

Report

	contigs
# contigs (≥ 0 bp)	319
# contigs (≥ 1000 bp)	128
# contigs (≥ 5000 bp)	92
# contigs (≥ 10000 bp)	87
# contigs (≥ 25000 bp)	75
# contigs (≥ 50000 bp)	58
Total length (≥ 0 bp)	9099742
Total length (≥ 1000 bp)	9024823
Total length (≥ 5000 bp)	8963653
Total length (≥ 10000 bp)	8923601
Total length (≥ 25000 bp)	8707088
Total length (≥ 50000 bp)	8133129
# contigs	172
Largest contig	527156
Total length	9055631
Reference length	9283304
N50	132545
N75	86976
L50	19
L75	39
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	82061
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.238
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	648.99
# indels per 100 kbp	1.13
Largest alignment	527156
NA50	132545
NA75	86976
LA50	19
LA75	39

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	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	82061
# local misassemblies	1
# mismatches	59186
# indels	103
# short indels	103
# long indels	0
Indels length	121

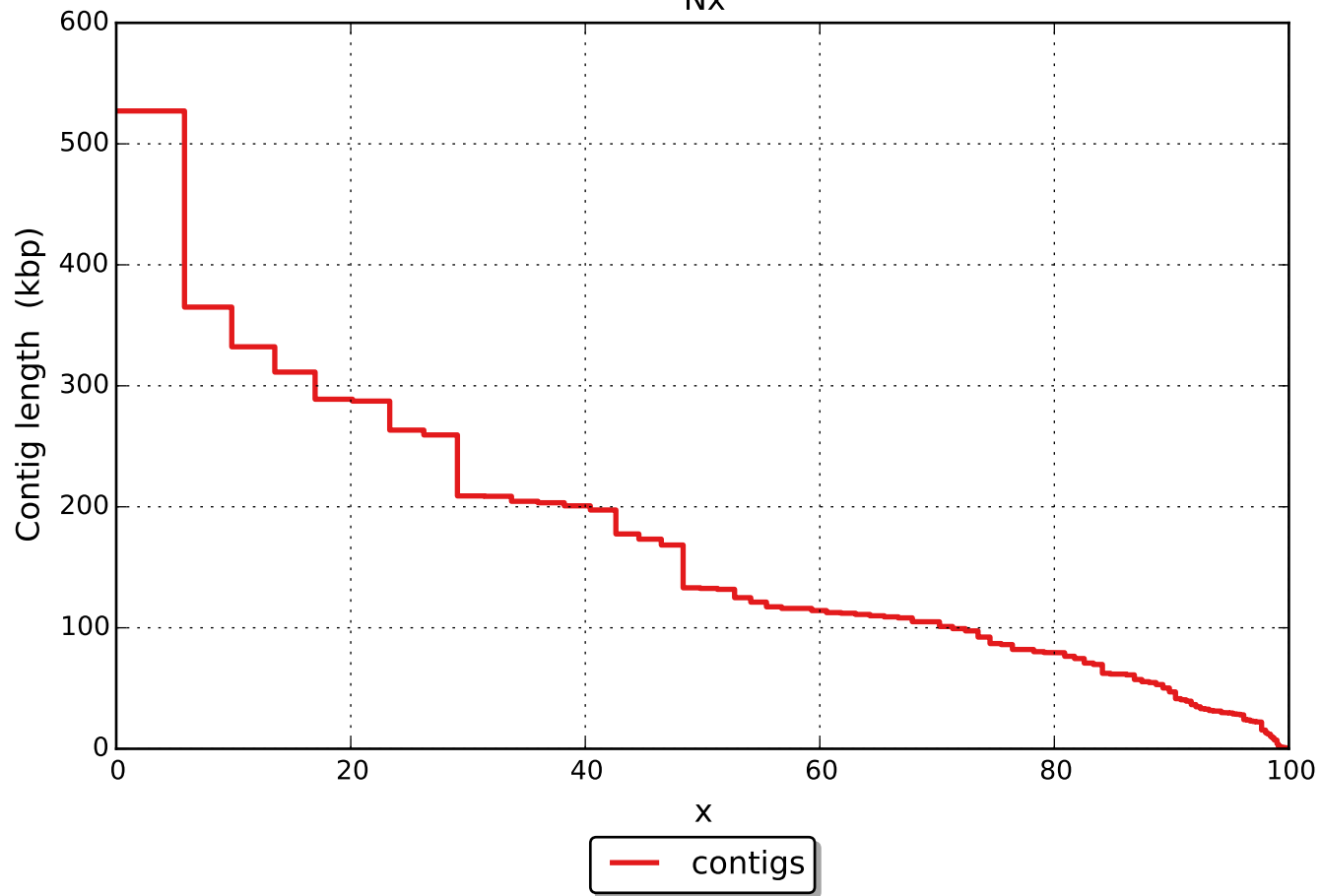
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

