

Report

	final.contigs
# contigs (≥ 0 bp)	801
# contigs (≥ 1000 bp)	647
# contigs (≥ 5000 bp)	464
# contigs (≥ 10000 bp)	320
# contigs (≥ 25000 bp)	110
# contigs (≥ 50000 bp)	15
Total length (≥ 0 bp)	9281077
Total length (≥ 1000 bp)	9217309
Total length (≥ 5000 bp)	8680679
Total length (≥ 10000 bp)	7648265
Total length (≥ 25000 bp)	4157605
Total length (≥ 50000 bp)	966351
# contigs	684
Largest contig	95788
Total length	9245899
Reference length	9283304
N50	23232
N75	13502
L50	130
L75	259
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	15109
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	99.051
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.20
# indels per 100 kbp	0.00
Largest alignment	95788
NA50	23232
NA75	13502
LA50	130
LA75	259

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

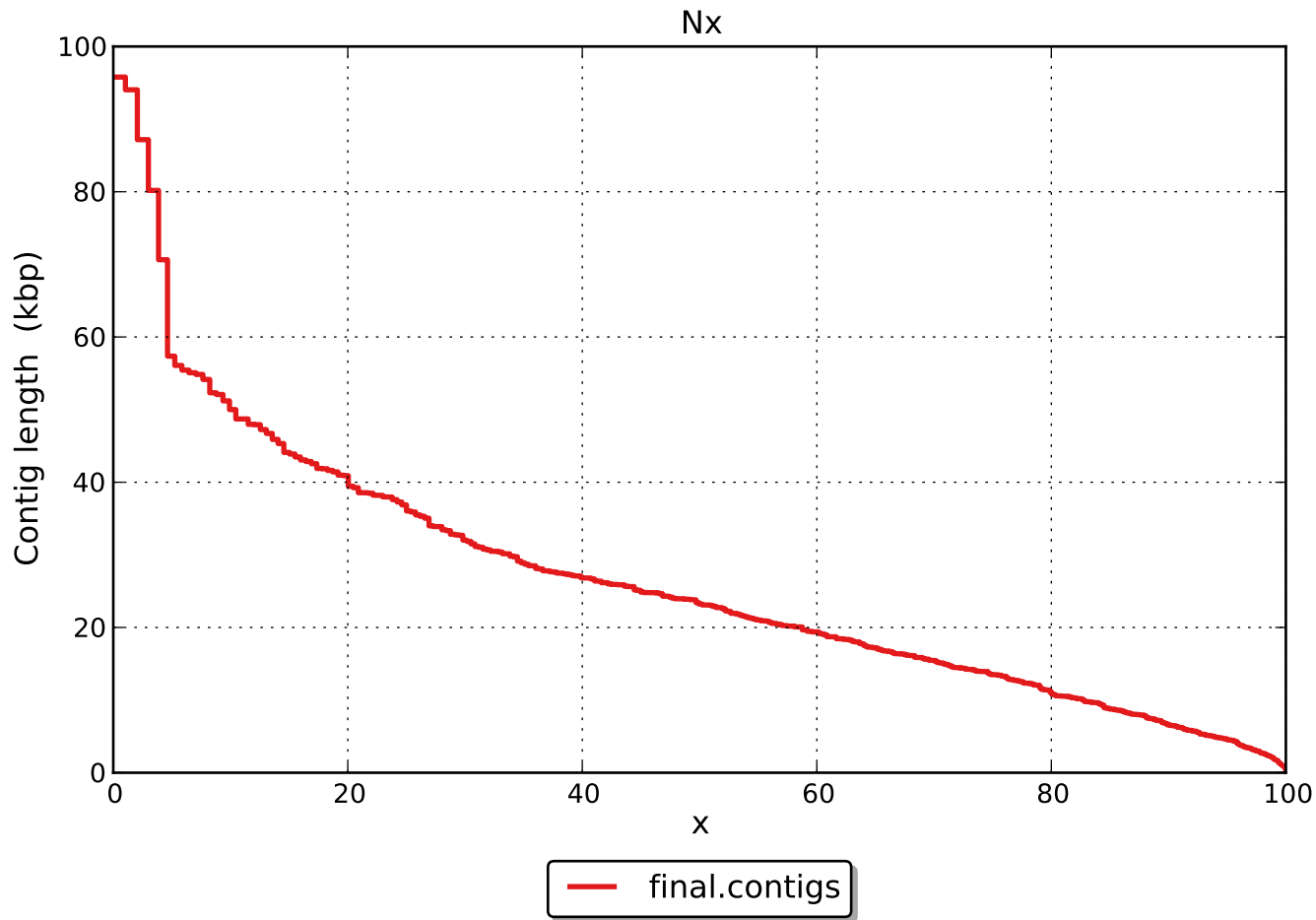
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	15109
# local misassemblies	0
# mismatches	18
# indels	0
# short indels	0
# long indels	0
Indels length	0

