

Report

	scaffolds
# contigs (≥ 0 bp)	1110
# contigs (≥ 1000 bp)	297
# contigs (≥ 5000 bp)	209
# contigs (≥ 10000 bp)	155
# contigs (≥ 25000 bp)	82
# contigs (≥ 50000 bp)	42
Total length (≥ 0 bp)	7356224
Total length (≥ 1000 bp)	7060857
Total length (≥ 5000 bp)	6844889
Total length (≥ 10000 bp)	6443865
Total length (≥ 25000 bp)	5259063
Total length (≥ 50000 bp)	3855778
# contigs	352
Largest contig	200996
Total length	7094731
Reference length	9283304
N50	54145
N75	24817
L50	37
L75	85
# misassemblies	115
# misassembled contigs	42
Misassembled contigs length	2166860
# local misassemblies	4
# unaligned contigs	21 + 4 part
Unaligned length	12653
Genome fraction (%)	49.159
Duplication ratio	1.552
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1200.60
# indels per 100 kbp	0.88
Largest alignment	200996
NA50	34010
NA75	15950
LA50	53
LA75	128

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	115
# relocations	97
# translocations	0
# inversions	17
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	42
Misassembled contigs length	2166860
# local misassemblies	4
# mismatches	54790
# indels	40
# short indels	40
# long indels	0
Indels length	45

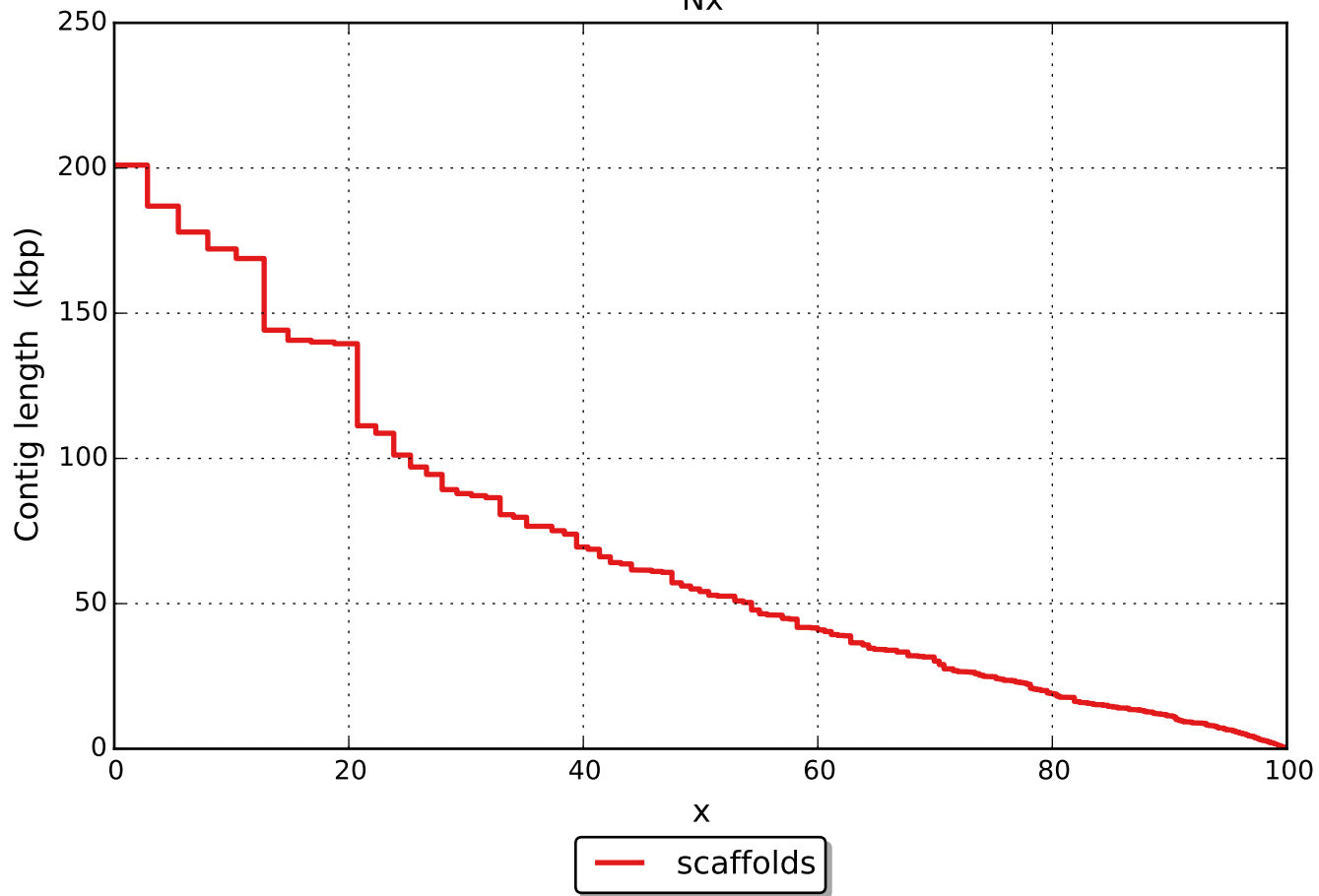
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

