Report

	final.contigs
# contigs (>= 0 bp)	522
# contigs (>= 1000 bp)	394
# contigs (>= 5000 bp)	318
# contigs (>= 10000 bp)	250
# contigs (>= 25000 bp)	142
# contigs (>= 50000 bp)	43
Total length (>= 0 bp)	9257773
Total length (>= 1000 bp)	9212498
Total length (>= 5000 bp)	8984058
Total length (>= 10000 bp)	8474619
Total length (>= 25000 bp)	6579906
Total length (>= 50000 bp)	3075392
# contigs	412
Largest contig	121705
Total length	9226211
Reference length	9283304
N50	38430
N75	23489
L50	79
L75	157
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.158
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.70
# indels per 100 kbp	0.00
Largest alignment	121705
NA50	38430
NA75	23489
LA50	79
LA75	157

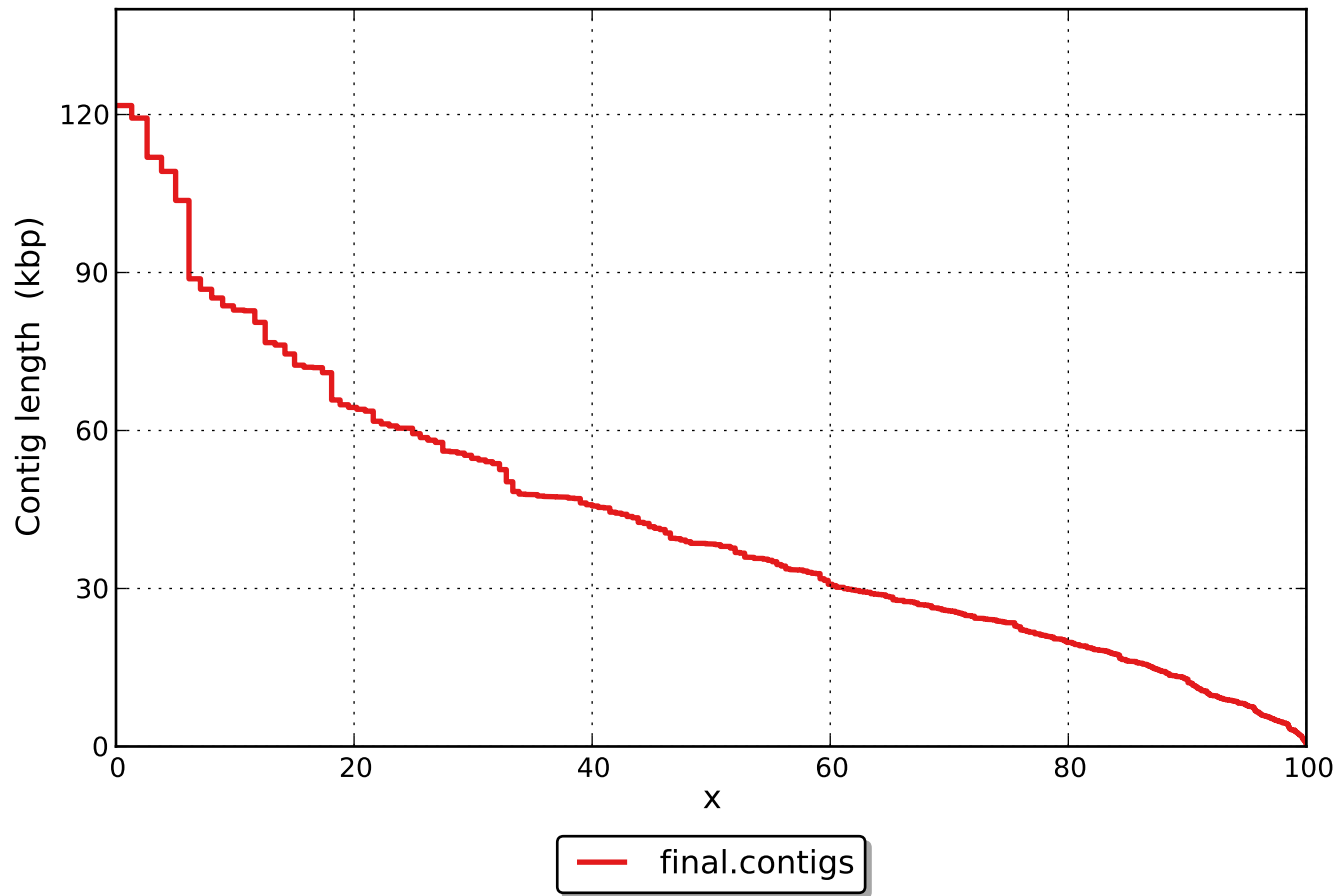All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	64
# indels	0
# short indels	0
# long indels	0
Indels length	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).
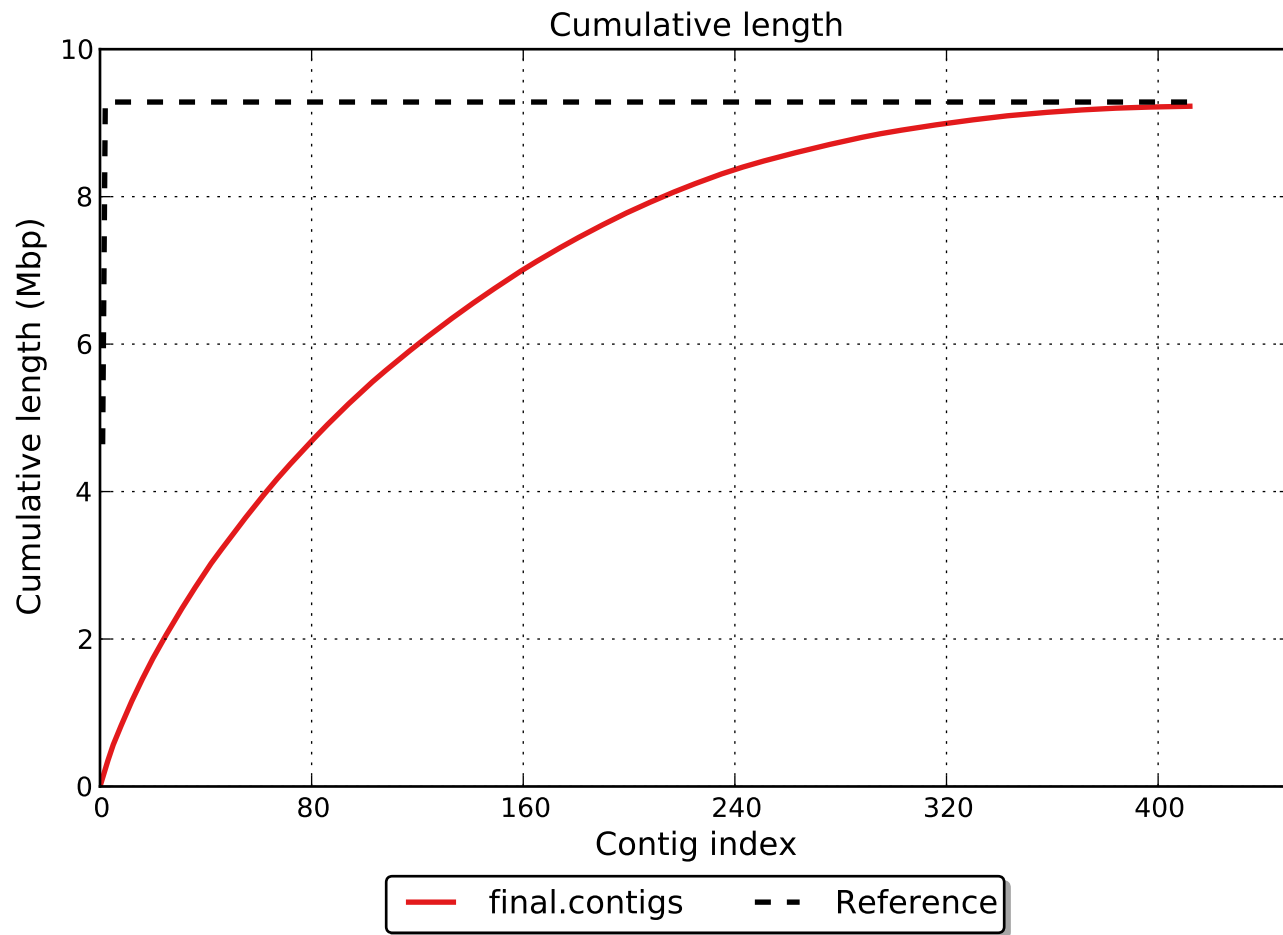
Unaligned report

	final.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).

