

Report

	scaffolds
# contigs (≥ 0 bp)	1003
# contigs (≥ 1000 bp)	802
# contigs (≥ 5000 bp)	325
# contigs (≥ 10000 bp)	102
# contigs (≥ 25000 bp)	2
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	4374169
Total length (≥ 1000 bp)	4264728
Total length (≥ 5000 bp)	2960601
Total length (≥ 10000 bp)	1385446
Total length (≥ 25000 bp)	66428
Total length (≥ 50000 bp)	0
# contigs	917
Largest contig	37682
Total length	4348006
Reference length	4641652
N50	7401
N75	4233
L50	195
L75	390
# misassemblies	16
# misassembled contigs	15
Misassembled contigs length	86787
# local misassemblies	10
# unaligned contigs	4 + 2 part
Unaligned length	4994
Genome fraction (▼)	93.360
Duplication ratio	1.002
# N's per 100 kbp	485.81
# mismatches per 100 kbp	166.82
# indels per 100 kbp	32.63
Largest alignment	37682
NA50	7226
NA75	4109
LA50	196
LA75	396

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

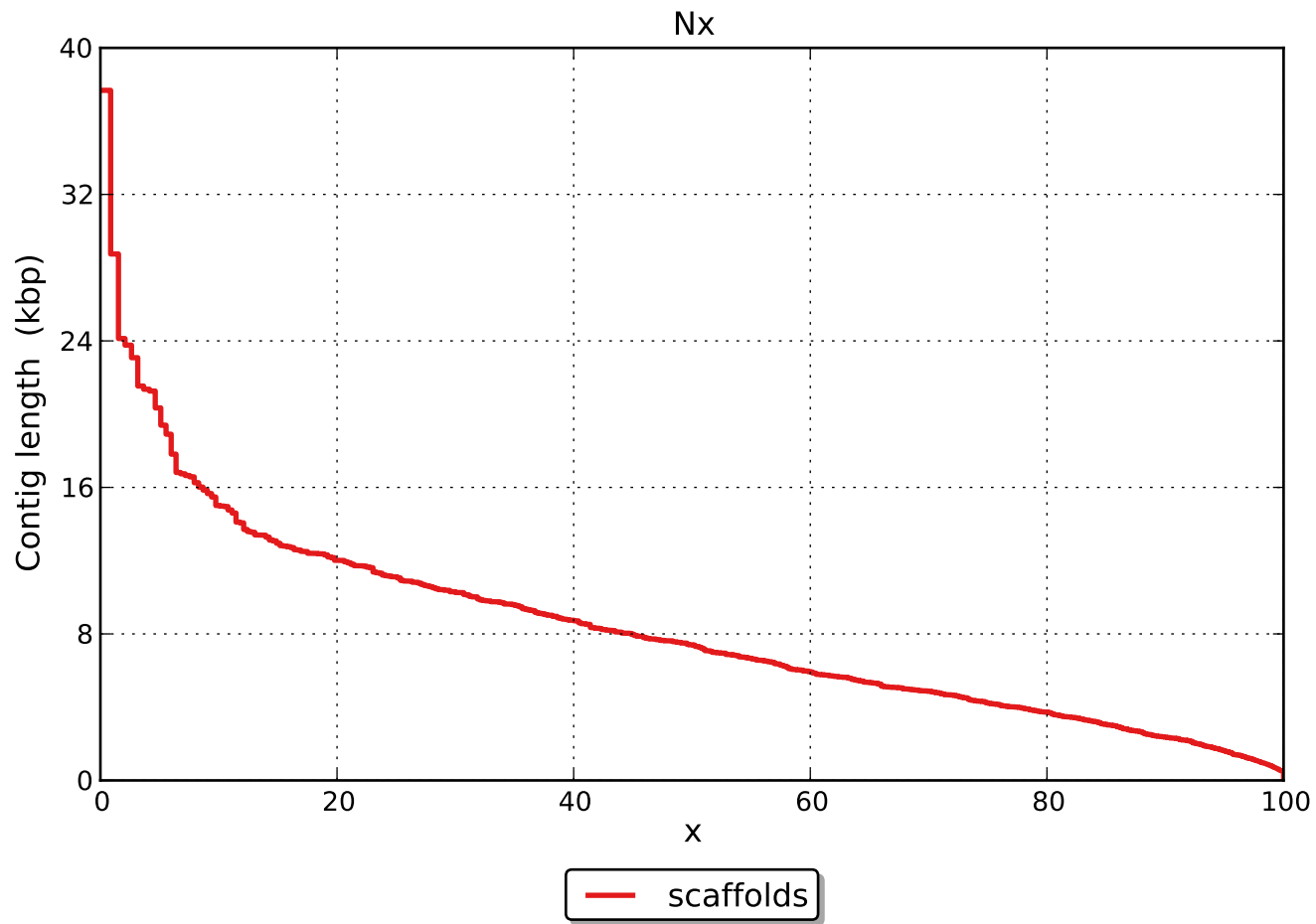
	scaffolds
# misassemblies	16
# relocations	16
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	1
# misassembled contigs	15
Misassembled contigs length	86787
# local misassemblies	10
# mismatches	7229
# indels	1414
# short indels	738
# long indels	676
Indels length	11527

