

Report

	scaffolds
# contigs (≥ 0 bp)	109
# contigs (≥ 1000 bp)	80
# contigs (≥ 5000 bp)	61
# contigs (≥ 10000 bp)	55
# contigs (≥ 25000 bp)	43
# contigs (≥ 50000 bp)	28
Total length (≥ 0 bp)	4561824
Total length (≥ 1000 bp)	4550585
Total length (≥ 5000 bp)	4507705
Total length (≥ 10000 bp)	4463142
Total length (≥ 25000 bp)	4275525
Total length (≥ 50000 bp)	3733992
# contigs	87
Largest contig	326979
Total length	4555927
Reference length	4641652
N50	132611
N75	60768
L50	11
L75	23
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	78666
# local misassemblies	14
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.114
Duplication ratio	1.000
# N's per 100 kbp	6.21
# mismatches per 100 kbp	62.82
# indels per 100 kbp	8.08
Largest alignment	326979
NA50	132611
NA75	60768
LA50	11
LA75	23

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	2
# relocations	2
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	78666
# local misassemblies	14
# mismatches	2861
# indels	368
# short indels	364
# long indels	4
Indels length	686

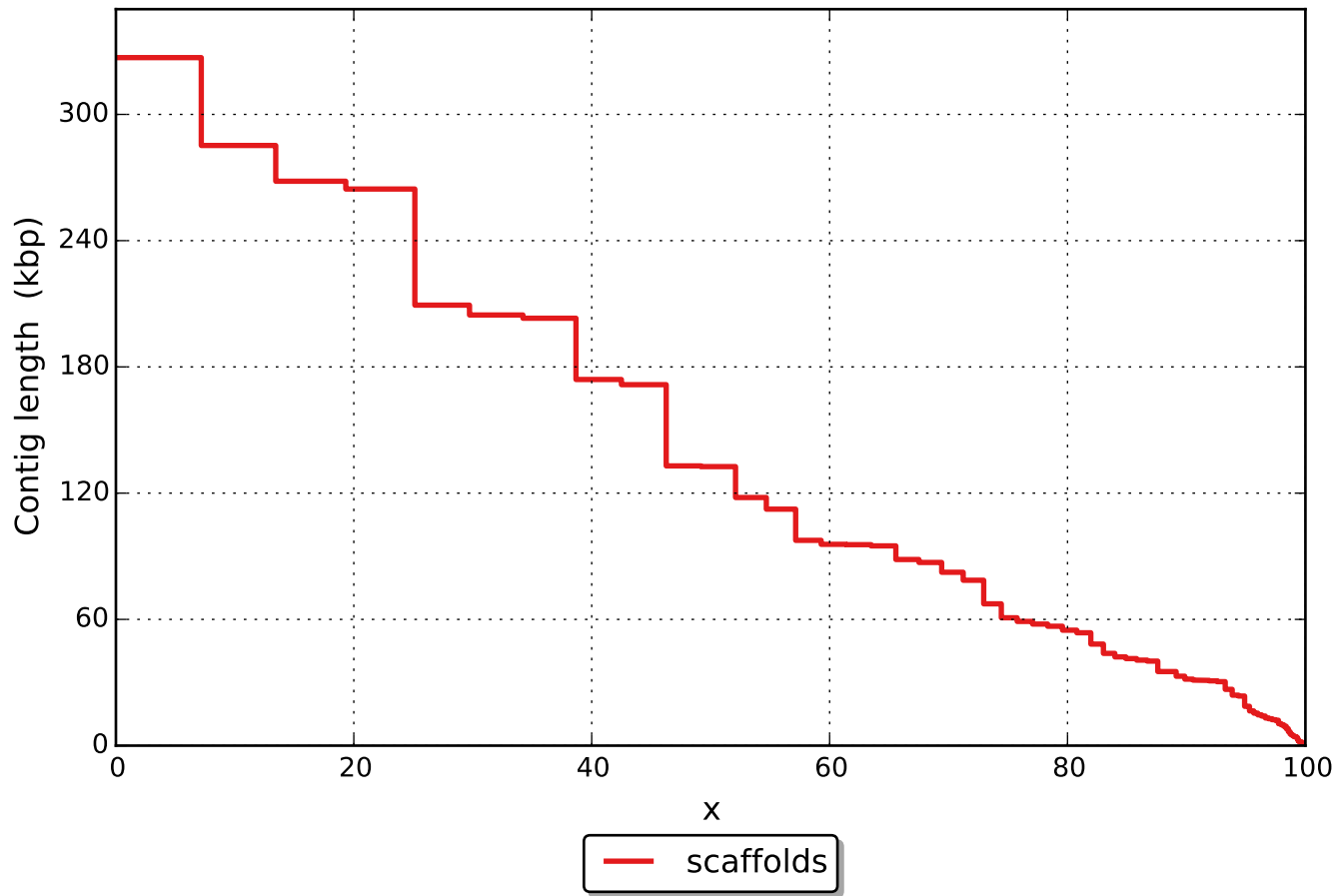
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

