Report

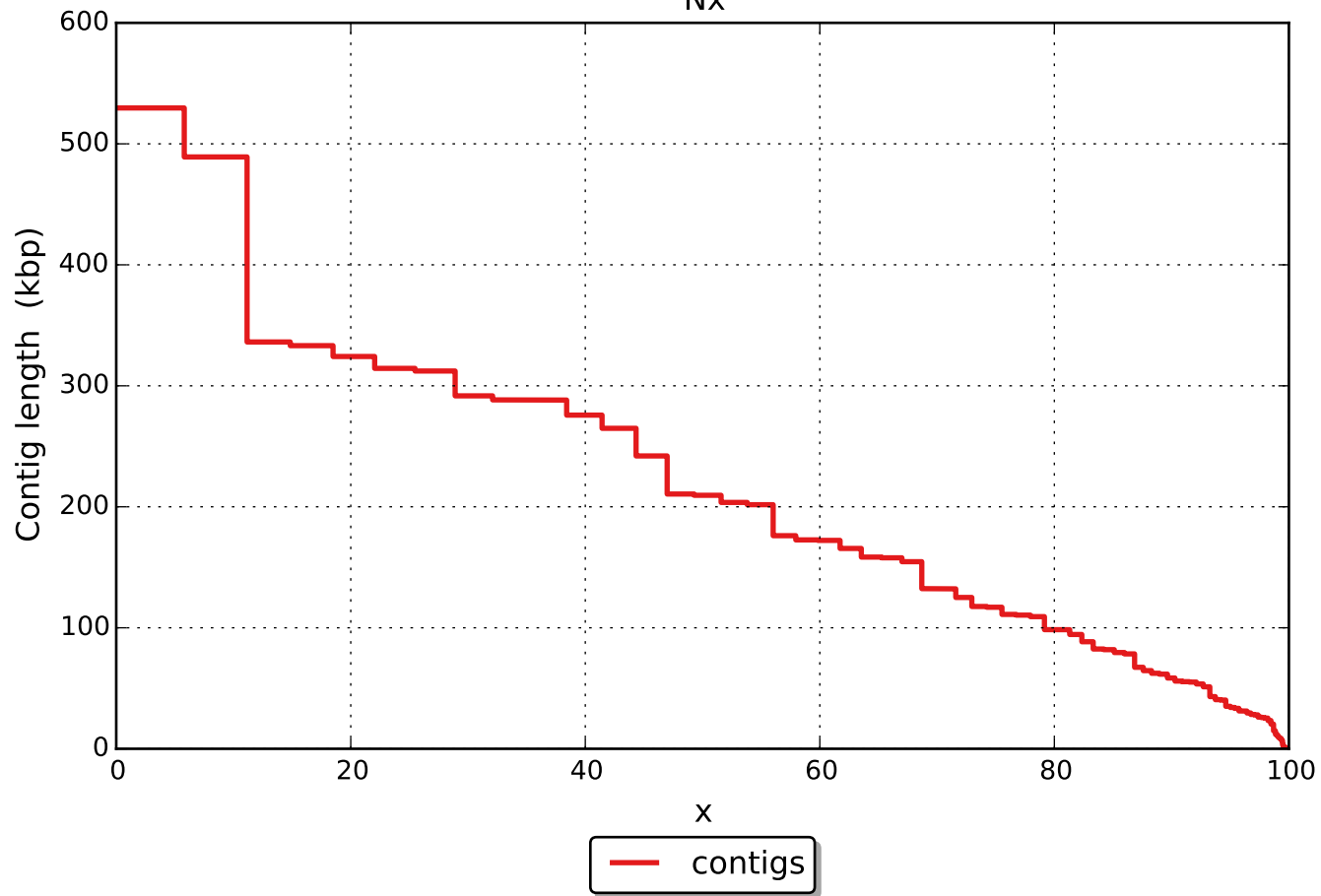|	contigs
# contigs (>= 0 bp)	203
# contigs (>= 1000 bp)	93
# contigs (>= 5000 bp)	73
# contigs (>= 10000 bp)	69
# contigs (>= 25000 bp)	64
# contigs (>= 50000 bp)	50
Total length (>= 0 bp)	9153923
Total length (>= 1000 bp)	9110901
Total length (>= 5000 bp)	9082212
Total length (>= 10000 bp)	9049427
Total length (>= 25000 bp)	8968196
Total length (>= 50000 bp)	8515834
# contigs	124
Largest contig	529642
Total length	9131439
Reference length	9283304
N50	209505
N75	116979
L50	15
L75	29
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	20404
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.862
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	403.59
# indels per 100 kbp	0.85
Largest alignment	529642
NA50	209505
NA75	116979
LA50	15
LA75	29

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	20404
# local misassemblies	0
# mismatches	37040
# indels	78
# short indels	78
# long indels	0
Indels length	78

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).
