

Report

	scaffolds
# contigs (≥ 0 bp)	137
# contigs (≥ 1000 bp)	78
# contigs (≥ 5000 bp)	66
# contigs (≥ 10000 bp)	62
# contigs (≥ 25000 bp)	55
# contigs (≥ 50000 bp)	41
Total length (≥ 0 bp)	9157004
Total length (≥ 1000 bp)	9135989
Total length (≥ 5000 bp)	9112641
Total length (≥ 10000 bp)	9079171
Total length (≥ 25000 bp)	8963305
Total length (≥ 50000 bp)	8497357
# contigs	89
Largest contig	657825
Total length	9144127
Reference length	9283304
N50	315111
N75	131793
L50	11
L75	24
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	48 + 18 part
Unaligned length	4507980
Genome fraction (%)	49.927
Duplication ratio	1.001
# N's per 100 kbp	0.84
# mismatches per 100 kbp	250.06
# indels per 100 kbp	1.01
Largest alignment	657825
NA50	27820
LA50	16

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	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	8
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	11590
# indels	47
# short indels	46
# long indels	1
Indels length	116

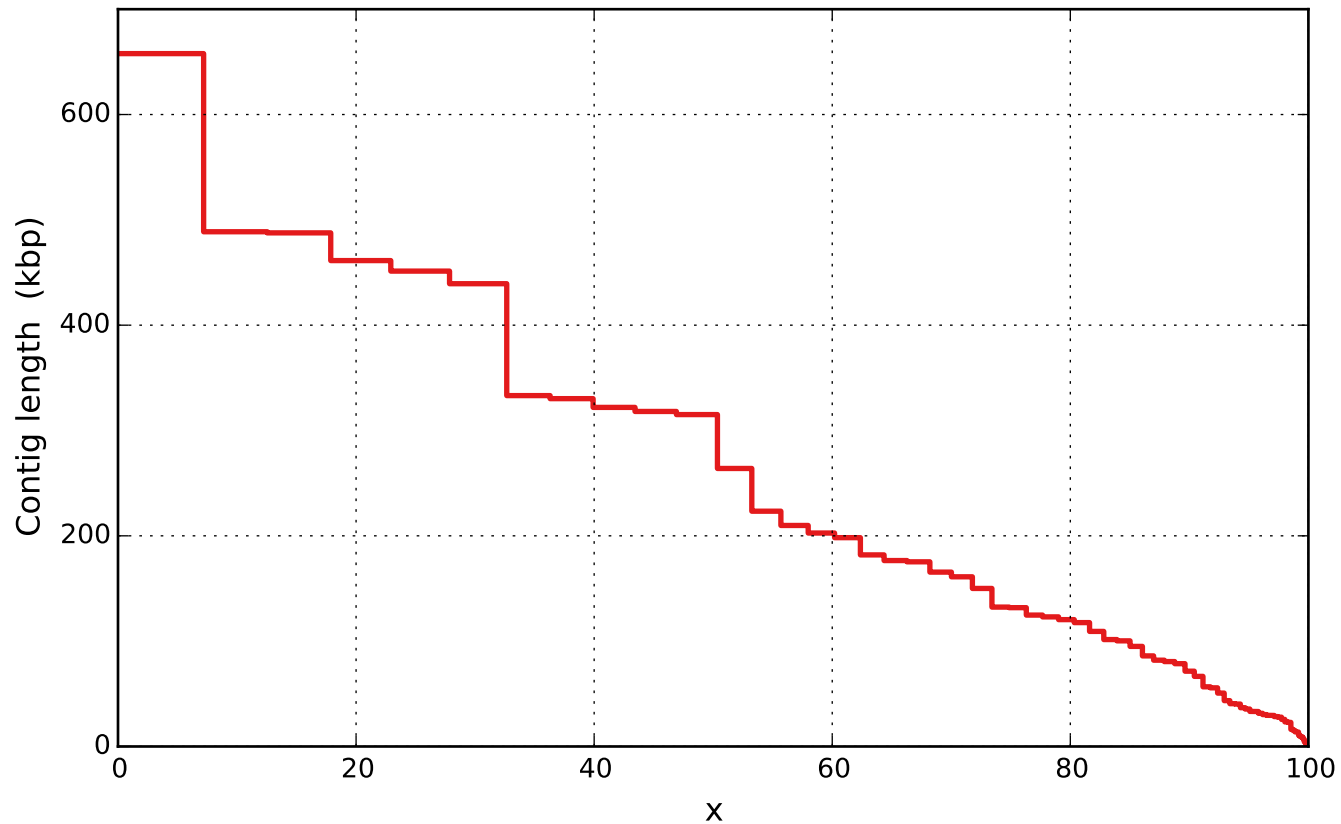
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

