

Report

	final.contigs
# contigs (≥ 0 bp)	2275
# contigs (≥ 1000 bp)	1774
# contigs (≥ 5000 bp)	719
# contigs (≥ 10000 bp)	193
# contigs (≥ 25000 bp)	2
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	9390939
Total length (≥ 1000 bp)	9124444
Total length (≥ 5000 bp)	6291708
Total length (≥ 10000 bp)	2704532
Total length (≥ 25000 bp)	56305
Total length (≥ 50000 bp)	0
# contigs	2022
Largest contig	30268
Total length	9307173
Reference length	9283304
N50	6635
N75	4132
L50	435
L75	871
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	98.699
Duplication ratio	1.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.22
# indels per 100 kbp	0.00
Largest alignment	30268
NA50	6635
NA75	4132
LA50	435
LA75	871

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

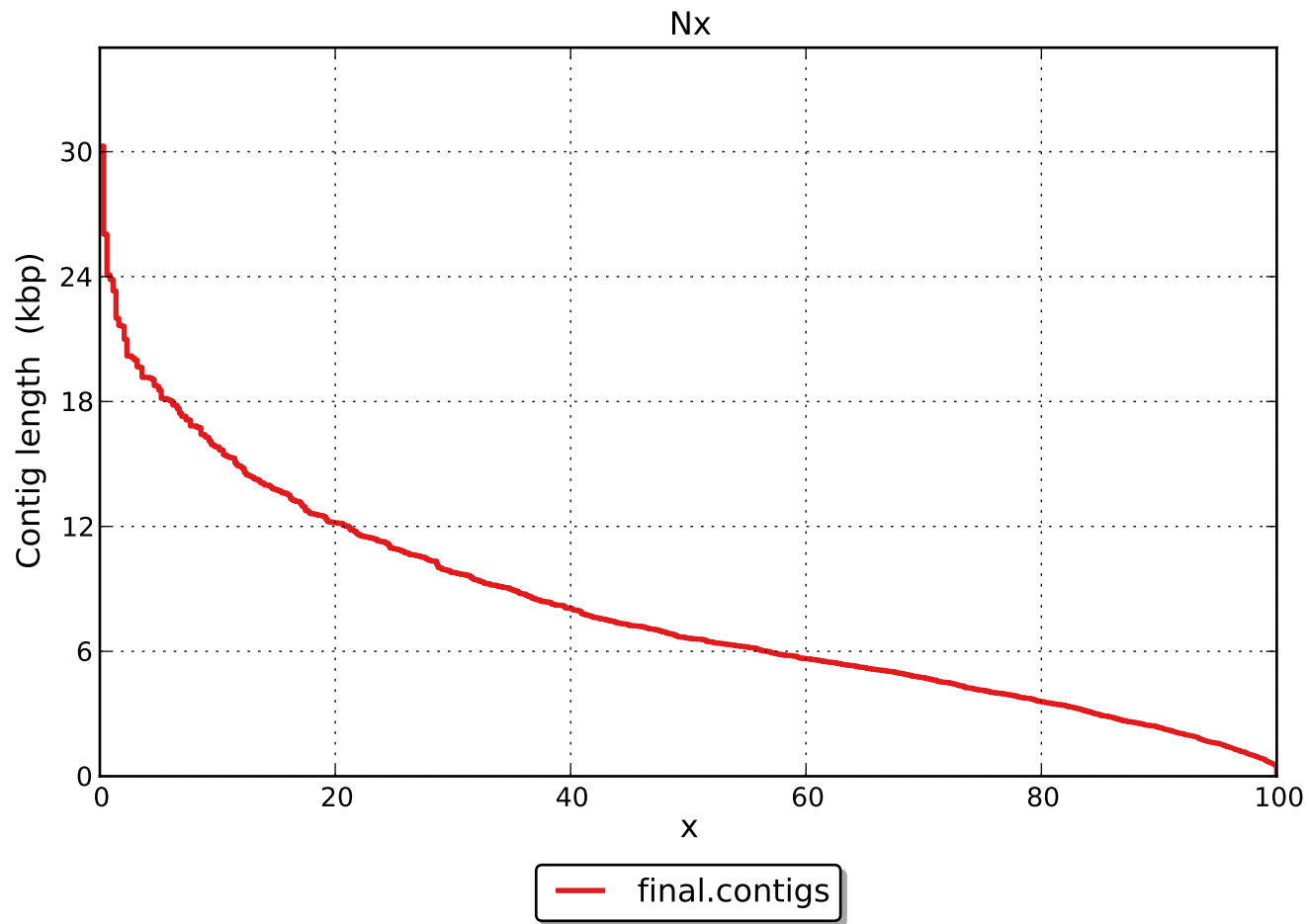
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	20
# indels	0
# short indels	0
# long indels	0
Indels length	0

