

Report

	final.contigs
# contigs (≥ 0 bp)	8094
# contigs (≥ 1000 bp)	1702
# contigs (≥ 5000 bp)	58
# contigs (≥ 10000 bp)	1
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	6542532
Total length (≥ 1000 bp)	3733123
Total length (≥ 5000 bp)	352686
Total length (≥ 10000 bp)	12848
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	3519
Largest contig	12848
Total length	4955551
Reference length	9283304
N50	1906
N75	1010
L50	793
L75	1686
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	3619
# local misassemblies	2
# unaligned contigs	2 + 6 part
Unaligned length	1812
Genome fraction (%)	51.681
Duplication ratio	1.033
# N's per 100 kbp	0.00
# mismatches per 100 kbp	400.56
# indels per 100 kbp	0.13
Largest alignment	12845
NA50	1906
NA75	1010
LA50	793
LA75	1686

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

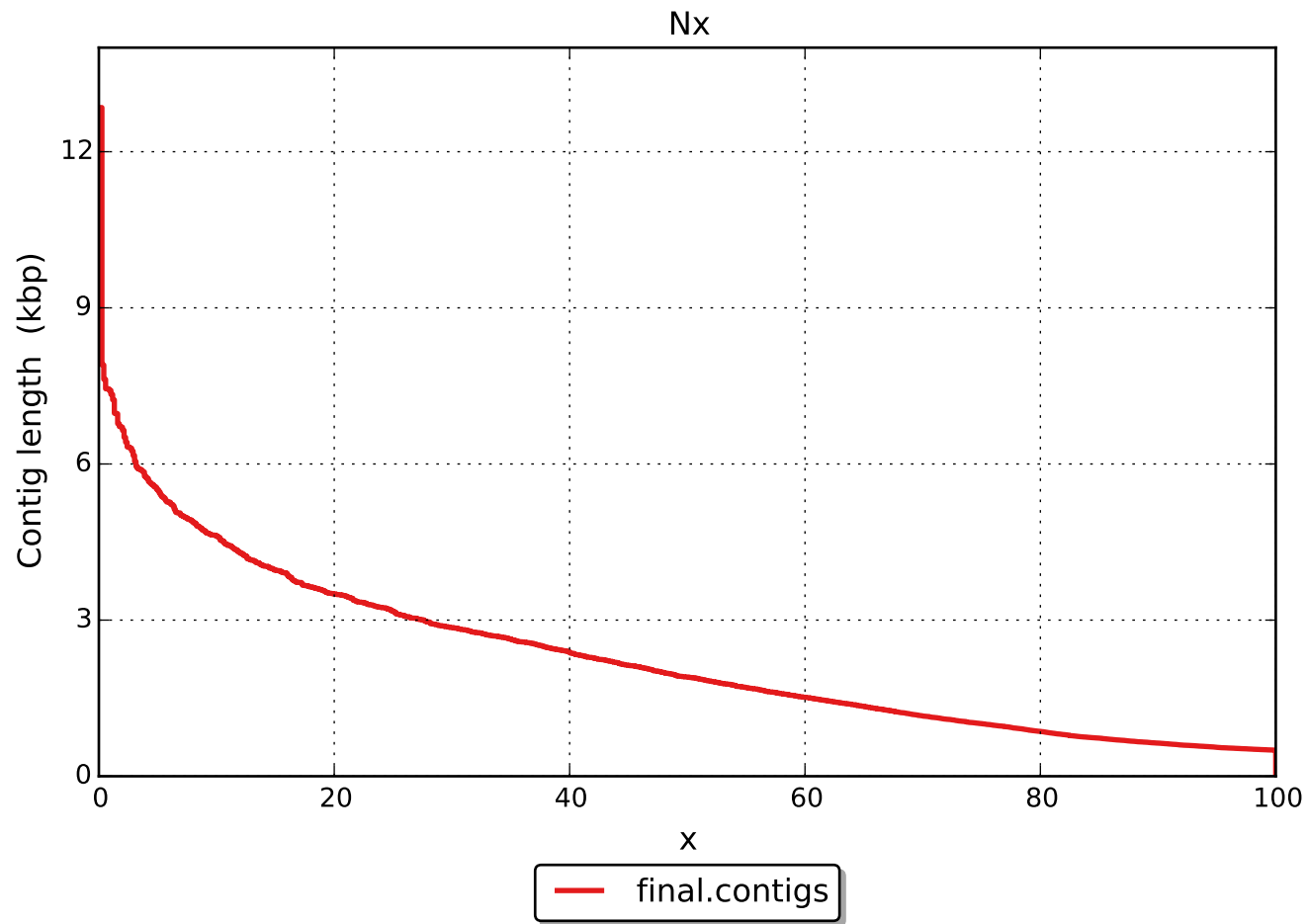
	final.contigs
# misassemblies	3
# relocations	2
# translocations	0
# inversions	1
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	3619
# local misassemblies	2
# mismatches	19218
# indels	6
# short indels	6
# long indels	0
Indels length	6

