87           N50         105935           N75         2041           L50         1           L75         14           # 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         10 + 41 part           Unaligned length         196465           Genome fraction (%)         0.022           Duplication ratio         4.719           # N's per 100 kbp         0.00           # mismatches per 100 kbp         14698.49           # indels per 100 kbp         0.00           Largest alignment         145           Total aligned length         3756	Total length (>= 50000 bp)	105935
Total length         200221           Reference length         3561038           GC (%)         41.62           Reference GC (%)         41.87           N50         105935           N75         2041           L50         1           L75         14           # 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         196465           Genome fraction (%)         0.022           Duplication ratio         4.719           # N's per 100 kbp         0.00           # mismatches per 100 kbp         14698.49           # indels per 100 kbp         0.00           Largest alignment         145           Total aligned length         3756	# contigs	51
Reference length         3561038           GC (%)         41.62           Reference GC (%)         41.87           N50         105935           N75         2041           L50         1           L75         14           # 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         196465           Genome fraction (%)         0.022           Duplication ratio         4.719           # N's per 100 kbp         0.00           # mismatches per 100 kbp         14698.49           # indels per 100 kbp         0.00           Largest alignment         145           Total aligned length         3756	Largest contig	105935
GC (%) 41.62  Reference GC (%) 41.87  N50 105935  N75 2041  L50 1  L75 14  # 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 10 + 41 part 196465  Genome fraction (%) 0.022  Duplication ratio 4.719  # N's per 100 kbp 0.00  # mismatches per 100 kbp 14698.49  # indels per 100 kbp 0.00  Largest alignment 145  Total aligned length 3756	Total length	200221
Reference GC (%)         41.87           N50         105935           N75         2041           L50         1           L75         14           # 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         196465           Genome fraction (%)         0.022           Duplication ratio         4.719           # N's per 100 kbp         0.00           # mismatches per 100 kbp         14698.49           # indels per 100 kbp         0.00           Largest alignment         145           Total aligned length         3756	Reference length	3561038
N50         105935           N75         2041           L50         1           L75         14           # 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         196465           Genome fraction (%)         0.022           Duplication ratio         4.719           # N's per 100 kbp         0.00           # mismatches per 100 kbp         14698.49           # indels per 100 kbp         0.00           Largest alignment         145           Total aligned length         3756	GC (%)	41.62
N75         2041           L50         1           L75         14           # 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         196465           Genome fraction (%)         0.022           Duplication ratio         4.719           # N's per 100 kbp         0.00           # mismatches per 100 kbp         14698.49           # indels per 100 kbp         0.00           Largest alignment         145           Total aligned length         3756	Reference GC (%)	41.87
L50         1           L75         14           # 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         10 + 41 part           Unaligned length         196465           Genome fraction (%)         0.022           Duplication ratio         4.719           # N's per 100 kbp         0.00           # mismatches per 100 kbp         14698.49           # indels per 100 kbp         0.00           Largest alignment         145           Total aligned length         3756	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 196465 Genome fraction (%) 0.022 Duplication ratio 4.719 # N's per 100 kbp 0.00 # mismatches per 100 kbp 14698.49 # indels per 100 kbp 0.00 Largest alignment 145 Total aligned length 3756	N75	2041
# 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 10 + 41 part  Unaligned length 196465  Genome fraction (%) 0.022  Duplication ratio 4.719  # N's per 100 kbp 0.00  # mismatches per 100 kbp 14698.49  # indels per 100 kbp 0.00  Largest alignment 145  Total aligned length 3756	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   10 + 41 part   Unaligned length   196465   Genome fraction (%)   0.022   Duplication ratio   4.719   # N's per 100 kbp   0.00   # mismatches per 100 kbp   14698.49   # indels per 100 kbp   0.00   Largest alignment   145   Total aligned length   3756	L75	14
Misassembled contigs length         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         1           # unaligned contigs         10 + 41 part           Unaligned length         196465           Genome fraction (%)         0.022           Duplication ratio         4.719           # N's per 100 kbp         0.00           # mismatches per 100 kbp         14698.49           # indels per 100 kbp         0.00           Largest alignment         145           Total aligned length         3756	# misassemblies	0
# local misassemblies 0  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 10 + 41 part  Unaligned length 196465  Genome fraction (%) 0.022  Duplication ratio 4.719  # N's per 100 kbp 0.00  # mismatches per 100 kbp 14698.49  # indels per 100 kbp 0.00  Largest alignment 145  Total aligned length 3756	# misassembled contigs	0
# scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 10 + 41 part  Unaligned length 196465  Genome fraction (%) 0.022  Duplication ratio 4.719  # N's per 100 kbp 0.00  # mismatches per 100 kbp 14698.49  # indels per 100 kbp 0.00  Largest alignment 145  Total aligned length 3756	Misassembled contigs length	0
# scaffold gap loc. mis. 0  # unaligned mis. contigs 10 + 41 part  Unaligned length 196465  Genome fraction (%) 0.022  Duplication ratio 4.719  # N's per 100 kbp 0.00  # mismatches per 100 kbp 14698.49  # indels per 100 kbp 0.00  Largest alignment 145  Total aligned length 3756	# local misassemblies	0
# unaligned mis. contigs 1  # unaligned contigs 10 + 41 part  Unaligned length 196465  Genome fraction (%) 0.022  Duplication ratio 4.719  # N's per 100 kbp 0.00  # mismatches per 100 kbp 14698.49  # indels per 100 kbp 0.00  Largest alignment 145  Total aligned length 3756	# scaffold gap ext. mis.	0
# unaligned contigs 10 + 41 part Unaligned length 196465 Genome fraction (%) 0.022 Duplication ratio 4.719 # N's per 100 kbp 0.00 # mismatches per 100 kbp 14698.49 # indels per 100 kbp 0.00 Largest alignment 145 Total aligned length 3756	# scaffold gap loc. mis.	0
Unaligned length         196465           Genome fraction (%)         0.022           Duplication ratio         4.719           # N's per 100 kbp         0.00           # mismatches per 100 kbp         14698.49           # indels per 100 kbp         0.00           Largest alignment         145           Total aligned length         3756	# unaligned mis. contigs	1
Genome fraction (%)         0.022           Duplication ratio         4.719           # N's per 100 kbp         0.00           # mismatches per 100 kbp         14698.49           # indels per 100 kbp         0.00           Largest alignment         145           Total aligned length         3756	# unaligned contigs	10 + 41 part
Duplication ratio         4.719           # N's per 100 kbp         0.00           # mismatches per 100 kbp         14698.49           # indels per 100 kbp         0.00           Largest alignment         145           Total aligned length         3756	Unaligned length	196465
# N's per 100 kbp 0.00  # mismatches per 100 kbp 14698.49  # indels per 100 kbp 0.00  Largest alignment 145  Total aligned length 3756	Genome fraction (%)	0.022
# mismatches per 100 kbp         14698.49           # indels per 100 kbp         0.00           Largest alignment         145           Total aligned length         3756	Duplication ratio	4.719
# indels per 100 kbp 0.00  Largest alignment 145  Total aligned length 3756	# N's per 100 kbp	0.00
Largest alignment 145 Total aligned length 3756	# mismatches per 100 kbp	14698.49
Total aligned length 3756	# indels per 100 kbp	0.00
	Largest alignment	145
NGA50 -	Total aligned length	3756
	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	49
# possible misassemblies	56
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	117
# 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_ANW_RAW
# fully unaligned contigs	10
Fully unaligned length	21714
# partially unaligned contigs	41
Partially unaligned length	174751
# 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).



















