

Report

	final.contigs
# contigs (≥ 0 bp)	10481
# contigs (≥ 1000 bp)	3838
# contigs (≥ 5000 bp)	33
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	10533556
Total length (≥ 1000 bp)	6964886
Total length (≥ 5000 bp)	184734
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	7132
Largest contig	6648
Total length	9351290
Reference length	9714864
N50	1521
N75	987
L50	1989
L75	3887
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1359
# local misassemblies	0
# unaligned contigs	1 + 1 part
Unaligned length	615
Genome fraction (%)	92.284
Duplication ratio	1.053
# N's per 100 kbp	0.00
# mismatches per 100 kbp	85.79
# indels per 100 kbp	0.07
Largest alignment	6648
NA50	1520
NA75	987
LA50	1989
LA75	3888

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

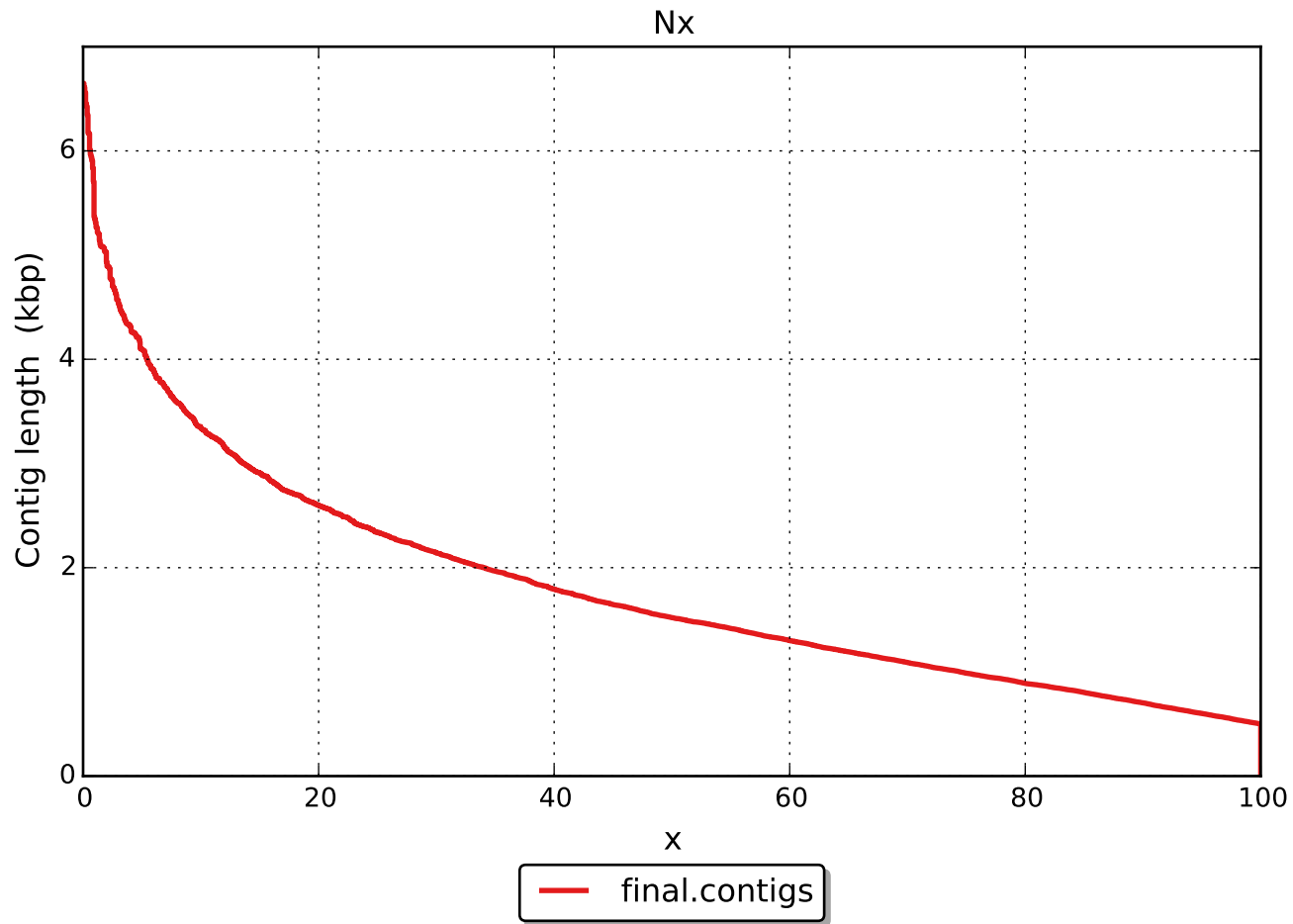
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1359
# local misassemblies	0
# mismatches	7691
# indels	6
# short indels	6
# long indels	0
Indels length	13