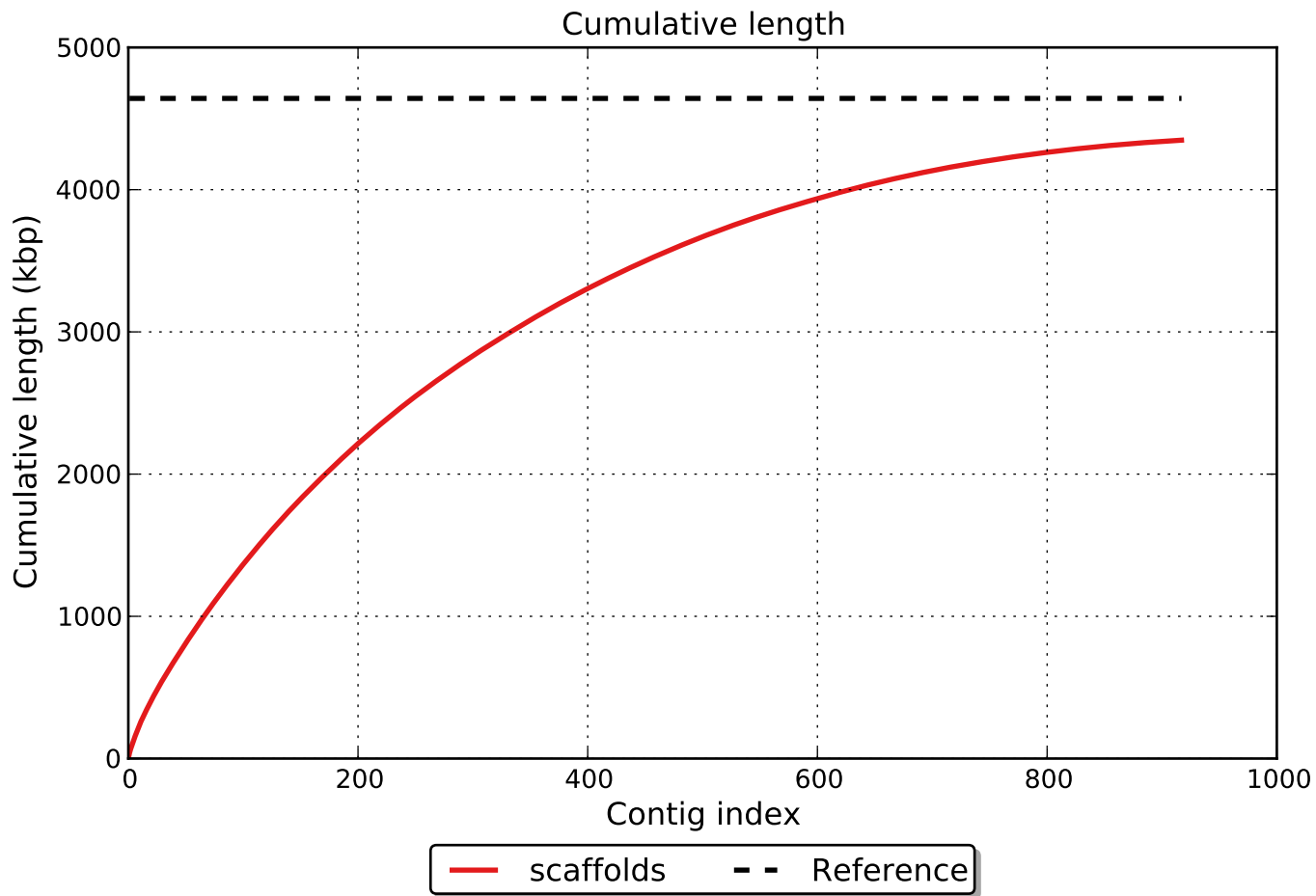
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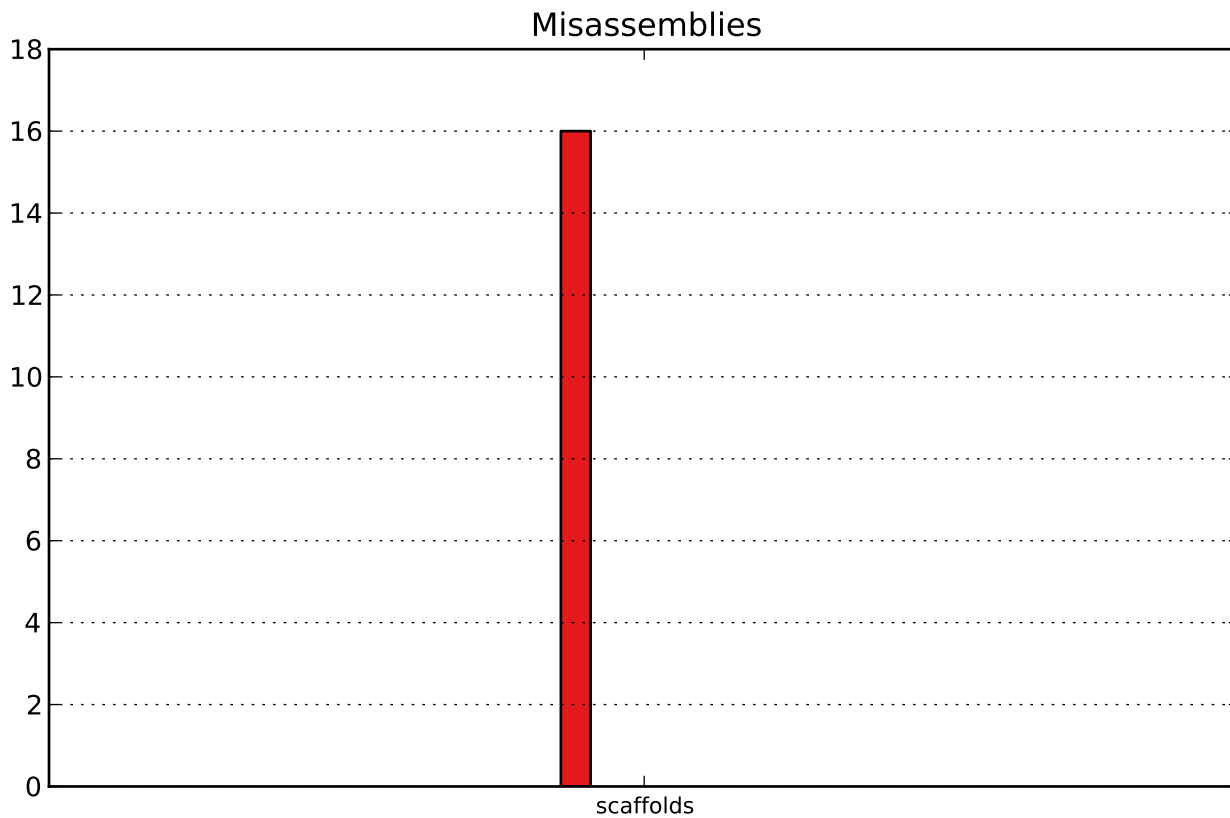
Unaligned report

	scaffolds
# fully unaligned contigs	4
Fully unaligned length	3466
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	1
Partially unaligned length	1528
# N's	21123

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Cumulative length (aligned contigs)

