

Report

	scaffolds
# contigs (≥ 0 bp)	206
# contigs (≥ 1000 bp)	179
# contigs (≥ 5000 bp)	140
# contigs (≥ 10000 bp)	102
# contigs (≥ 25000 bp)	62
# contigs (≥ 50000 bp)	24
Total length (≥ 0 bp)	4547906
Total length (≥ 1000 bp)	4537084
Total length (≥ 5000 bp)	4425493
Total length (≥ 10000 bp)	4123960
Total length (≥ 25000 bp)	3462834
Total length (≥ 50000 bp)	2085767
# contigs	187
Largest contig	255476
Total length	4542889
Reference length	4641652
N50	46912
N75	26834
L50	28
L75	60
# misassemblies	14
# misassembled contigs	13
Misassembled contigs length	613325
# local misassemblies	7
# unaligned contigs	0 + 2 part
Unaligned length	113
Genome fraction (%)	97.767
Duplication ratio	1.001
# N's per 100 kbp	15.47
# mismatches per 100 kbp	88.63
# indels per 100 kbp	10.36
Largest alignment	255473
NA50	46087
NA75	23452
LA50	30
LA75	65

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

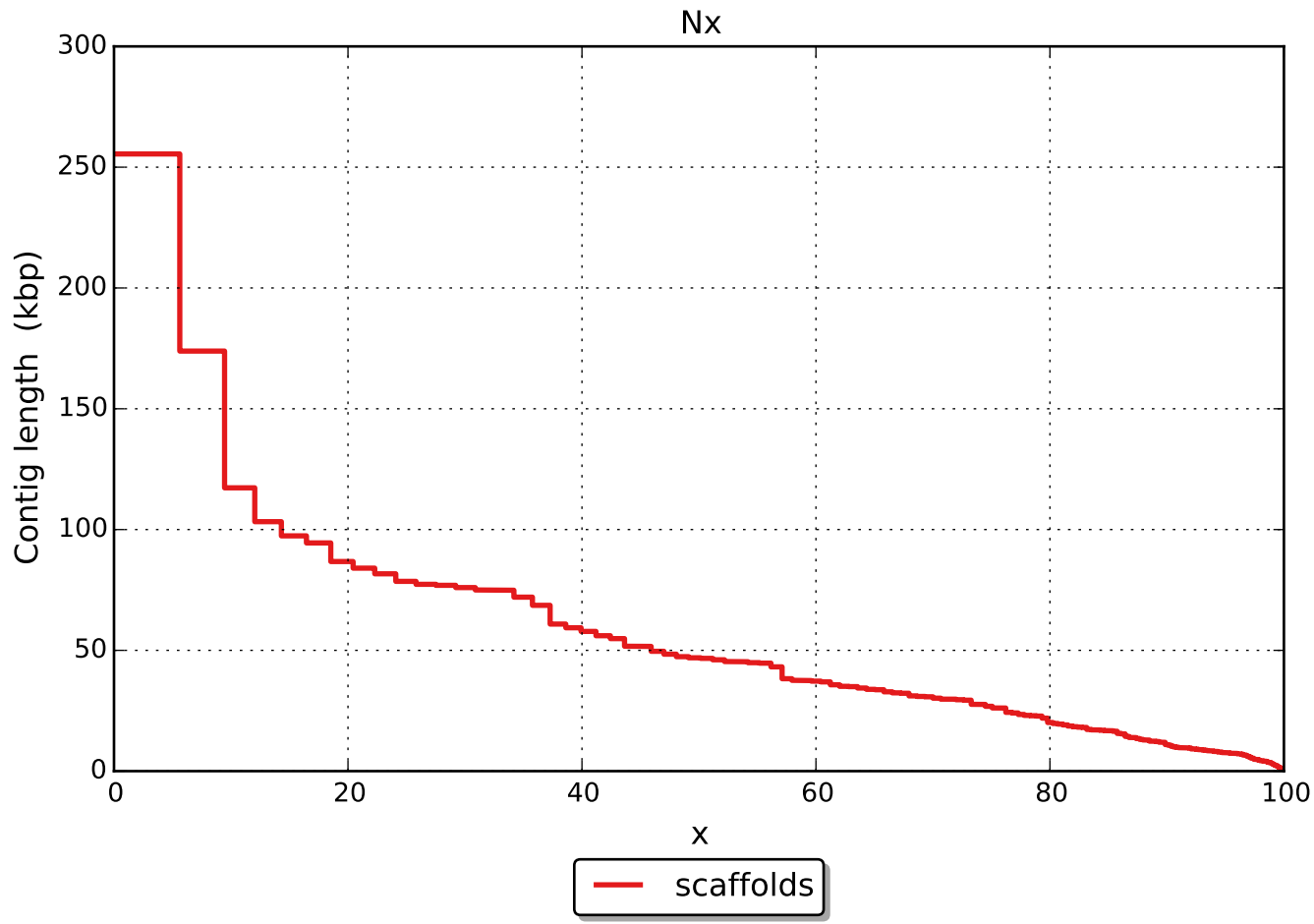
	scaffolds
# misassemblies	14
# relocations	14
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	13
Misassembled contigs length	613325
# local misassemblies	7
# mismatches	4022
# indels	470
# short indels	431
# long indels	39
Indels length	1216