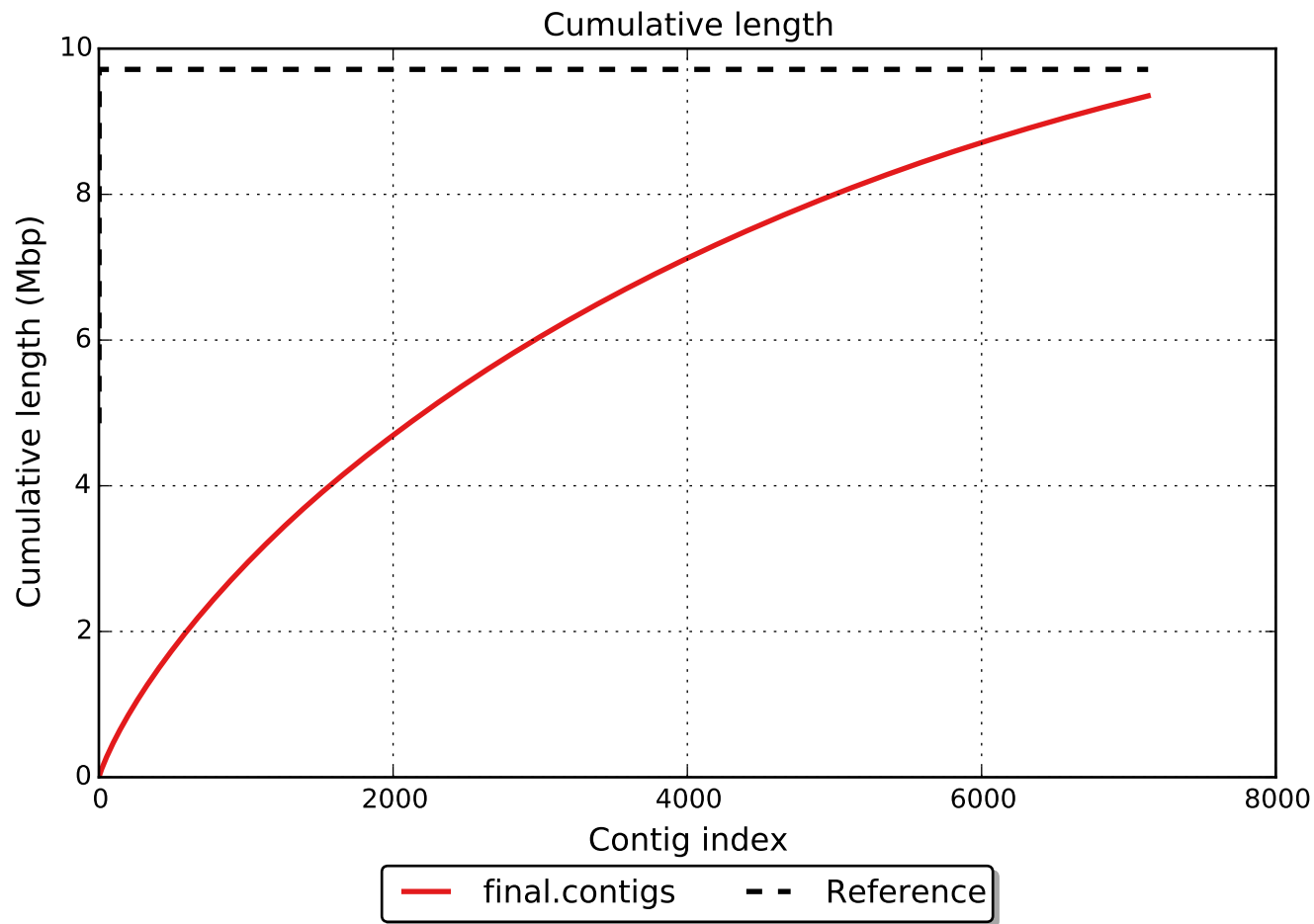
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