

Report

	scaffolds
# contigs (≥ 0 bp)	416
# contigs (≥ 1000 bp)	364
# contigs (≥ 5000 bp)	241
# contigs (≥ 10000 bp)	154
# contigs (≥ 25000 bp)	41
# contigs (≥ 50000 bp)	9
Total length (≥ 0 bp)	4482744
Total length (≥ 1000 bp)	4454441
Total length (≥ 5000 bp)	4103011
Total length (≥ 10000 bp)	3446895
Total length (≥ 25000 bp)	1653950
Total length (≥ 50000 bp)	574446
# contigs	393
Largest contig	95483
Total length	4476694
Reference length	4641652
N50	18571
N75	10727
L50	69
L75	146
# misassemblies	7
# misassembled contigs	7
Misassembled contigs length	156454
# local misassemblies	12
# unaligned contigs	0 + 2 part
Unaligned length	531
Genome fraction (▼)	96.280
Duplication ratio	1.002
# N's per 100 kbp	267.38
# mismatches per 100 kbp	99.51
# indels per 100 kbp	22.69
Largest alignment	95385
NA50	18206
NA75	10403
LA50	70
LA75	149

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

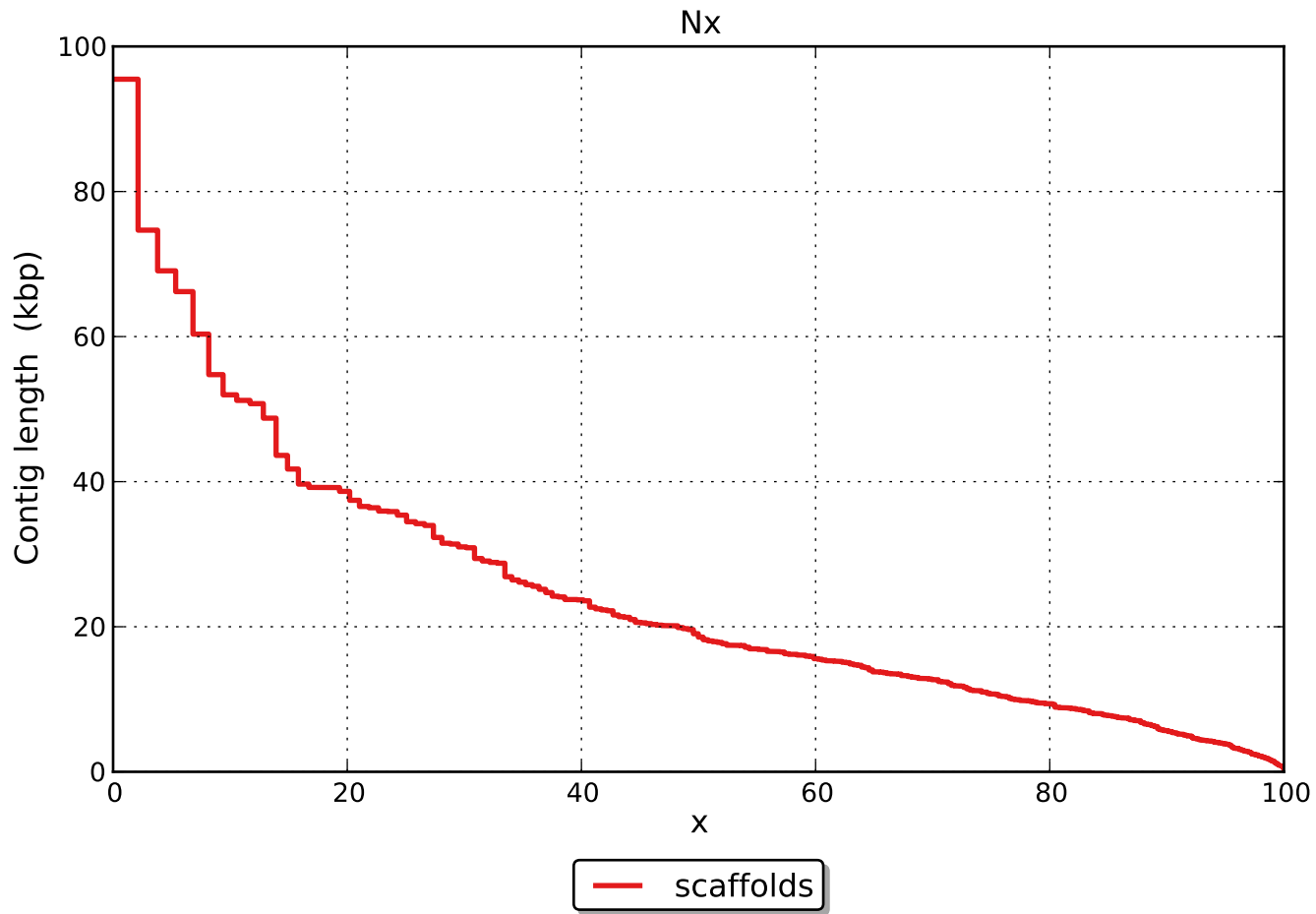
	scaffolds
# misassemblies	7
# relocations	7
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	7
Misassembled contigs length	156454
# local misassemblies	12
# mismatches	4447
# indels	1014
# short indels	683
# long indels	331
Indels length	6037

