## Report

# contigs (>= 0 bp)		
# contigs (>= 1000 bp) 749 # contigs (>= 5000 bp) 749 # contigs (>= 10000 bp) 221 # contigs (>= 25000 bp) 5 # contigs (>= 25000 bp) 6 # contigs (>= 50000 bp) 7 Total length (>= 0 bp) 9840987 Total length (>= 1000 bp) 9601076 Total length (>= 5000 bp) 6834637 Total length (>= 10000 bp) 3175832 Total length (>= 25000 bp) 133677 Total length (>= 50000 bp) 0 # contigs 2023 Largest contig 31188 Total length (>= 50000 bp) 0 # contigs 2023 Largest contig 31188 Total length 9769814 Reference length 9714864 N50 7229 N75 4304 L50 424 L75 855 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 # unaligned length 0 Genome fraction (%) 99.040 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.07 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304		_
# contigs (>= 5000 bp) 749 # contigs (>= 10000 bp) 221 # contigs (>= 25000 bp) 5 # contigs (>= 50000 bp) 0 Total length (>= 0 bp) 9840987 Total length (>= 1000 bp) 9601076 Total length (>= 5000 bp) 6834637 Total length (>= 10000 bp) 3175832 Total length (>= 25000 bp) 133677 Total length (>= 5000 bp) 0 # contigs 2023 Largest contig 31188 Total length (>= 50000 bp) 0 # contigs 2023 Largest contig 31188 Total length 9769814 Reference length 9714864 N50 7229 N75 4304 L50 424 L75 855 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 # unaligned length 0 Genome fraction (%) 99.040 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.07 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304	_	
# contigs (>= 10000 bp)		1794
# contigs (>= 25000 bp)  # contigs (>= 50000 bp)  Total length (>= 0 bp)  Total length (>= 1000 bp)  Total length (>= 5000 bp)  Total length (>= 25000 bp)  Total length (>= 25000 bp)  Total length (>= 50000 bp)  # contigs  Largest contig  Total length  Reference length  N50  N75  A304  L50  L75  # misassemblies  # misassembled contigs  # misassembled contigs  # unaligned contigs  Unaligned length  Genome fraction (%)  Duplication ratio  # N's per 100 kbp  # indels per 100 kbp  Largest alignment  NA50  N229  NA75  A304  L304  L304  L304  L306  L306  L307  L307  L308	_	749
# contigs (>= 50000 bp) Total length (>= 0 bp) Total length (>= 1000 bp) 9840987 Total length (>= 1000 bp) 9601076 Total length (>= 5000 bp) 6834637 Total length (>= 10000 bp) 3175832 Total length (>= 25000 bp) 133677 Total length (>= 50000 bp) 60 # contigs 2023 Largest contig 31188 Total length 8eference length 9769814 Reference length 9714864 N50 7229 N75 4304 L50 424 L75 855 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs Unaligned length 0 Genome fraction (%) 99.040 Duplication ratio # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.07 # indels per 100 kbp 1.07	_	221
Total length (>= 0 bp)         9840987           Total length (>= 1000 bp)         9601076           Total length (>= 5000 bp)         6834637           Total length (>= 10000 bp)         3175832           Total length (>= 25000 bp)         133677           Total length (>= 50000 bp)         0           # contigs         2023           Largest contig         31188           Total length         9769814           Reference length         9714864           N50         7229           N75         4304           L50         424           L75         855           # misassemblies         0           # sessembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         99.040           Duplication ratio         1.015           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         31188           NA50         7229           NA75         4304	_	5
Total length (>= 1000 bp)         9601076           Total length (>= 5000 bp)         6834637           Total length (>= 10000 bp)         3175832           Total length (>= 25000 bp)         133677           Total length (>= 50000 bp)         0           # contigs         2023           Largest contig         31188           Total length         9769814           Reference length         9714864           N50         7229           N75         4304           L50         424           L75         855           # misassemblies         0           # sessembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         99.040           Duplication ratio         1.015           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         31188           NA50         7229           NA75         4304	# contigs (>= 50000 bp)	0
Total length (>= 5000 bp) 6834637  Total length (>= 10000 bp) 3175832  Total length (>= 25000 bp) 133677  Total length (>= 50000 bp) 0  # contigs 2023  Largest contig 31188  Total length 9769814  Reference length 9714864  N50 7229  N75 4304  L50 424  L75 855  # misassemblies 0  # misassembled contigs 0  Misassembled contigs 0  # local misassemblies 0  # unaligned contigs 0  # unaligned length 0  Genome fraction (%) 99.040  Duplication ratio 1.015  # N's per 100 kbp 0.00  # mismatches per 100 kbp 1.07  # indels per 100 kbp 0.00  Largest alignment 31188  NA50 7229  NA75 4304	_	9840987
Total length (>= 10000 bp) 3175832  Total length (>= 25000 bp) 133677  Total length (>= 50000 bp) 0  # contigs 2023  Largest contig 31188  Total length 9769814  Reference length 9714864  N50 7229  N75 4304  L50 424  L75 855  # misassemblies 0  # misassembled contigs 0  Misassembled contigs 0  # local misassemblies 0  # unaligned contigs 0  Genome fraction (%) 99.040  Duplication ratio 1.015  # N's per 100 kbp 0.00  # mismatches per 100 kbp 1.07  # indels per 100 kbp 0.00  Largest alignment 31188  NA50 7229  NA75 4304	Total length (>= 1000 bp)	9601076
Total length (>= 25000 bp) 133677  Total length (>= 50000 bp) 0  # contigs 2023  Largest contig 31188  Total length 9769814  Reference length 9714864  N50 7229  N75 4304  L50 424  L75 855  # misassemblies 0  # misassembled contigs 0  Misassembled contigs 10  # local misassemblies 0  # unaligned contigs 0  Genome fraction (♥) 99.040  Duplication ratio 1.015  # N's per 100 kbp 0.000  # mismatches per 100 kbp 1.07  # indels per 100 kbp 0.00  Largest alignment 31188  NA50 7229  NA75 4304	Total length (>= 5000 bp)	6834637
Total length (>= 50000 bp)         0           # contigs         2023           Largest contig         31188           Total length         9769814           Reference length         9714864           N50         7229           N75         4304           L50         424           L75         855           # misassemblies         0           # insassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         99.040           Duplication ratio         1.015           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           # mindels per 100 kbp         0.00           Largest alignment         31188           NA50         7229           NA75         4304	Total length (>= 10000 bp)	3175832
