

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	2
# misassembled contigs	2
Misassembled contigs length	804418
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.527
Duplication ratio	1.000
# N's per 100 kbp	1.05
# mismatches per 100 kbp	247.84
# indels per 100 kbp	0.80
Largest alignment	594540
NA50	248289
NA75	131763
LA50	12
LA75	25

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	2
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	804418
# local misassemblies	3
# mismatches	22669
# indels	73
# short indels	73
# long indels	0
Indels length	83

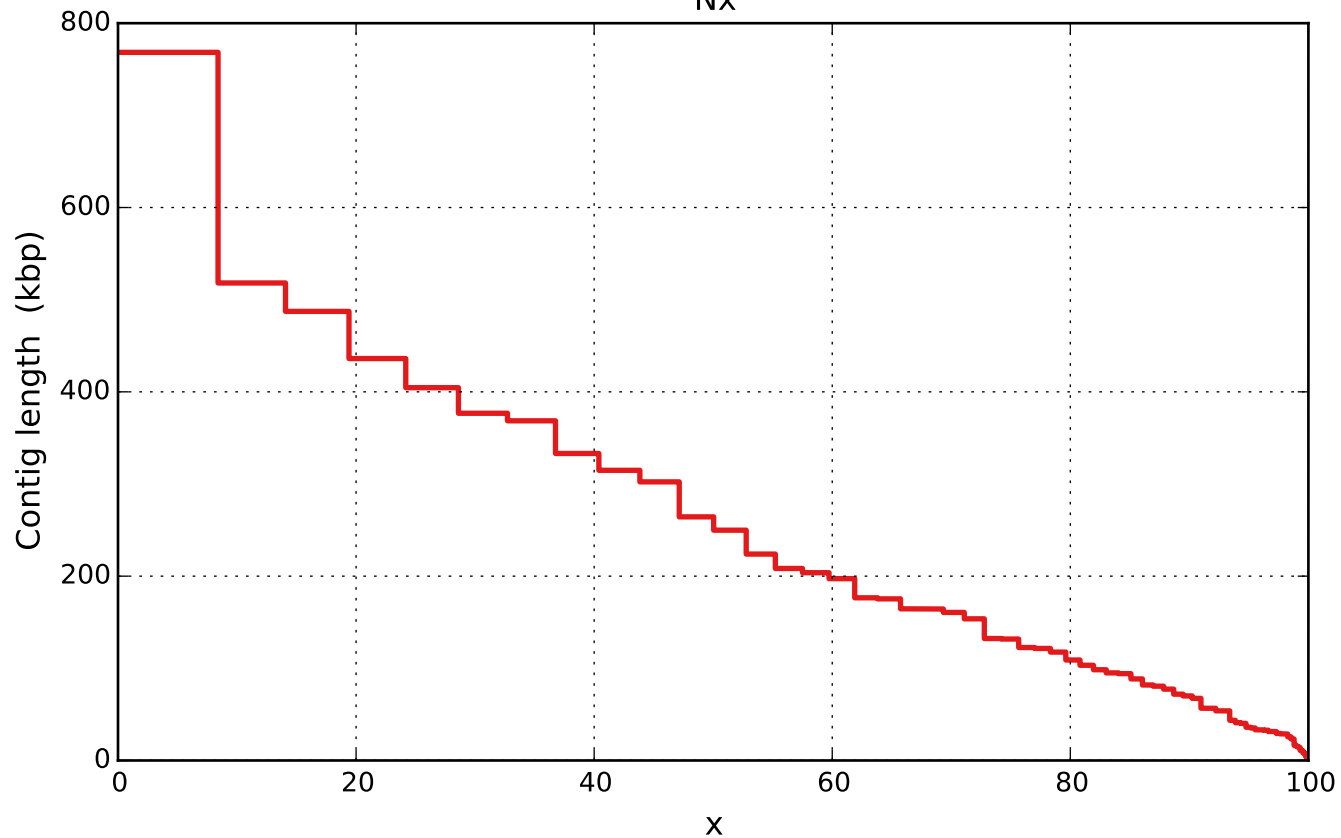
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

