

Report

	final.contigs
# contigs (≥ 0 bp)	14268
# contigs (≥ 1000 bp)	2027
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	9098460
Total length (≥ 1000 bp)	2922422
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	7414
Largest contig	4191
Total length	6632596
Reference length	9714864
N50	923
N75	673
L50	2438
L75	4551
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1221
# local misassemblies	0
# unaligned contigs	0 + 3 part
Unaligned length	209
Genome fraction (%)	76.893
Duplication ratio	1.087
# N's per 100 kbp	0.00
# mismatches per 100 kbp	404.58
# indels per 100 kbp	0.05
Largest alignment	4191
NA50	923
NA75	673
LA50	2438
LA75	4551

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	0
# translocations	0
# inversions	1
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1221
# local misassemblies	0
# mismatches	30222
# indels	4
# short indels	4
# long indels	0
Indels length	4

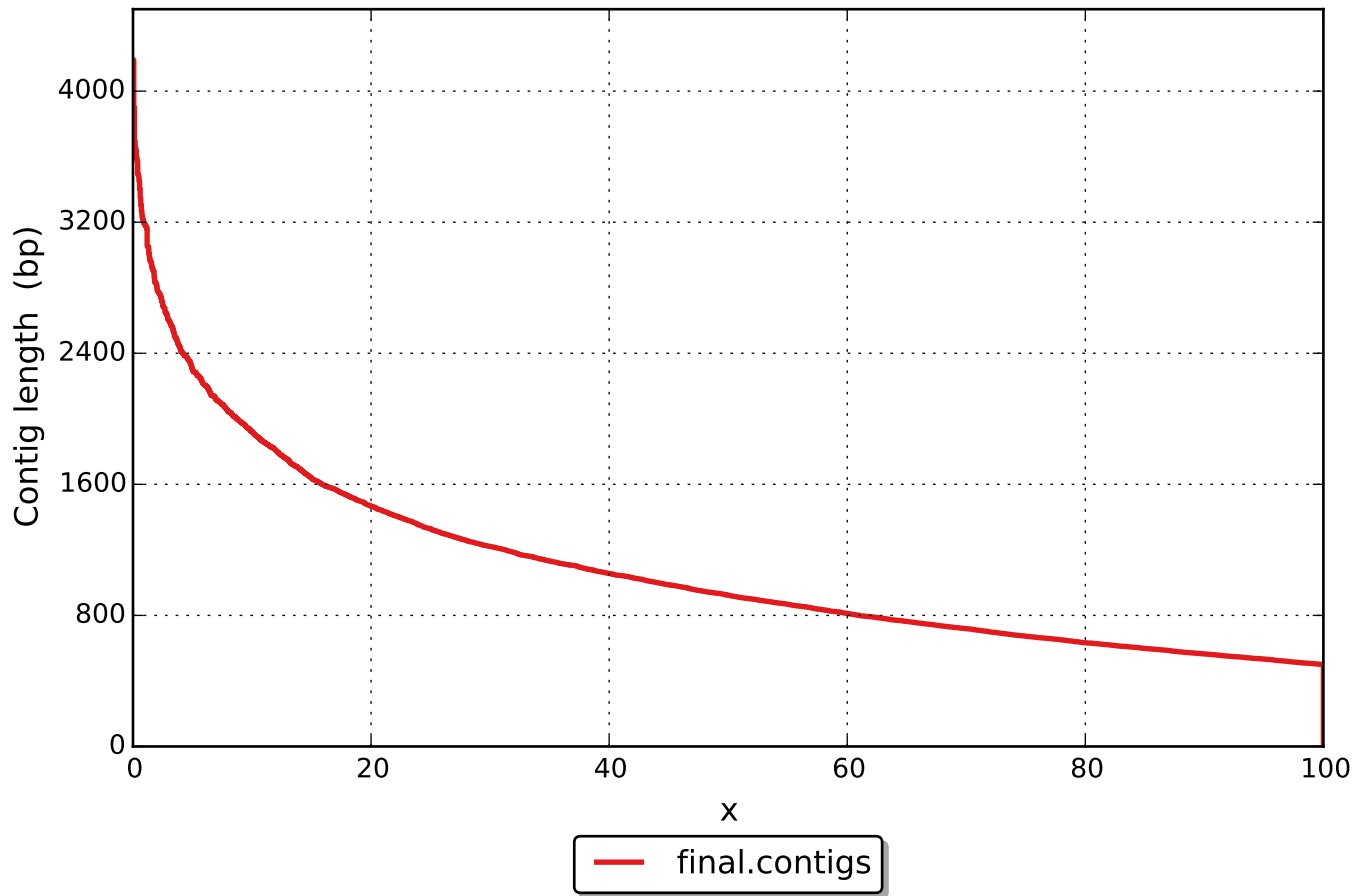
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

