

Report

	contigs
# contigs (≥ 0 bp)	134
# contigs (≥ 1000 bp)	80
# contigs (≥ 5000 bp)	67
# contigs (≥ 10000 bp)	64
# contigs (≥ 25000 bp)	58
# contigs (≥ 50000 bp)	44
Total length (≥ 0 bp)	9165353
Total length (≥ 1000 bp)	9144973
Total length (≥ 5000 bp)	9120514
Total length (≥ 10000 bp)	9097881
Total length (≥ 25000 bp)	9006646
Total length (≥ 50000 bp)	8535794
# contigs	92
Largest contig	601815
Total length	9153565
Reference length	9283304
N50	248289
N75	131763
L50	12
L75	25
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	36059
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.224
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	242.57
# indels per 100 kbp	0.86
Largest alignment	601815
NA50	248289
NA75	131763
LA50	12
LA75	25

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

	contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	36059
# local misassemblies	3
# mismatches	22344
# indels	79
# short indels	79
# long indels	0
Indels length	83

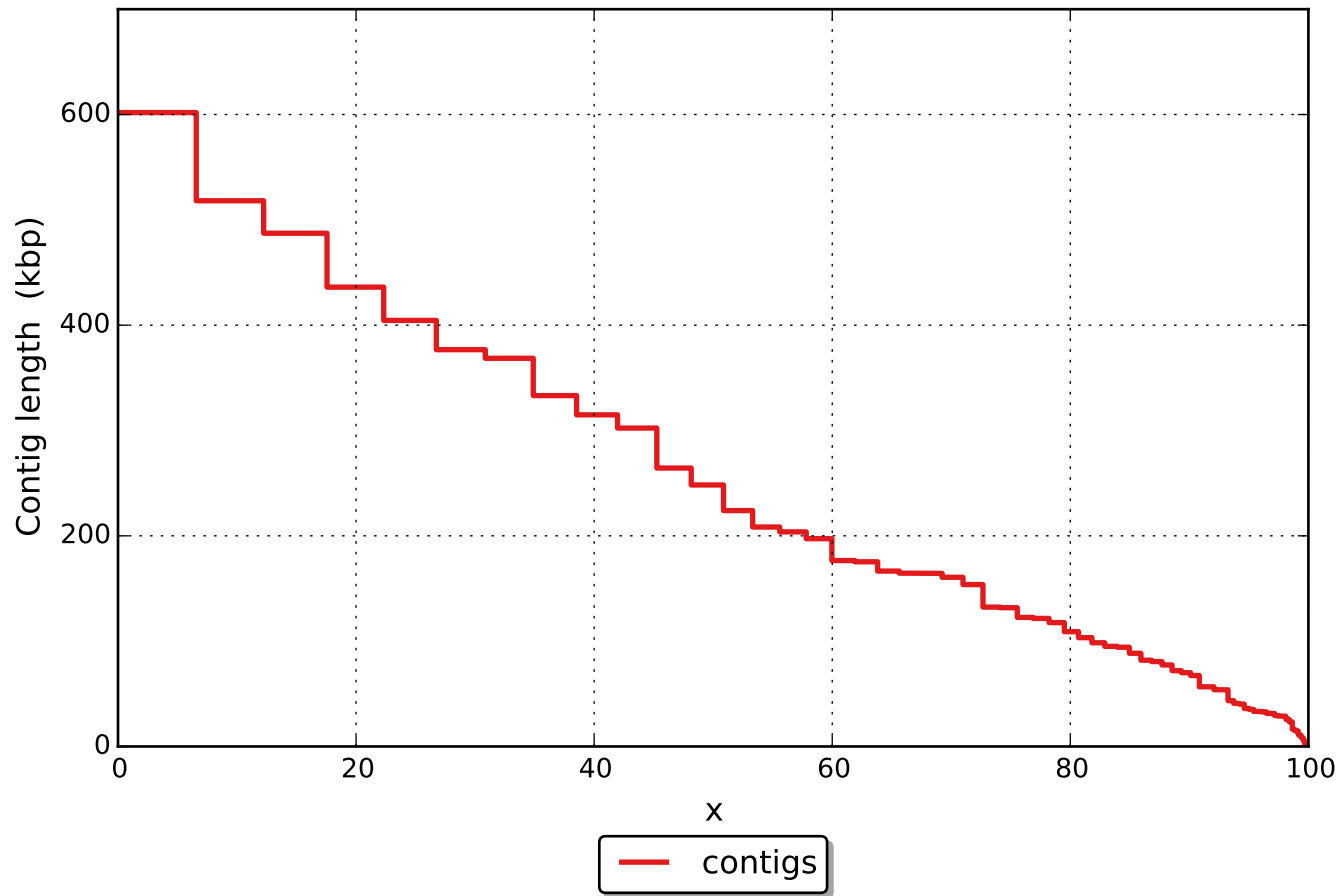
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

