

Report

	final.contigs
# contigs (≥ 0 bp)	271
# contigs (≥ 1000 bp)	217
# contigs (≥ 5000 bp)	172
# contigs (≥ 10000 bp)	143
# contigs (≥ 25000 bp)	66
# contigs (≥ 50000 bp)	20
Total length (≥ 0 bp)	4573421
Total length (≥ 1000 bp)	4549760
Total length (≥ 5000 bp)	4445537
Total length (≥ 10000 bp)	4223740
Total length (≥ 25000 bp)	2959535
Total length (≥ 50000 bp)	1358550
# contigs	235
Largest contig	105740
Total length	4562347
Reference length	4641652
N50	33685
N75	19315
L50	43
L75	88
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	7
# unaligned contigs	0 + 1 part
Unaligned length	53
Genome fraction (▼)	98.209
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	57.65
# indels per 100 kbp	9.59
Largest alignment	105740
NA50	33685
NA75	19315
LA50	43
LA75	88

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

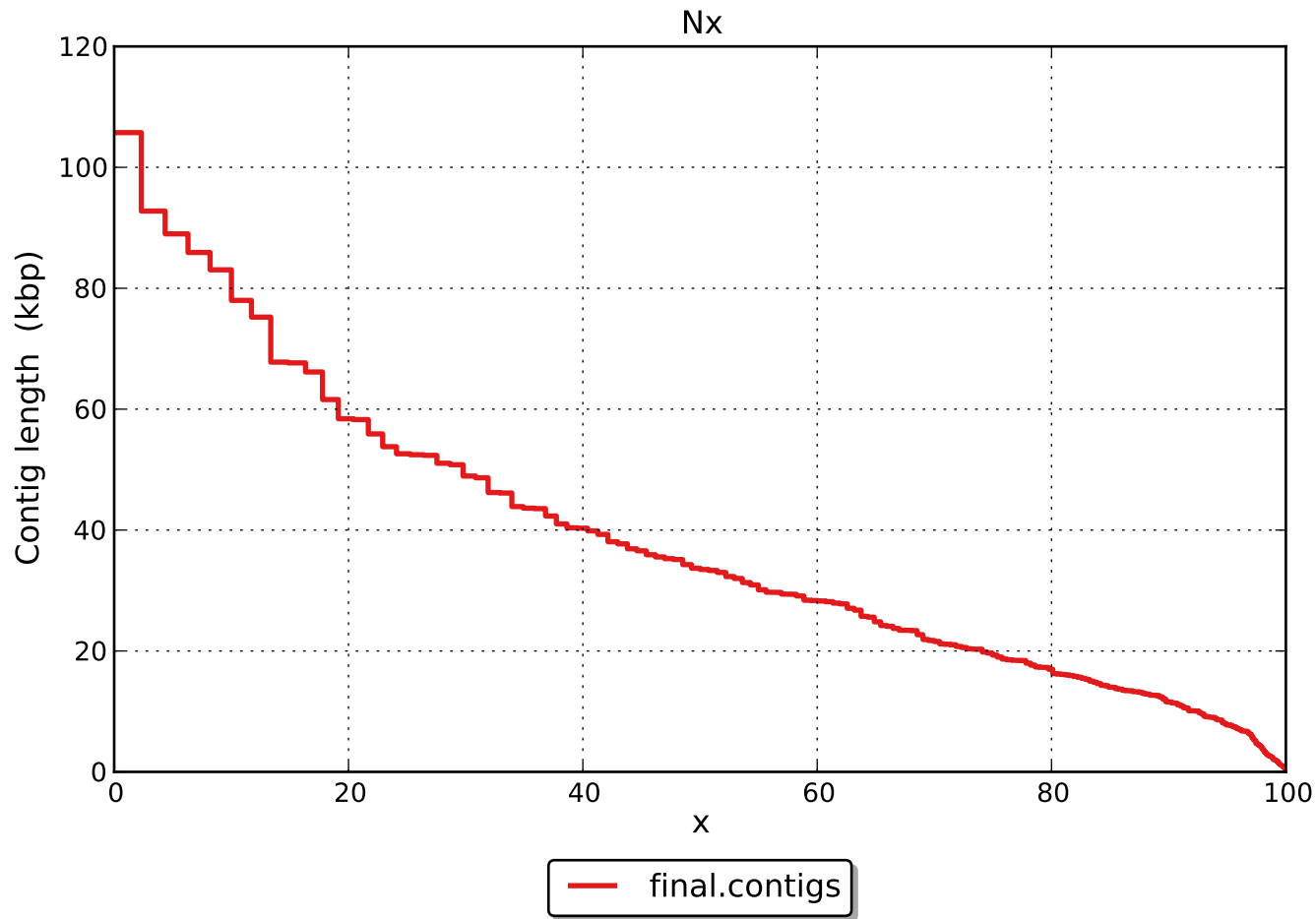
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	7
# mismatches	2628
# indels	437
# short indels	431
# long indels	6
Indels length	757

