Report

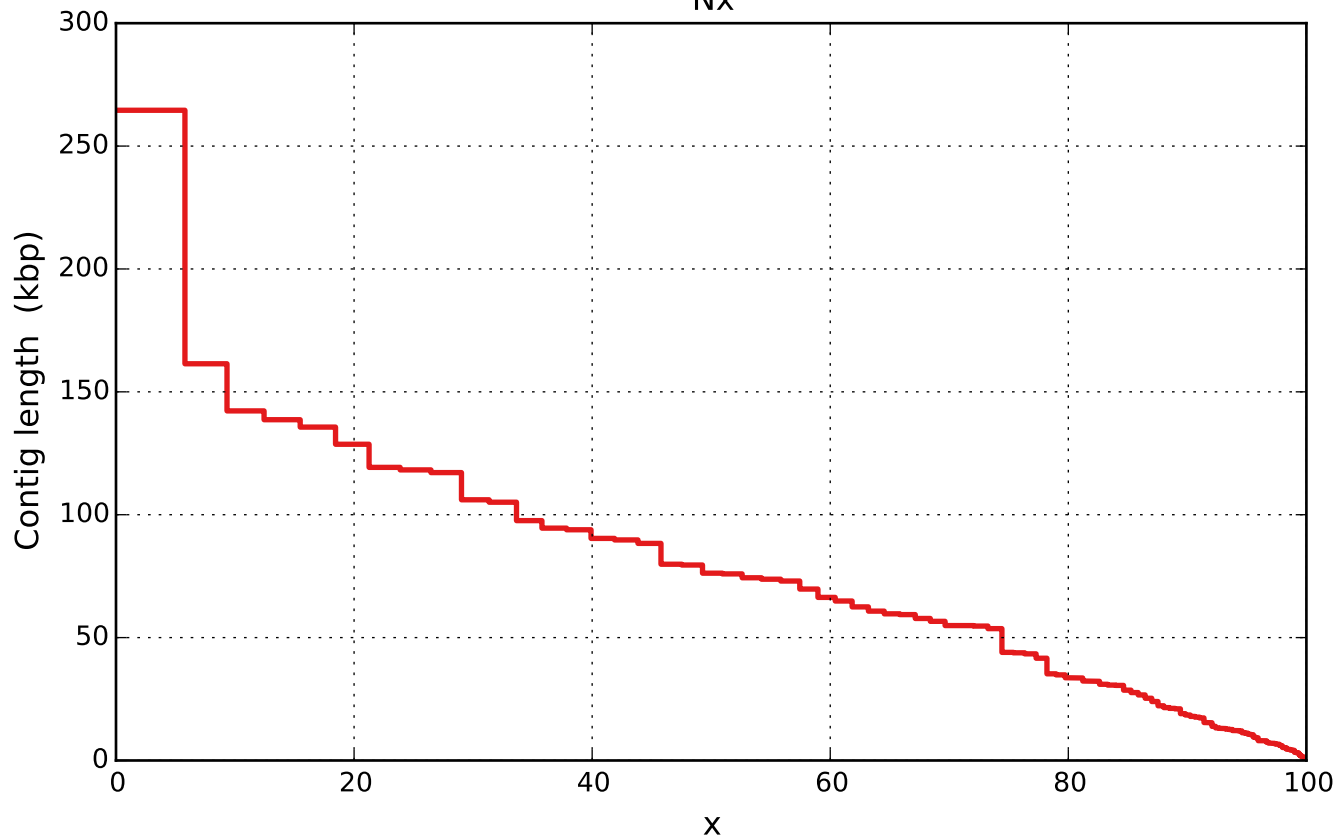|	scaffolds
# contigs (>= 0 bp)	308
# contigs (>= 1000 bp)	124
# contigs (>= 5000 bp)	97
# contigs (>= 10000 bp)	79
# contigs (>= 25000 bp)	54
# contigs (>= 50000 bp)	37
Total length (>= 0 bp)	4603571
Total length (>= 1000 bp)	4562517
Total length (>= 5000 bp)	4491950
Total length (>= 10000 bp)	4364624
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	14
# misassembled contigs	11
Misassembled contigs length	1018010
# local misassemblies	3
# unaligned contigs	0 + 2 part
Unaligned length	126
Genome fraction (%)	49.734
Duplication ratio	1.002
# N's per 100 kbp	13.44
# mismatches per 100 kbp	560.49
# indels per 100 kbp	0.65
Largest alignment	183386
NA50	73703
NA75	34543
LA50	22
LA75	43

