Report

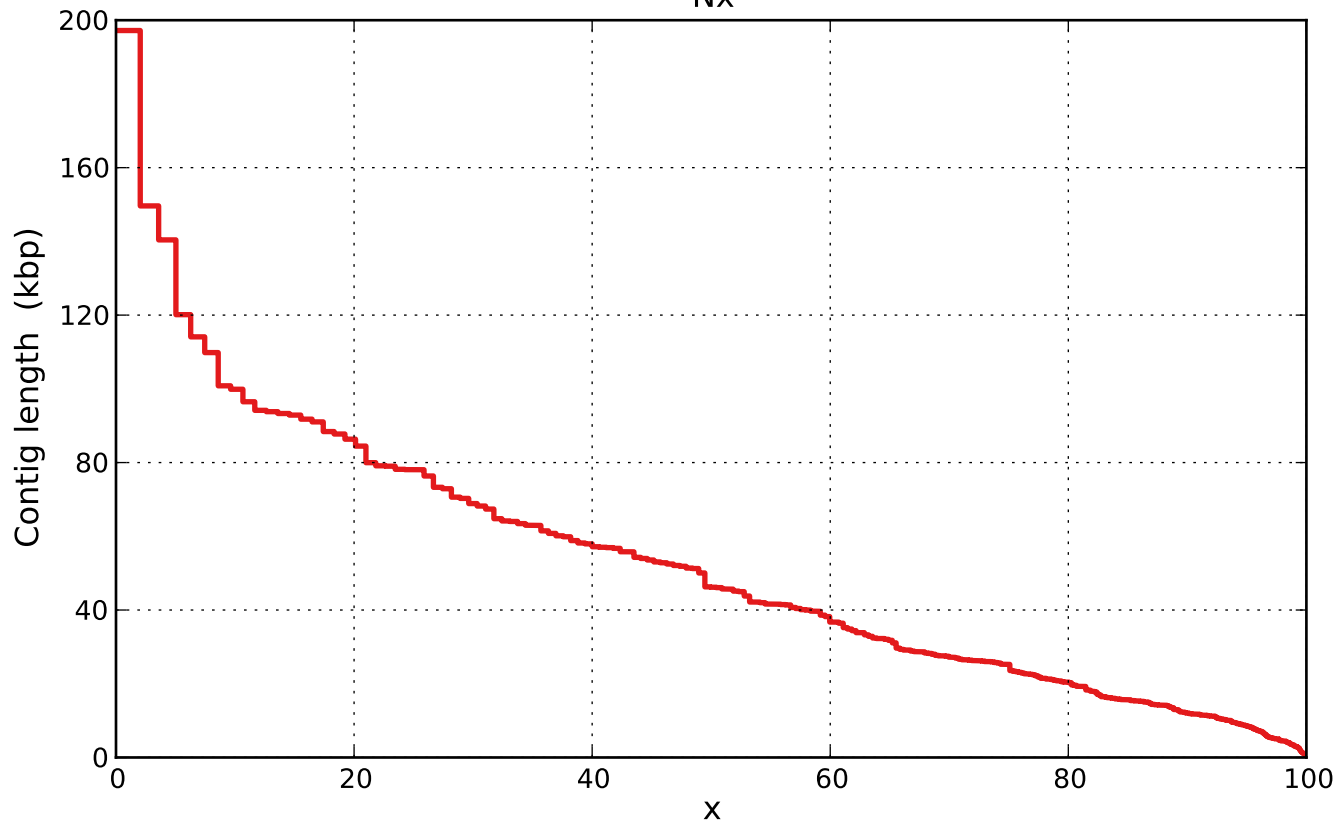|	final.contigs
# contigs (>= 0 bp)	492
# contigs (>= 1000 bp)	379
# contigs (>= 5000 bp)	307
# contigs (>= 10000 bp)	253
# contigs (>= 25000 bp)	137
# contigs (>= 50000 bp)	63
Total length (>= 0 bp)	9704872
Total length (>= 1000 bp)	9660643
Total length (>= 5000 bp)	9453397
Total length (>= 10000 bp)	9068324
Total length (>= 25000 bp)	7268360
Total length (>= 50000 bp)	4788544
# contigs	406
Largest contig	197199
Total length	9679992
Reference length	9714864
N50	46181
N75	25244
L50	65
L75	137
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.506
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.52
# indels per 100 kbp	0.00
Largest alignment	197199
NA50	46181
NA75	25244
LA50	65
LA75	137

