Report

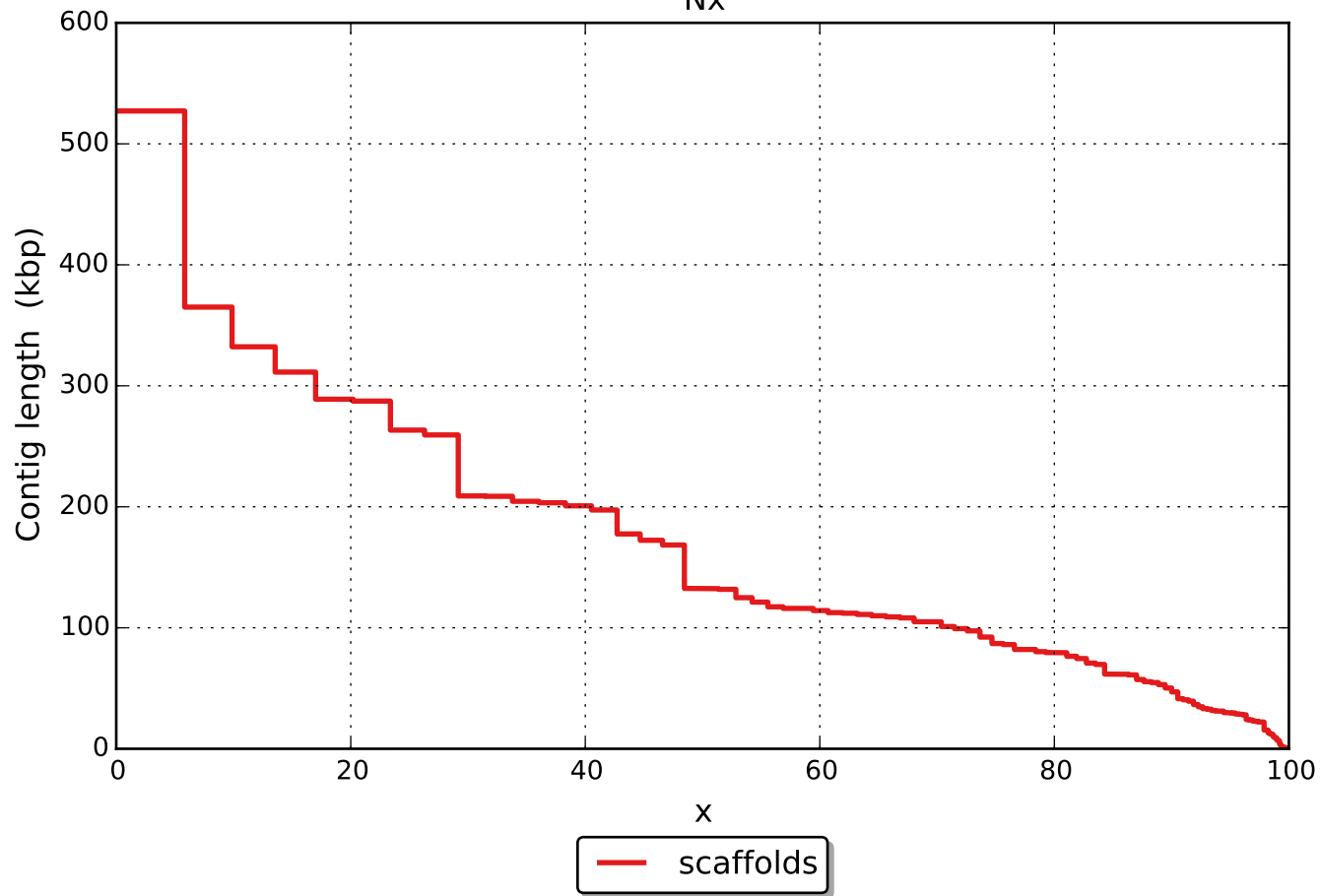|	scaffolds
# contigs (>= 0 bp)	302
# contigs (>= 1000 bp)	121
# contigs (>= 5000 bp)	92
# contigs (>= 10000 bp)	87
# contigs (>= 25000 bp)	75
# contigs (>= 50000 bp)	58
Total length (>= 0 bp)	9077926
Total length (>= 1000 bp)	9011157
Total length (>= 5000 bp)	8960493
Total length (>= 10000 bp)	8921146
Total length (>= 25000 bp)	8704633
Total length (>= 50000 bp)	8130674
# contigs	154
Largest contig	527156
Total length	9033467
Reference length	9283304
N50	132337
N75	86976
L50	19
L75	39
# misassemblies	268
# misassembled contigs	42
Misassembled contigs length	4251762
# local misassemblies	4
# unaligned contigs	17 + 2 part
Unaligned length	20728
Genome fraction (%)	49.375
Duplication ratio	1.966
# N's per 100 kbp	0.00
# mismatches per 100 kbp	858.20
# indels per 100 kbp	1.27
Largest alignment	527156
NA50	61543
NA75	20909
LA50	33
LA75	98

