

Report

	final.contigs
# contigs (≥ 0 bp)	2700
# contigs (≥ 1000 bp)	1772
# contigs (≥ 5000 bp)	718
# contigs (≥ 10000 bp)	222
# contigs (≥ 25000 bp)	13
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	10019364
Total length (≥ 1000 bp)	9618866
Total length (≥ 5000 bp)	6784288
Total length (≥ 10000 bp)	3314448
Total length (≥ 25000 bp)	357921
Total length (≥ 50000 bp)	0
# contigs	2005
Largest contig	32238
Total length	9786477
Reference length	9714864
N50	7435
N75	4359
L50	406
L75	837
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	6932
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.931
Duplication ratio	1.018
# N's per 100 kbp	0.00
# mismatches per 100 kbp	22.47
# indels per 100 kbp	0.00
Largest alignment	32238
NA50	7435
NA75	4359
LA50	406
LA75	837

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

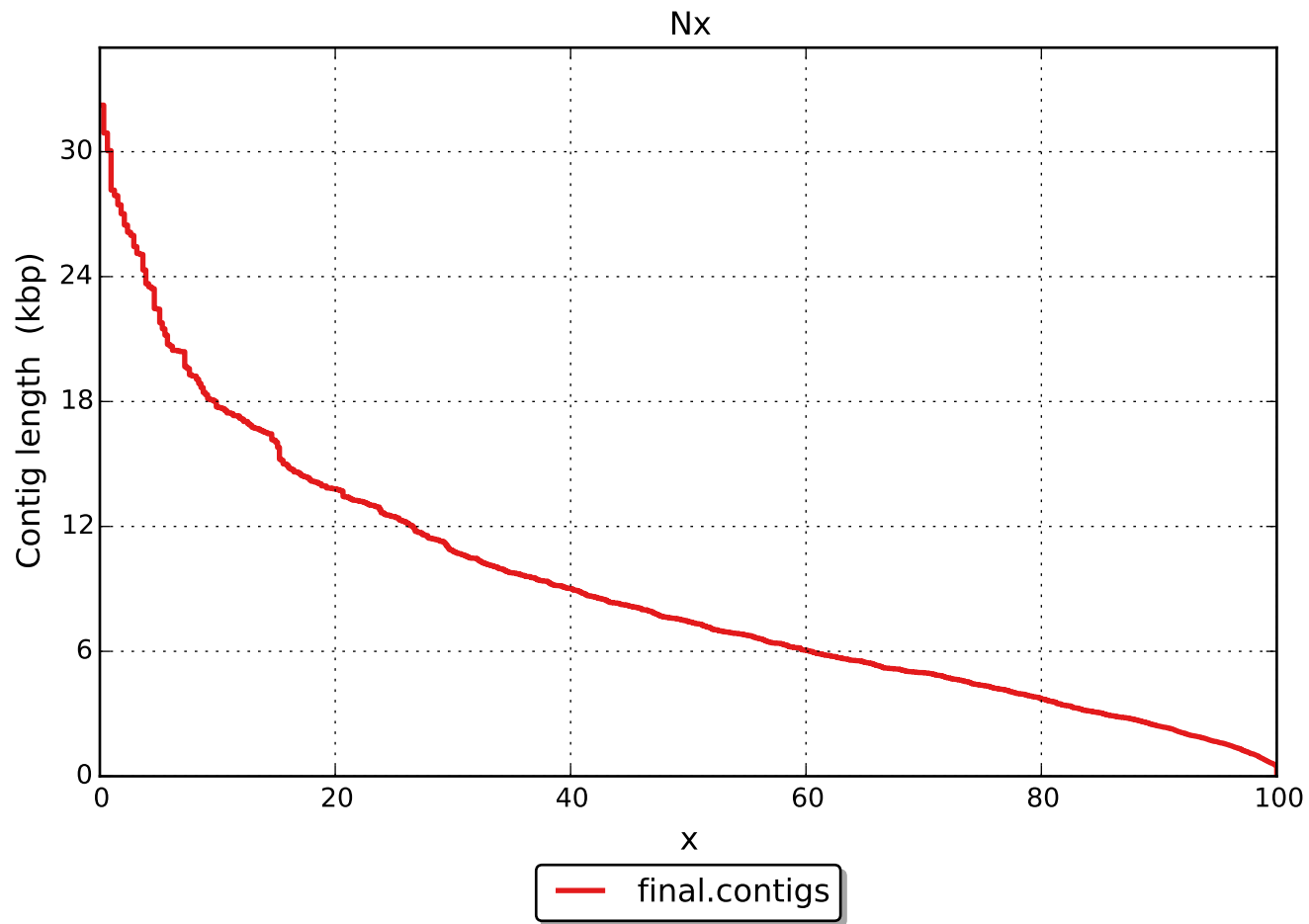
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	6932
# local misassemblies	2
# mismatches	2160
# indels	0
# short indels	0
# long indels	0
Indels length	0

