Report

	final.contigs
# contigs (>= 0 bp)	8478
# contigs (>= 1000 bp)	1780
# contigs (>= 5000 bp)	63
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	6861032
Total length (>= 1000 bp)	3904323
Total length (>= 5000 bp)	396789
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3727
Largest contig	9194
Total length	5216997
Reference length	9714864
N50	1865
N75	998
L50	839
L75	1789
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1540
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	52.068
Duplication ratio	1.031
# N's per 100 kbp	0.00
# mismatches per 100 kbp	398.07
# indels per 100 kbp	0.16
Largest alignment	9194
NA50	1865
NA75	998
LA50	839
LA75	1789

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

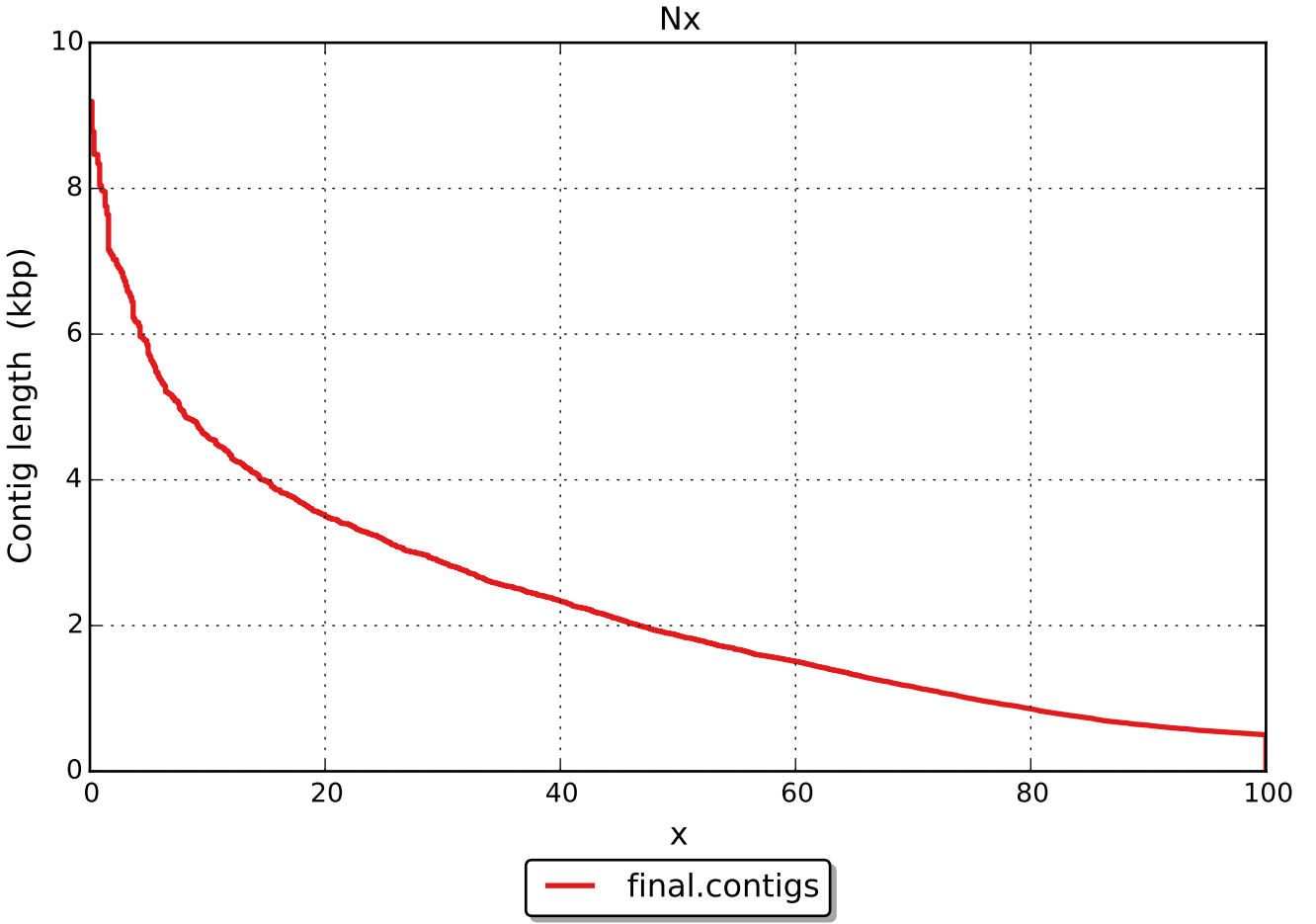
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1540
# local misassemblies	2
# mismatches	20136
# indels	8
# short indels	8
# long indels	0
Indels length	11