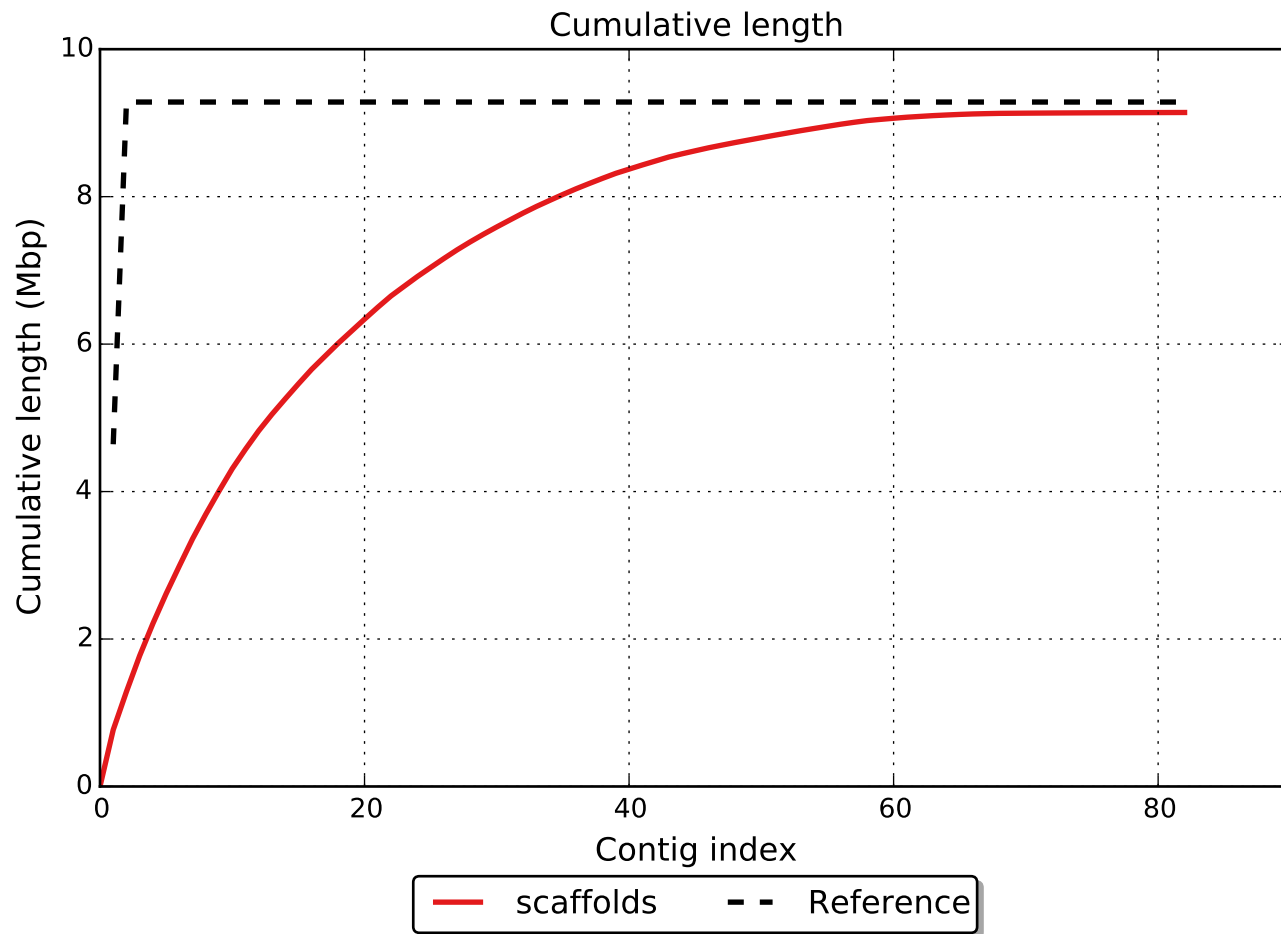
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	96