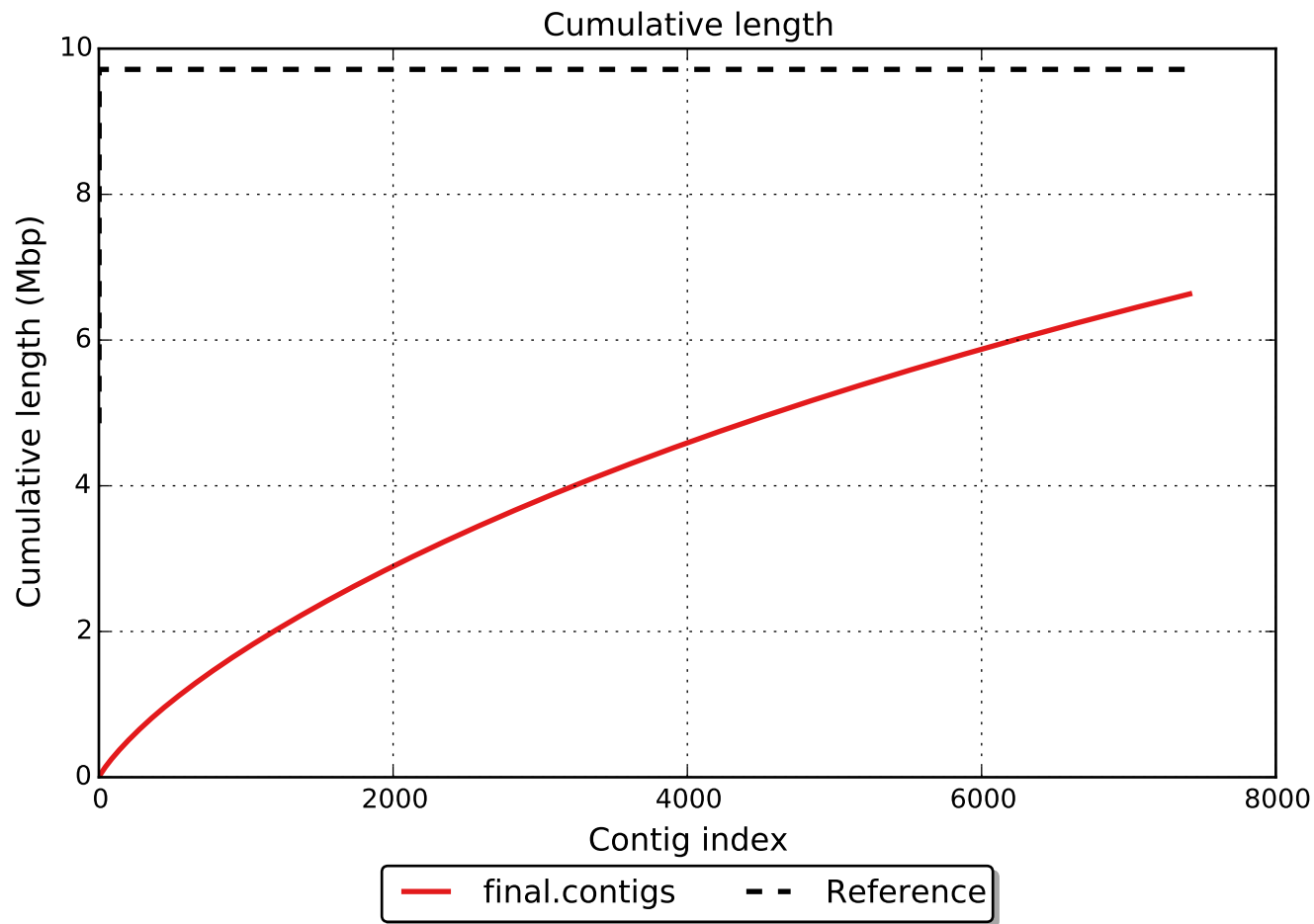
Unaligned report

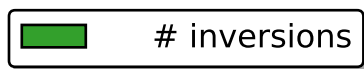