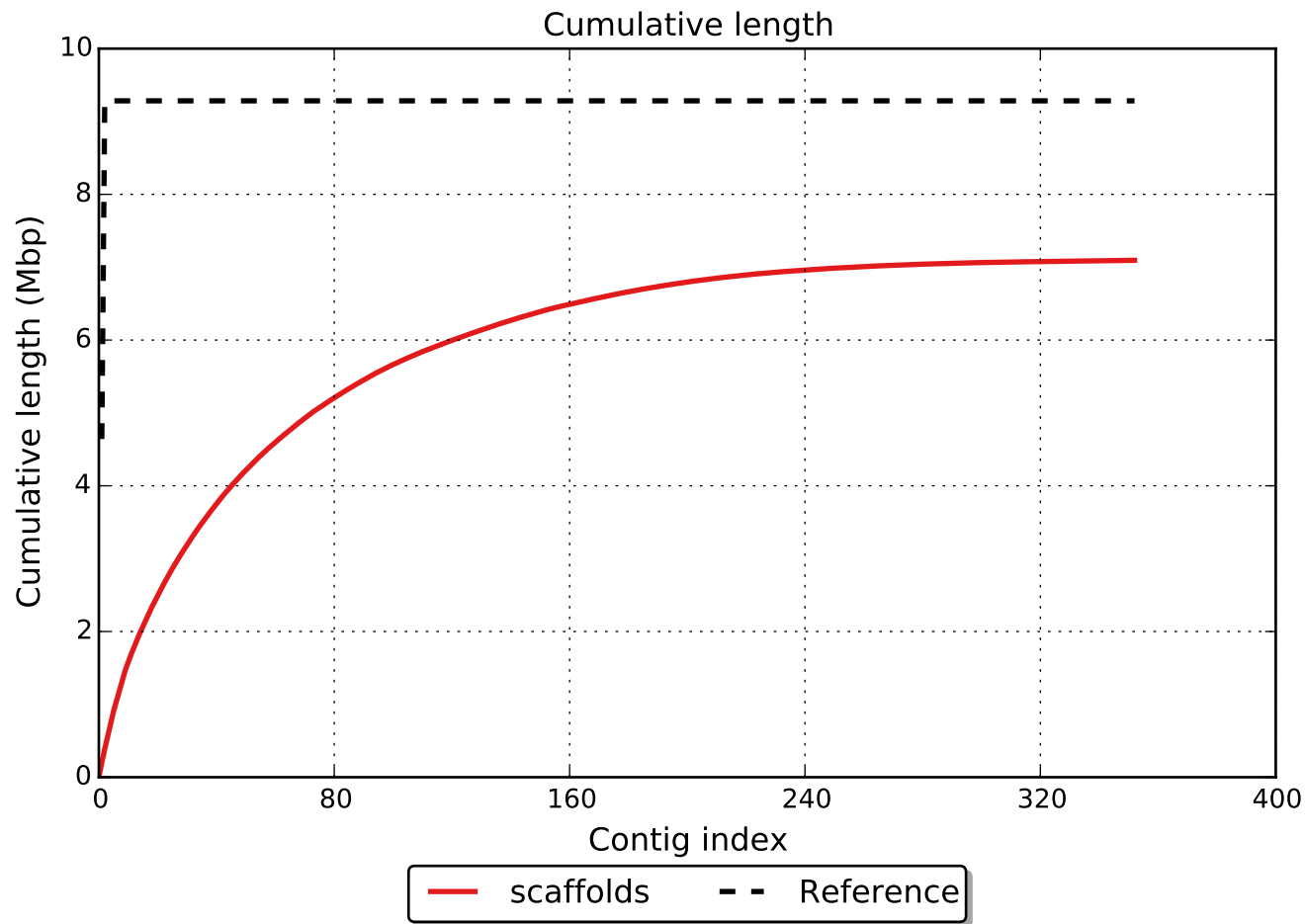
Unaligned report

	scaffolds
# fully unaligned contigs	21
Fully unaligned length	11824
# partially unaligned contigs	4
# with misassembly	0
# both parts