

Report

	scaffolds
# contigs (≥ 0 bp)	3916
# contigs (≥ 1000 bp)	947
# contigs (≥ 5000 bp)	3
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	3001064
Total length (≥ 1000 bp)	1494199
Total length (≥ 5000 bp)	21011
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	2327
Largest contig	8898
Total length	2476014
Reference length	4641652
N50	1171
N75	802
L50	710
L75	1351
# misassemblies	18
# misassembled contigs	17
Misassembled contigs length	37784
# local misassemblies	3
# unaligned contigs	172 + 22 part
Unaligned length	187873
Genome fraction (‰)	49.096
Duplication ratio	1.004
# N's per 100 kbp	1195.91
# mismatches per 100 kbp	225.90
# indels per 100 kbp	48.18
Largest alignment	6590
NA50	1083
NA75	707
LA50	745
LA75	1451

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

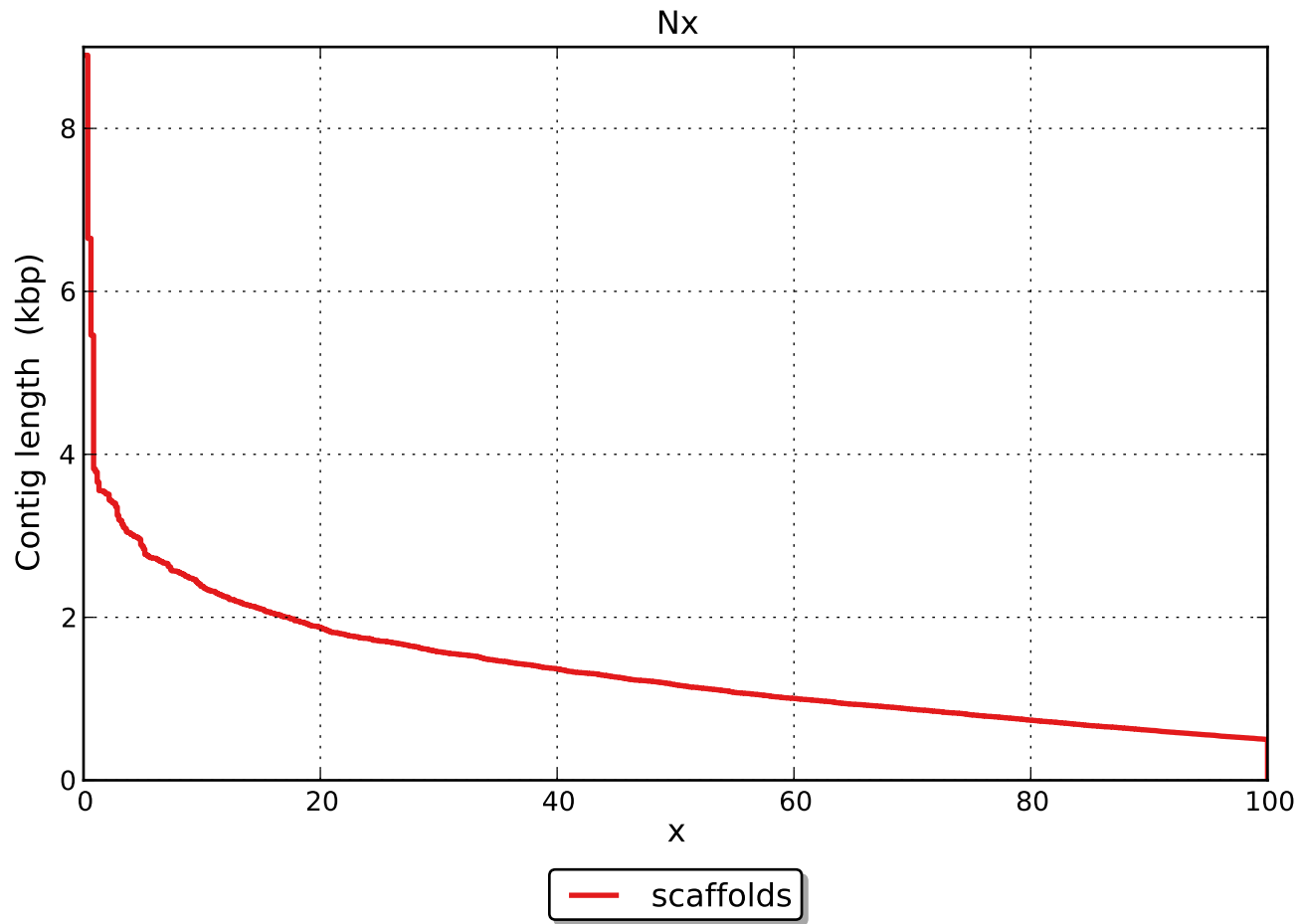
	scaffolds
# misassemblies	18
# relocations	18
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	8
# misassembled contigs	17
Misassembled contigs length	37784
# local misassemblies	3
# mismatches	5148
# indels	1098
# short indels	531
# long indels	567
Indels length	9465

