

Report

	scaffolds
# contigs (≥ 0 bp)	187
# contigs (≥ 1000 bp)	86
# contigs (≥ 5000 bp)	71
# contigs (≥ 10000 bp)	67
# contigs (≥ 25000 bp)	62
# contigs (≥ 50000 bp)	48
Total length (≥ 0 bp)	9140317
Total length (≥ 1000 bp)	9103206
Total length (≥ 5000 bp)	9082242
Total length (≥ 10000 bp)	9049457
Total length (≥ 25000 bp)	8968226
Total length (≥ 50000 bp)	8515864
# contigs	110
Largest contig	529642
Total length	9118481
Reference length	9283304
N50	210553
N75	117600
L50	14
L75	28
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	42 + 33 part
Unaligned length	4078123
Genome fraction (%)	49.789
Duplication ratio	1.091
# N's per 100 kbp	0.33
# mismatches per 100 kbp	464.78
# indels per 100 kbp	0.97
Largest alignment	529642
NA50	28010
LA50	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).

Misassemblies report

	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	32
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	21482
# indels	45
# short indels	45
# long indels	0
Indels length	48

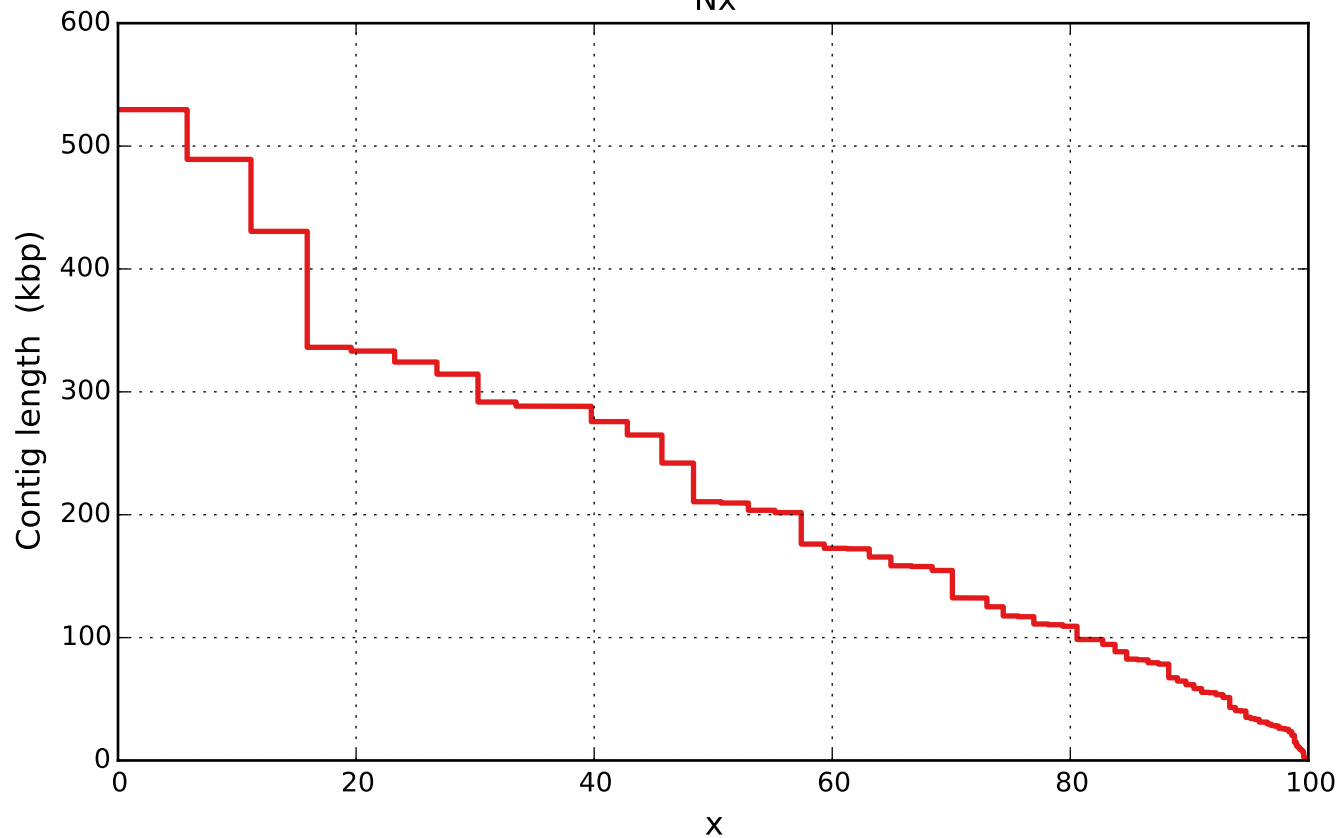
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