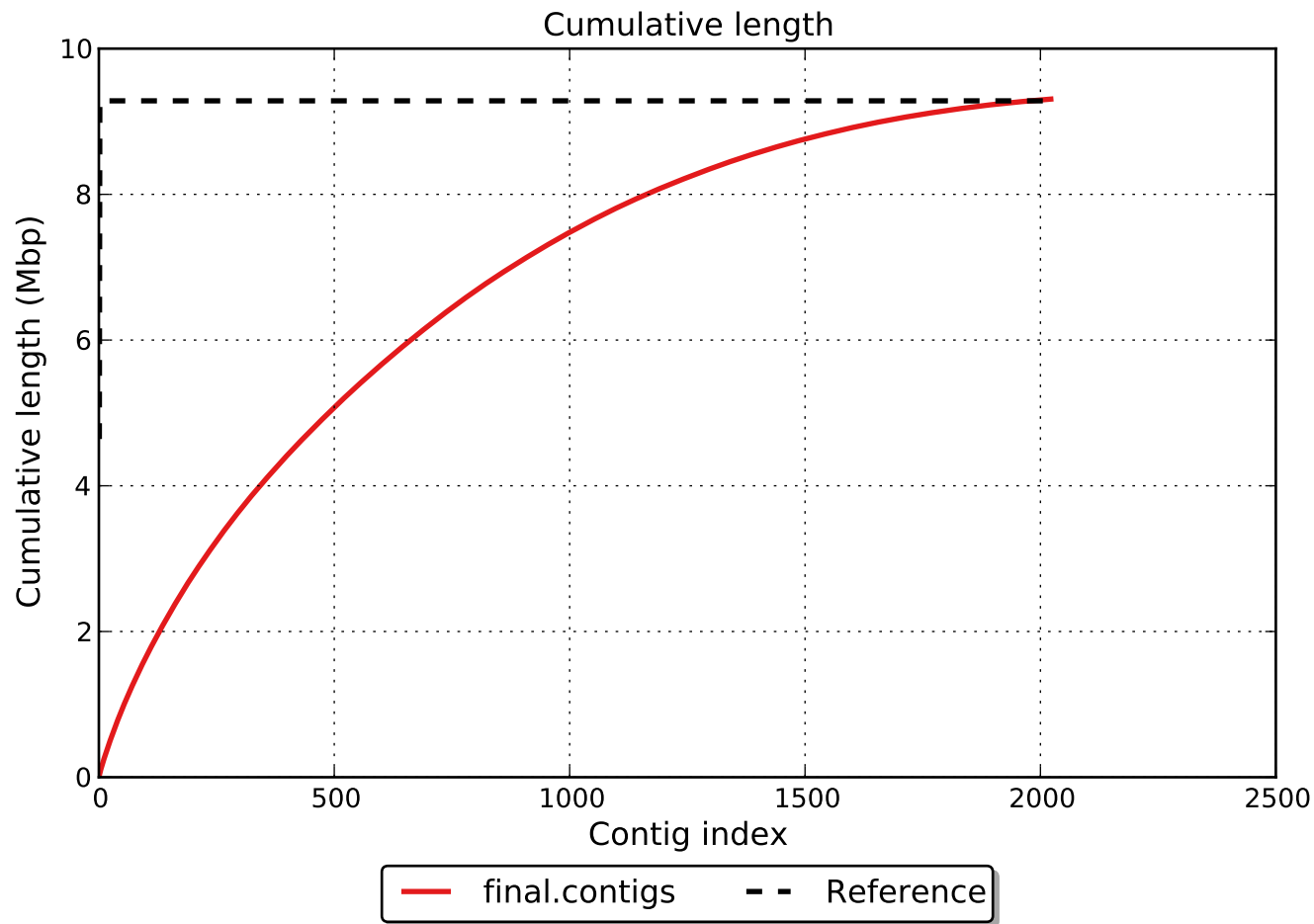
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

