

Report

	scaffolds
# contigs (≥ 0 bp)	308
# contigs (≥ 1000 bp)	124
# contigs (≥ 5000 bp)	97
# contigs (≥ 10000 bp)	79
# contigs (≥ 25000 bp)	54
# contigs (≥ 50000 bp)	37
Total length (≥ 0 bp)	4603571
Total length (≥ 1000 bp)	4562517
Total length (≥ 5000 bp)	4491950
Total length (≥ 10000 bp)	4364624
Total length (≥ 25000 bp)	3974973
Total length (≥ 50000 bp)	3399888
# contigs	132
Largest contig	264572
Total length	4568391
Reference length	9283304
N50	76208
N75	43987
L50	20
L75	38
# misassemblies	5
# misassembled contigs	5
Misassembled contigs length	310368
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	49.176
Duplication ratio	1.001
# N's per 100 kbp	13.44
# mismatches per 100 kbp	541.63
# indels per 100 kbp	0.53
Largest alignment	264572
NA50	76208
NA75	43392
LA50	20
LA75	39

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	5
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	4
# possibly misassembled contigs	0
# misassembled contigs	5
Misassembled contigs length	310368
# local misassemblies	3
# mismatches	24726
# indels	24
# short indels	22
# long indels	2
Indels length	139

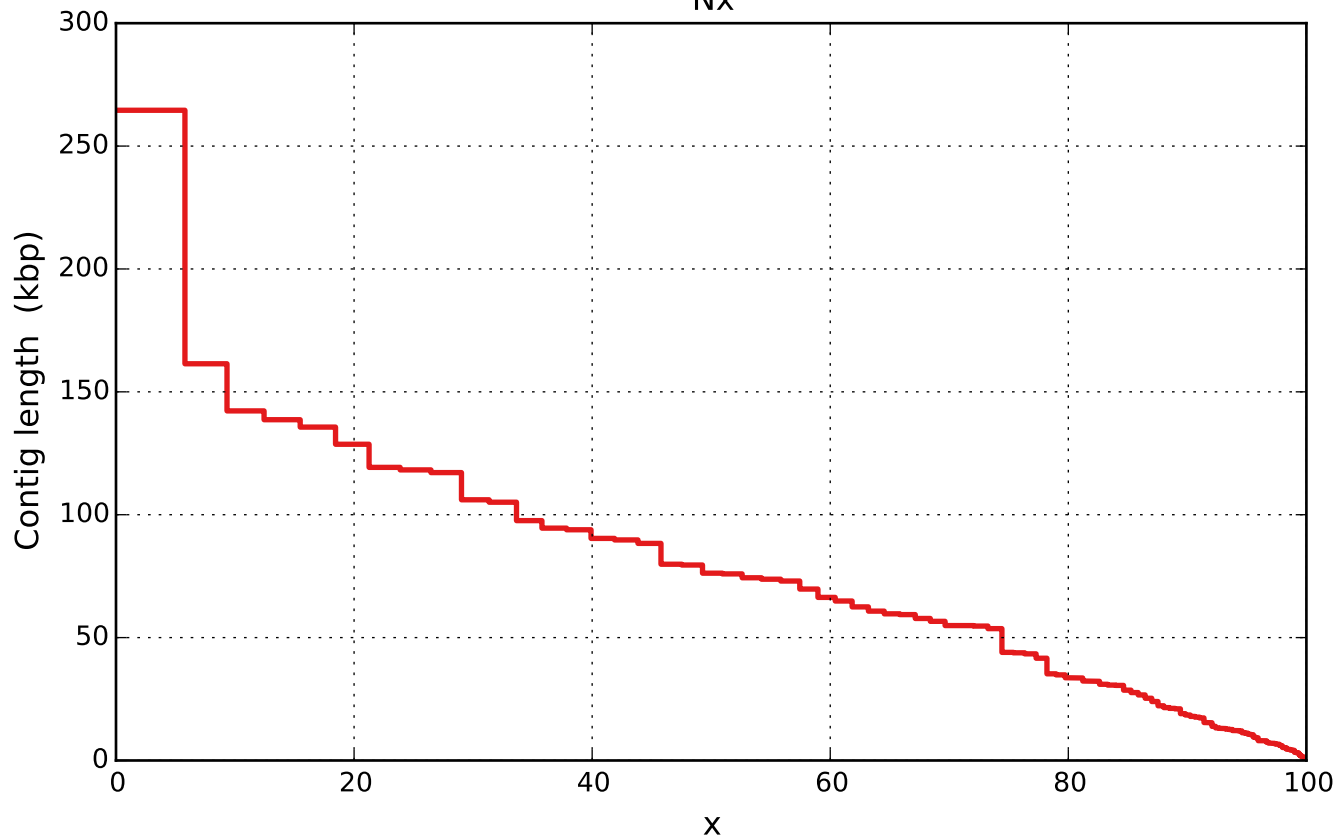
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