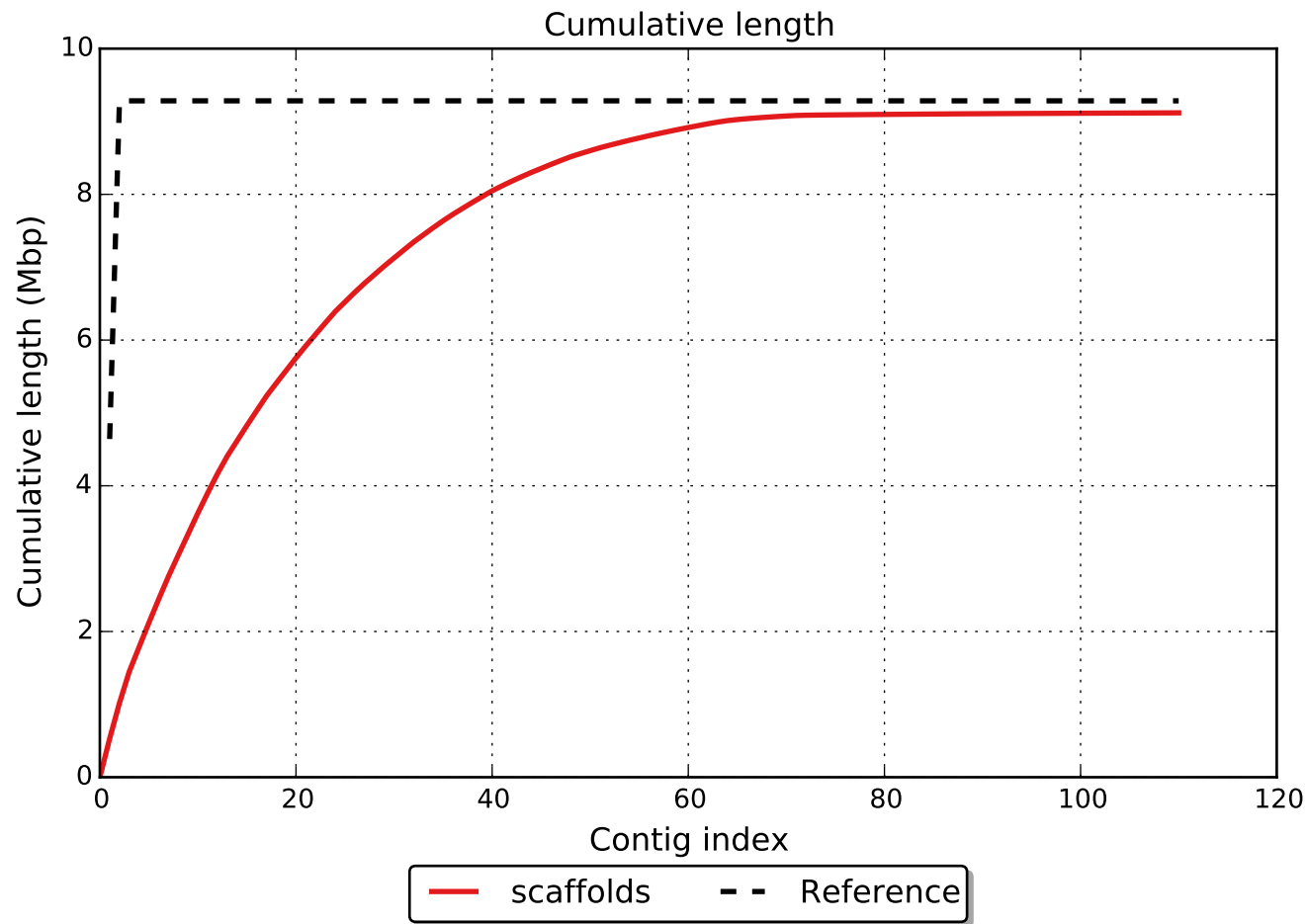
	scaffolds
# fully unaligned contigs	42
Fully unaligned length	733649
# partially unaligned contigs	33
# with misassembly	22
# both parts are significant	32
Partially unaligned length	3344474
# N's	30

