Report

	contigs
# contigs (>= 0 bp)	1050
# contigs (>= 1000 bp)	272
# contigs (>= 5000 bp)	167
# contigs (>= 10000 bp)	125
# contigs (>= 25000 bp)	85
# contigs (>= 50000 bp)	51
Total length (>= 0 bp)	8184822
Total length (>= 1000 bp)	7885006
Total length (>= 5000 bp)	7603923
Total length (>= 10000 bp)	7313364
Total length (>= 25000 bp)	6634529
Total length (>= 50000 bp)	5466396
# contigs	341
Largest contig	347033
Total length	7930445
Reference length	9283304
N50	76984
N75	34790
L50	27
L75	63
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	139104
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	84.491
Duplication ratio	1.011
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1007.63
# indels per 100 kbp	0.62
Largest alignment	347033
NA50	76984
NA75	34689
LA50	27
LA75	64

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

	contigs
# misassemblies	2
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	2
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	139104
# local misassemblies	2
# mismatches	79034
# indels	49
# short indels	49
# long indels	0
Indels length	57

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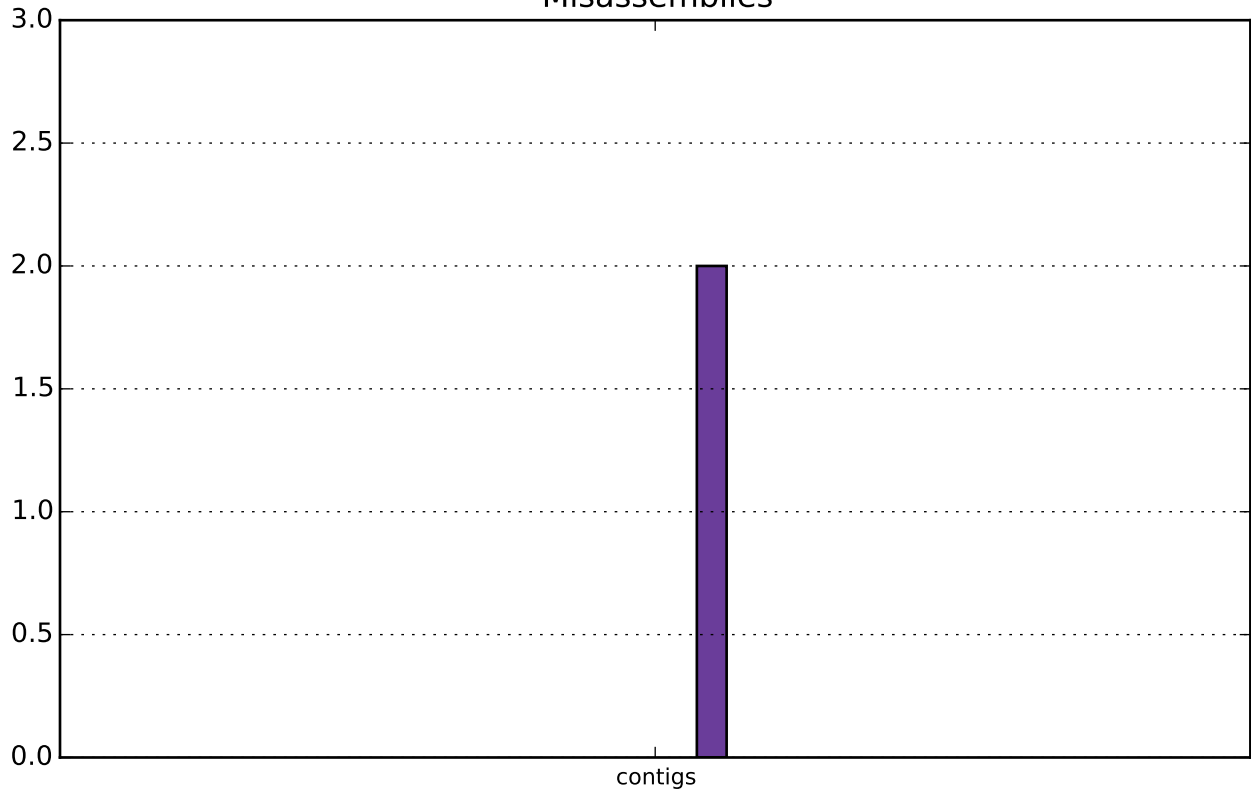(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	contigs
