Report

	scaffolds
# contigs (>= 0 bp)	2779
# contigs (>= 1000 bp)	1575
# contigs (>= 5000 bp)	119
# contigs (>= 10000 bp)	3
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4574218
Total length (>= 1000 bp)	3924493
Total length (>= 5000 bp)	764485
Total length (>= 10000 bp)	38155
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2212
Largest contig	13882
Total length	4391106
Reference length	4641652
N50	2615
N75	1537
L50	529
L75	1076
# misassemblies	25
# misassembled contigs	24
Misassembled contigs length	80849
# local misassemblies	5
# unaligned contigs	2 + 24 part
Unaligned length	4872
Genome fraction (%)	93.088
Duplication ratio	1.015
# N's per 100 kbp	18.65
# mismatches per 100 kbp	680.68
# indels per 100 kbp	12.06
Largest alignment	13882
NA50	2588
NA75	1521
LA50	534
LA75	1089

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).
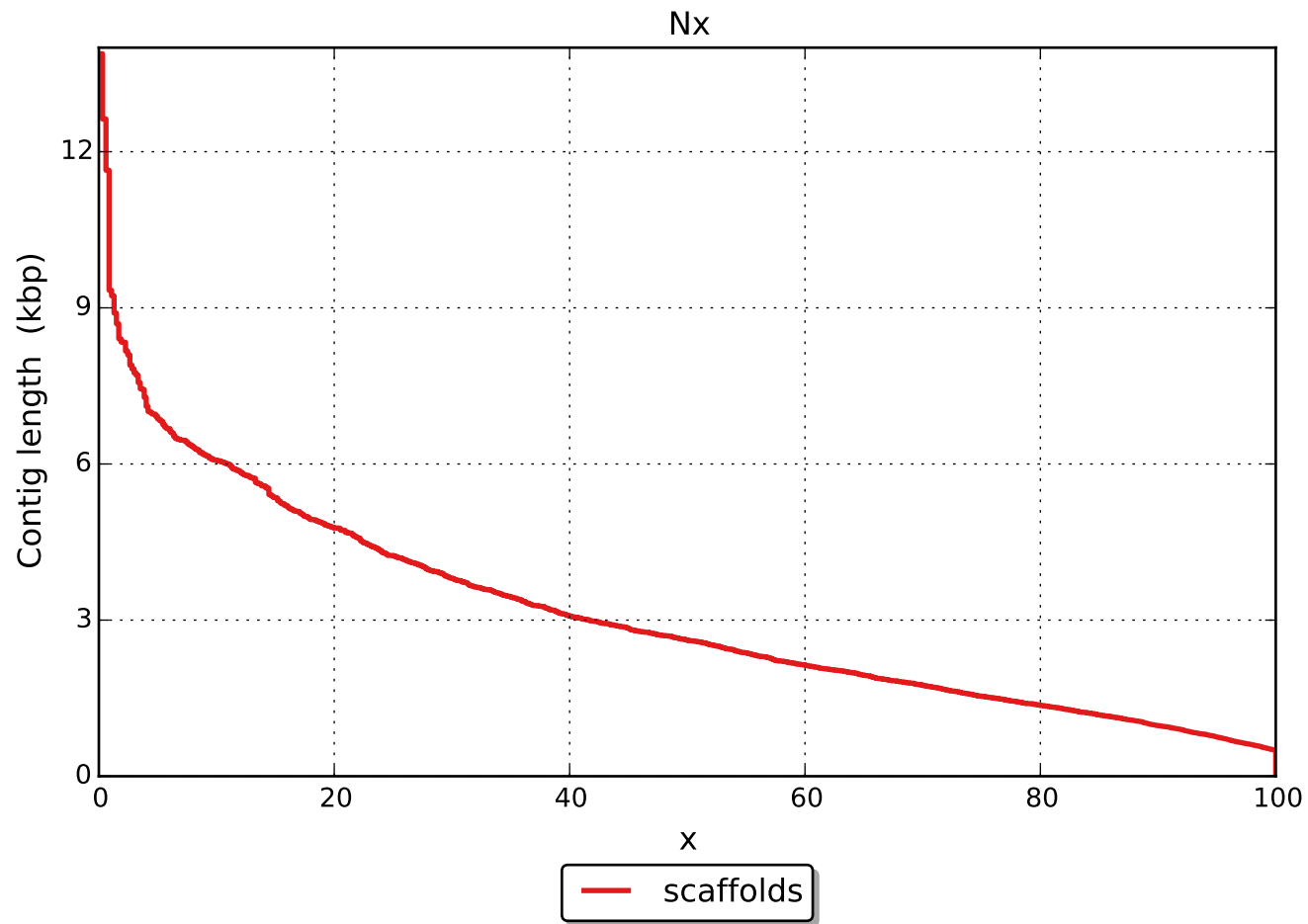
Misassemblies report