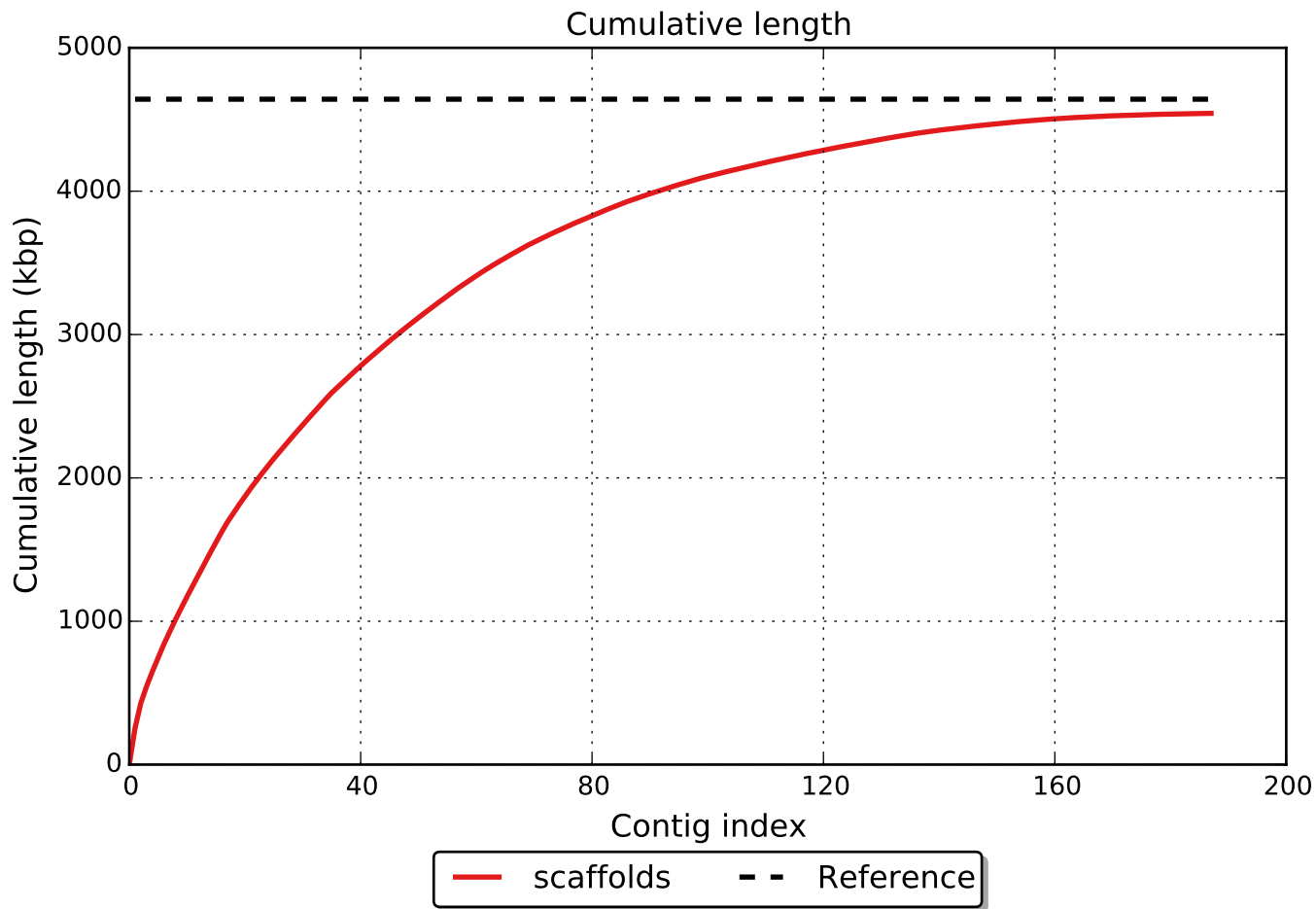
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