are significant	0
Partially unaligned length	829
# N's	0

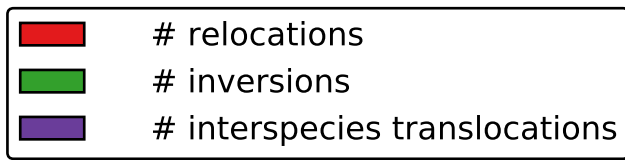
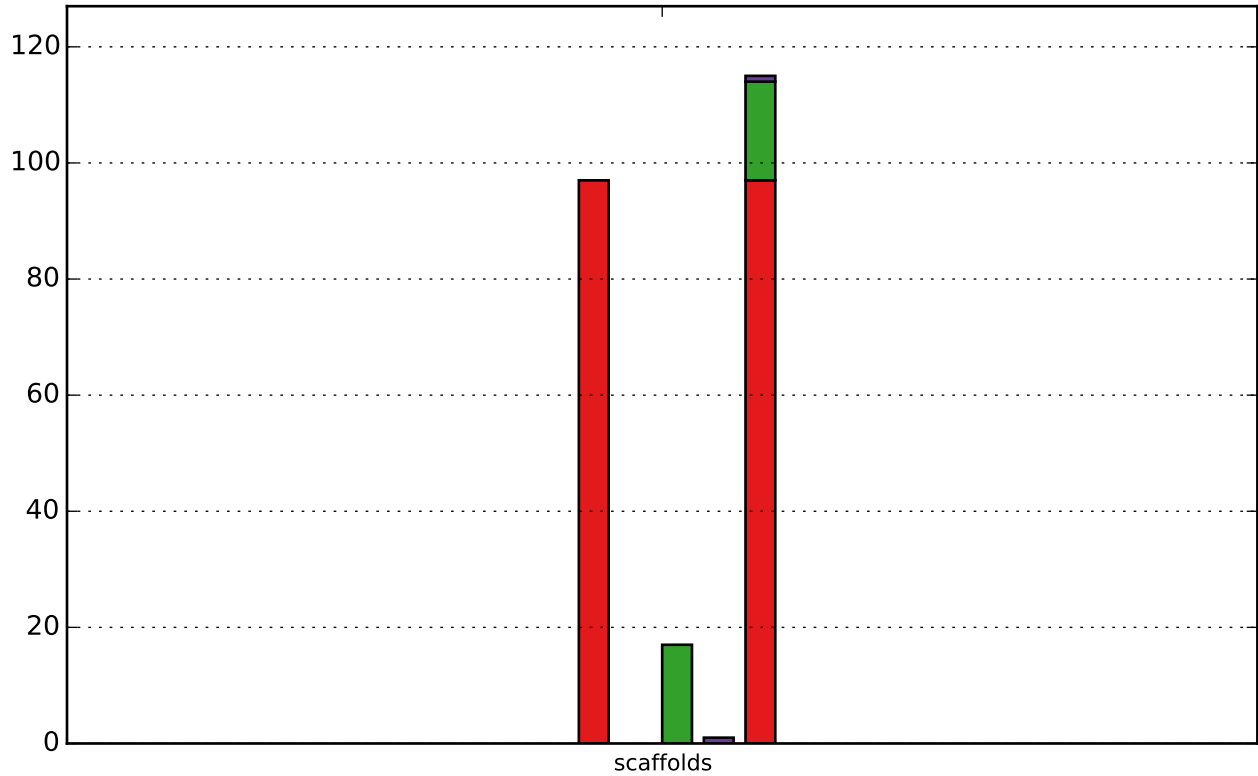
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