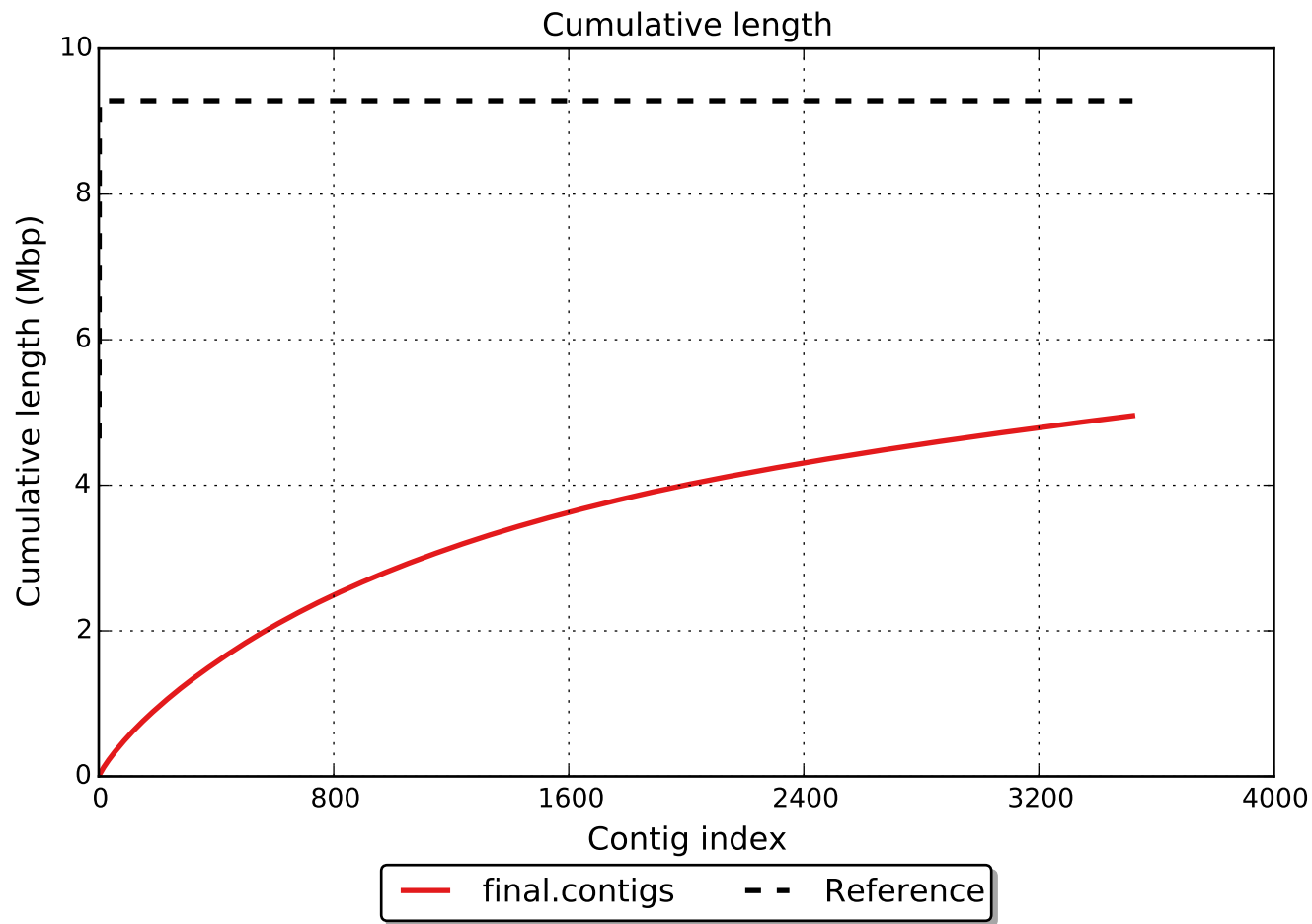
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