|	scaffolds
# misassemblies	25
# relocations	25
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	1
# misassembled contigs	24
Misassembled contigs length	80849
# local misassemblies	5
# mismatches	29411
# indels	521
# short indels	474
# long indels	47
Indels length	1402

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).
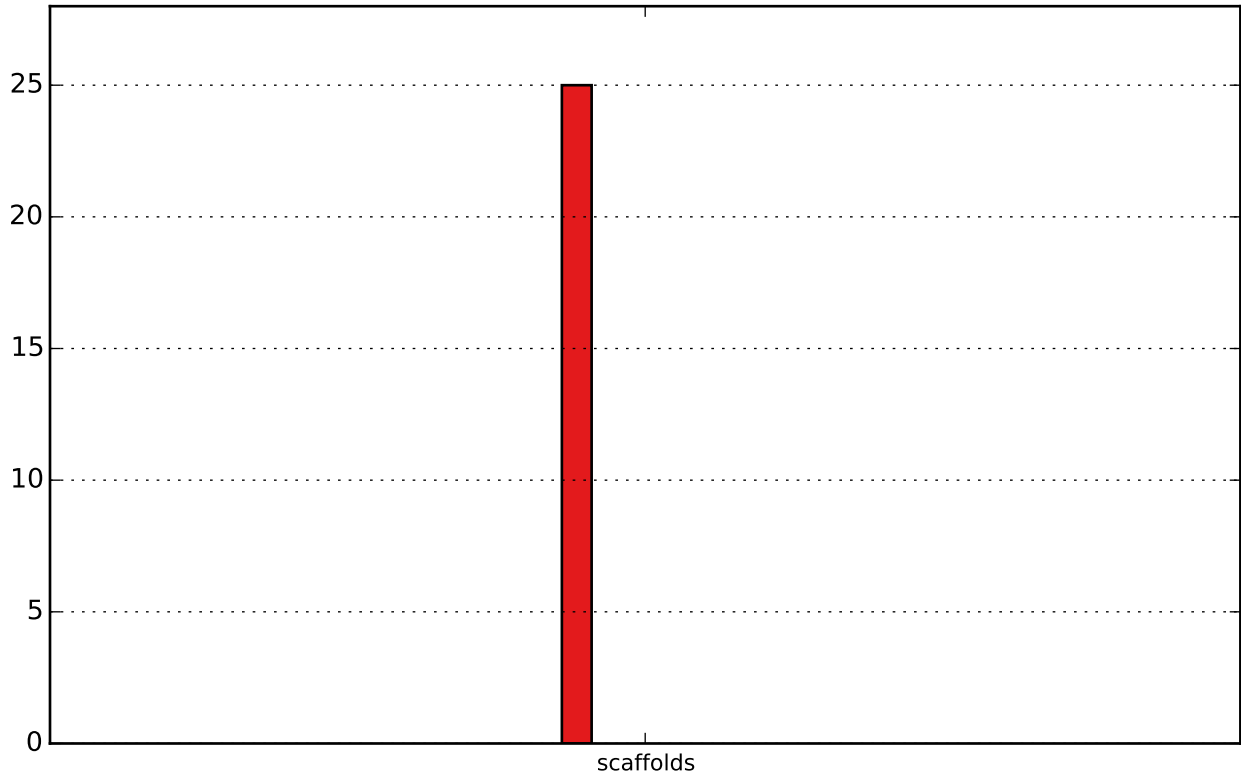
Unaligned report

	scaffolds
# fully unaligned contigs	2
Fully unaligned length	2345
# partially unaligned contigs	24
# with misassembly	0
# both parts are significant	1
Partially unaligned length	2527
# N's	819