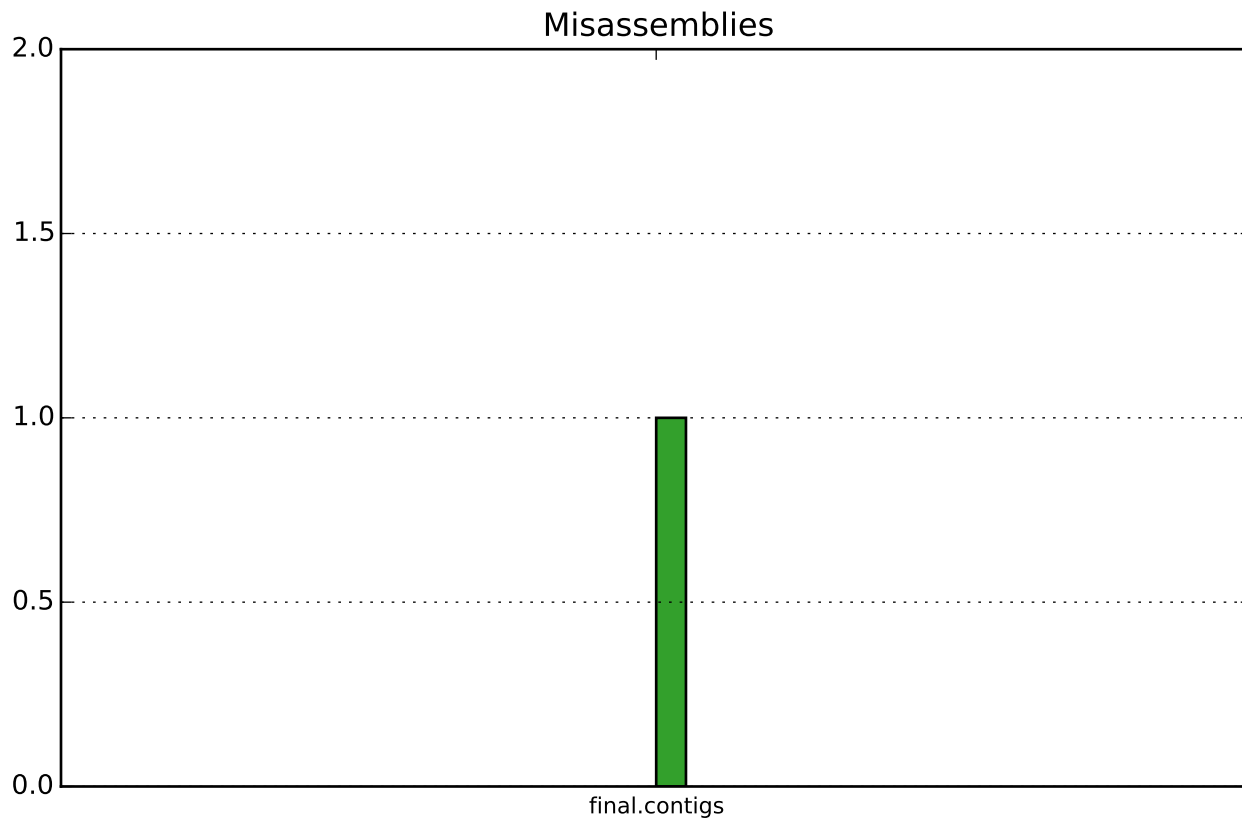
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	0
Partially unaligned length	209
# N's	0