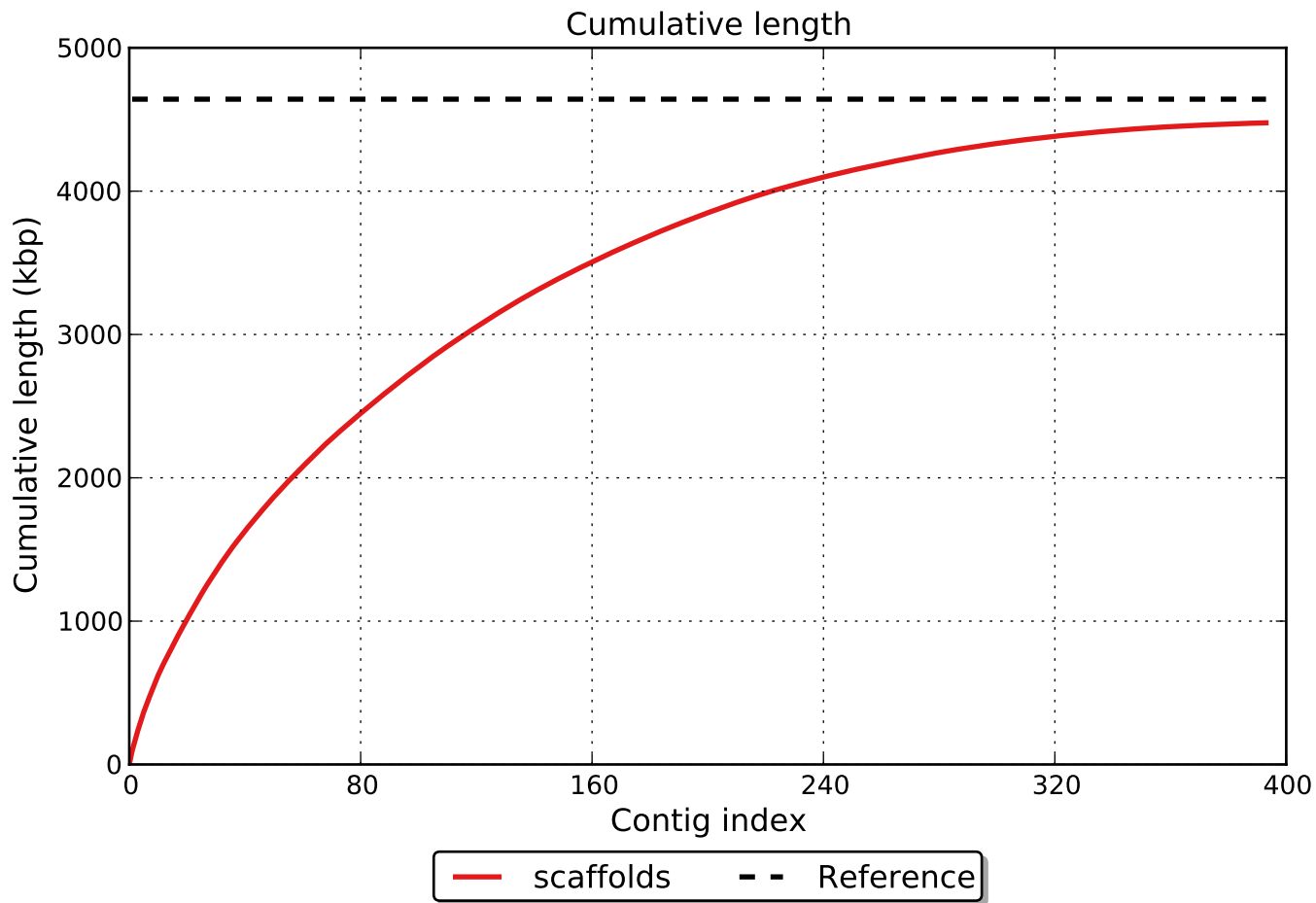
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