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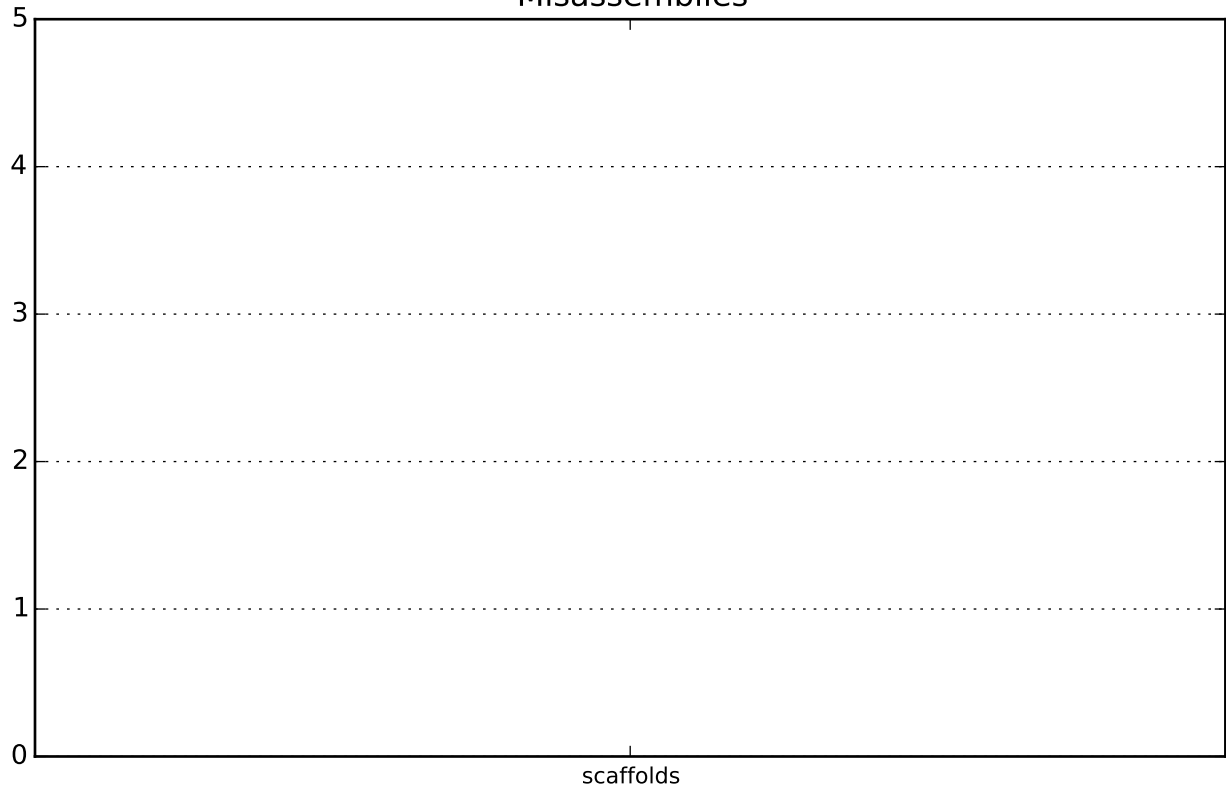
Nx

