Report

	final.contigs
# contigs (>= 0 bp)	777
# contigs (>= 1000 bp)	641
# contigs (>= 5000 bp)	477
# contigs (>= 10000 bp)	319
# contigs (>= 25000 bp)	105
# contigs (>= 50000 bp)	27
Total length (>= 0 bp)	9729578
Total length (>= 1000 bp)	9673156
Total length (>= 5000 bp)	9163679
Total length (>= 10000 bp)	7975994
Total length (>= 25000 bp)	4580184
Total length (>= 50000 bp)	1932214
# contigs	682
Largest contig	119580
Total length	9702732
Reference length	9714864
N50	23406
N75	12507
L50	117
L75	257
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.501
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.50
# indels per 100 kbp	0.00
Largest alignment	119580
NA50	23406
NA75	12507
LA50	117
LA75	257

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).
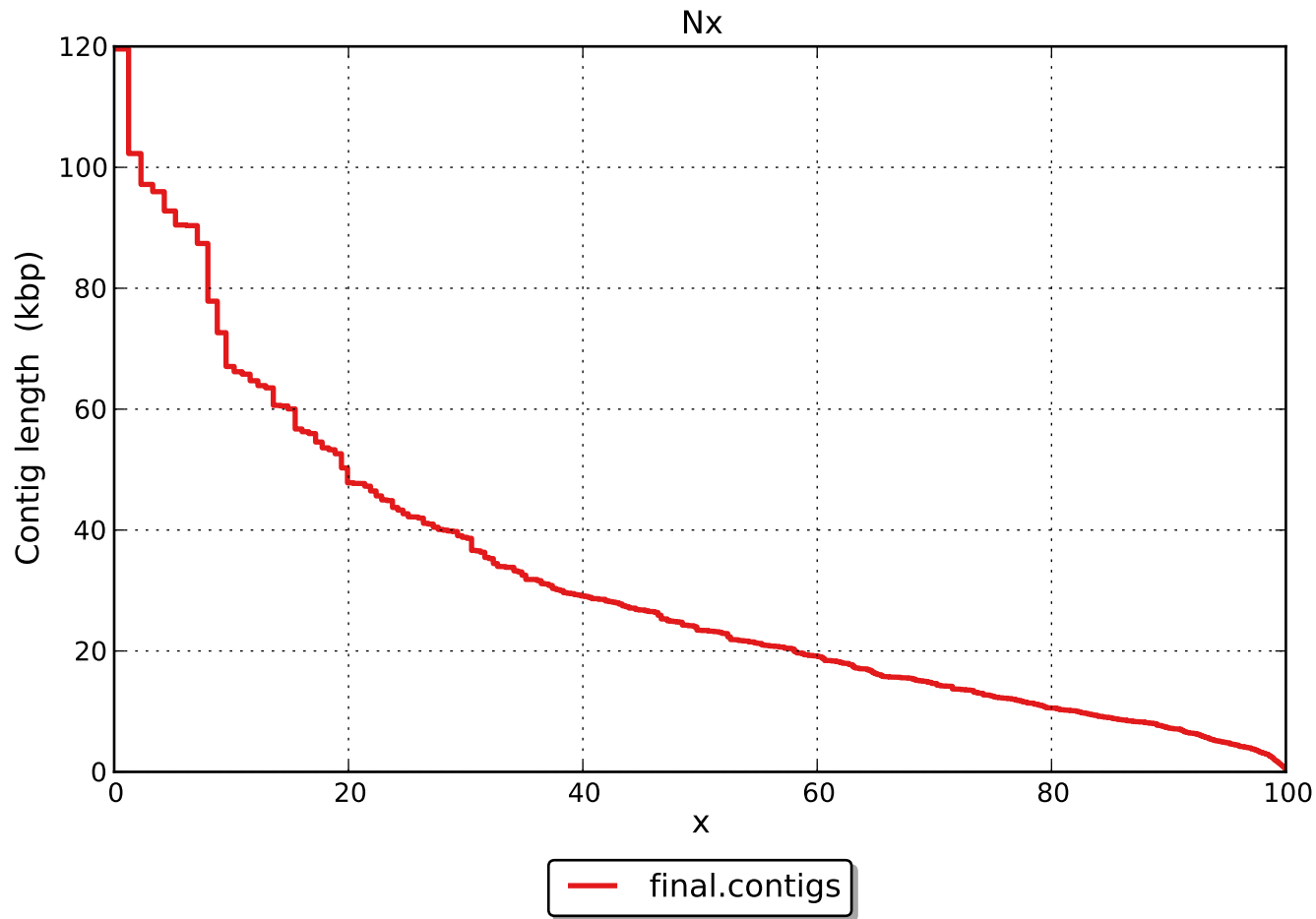