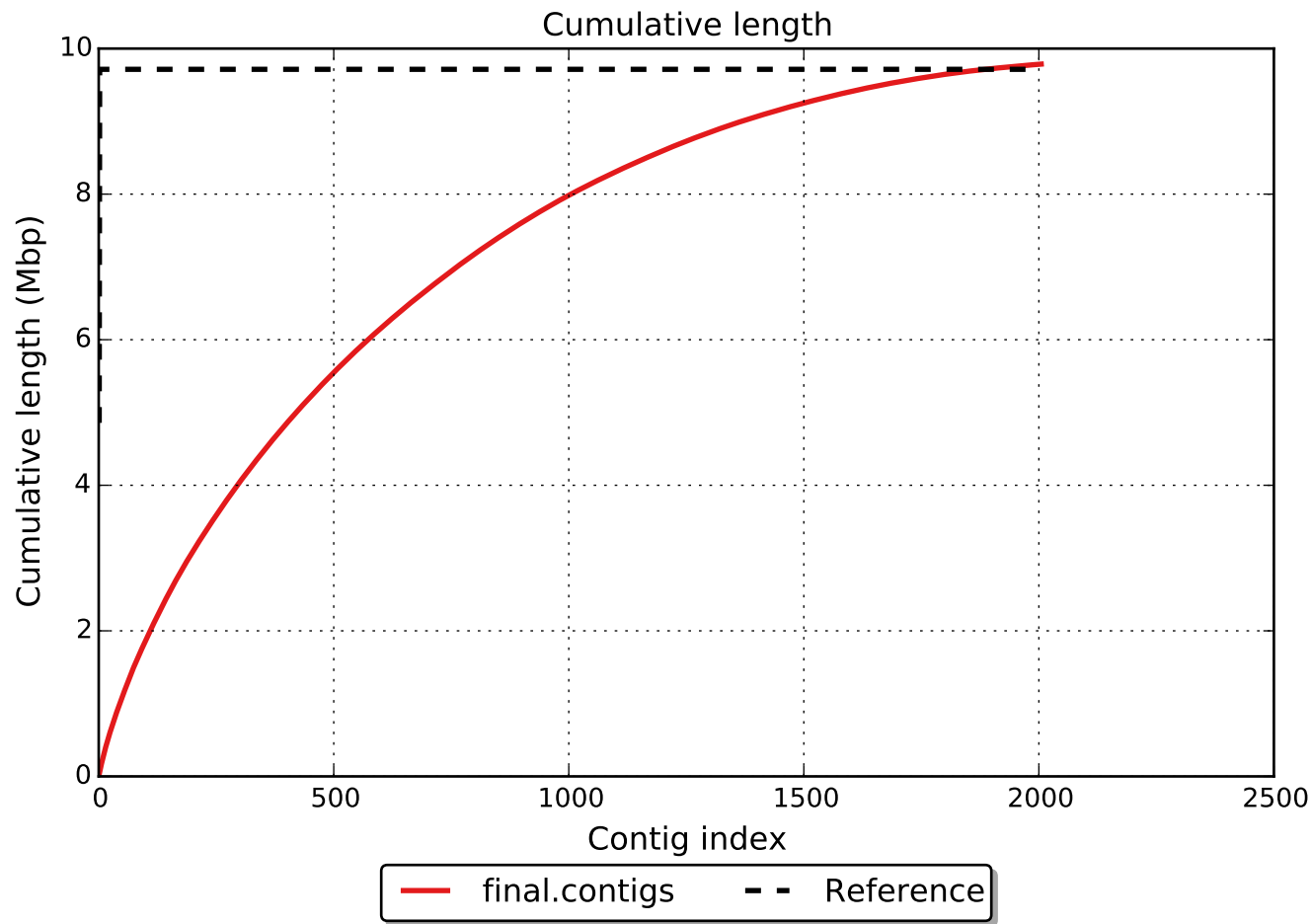
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