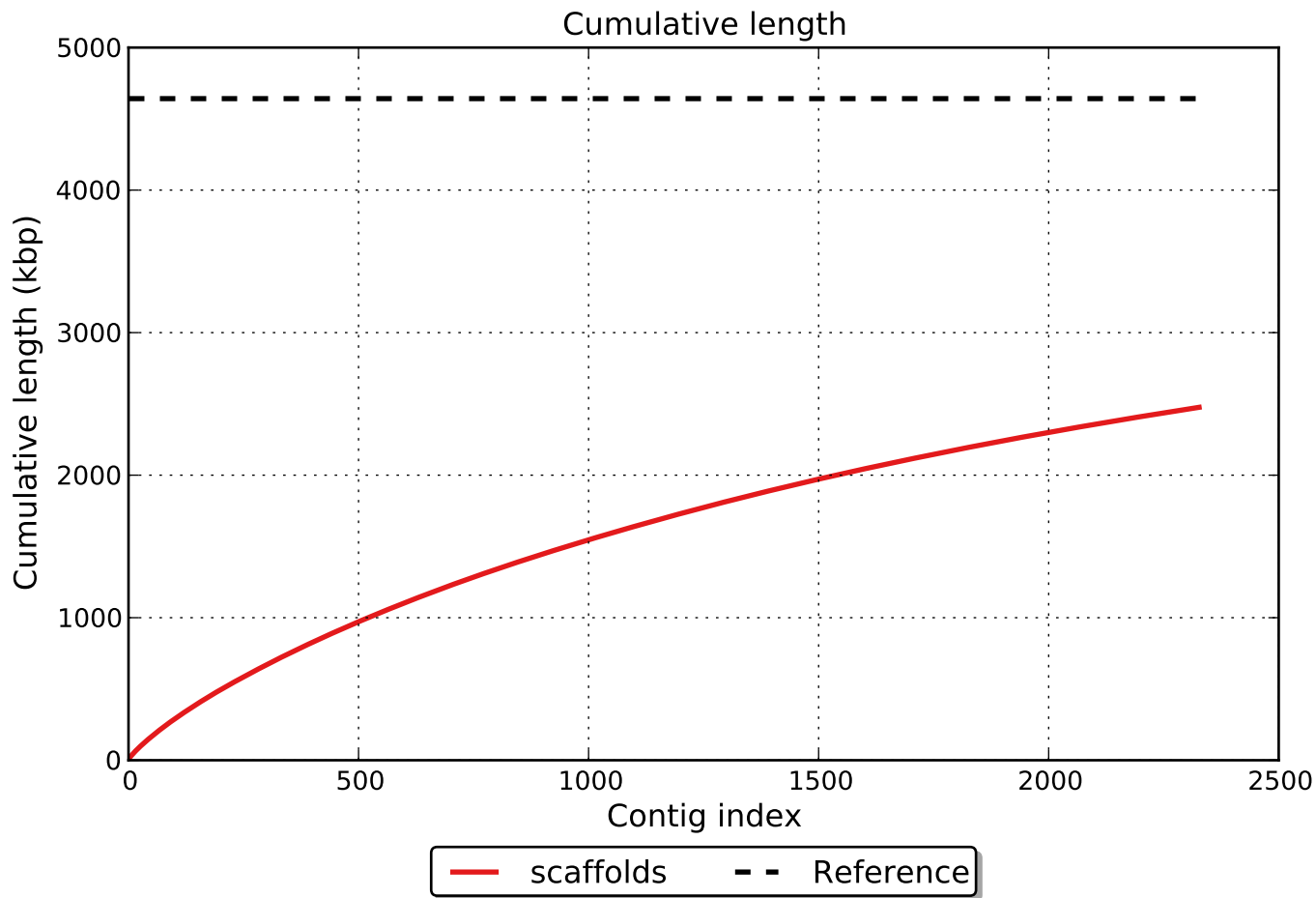
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

