

Report

	final.contigs
# contigs (>= 0 bp)	8195
# contigs (>= 1000 bp)	3603
# contigs (>= 5000 bp)	108
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	9994134
Total length (>= 1000 bp)	7571441
Total length (>= 5000 bp)	662302
Total length (>= 10000 bp)	14787
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	5764
Largest contig	14787
Total length	9148653
Reference length	9283304
N50	1968
N75	1227
L50	1497
L75	2964
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	94.692
Duplication ratio	1.046
# N's per 100 kbp	0.00
# mismatches per 100 kbp	62.43
# indels per 100 kbp	0.07
Largest alignment	14787
NA50	1968
NA75	1227
LA50	1497
LA75	2965

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

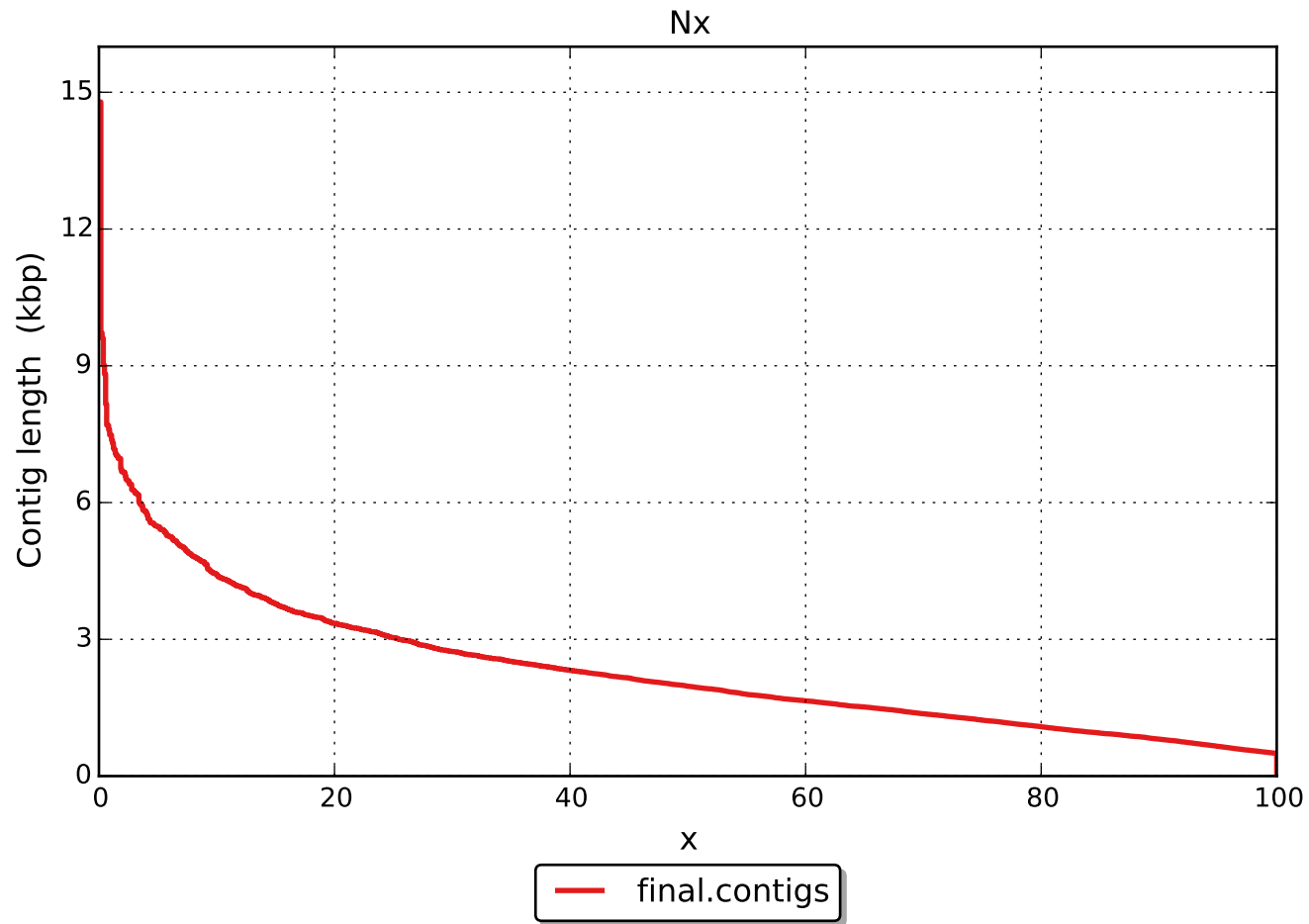
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	5488
# indels	6
# short indels	6
# long indels	0
Indels length	6

