Report

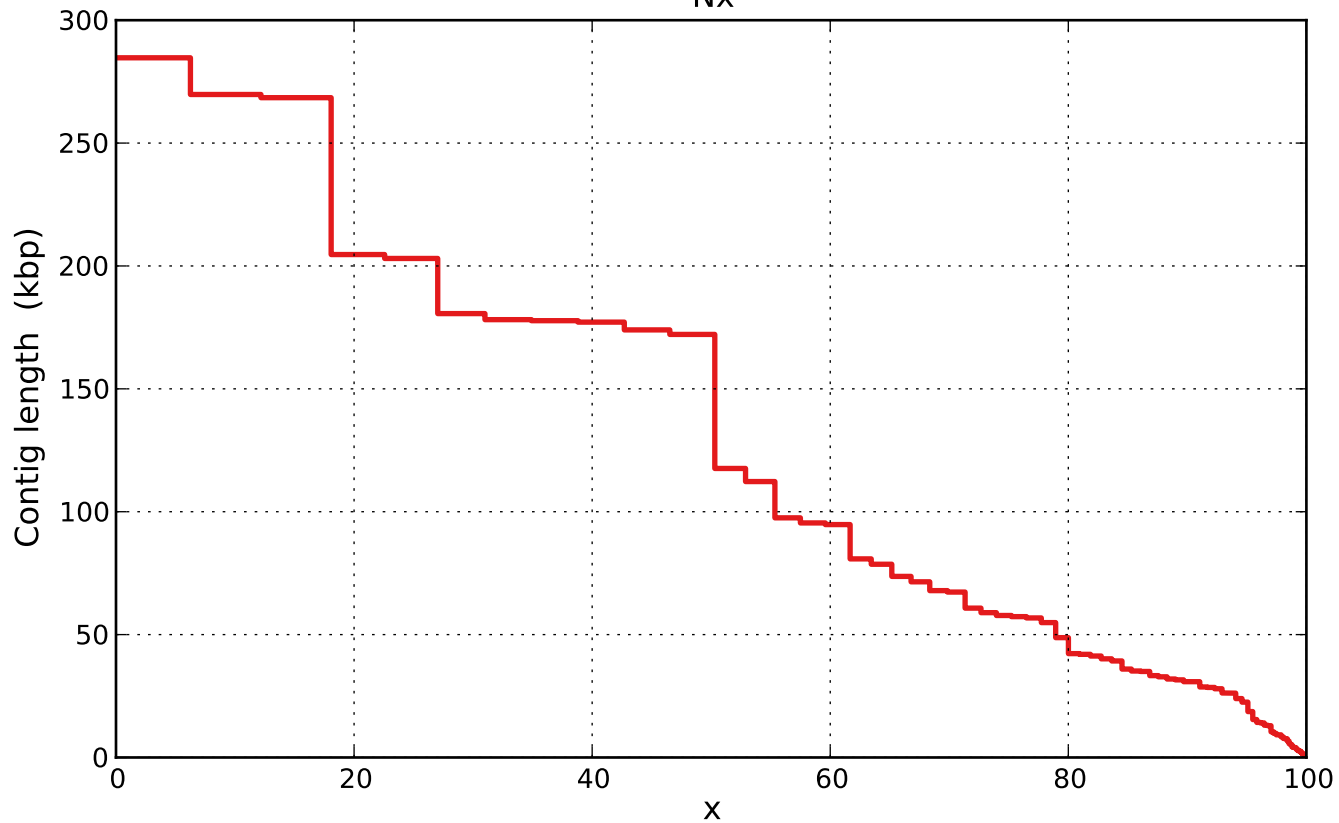|	scaffolds
# contigs (>= 0 bp)	113
# contigs (>= 1000 bp)	87
# contigs (>= 5000 bp)	66
# contigs (>= 10000 bp)	57
# contigs (>= 25000 bp)	48
# contigs (>= 50000 bp)	28
Total length (>= 0 bp)	4557171
Total length (>= 1000 bp)	4547503
Total length (>= 5000 bp)	4497765
