

Report

	final.contigs
# contigs (≥ 0 bp)	473
# contigs (≥ 1000 bp)	362
# contigs (≥ 5000 bp)	291
# contigs (≥ 10000 bp)	243
# contigs (≥ 25000 bp)	135
# contigs (≥ 50000 bp)	60
Total length (≥ 0 bp)	9703527
Total length (≥ 1000 bp)	9660026
Total length (≥ 5000 bp)	9460101
Total length (≥ 10000 bp)	9102685
Total length (≥ 25000 bp)	7355472
Total length (≥ 50000 bp)	4763656
# contigs	391
Largest contig	160557
Total length	9680848
Reference length	9714864
N50	48729
N75	25894
L50	62
L75	132
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	99.564
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.57
# indels per 100 kbp	0.00
Largest alignment	160557
NA50	48729
NA75	25894
LA50	62
LA75	132

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

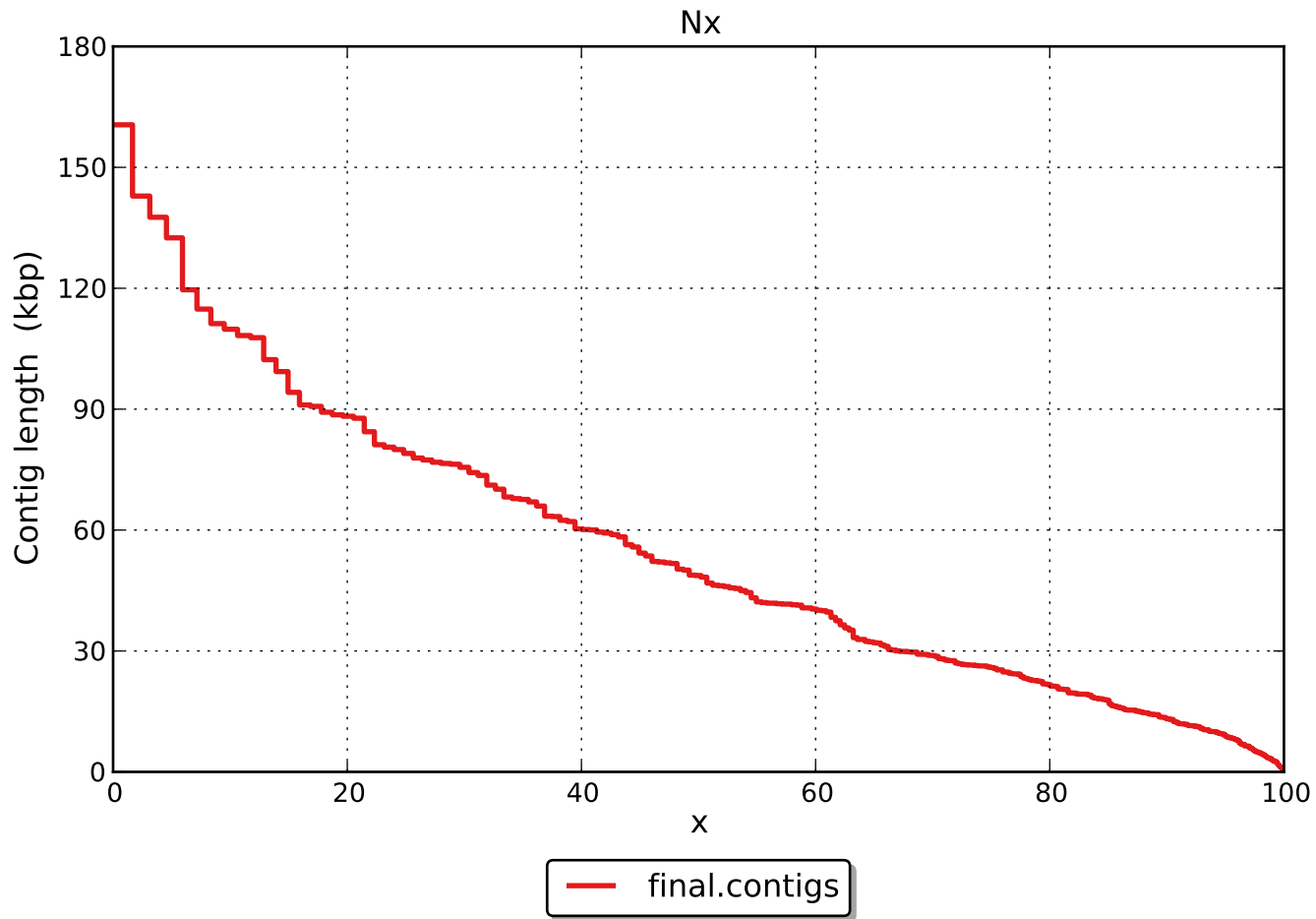
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	152
# indels	0
# short indels	0
# long indels	0
Indels length	0