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	14
# relocations	11
# translocations	0
# inversions	3
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	11
Misassembled contigs length	1018010
# local misassemblies	3
# mismatches	25878
# indels	30
# short indels	28
# long indels	2
Indels length	144

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).
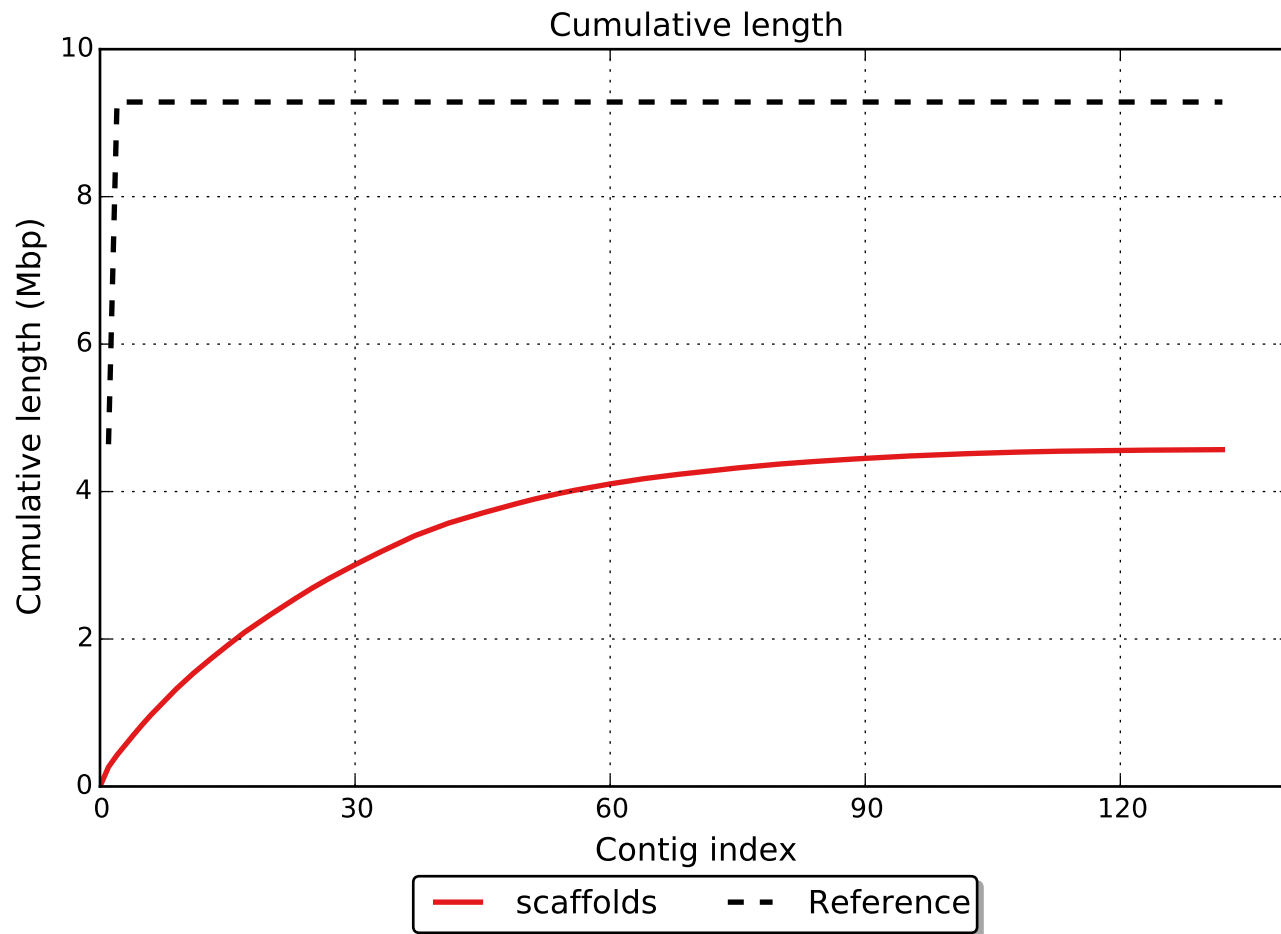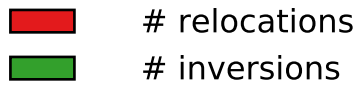
Unaligned report