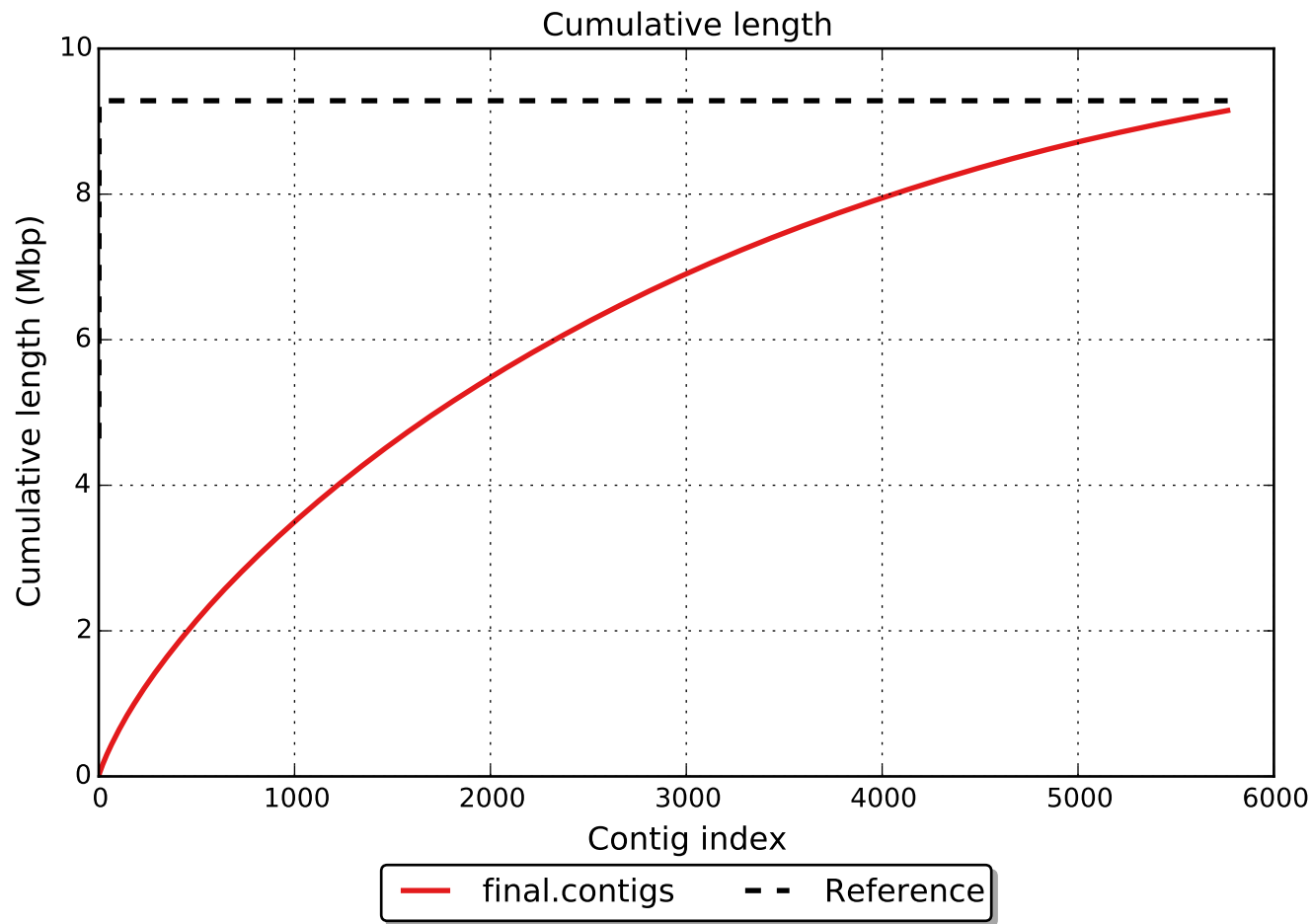
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