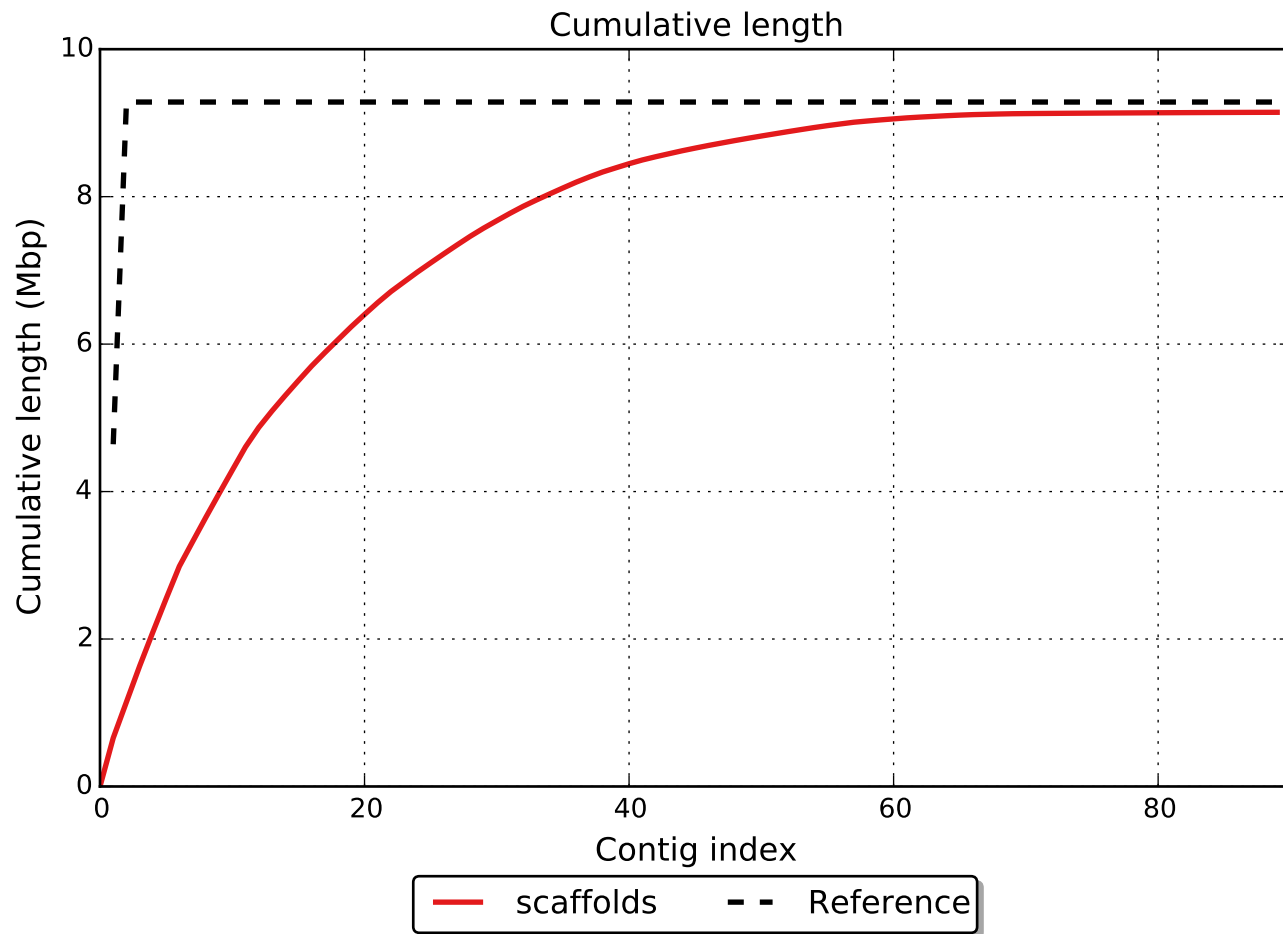
Unaligned report

	scaffolds
# fully unaligned contigs	48
Fully unaligned length	2812320
# partially unaligned contigs	18
# with misassembly	