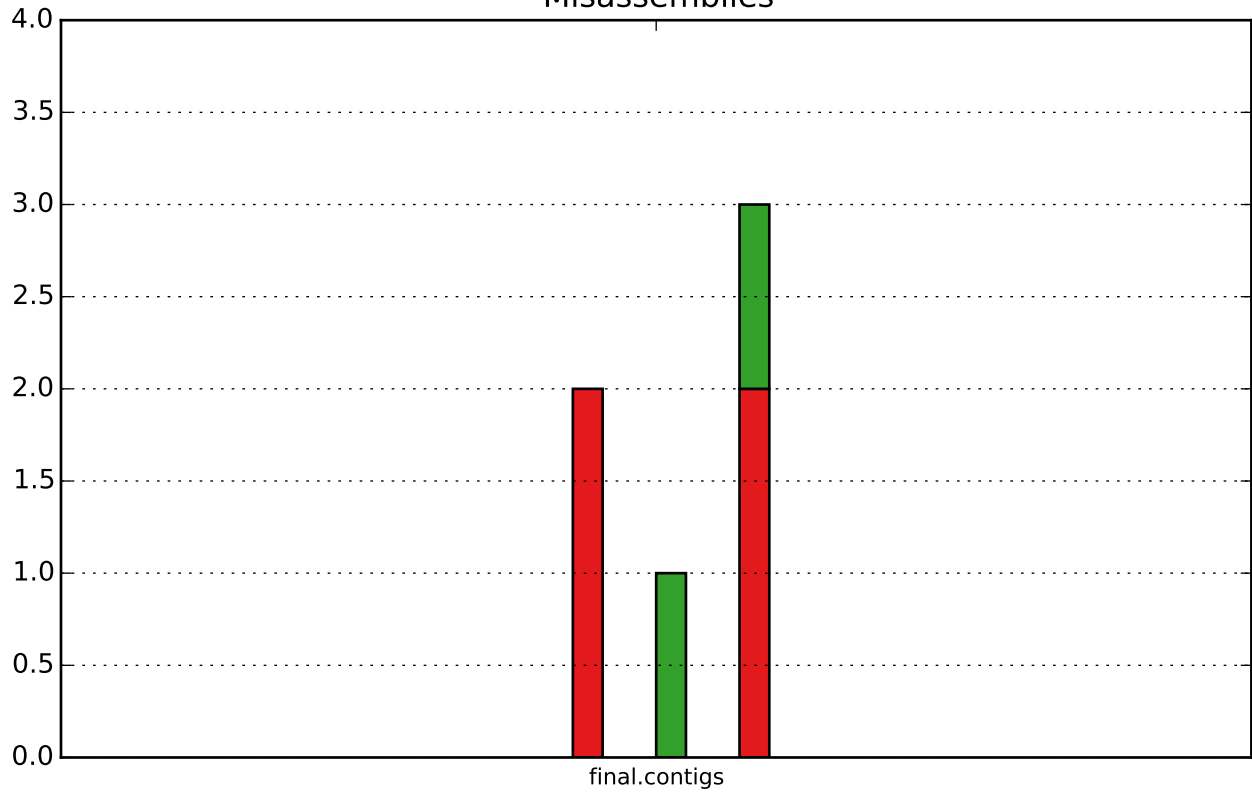
	final.contigs
# fully unaligned contigs	2
Fully unaligned length	1029
# partially unaligned contigs	6
# with misassembly	0
# both parts are significant	0
Partially unaligned length	783
# N's	0