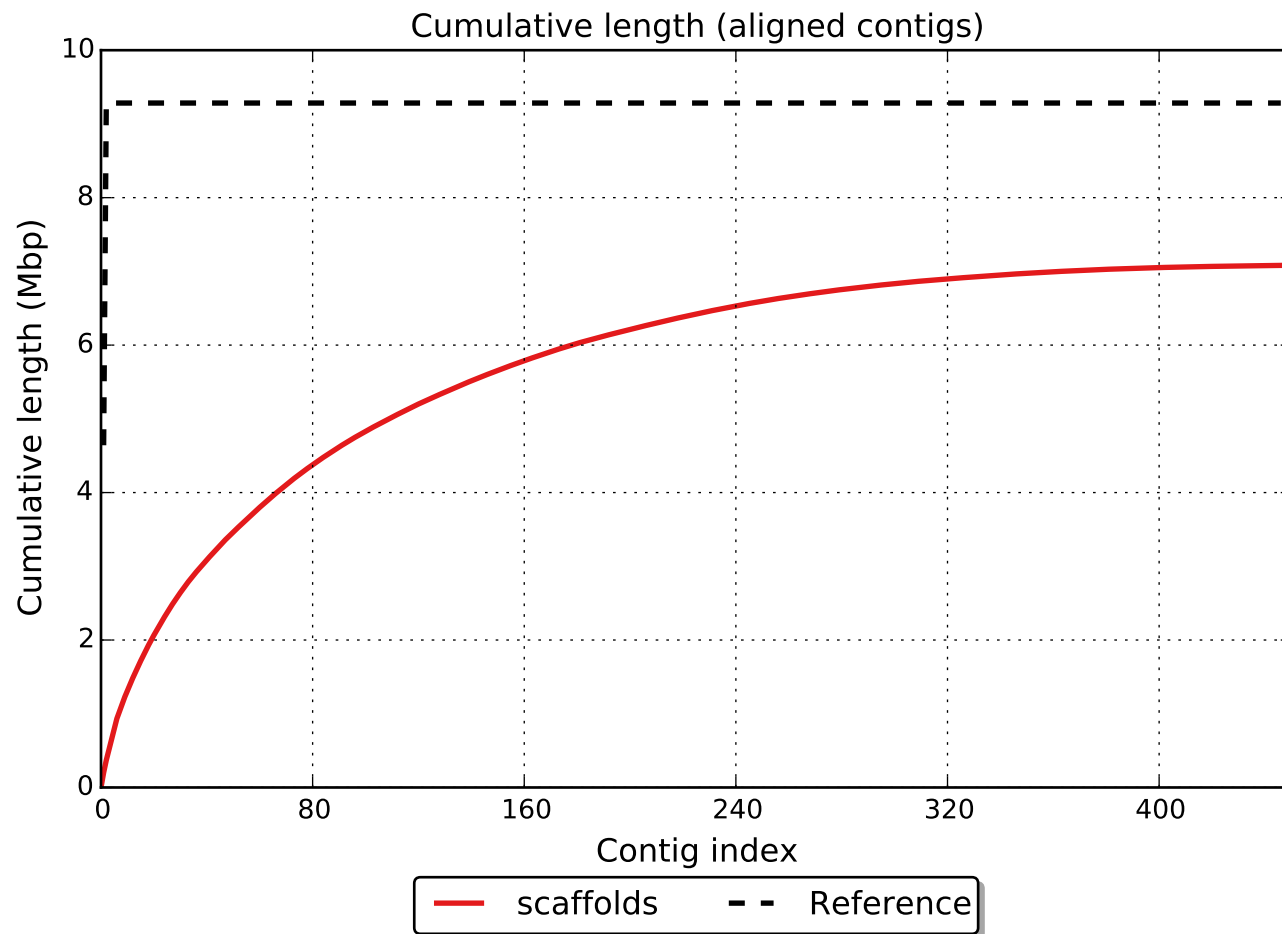
Nx



