

Report

	final.contigs
# contigs (≥ 0 bp)	1051
# contigs (≥ 1000 bp)	604
# contigs (≥ 5000 bp)	446
# contigs (≥ 10000 bp)	313
# contigs (≥ 25000 bp)	132
# contigs (≥ 50000 bp)	28
Total length (≥ 0 bp)	9844930
Total length (≥ 1000 bp)	9683354
Total length (≥ 5000 bp)	9227570
Total length (≥ 10000 bp)	8219037
Total length (≥ 25000 bp)	5352810
Total length (≥ 50000 bp)	1864189
# contigs	639
Largest contig	110430
Total length	9707673
Reference length	9714864
N50	27264
N75	13773
L50	113
L75	234
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.281
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	9.96
# indels per 100 kbp	0.02
Largest alignment	110430
NA50	27264
NA75	13773
LA50	113
LA75	234

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

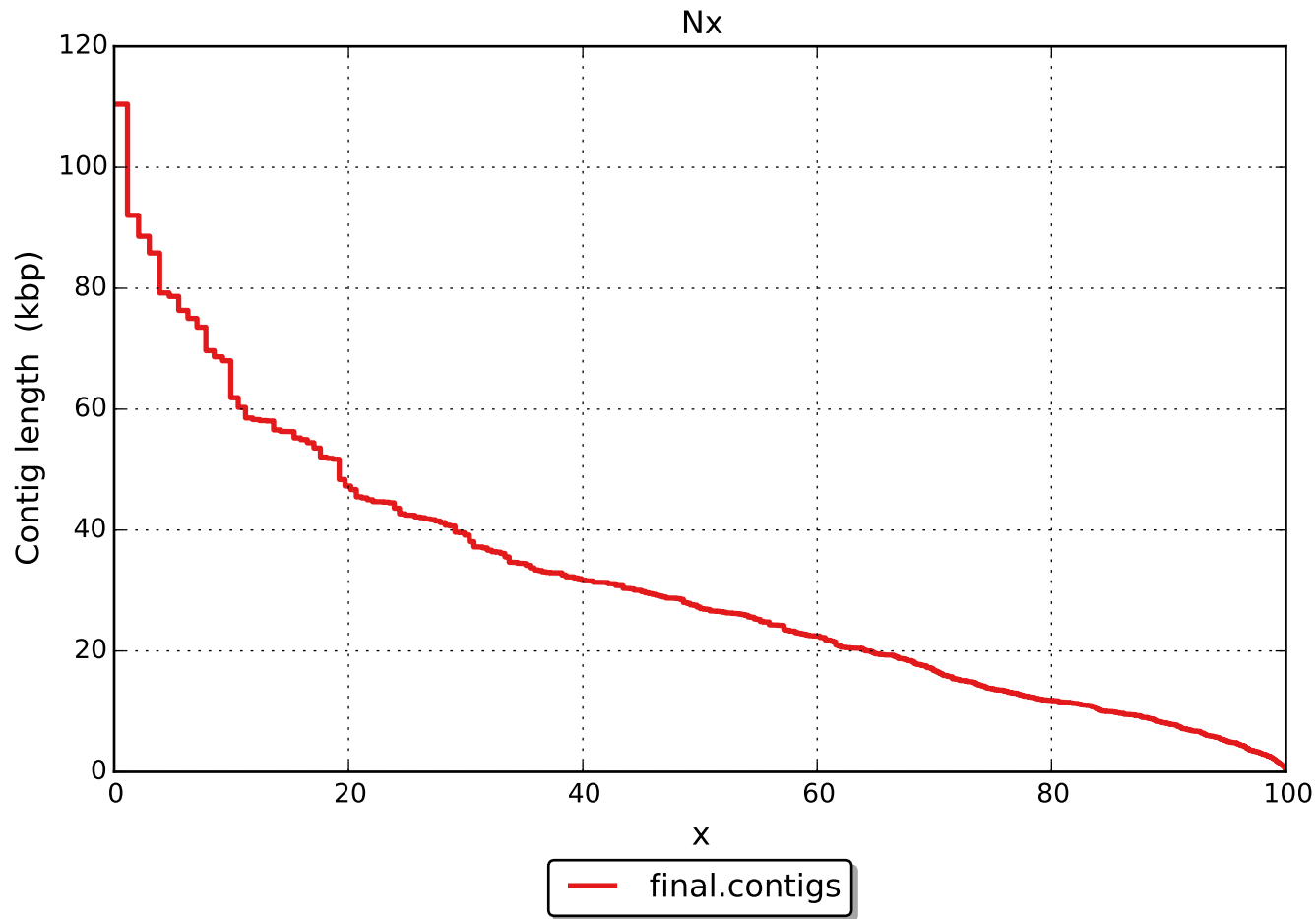
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	961
# indels	2
# short indels	2
# long indels	0
Indels length	2

