Report

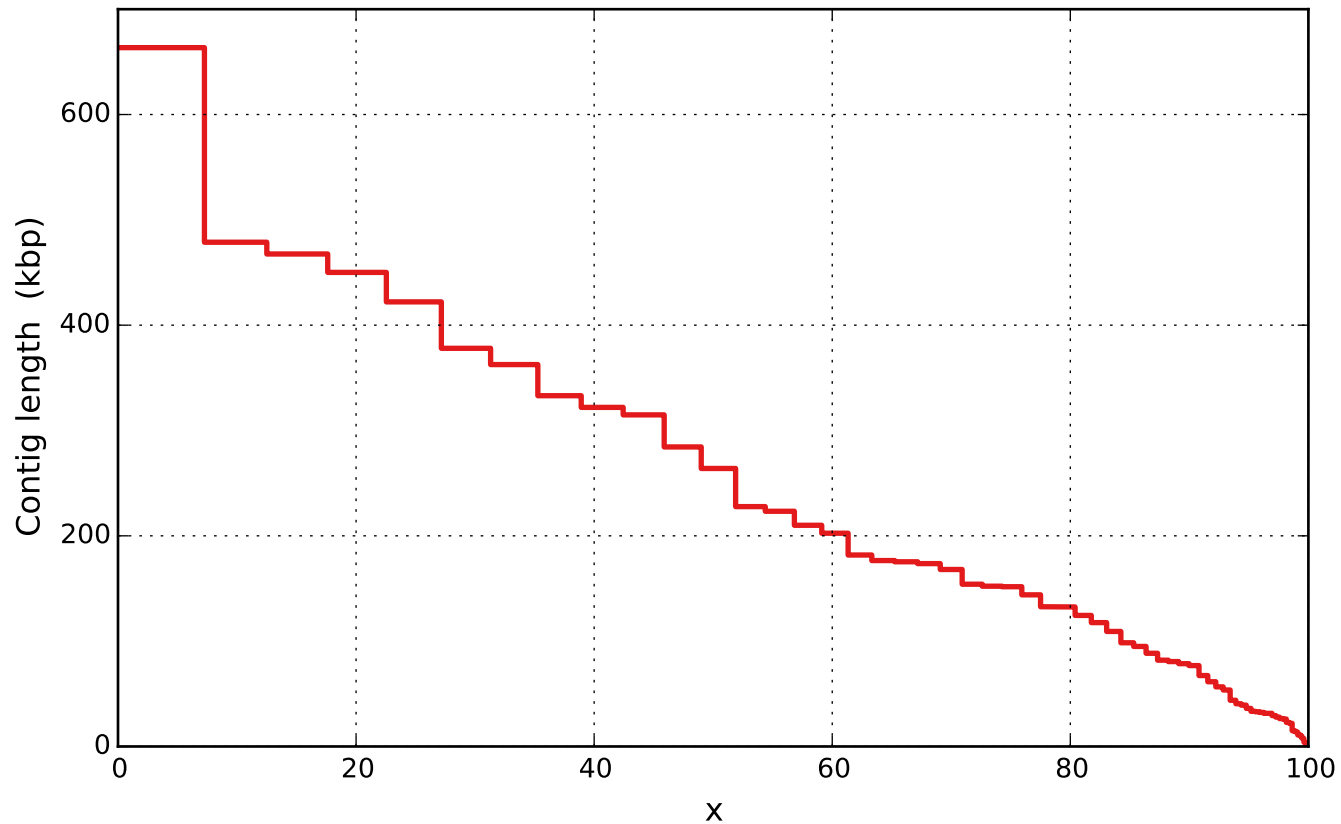|	scaffolds
# contigs (>= 0 bp)	125
# contigs (>= 1000 bp)	77
# contigs (>= 5000 bp)	64
# contigs (>= 10000 bp)	61
# contigs (>= 25000 bp)	54
# contigs (>= 50000 bp)	41
Total length (>= 0 bp)	9146130
Total length (>= 1000 bp)	9129851
Total length (>= 5000 bp)	9102772
Total length (>= 10000 bp)	9077538
Total length (>= 25000 bp)	8967925
Total length (>= 50000 bp)	8536857
# contigs	86
Largest contig	663492
Total length	9137424
Reference length	9283304
N50	263950
N75	151678
L50	12
L75	24
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	478751
# local misassemblies	0
# unaligned contigs	54 + 9 part
Unaligned length	4348582
Genome fraction (%)	50.106
Duplication ratio	1.030
# N's per 100 kbp	0.51
# mismatches per 100 kbp	238.80
# indels per 100 kbp	0.67
Largest alignment	663492
NA50	27851
LA50	17