# contigs 2023 Largest contig 31188 Total length 9769814 Reference length 9714864 N50 7229 N75 4304 L50 424 L75 855 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # unaligned contigs 0 H unaligned length 0 Genome fraction (%) 99.040 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.07 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304	Total length (>= 25000 bp)	133677
Largest contig       31188         Total length       9769814         Reference length       9714864         N50       7229         N75       4304         L50       424         L75       855         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.040         Duplication ratio       1.015         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1.07         # indels per 100 kbp       0.00         Largest alignment       31188         NA50       7229         NA75       4304	Total length (>= 50000 bp)	0
Total length       9769814         Reference length       9714864         N50       7229         N75       4304         L50       424         L75       855         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (♥)       99.040         Duplication ratio       1.015         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1.07         # indels per 100 kbp       0.00         Largest alignment       31188         NA50       7229         NA75       4304	# contigs	2023
Reference length       9714864         N50       7229         N75       4304         L50       424         L75       855         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.040         Duplication ratio       1.015         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1.07         # indels per 100 kbp       0.00         Largest alignment       31188         NA50       7229         NA75       4304	Largest contig	31188
N50       7229         N75       4304         L50       424         L75       855         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.040         Duplication ratio       1.015         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1.07         # indels per 100 kbp       0.00         Largest alignment       31188         NA50       7229         NA75       4304	Total length	9769814
N75       4304         L50       424         L75       855         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.040         Duplication ratio       1.015         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1.07         # indels per 100 kbp       0.00         Largest alignment       31188         NA50       7229         NA75       4304	Reference length	9714864
L50       424         L75       855         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       99.040         Duplication ratio       1.015         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1.07         # indels per 100 kbp       0.00         Largest alignment       31188         NA50       7229         NA75       4304	N50	7229
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.040 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.07 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304	N75	4304
# misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.040 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.07 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304	L50	424
# misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.040 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.07 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304	L75	855
Misassembled contigs length  # local misassemblies  # unaligned contigs  Unaligned length  Genome fraction (%)  Duplication ratio  # N's per 100 kbp  # mismatches per 100 kbp  1.07  # indels per 100 kbp  Largest alignment  NA50  NA75  0 + 0 part  0 + 0 part  0 - 0 pont  99.040  99.040  1.015  # N's per 100 kbp  0.00  7.000  1.0000  1.0000  1.0000  1.0000  1.0000  1.0000	# misassemblies	0
# local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.040 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.07 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304	# misassembled contigs	0
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 99.040 Duplication ratio 1.015 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1.07 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304	Misassembled contigs length	0
Unaligned length       0         Genome fraction (%)       99.040         Duplication ratio       1.015         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1.07         # indels per 100 kbp       0.00         Largest alignment       31188         NA50       7229         NA75       4304	# local misassemblies	0
Genome fraction (♥)       99.040         Duplication ratio       1.015         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1.07         # indels per 100 kbp       0.00         Largest alignment       31188         NA50       7229         NA75       4304	# unaligned contigs	0 + 0 part
Duplication ratio       1.015         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1.07         # indels per 100 kbp       0.00         Largest alignment       31188         NA50       7229         NA75       4304	Unaligned length	0
# N's per 100 kbp 0.00 # mismatches per 100 kbp 1.07 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304	Genome fraction (%)	99.040
# mismatches per 100 kbp 1.07 # indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304	Duplication ratio	1.015
# indels per 100 kbp 0.00 Largest alignment 31188 NA50 7229 NA75 4304	# N's per 100 kbp	0.00
Largest alignment       31188         NA50       7229         NA75       4304	# mismatches per 100 kbp	1.07
NA50 7229 NA75 4304	# indels per 100 kbp	0.00
NA75 4304	Largest alignment	31188
	NA50	7229
LA50 424	NA75	4304
	LA50	424
LA75 855	LA75	

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

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	103
# indels	0
# short indels	0
# long indels	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

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# 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).