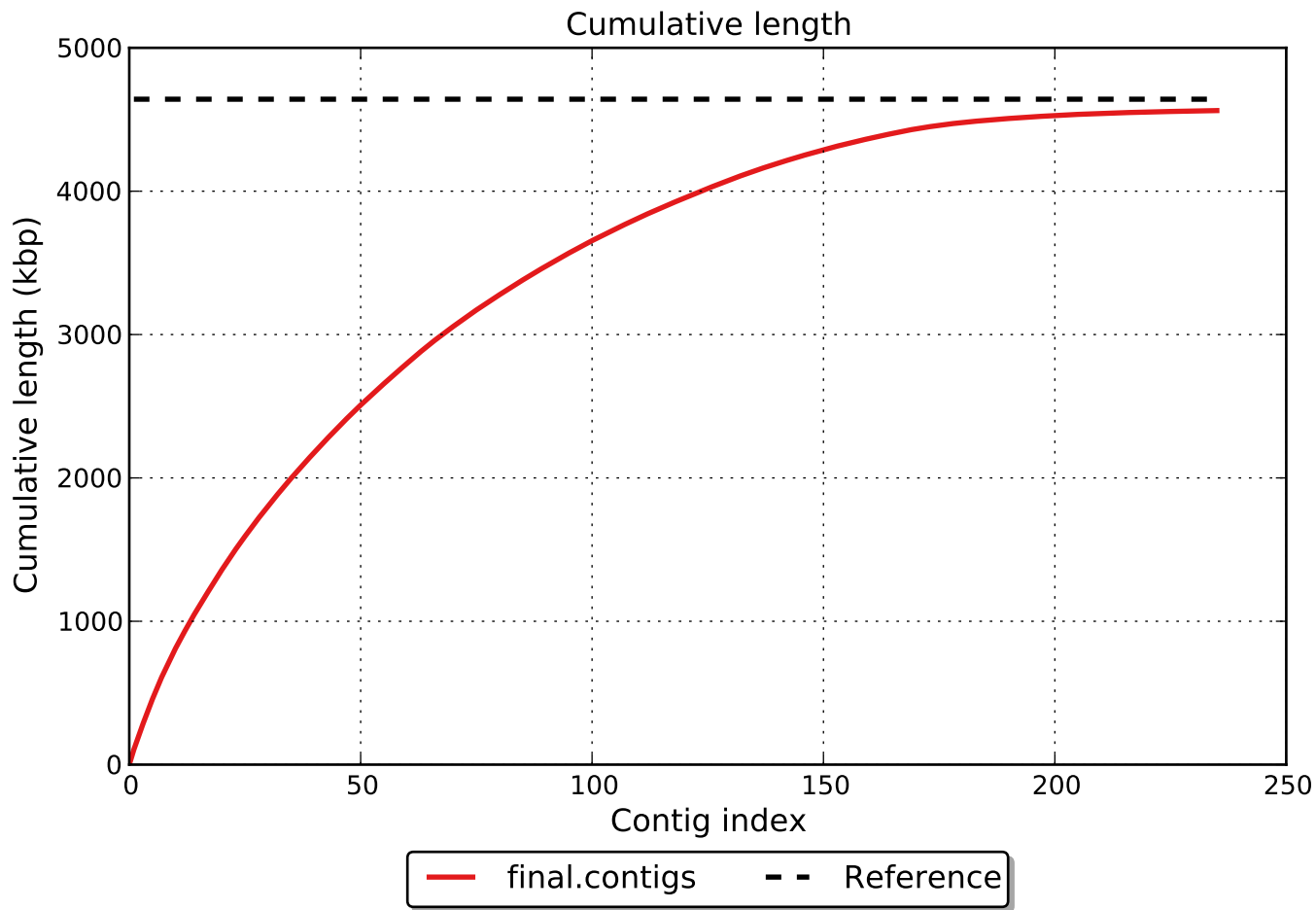
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

