

Report

	contigs
# contigs (≥ 0 bp)	139
# contigs (≥ 1000 bp)	76
# contigs (≥ 5000 bp)	65
# contigs (≥ 10000 bp)	62
# contigs (≥ 25000 bp)	58
# contigs (≥ 50000 bp)	43
Total length (≥ 0 bp)	9169904
Total length (≥ 1000 bp)	9146822
Total length (≥ 5000 bp)	9126183
Total length (≥ 10000 bp)	9103238
Total length (≥ 25000 bp)	9045107
Total length (≥ 50000 bp)	8515013
# contigs	88
Largest contig	700824
Total length	9156211
Reference length	9283304
N50	264356
N75	131763
L50	12
L75	24
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	711322
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.912
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	300.91
# indels per 100 kbp	0.77
Largest alignment	700544
NA50	256361
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	3
# relocations	2
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	711322
# local misassemblies	2
# mismatches	27630
# indels	71
# short indels	71
# long indels	0
Indels length	71

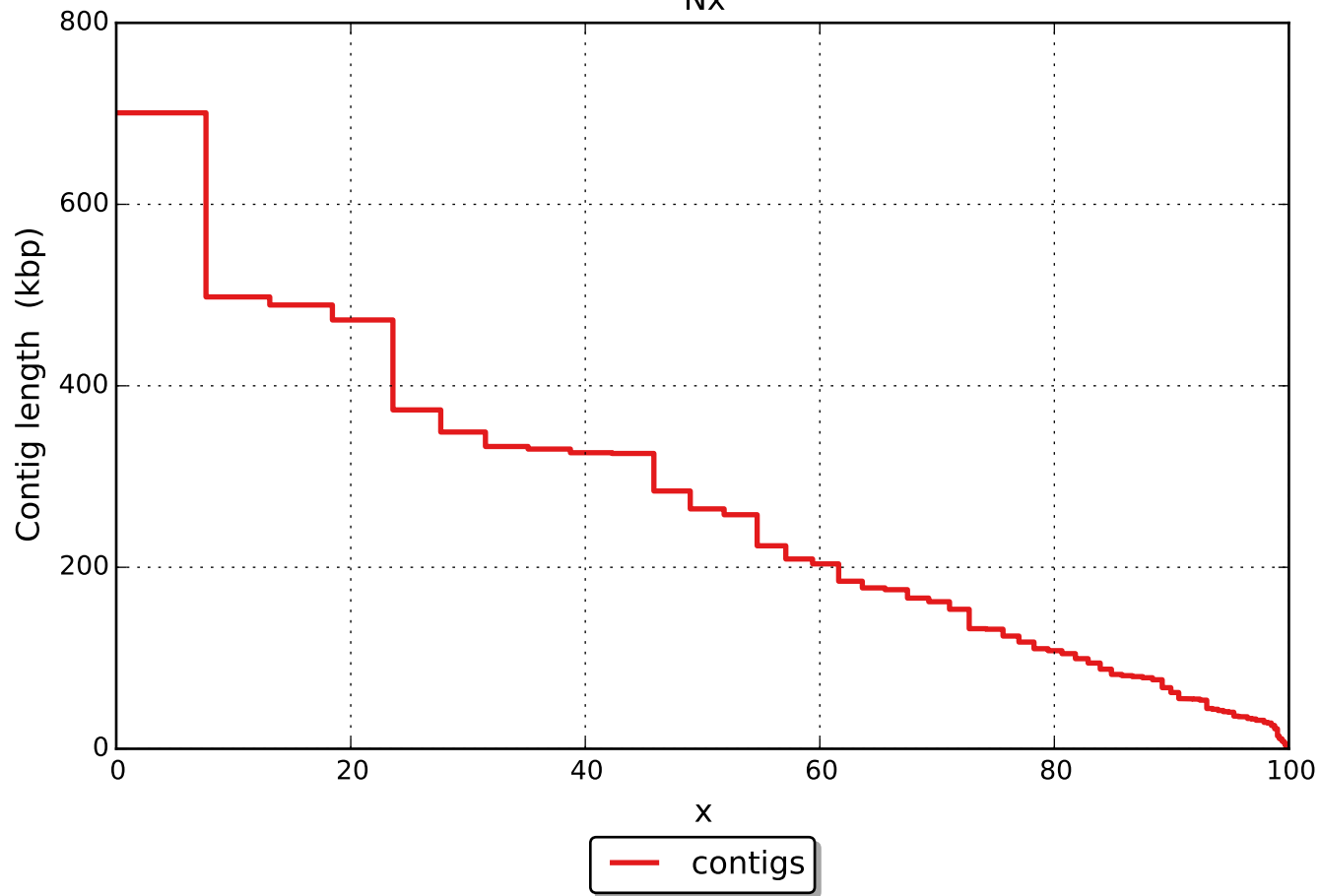
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

