

Report

	final.contigs
# contigs (≥ 0 bp)	5331
# contigs (≥ 1000 bp)	150
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	2782025
Total length (≥ 1000 bp)	180665
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	2313
Largest contig	1993
Total length	1593036
Reference length	4641652
N50	673
N75	577
L50	929
L75	1569
# misassemblies	10
# misassembled contigs	10
Misassembled contigs length	9513
# local misassemblies	0
# unaligned contigs	1 + 12 part
Unaligned length	1356
Genome fraction (%)	33.596
Duplication ratio	1.021
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1539.92
# indels per 100 kbp	9.94
Largest alignment	1885
NA50	670
NA75	575
LA50	932
LA75	1574

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	10
# relocations	9
# translocations	0
# inversions	1
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	10
Misassembled contigs length	9513
# local misassemblies	0
# mismatches	24014
# indels	155
# short indels	155
# long indels	0
Indels length	210

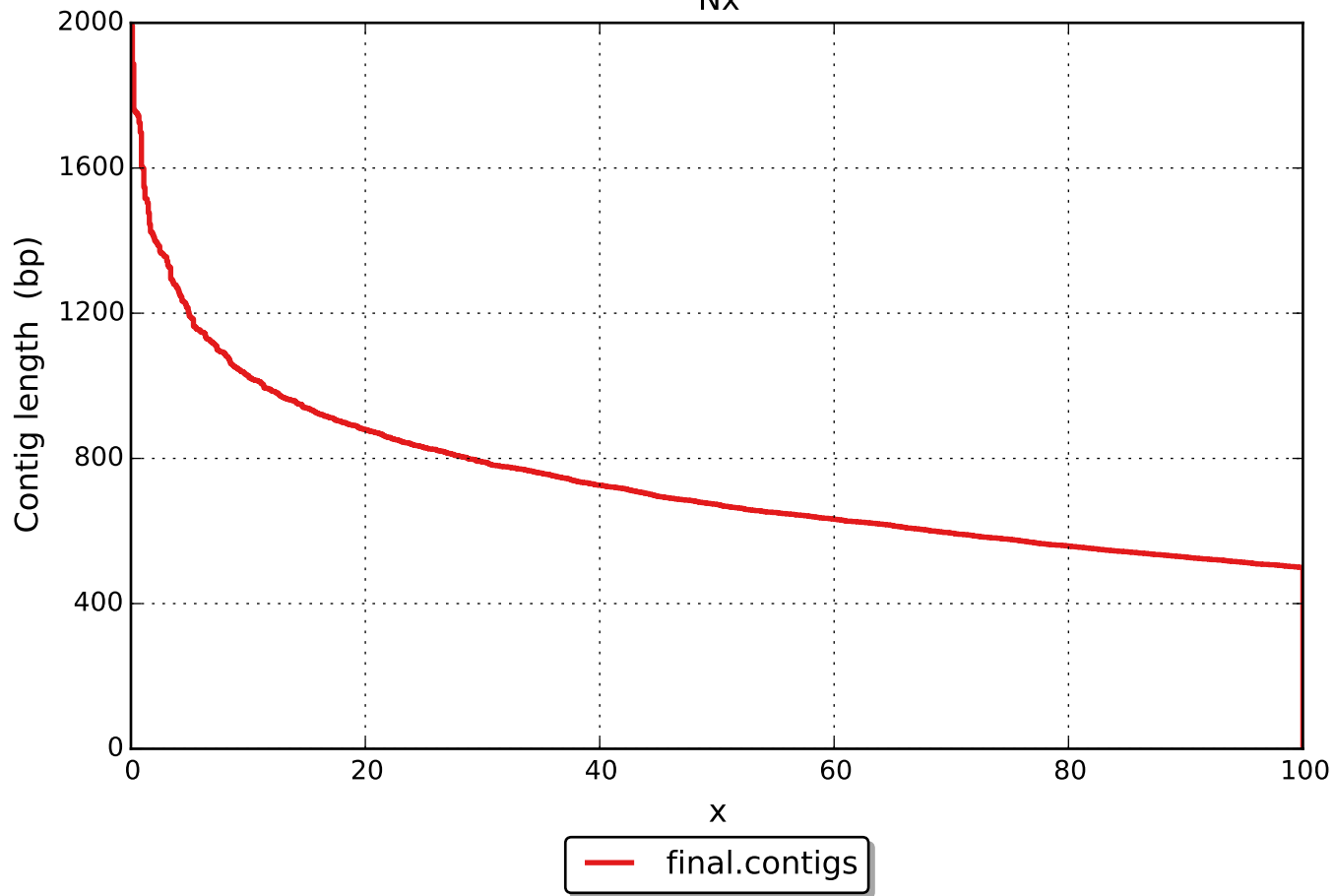
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