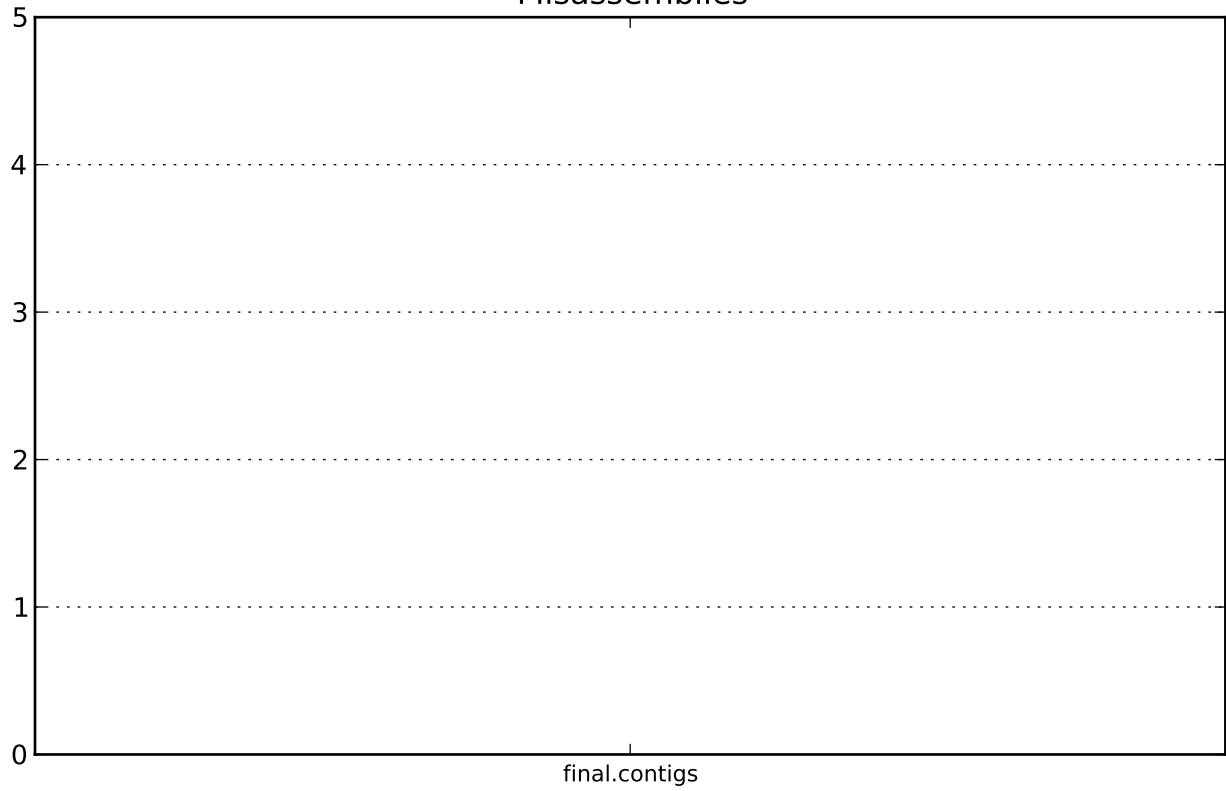
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	53
# N's	0

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).