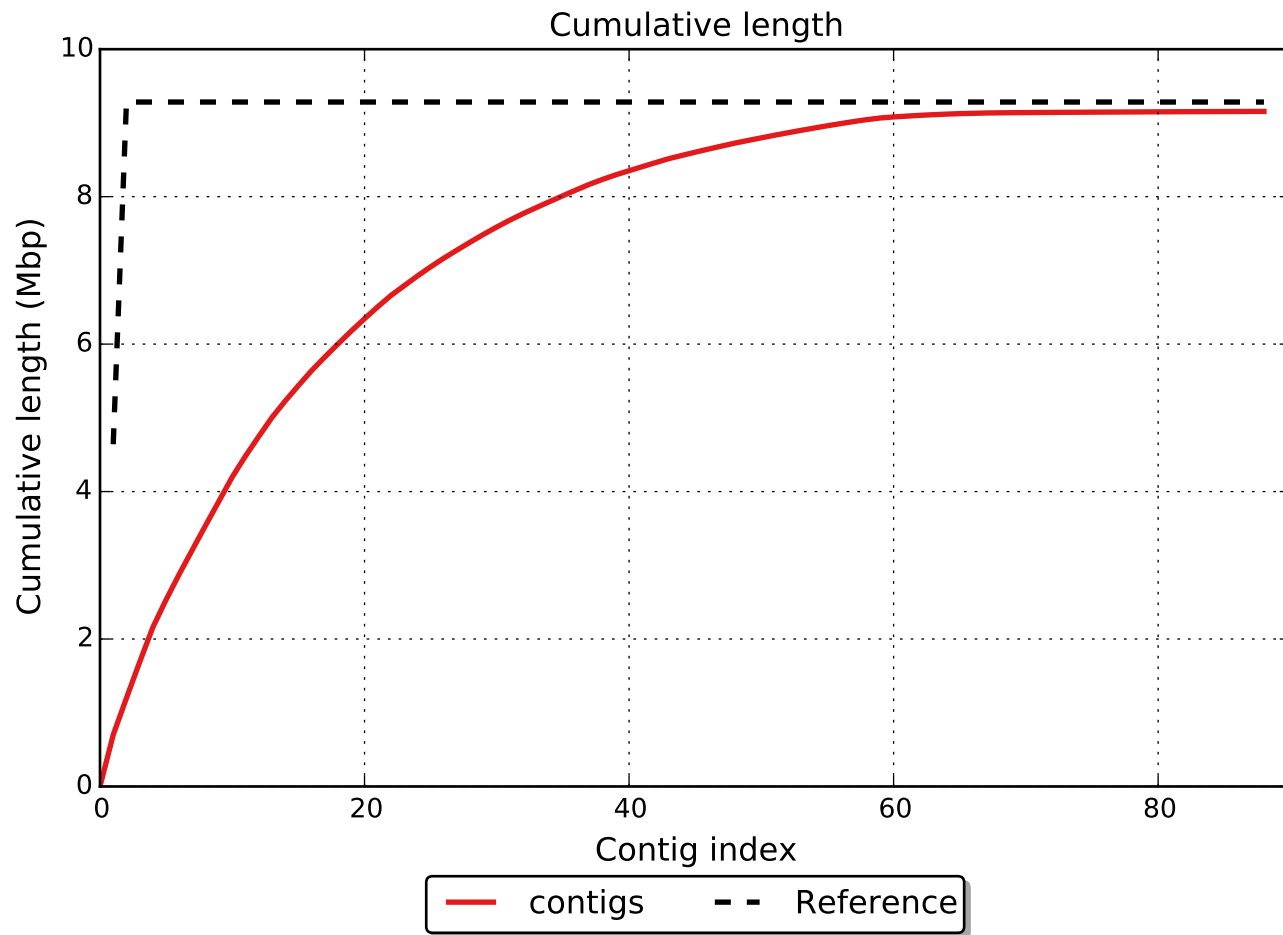
Unaligned report

	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

