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 (%)	86.537
Duplication ratio	1.061
# N's per 100 kbp	0.00
# mismatches per 100 kbp	600.85
# indels per 100 kbp	0.15
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

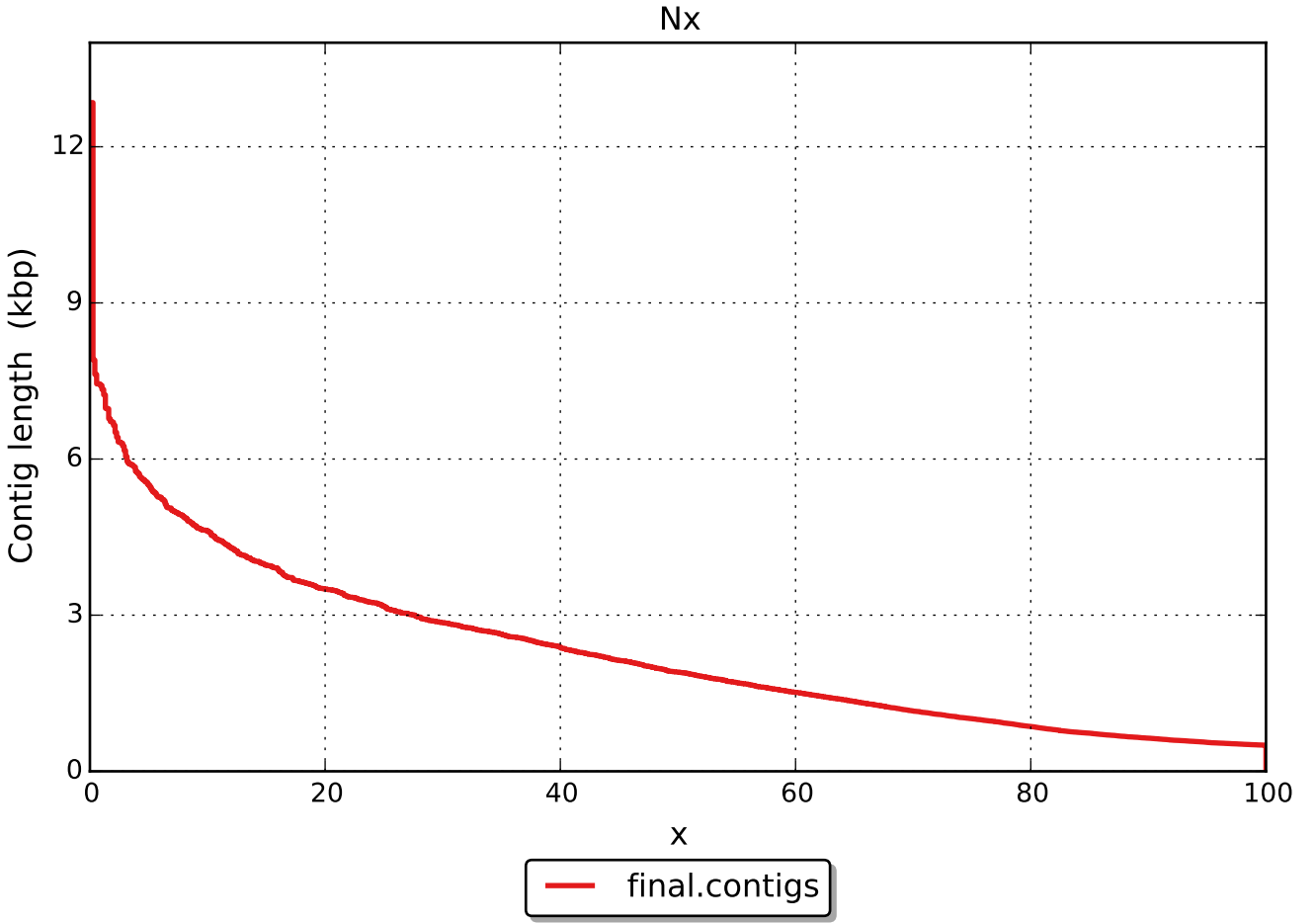