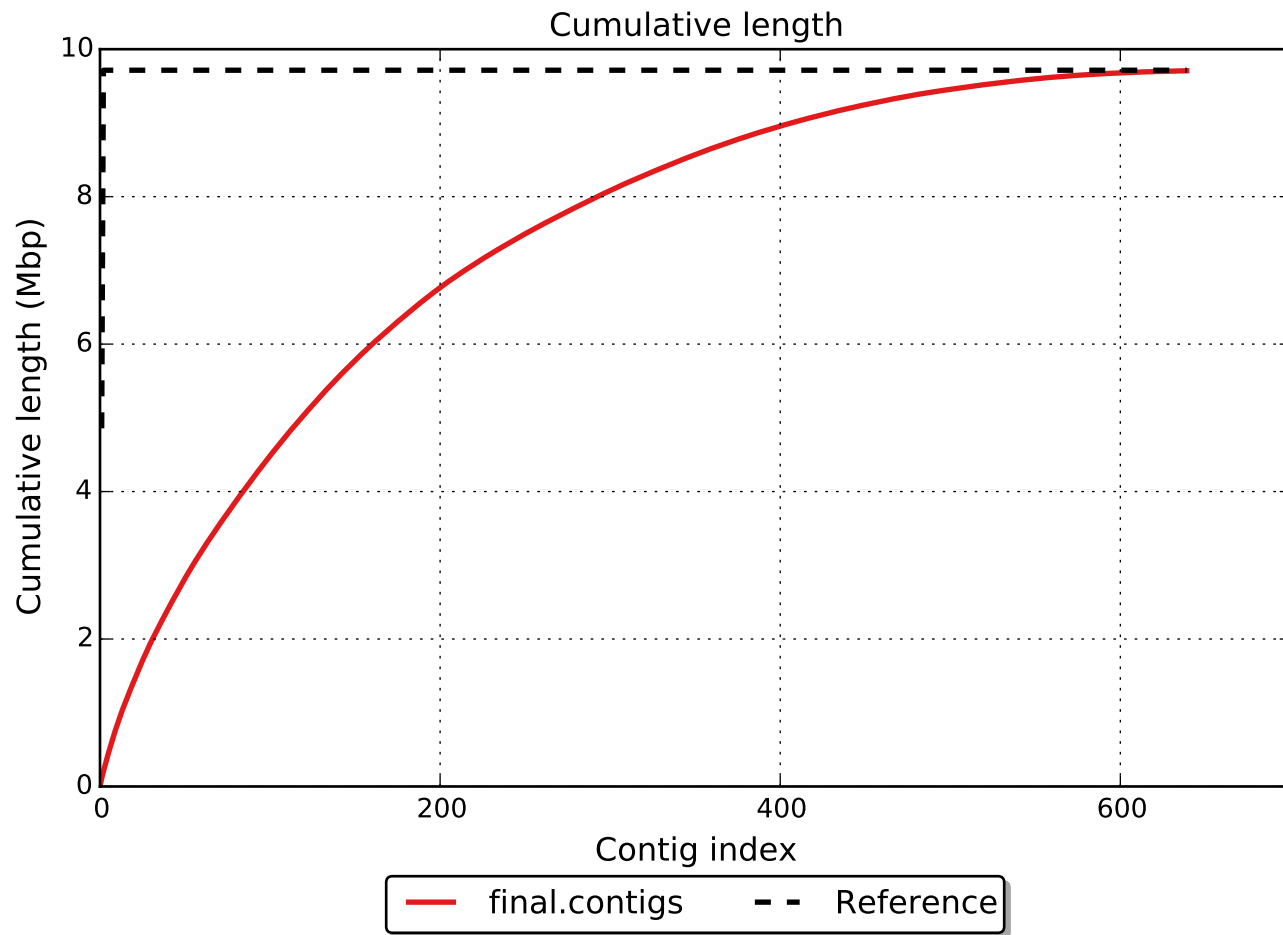
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