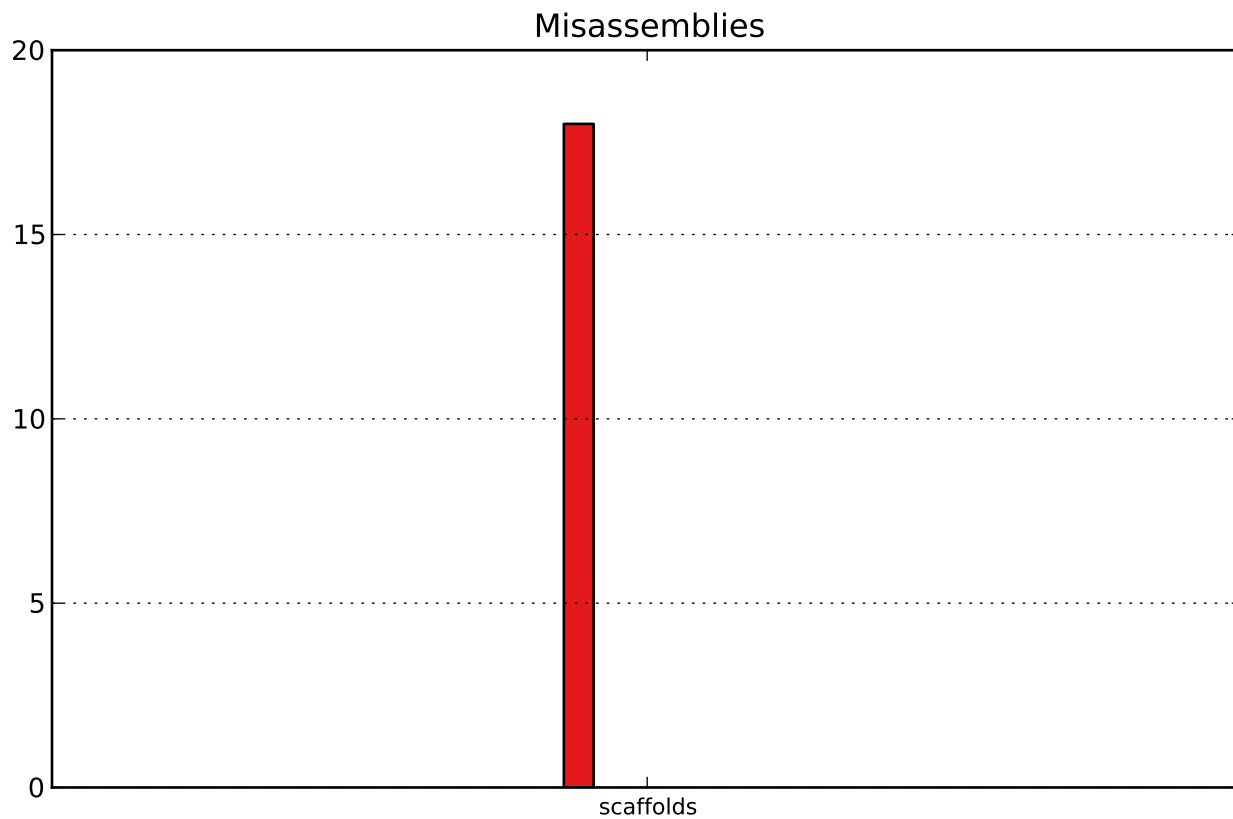
Unaligned report

	scaffolds
# fully unaligned contigs	172
Fully unaligned length	173377
# partially unaligned contigs	22
# with misassembly	0
# both parts are significant	6
Partially unaligned length	14496
# N's	29611