	final.contigs
# misassemblies	3
# relocations	2
# translocations	0
# inversions	1
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	3619
# local misassemblies	2
# mismatches	48269
# indels	12
# short indels	12
# long indels	0
Indels length	12

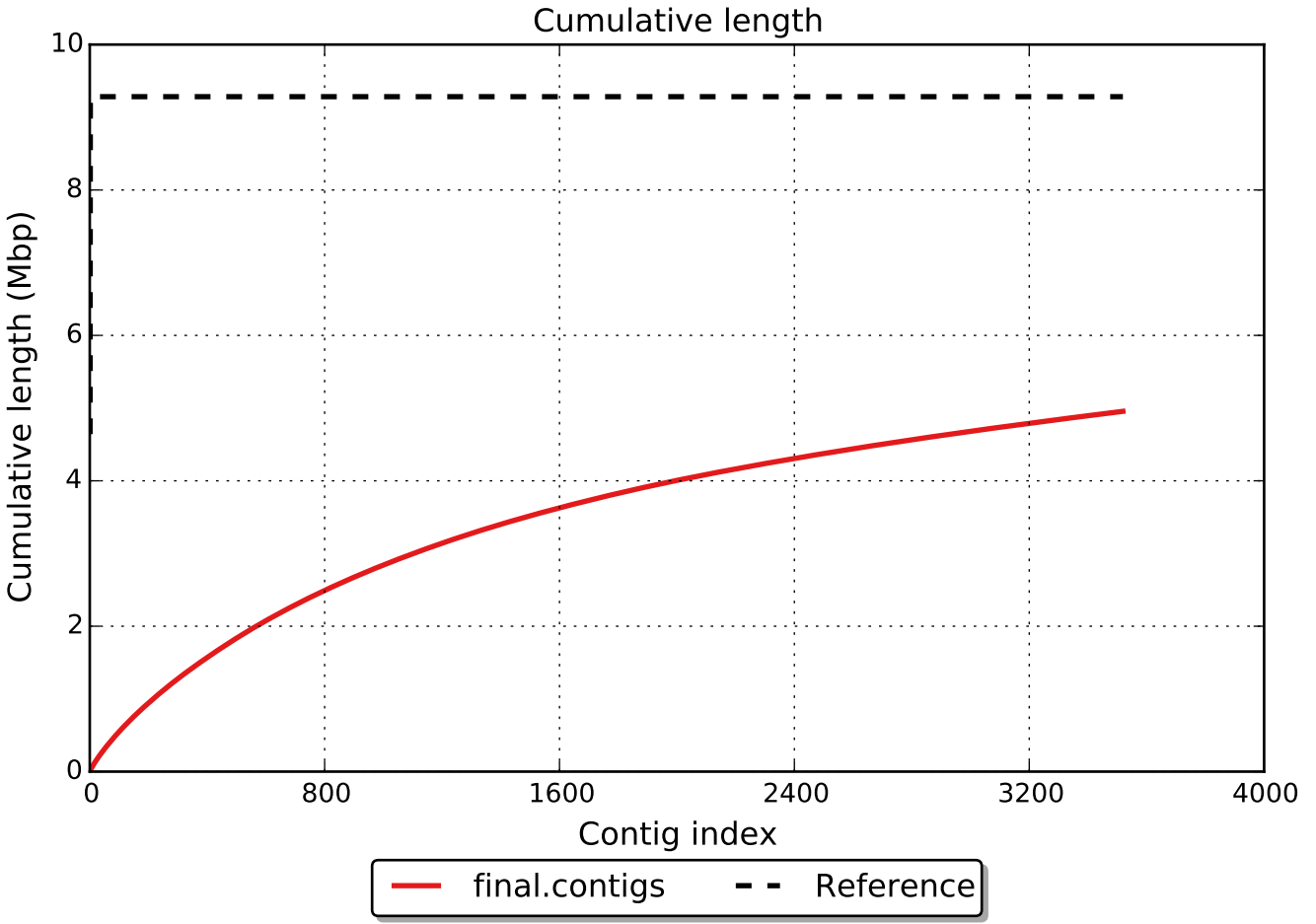
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

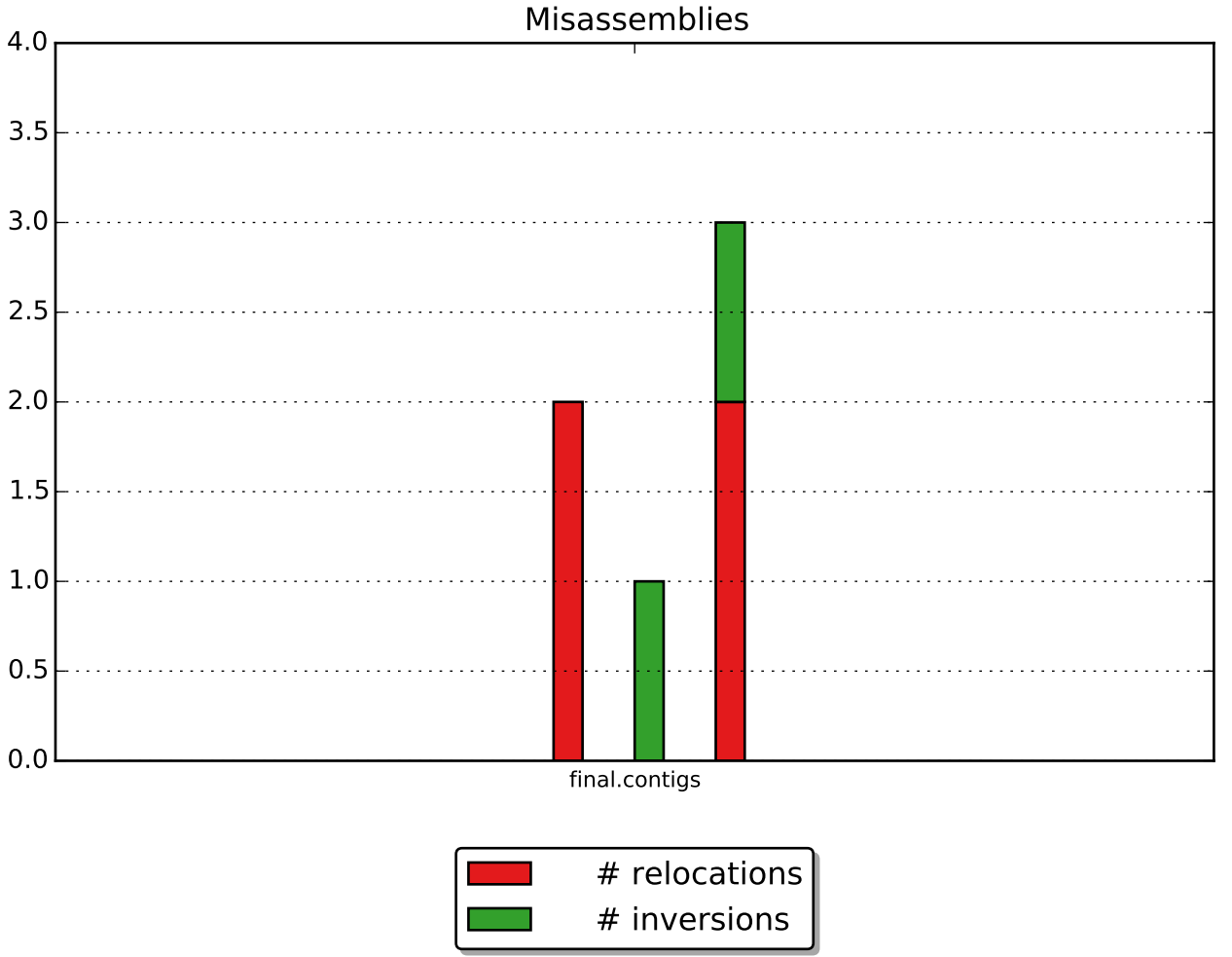
Unaligned report

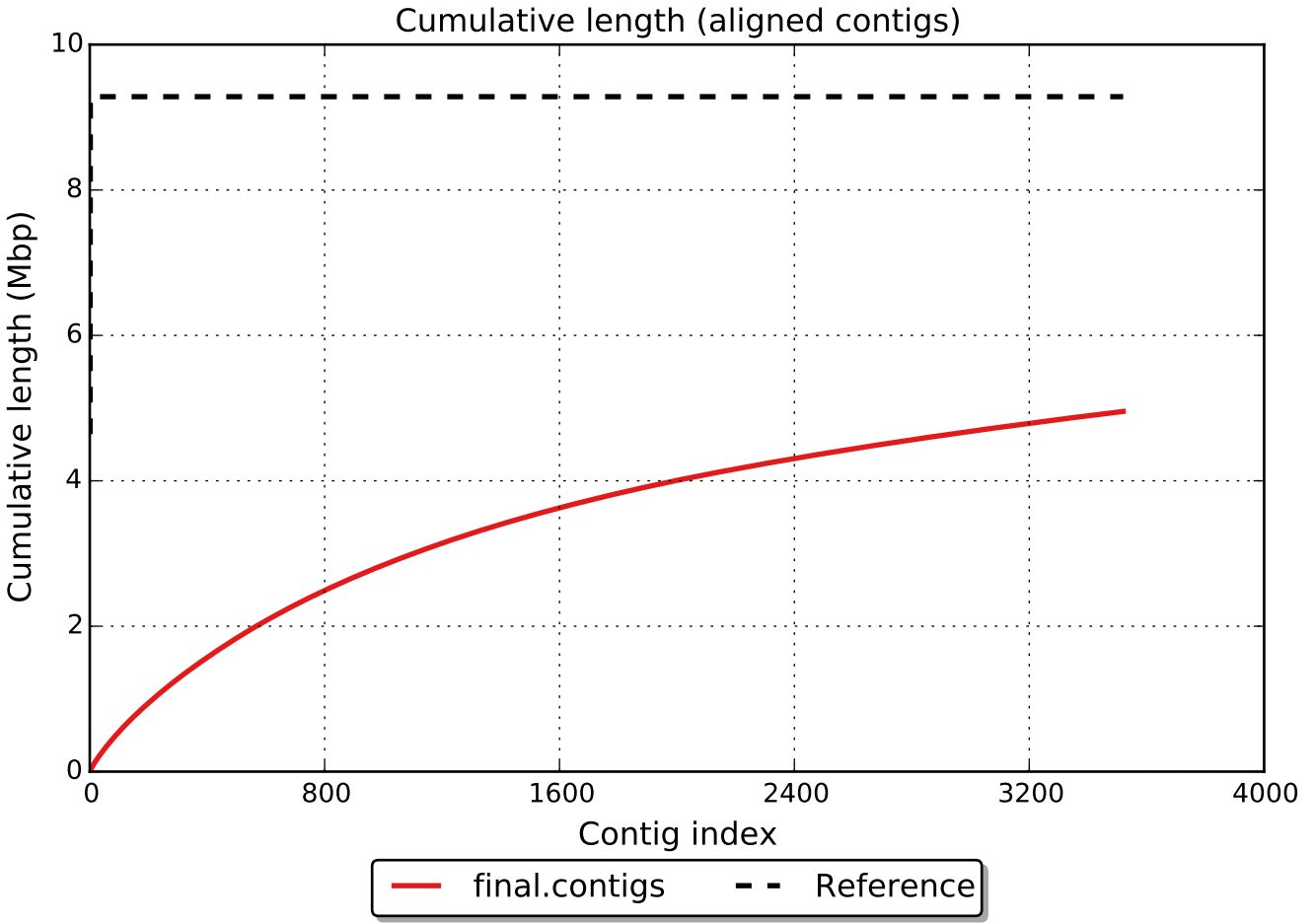
	final.contigs
# fully unaligned contigs	2
Fully unaligned length	1029