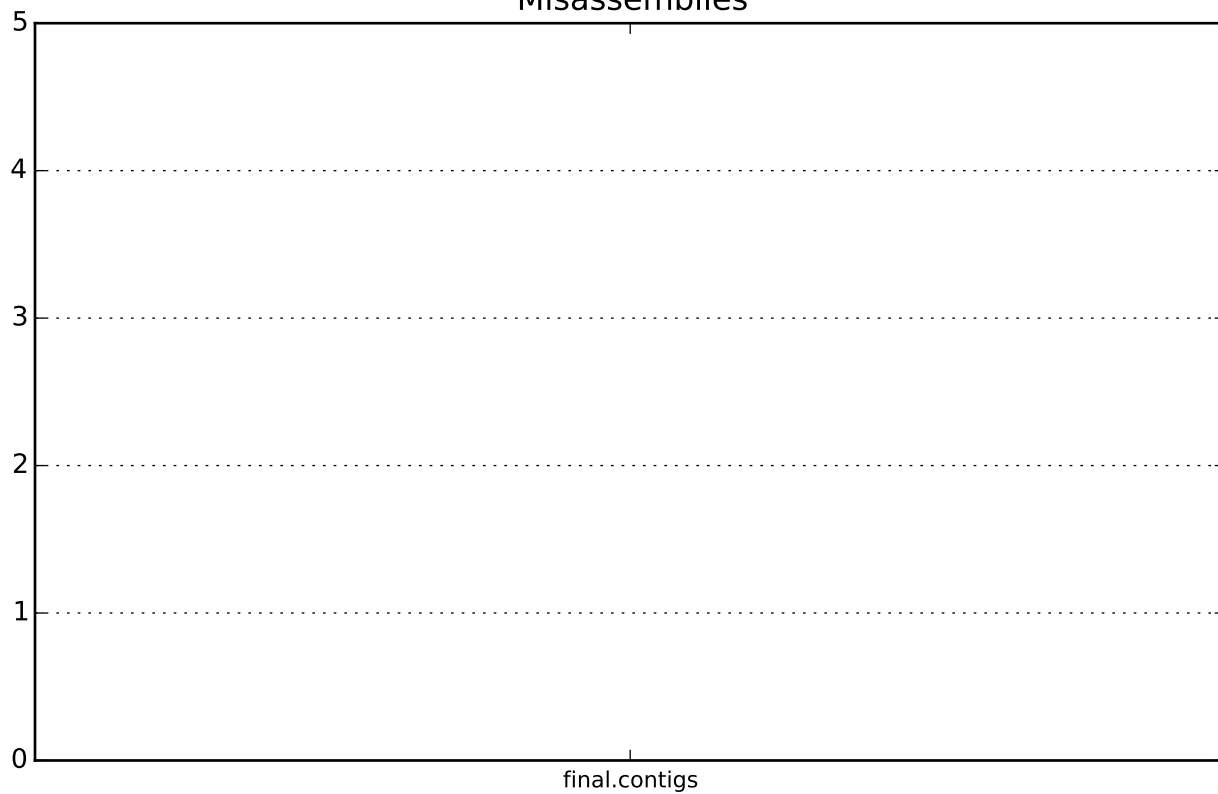
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