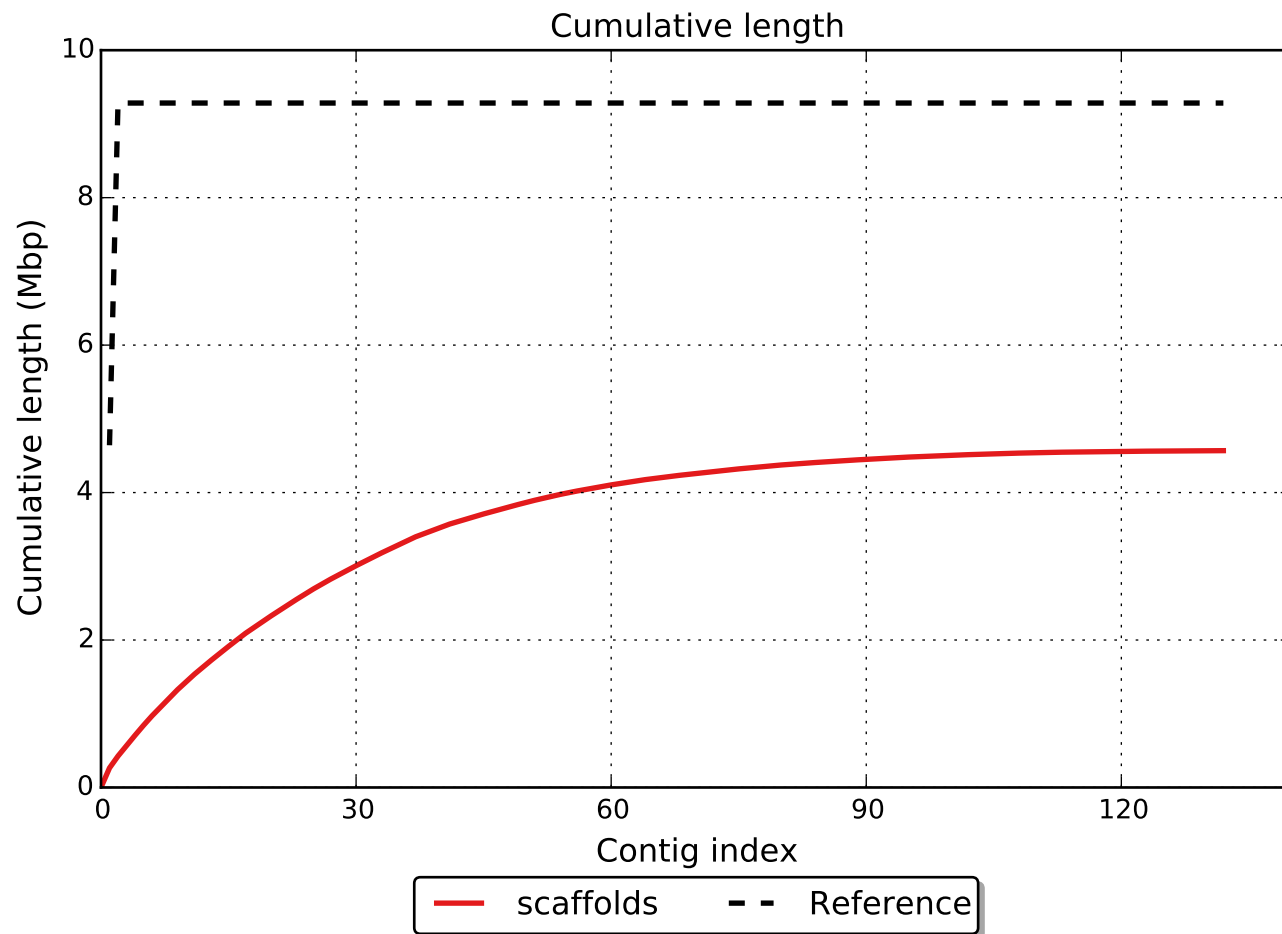
Unaligned report

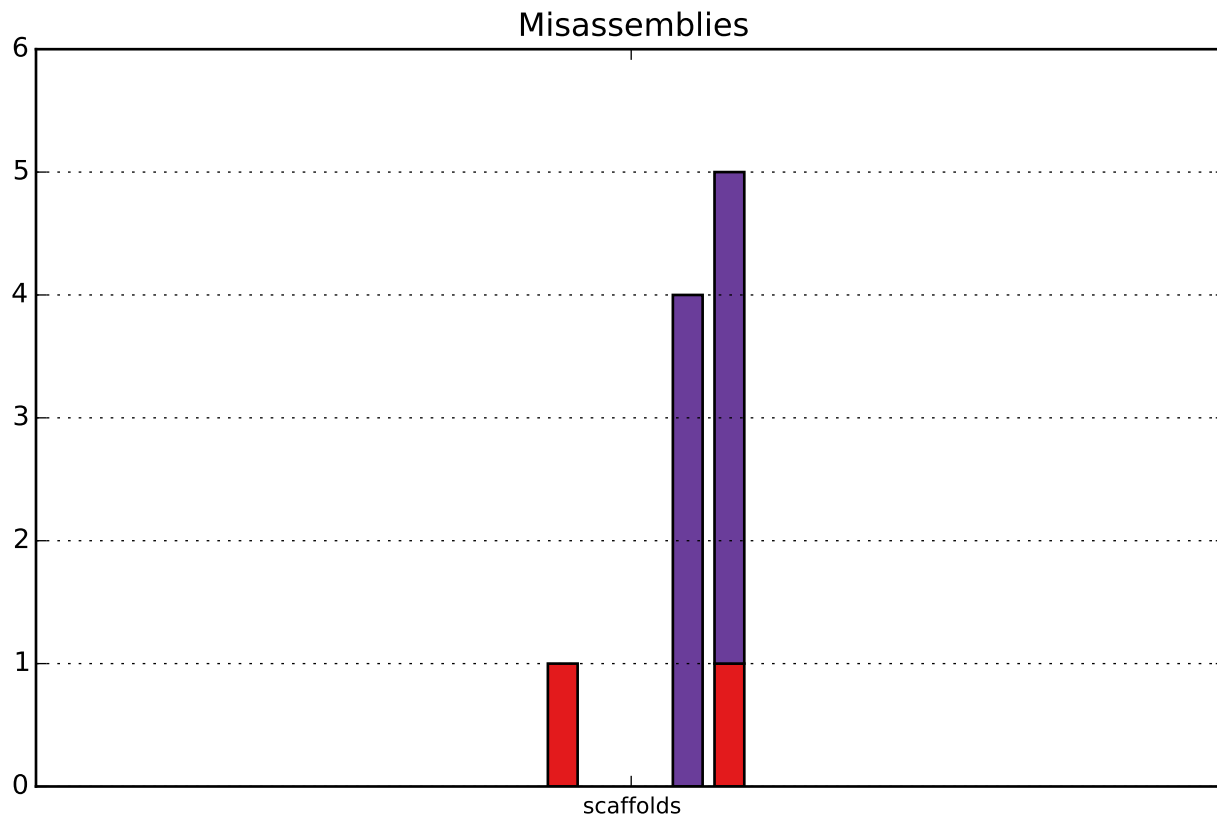
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	614