4
# both parts are significant	8
Partially unaligned length	1695660
# N's	77

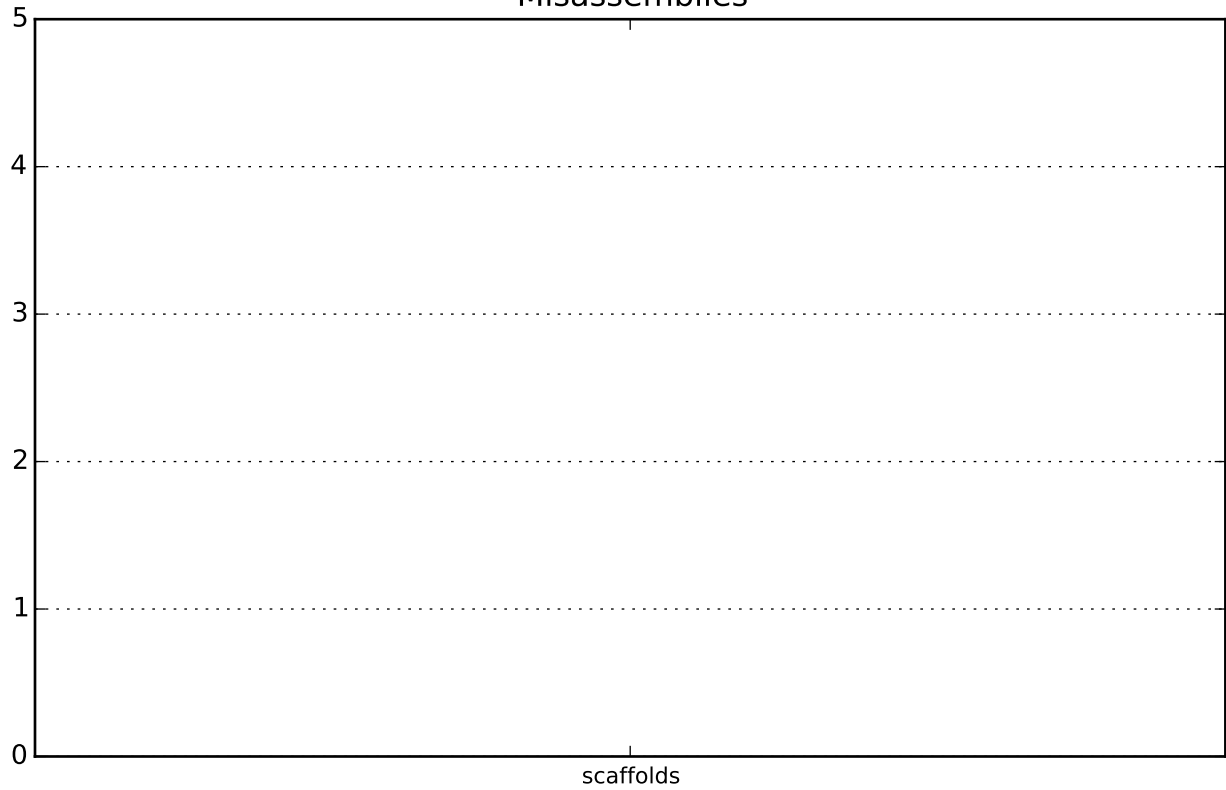
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