# 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	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).
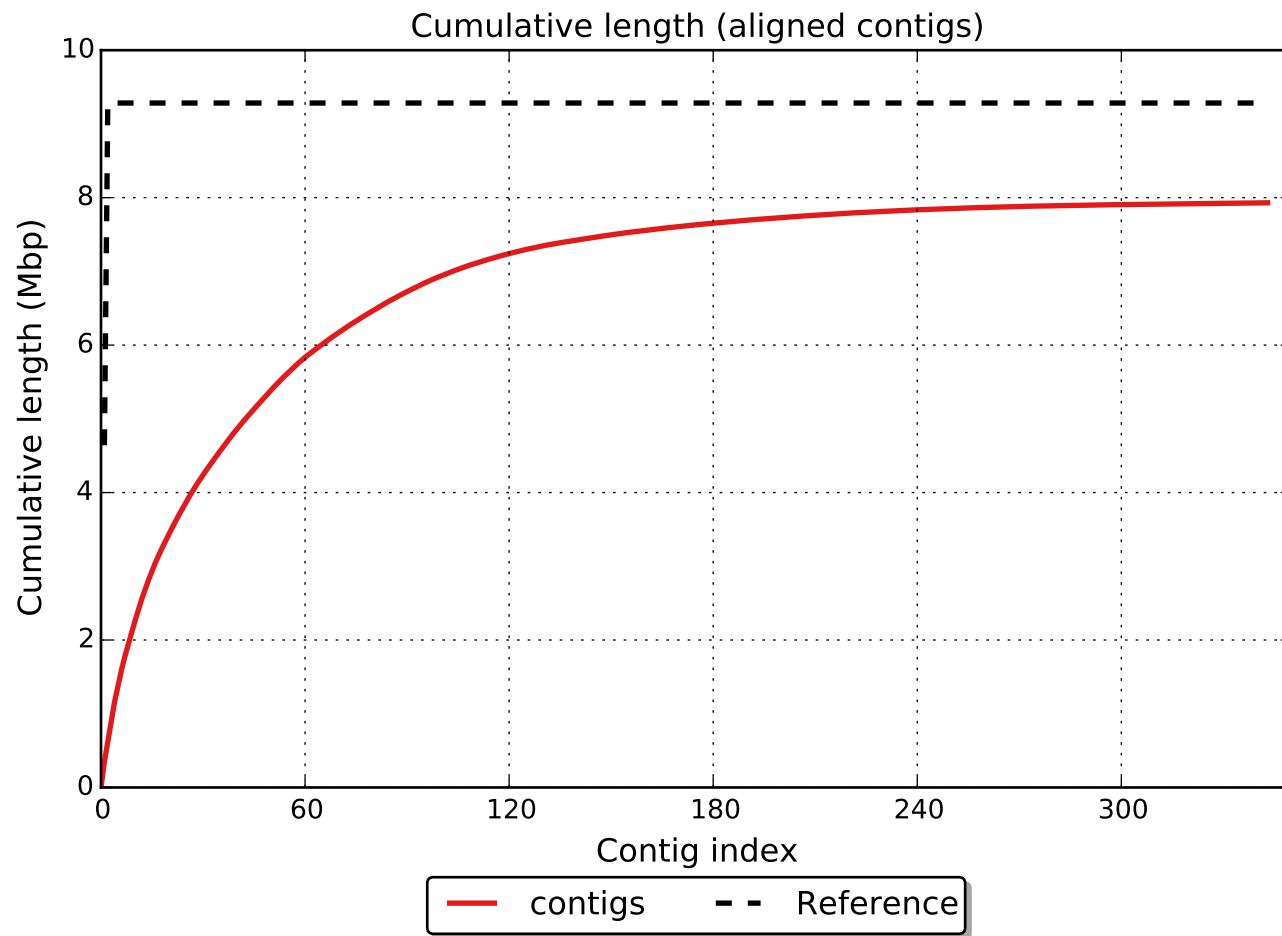
Cumulative length
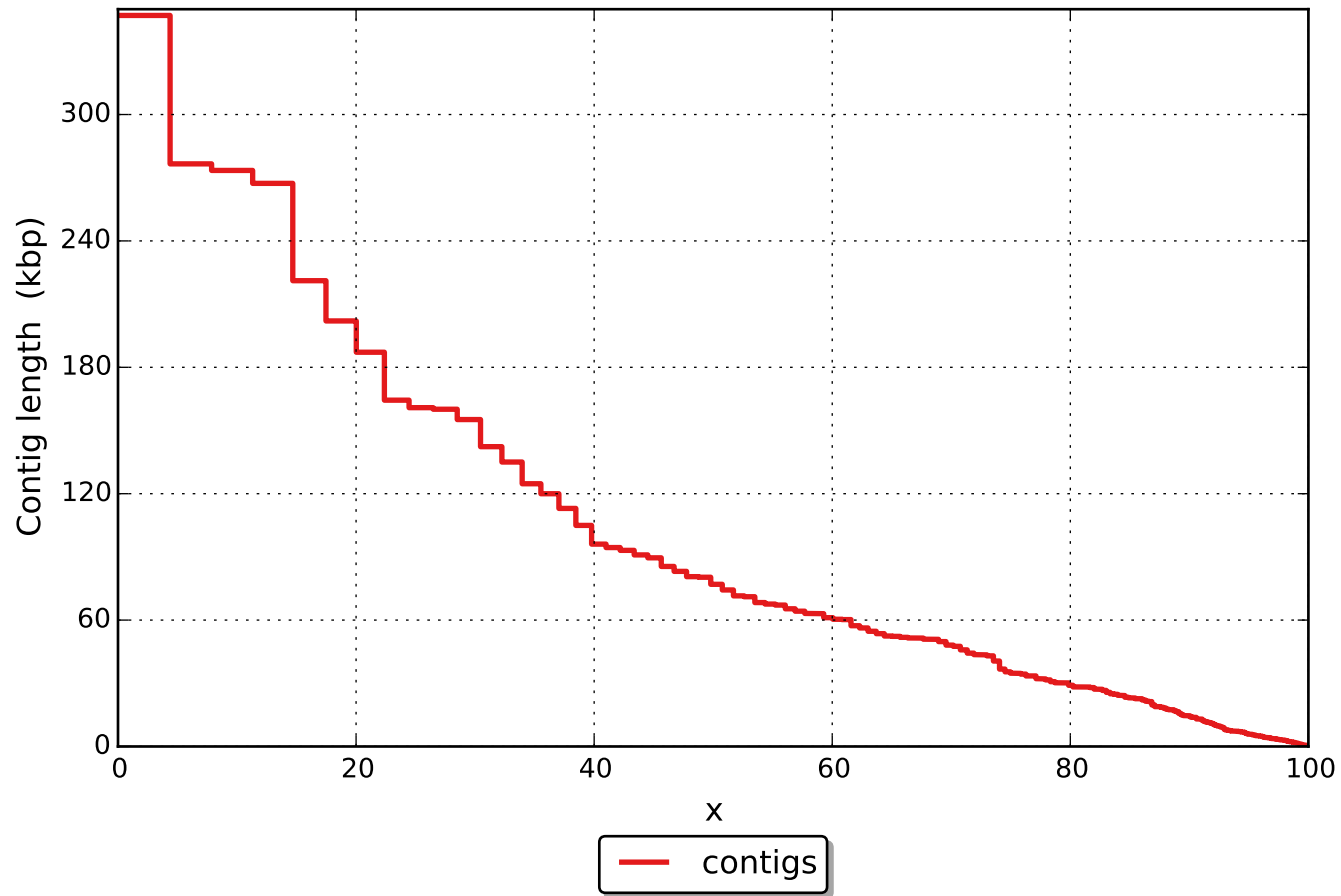