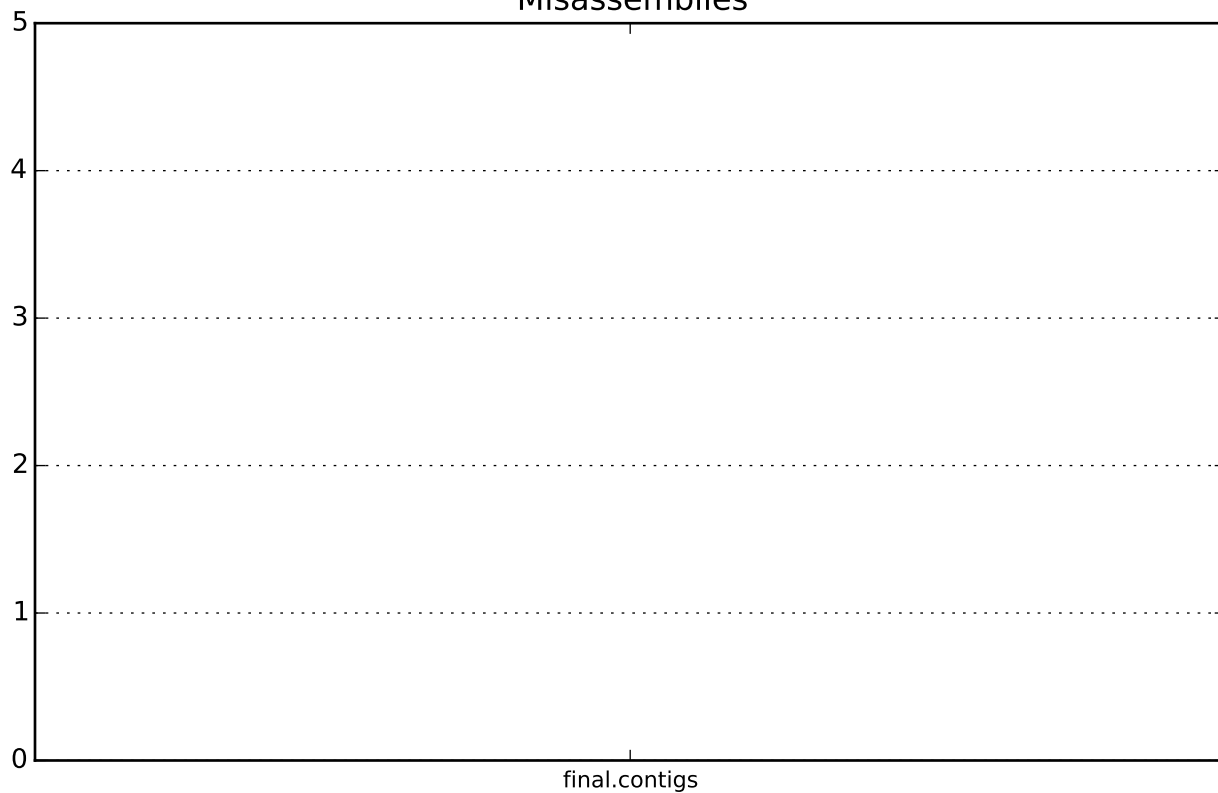
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

