

Report

	scaffolds
# contigs (≥ 0 bp)	123
# contigs (≥ 1000 bp)	72
# contigs (≥ 5000 bp)	66
# contigs (≥ 10000 bp)	63
# contigs (≥ 25000 bp)	57
# contigs (≥ 50000 bp)	43
Total length (≥ 0 bp)	9152926
Total length (≥ 1000 bp)	9134576
Total length (≥ 5000 bp)	9121767
Total length (≥ 10000 bp)	9099134
Total length (≥ 25000 bp)	9008253
Total length (≥ 50000 bp)	8537401
# contigs	82
Largest contig	768359
Total length	9141550
Reference length	9283304
N50	264356
N75	131763
L50	11
L75	24
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	768359
# local misassemblies	1
# unaligned contigs	44 + 15 part
Unaligned length	4340680
Genome fraction (%)	49.867
Duplication ratio	1.038
# N's per 100 kbp	1.05
# mismatches per 100 kbp	308.36
# indels per 100 kbp	1.04
Largest alignment	607862
NA50	53885
LA50	17

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	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	8
# misassembled contigs	1
Misassembled contigs length	768359
# local misassemblies	1
# mismatches	14275
# indels	48
# short indels	48
# long indels	0
Indels length	55

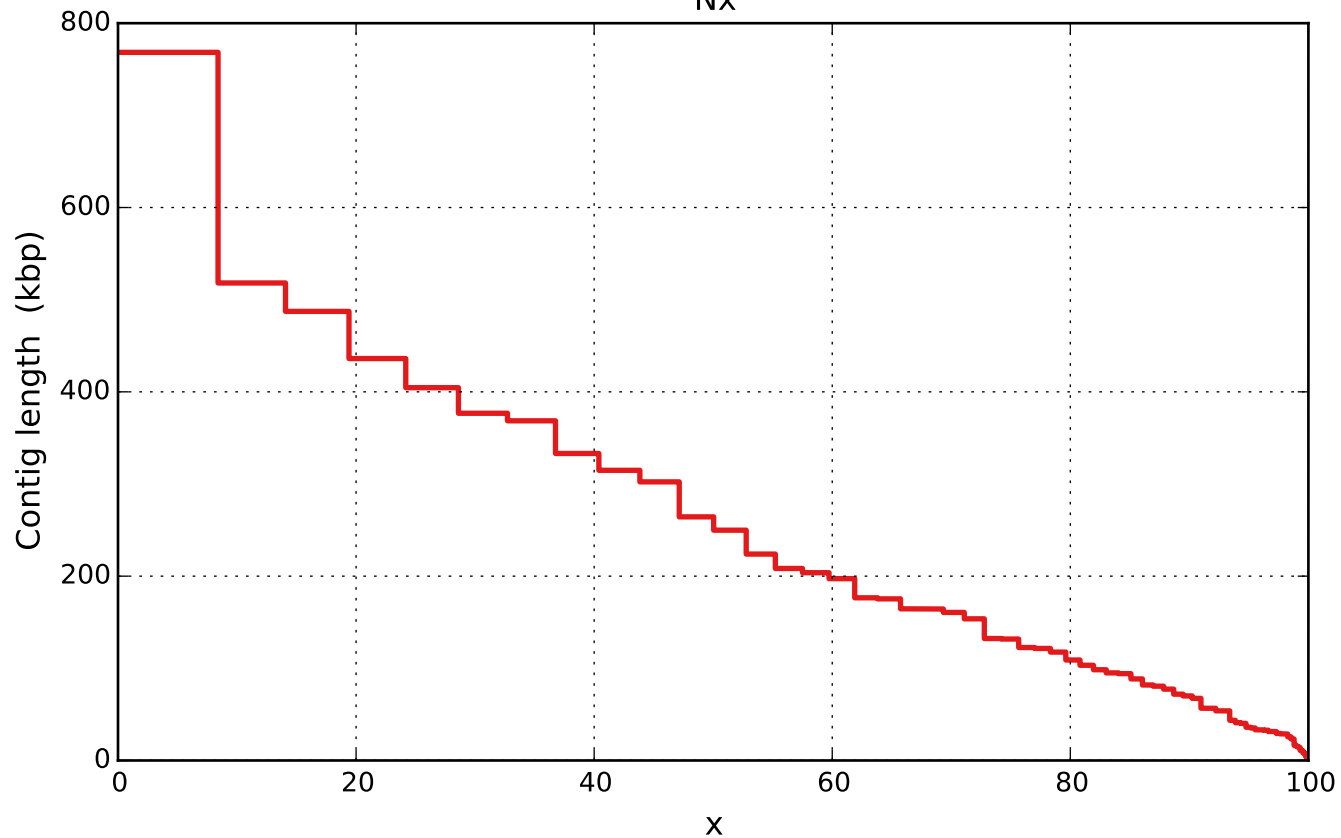
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

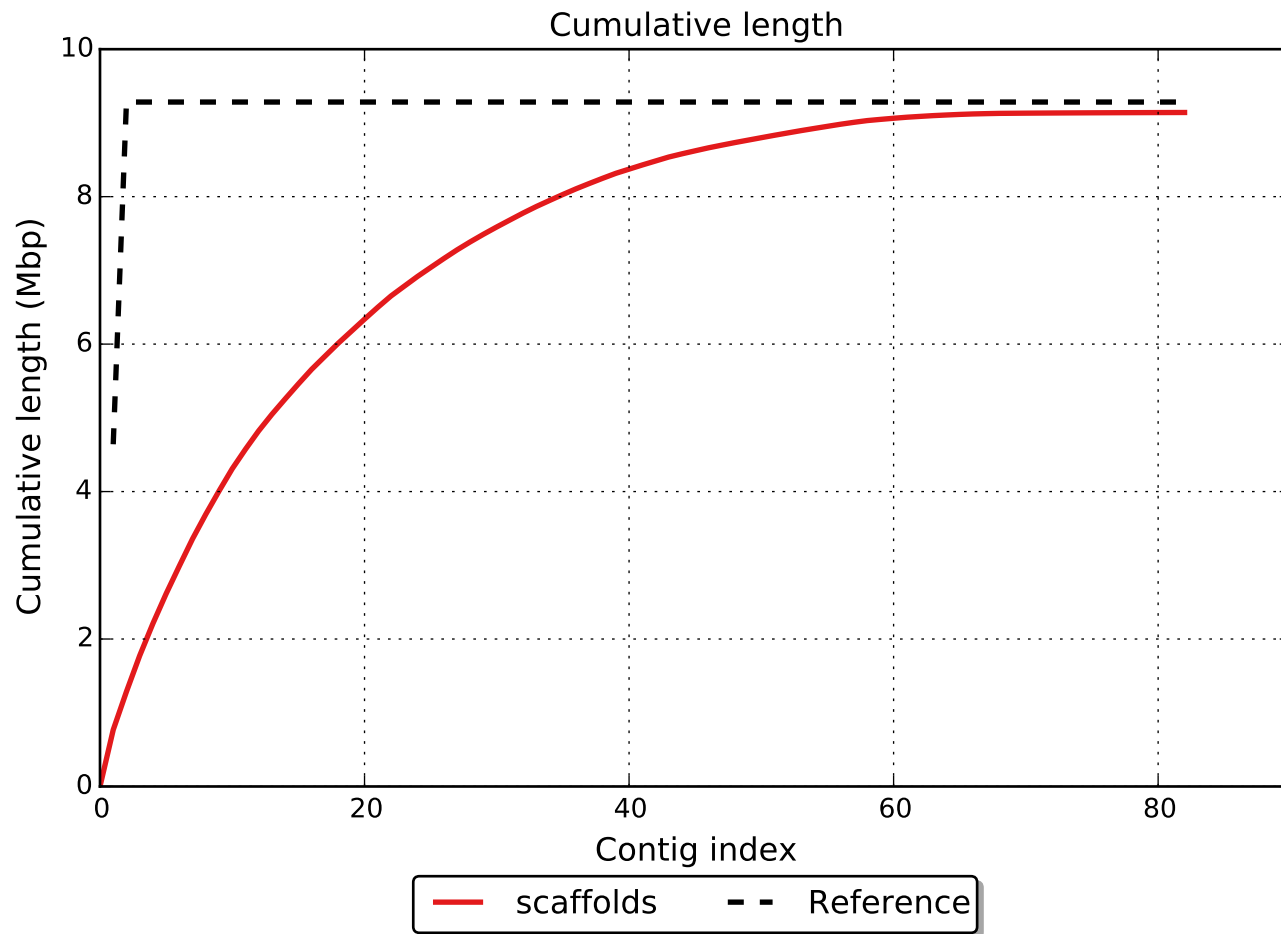
	scaffolds
# fully unaligned contigs	44
Fully unaligned length	2557407
# partially unaligned contigs	15
# with misassembly	3
# both parts are significant	7
Partially unaligned length	1783273
# N's	96

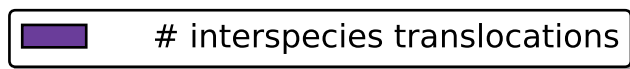
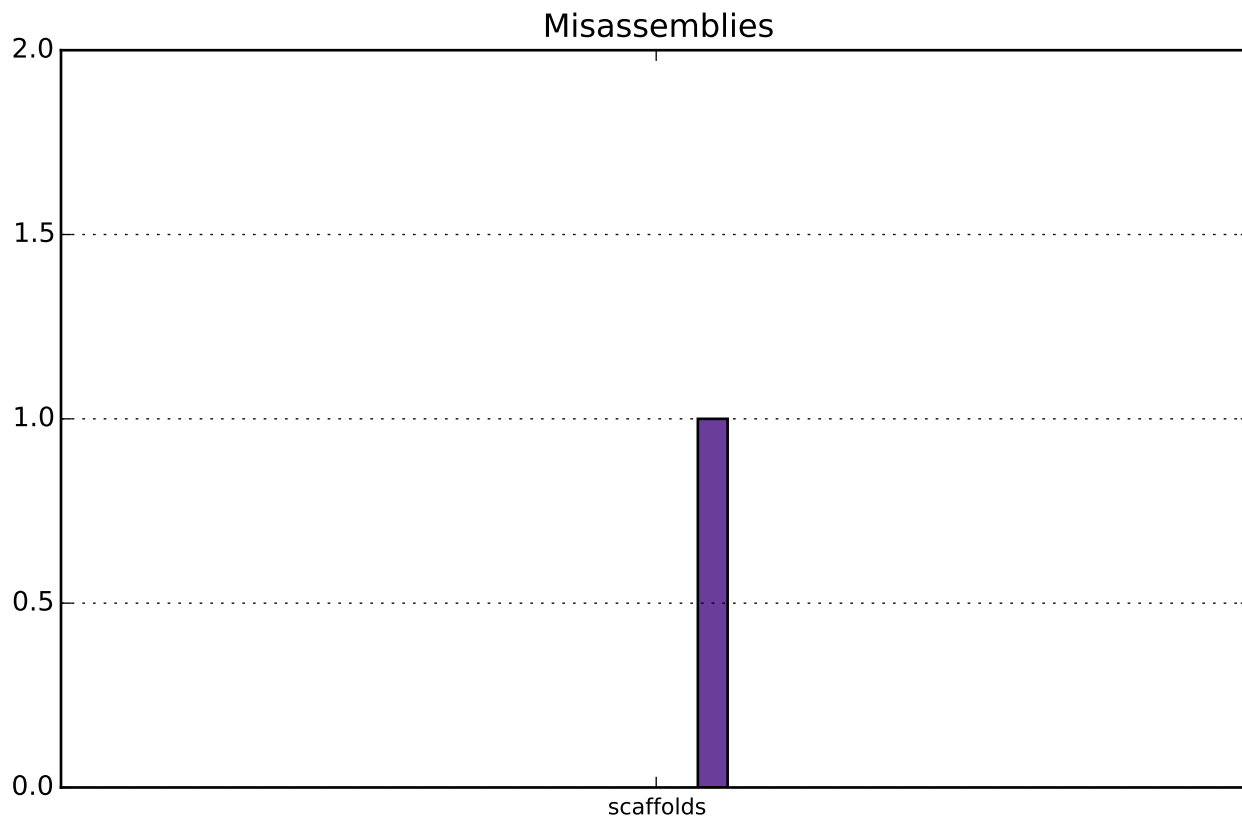
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

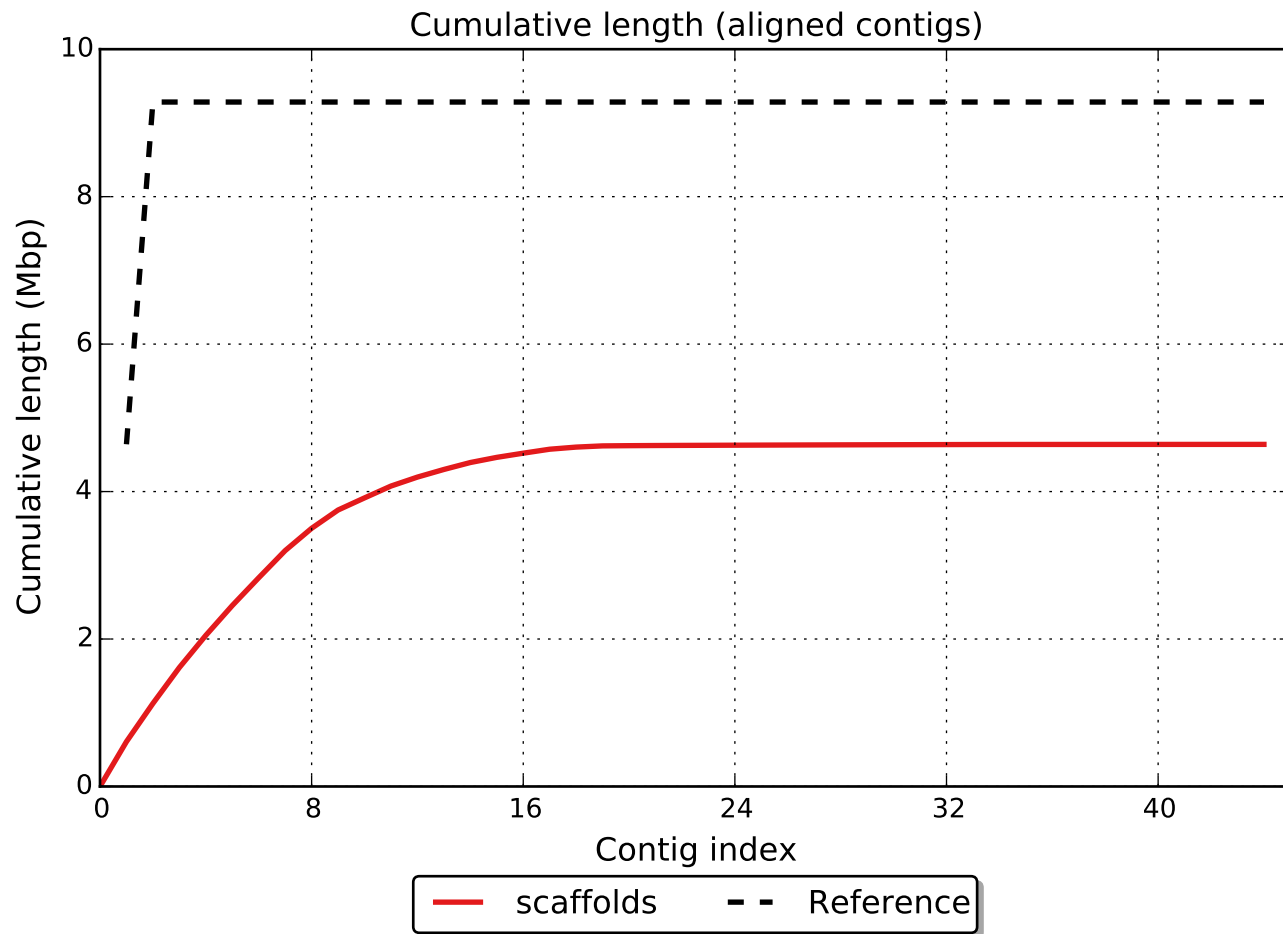
Nx



scaffolds







NAx