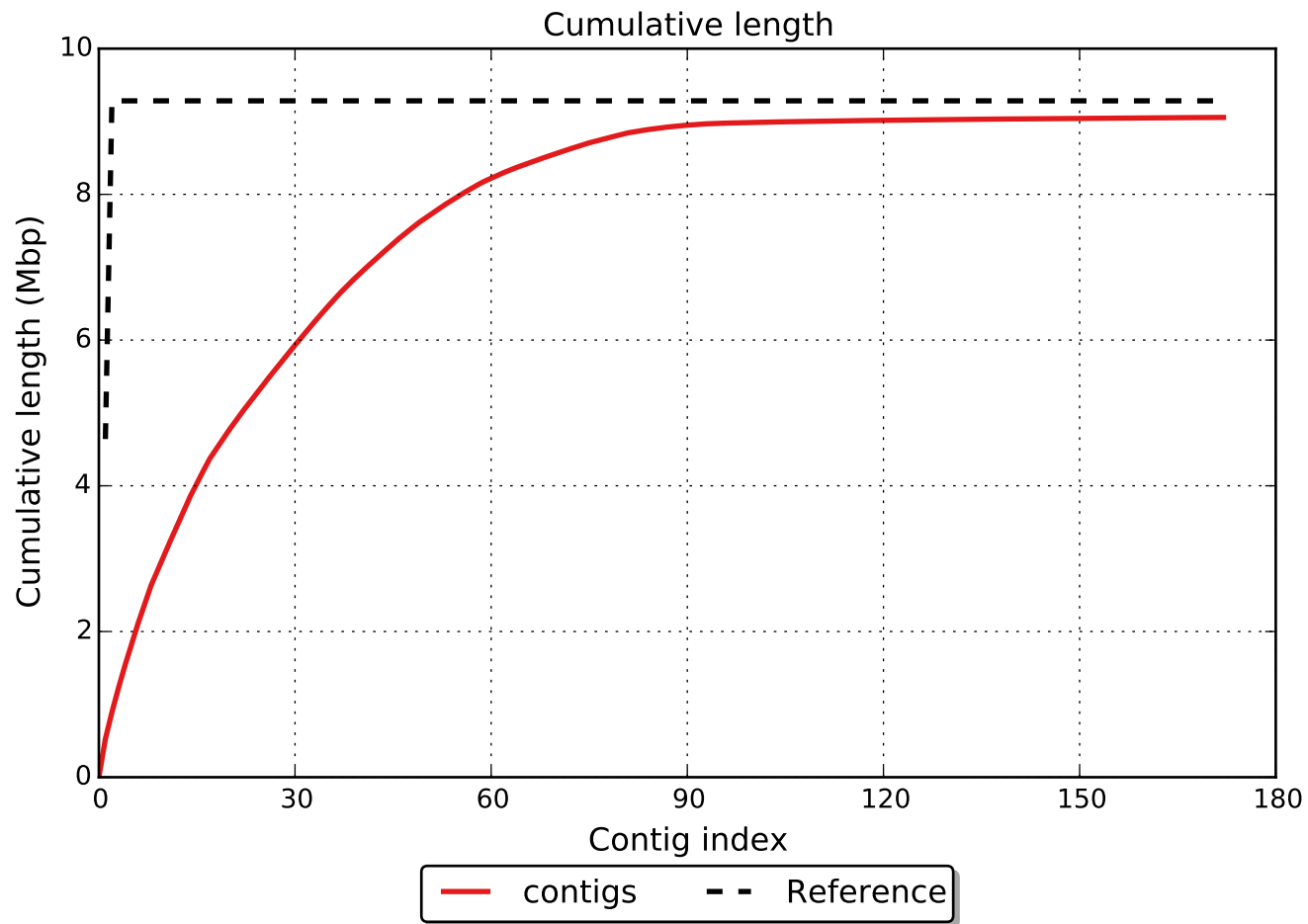
Unaligned report

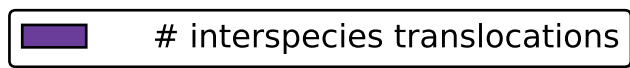