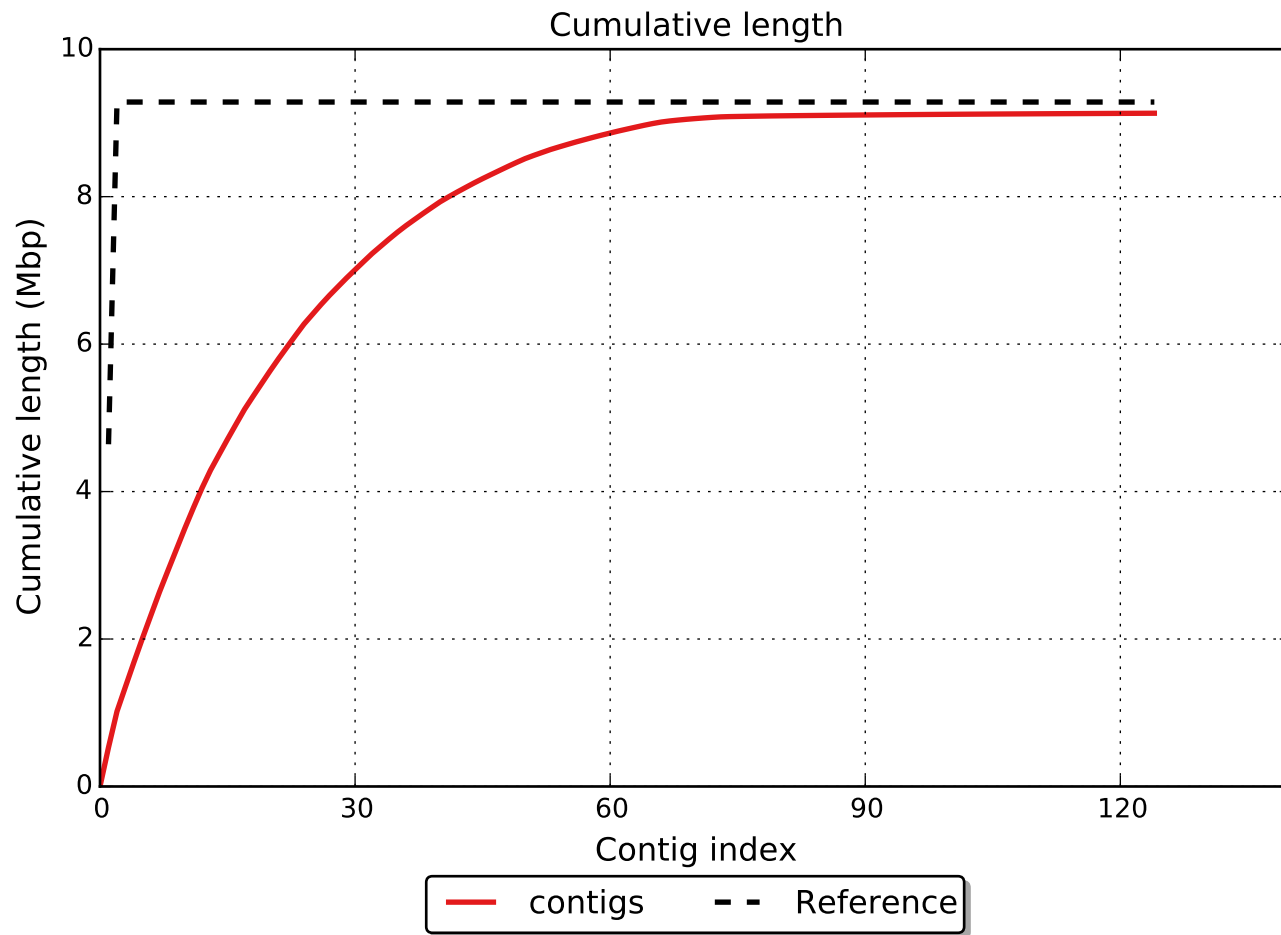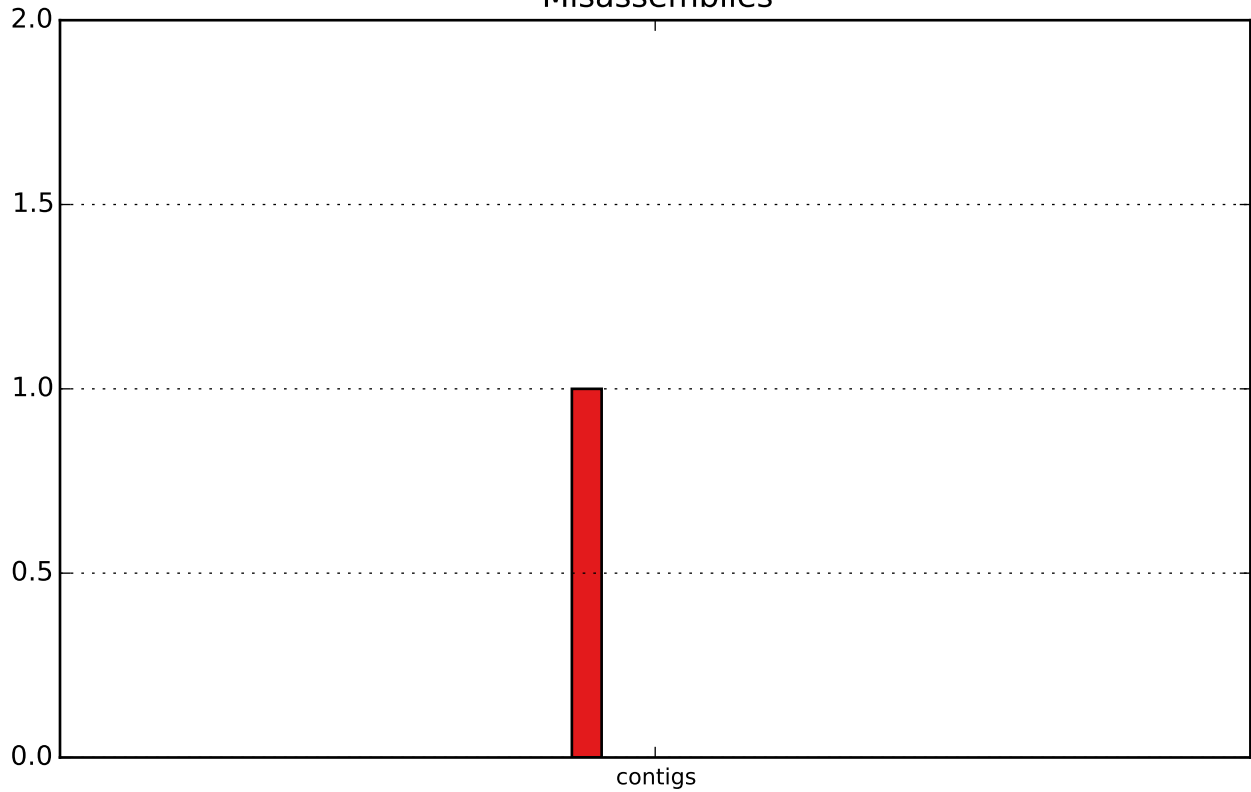
Unaligned report

	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).