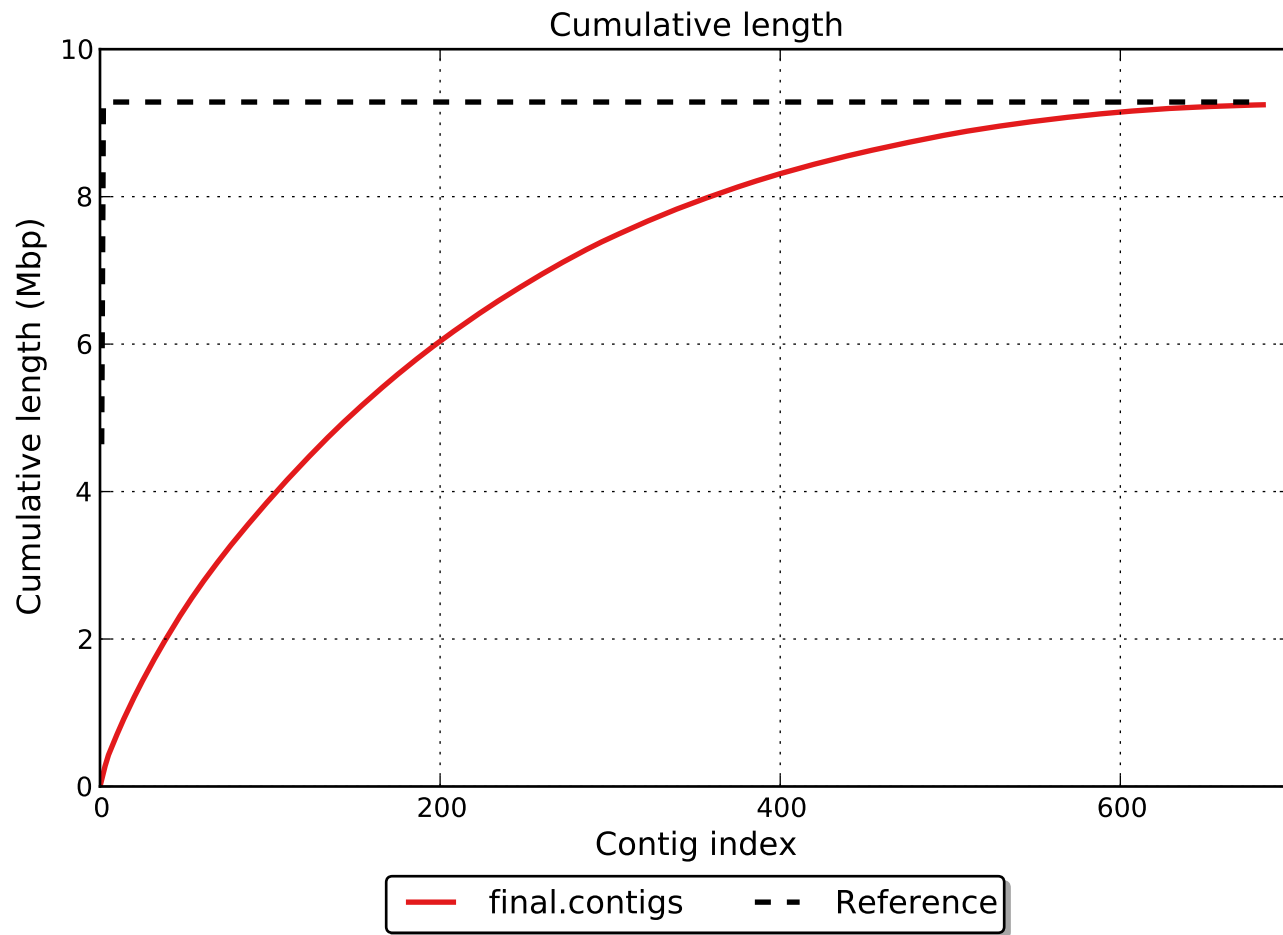
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