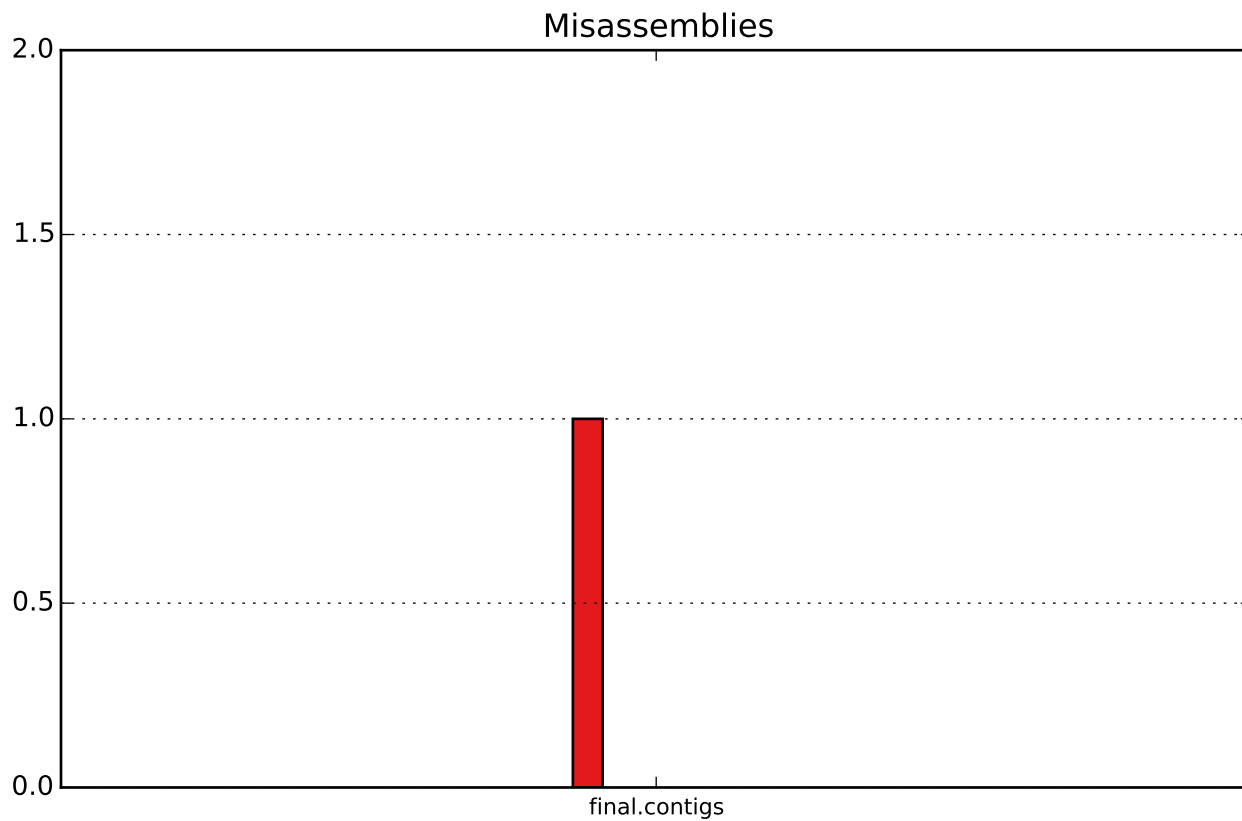
Unaligned report

