

Report

	scaffolds
# contigs (≥ 0 bp)	8119
# contigs (≥ 1000 bp)	74
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	2880563
Total length (≥ 1000 bp)	94579
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	1240
Largest contig	3978
Total length	842840
Reference length	4641652
N50	657
N75	566
L50	497
L75	845
# misassemblies	22
# misassembled contigs	22
Misassembled contigs length	24093
# local misassemblies	0
# unaligned contigs	25 + 21 part
Unaligned length	19260
Genome fraction (%)	17.670
Duplication ratio	1.004
# N's per 100 kbp	108.44
# mismatches per 100 kbp	1819.59
# indels per 100 kbp	14.27
Largest alignment	3704
NA50	644
NA75	555
LA50	508
LA75	861

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	22
# relocations	22
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	1
# misassembled contigs	22
Misassembled contigs length	24093
# local misassemblies	0
# mismatches	14924
# indels	117
# short indels	108
# long indels	9
Indels length	247

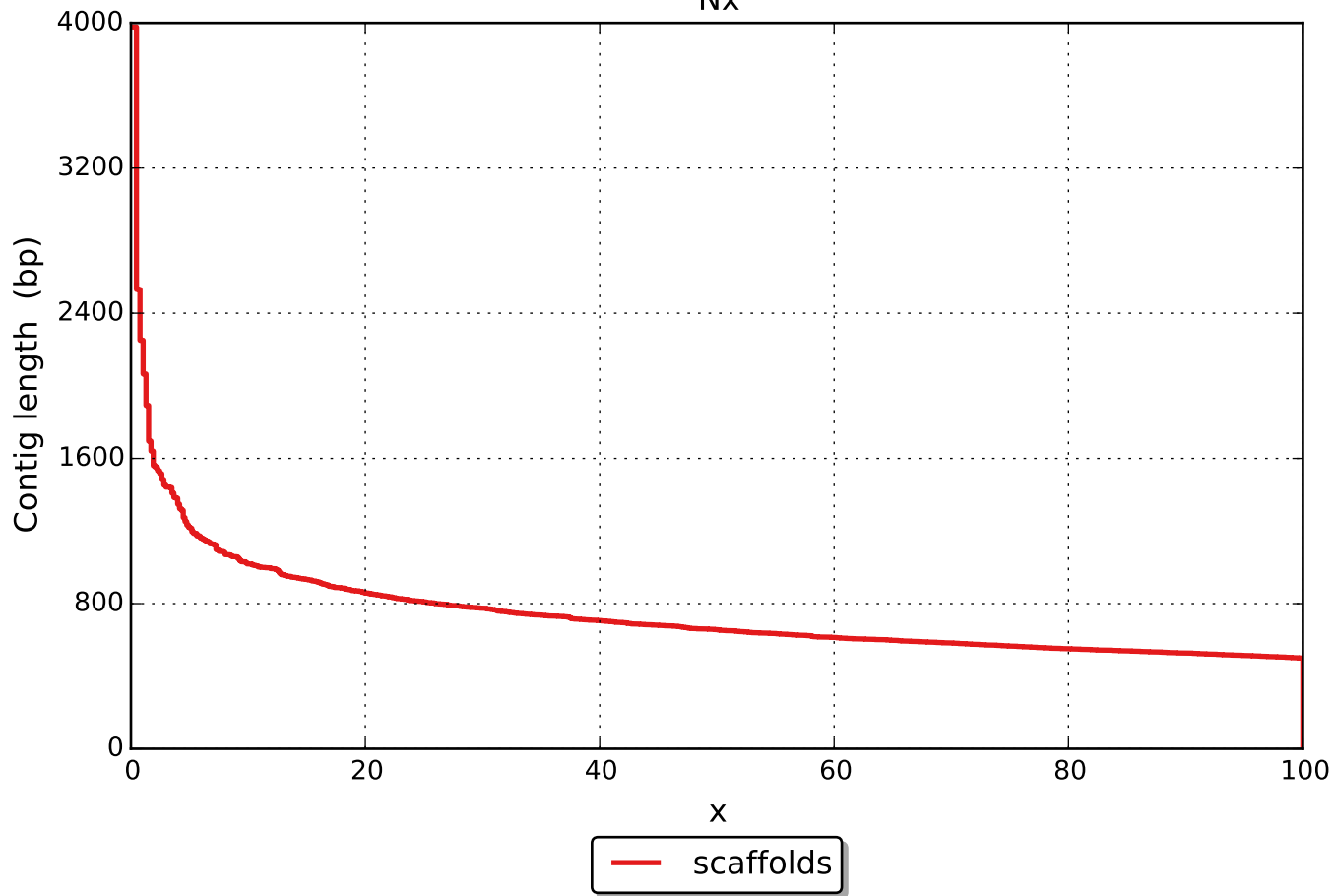
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