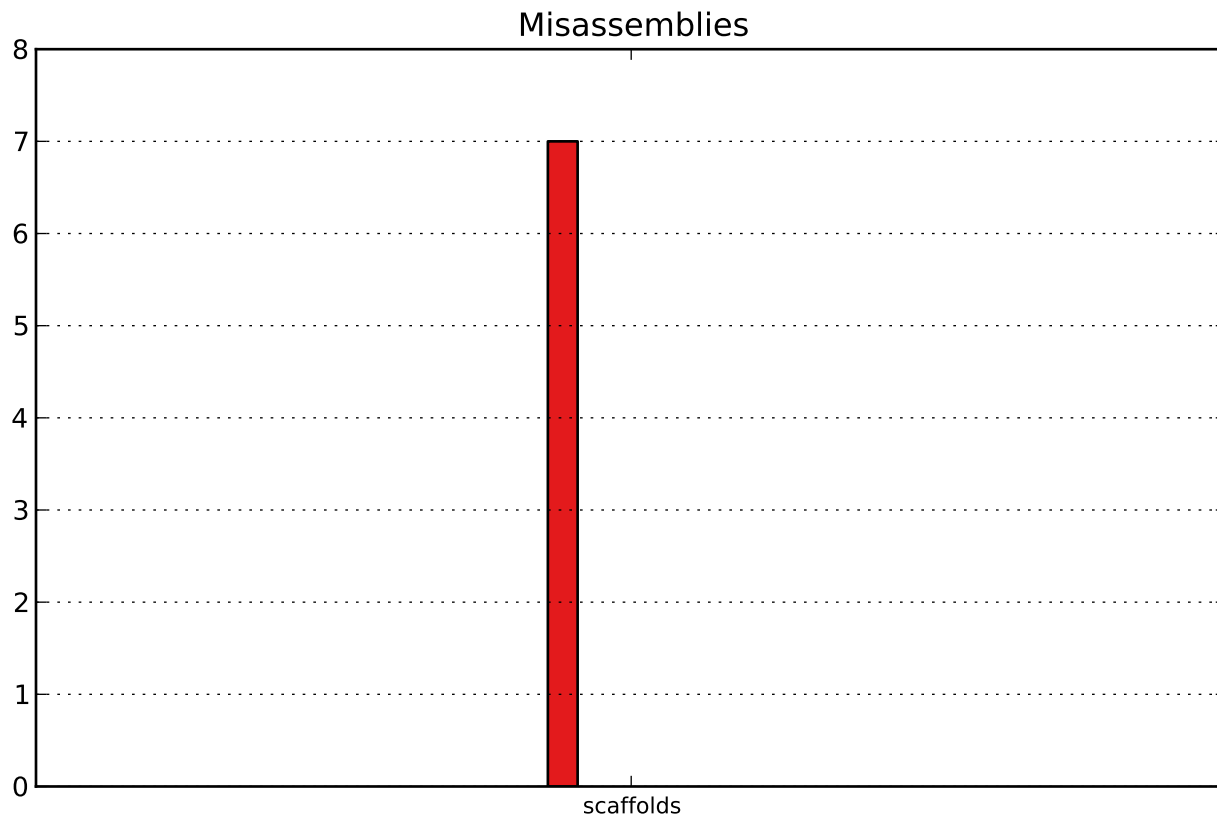
Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	531
# N's	11970