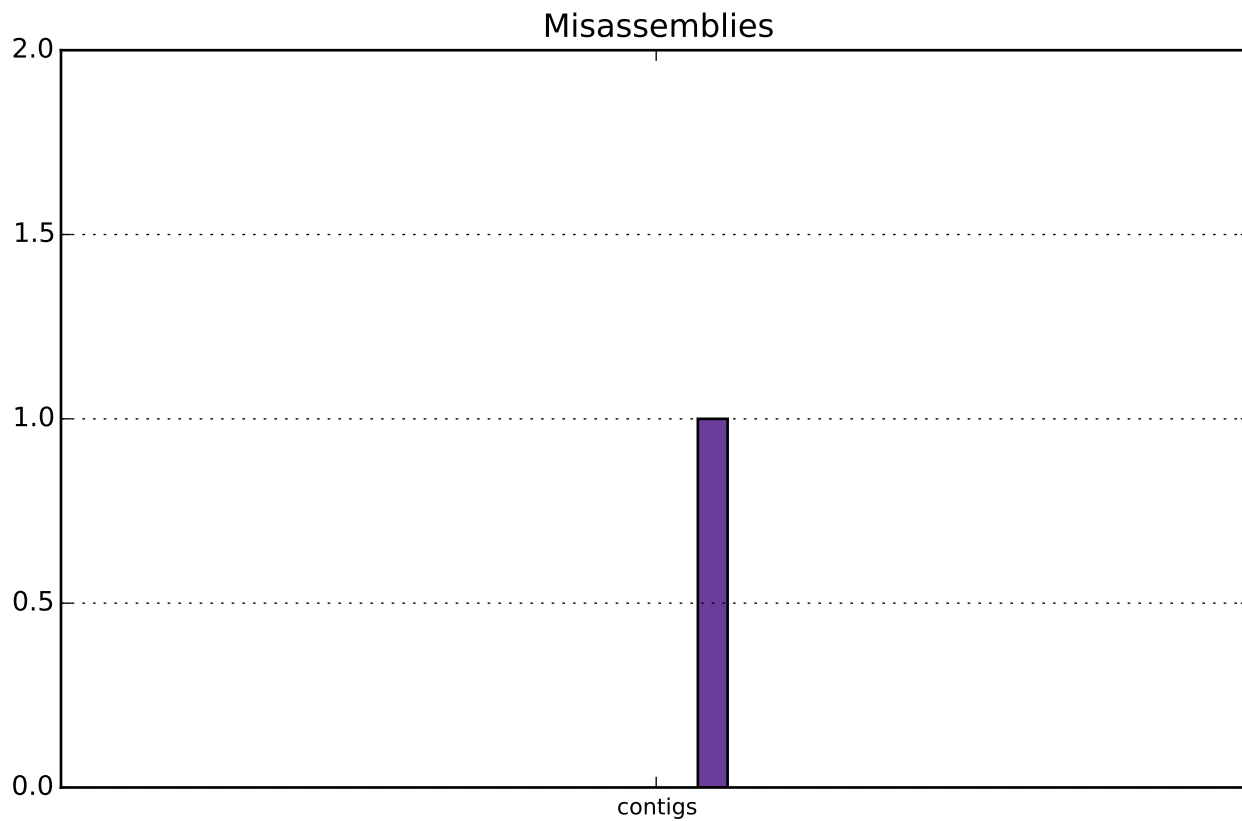
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