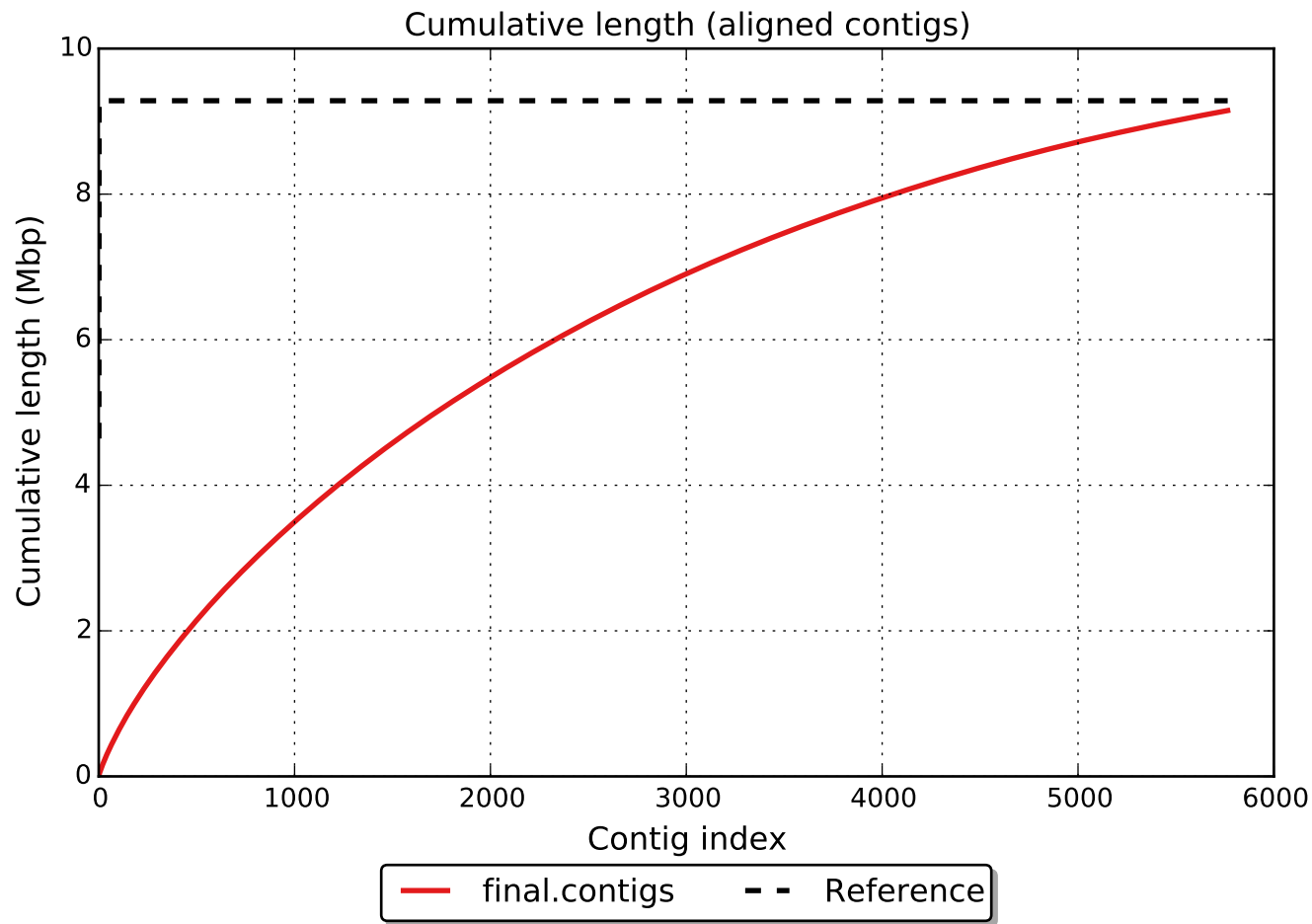
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).





Misassemblies





NAx