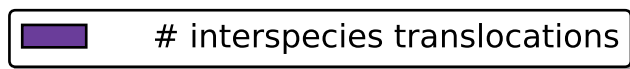
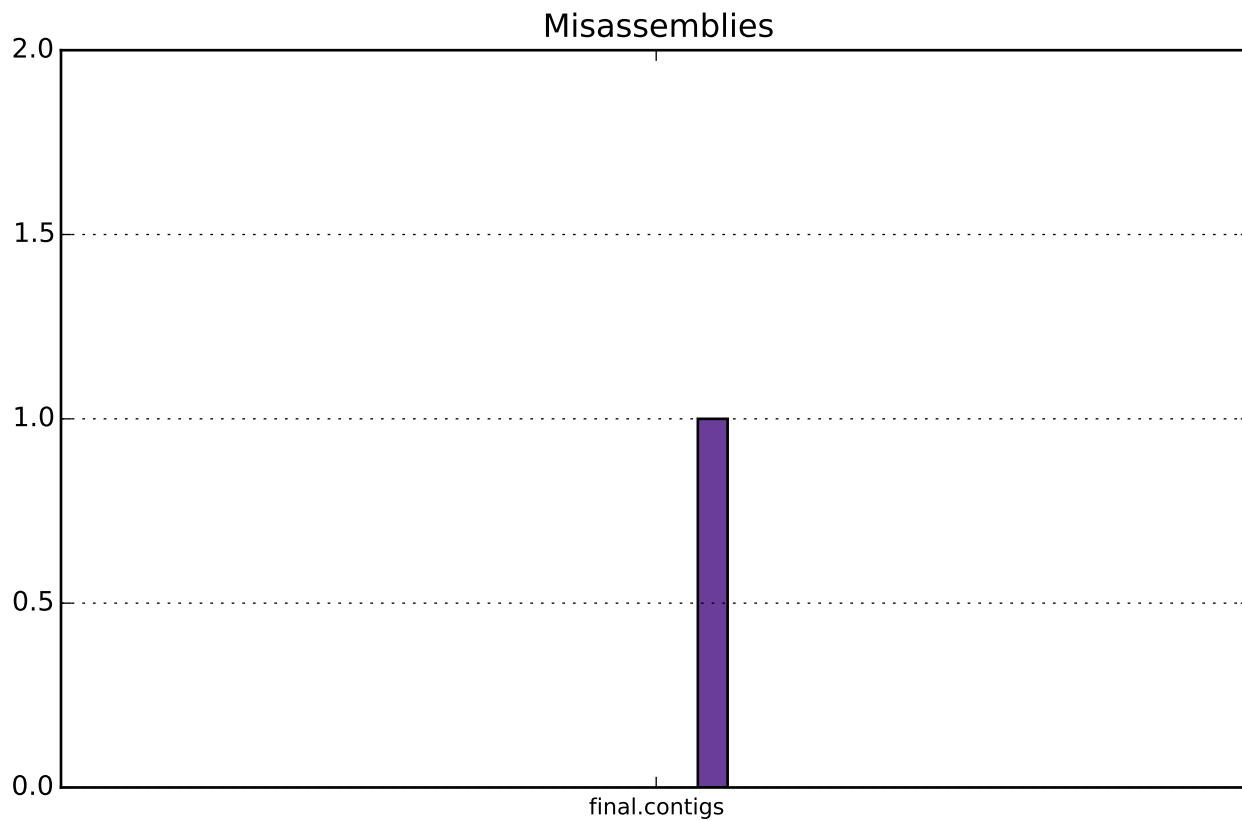
Unaligned report