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	268
# relocations	221
# translocations	0
# inversions	45
# interspecies translocations	2
# possibly misassembled contigs	13
# misassembled contigs	42
Misassembled contigs length	4251762
# local misassemblies	4
# mismatches	39337
# indels	58
# short indels	58
# long indels	0
Indels length	59

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).
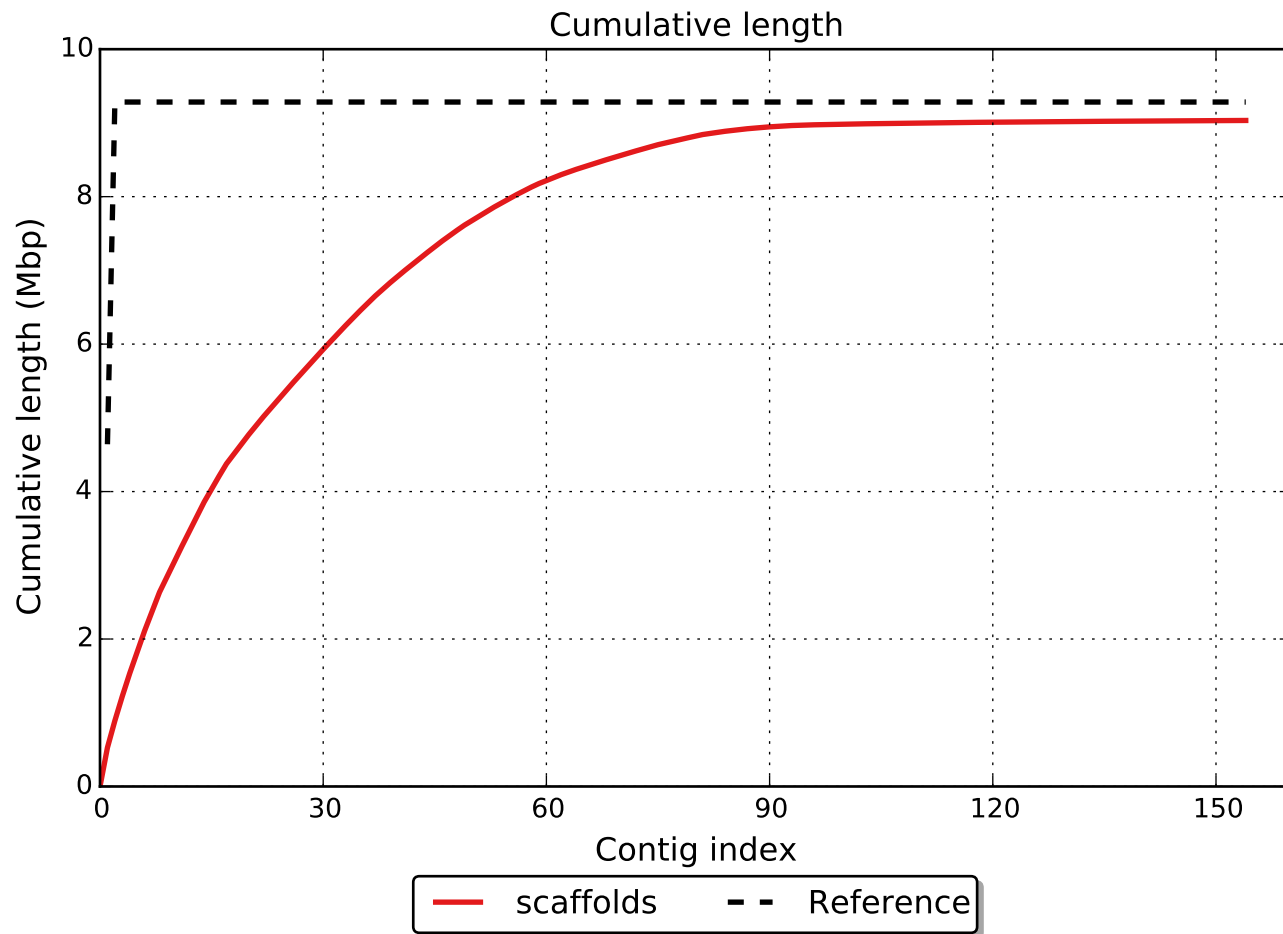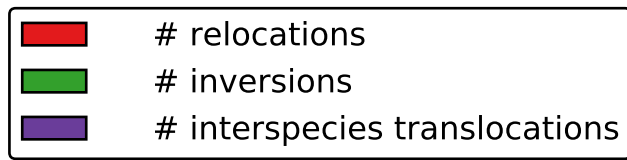
Unaligned report