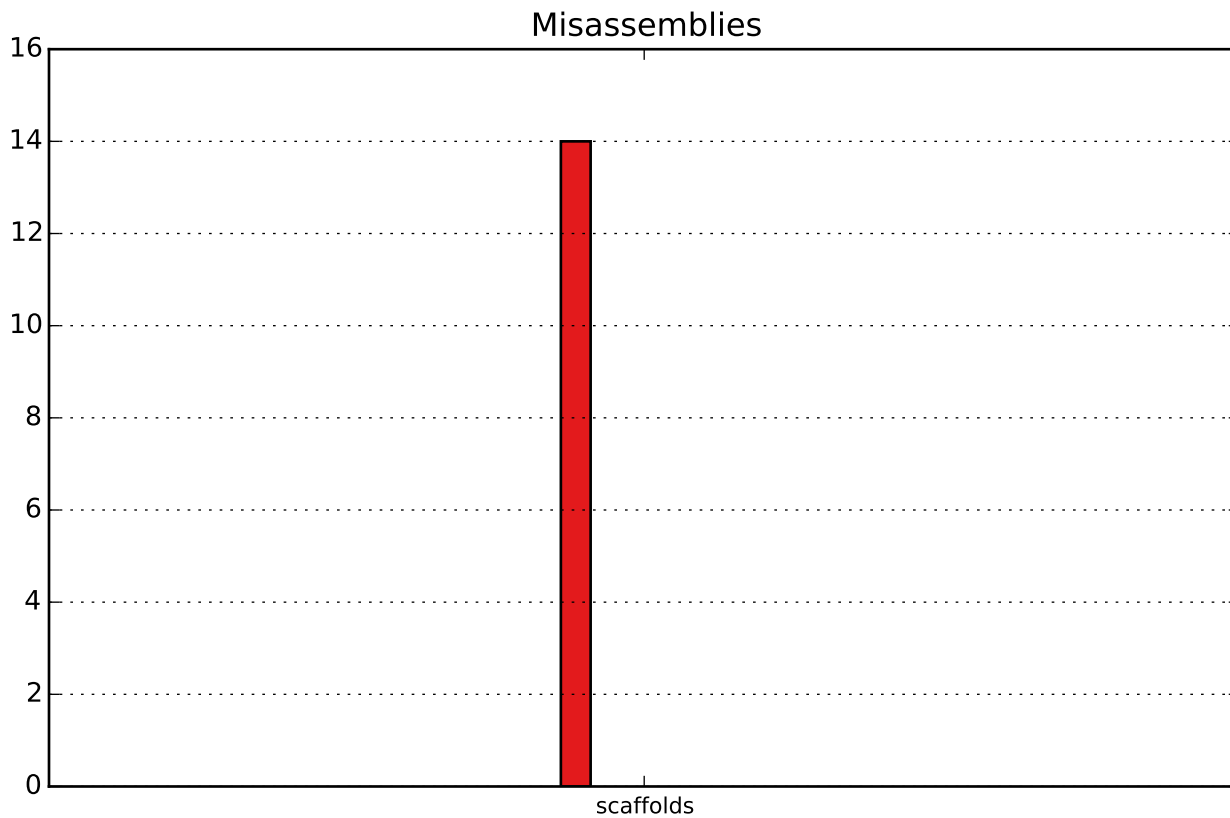
Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	113
# N's	703