Cumulative length
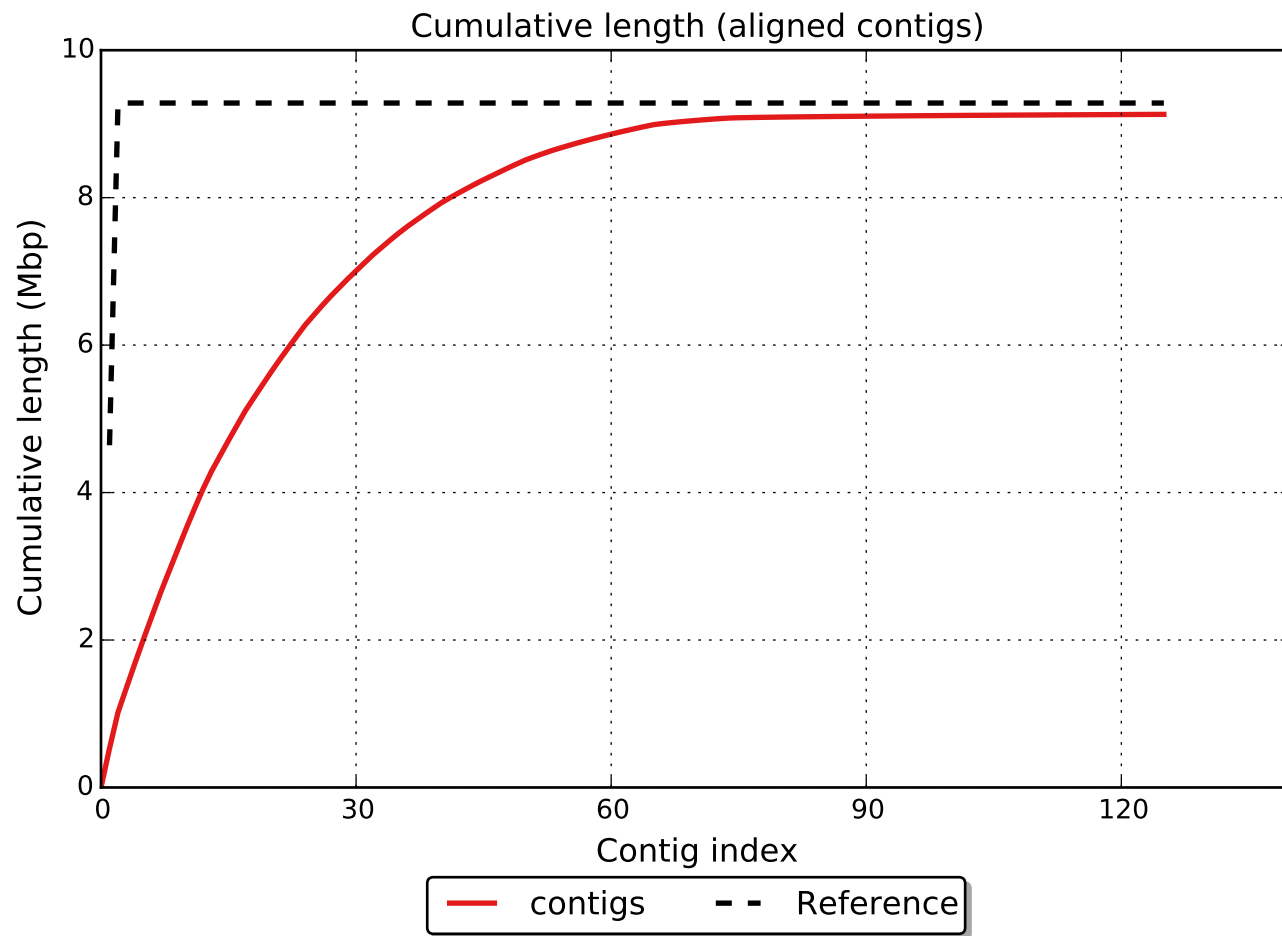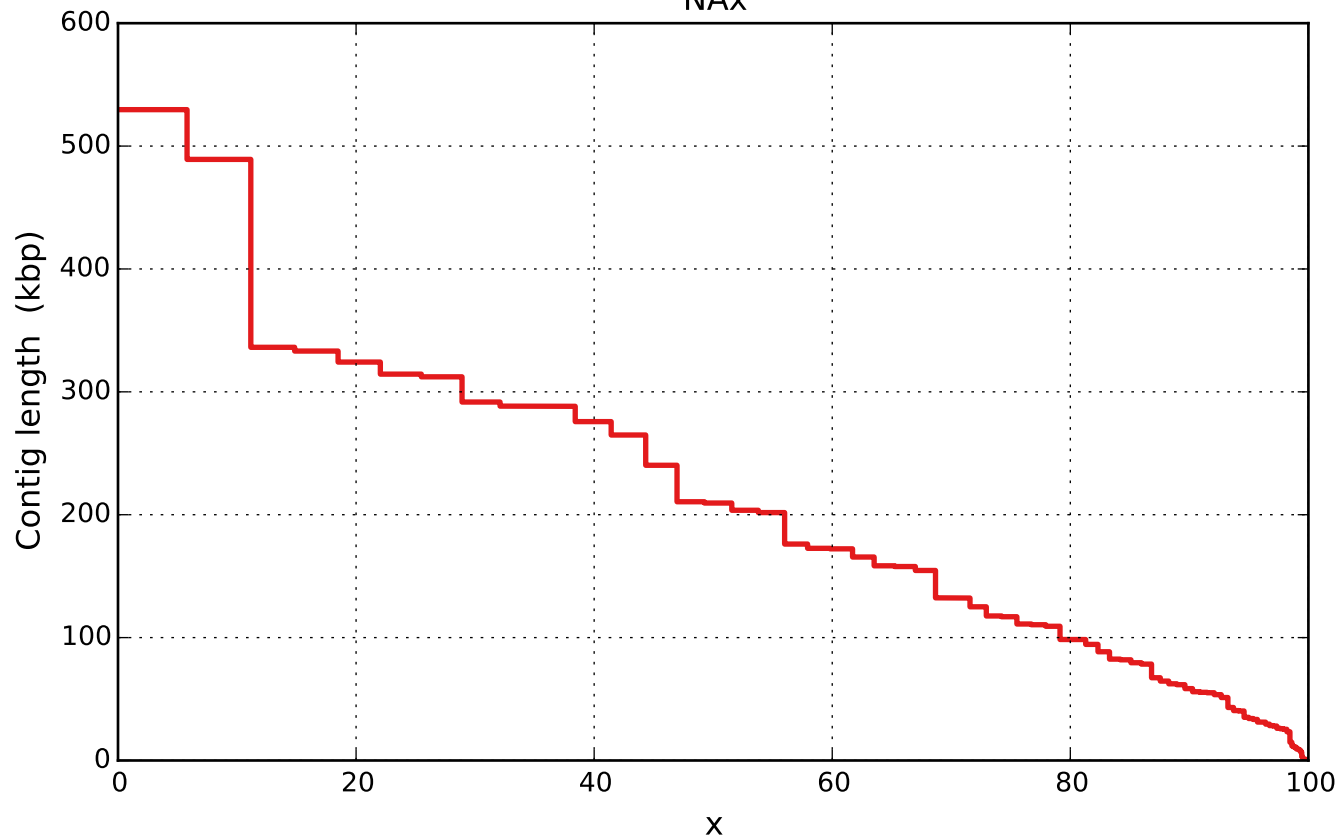
Misassemblies

contigs

relocations

Cumulative length (aligned contigs)