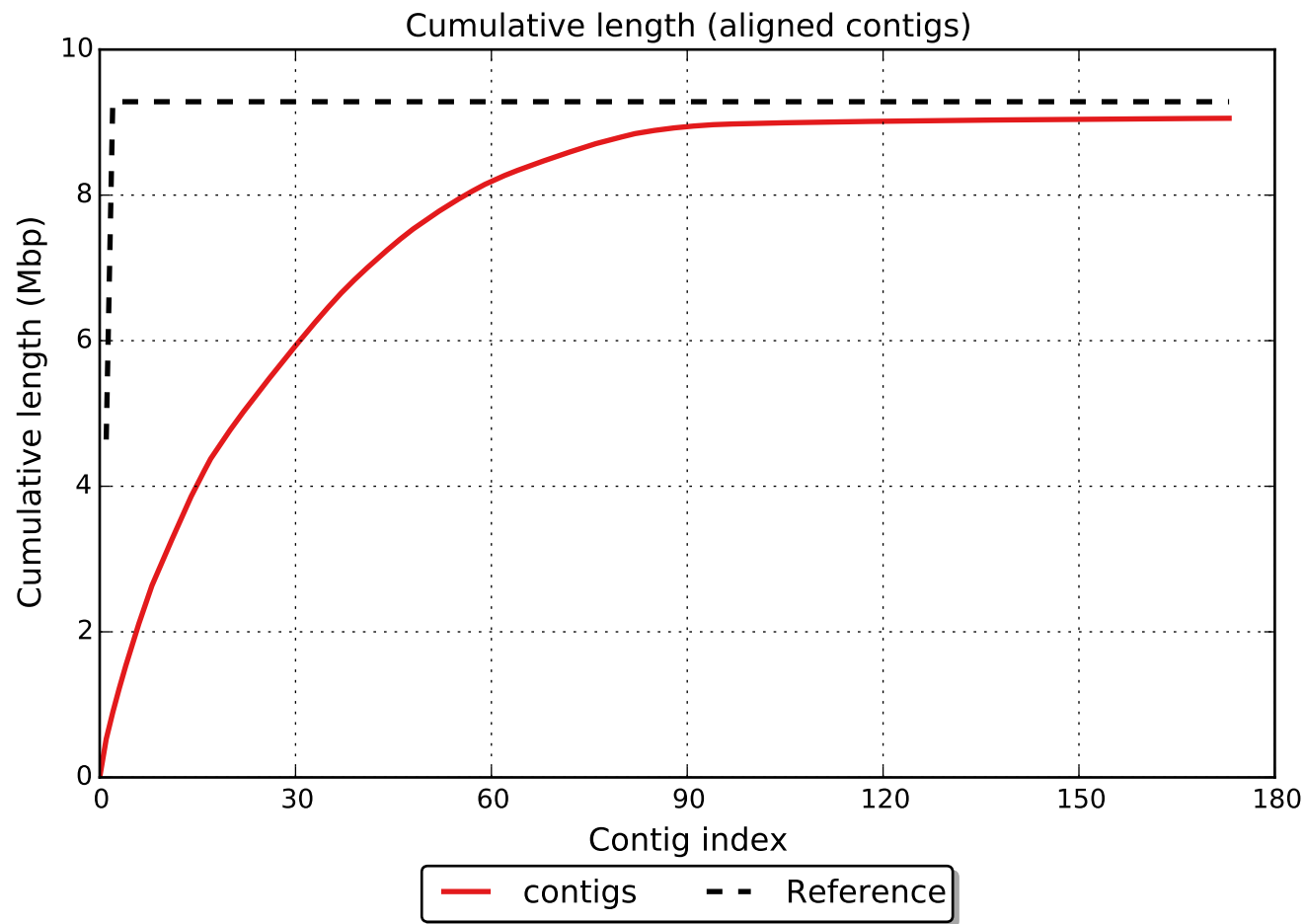
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