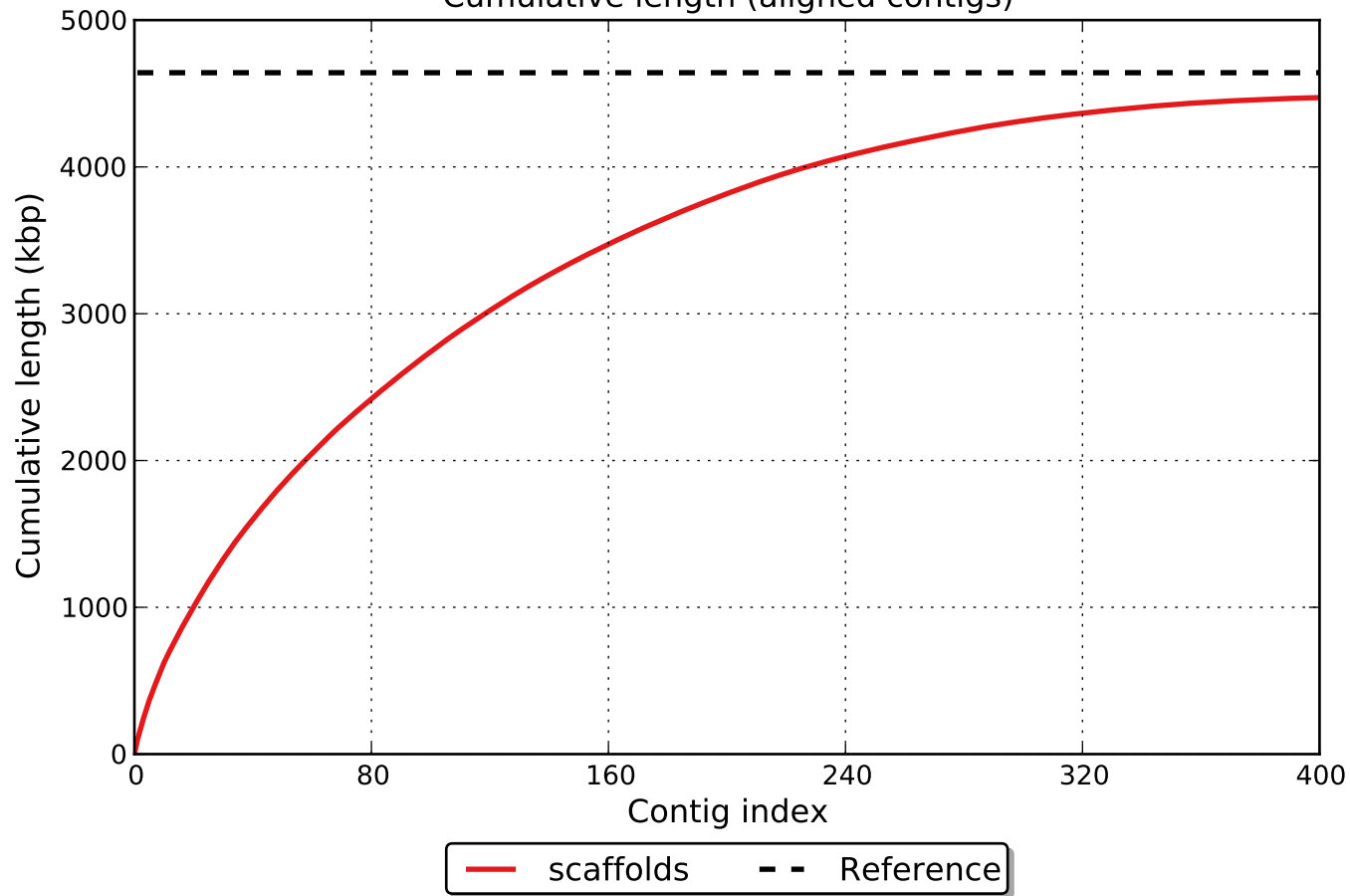
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



