

Report

	final.contigs
# contigs (≥ 0 bp)	3359
# contigs (≥ 1000 bp)	2156
# contigs (≥ 5000 bp)	659
# contigs (≥ 10000 bp)	121
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	9628168
Total length (≥ 1000 bp)	9074409
Total length (≥ 5000 bp)	5200261
Total length (≥ 10000 bp)	1582168
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	2536
Largest contig	20716
Total length	9353930
Reference length	9283304
N50	5438
N75	3233
L50	559
L75	1114
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 1 part
Unaligned length	29
Genome fraction (%)	98.366
Duplication ratio	1.024
# N's per 100 kbp	0.00
# mismatches per 100 kbp	25.78
# indels per 100 kbp	0.05
Largest alignment	20716
NA50	5438
NA75	3233
LA50	559
LA75	1114

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

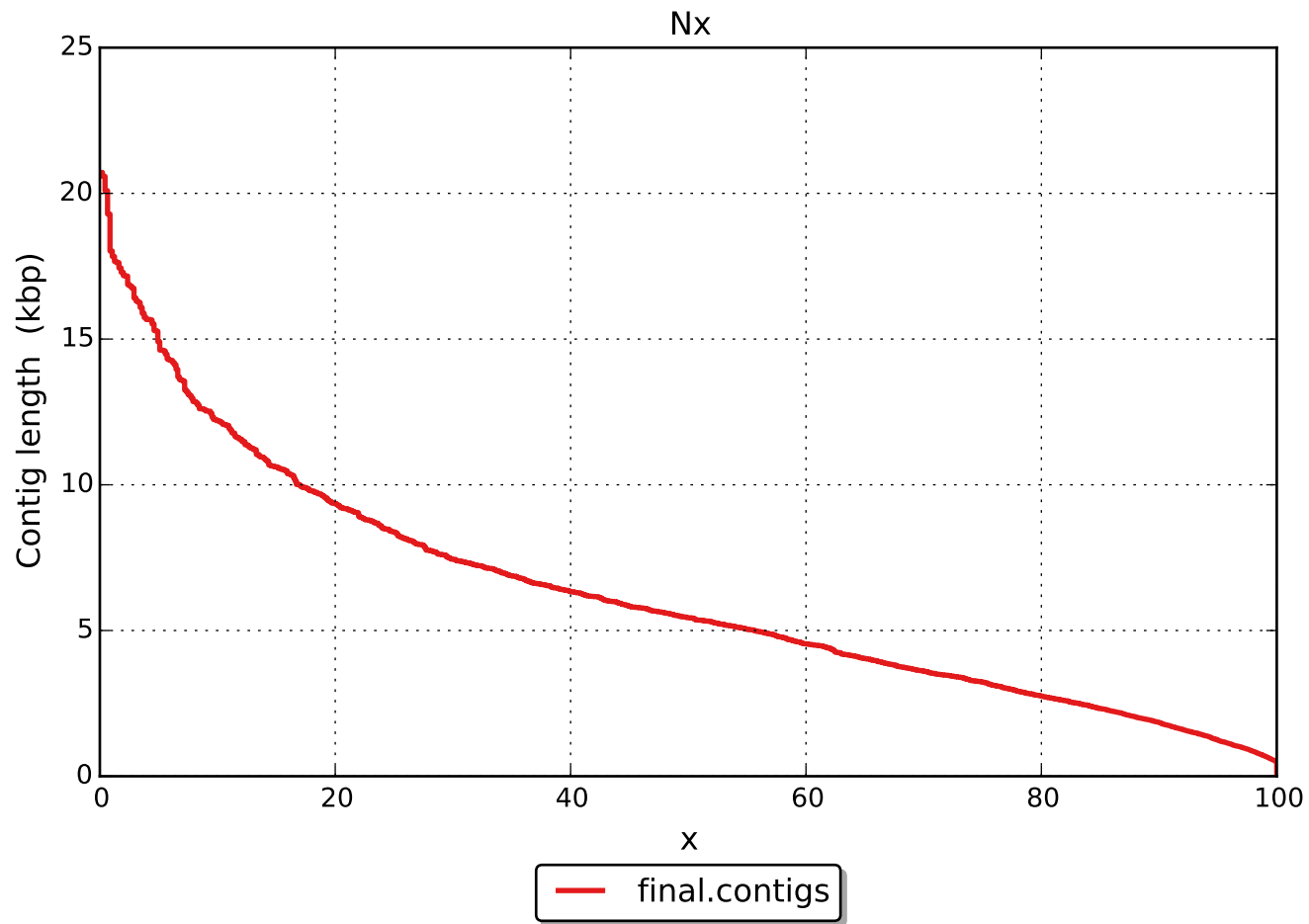
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	2354
# indels	5
# short indels	5
# long indels	0
Indels length	5