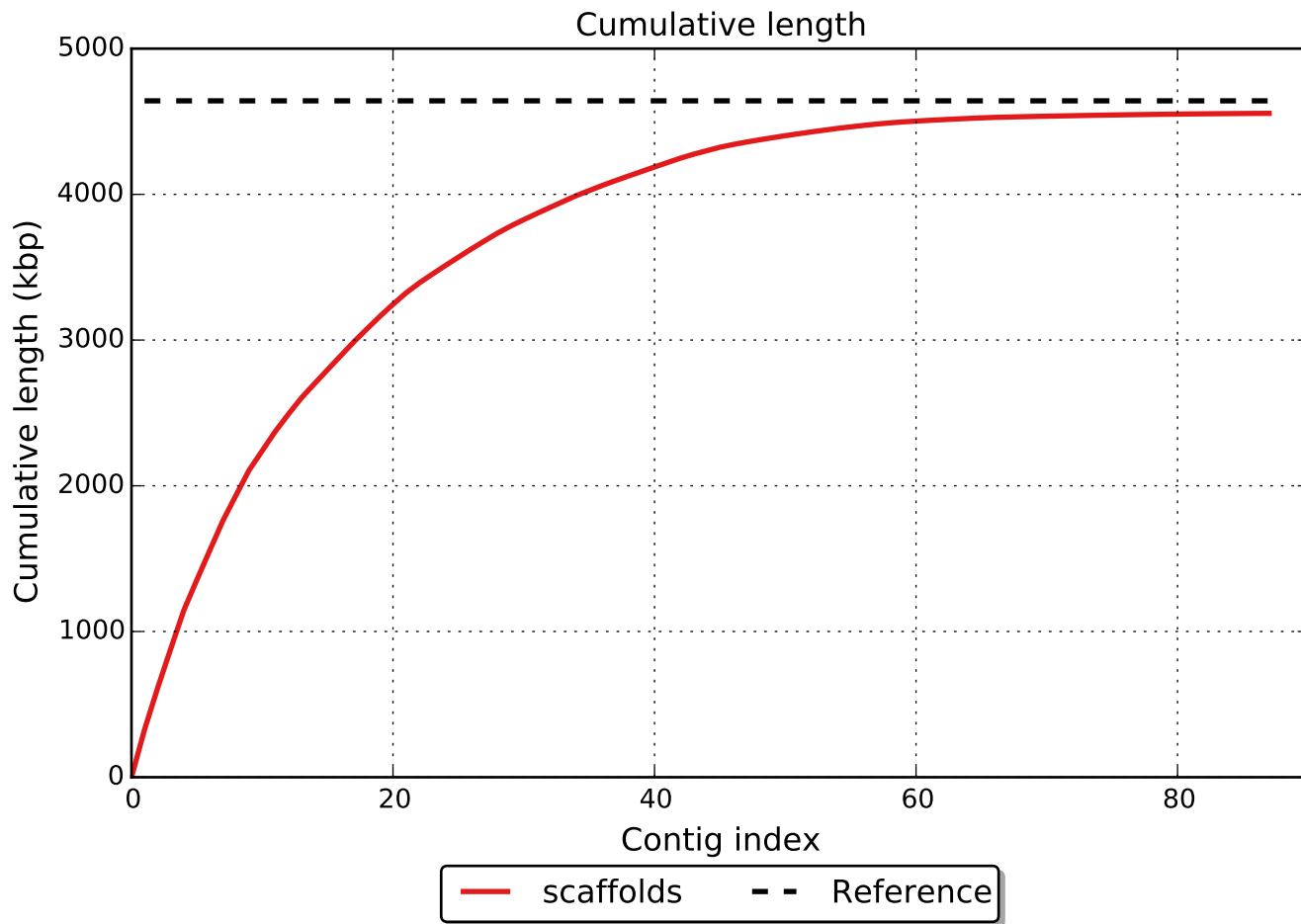
Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	283

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).