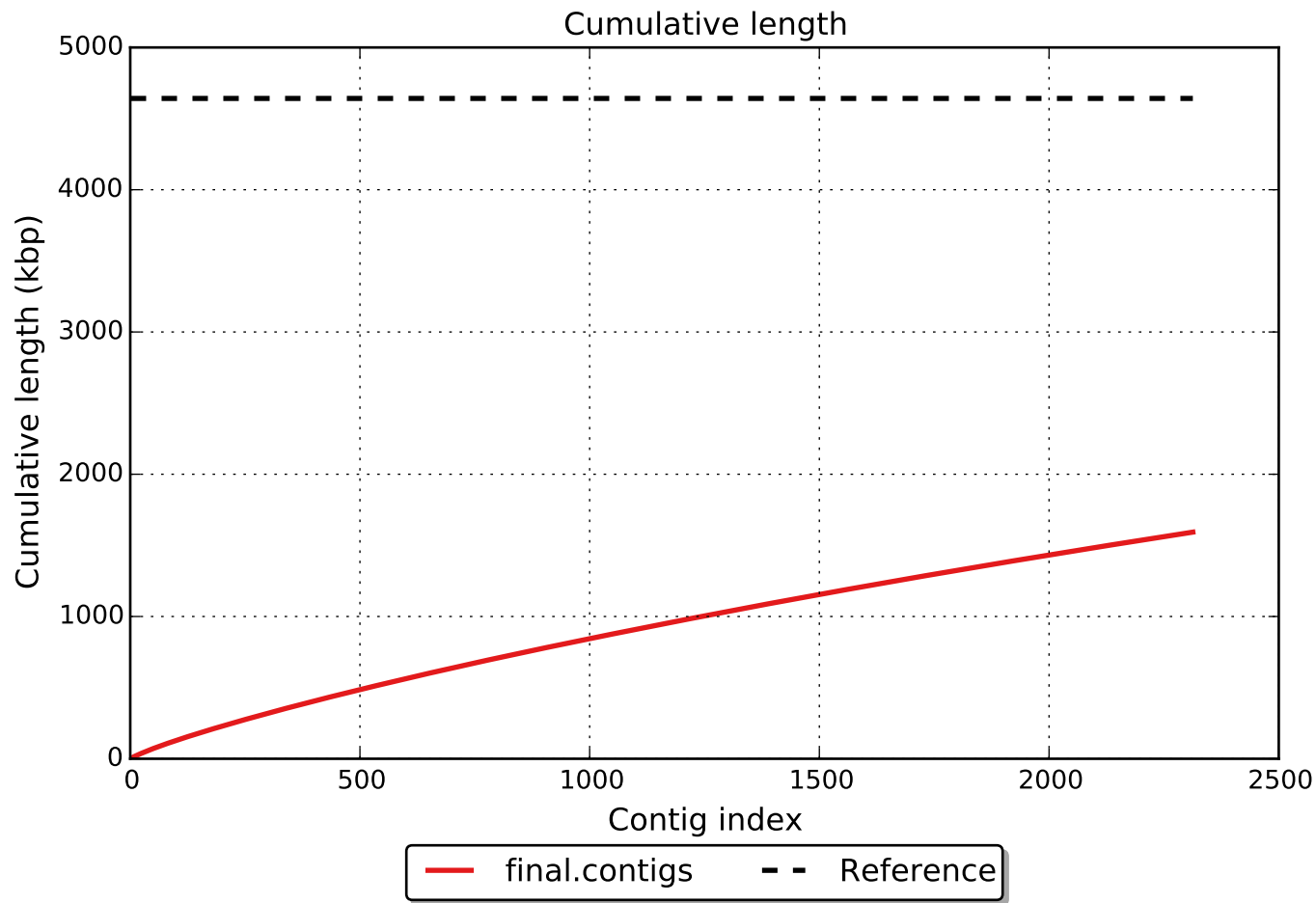
Unaligned report

	final.contigs
# fully unaligned contigs	1
Fully unaligned length	609
# partially unaligned contigs	12
# with