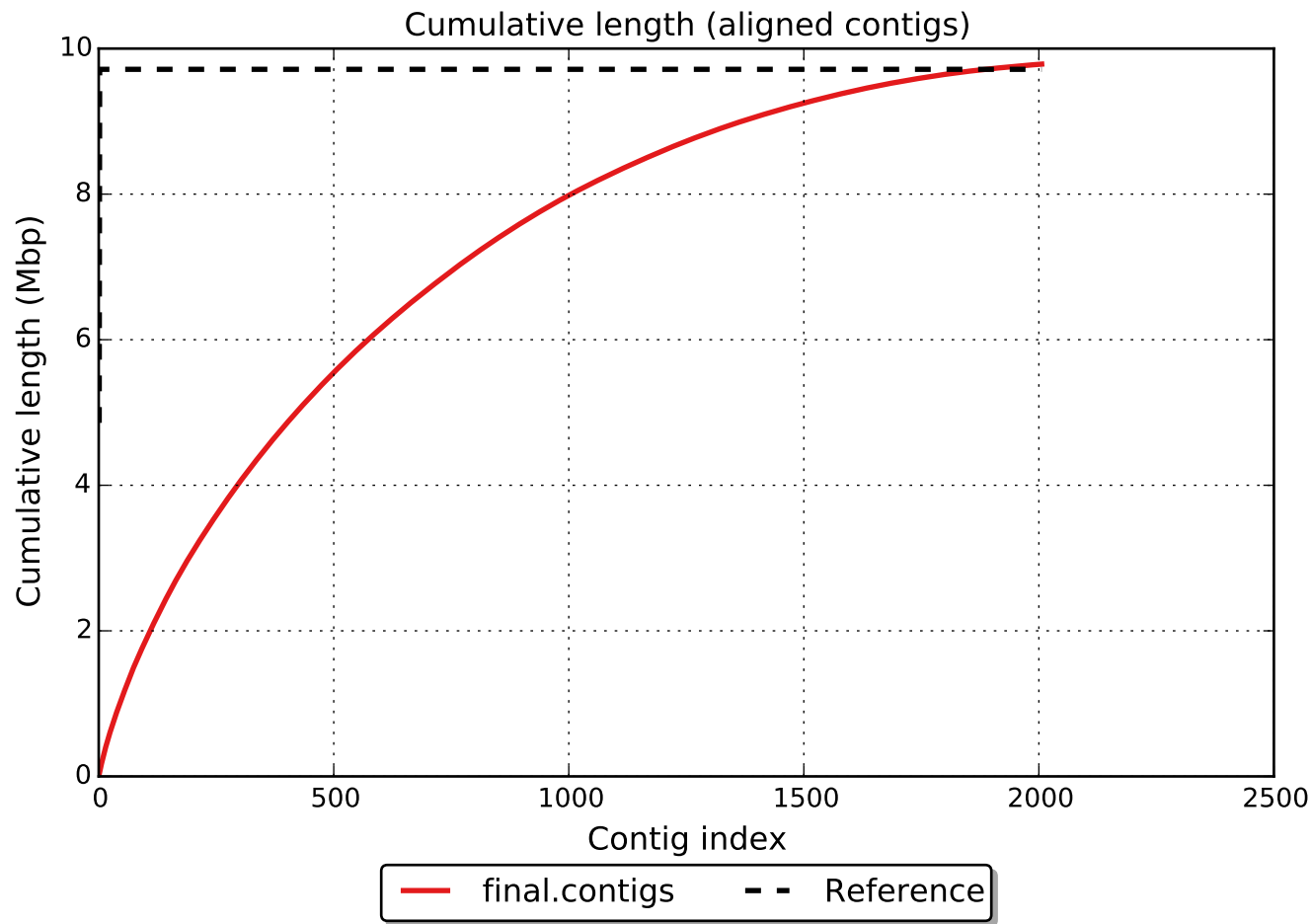
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).









NAx