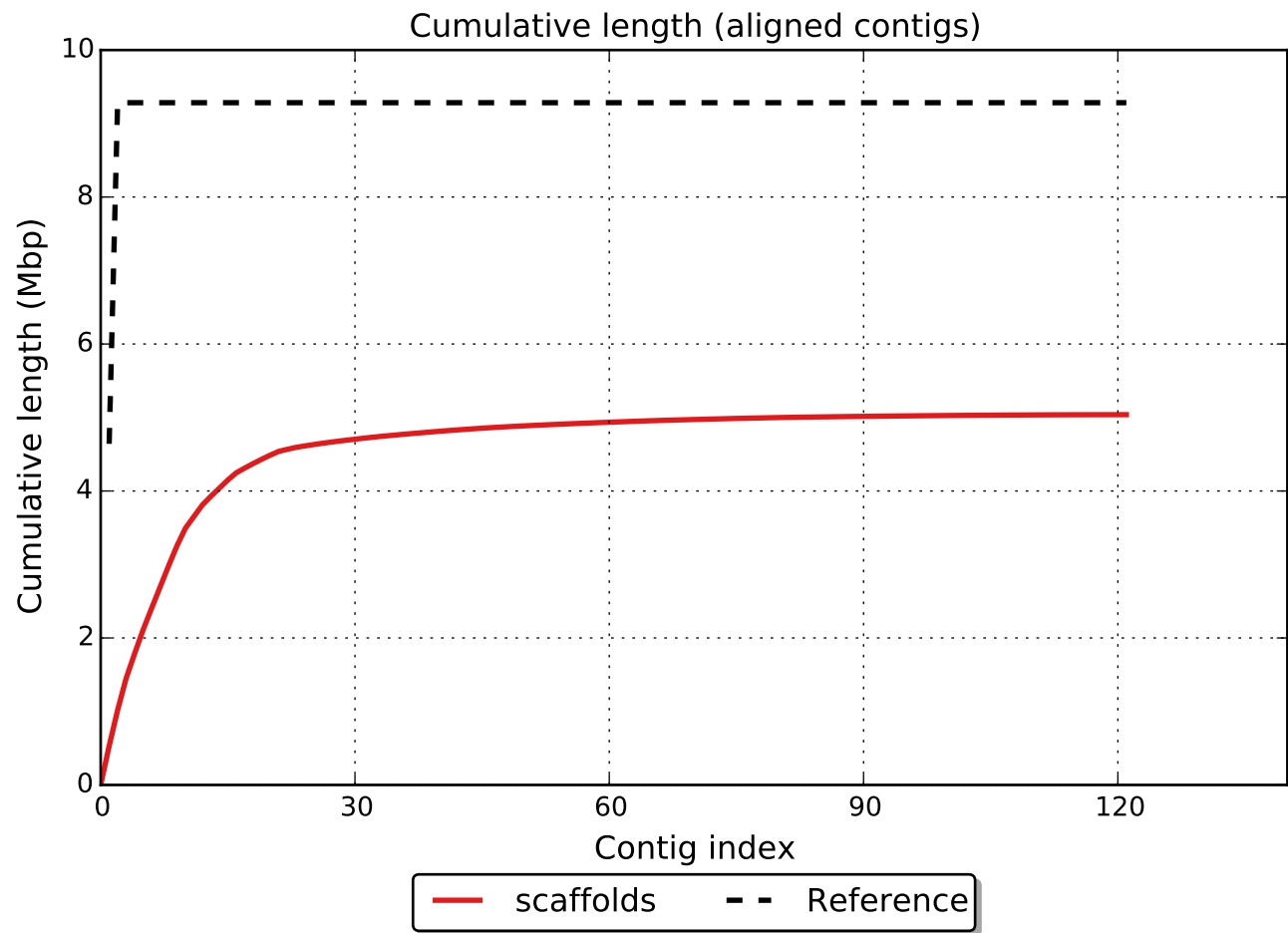


— scaffolds

