

Report

	scaffolds
# contigs (≥ 0 bp)	132
# contigs (≥ 1000 bp)	74
# contigs (≥ 5000 bp)	65
# contigs (≥ 10000 bp)	62
# contigs (≥ 25000 bp)	58
# contigs (≥ 50000 bp)	43
Total length (≥ 0 bp)	9161853
Total length (≥ 1000 bp)	9142481
Total length (≥ 5000 bp)	9125370
Total length (≥ 10000 bp)	9102425
Total length (≥ 25000 bp)	9045107
Total length (≥ 50000 bp)	8515013
# contigs	82
Largest contig	700824
Total length	9148773
Reference length	9283304
N50	264356
N75	131763
L50	12
L75	24
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	349059
# local misassemblies	1
# unaligned contigs	48 + 8 part
Unaligned length	4339565
Genome fraction (%)	49.791
Duplication ratio	1.040
# N's per 100 kbp	0.00
# mismatches per 100 kbp	352.62
# indels per 100 kbp	1.10
Largest alignment	700544
NA50	42185
LA50	20

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	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	8
# misassembled contigs	1
Misassembled contigs length	349059
# local misassemblies	1
# mismatches	16299
# indels	51
# short indels	51
# long indels	0
Indels length	51

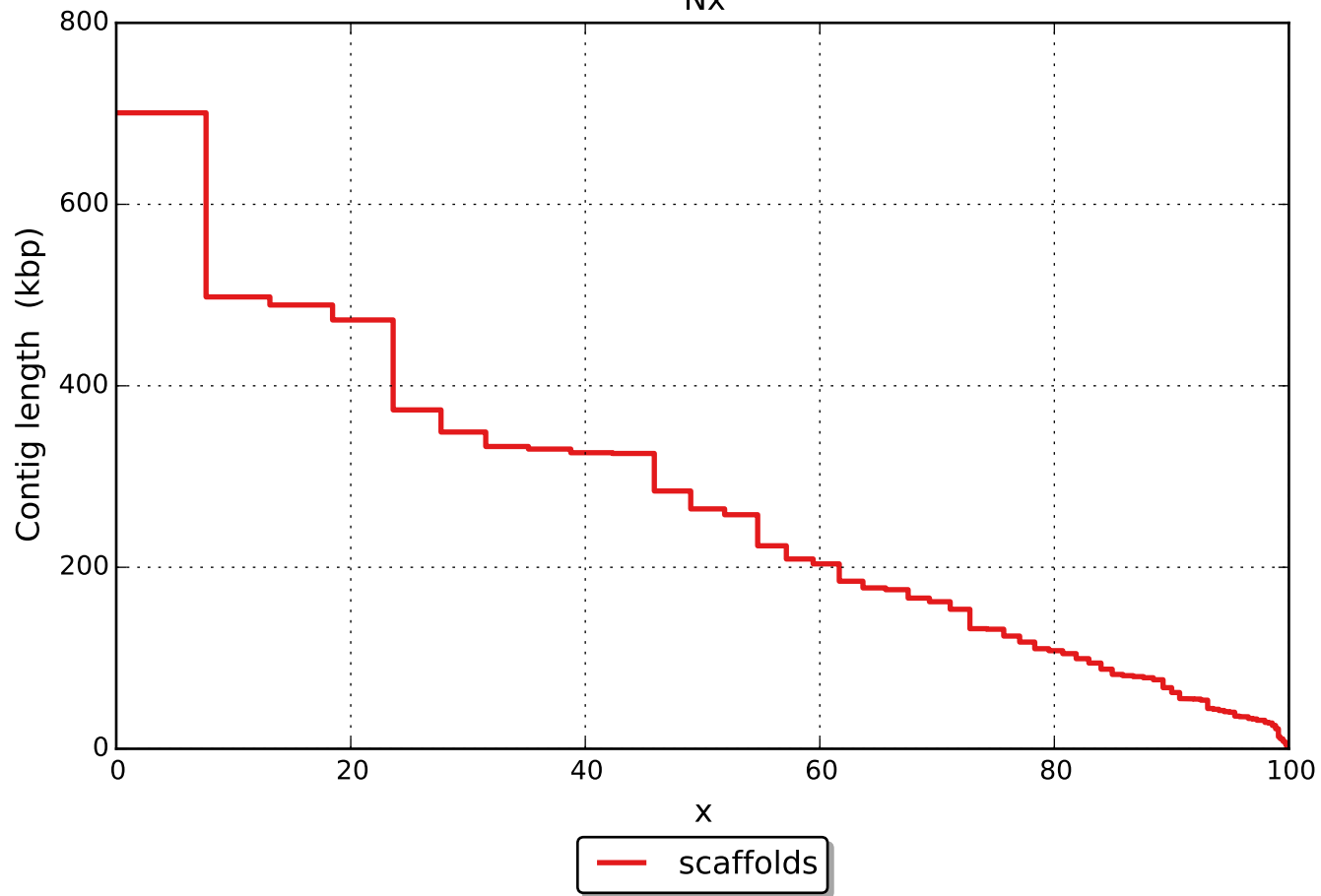
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