misassembly	0
# both parts are significant	0
Partially unaligned length	747
# N's	0

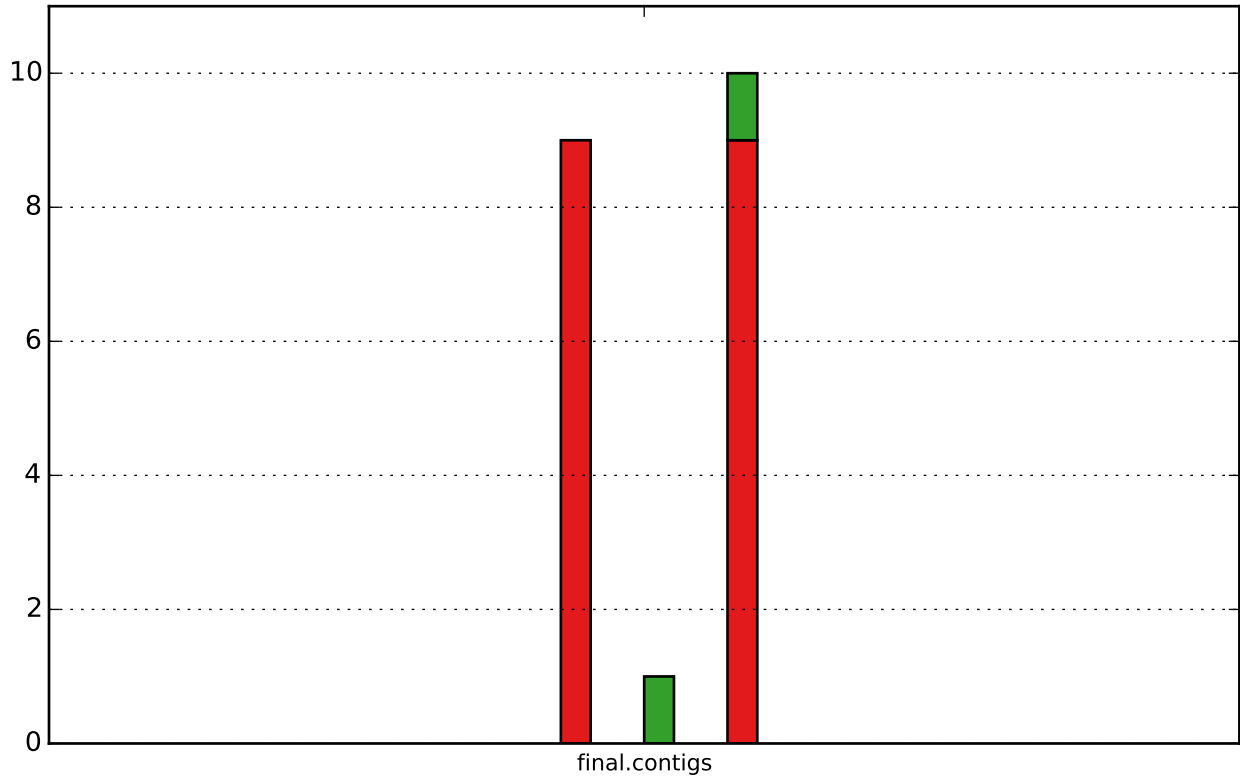
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