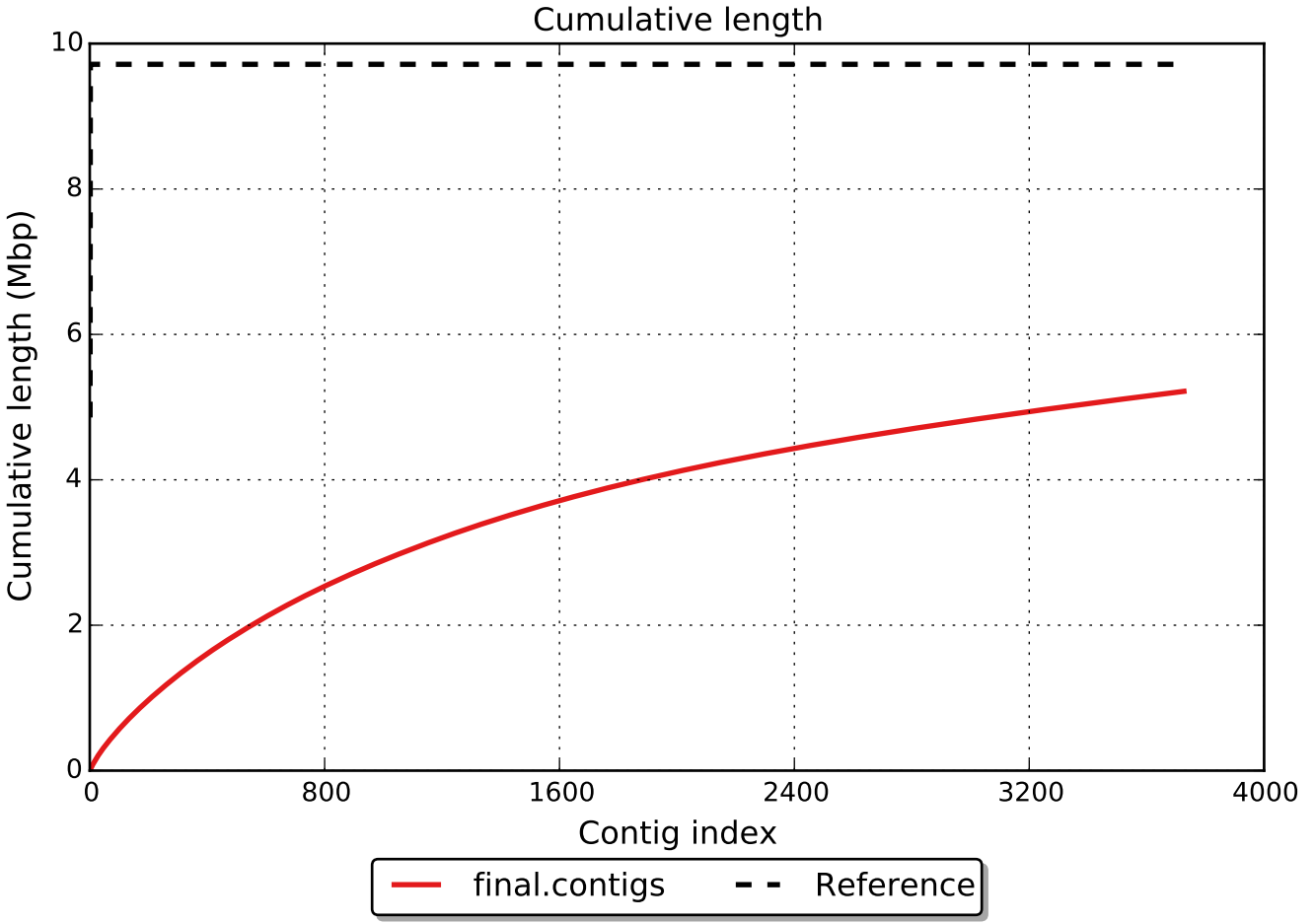
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