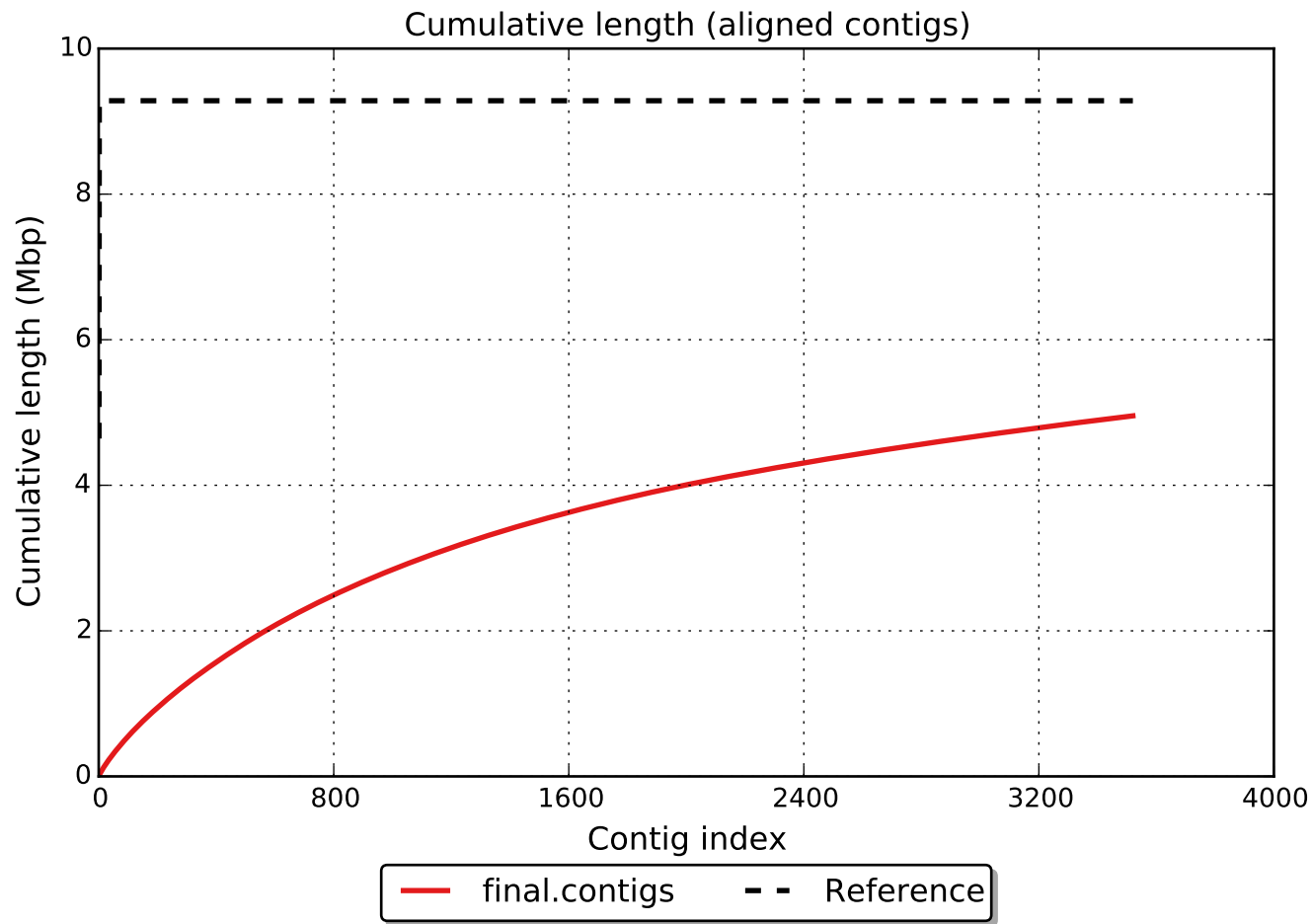
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).





Misassemblies





NAx