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	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	7
# misassembled contigs	1
Misassembled contigs length	478751
# local misassemblies	0
# mismatches	11108
# indels	31
# short indels	28
# long indels	3
Indels length	106

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).
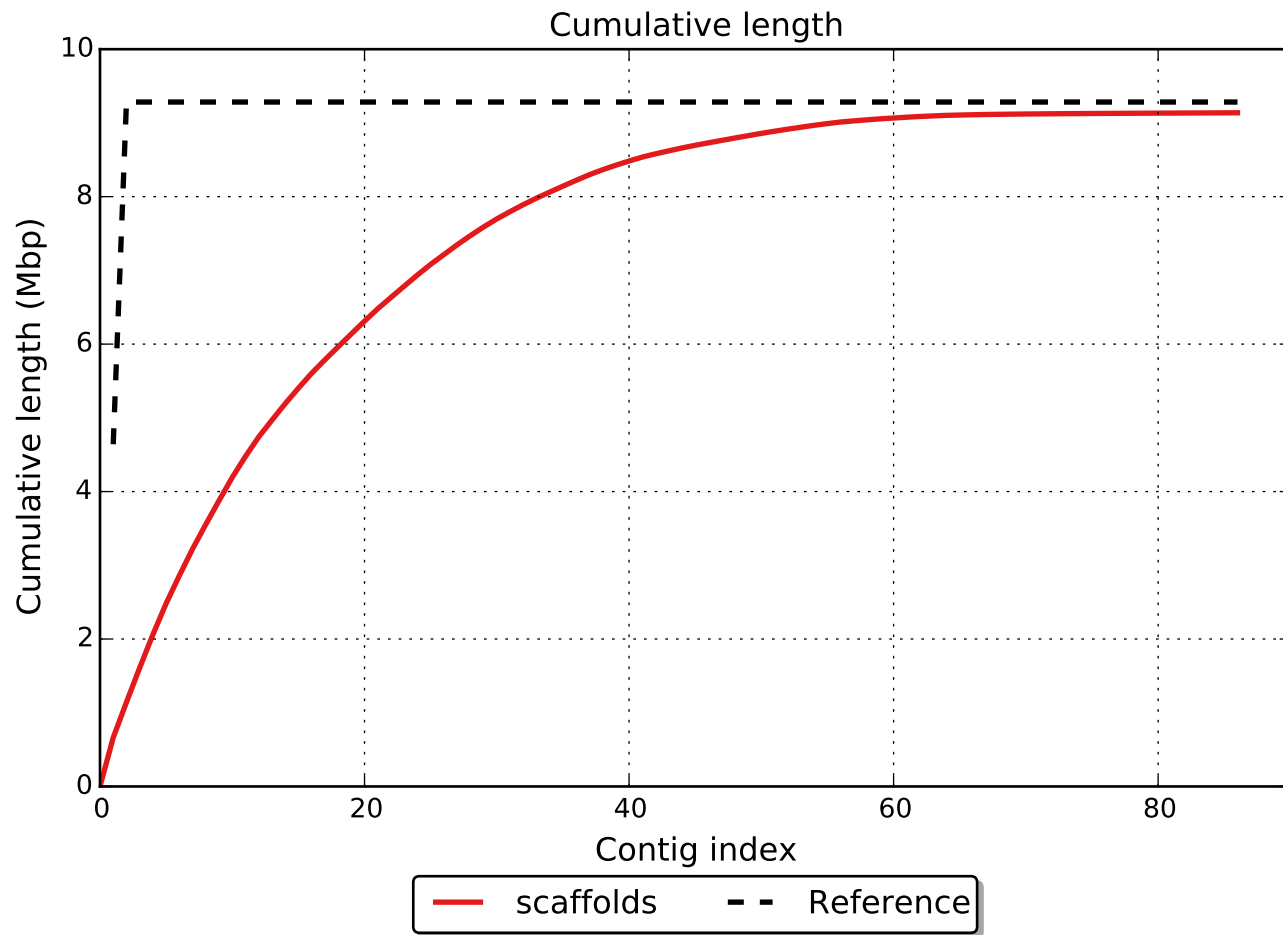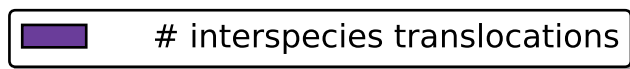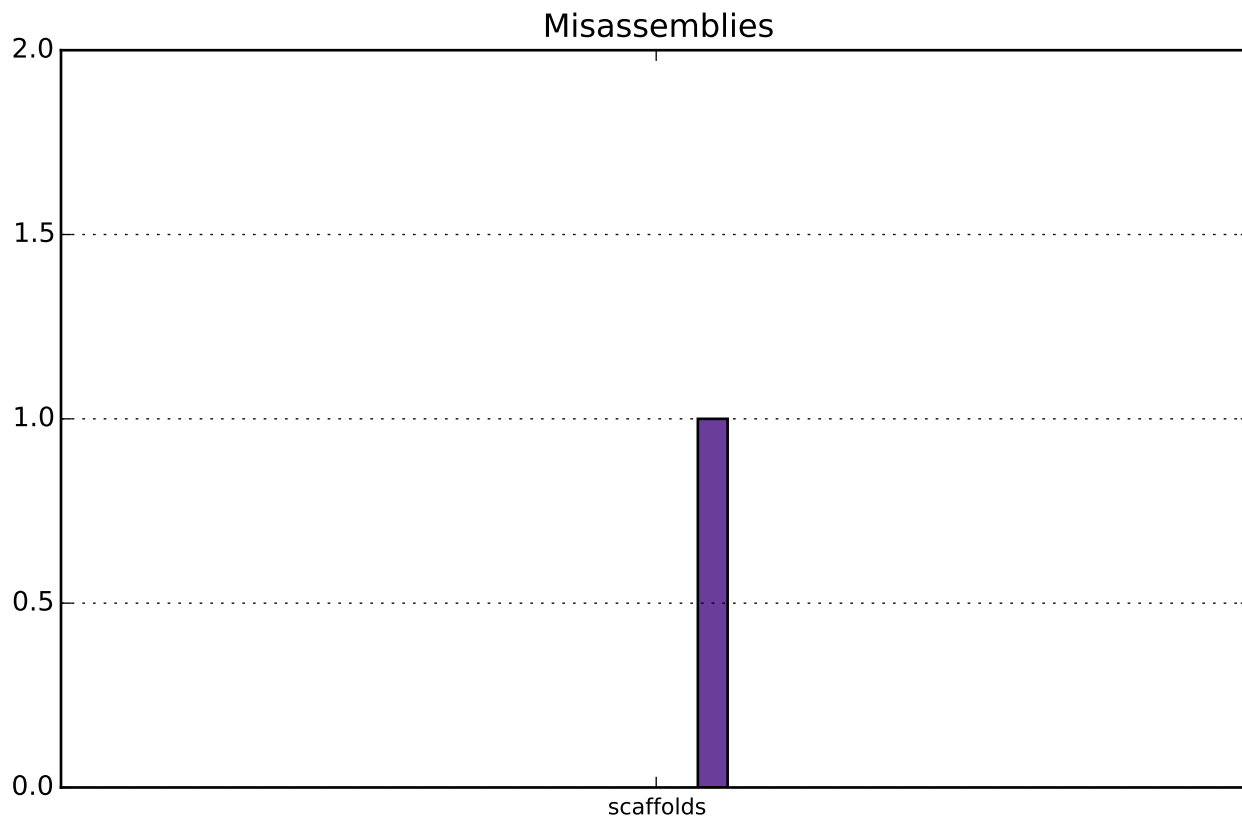
Unaligned report