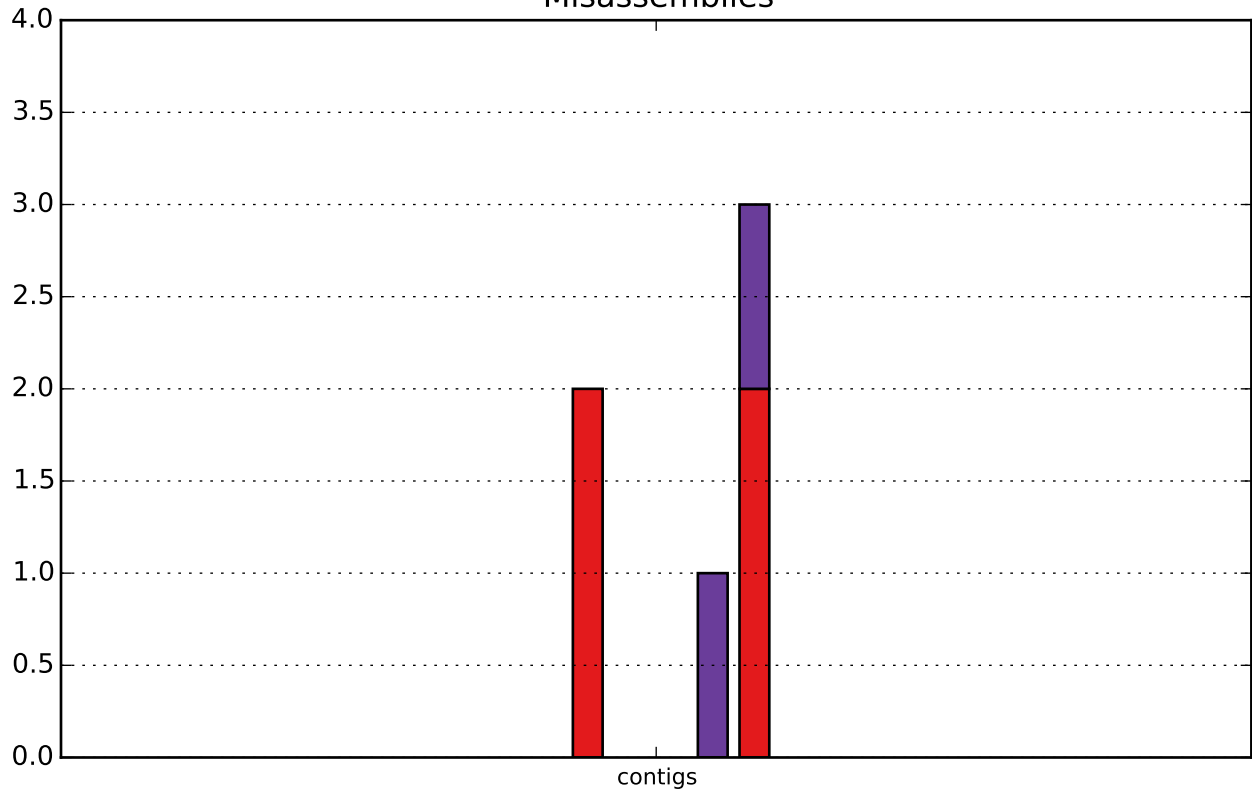
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

