Report

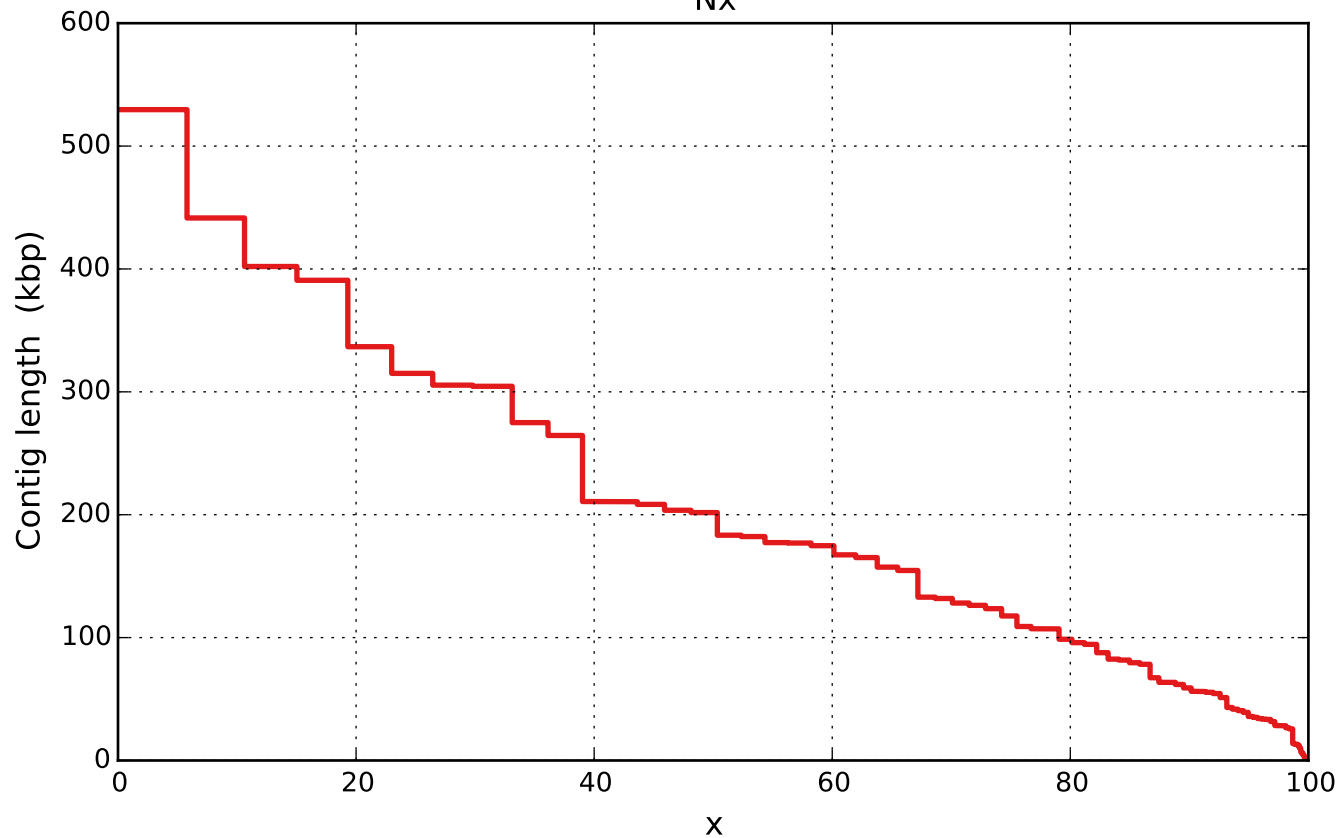|	contigs
# contigs (>= 0 bp)	166
# contigs (>= 1000 bp)	90
# contigs (>= 5000 bp)	74
# contigs (>= 10000 bp)	70
# contigs (>= 25000 bp)	66
# contigs (>= 50000 bp)	51
Total length (>= 0 bp)	9152051
Total length (>= 1000 bp)	9123821
Total length (>= 5000 bp)	9096558
Total length (>= 10000 bp)	9068065
Total length (>= 25000 bp)	9015948
Total length (>= 50000 bp)	8510358
# contigs	108
Largest contig	529644
Total length	9136507
Reference length	9283304
N50	201734
N75	117603
L50	15
L75	30
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	648881
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.401
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	340.90
# indels per 100 kbp	0.83
Largest alignment	529644
NA50	183318
NA75	107192
LA50	16
LA75	32

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	4
# relocations	3
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	648881
# local misassemblies	3
# mismatches	31141
# indels	76
# short indels	76
# long indels	0
Indels length	82

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).