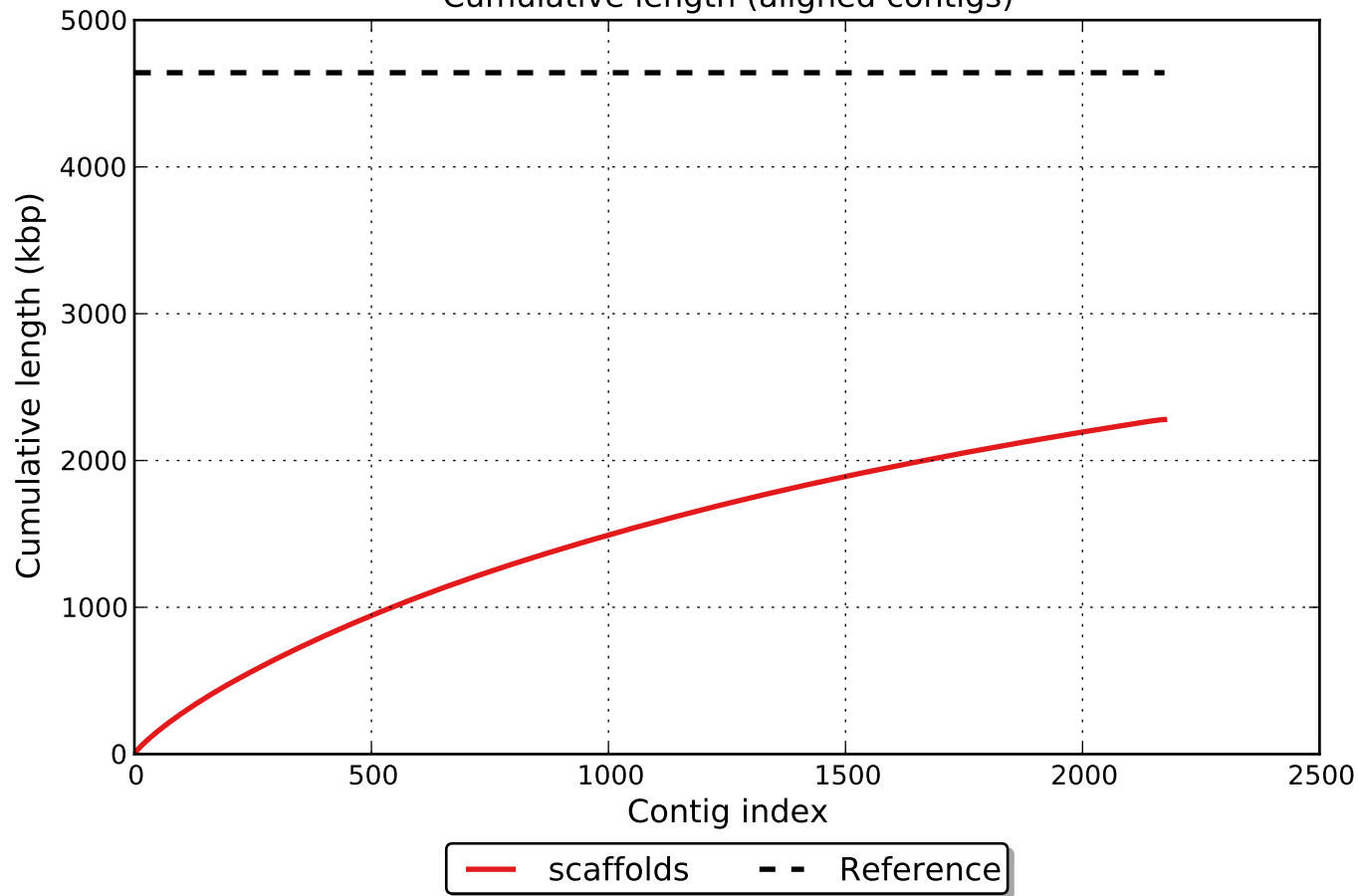
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