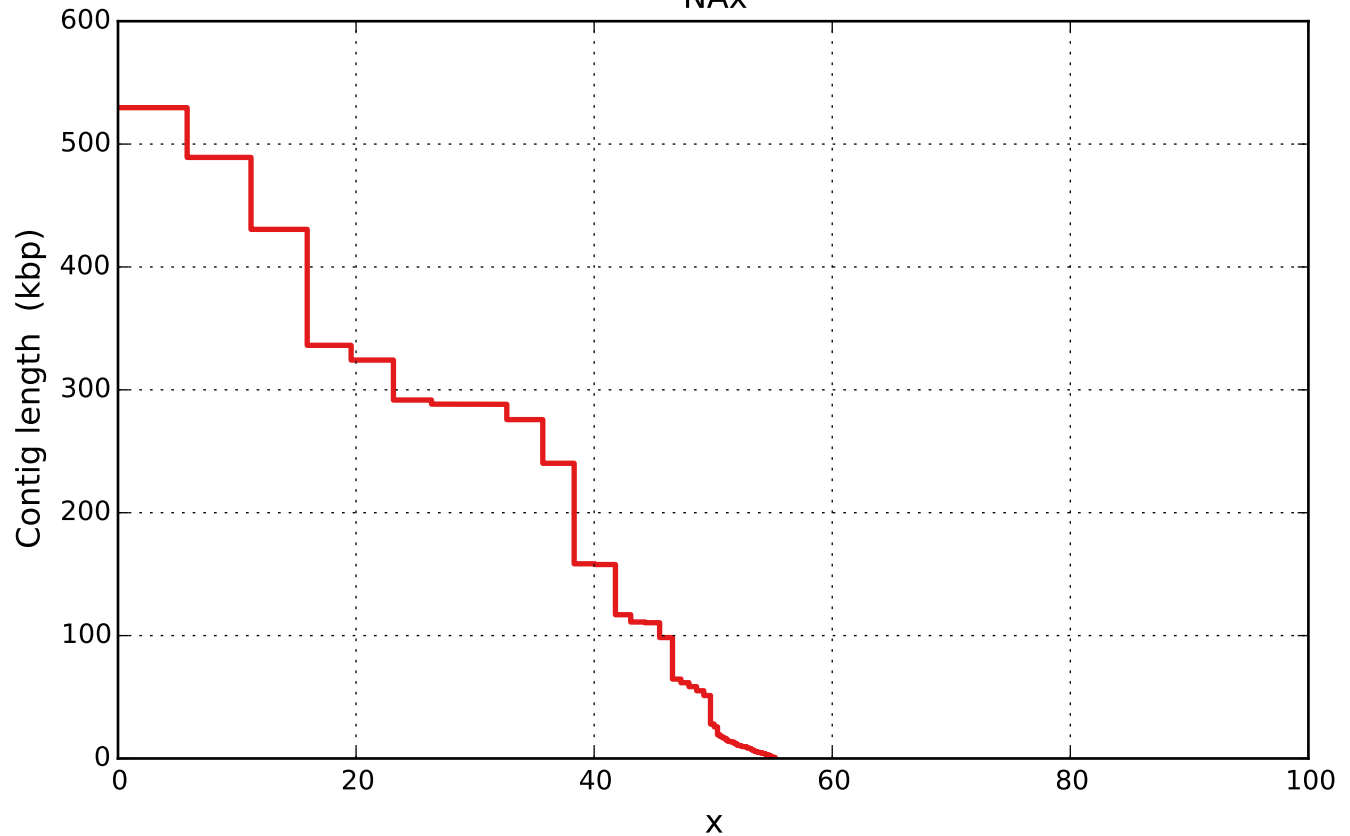


Misassemblies





NAx



— scaffolds