Nx

Cumulative length
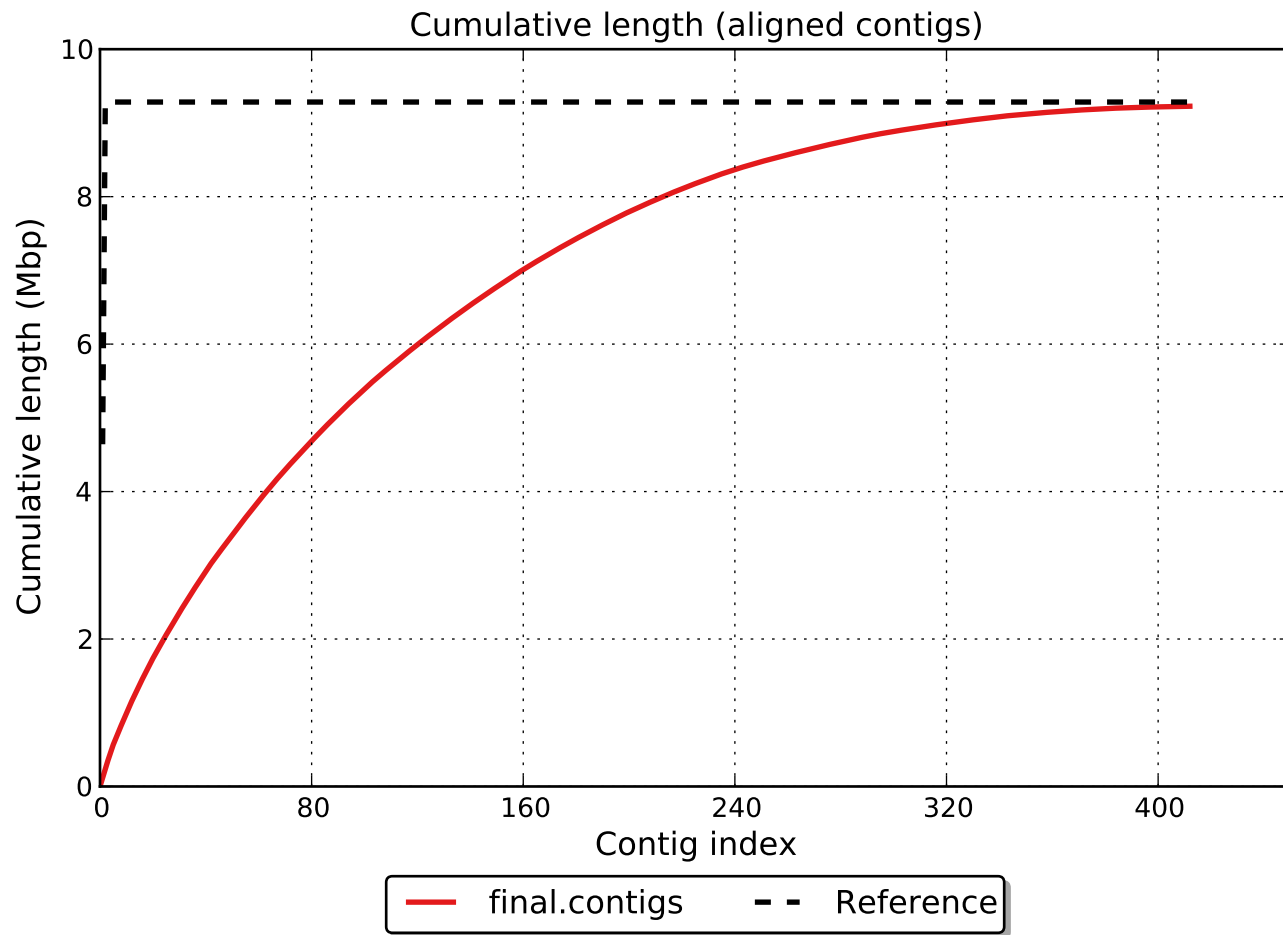
Misassemblies

final.contigs

Cumulative length (aligned contigs)