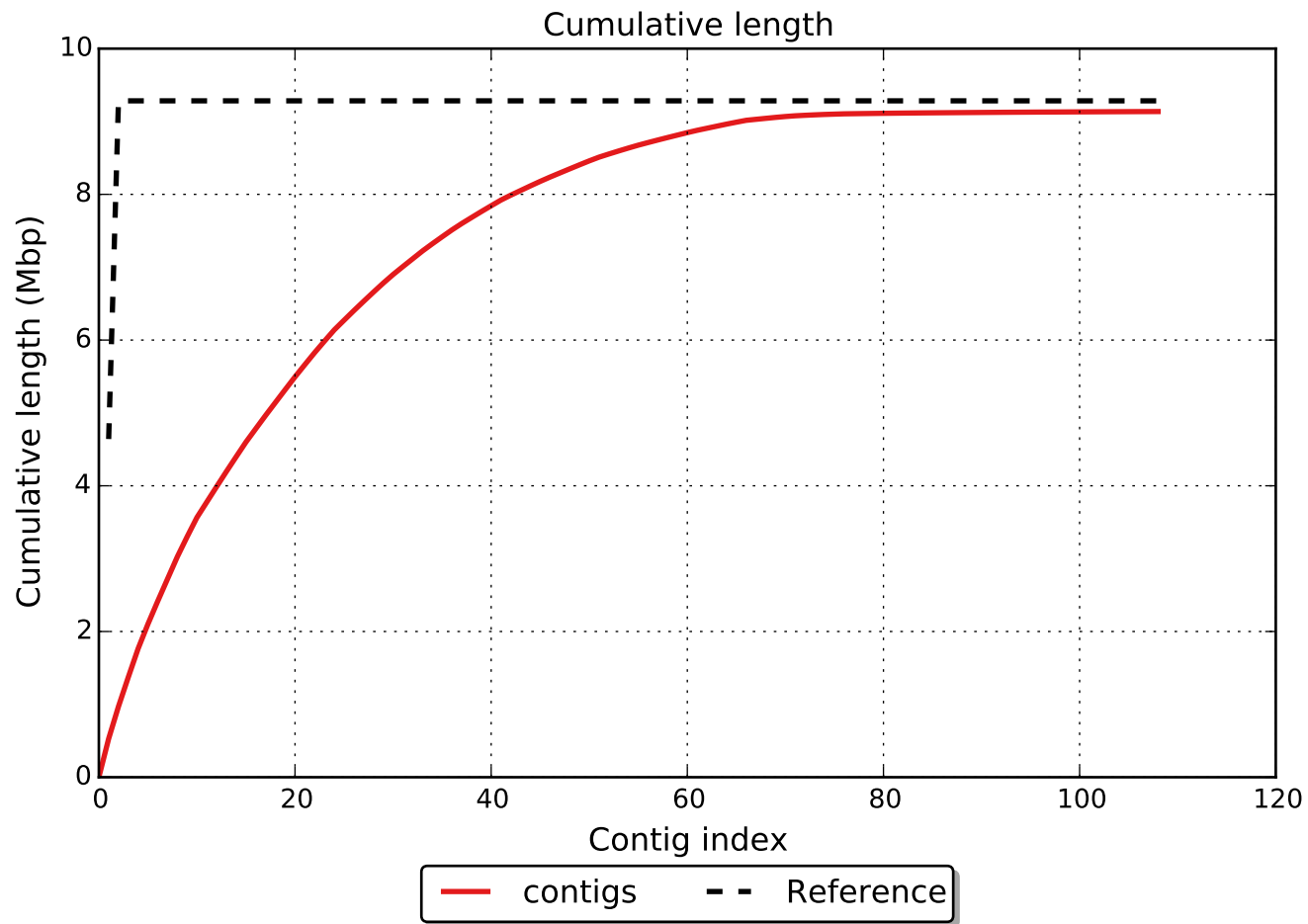
Unaligned report

	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).