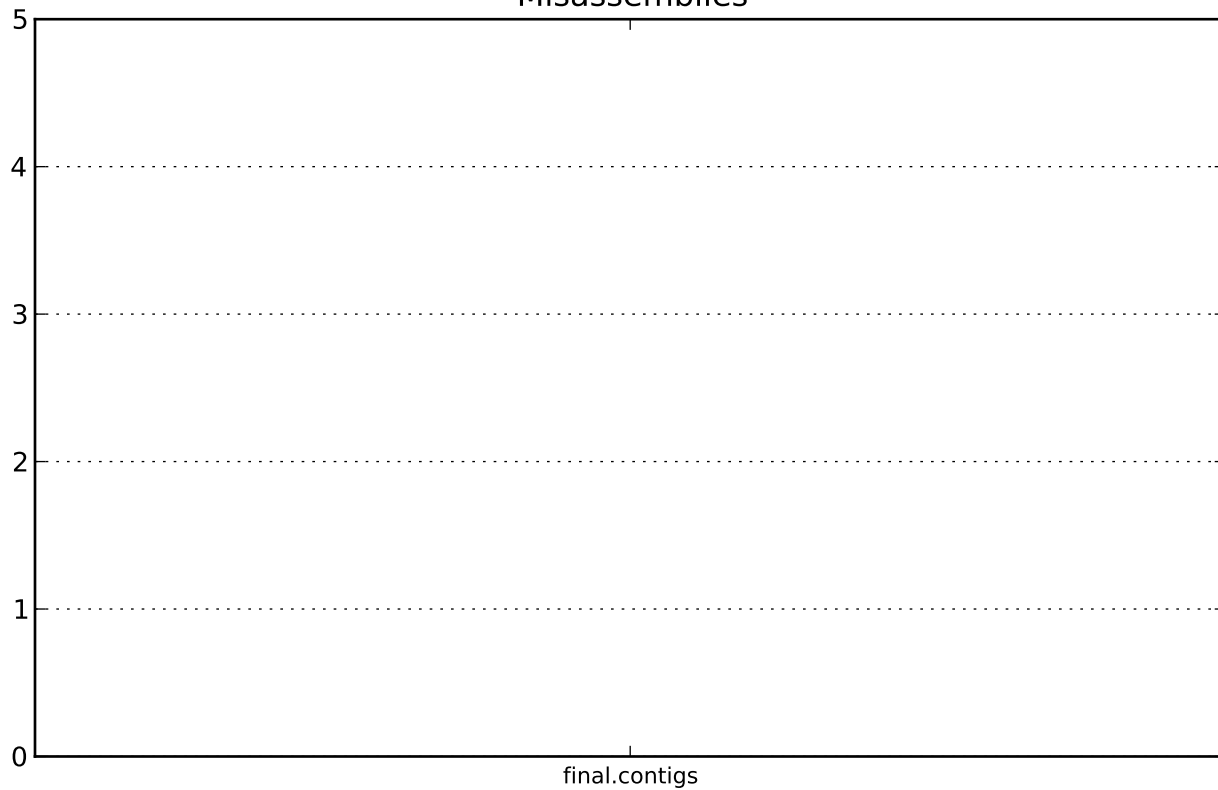
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