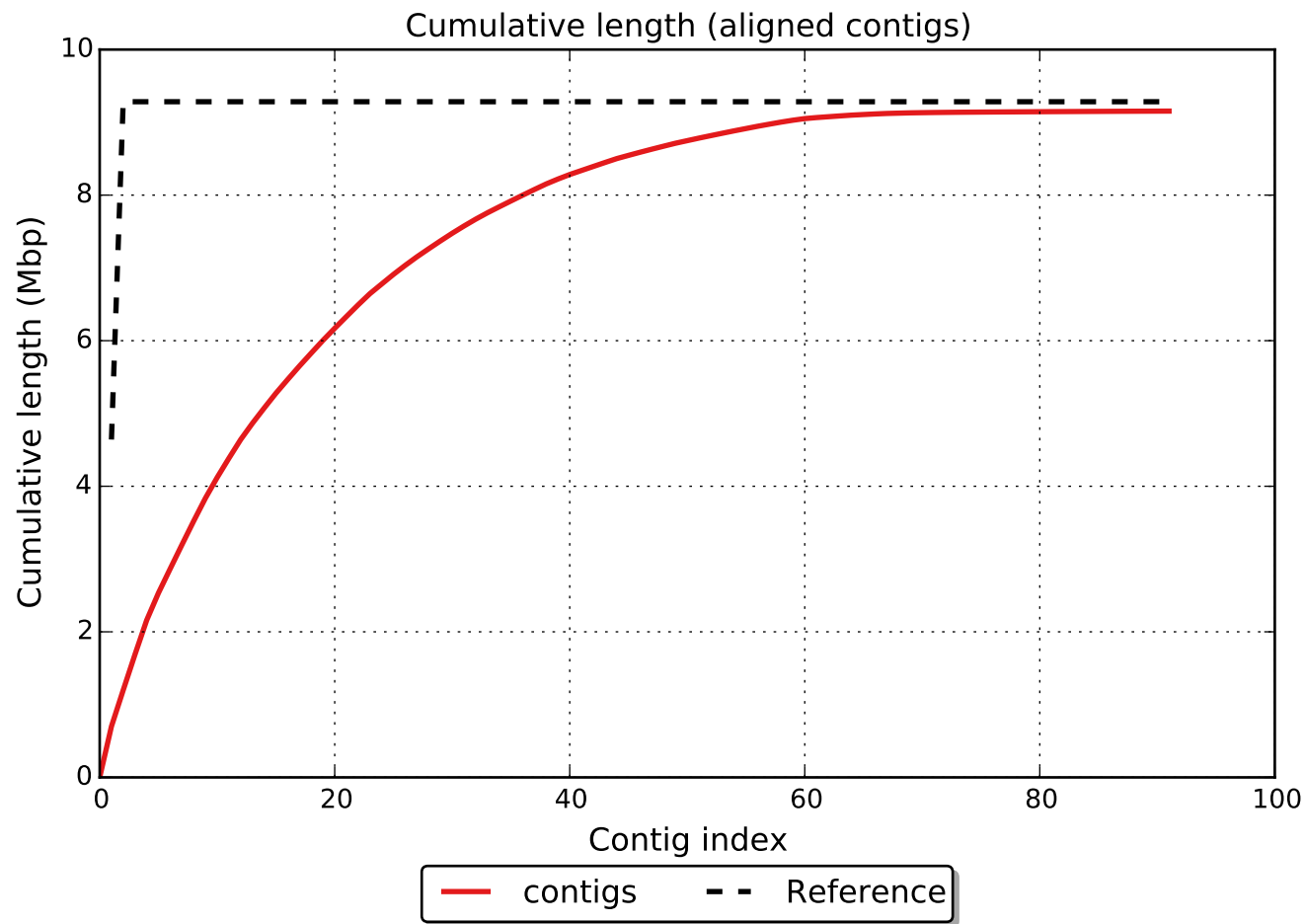
Nx



