

# Report

	final.contigs
# contigs (>= 0 bp)	11685
# contigs (>= 1000 bp)	3373
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	10000884
Total length (>= 1000 bp)	5579757
Total length (>= 5000 bp)	10290
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	7447
Largest contig	5156
Total length	8493193
Reference length	9283304
N50	1299
N75	860
L50	2204
L75	4227
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	1 + 4 part
Unaligned length	777
Genome fraction (%)	87.989
Duplication ratio	1.060
# N's per 100 kbp	0.00
# mismatches per 100 kbp	122.98
# indels per 100 kbp	0.10
Largest alignment	5156
NA50	1299
NA75	860
LA50	2205
LA75	4227

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

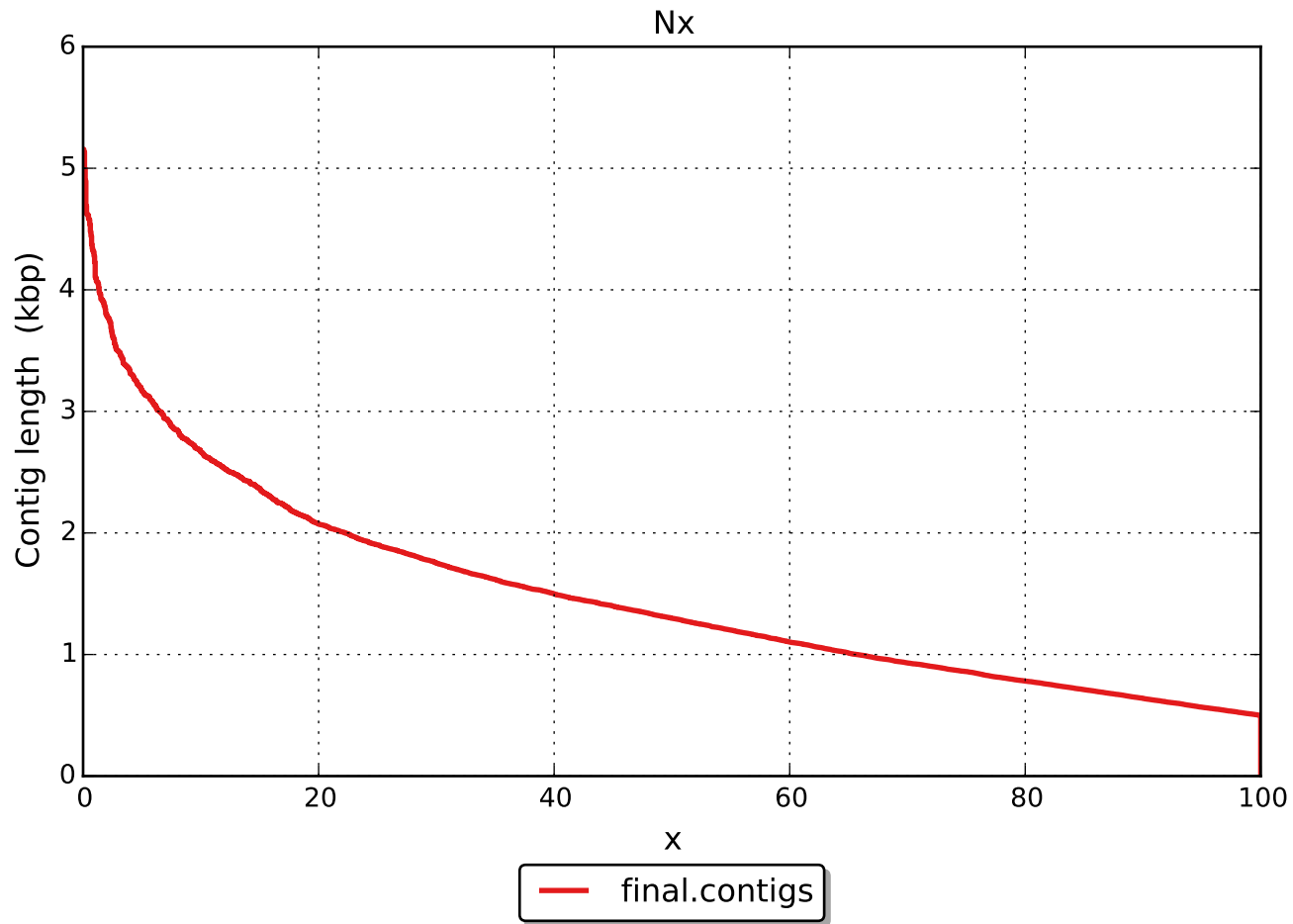
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	10045
# indels	8
# short indels	8
# long indels	0
Indels length	8