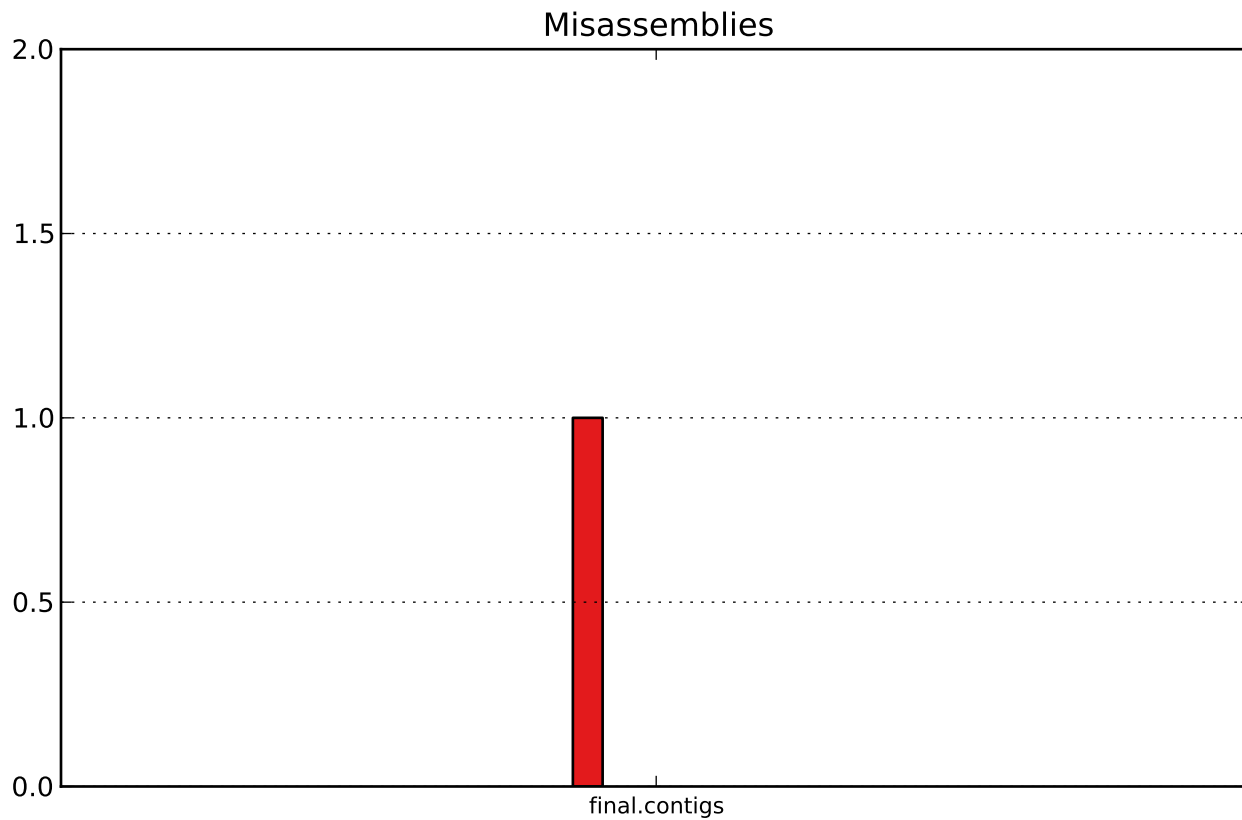
Unaligned report