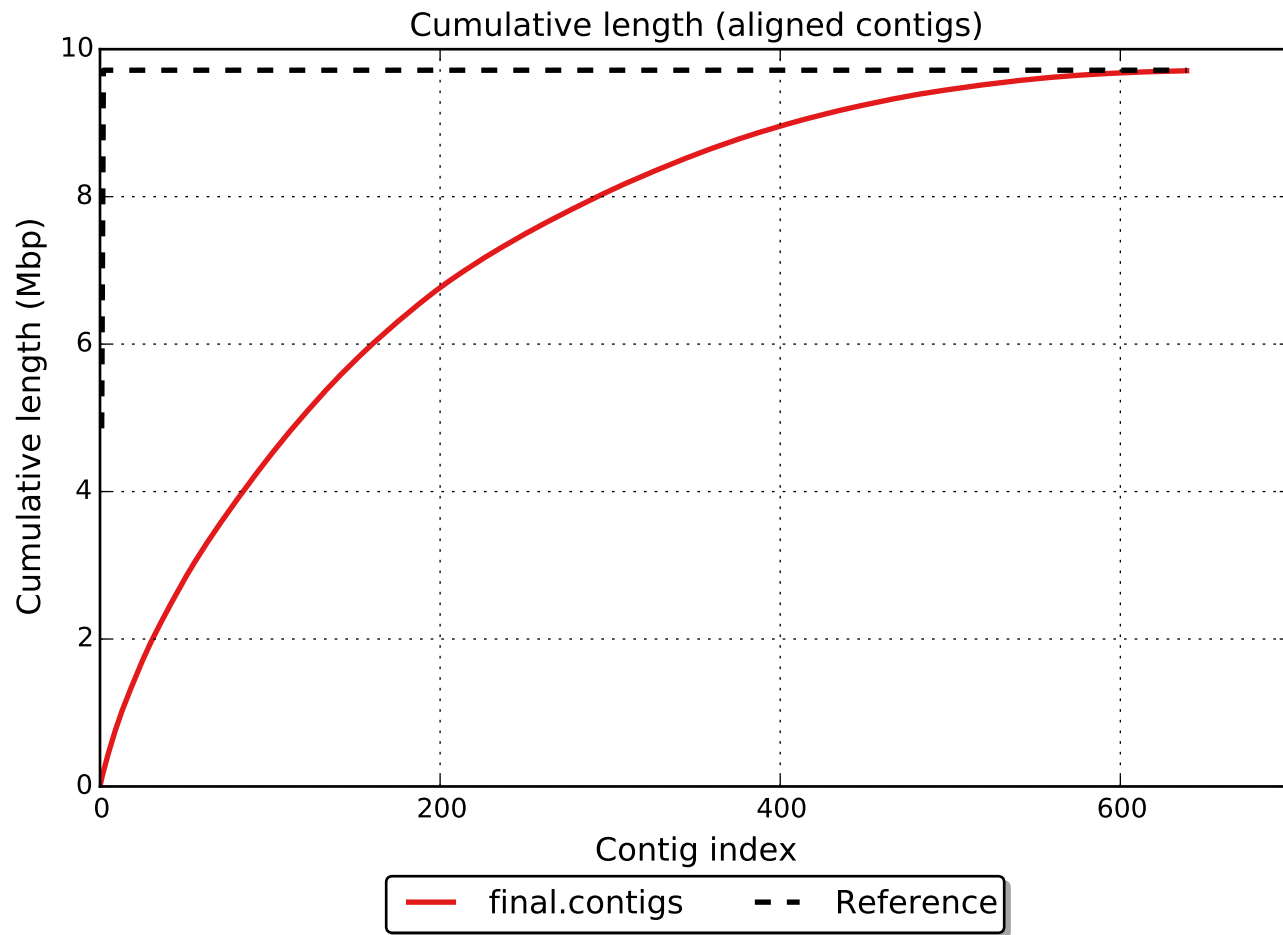
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



