

Report

	scaffolds
# contigs (≥ 0 bp)	137
# contigs (≥ 1000 bp)	78
# contigs (≥ 5000 bp)	66
# contigs (≥ 10000 bp)	62
# contigs (≥ 25000 bp)	55
# contigs (≥ 50000 bp)	41
Total length (≥ 0 bp)	9157004
Total length (≥ 1000 bp)	9135989
Total length (≥ 5000 bp)	9112641
Total length (≥ 10000 bp)	9079171
Total length (≥ 25000 bp)	8963305
Total length (≥ 50000 bp)	8497357
# contigs	89
Largest contig	657825
Total length	9144127
Reference length	9283304
N50	315111
N75	131793
L50	11
L75	24
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	36823
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.493
Duplication ratio	1.000
# N's per 100 kbp	0.84
# mismatches per 100 kbp	191.91
# indels per 100 kbp	0.68
Largest alignment	657825
NA50	315111
NA75	131793
LA50	11
LA75	24

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	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	36823
# local misassemblies	1
# mismatches	17547
# indels	62
# short indels	61
# long indels	1
Indels length	132

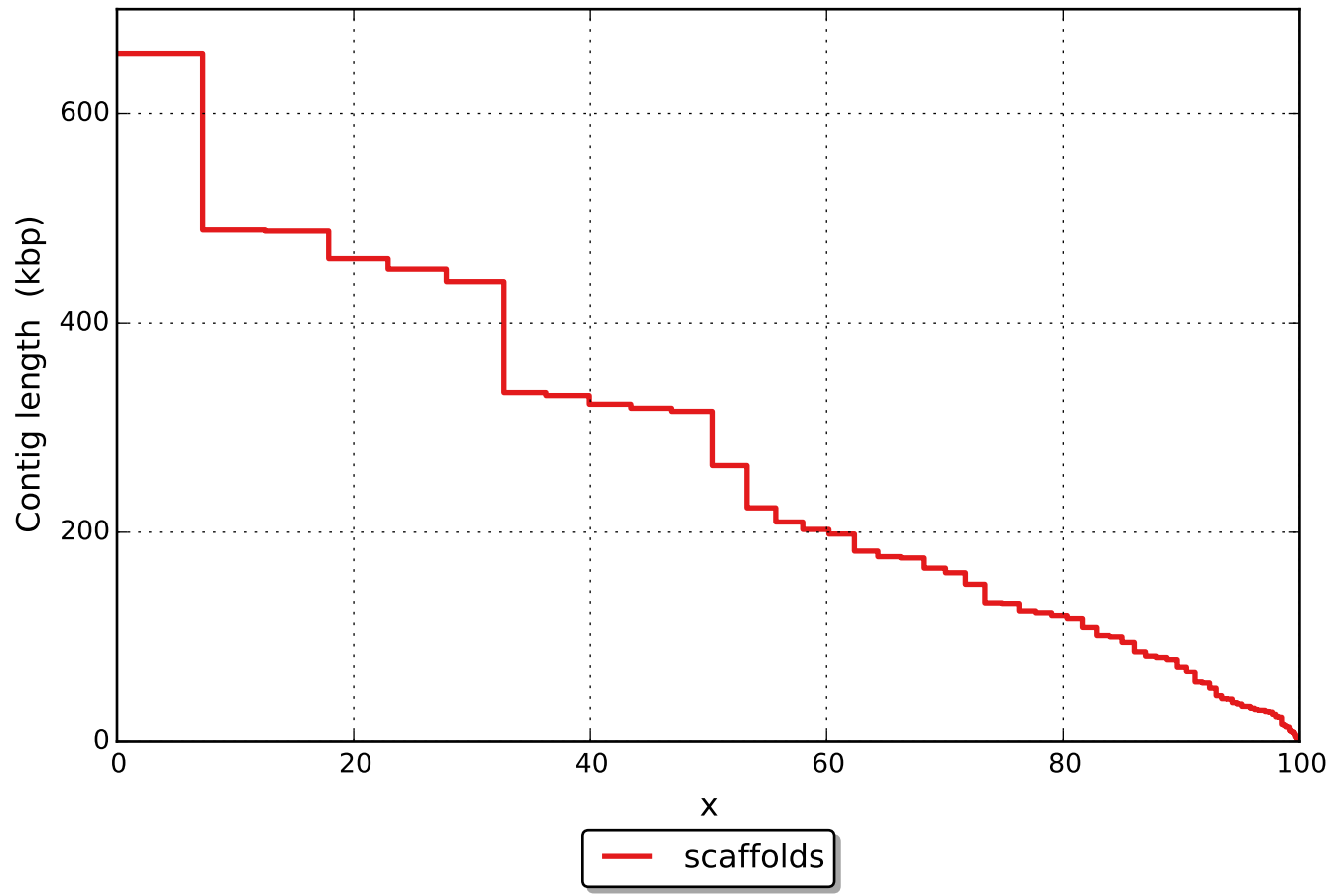
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