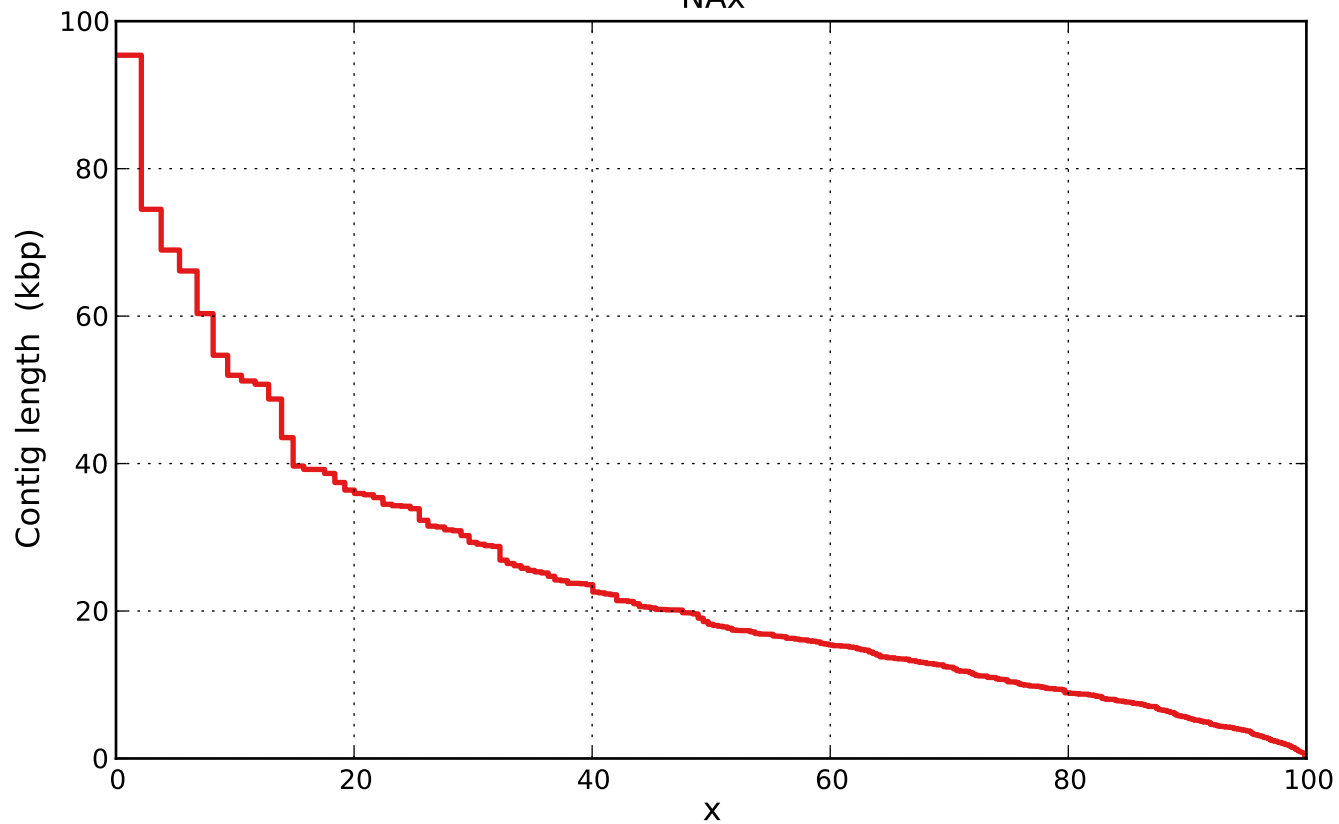




Cumulative length (aligned contigs)



NAx



— scaffolds