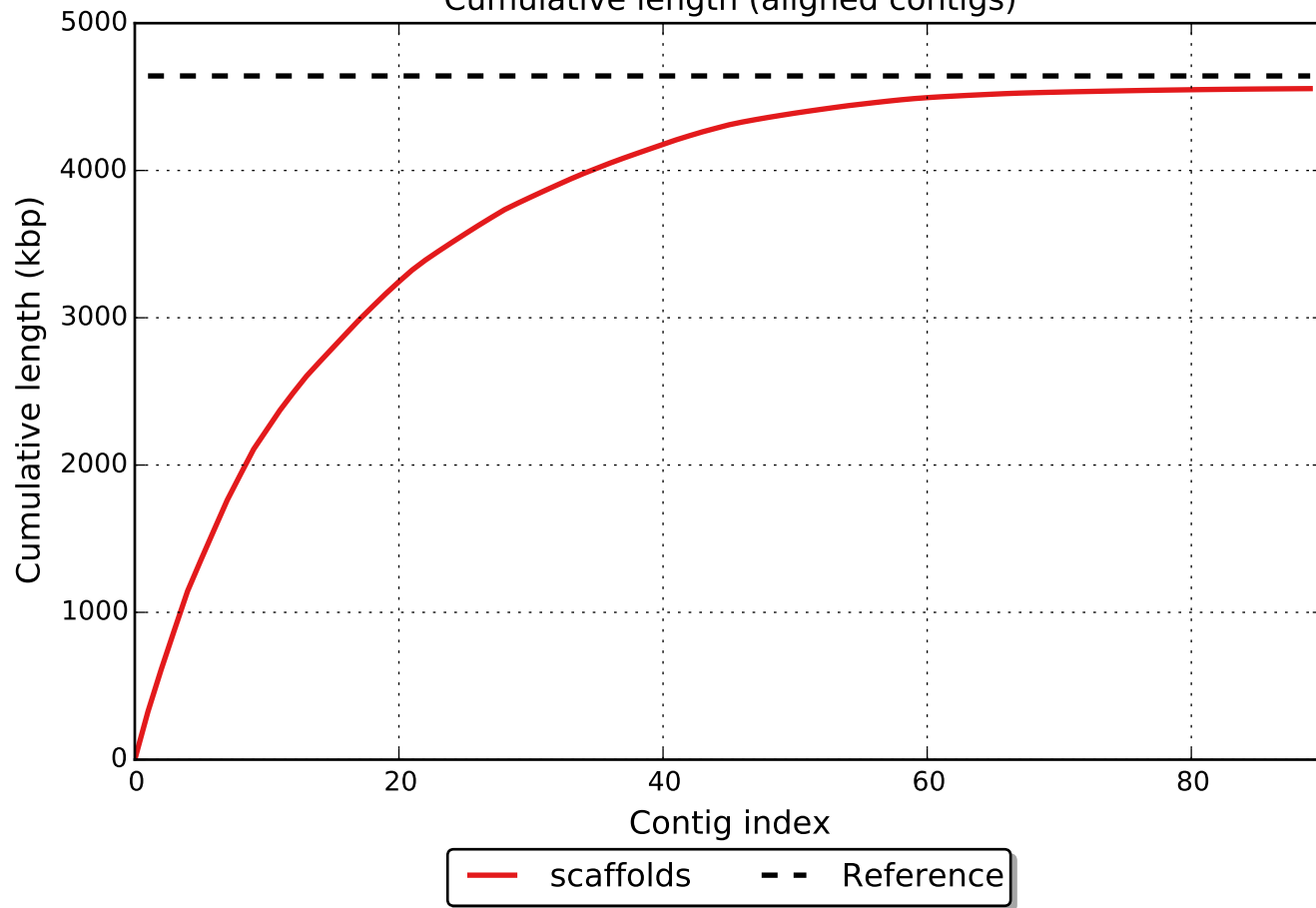
Nx







Cumulative length (aligned contigs)



NAx