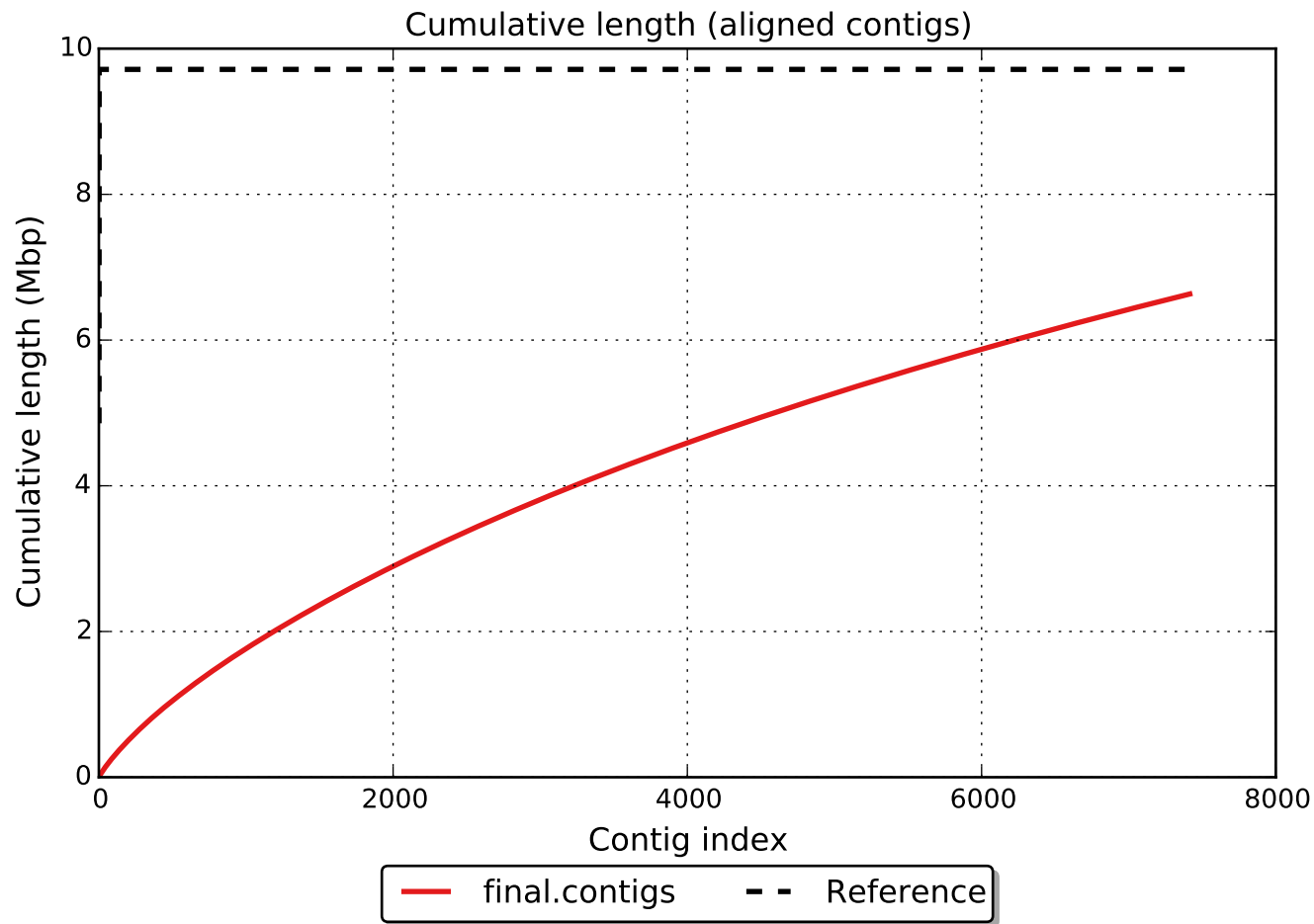
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx









NAx