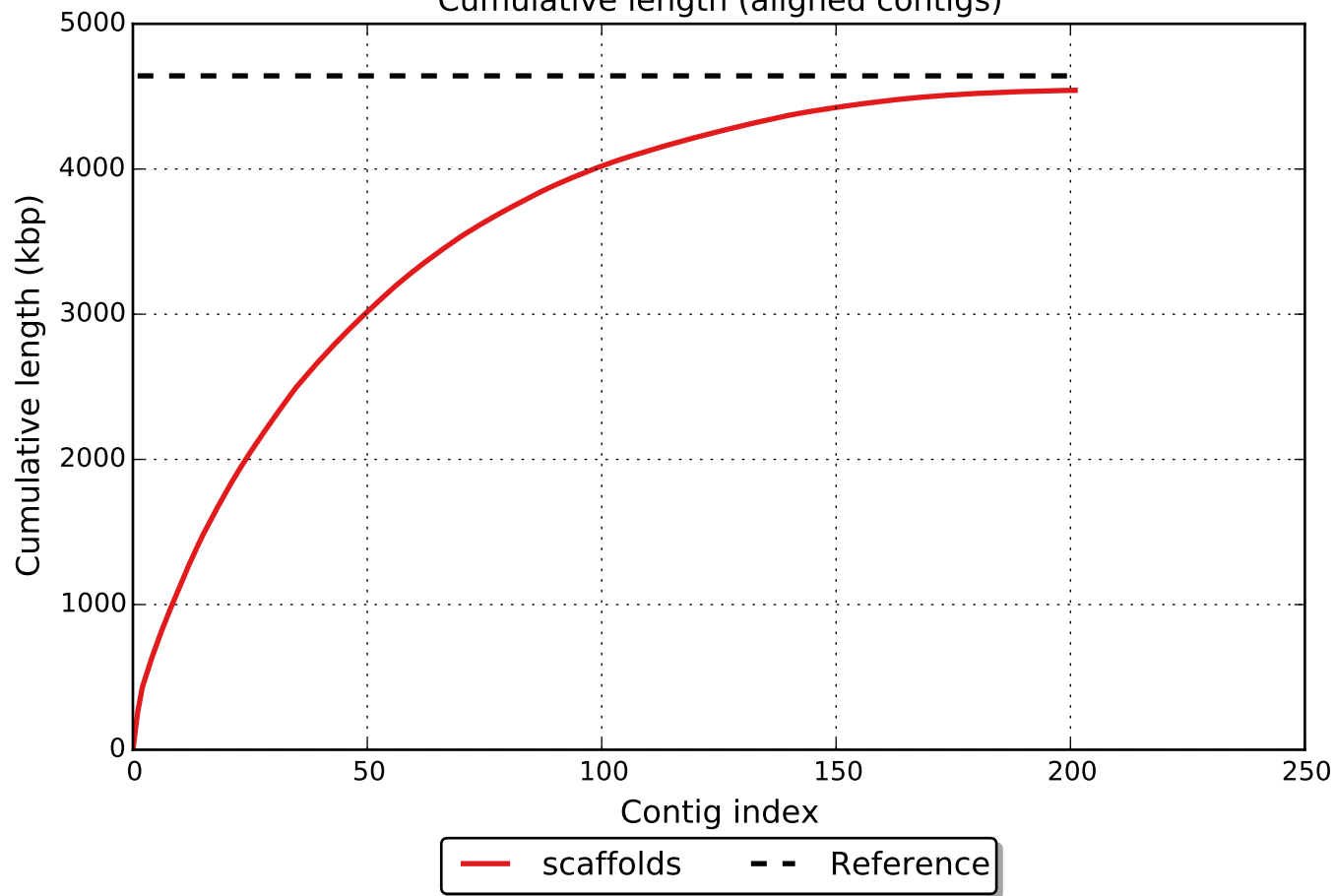
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