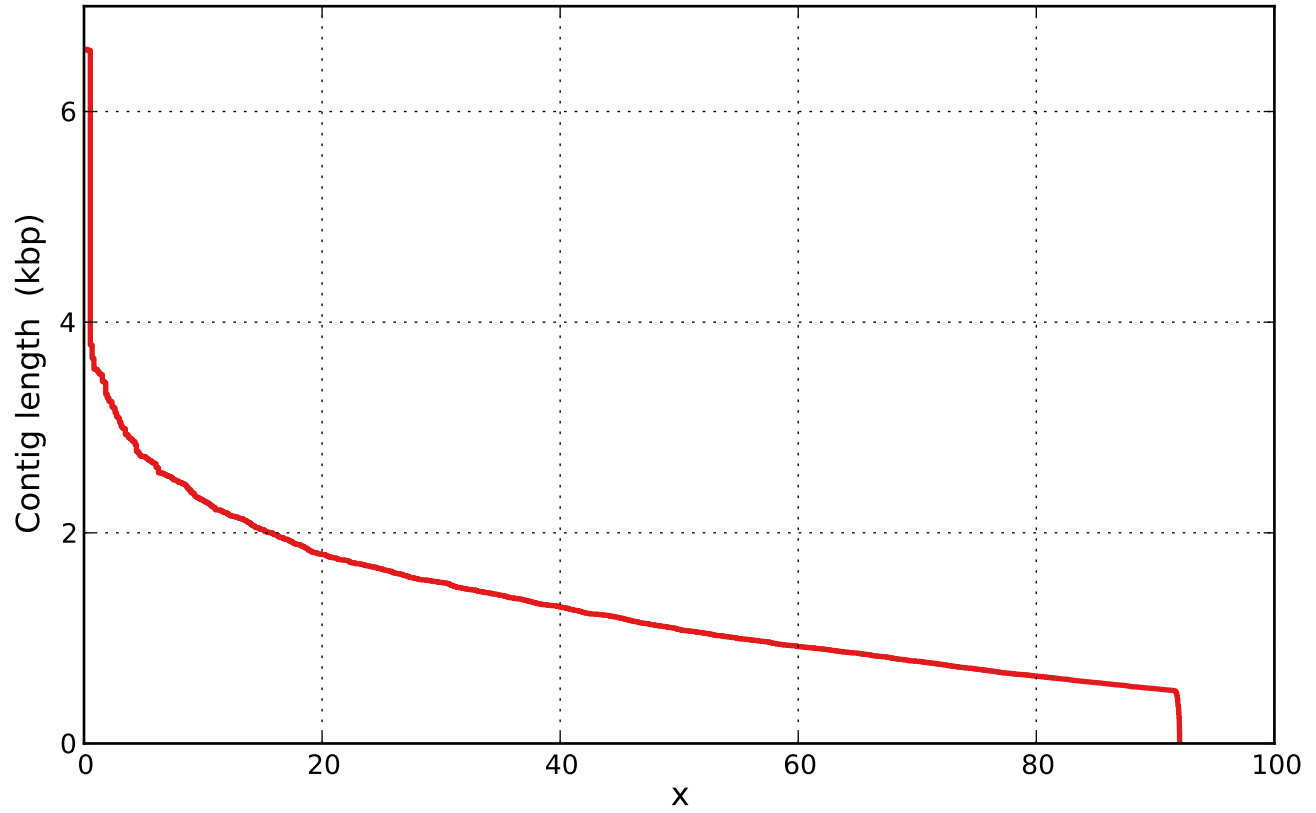




Cumulative length (aligned contigs)



NAx



— scaffolds