Total length (>= 10000 bp)	4428326
Total length (>= 25000 bp)	4282915
Total length (>= 50000 bp)	3594211
# contigs	94
Largest contig	284701
Total length	4553225
Reference length	4641652
N50	172142
N75	57777
L50	11
L75	25
# misassemblies	7
# misassembled contigs	5
Misassembled contigs length	422276
# local misassemblies	15
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.032
Duplication ratio	1.001
# N's per 100 kbp	3.73
# mismatches per 100 kbp	7.25
# indels per 100 kbp	0.66
Largest alignment	284701
NA50	112272
NA75	57309
LA50	12
LA75	27

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	7
# relocations	7
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	5
Misassembled contigs length	422276
# local misassemblies	15
# mismatches	330
# indels	30
# short indels	28
# long indels	2
Indels length	129

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	170

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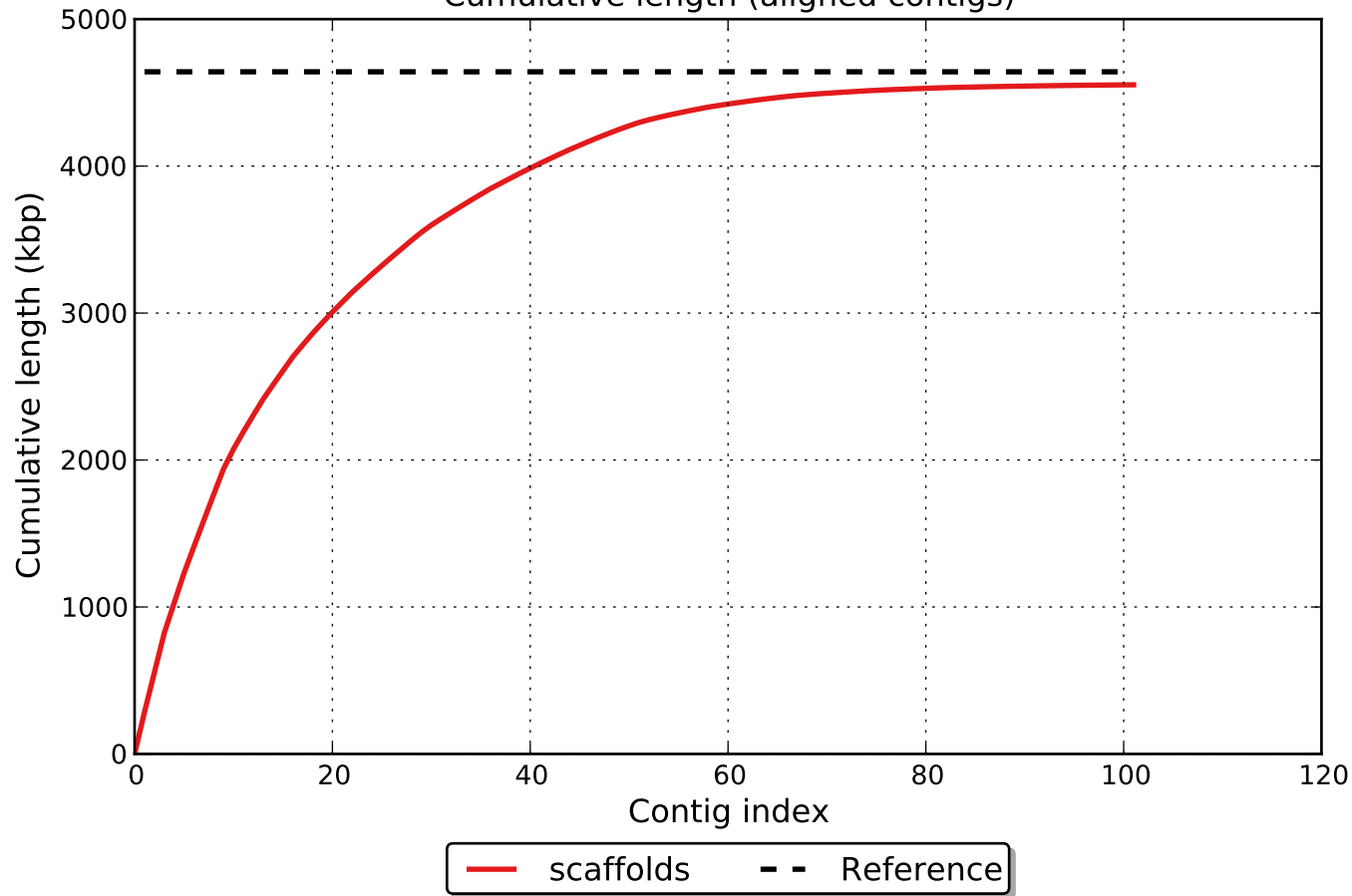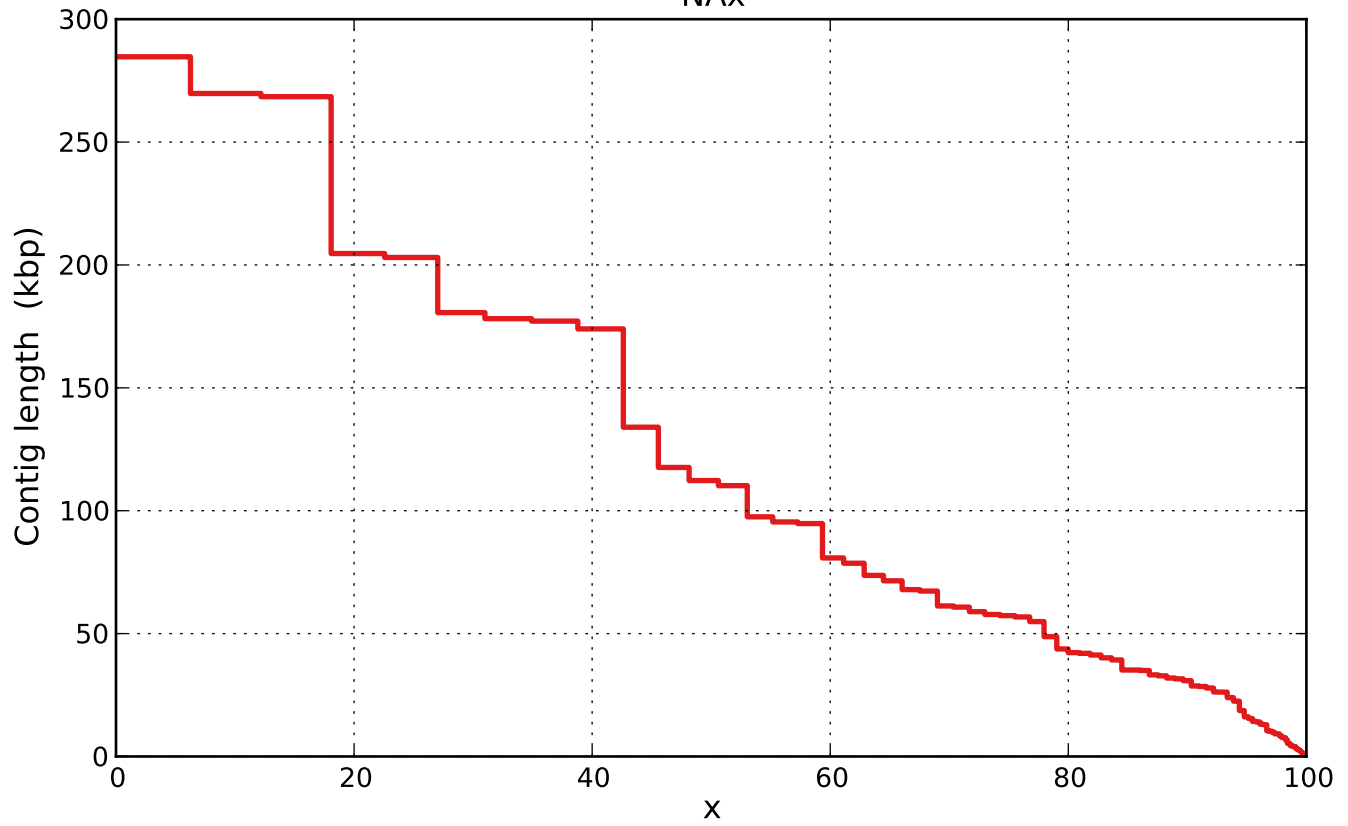(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

Cumulative length

Misassemblies

relocations
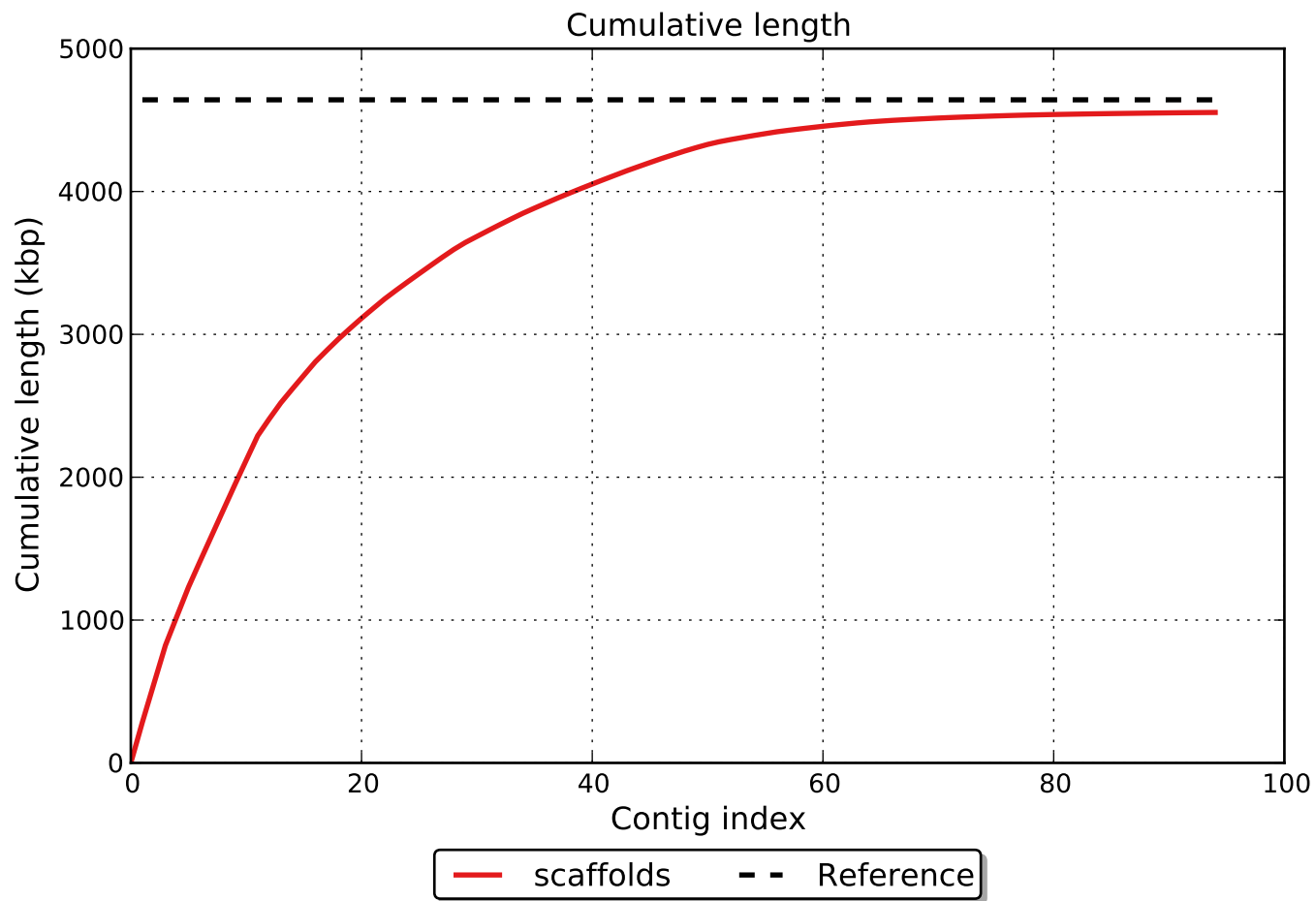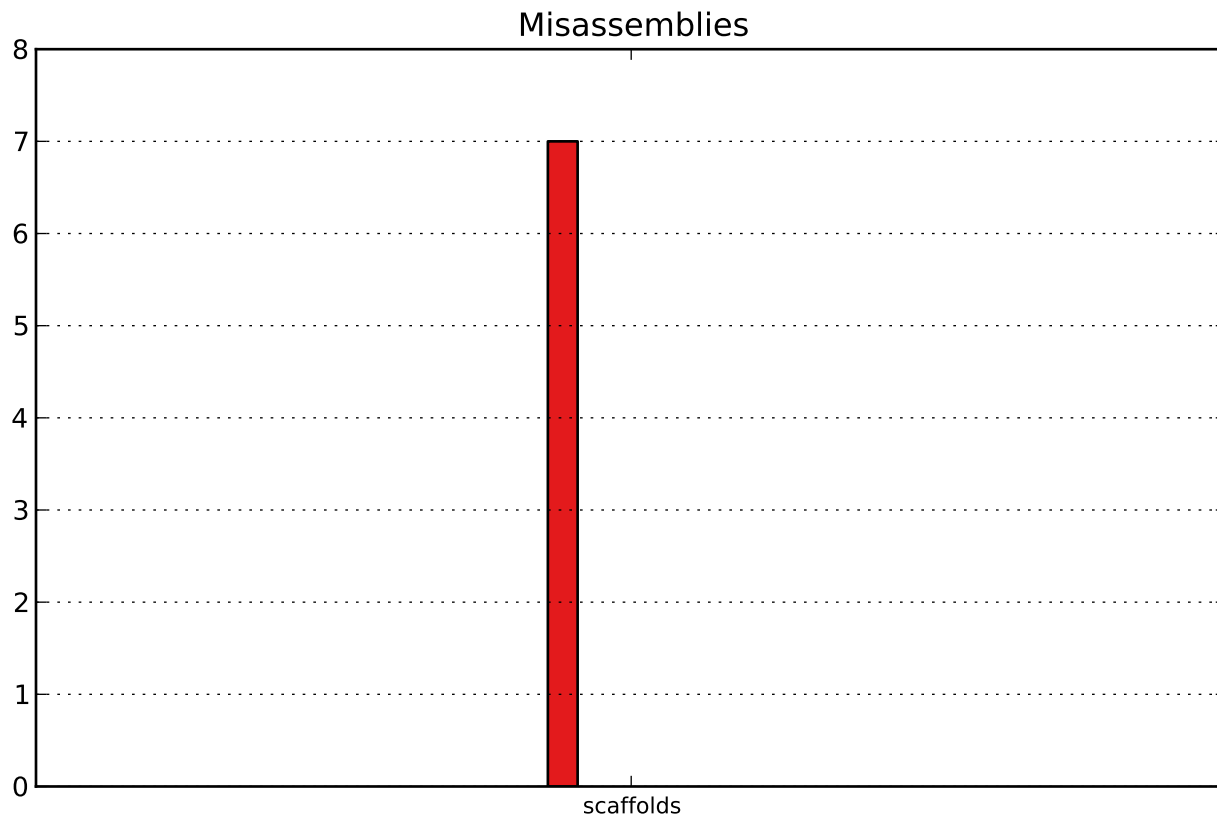
Cumulative length (aligned contigs)