Misassemblies report

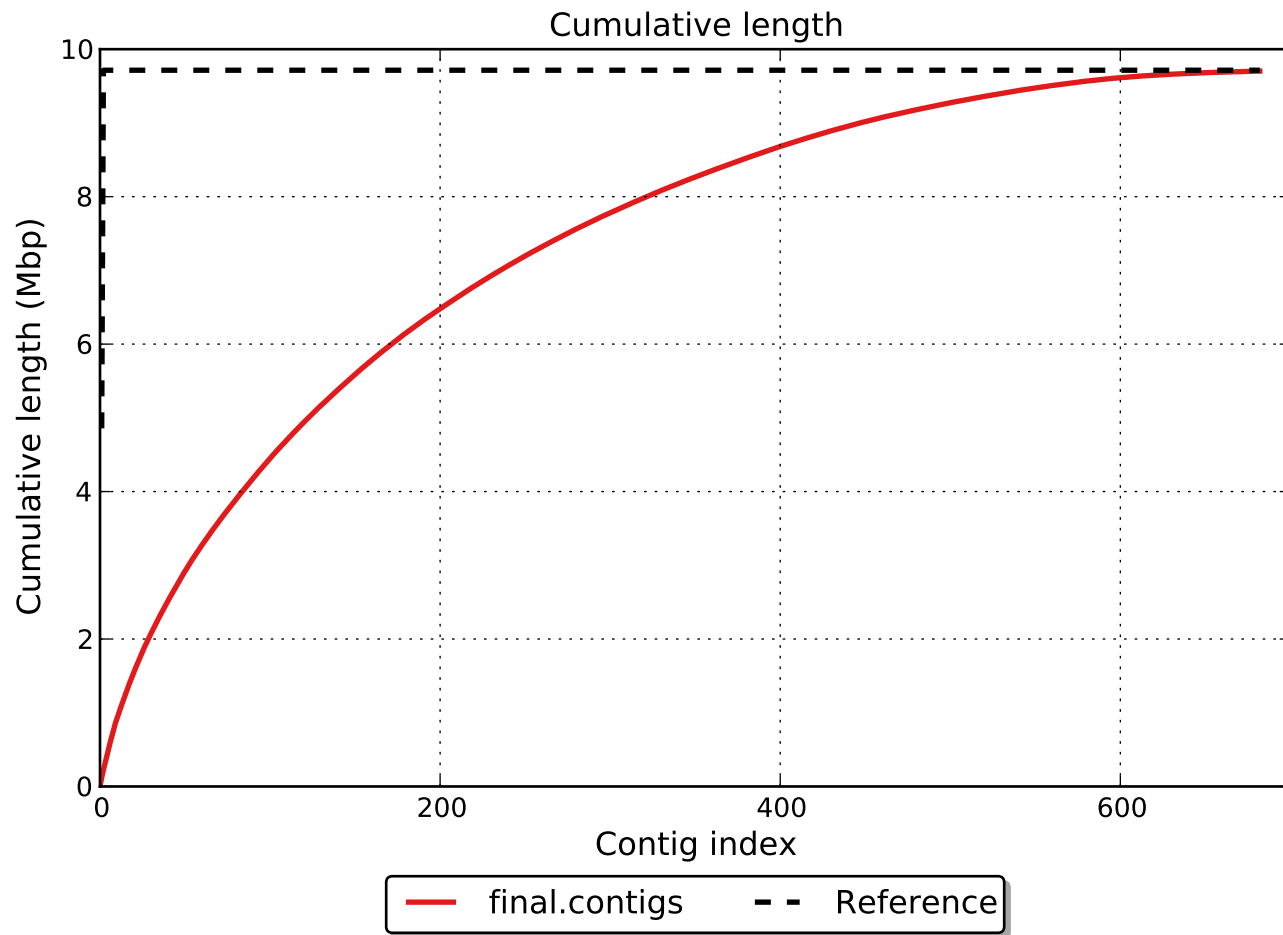|	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	145
# indels	0
# short indels	0
# long indels	0
Indels length	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

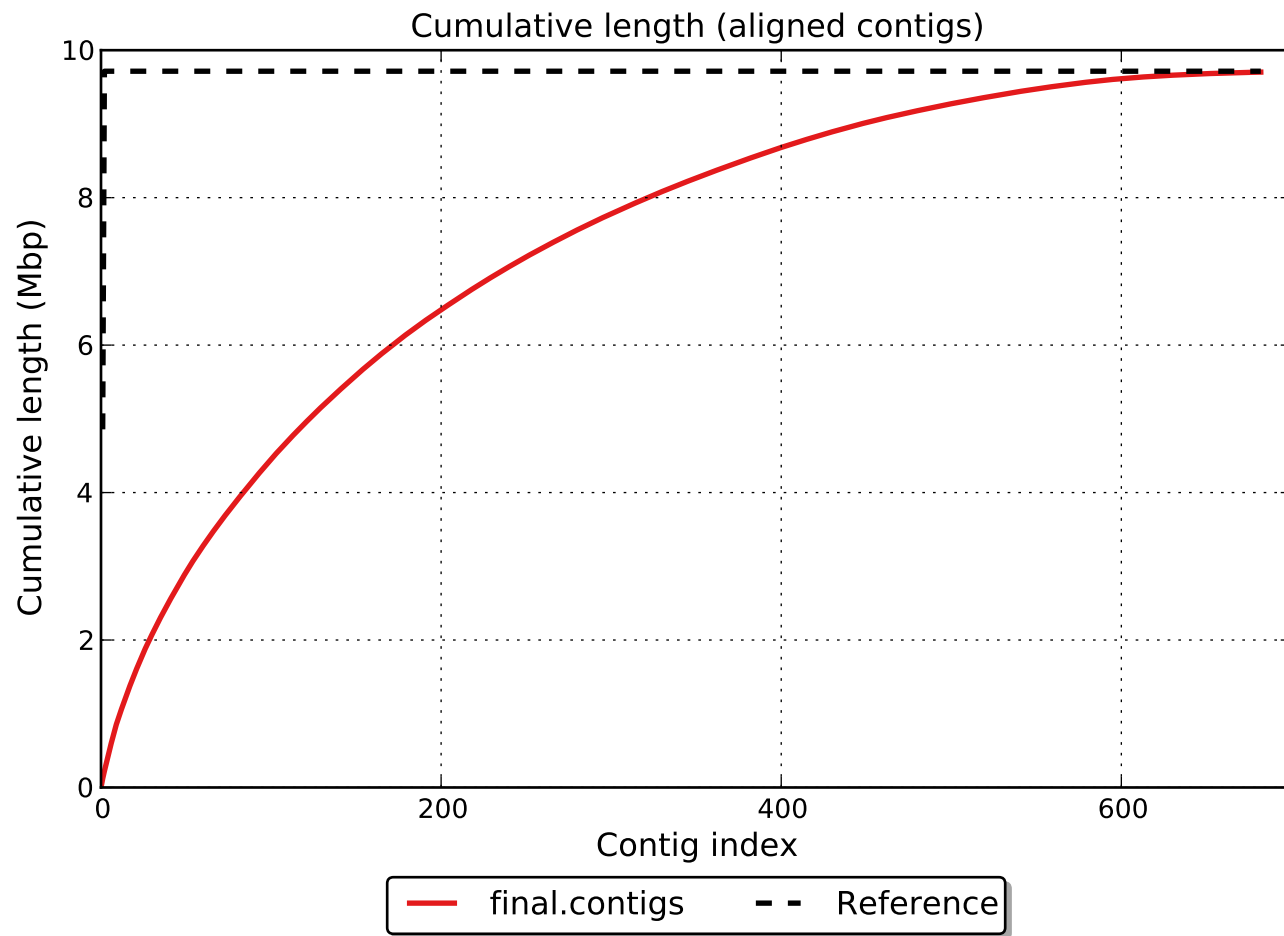|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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)