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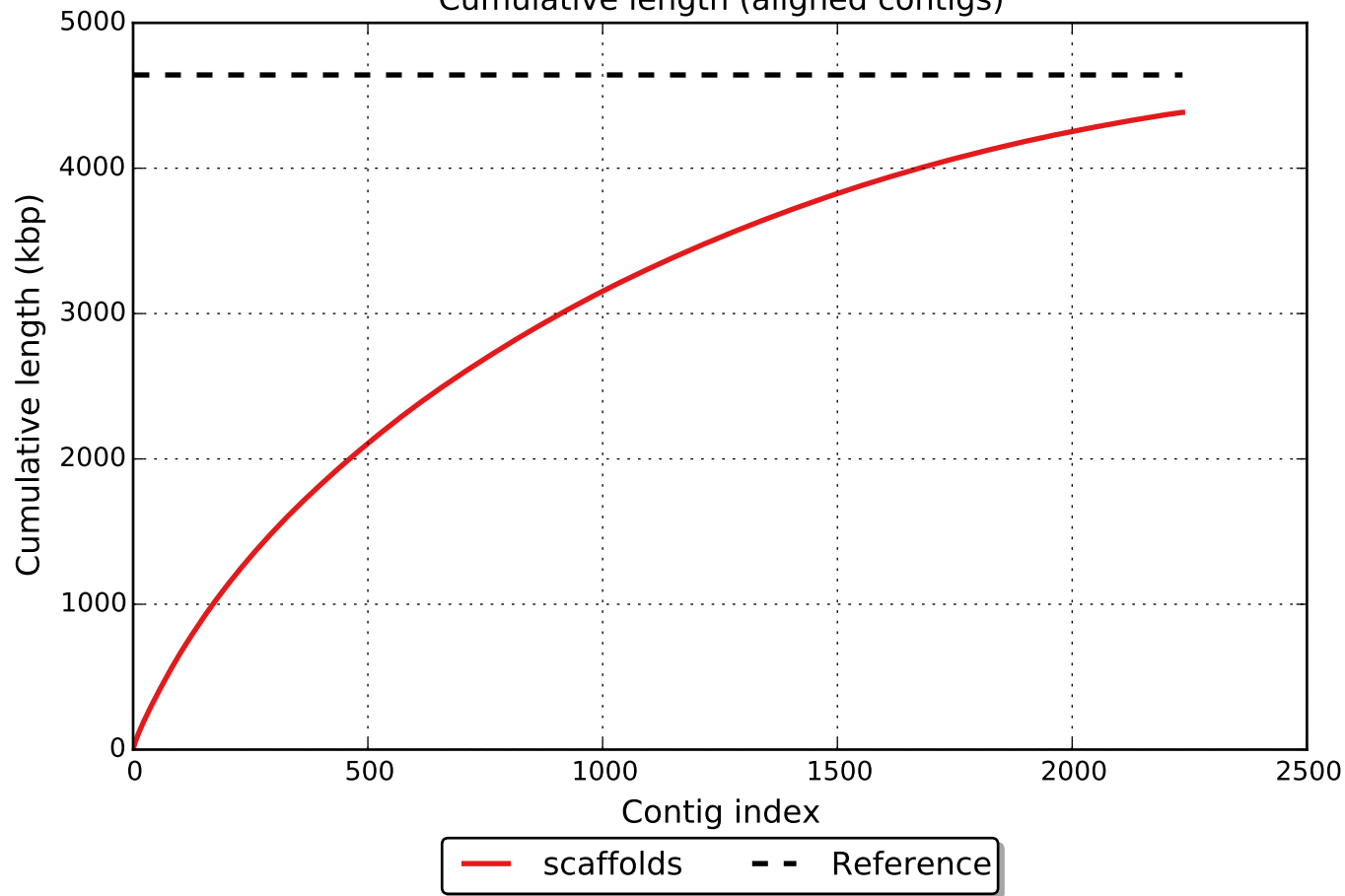(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