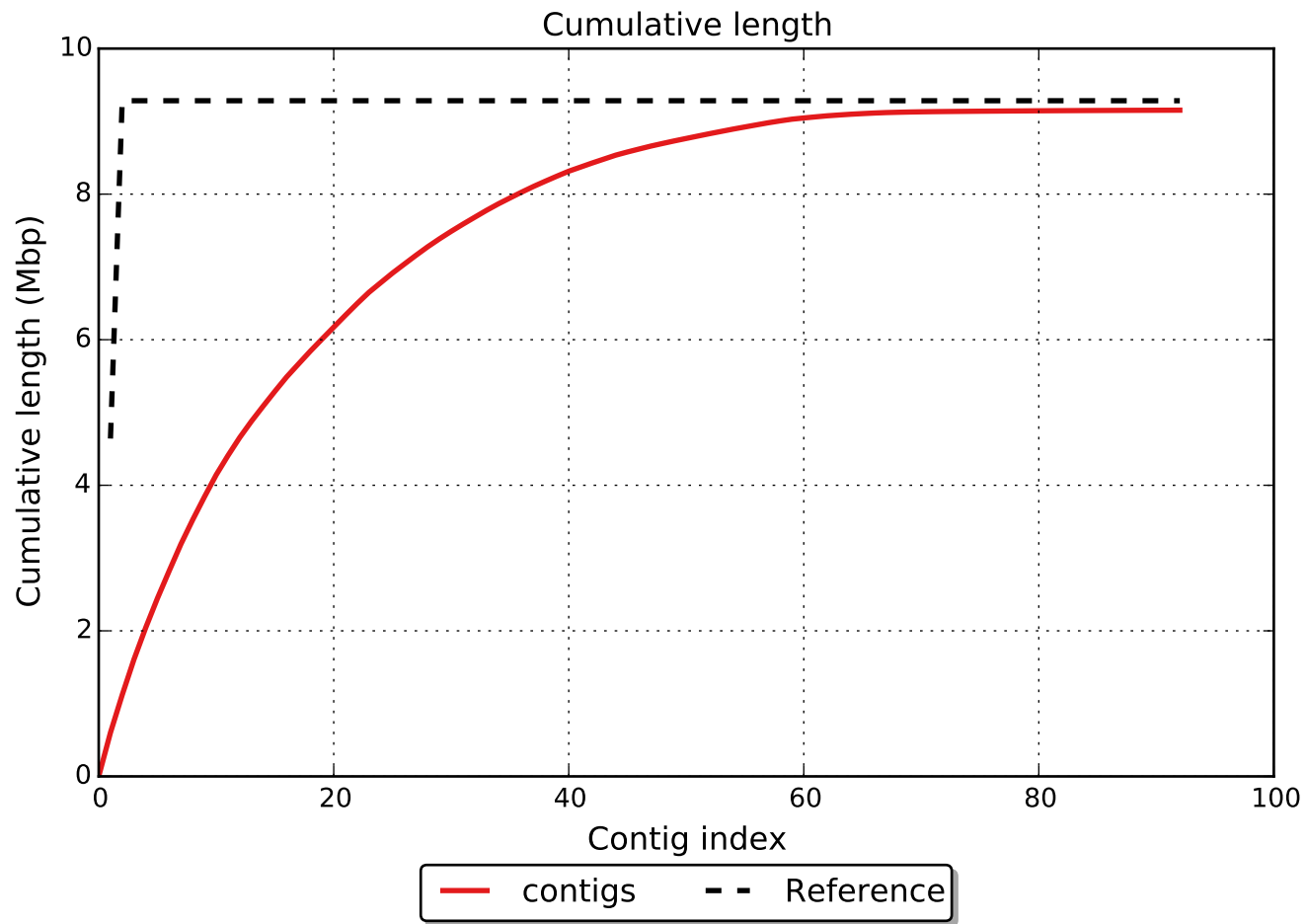
Unaligned report

	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

