Report

	scaffolds
# contigs (>= 1000 bp)	1574
# contigs (>= 5000 bp)	119
# contigs (>= 10000 bp)	3
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3923025
Total length (>= 5000 bp)	764485
Total length (>= 10000 bp)	38155
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2210
Largest contig	13882
Total length	4388761
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	2615
NG50	2486
N75	1538
NG75	1393
L50	529
LG50	578
L75	1075
LG75	1204
# misassemblies	25
# misassembled contigs	24
Misassembled contigs length	80849
# local misassemblies	5
# unaligned contigs	0 + 24 part
Unaligned length	2527
Genome fraction (%)	93.088
Duplication ratio	1.015
# N's per 100 kbp	18.66
# mismatches per 100 kbp	680.68
# indels per 100 kbp	12.06
Largest alignment	13882
NA50	2588
NGA50	2441
NA75	1523
NGA75	1372
LA50	534
LGA50	584
LA75	1088
LGA75	1219

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

|	scaffolds
# misassemblies	25
# relocations	25
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	24
Misassembled contigs length	80849
# local misassemblies	5
# mismatches	29411
# indels	521
# short indels	474
# long indels	47
Indels length	1402

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

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	24
# with misassembly	0
# both parts are significant	1
Partially unaligned length	2527
# N's	819

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).
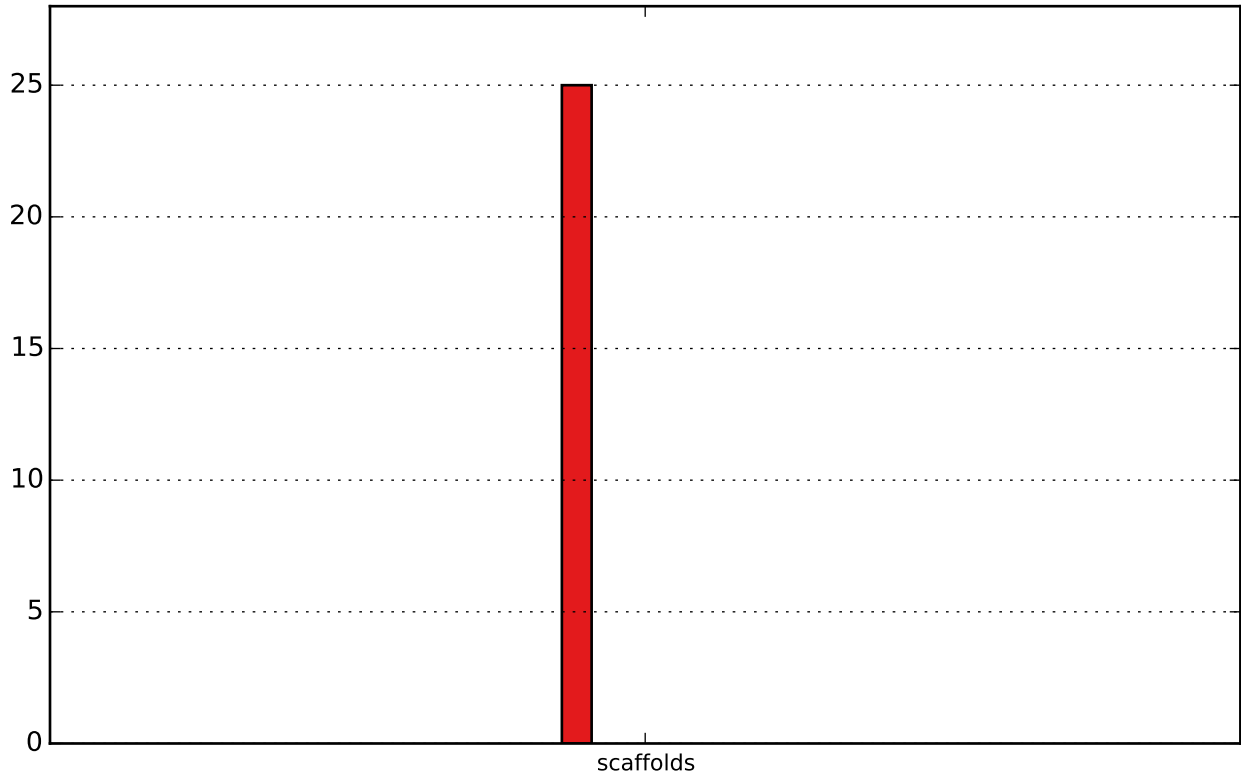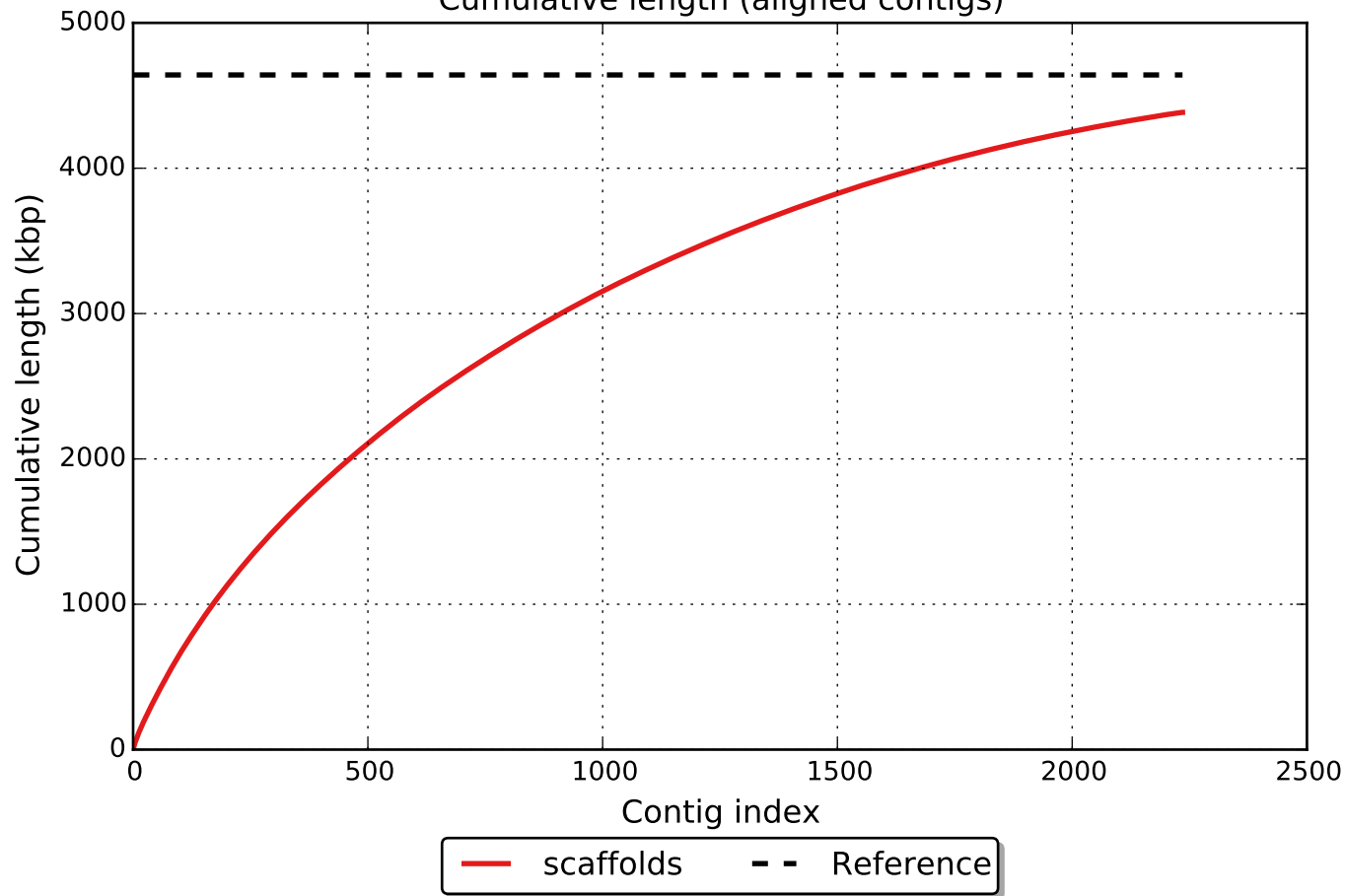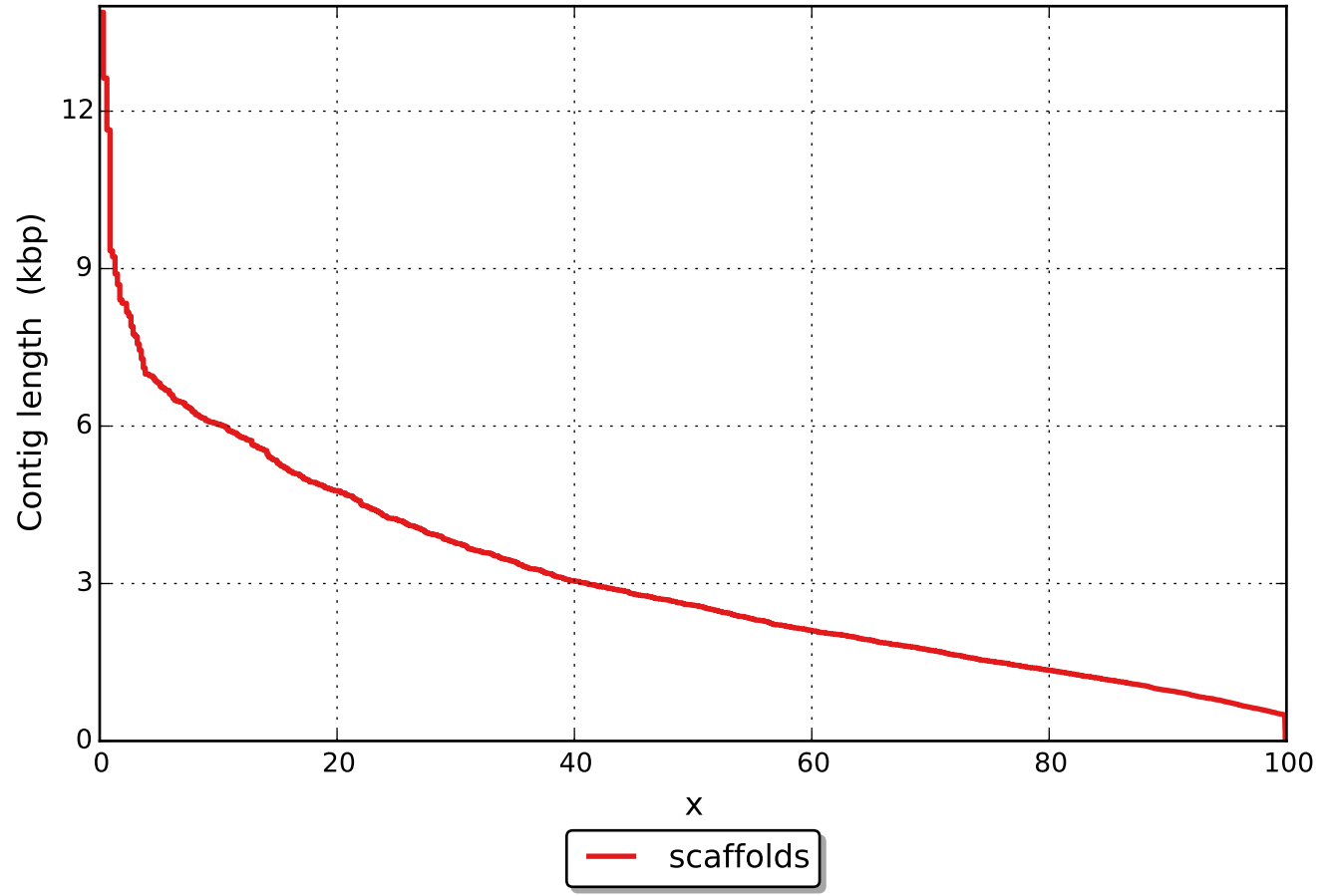
Nx