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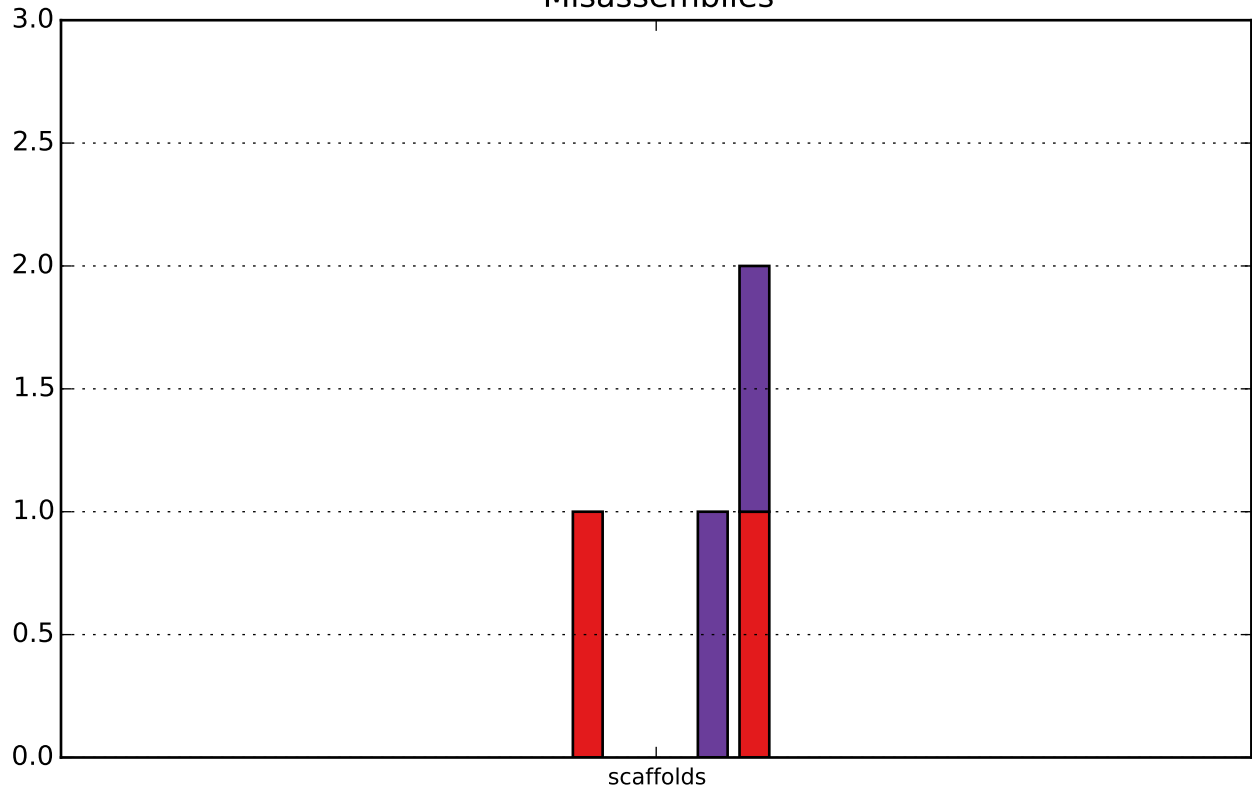
Nx