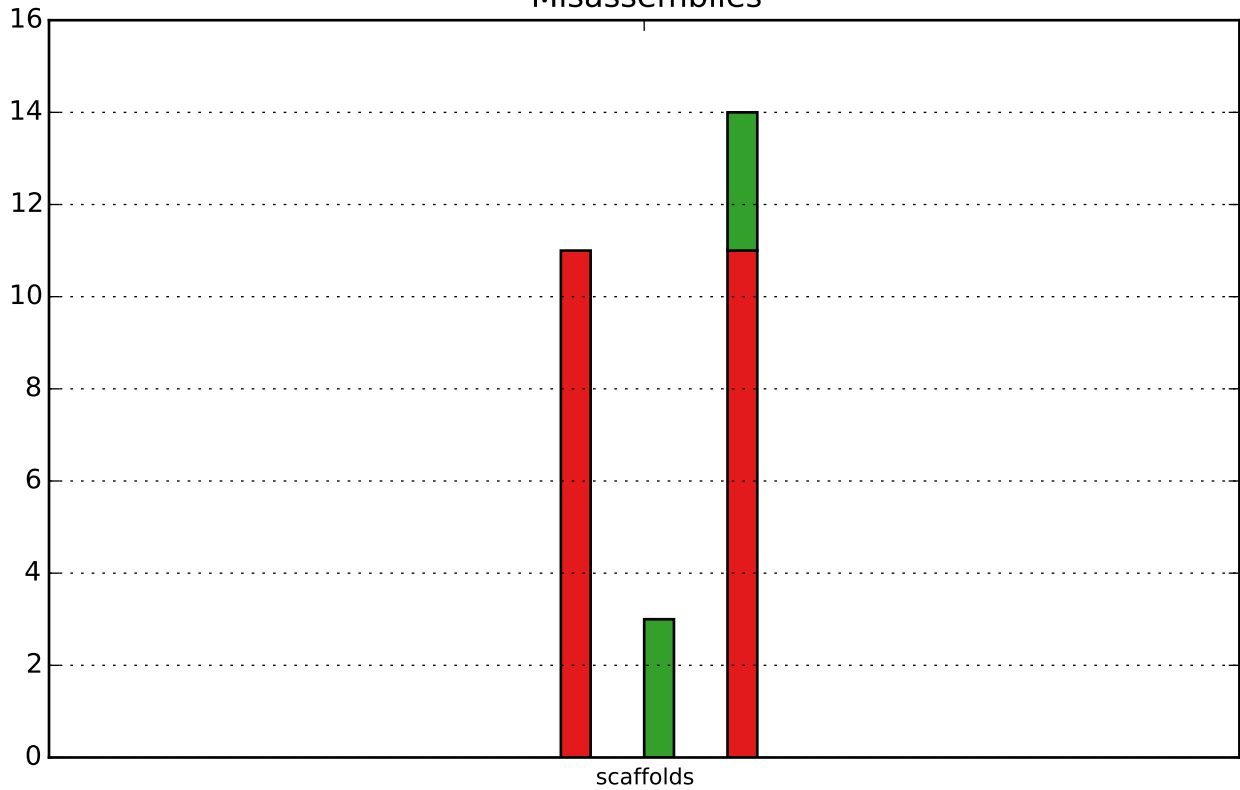|	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	126
# N's	614