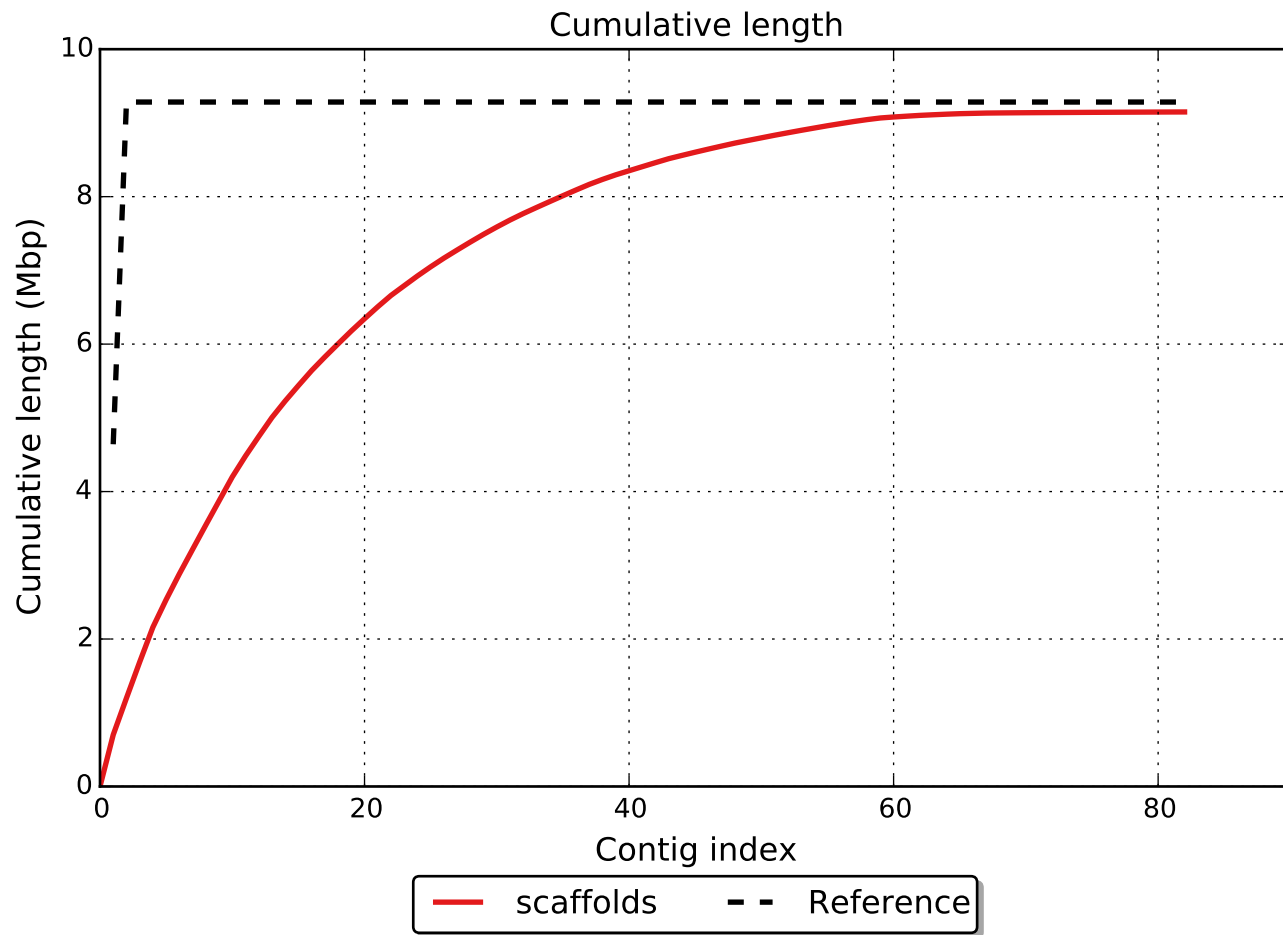
Unaligned report

	scaffolds
# fully unaligned contigs	48
Fully unaligned length	3145448
# partially unaligned contigs	8
# with misassembly	3
# both parts are significant	7
Partially unaligned length	1194117
# N's	0

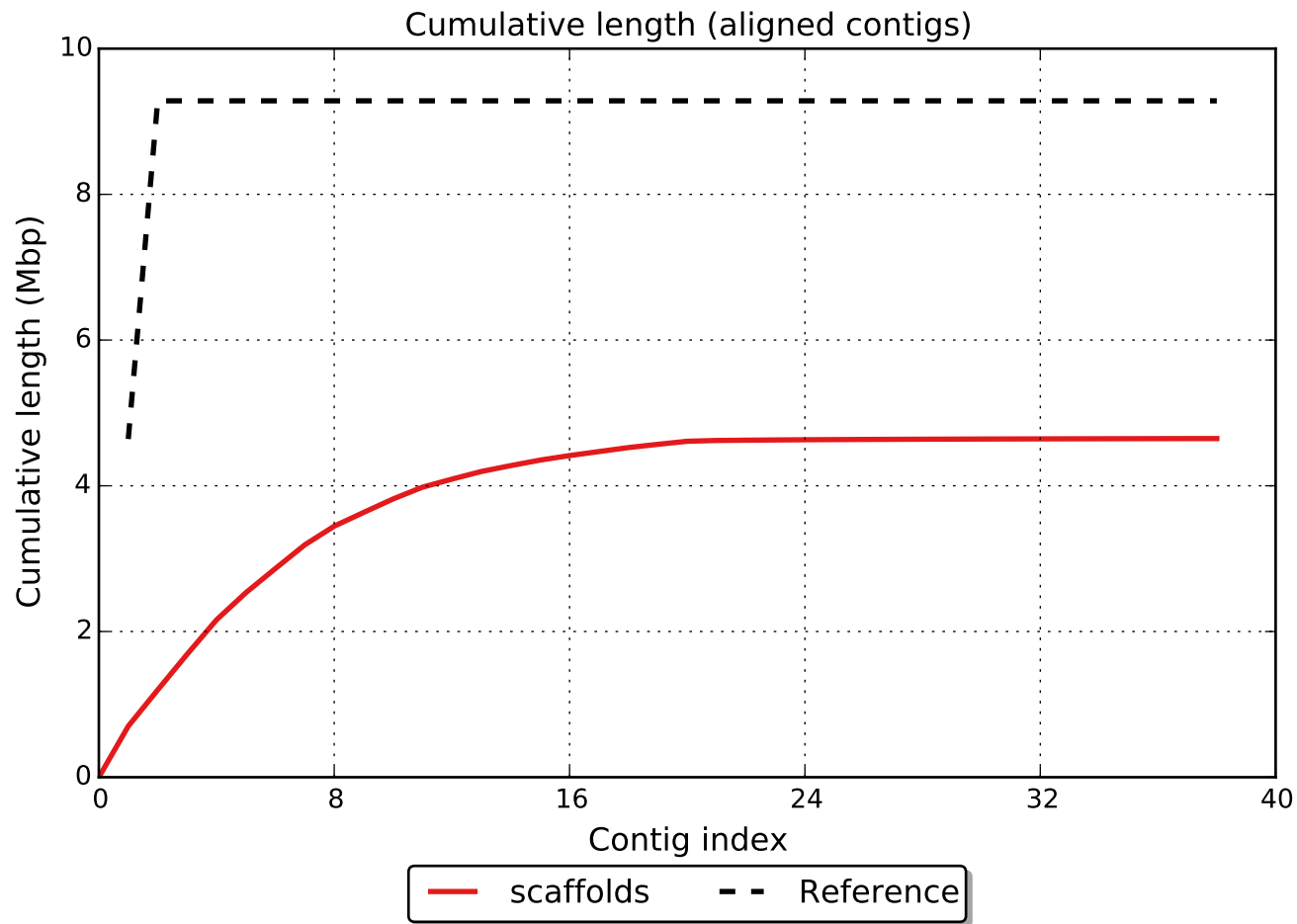
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

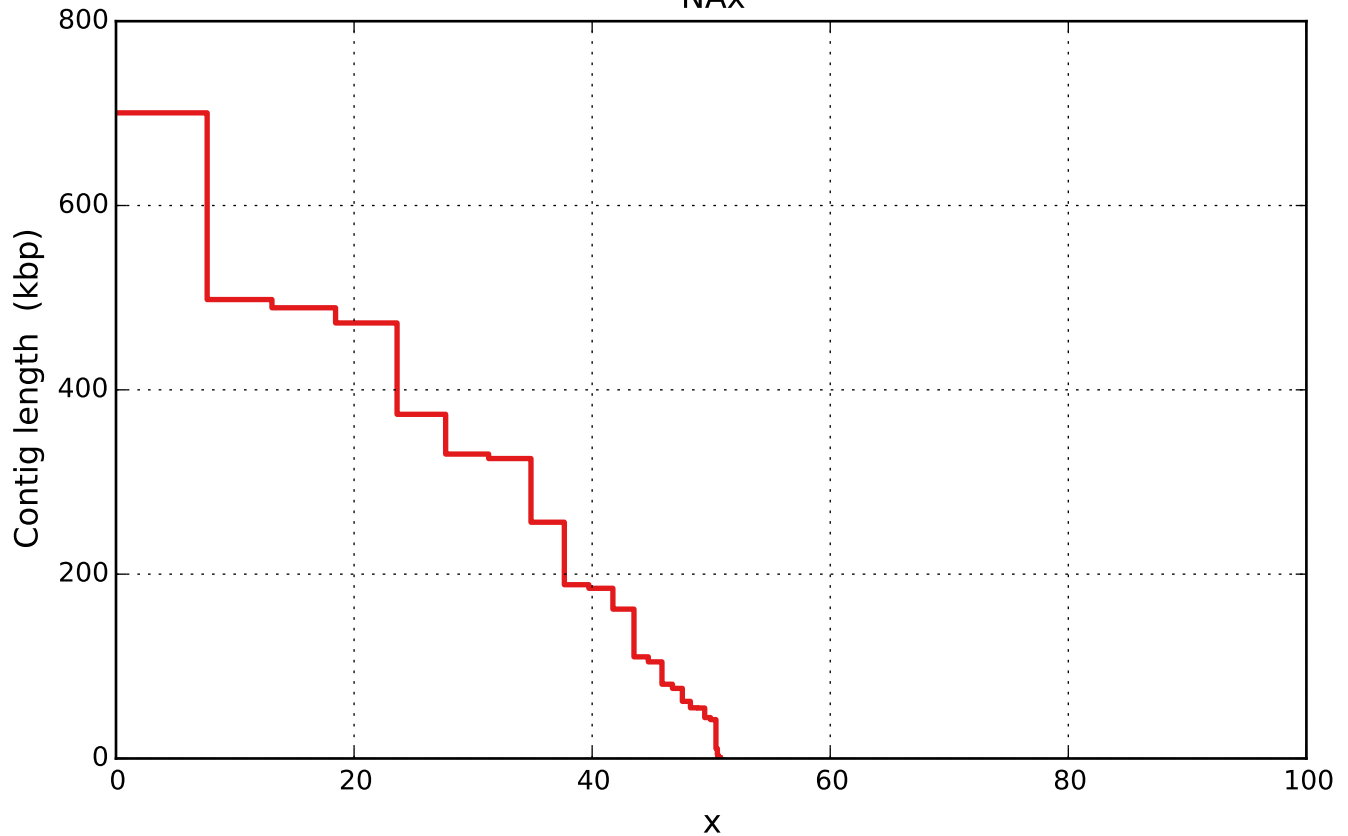








NAx



— scaffolds