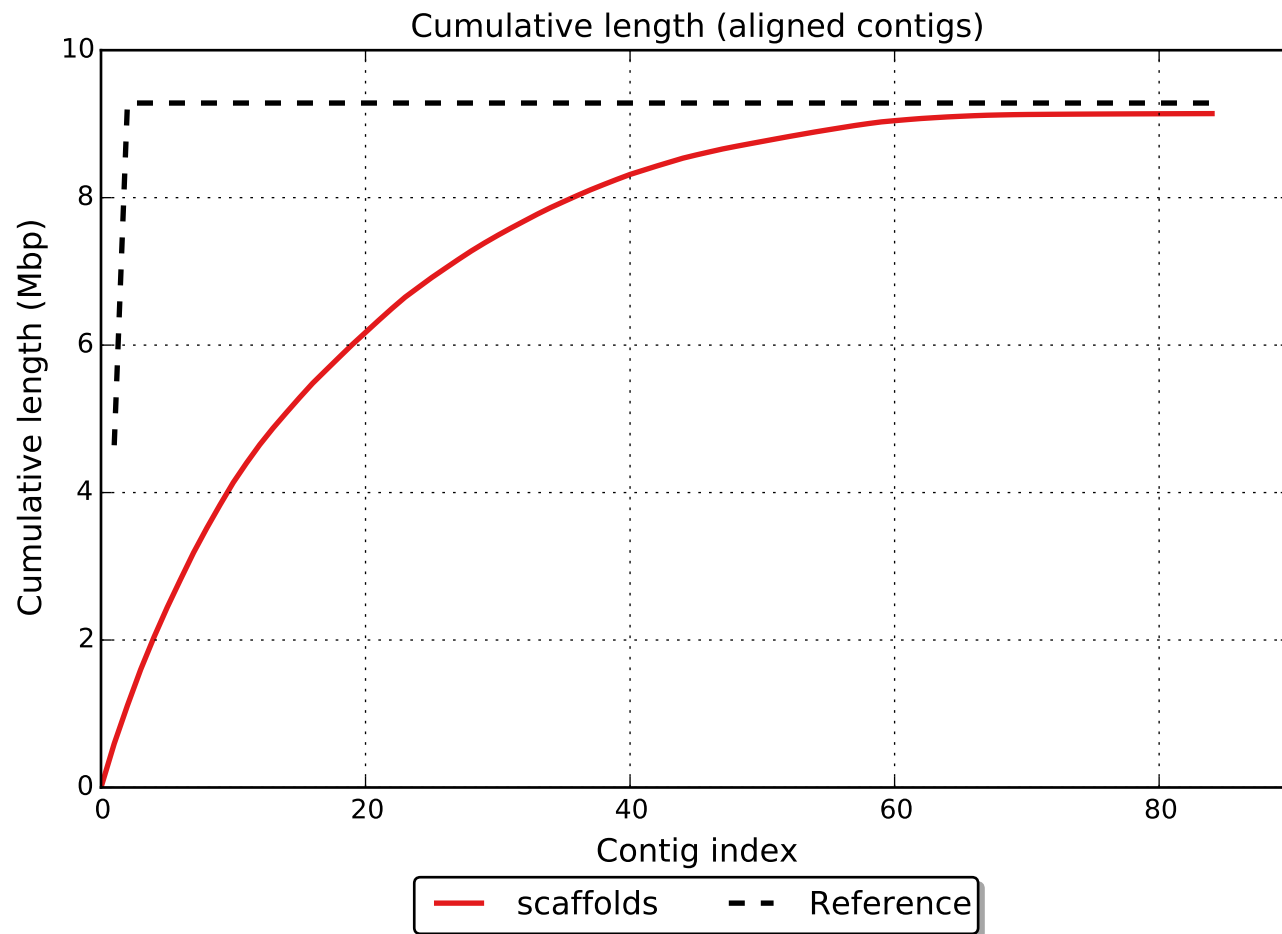


— scaffolds

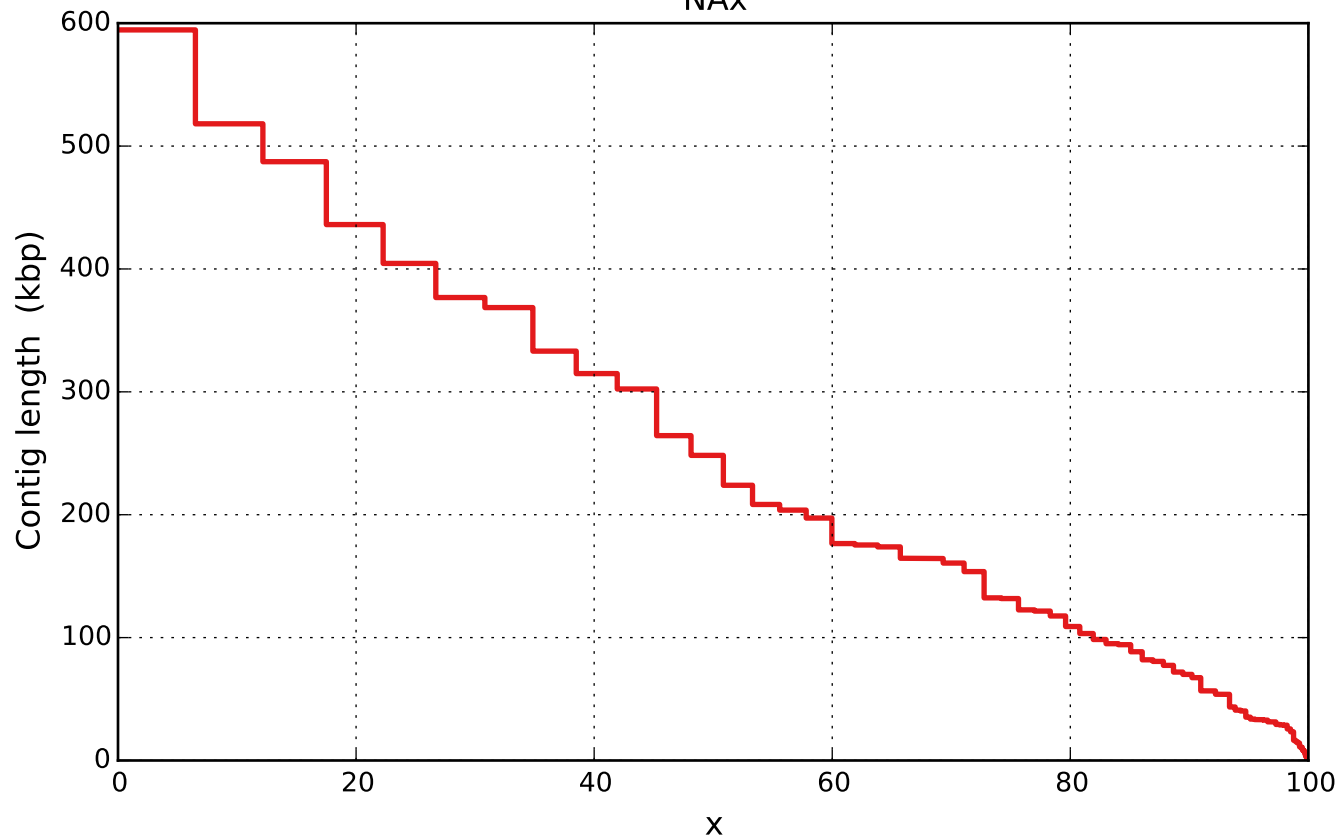


Misassemblies





NAx



— scaffolds