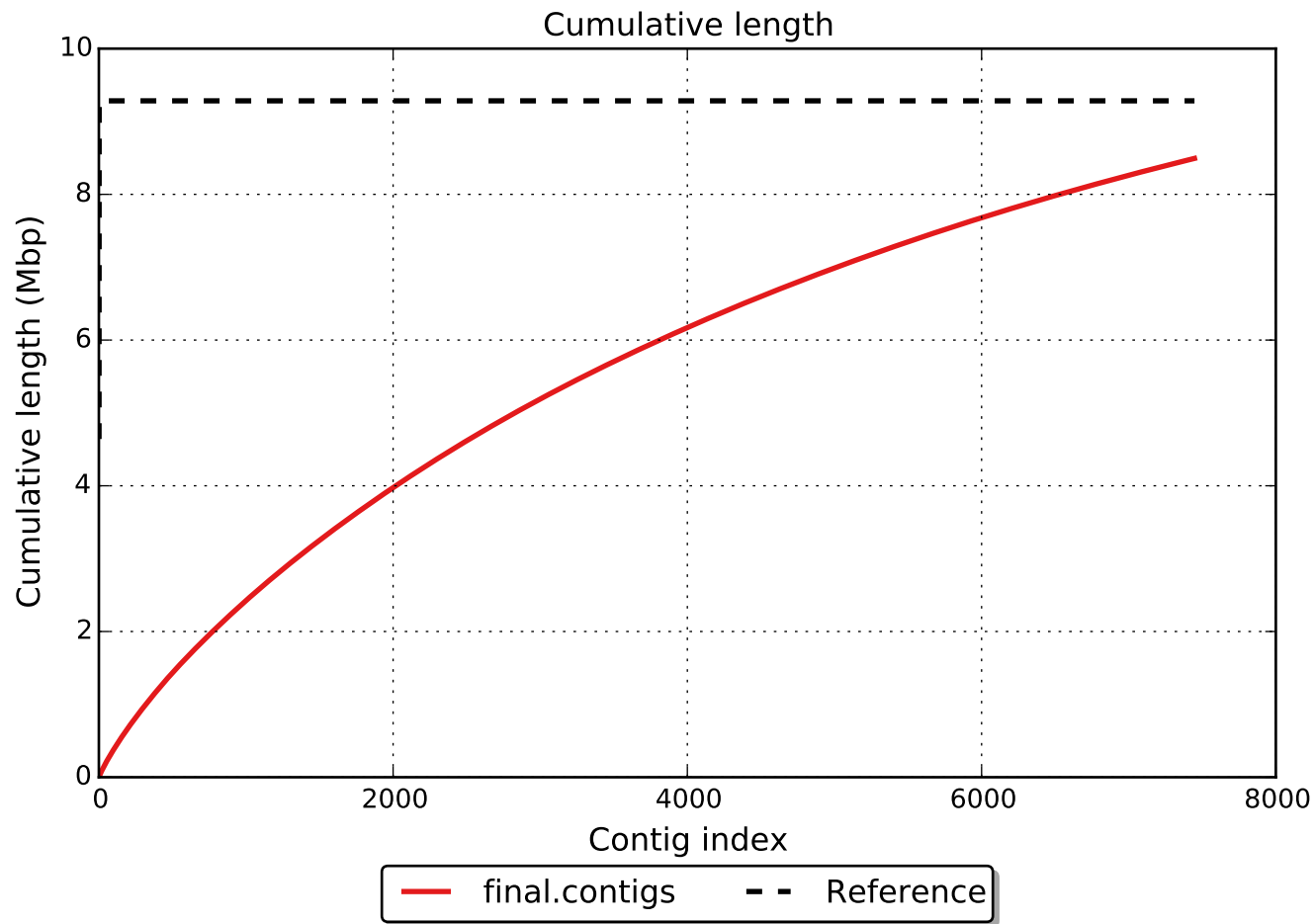
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	final.contigs
# fully unaligned contigs	1
Fully unaligned length	514
# partially unaligned contigs	4
# with misassembly	0
# both parts are significant	0
Partially unaligned length	263
# N's	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).





# Misassemblies