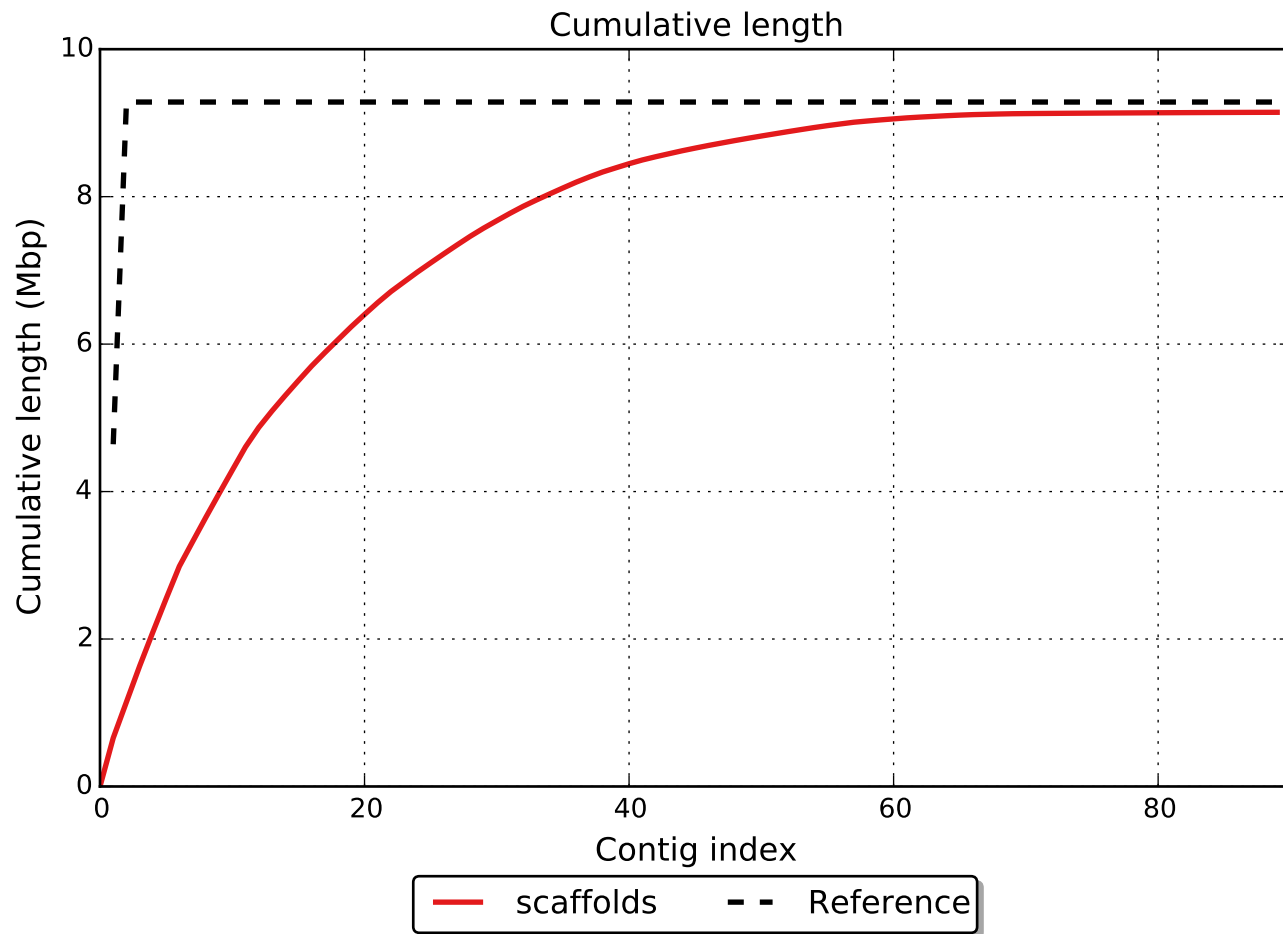
Unaligned report