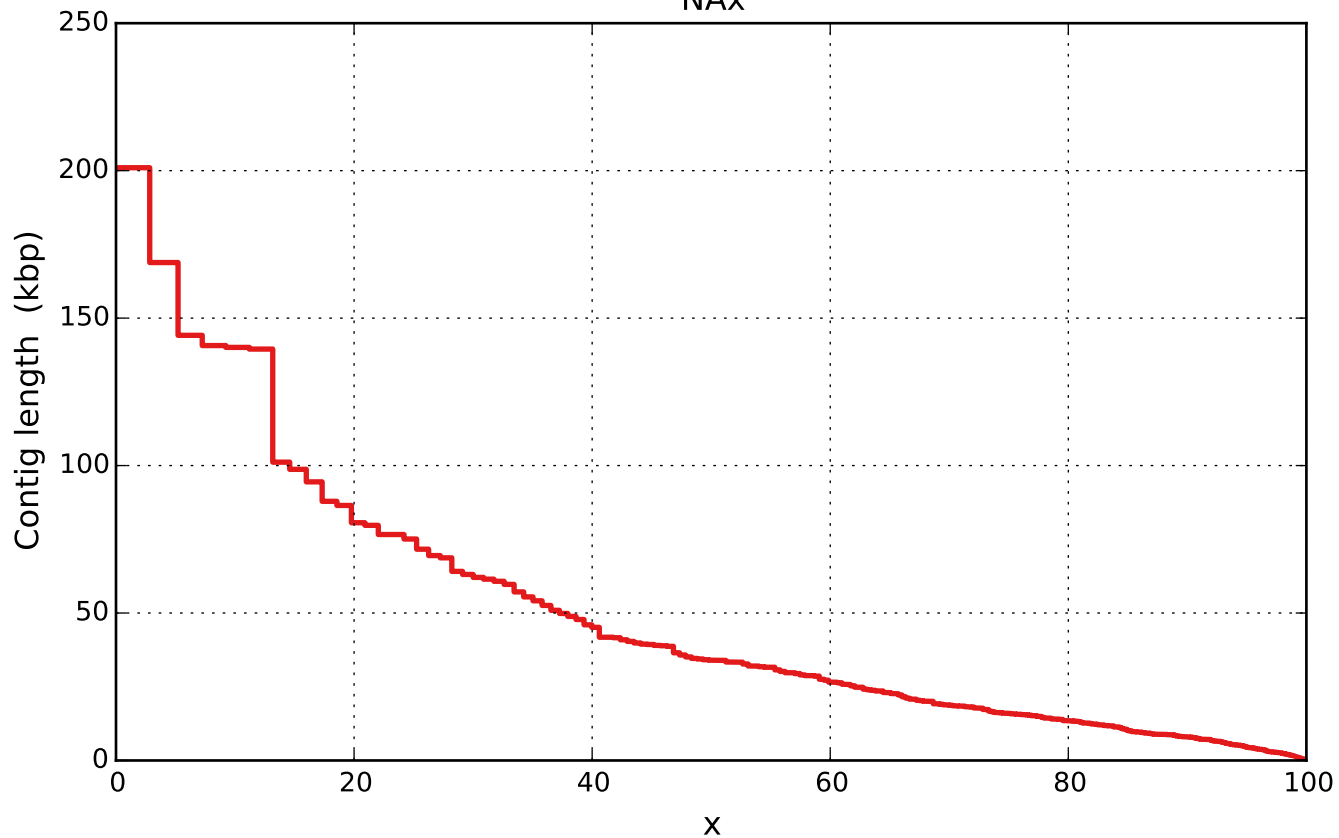


Misassemblies





NAx



— scaffolds