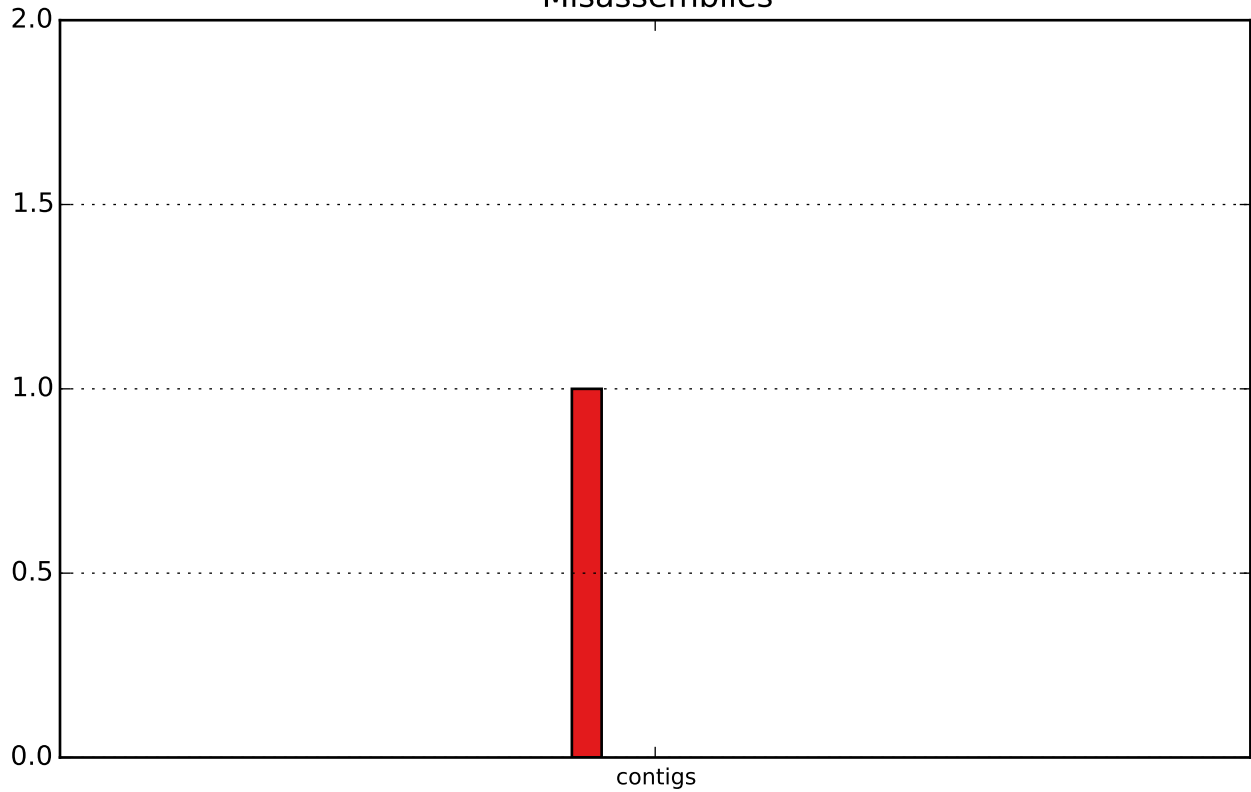
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