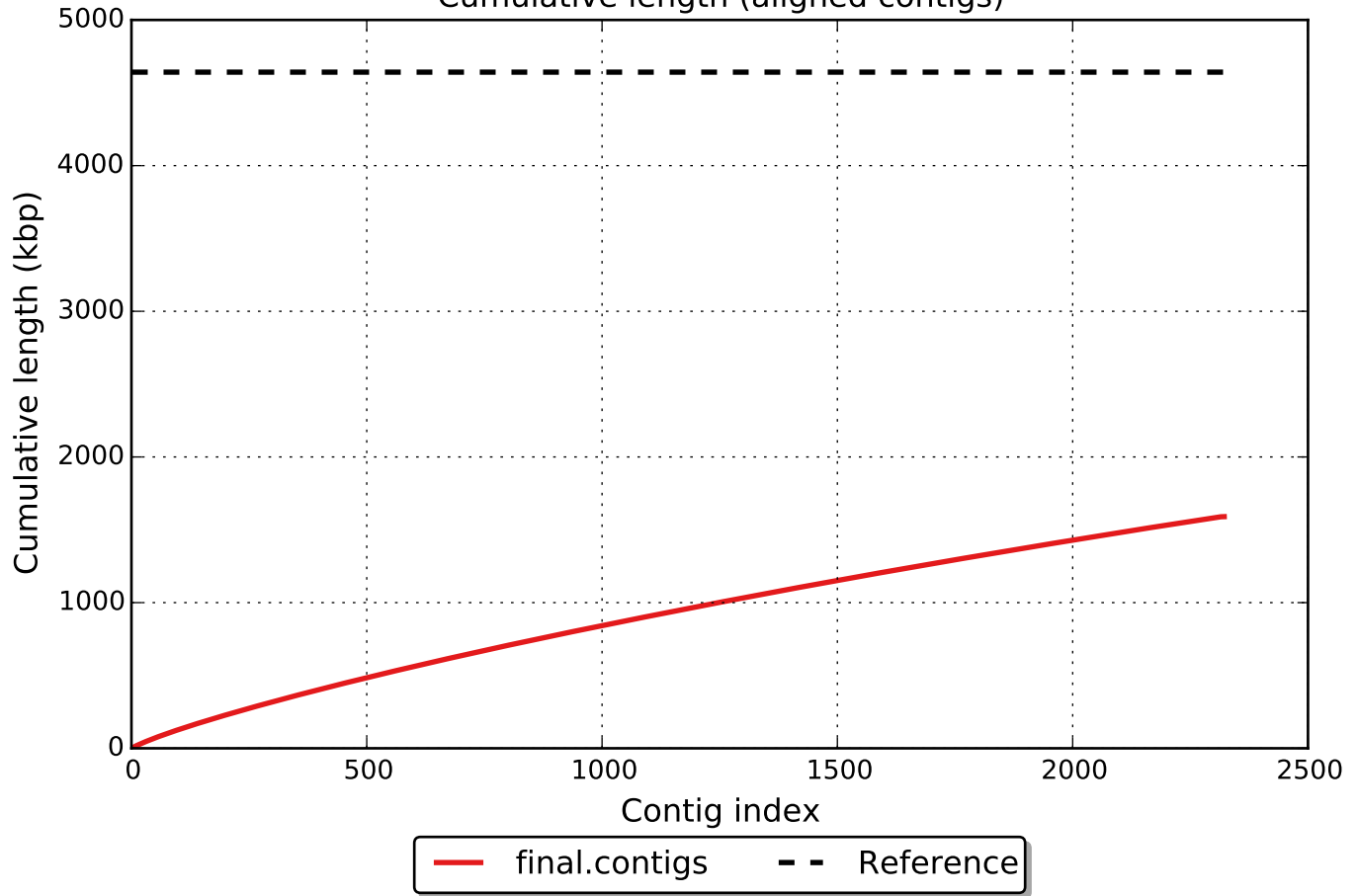




Misassemblies



Cumulative length (aligned contigs)



NAx