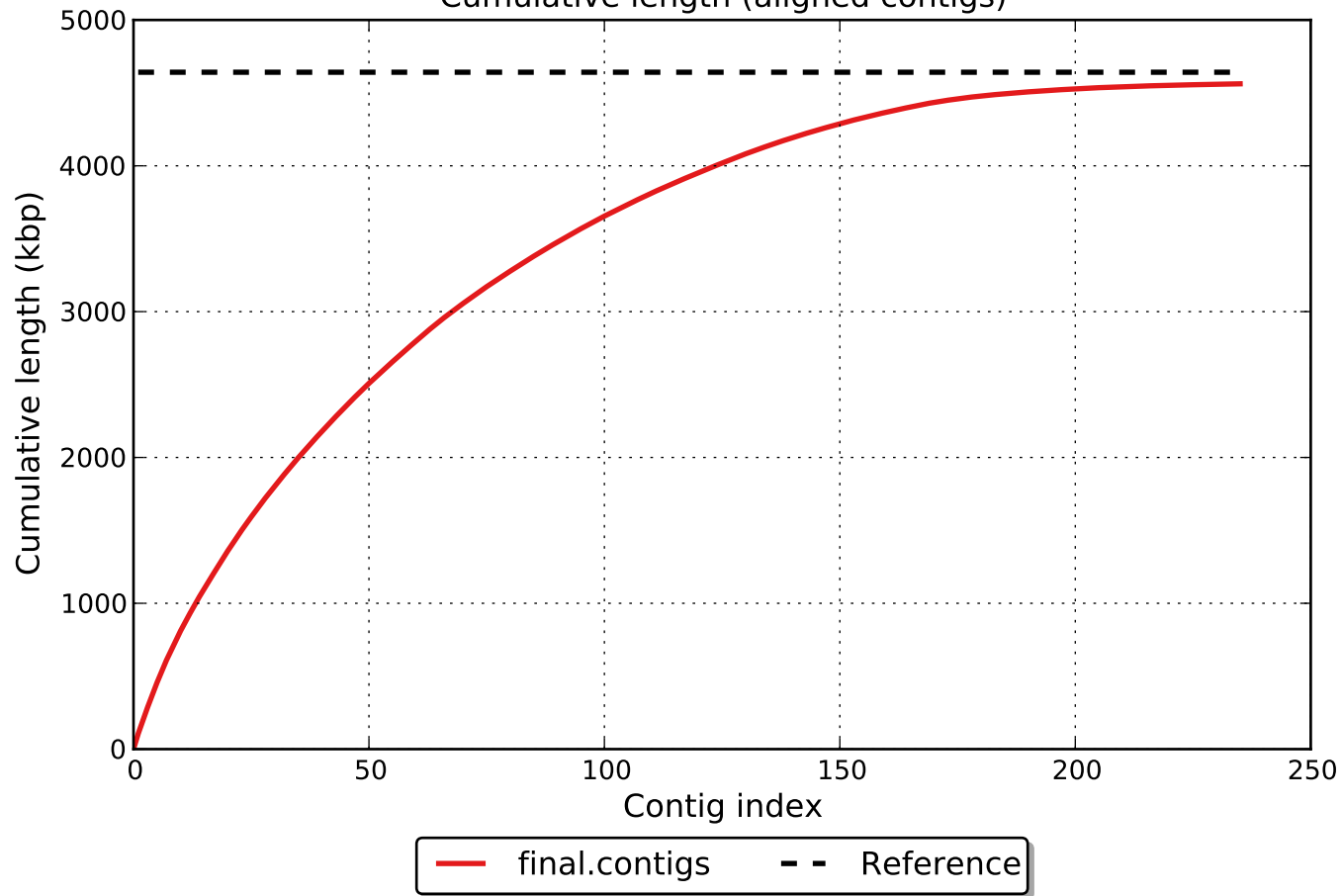




Misassemblies



Cumulative length (aligned contigs)



NAx