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	147
# 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).
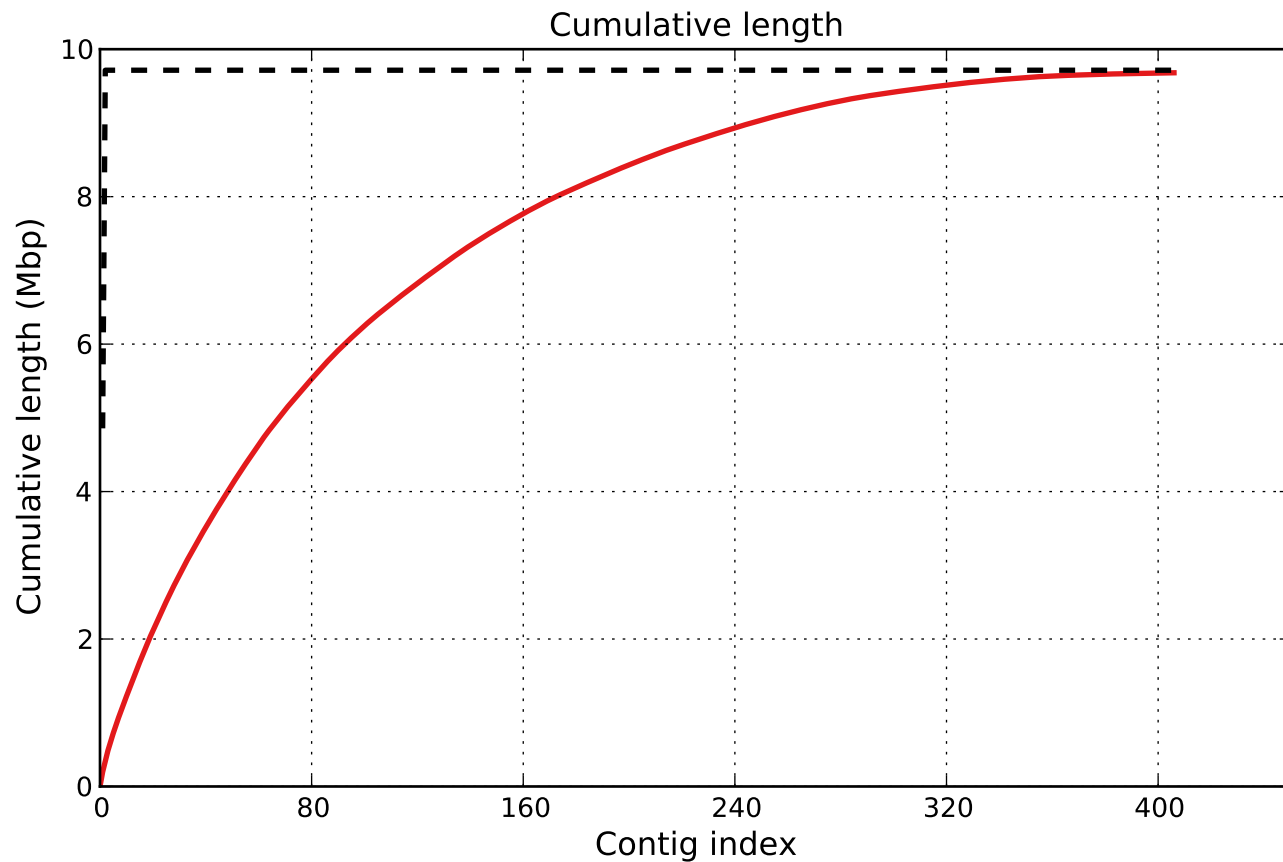
Unaligned report

	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).