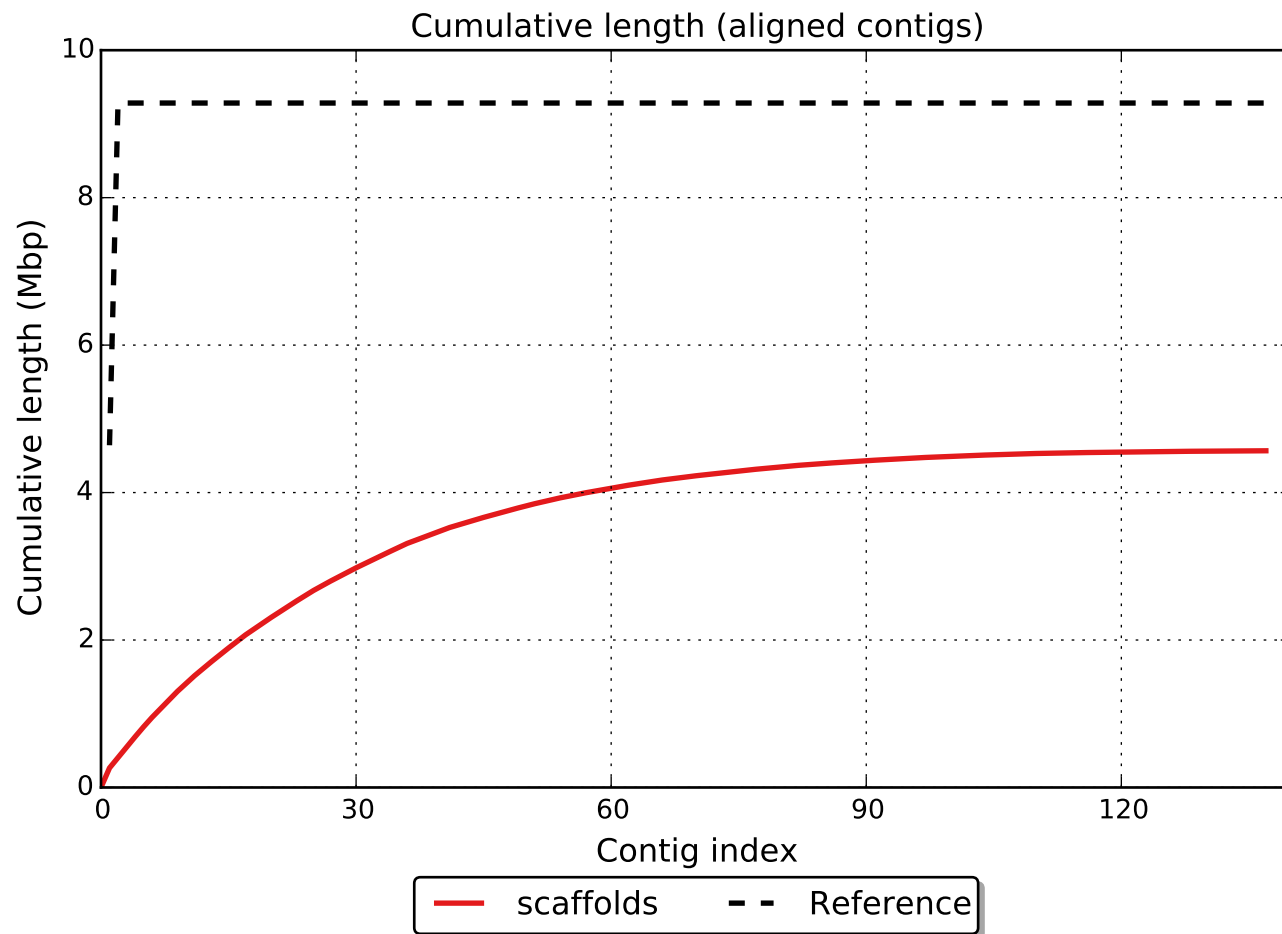
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx









NAx