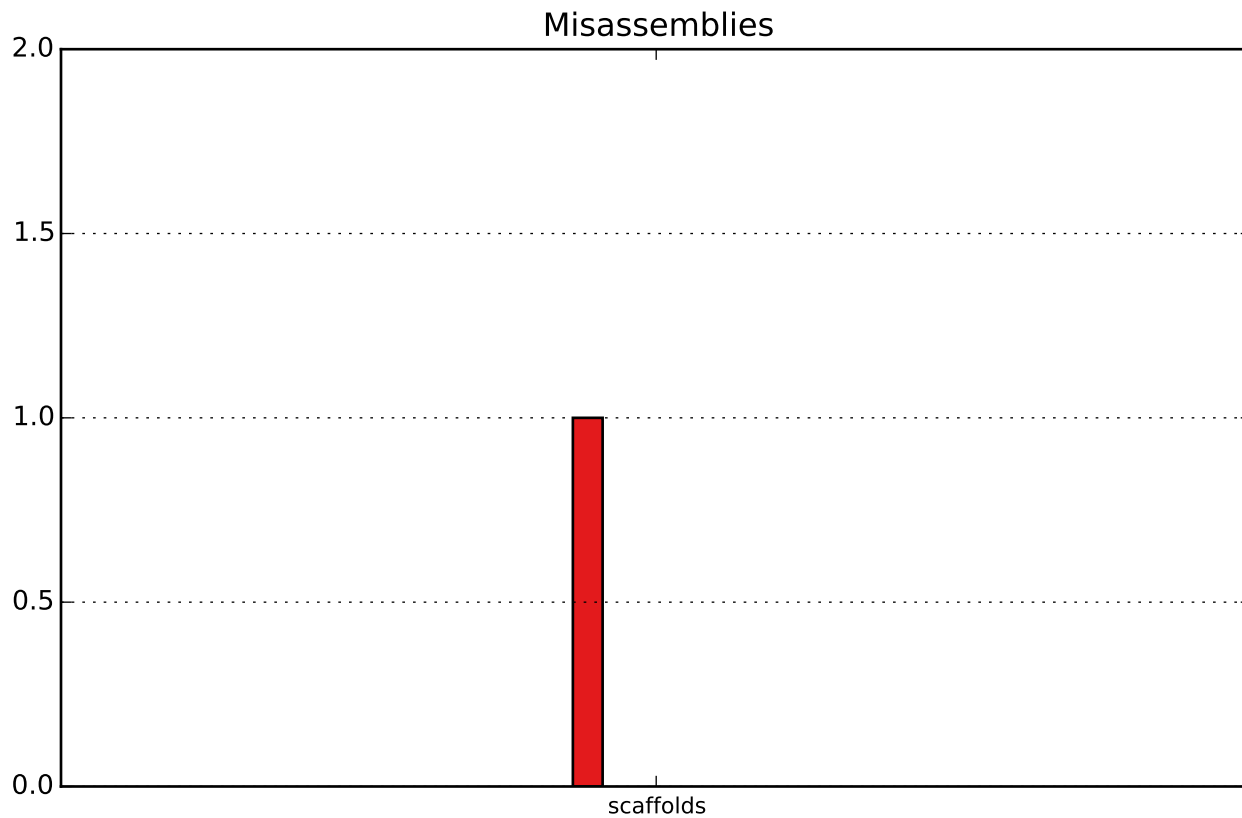
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	77