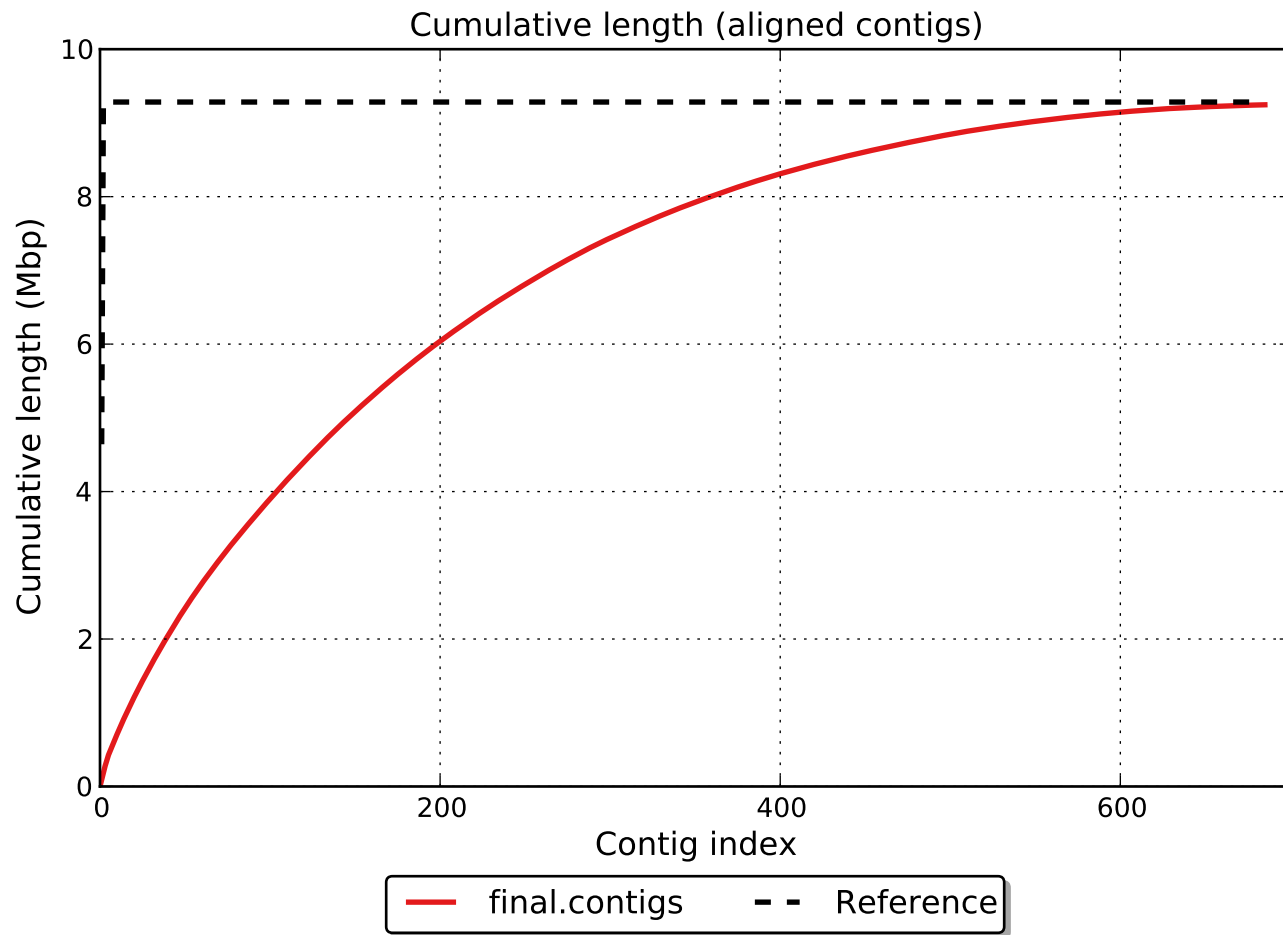
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