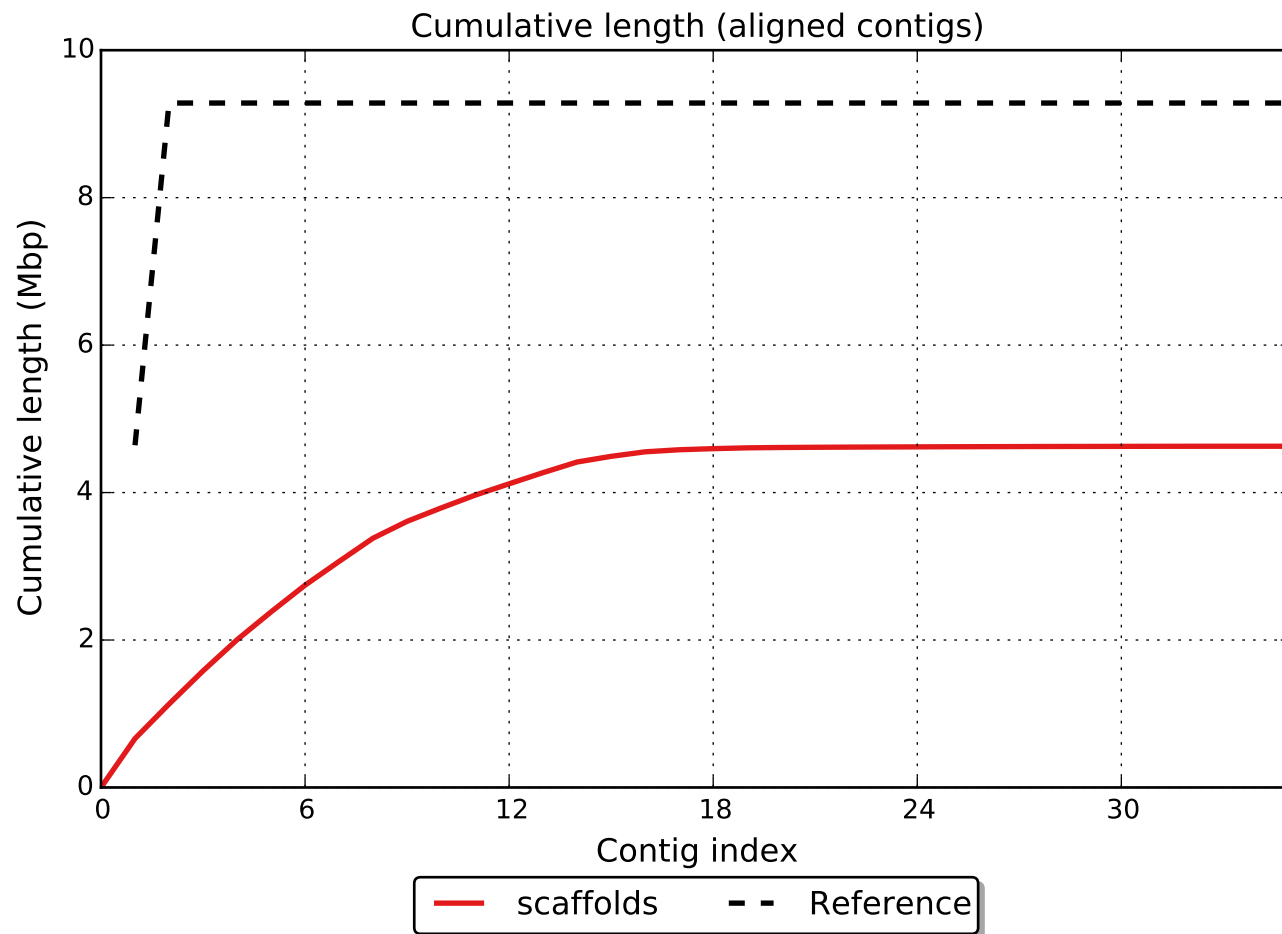|	scaffolds
# fully unaligned contigs	54
Fully unaligned length	3304638
# partially unaligned contigs	9
# with misassembly	2
# both parts are significant	6
Partially unaligned length	1043944
# N's	47