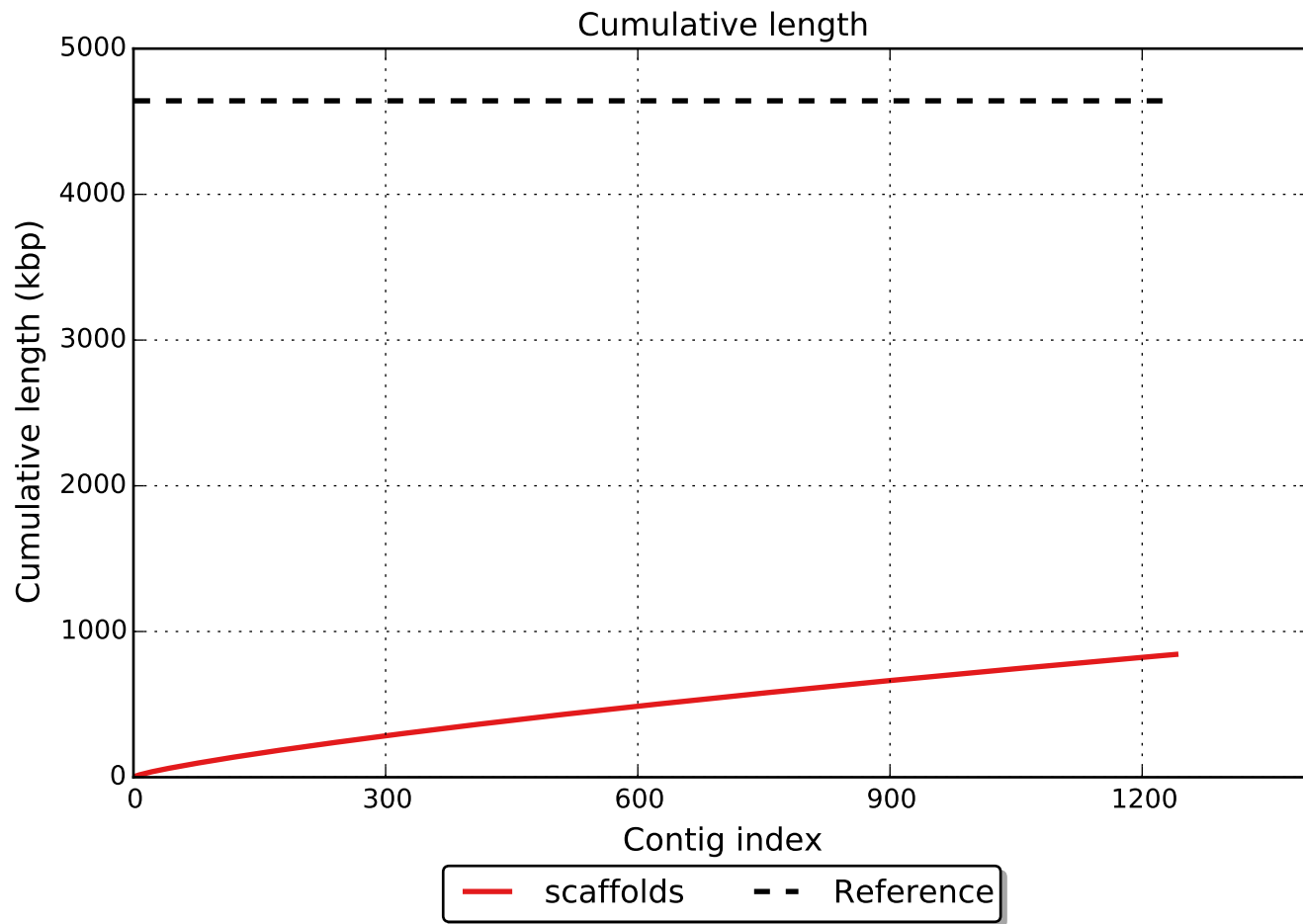
Unaligned report

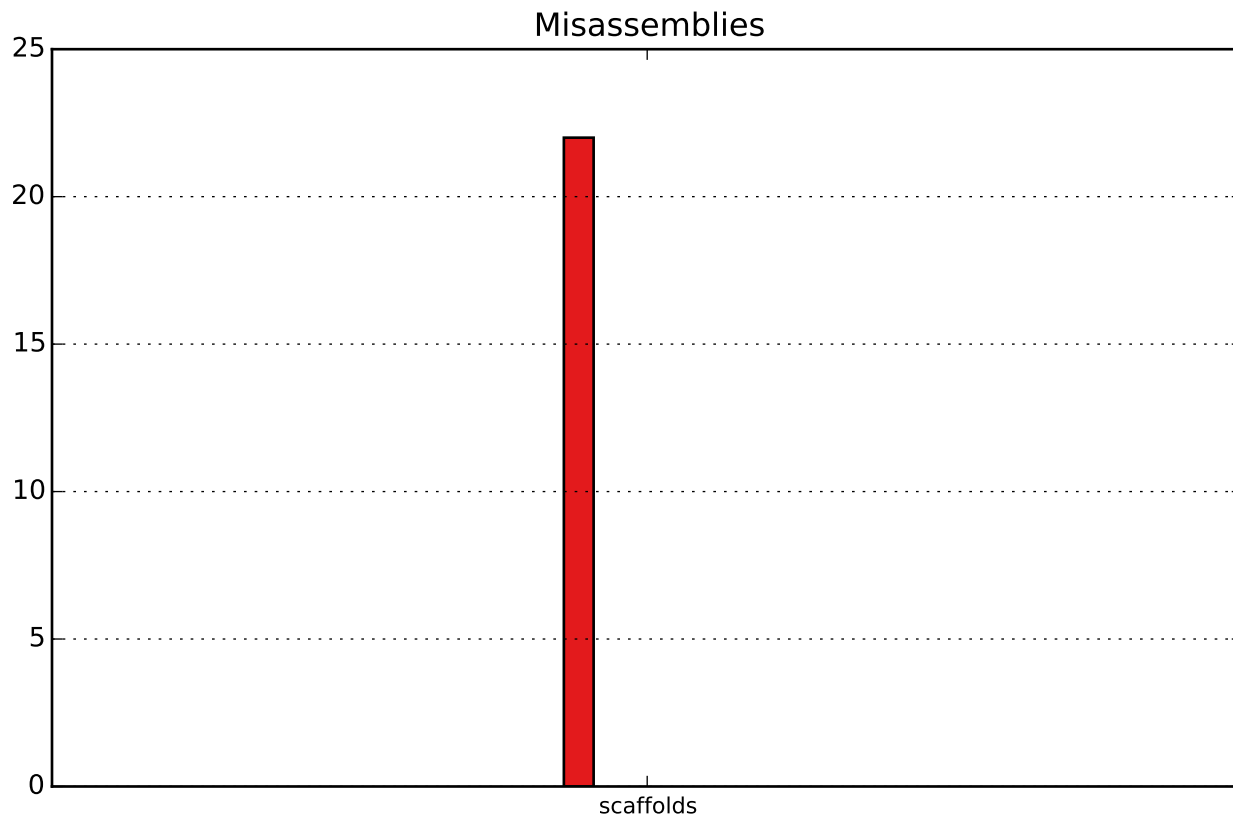
	scaffolds
# fully unaligned contigs	25
Fully unaligned length	17304
# partially unaligned contigs	21
# with misassembly	0
# both parts are significant	1
Partially unaligned length	1956
# N's	914