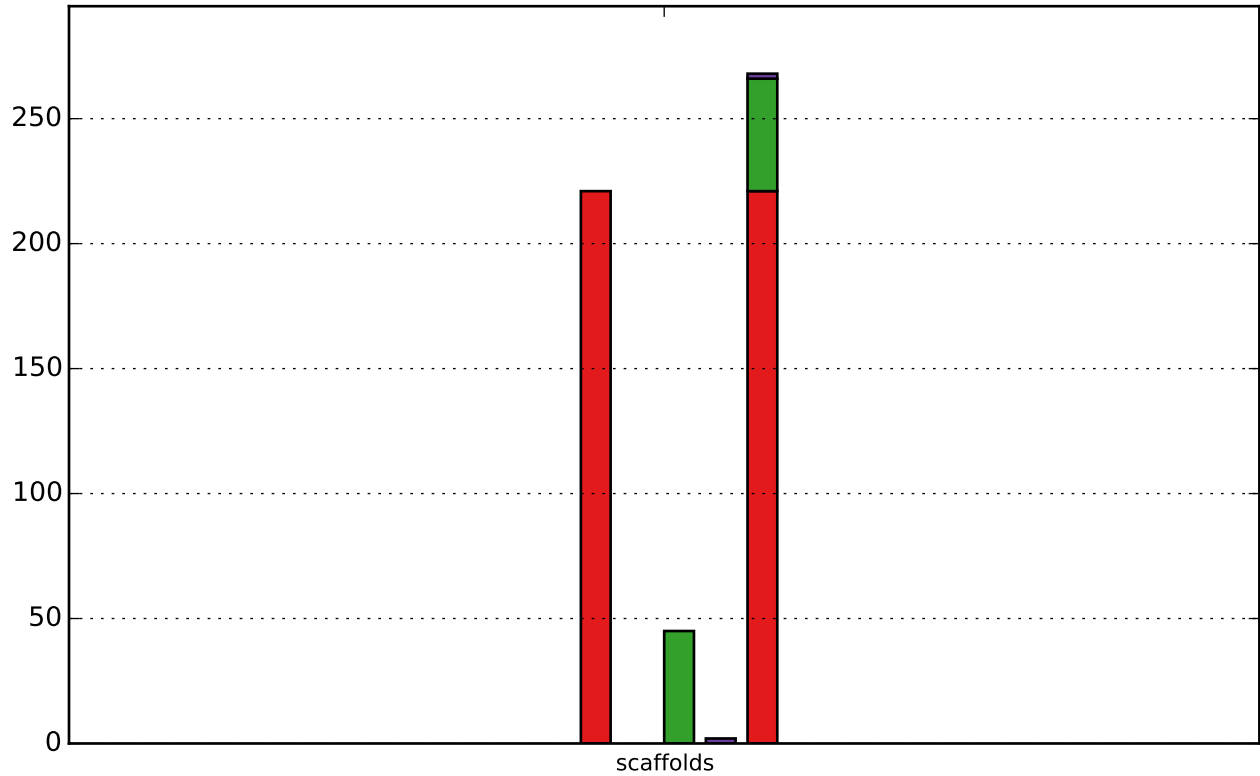|	scaffolds
# fully unaligned contigs	17
Fully unaligned length	13548
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	1
Partially unaligned length	7180
# N's	0

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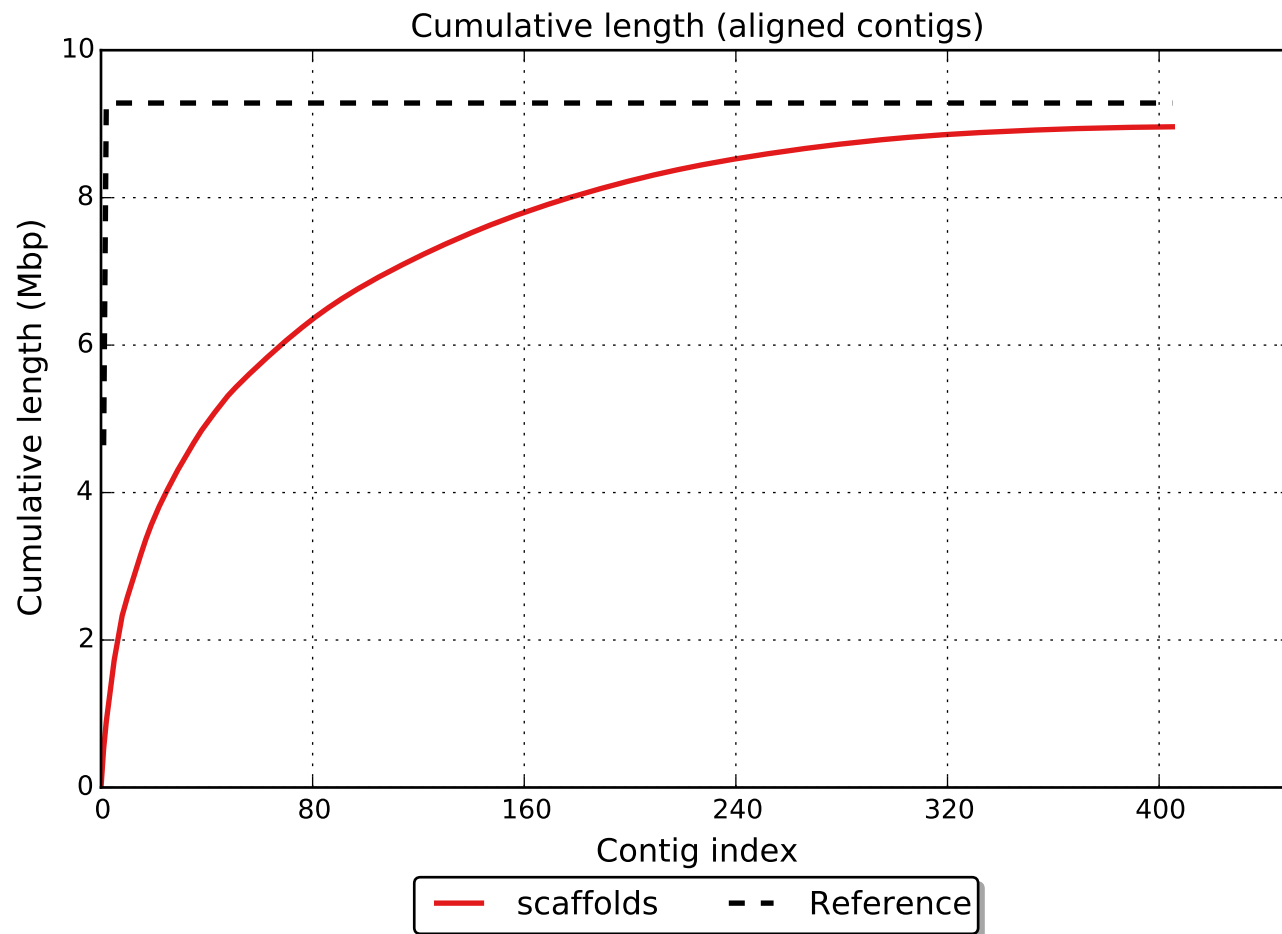(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

Misassemblies

Cumulative length (aligned contigs)