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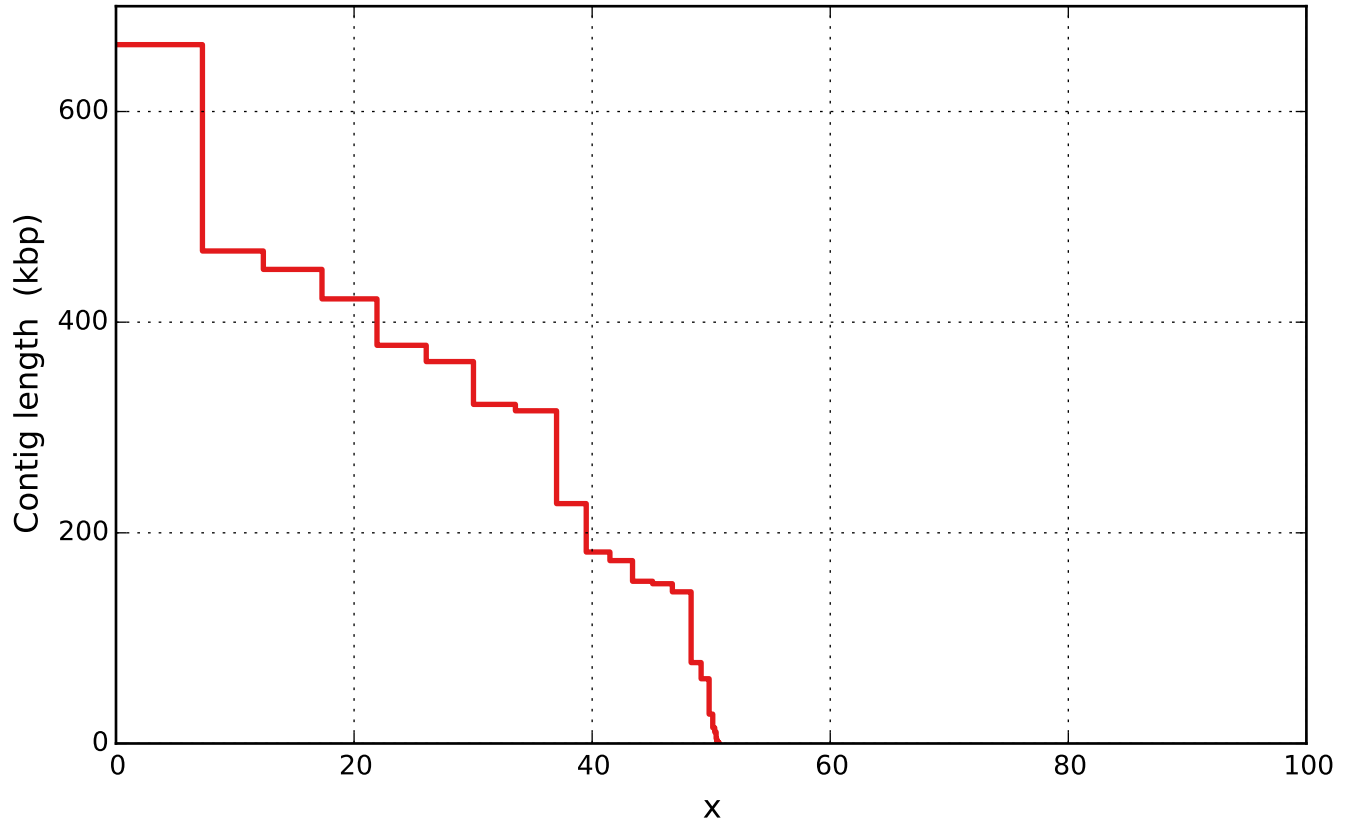(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

Misassemblies

scaffolds

interspecies translocations

Cumulative length (aligned contigs)