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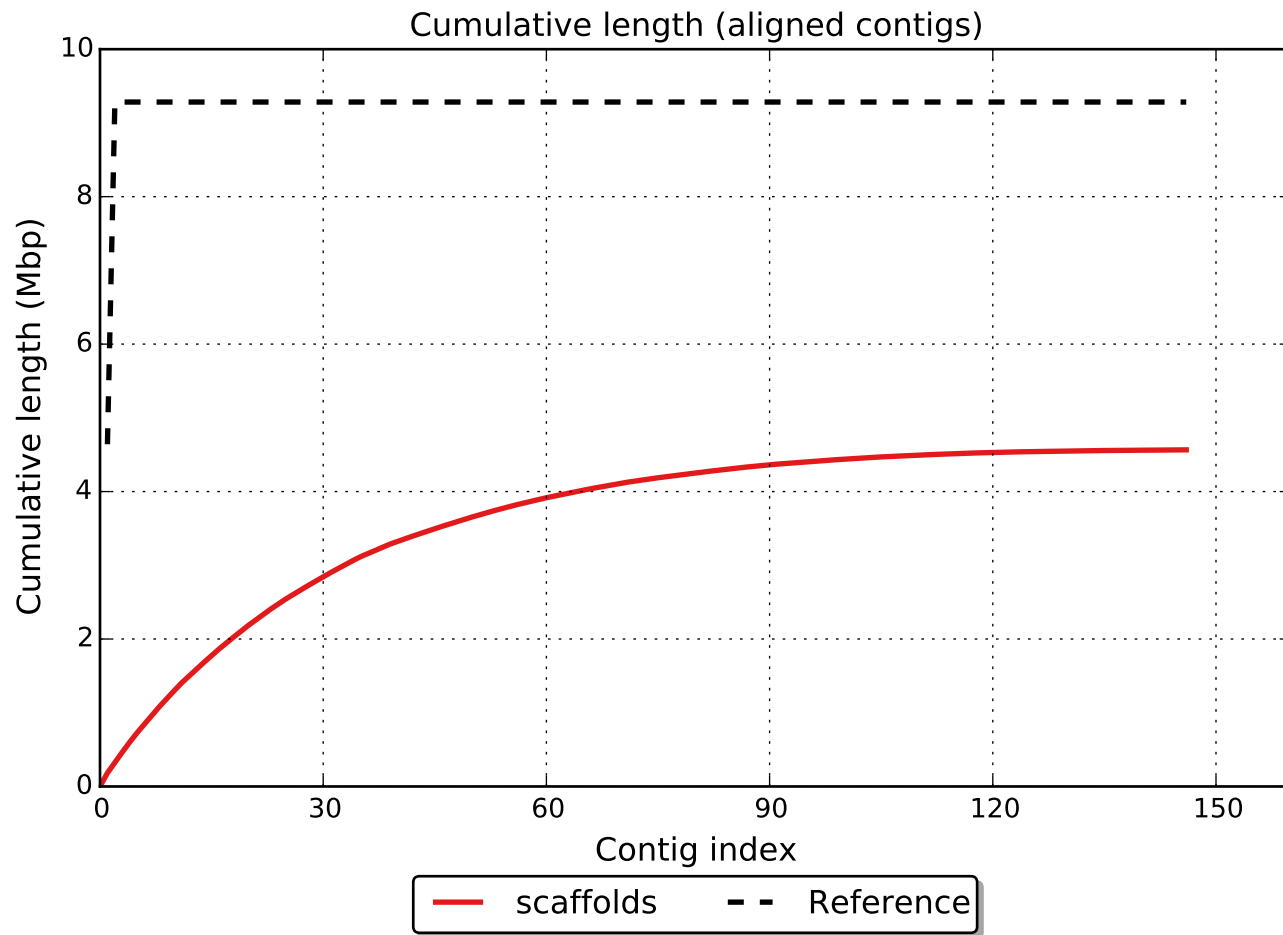(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

Misassemblies

Cumulative length (aligned contigs)