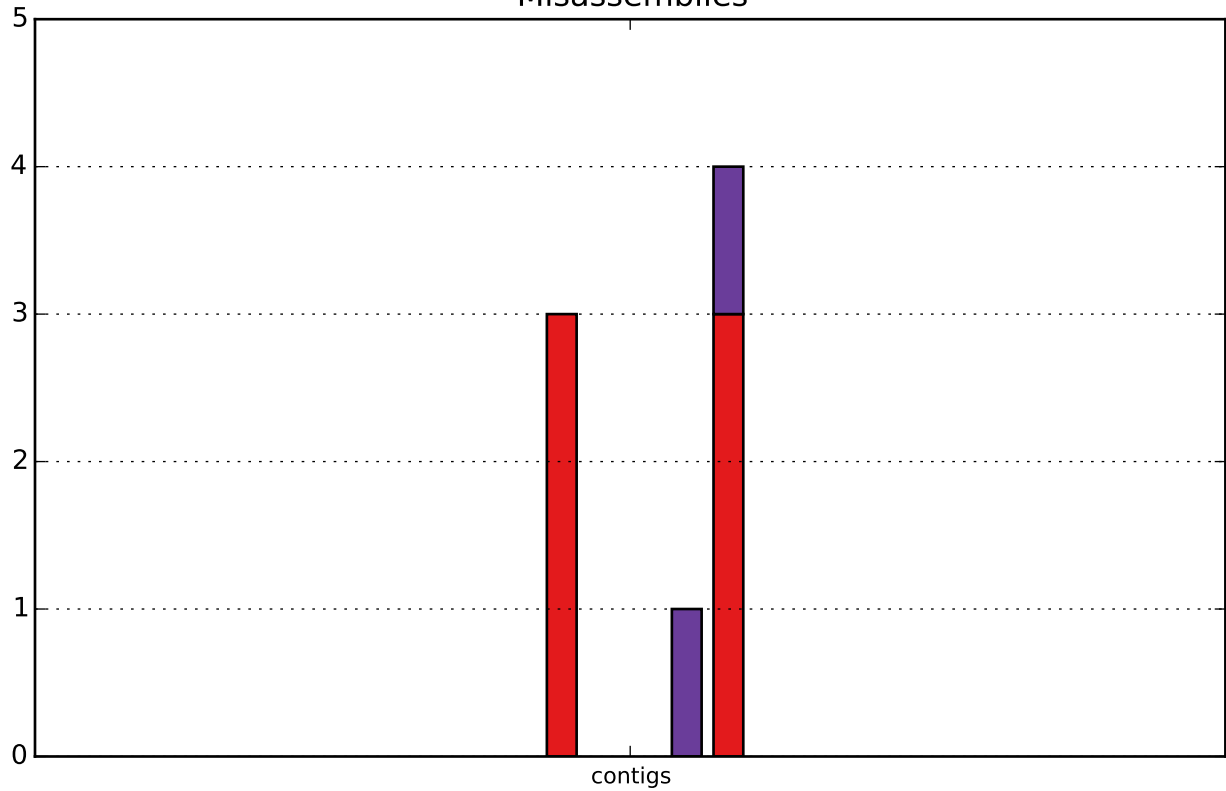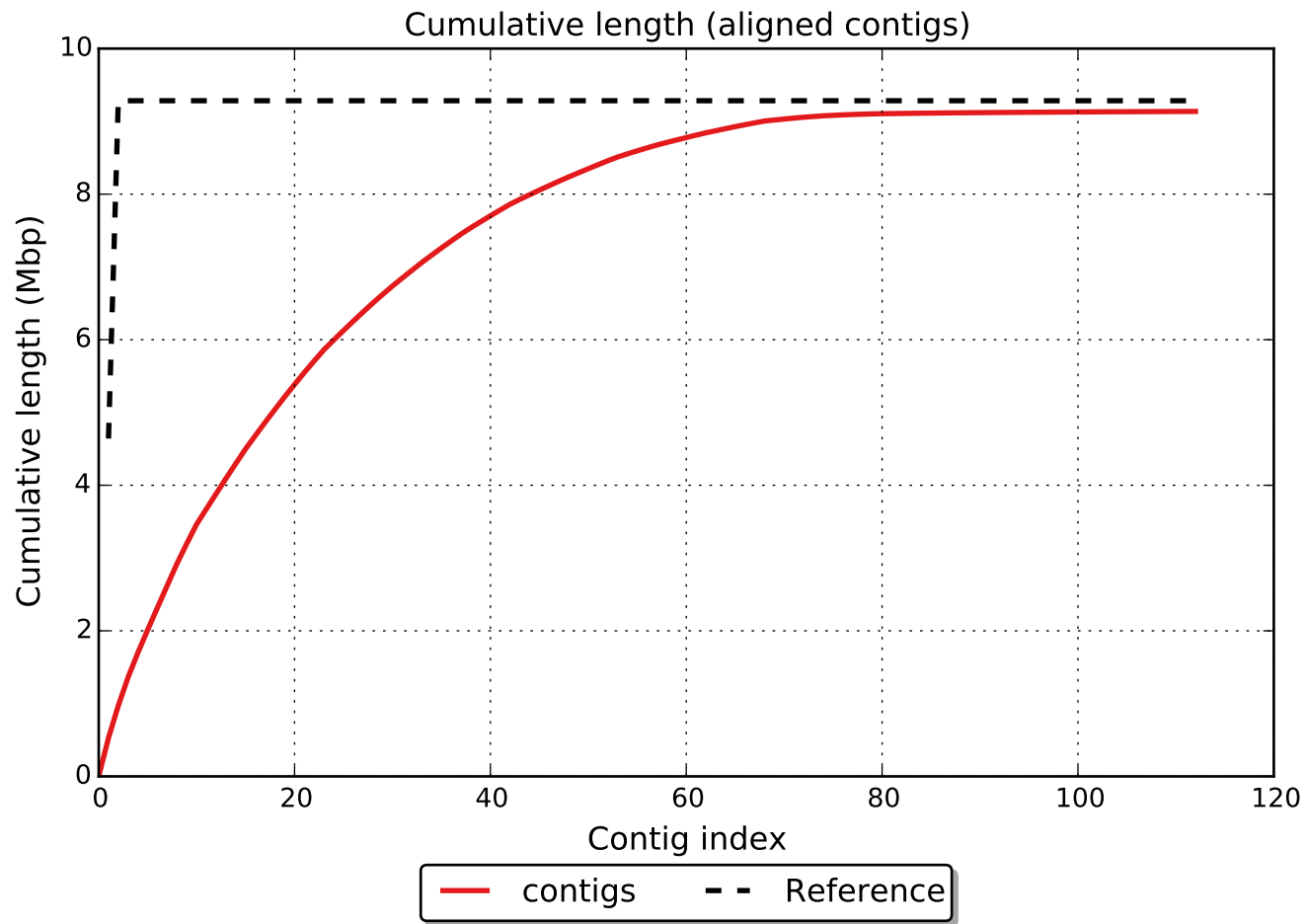
Cumulative length

Misassemblies

Cumulative length (aligned contigs)