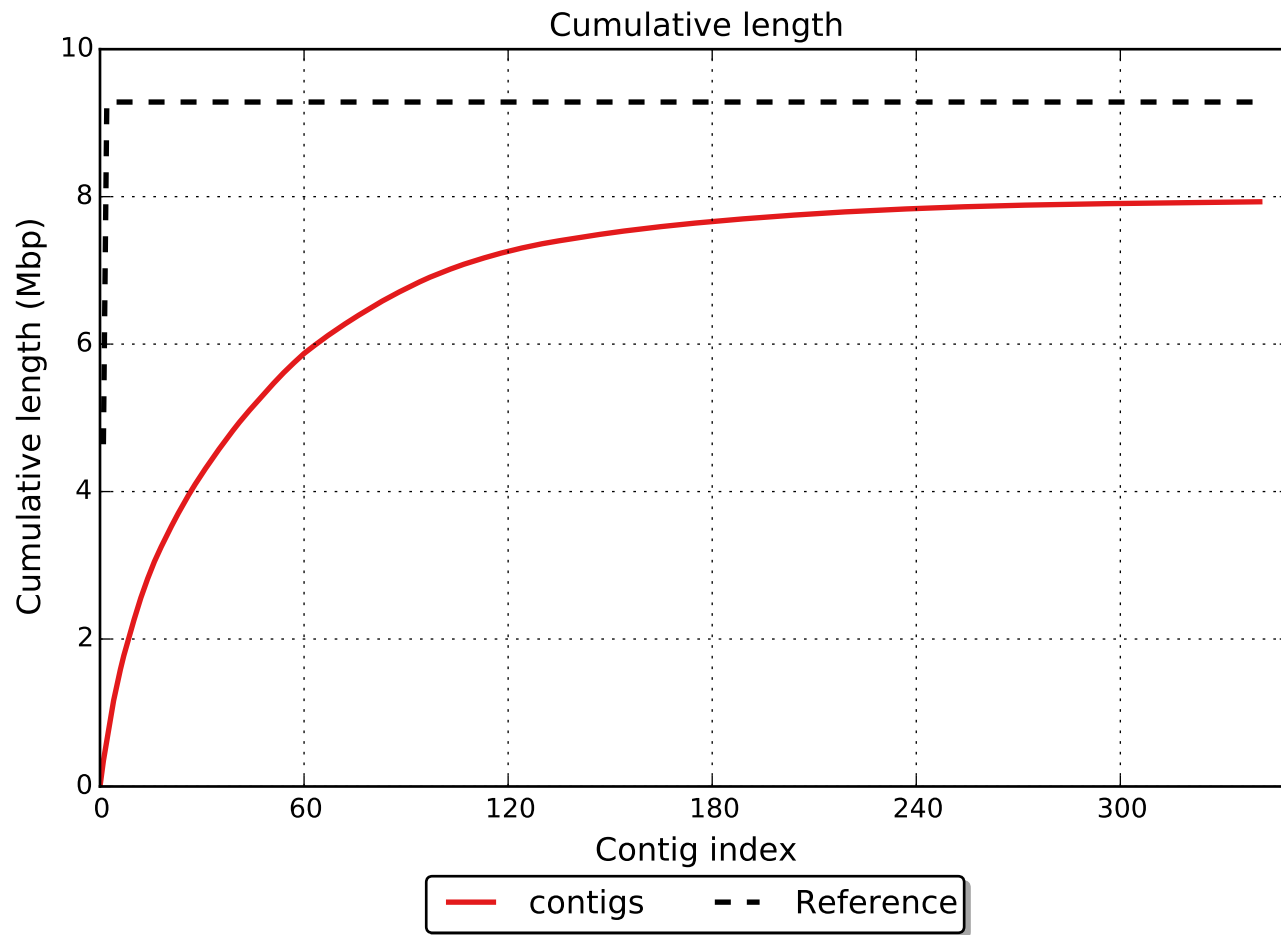
Misassemblies

interspecies translocations

Cumulative length (aligned contigs)