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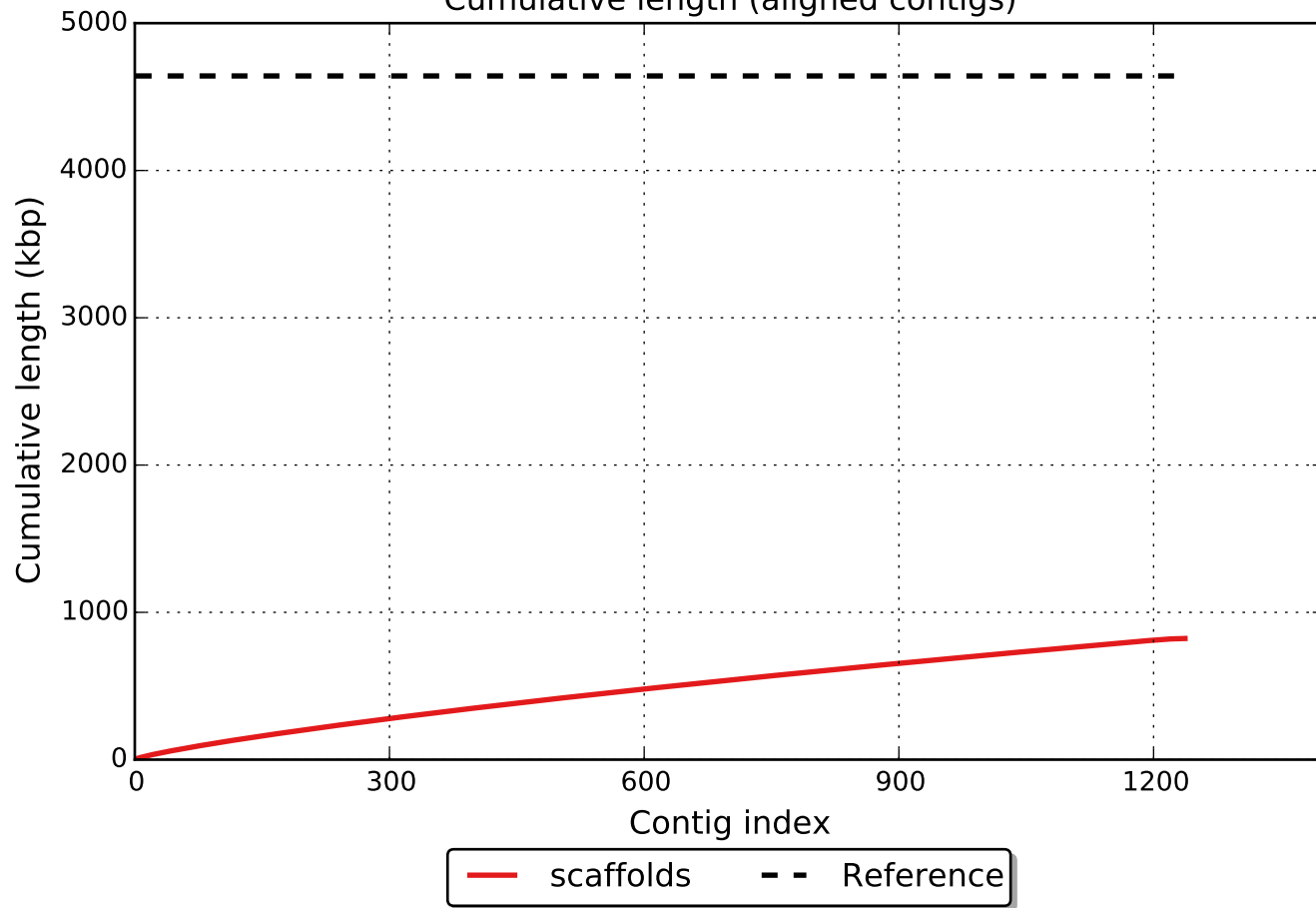
Nx







Cumulative length (aligned contigs)



NAx