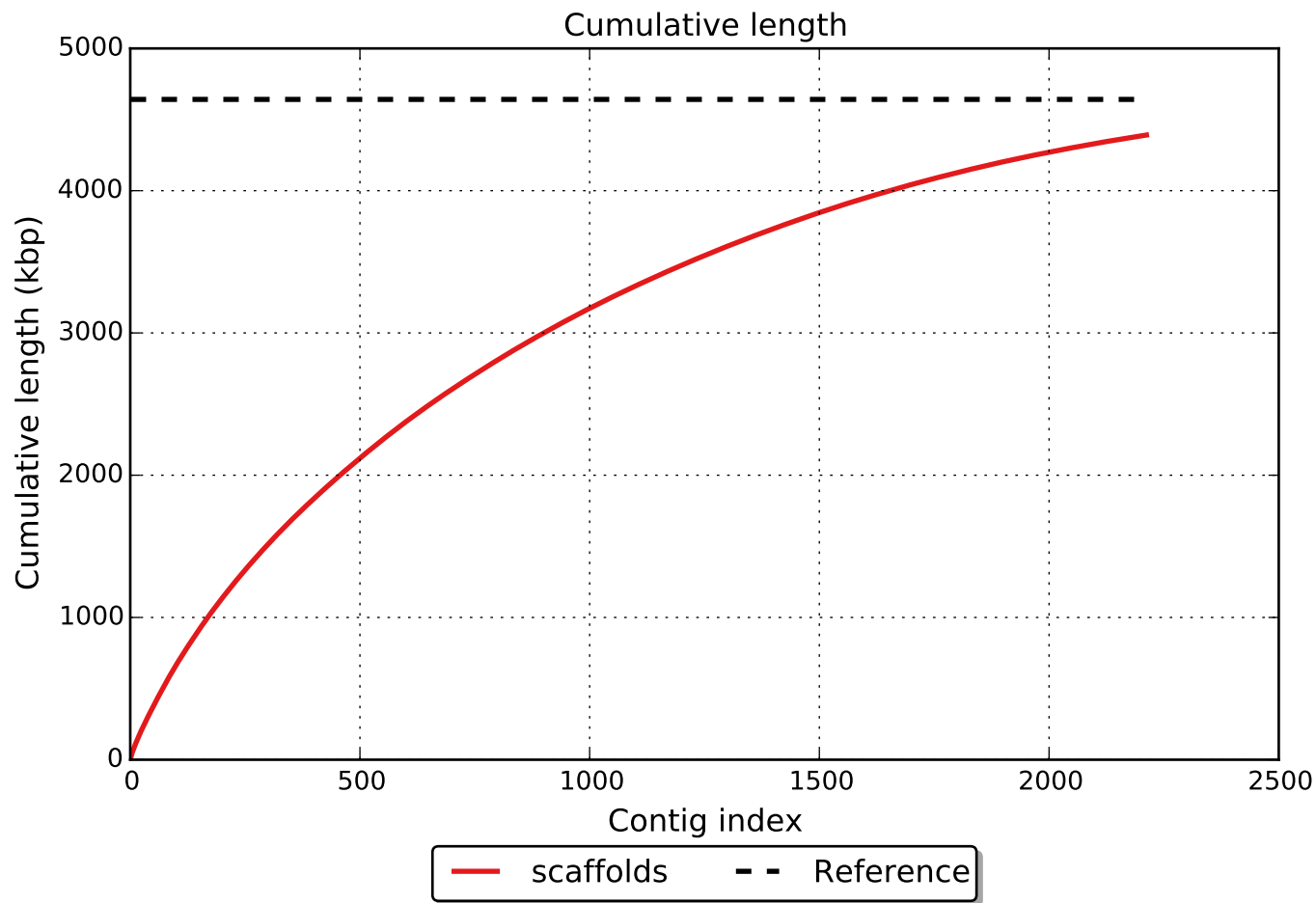
Cumulative length

Misassemblies

Cumulative length (aligned contigs)