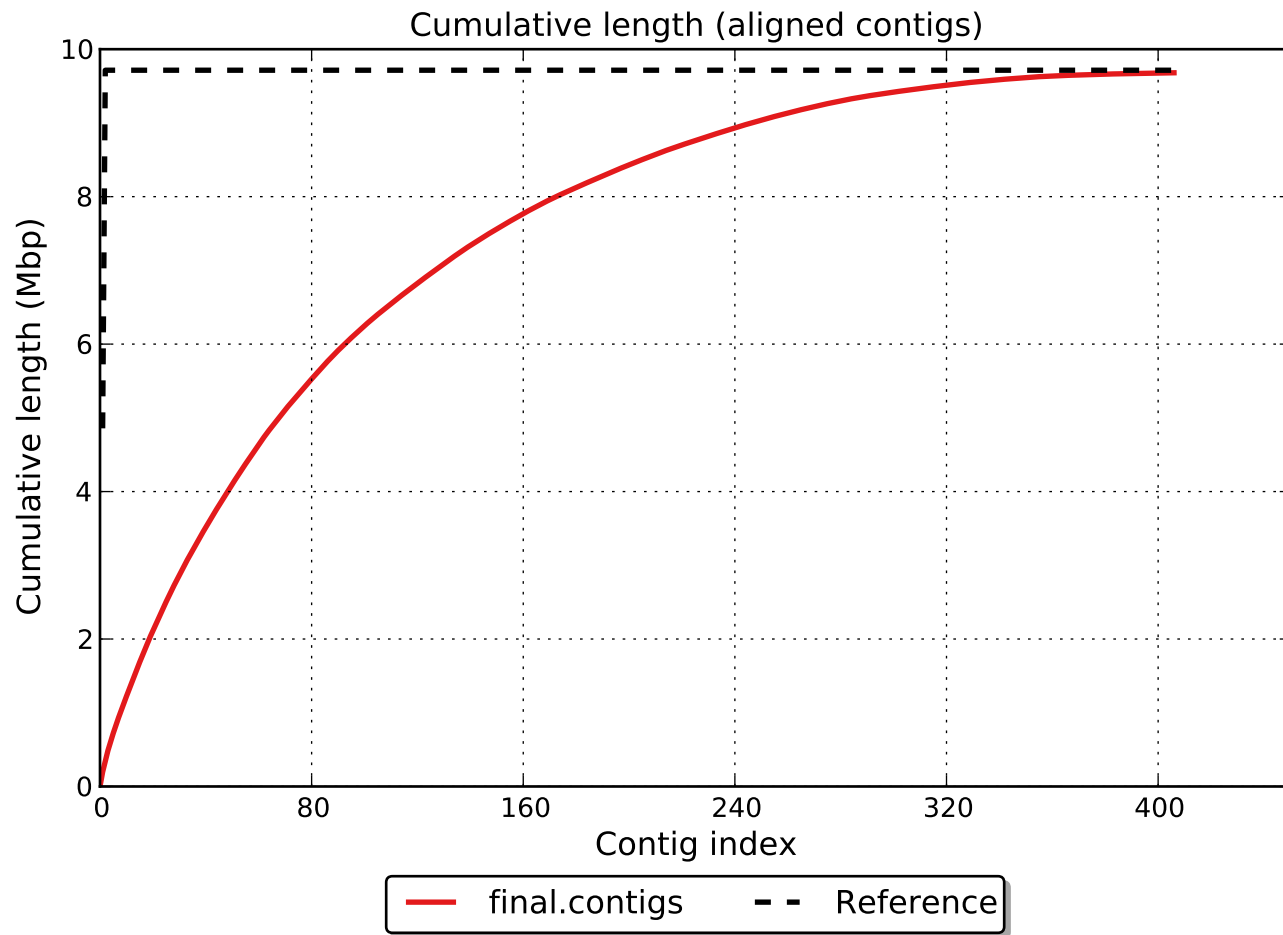
Cumulative length
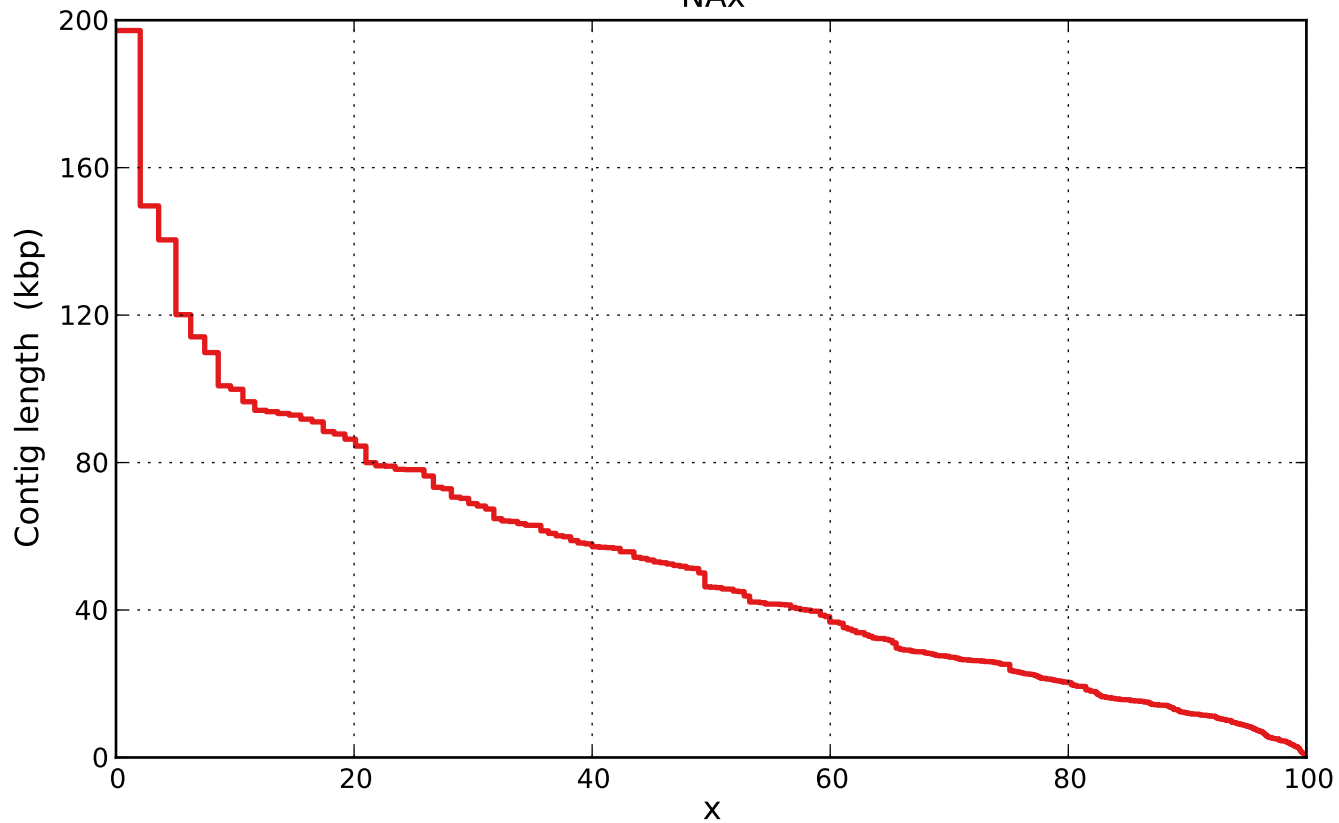
Misassemblies

final.contigs

Cumulative length (aligned contigs)

NAx