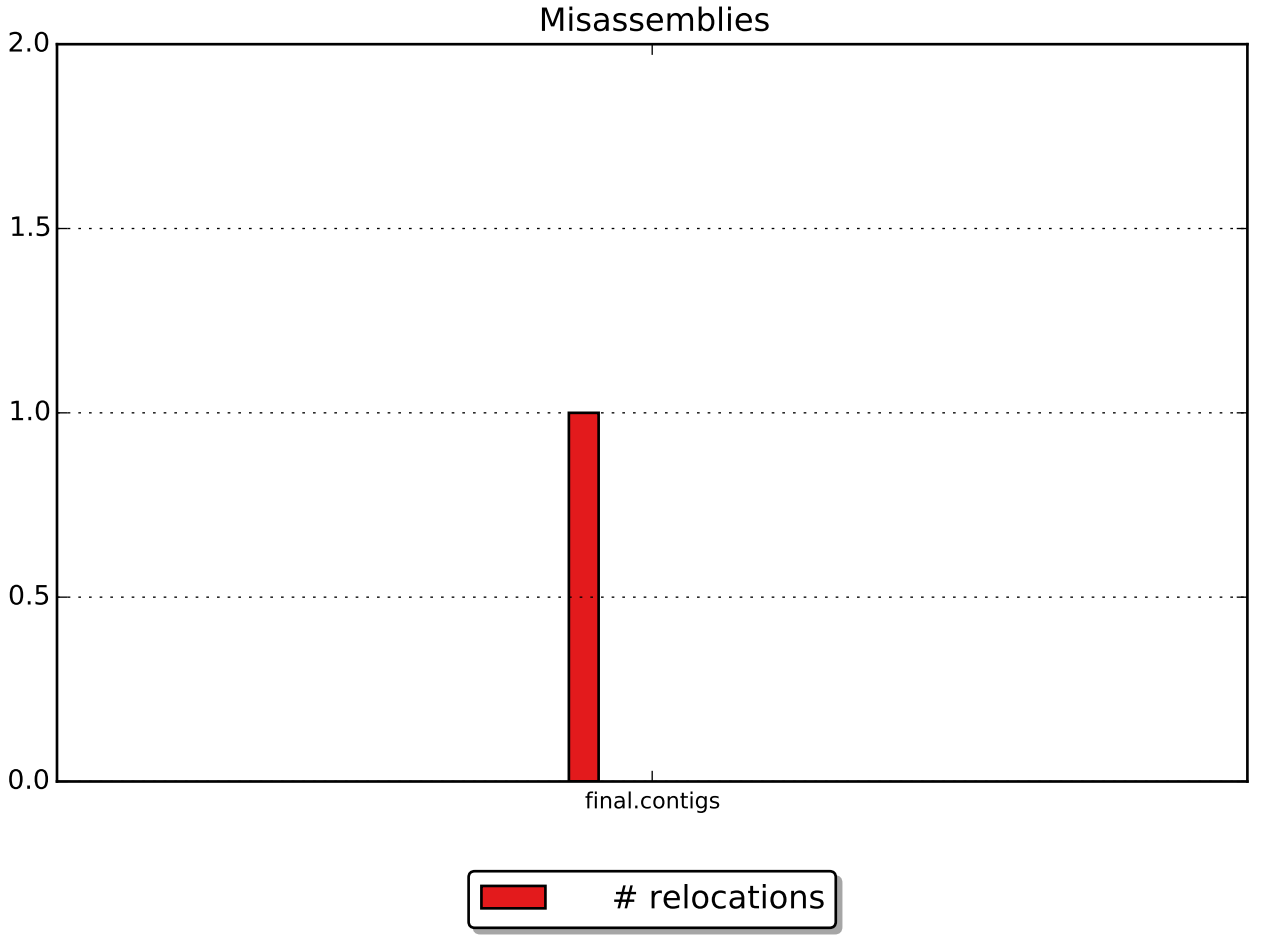
Unaligned report