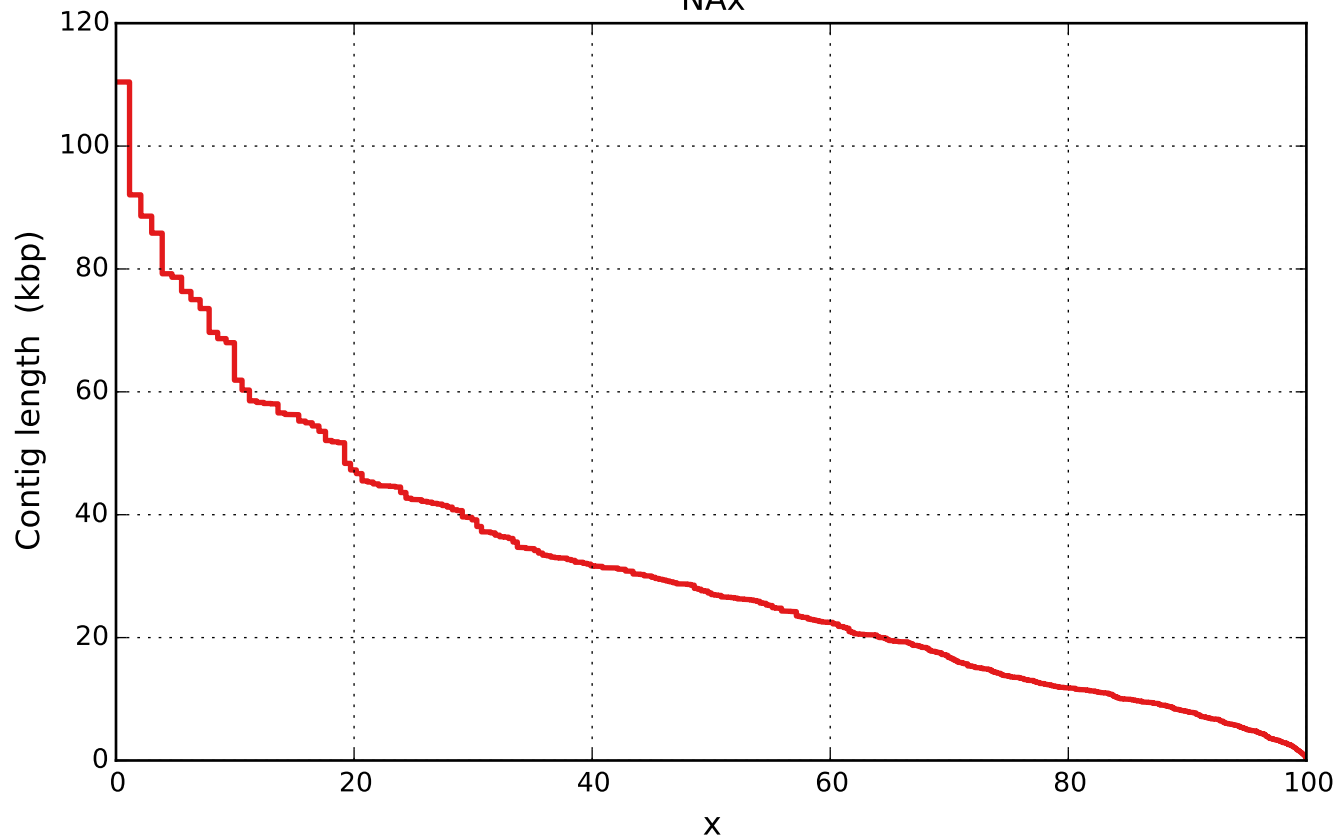


Misassemblies





NAx



— final.contigs