NGx
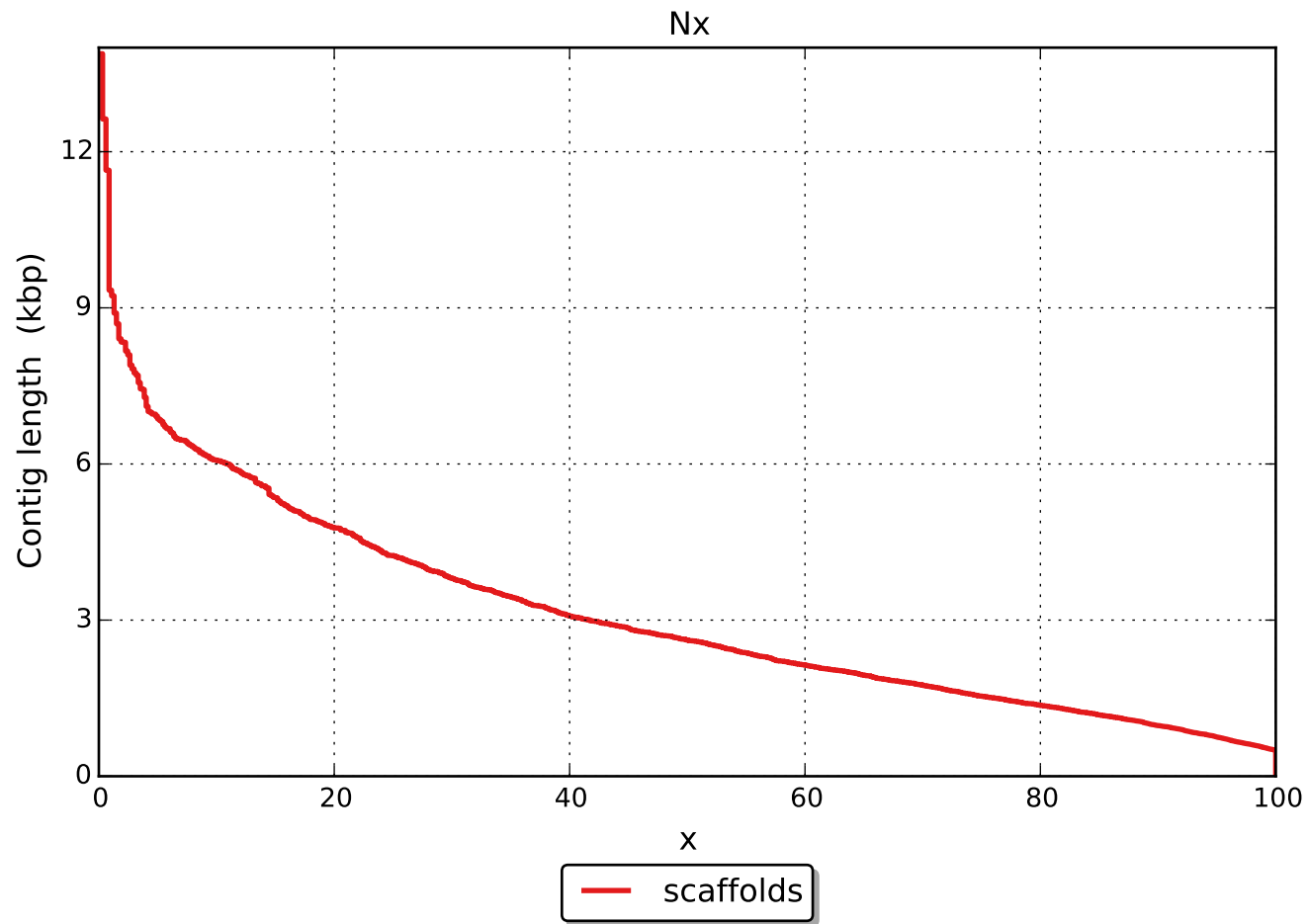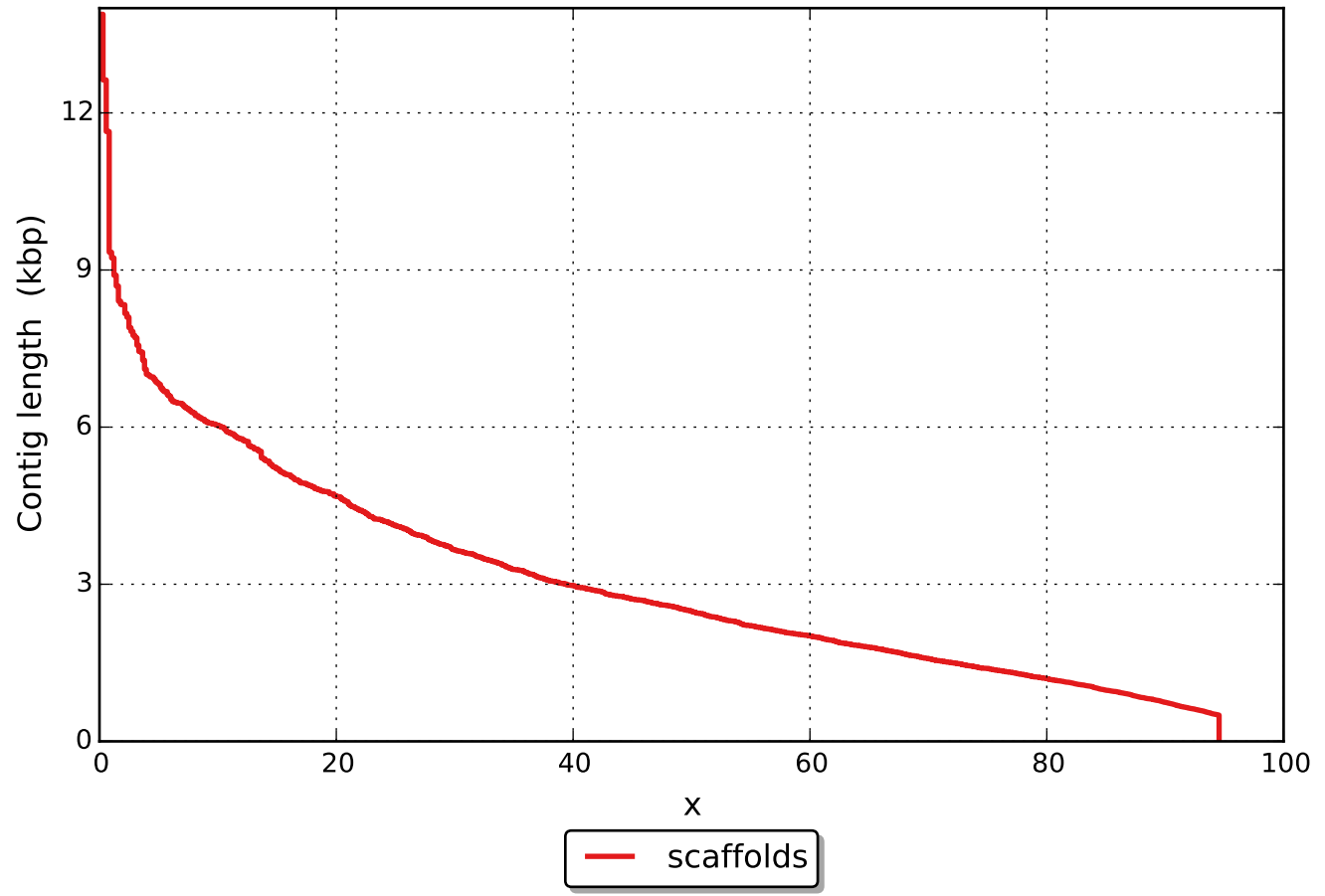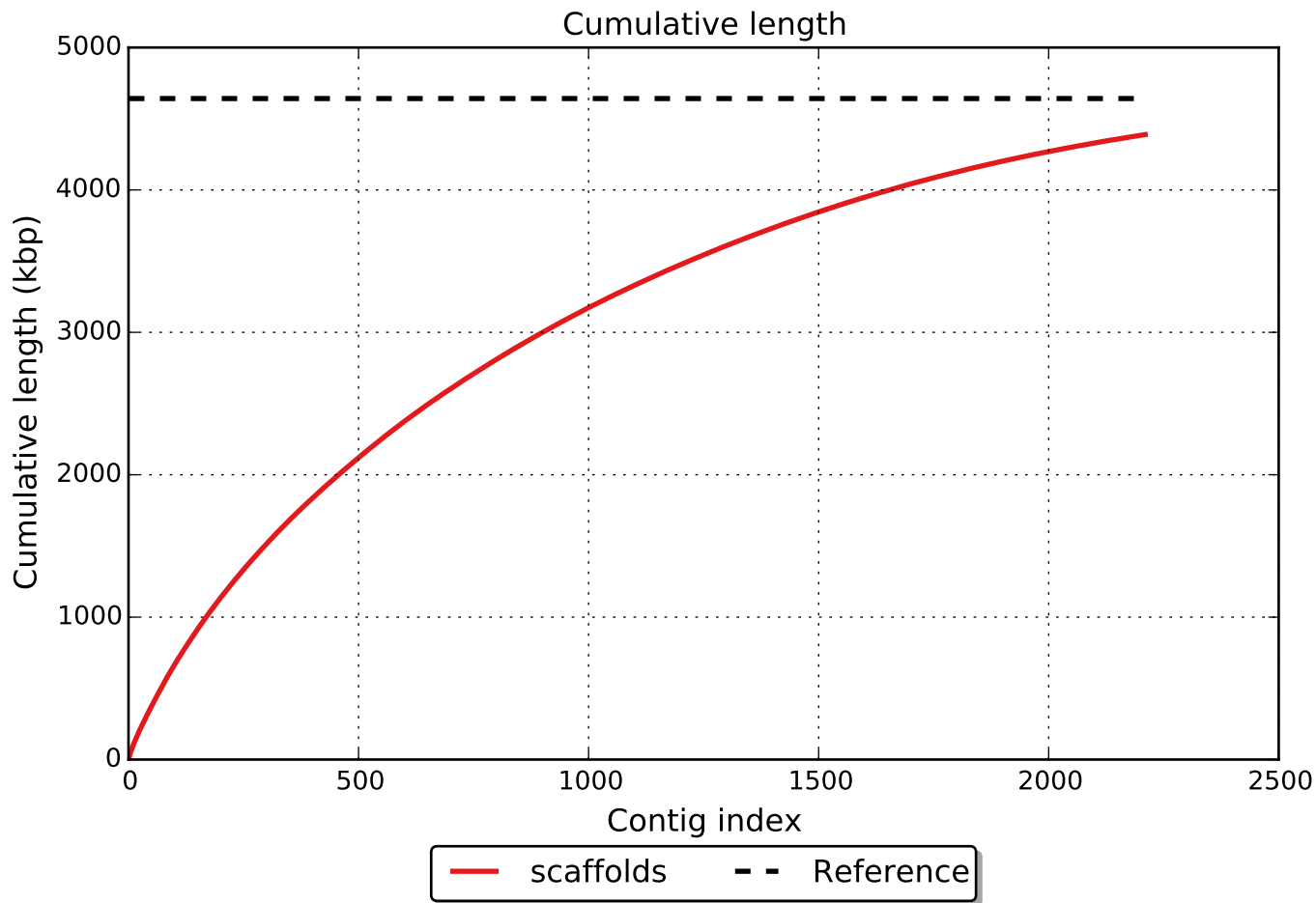
Cumulative length

GC content
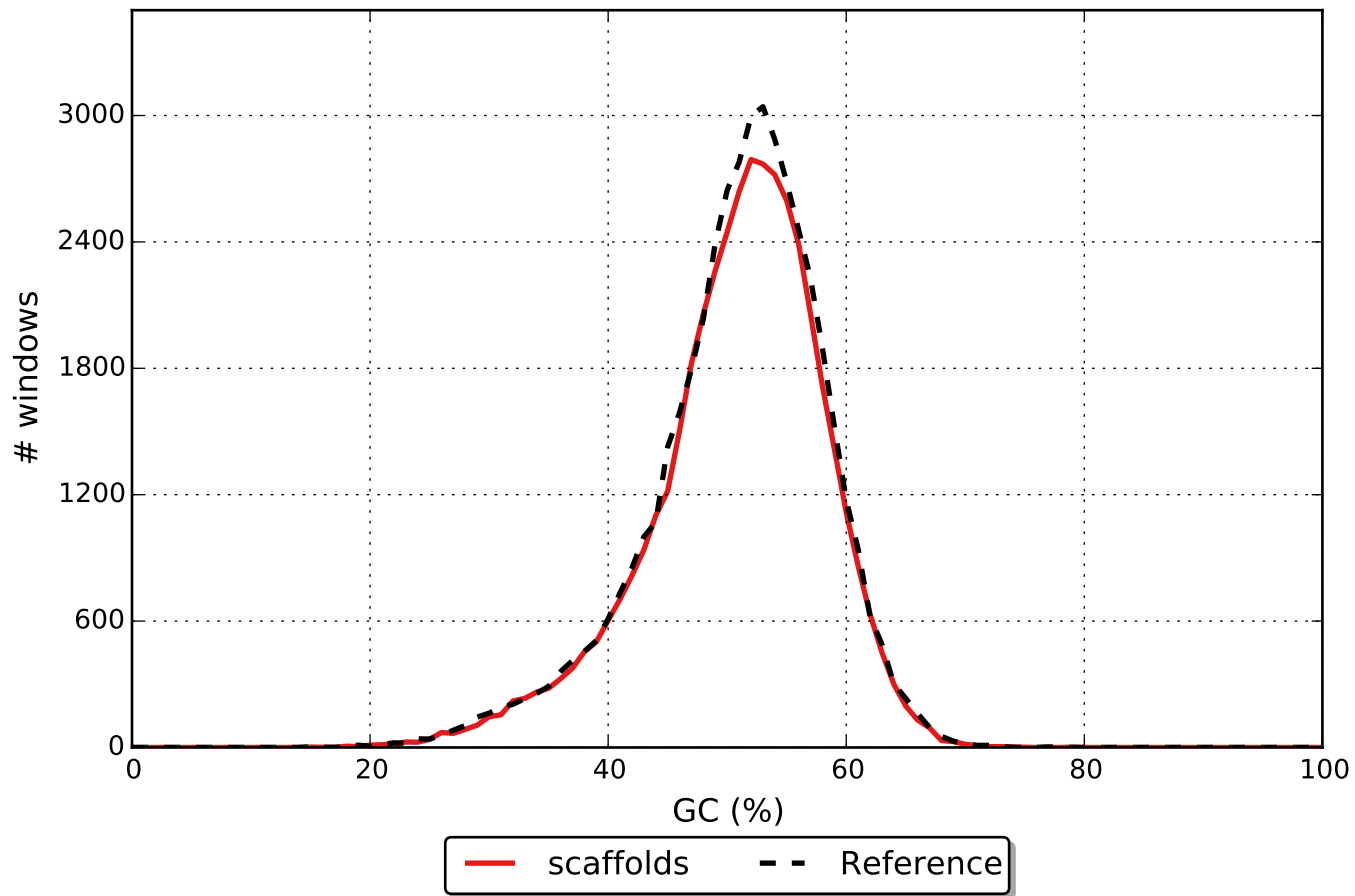
Misassemblies

Cumulative length (aligned contigs)

NAx

NGAx