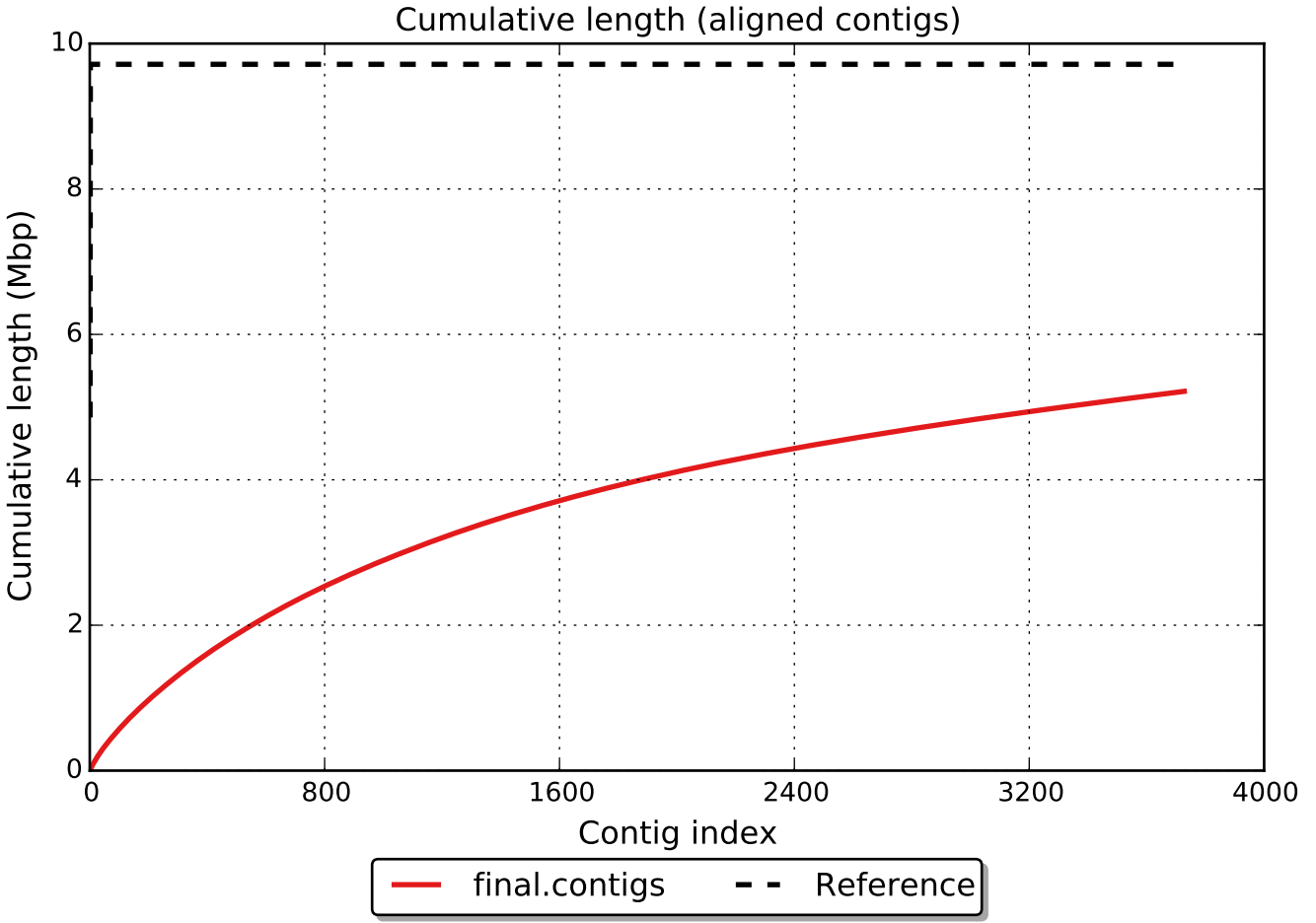
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