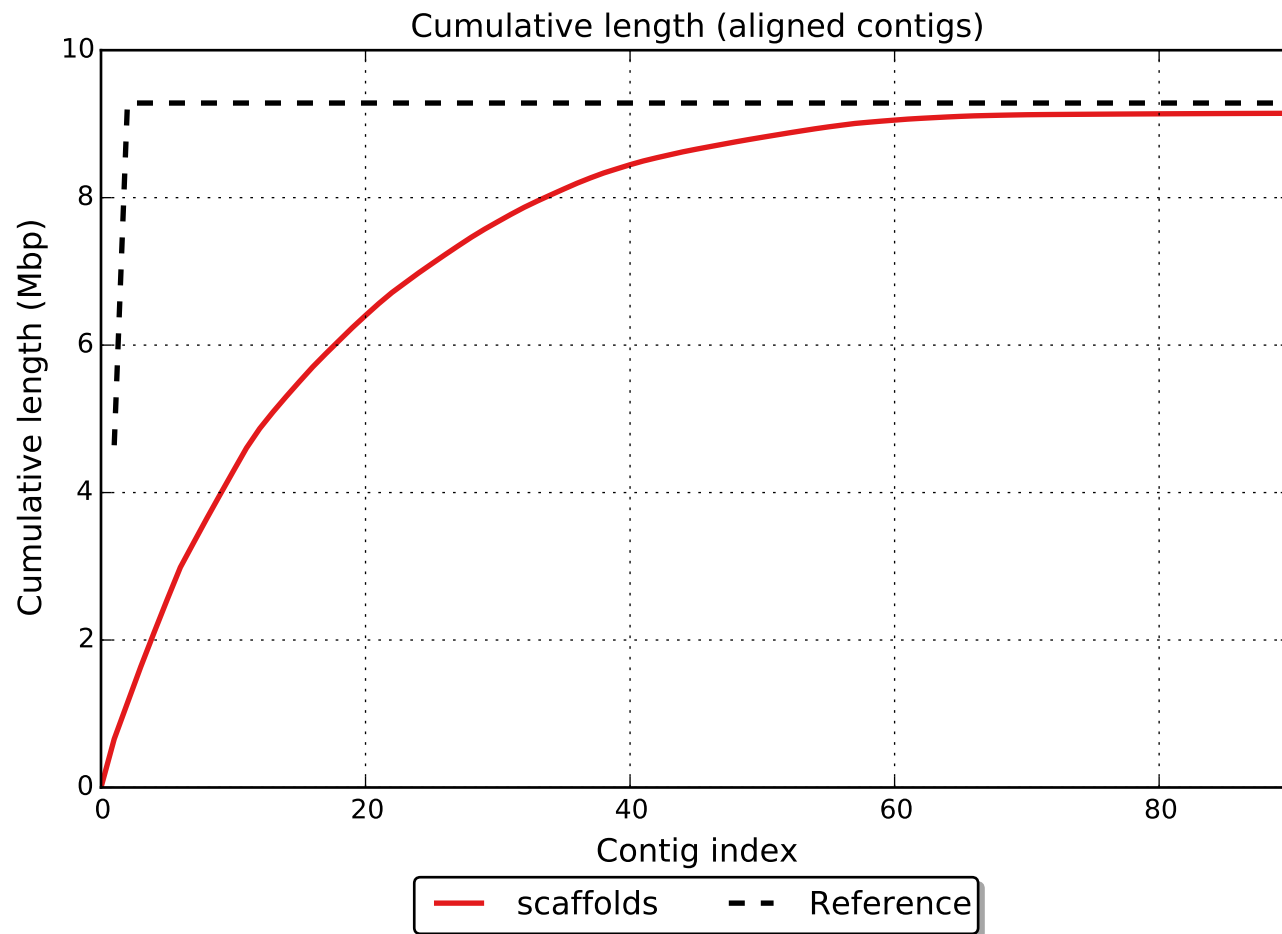
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx









NAx