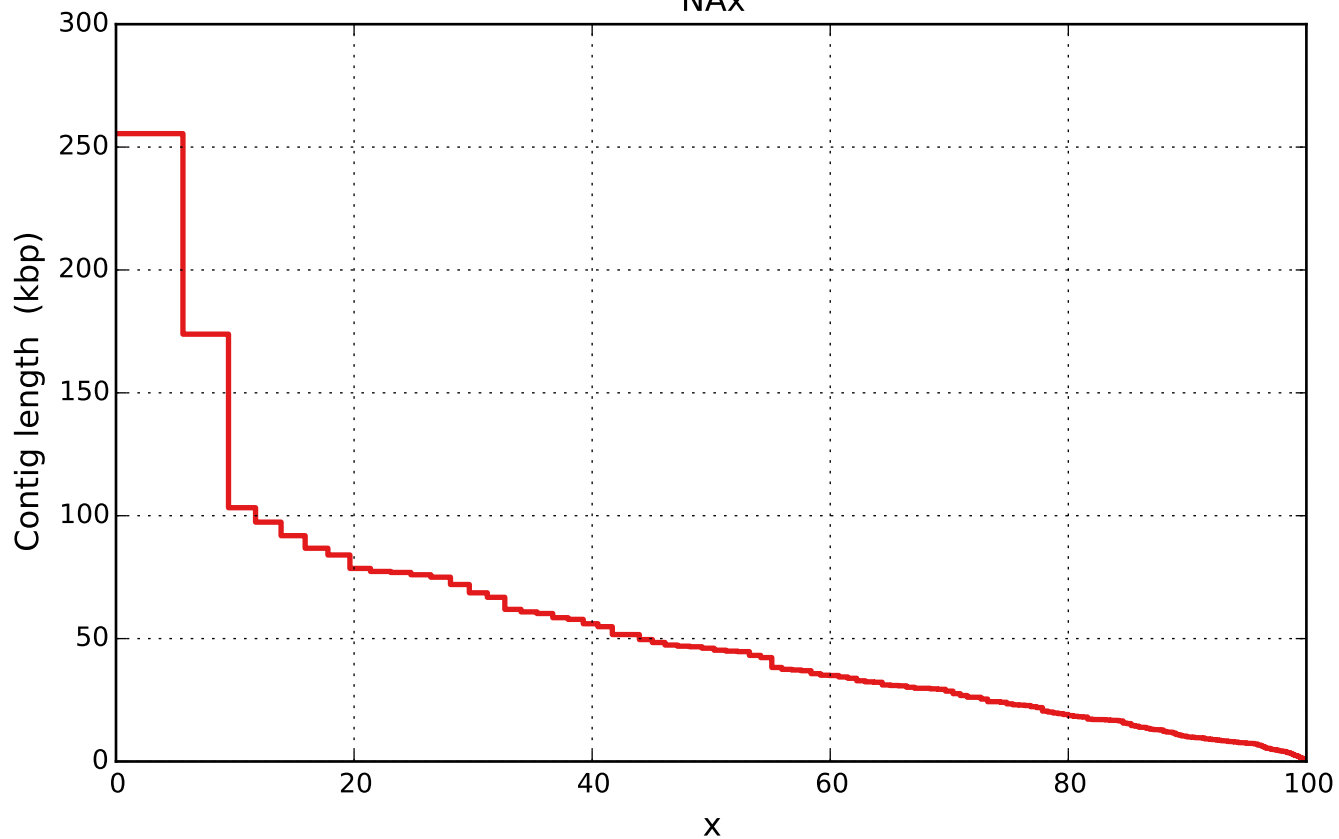




Cumulative length (aligned contigs)



NAx



— scaffolds