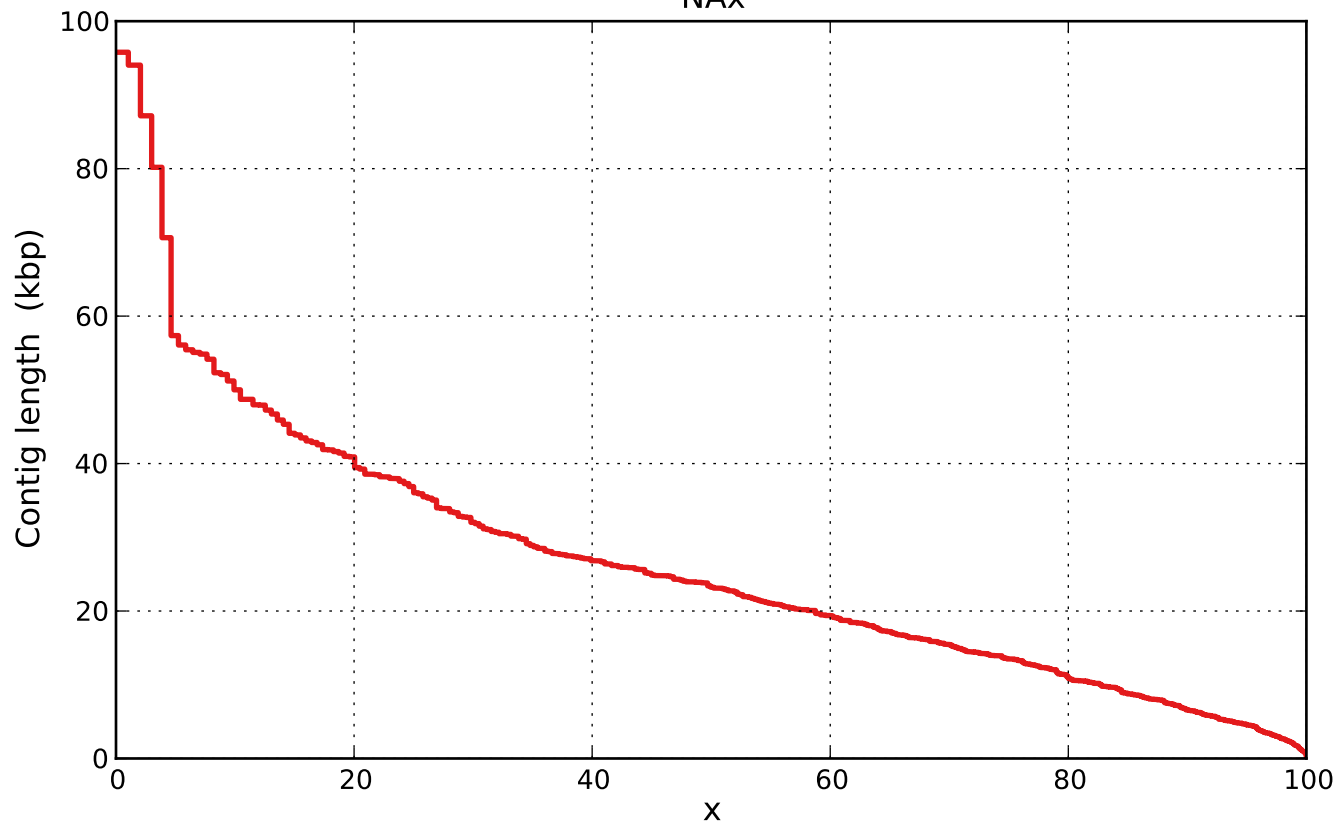








NAx



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