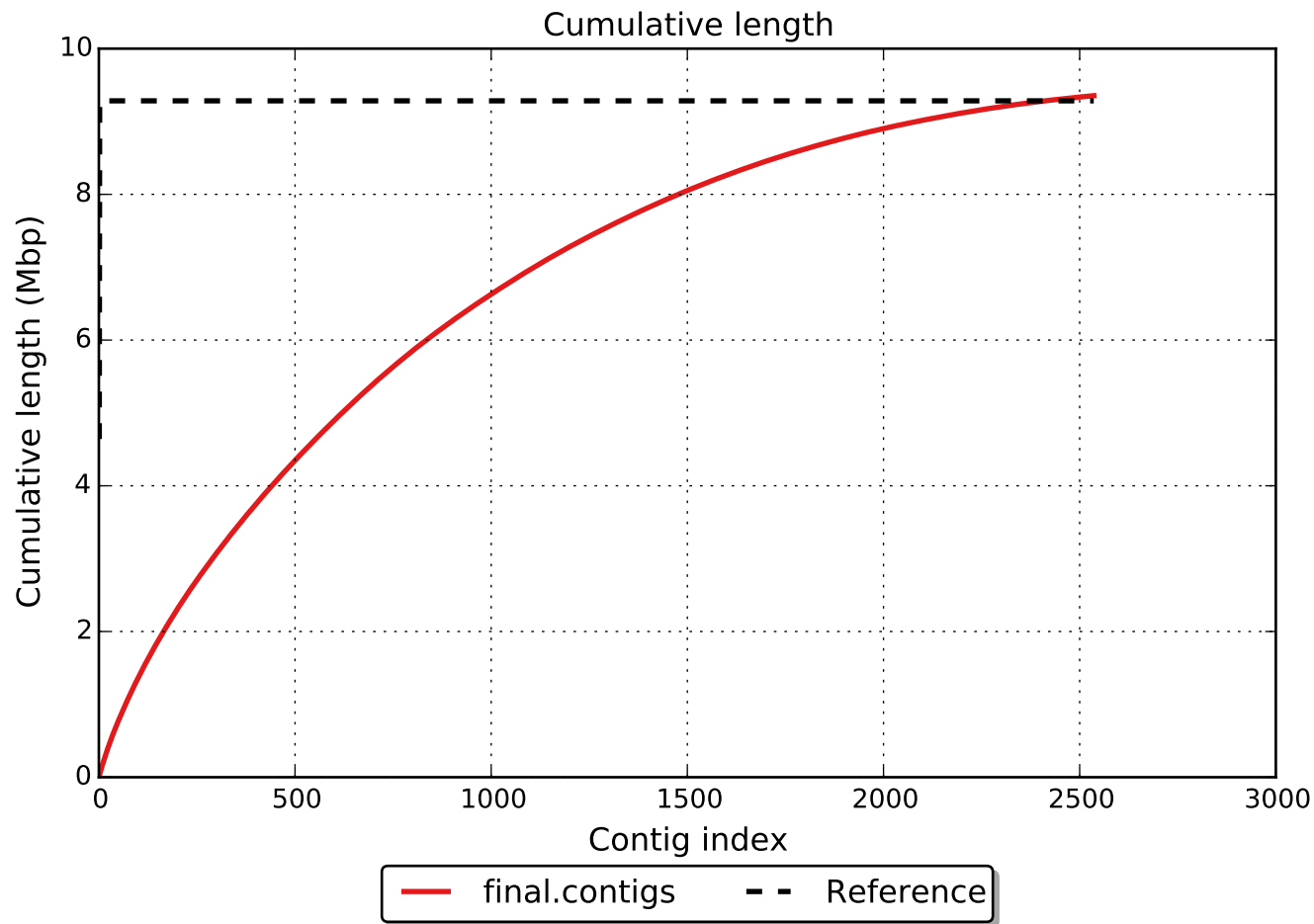
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	29
# 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).





Misassemblies