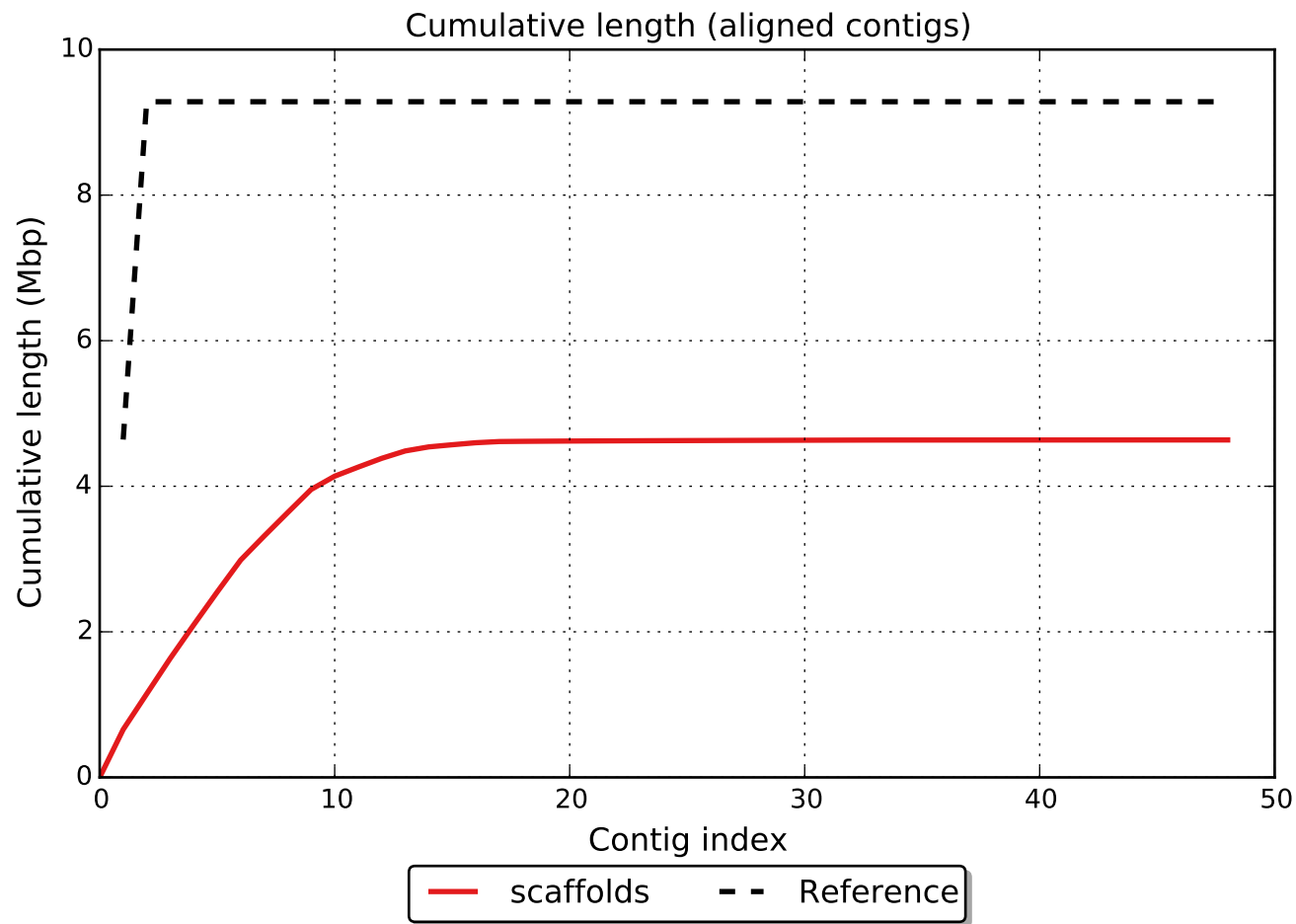
Nx



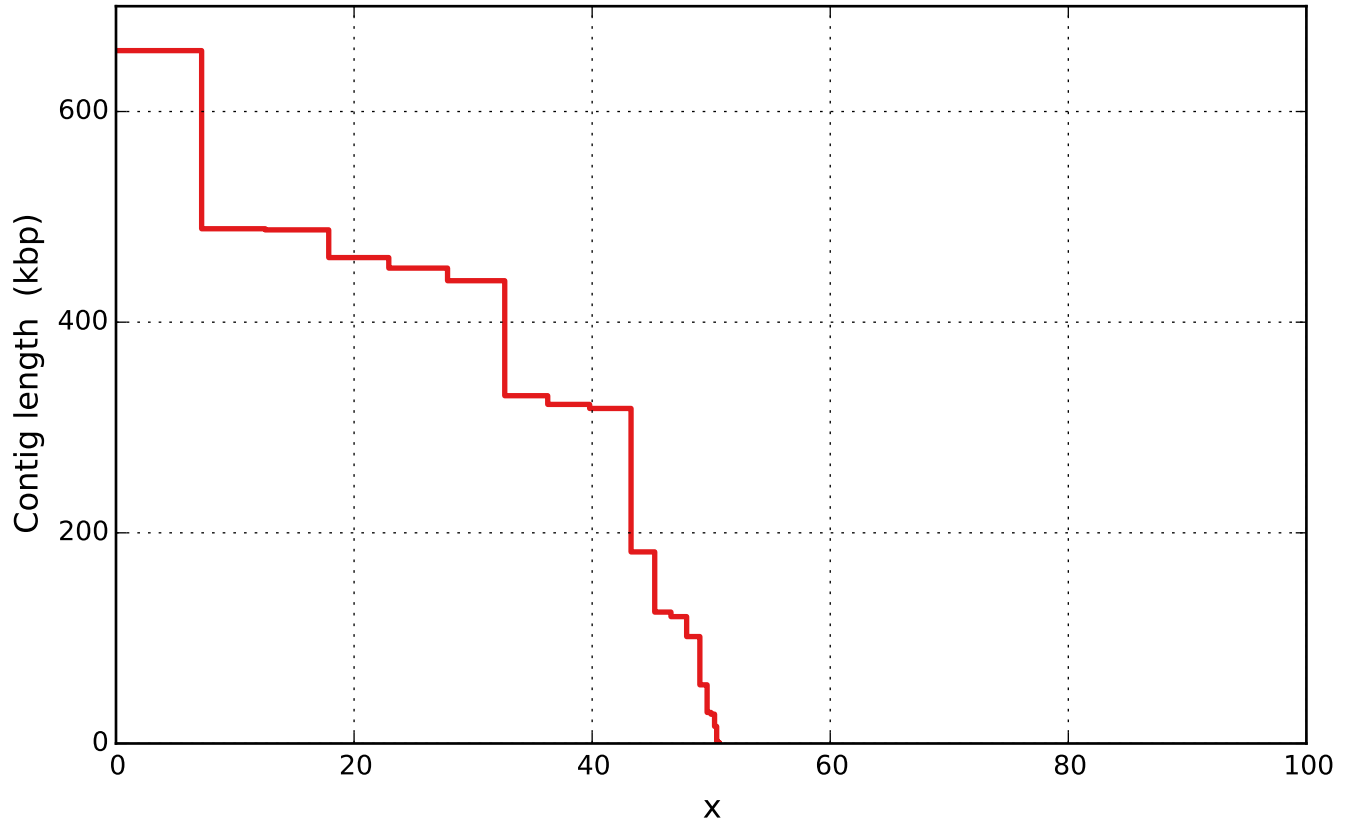


Misassemblies





NAx



— scaffolds