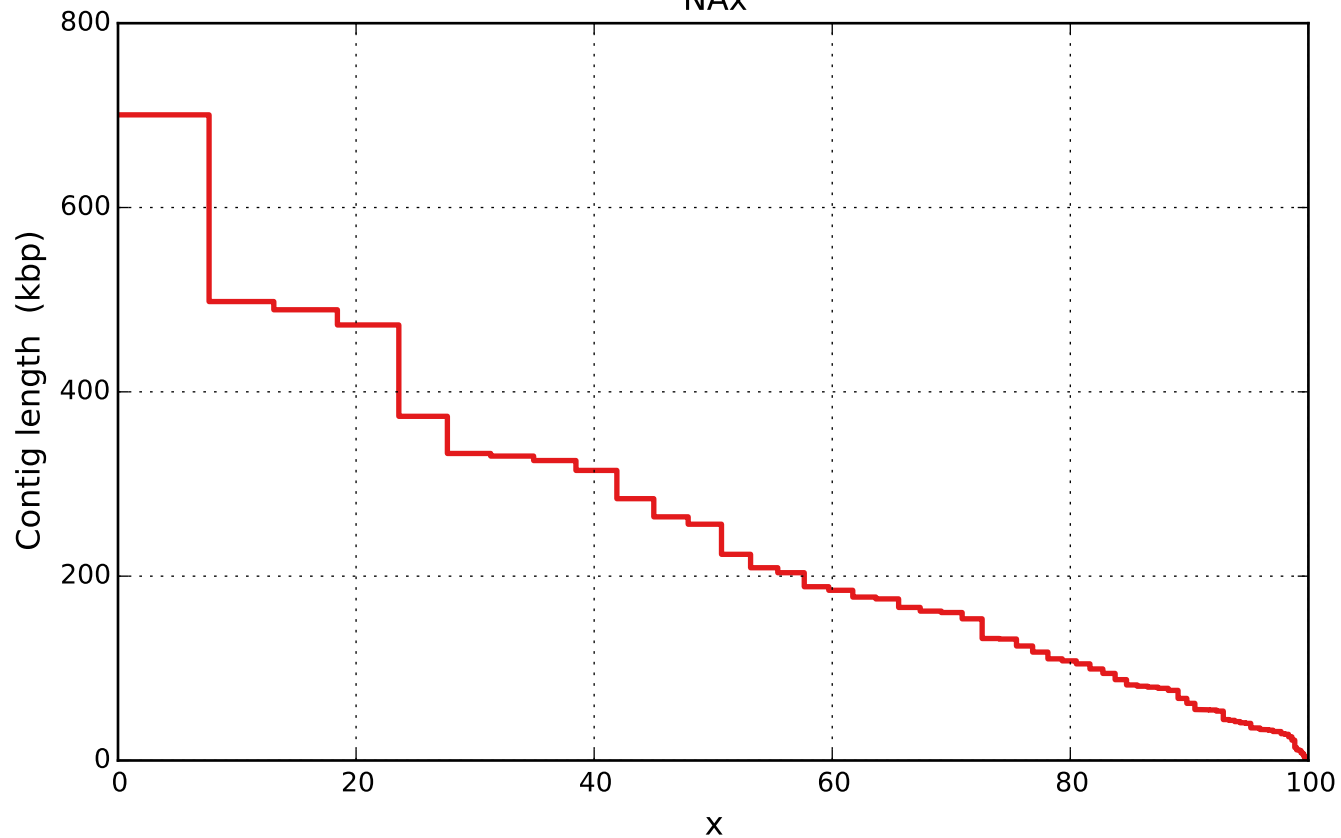


Misassemblies





NAx



contigs