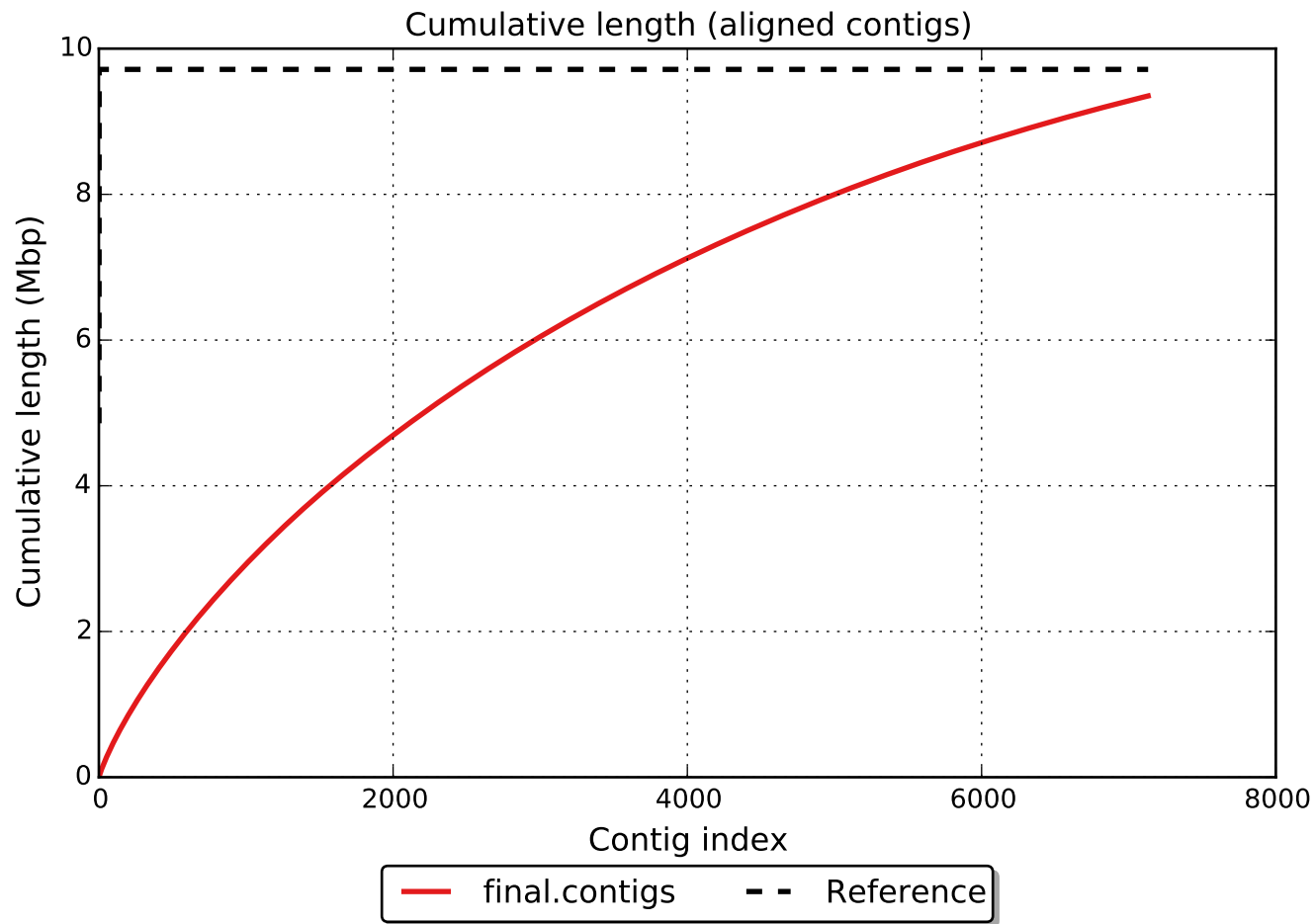
	final.contigs
# fully unaligned contigs	1
Fully unaligned length	556
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	59
# N's	0

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