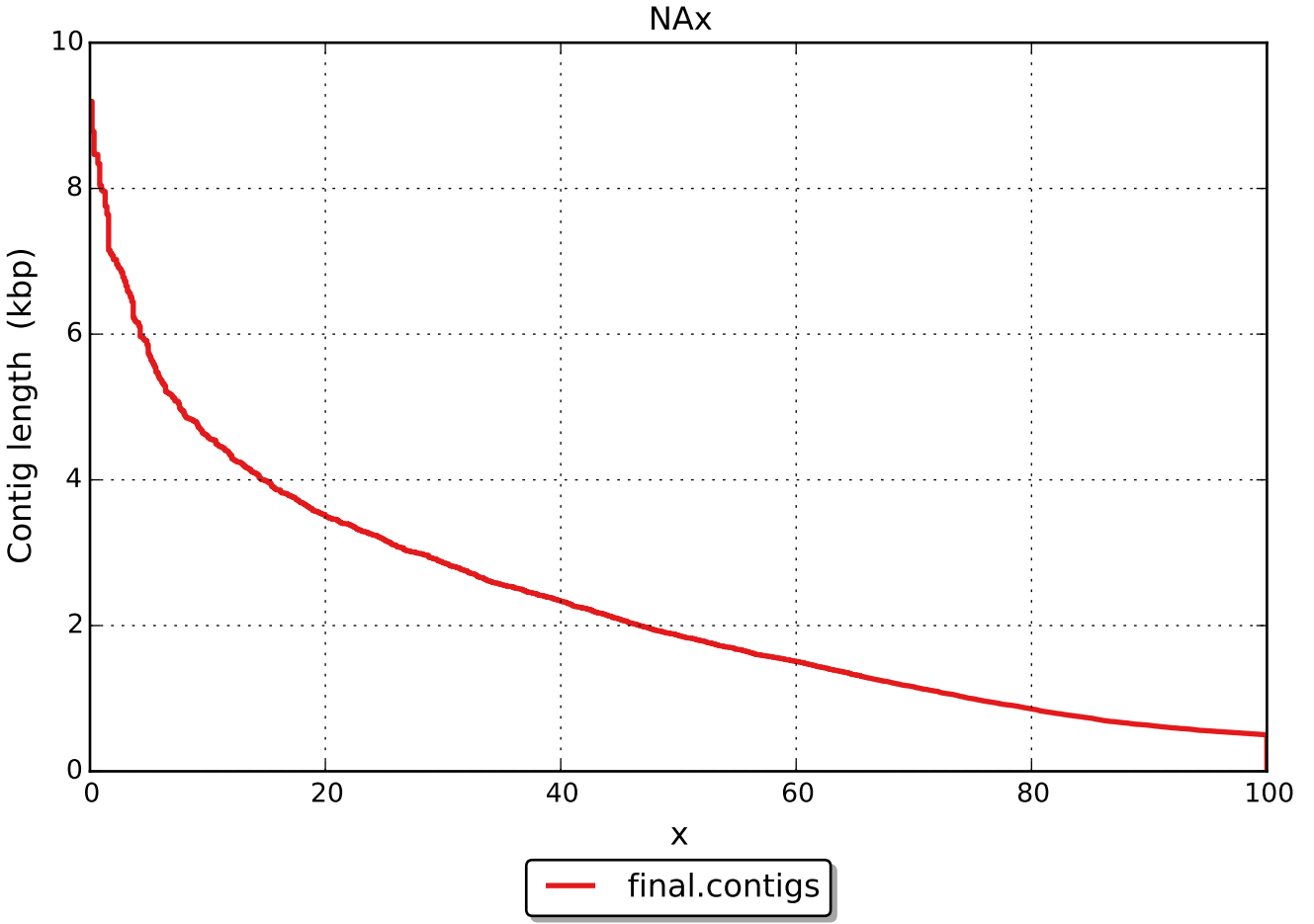
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
Contig length (kbp)
10
8
6
4
2
0
0
20
40
60
80
100
x
final.contigs


Cumulative length
Cumulative length (Mbp)
10
8
6
4
2
0
0
800
1600
2400
3200
4000
Contig index
final.contigs
Reference


Misassemblies
2.0
1.5
1.0
0.5
0.0
final.contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (Mbp)
10
8
6
4
2
0
0
800
1600
2400
3200
4000
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
10
8
6
4
2
0
0
20
40
60
80
100
x
final.contigs