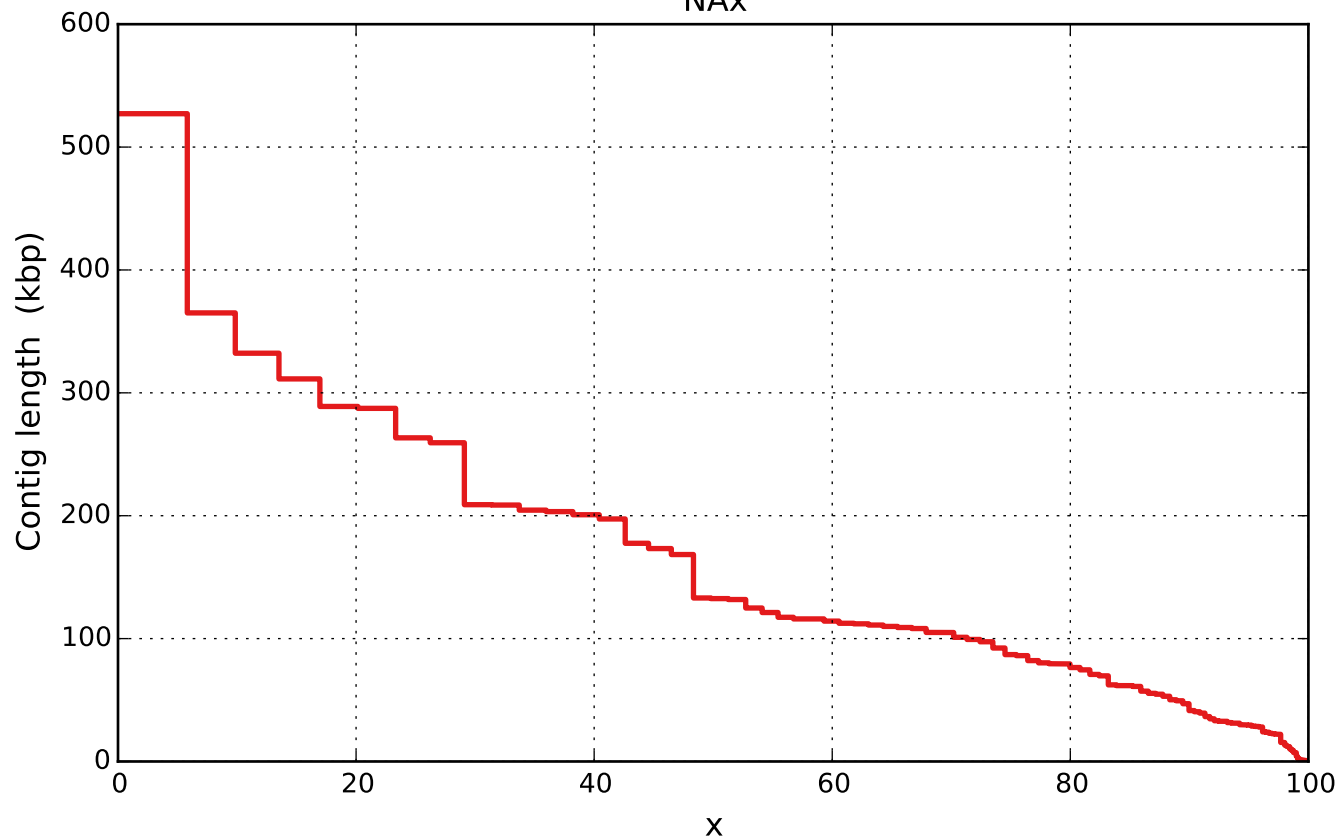








NAx



contigs