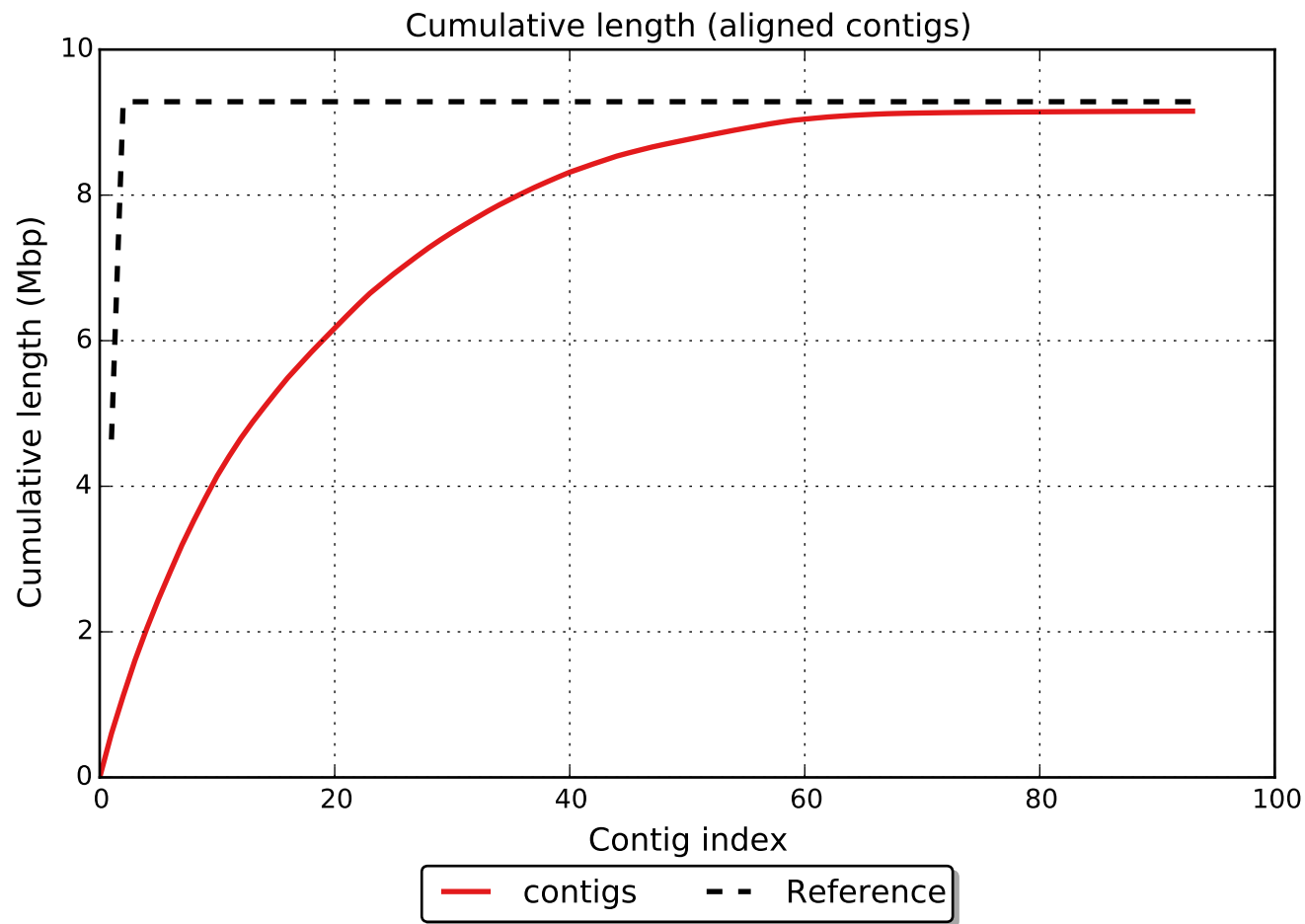
Nx





Misassemblies





NAx