# partially unaligned contigs	6
# with misassembly	0
# both parts are significant	0
Partially unaligned length	783
# N's	0

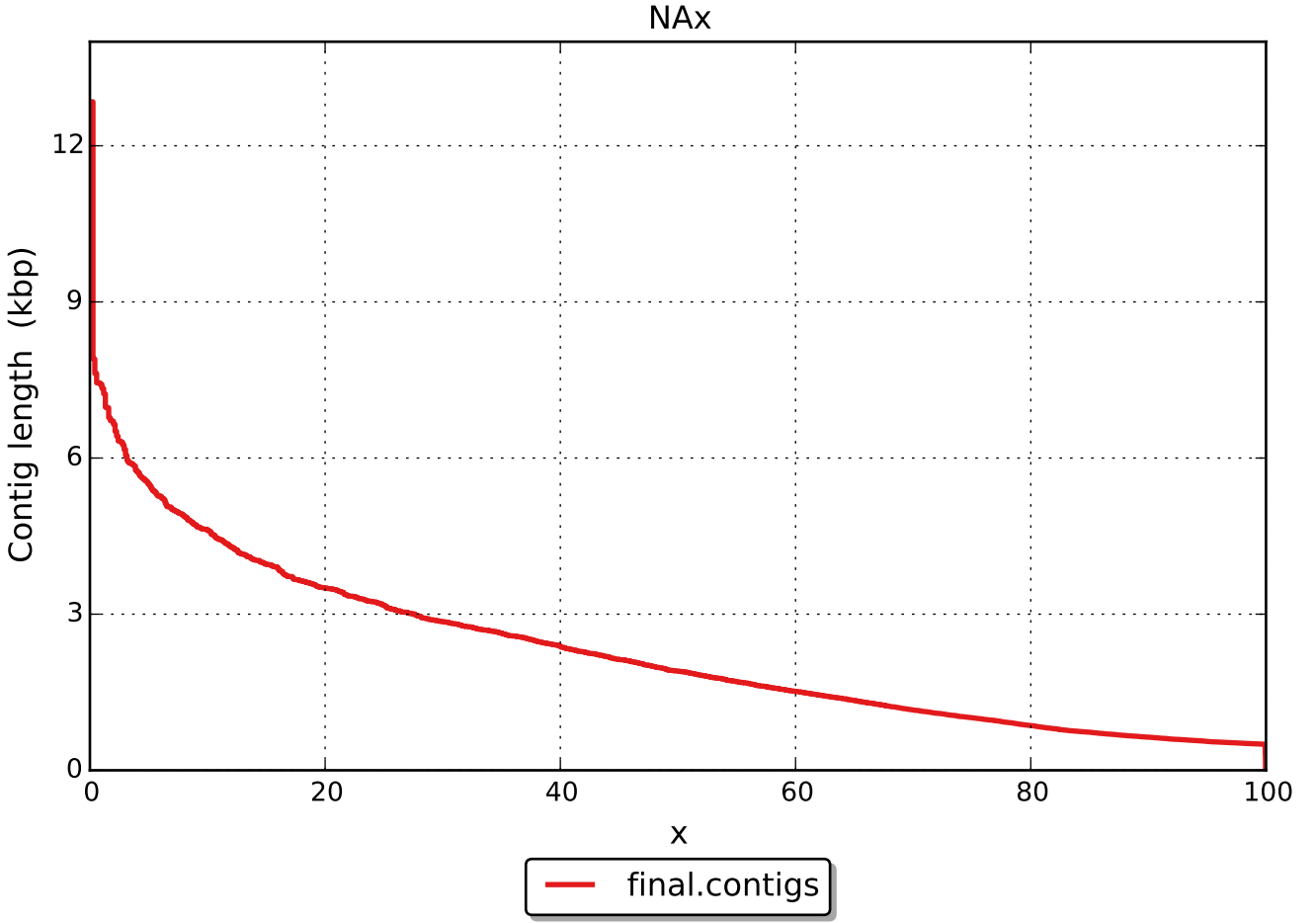
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
Contig length (kbp)
12
9
6
3
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
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
final.contigs
relocations
inversions


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)
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs