Report

	contigs
# contigs (>= 0 bp)	296
# contigs (>= 1000 bp)	123
# contigs (>= 5000 bp)	90
# contigs (>= 10000 bp)	86
# contigs (>= 25000 bp)	76
# contigs (>= 50000 bp)	60
Total length (>= 0 bp)	9085165
Total length (>= 1000 bp)	9015877
Total length (>= 5000 bp)	8952166
Total length (>= 10000 bp)	8919890
Total length (>= 25000 bp)	8755457
Total length (>= 50000 bp)	8229377
# contigs	168
Largest contig	332068
Total length	9046735
Reference length	9283304
N50	164195
N75	87060
L50	21
L75	40
# misassemblies	2
# misassembled contigs	1
Misassembled contigs length	210680
# local misassemblies	5
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.176
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	753.19
# indels per 100 kbp	1.11
Largest alignment	332068
NA50	164195
NA75	87060
LA50	21
LA75	40

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

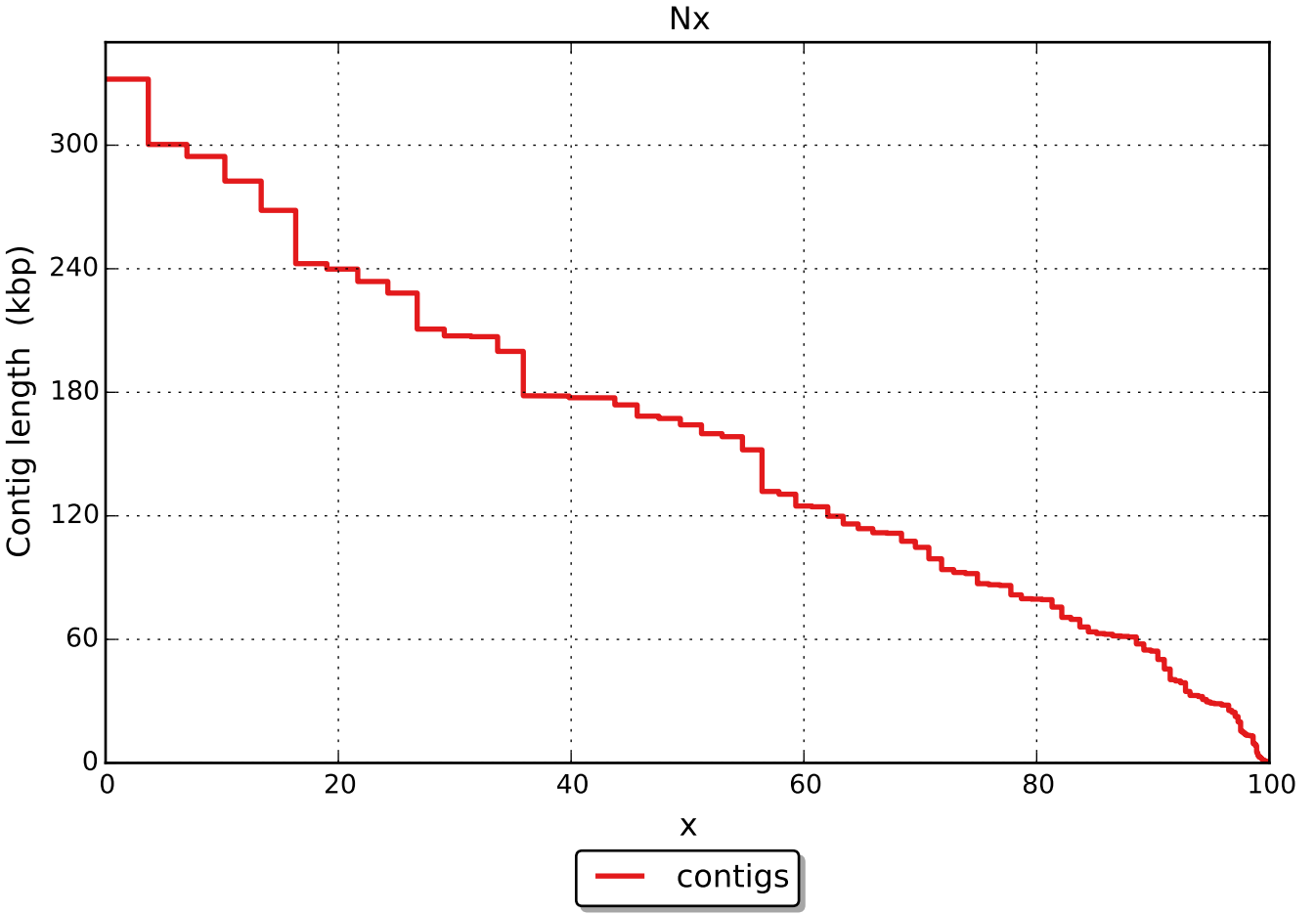
	contigs
# misassemblies	2
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	2
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	210680
# local misassemblies	5
# mismatches	68645
# indels	101
# short indels	100
# long indels	1
Indels length	122

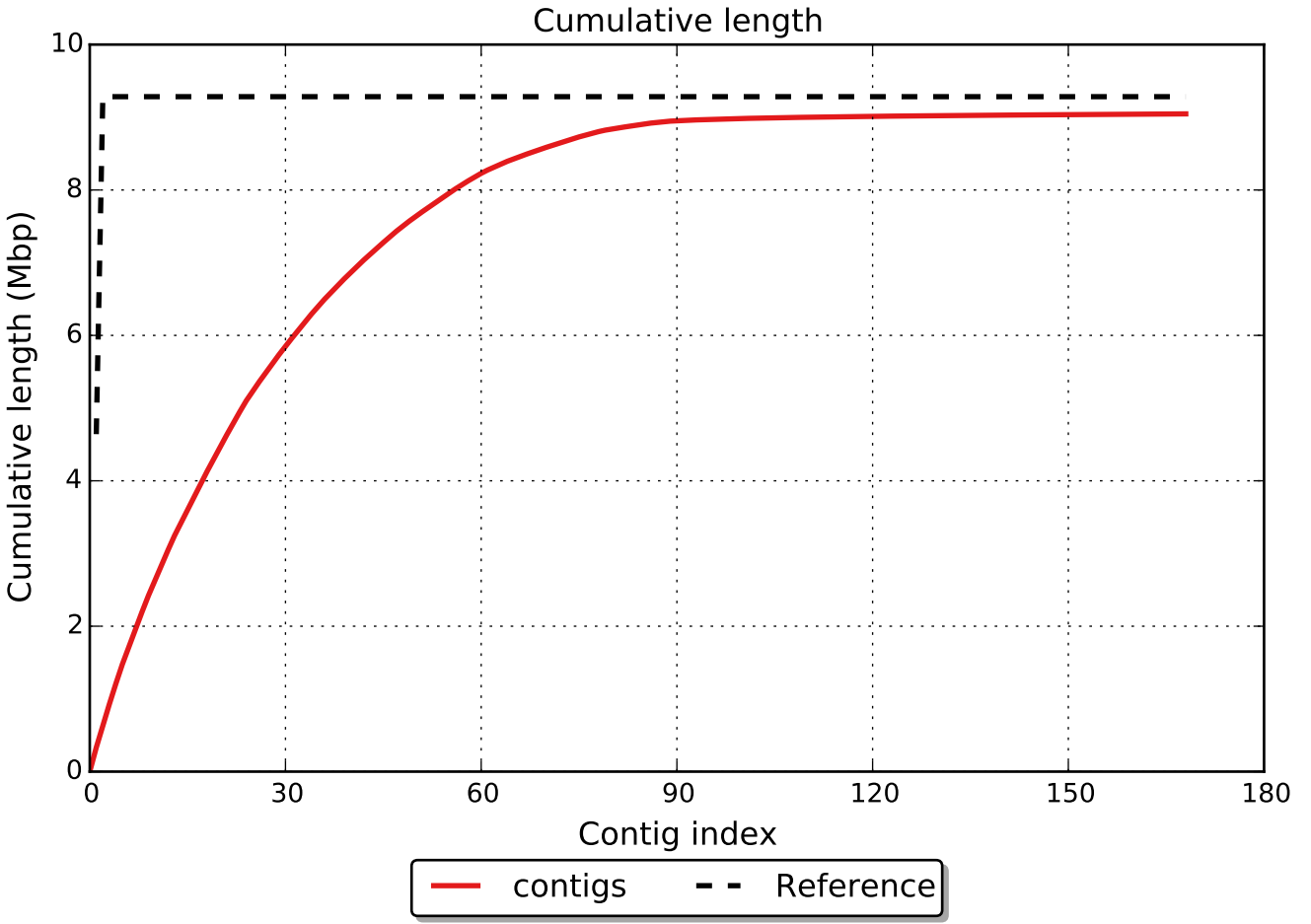
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

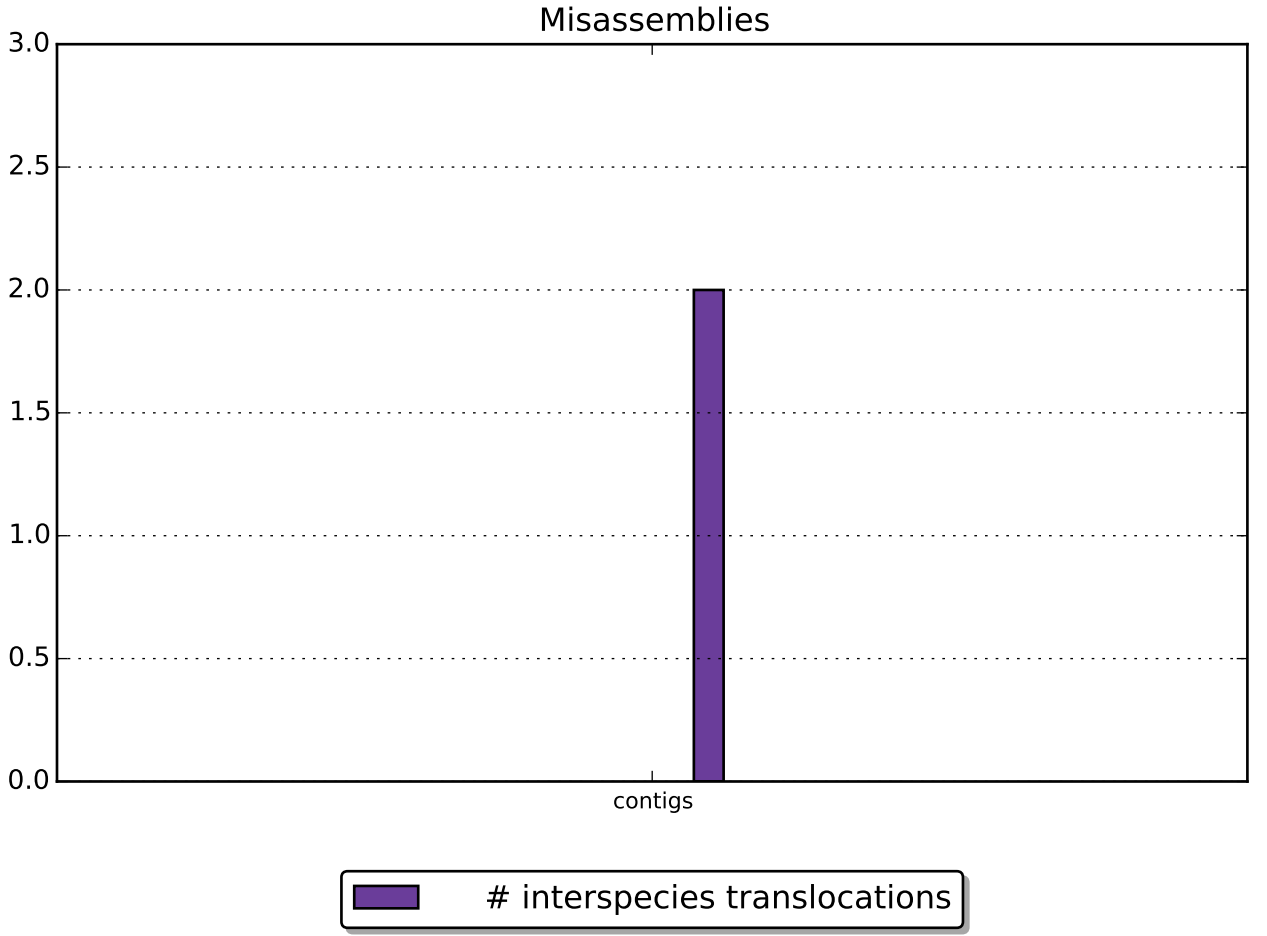
Unaligned report

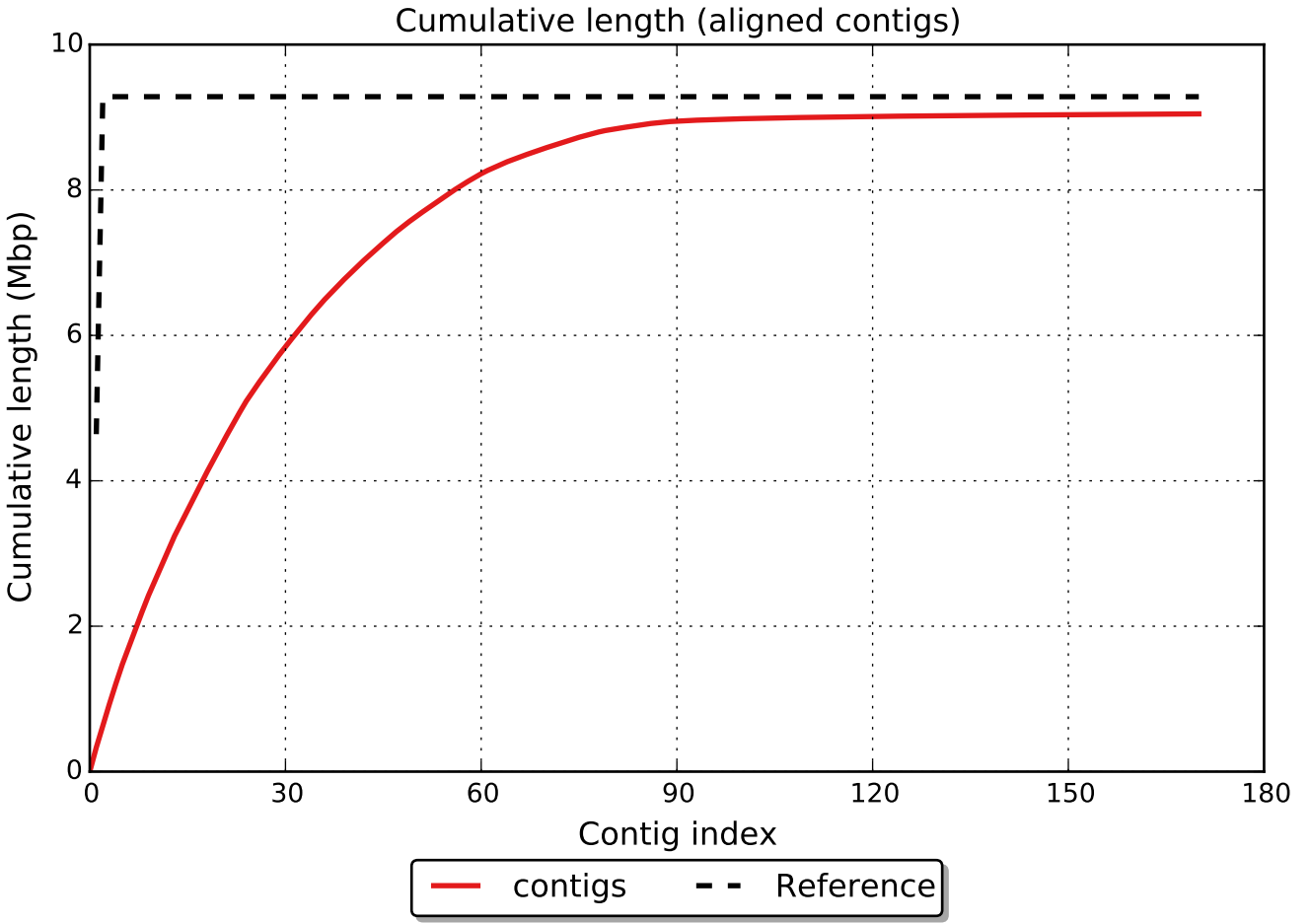
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

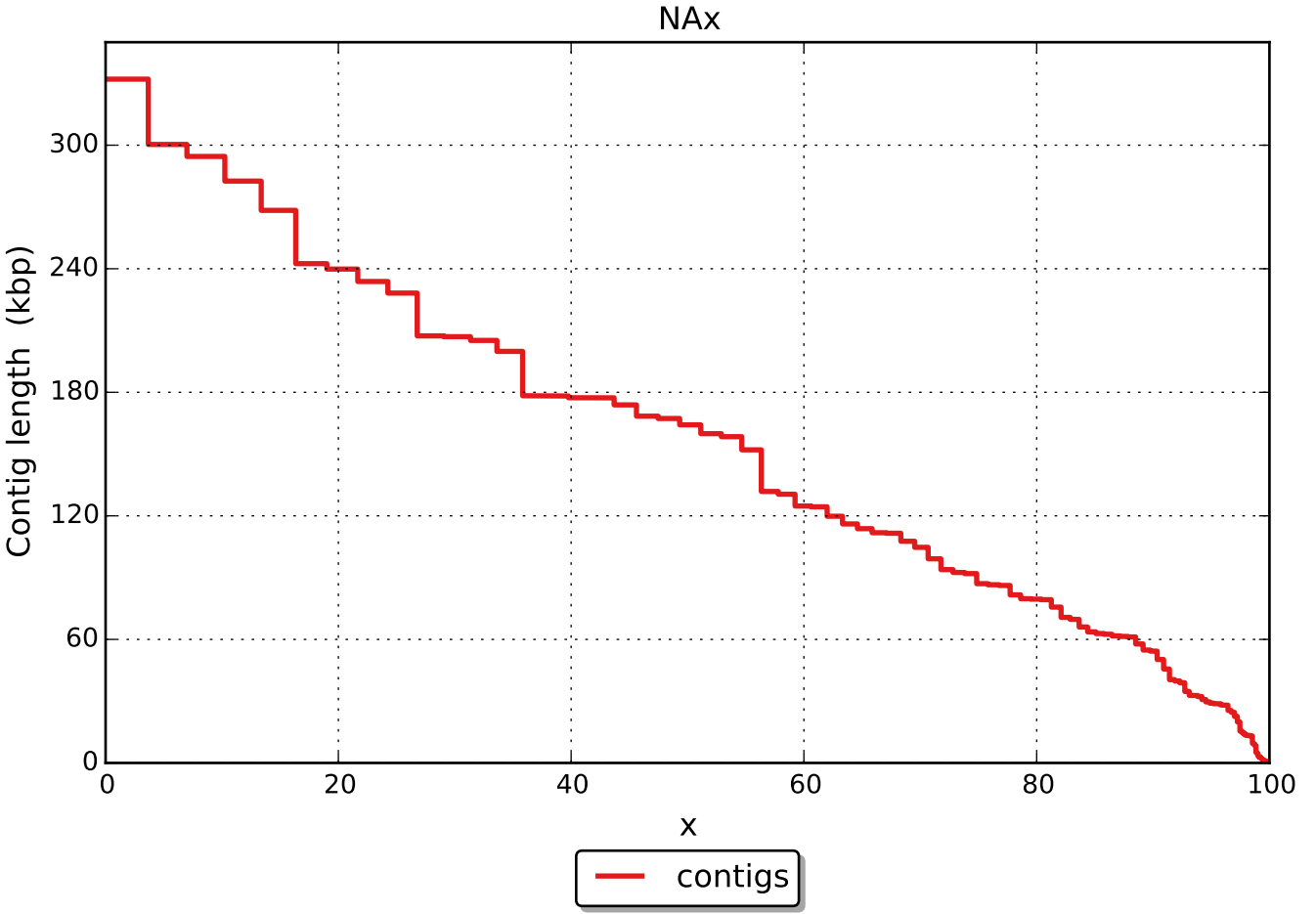
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs


Cumulative length
Cumulative length (Mbp)
10
8
6
4
2
0
0
30
60
90
120
150
180
Contig index
contigs
Reference


Misassemblies
3.0
2.5
2.0
1.5
1.0
0.5
0.0
contigs
interspecies translocations


Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
2
4
6
8
10
0
30
60
90
120
150
180
contigs
Reference


NAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs