

Report

	scaffolds
# contigs (≥ 0 bp)	159
# contigs (≥ 1000 bp)	86
# contigs (≥ 5000 bp)	73
# contigs (≥ 10000 bp)	69
# contigs (≥ 25000 bp)	65
# contigs (≥ 50000 bp)	50
Total length (≥ 0 bp)	9142640
Total length (≥ 1000 bp)	9118271
Total length (≥ 5000 bp)	9095669
Total length (≥ 10000 bp)	9067176
Total length (≥ 25000 bp)	9015059
Total length (≥ 50000 bp)	8509469
# contigs	99
Largest contig	529644
Total length	9127470
Reference length	9283304
N50	203618
N75	117603
L50	15
L75	30
# misassemblies	3
# misassembled contigs	2
Misassembled contigs length	578950
# local misassemblies	1
# unaligned contigs	31 + 23 part
Unaligned length	4344666
Genome fraction (%)	50.402
Duplication ratio	1.035
# N's per 100 kbp	0.24
# mismatches per 100 kbp	407.70
# indels per 100 kbp	1.03
Largest alignment	529644
NA50	26584
LA50	26

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	3
# relocations	3
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	21
# misassembled contigs	2
Misassembled contigs length	578950
# local misassemblies	1
# mismatches	19076
# indels	48
# short indels	47
# long indels	1
Indels length	69

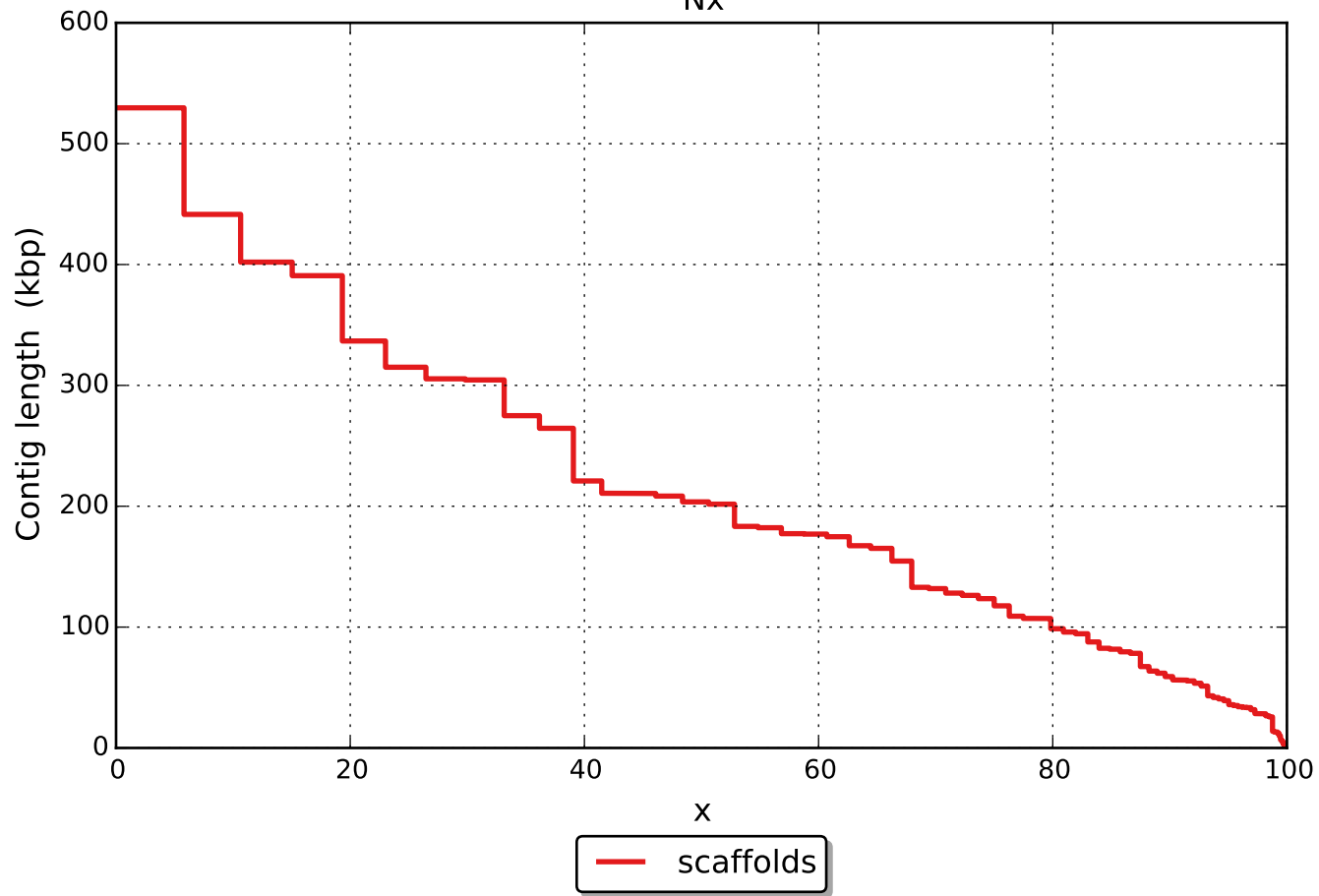
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

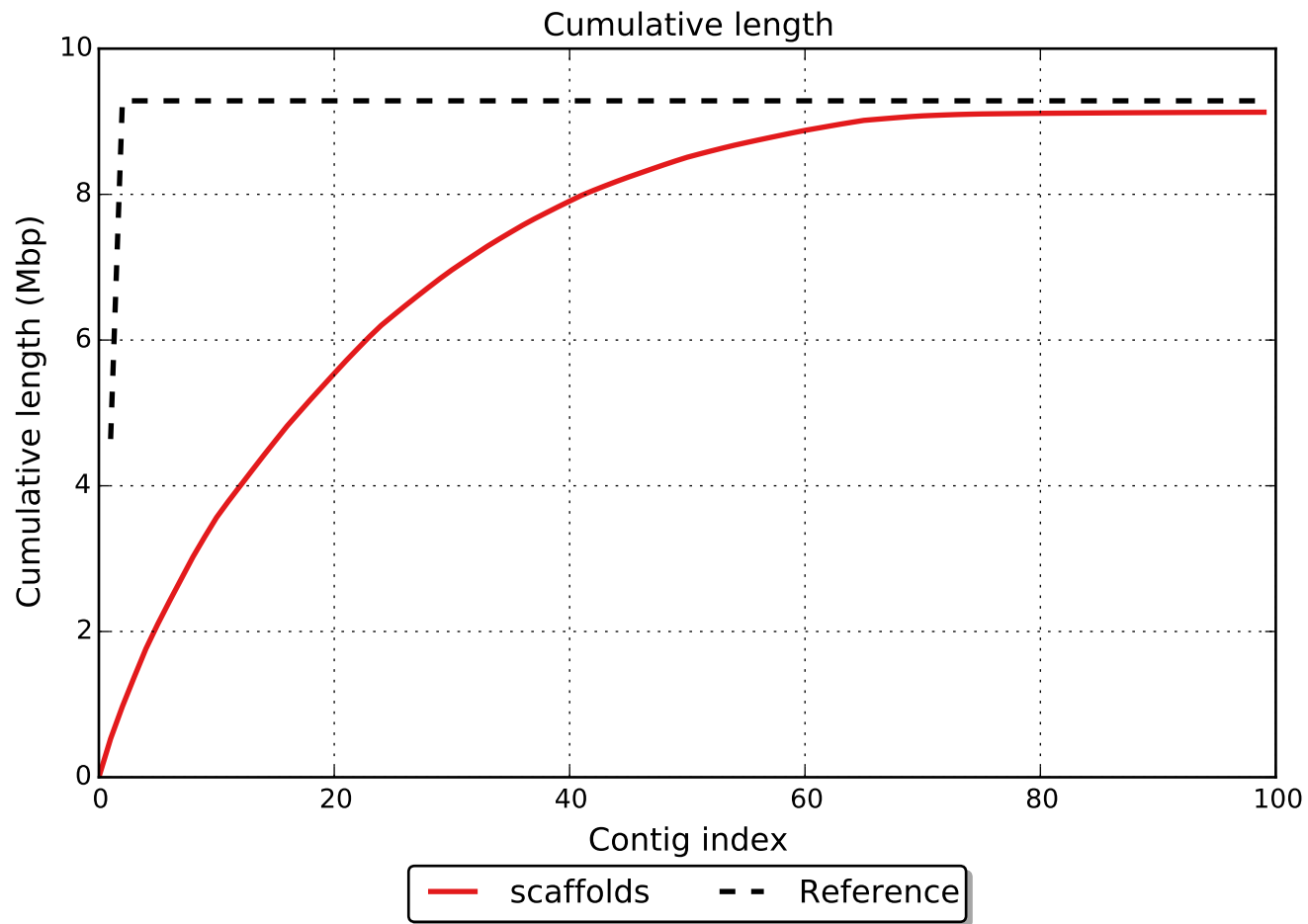
Unaligned report

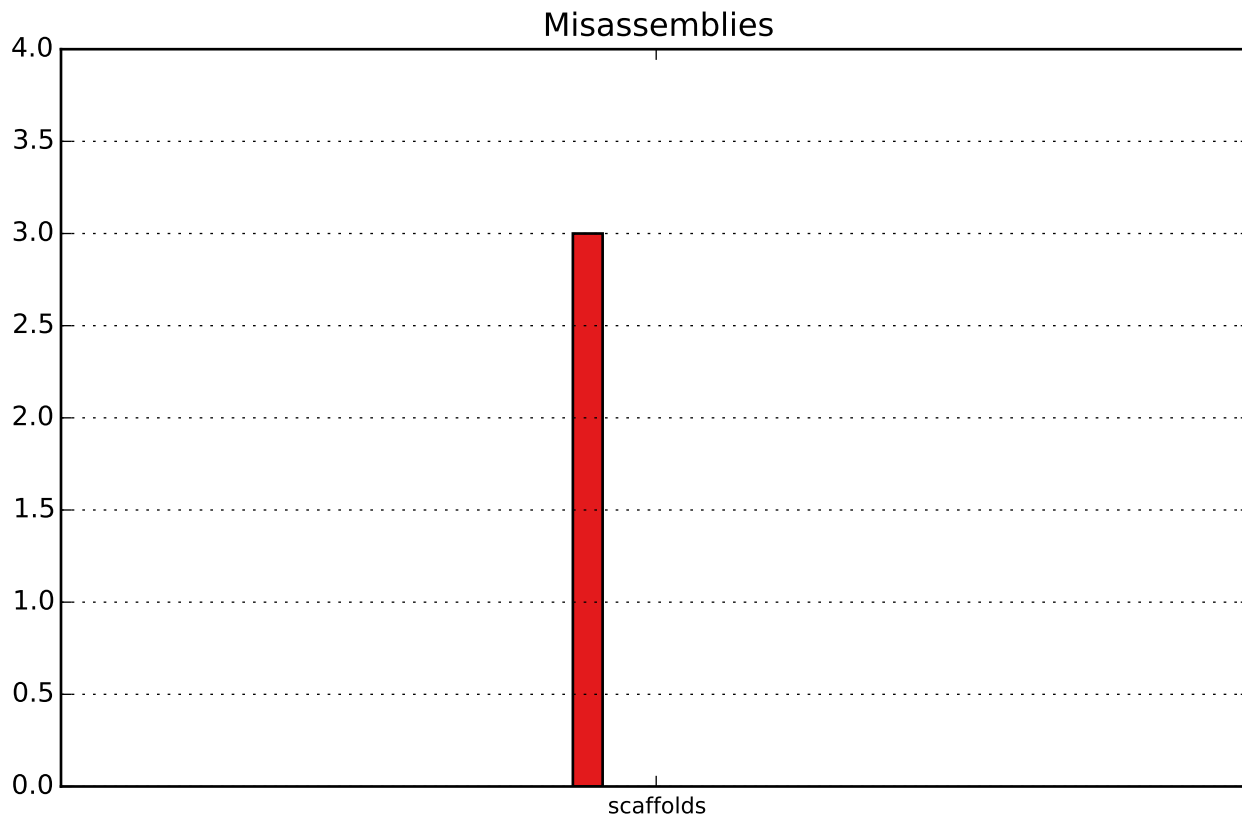
	scaffolds
# fully unaligned contigs	31
Fully unaligned length	1830654
# partially unaligned contigs	23
# with misassembly	7
# both parts are significant	20
Partially unaligned length	2514012
# N's	22

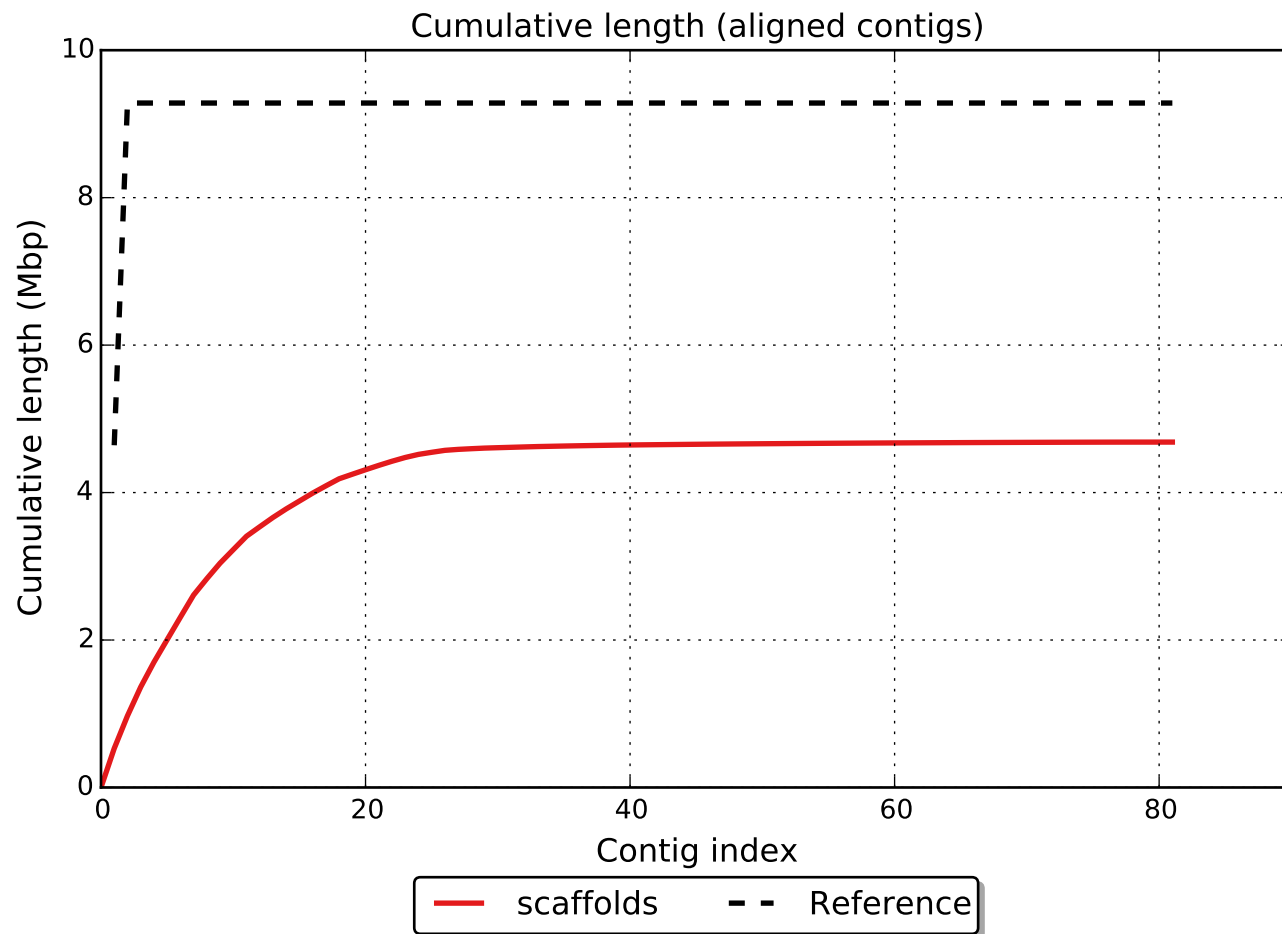
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

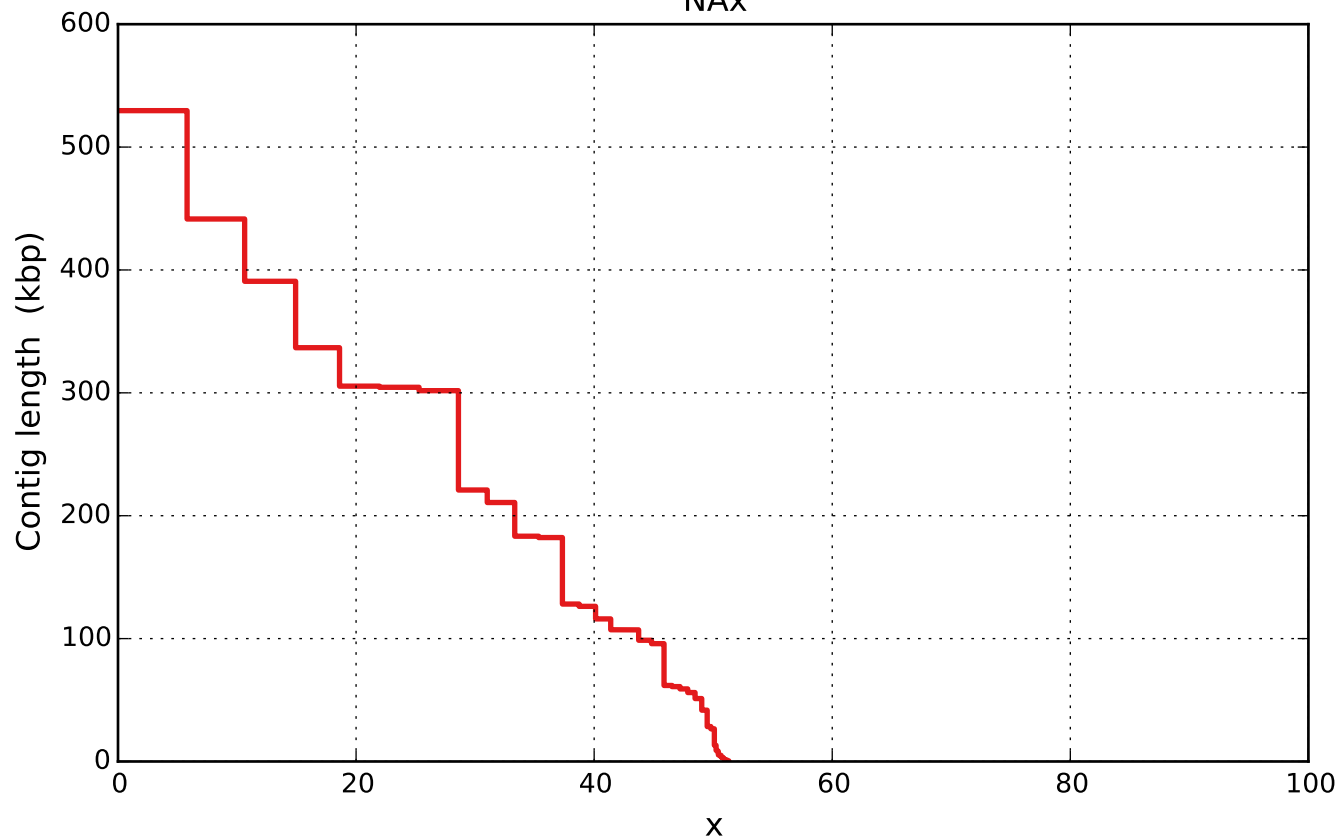








NAx



— scaffolds