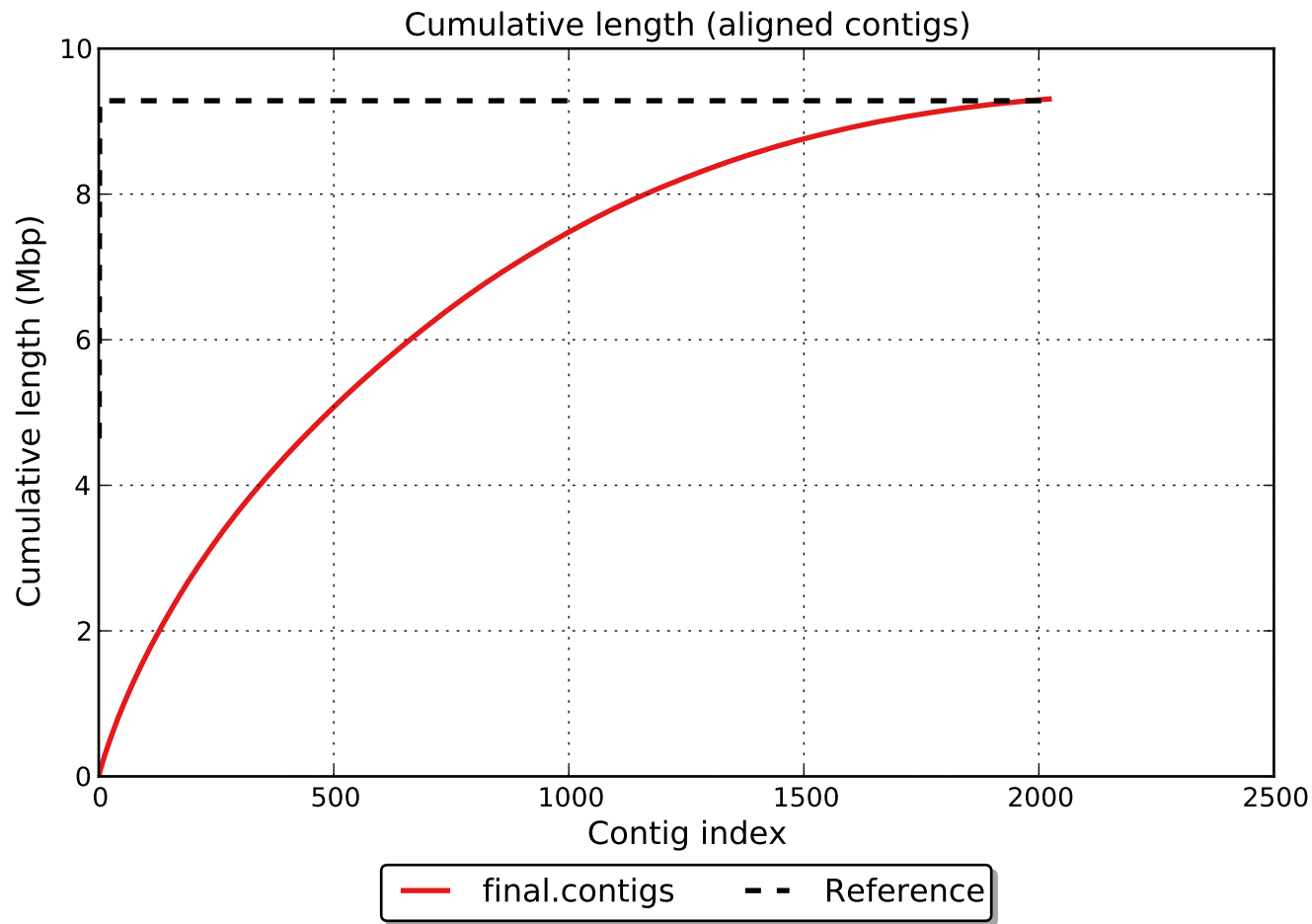
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).





Misassemblies





NAx