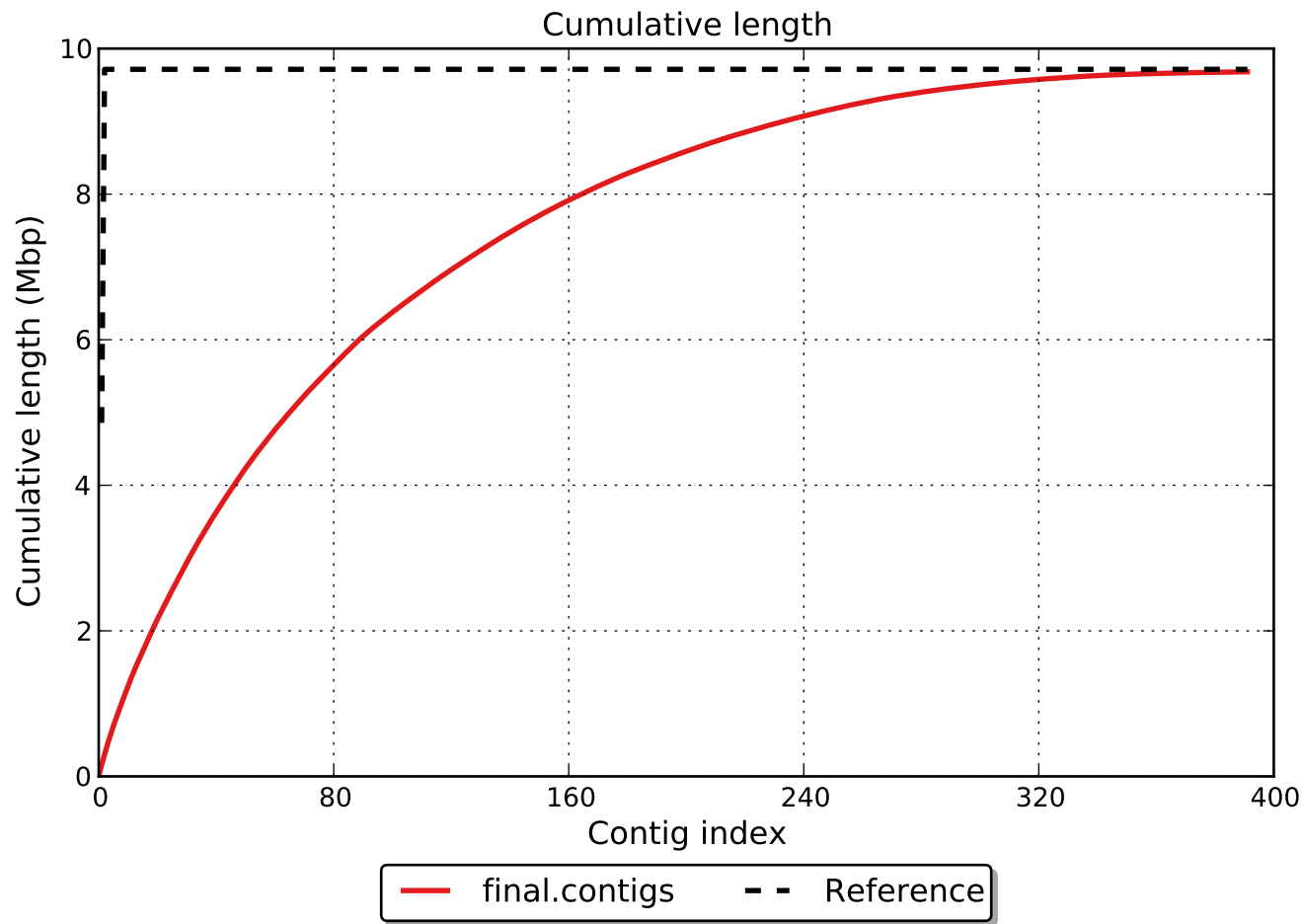
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

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

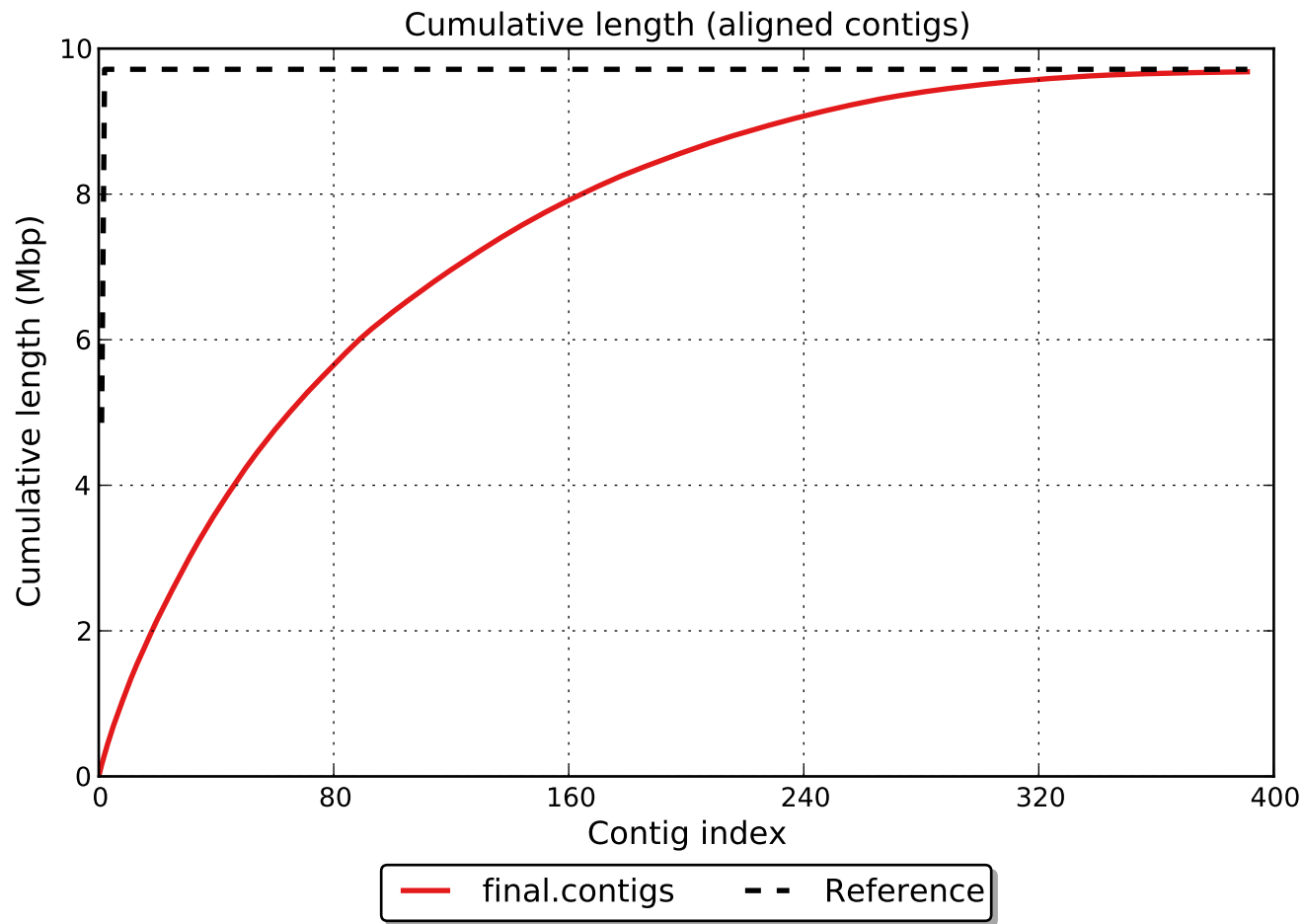
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).





Misassemblies





NAx

