Report

	scaffolds
# contigs (>= 1000 bp)	443
# contigs (>= 5000 bp)	257
# contigs (>= 10000 bp)	143
# contigs (>= 25000 bp)	34
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	4141110
Total length (>= 5000 bp)	3696371
Total length (>= 10000 bp)	2853582
Total length (>= 25000 bp)	1180594
Total length (>= 50000 bp)	61819
# contigs	596
Largest contig	61819
Total length	4245988
Reference length	4641652
GC (%)	50.70
Reference GC (%)	50.79
N50	15354
NG50	13762
N75	8143
NG75	6662
L50	84
LG50	98
L75	180
LG75	220
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	87.664
Duplication ratio	1.043
# N's per 100 kbp	3420.00
# mismatches per 100 kbp	1022.76
# indels per 100 kbp	10.10
Largest alignment	59611
NA50	14248
NGA50	12484
NA75	7280
NGA75	5423
LA50	91
LGA50	105
LA75	197
LGA75	243

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).
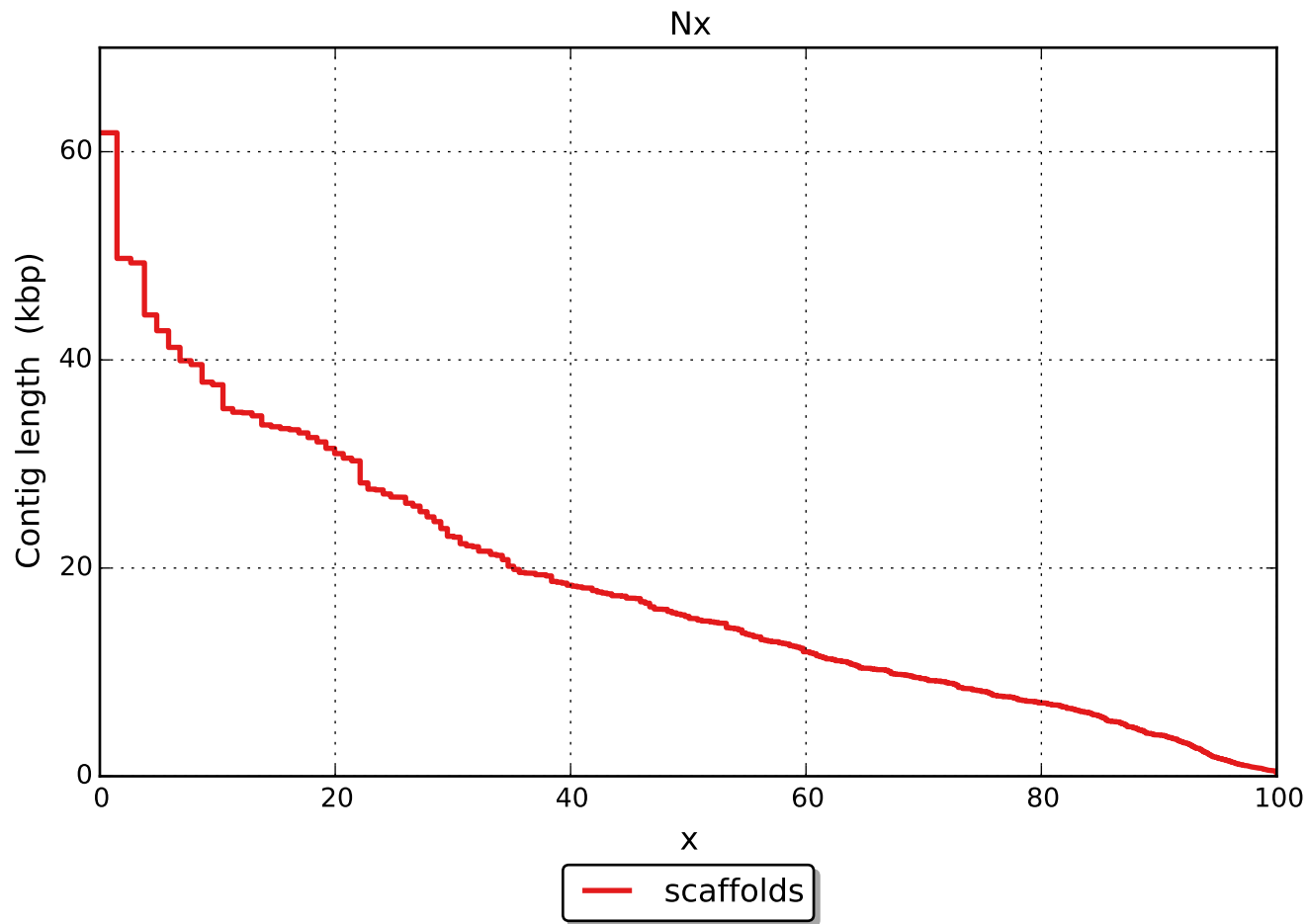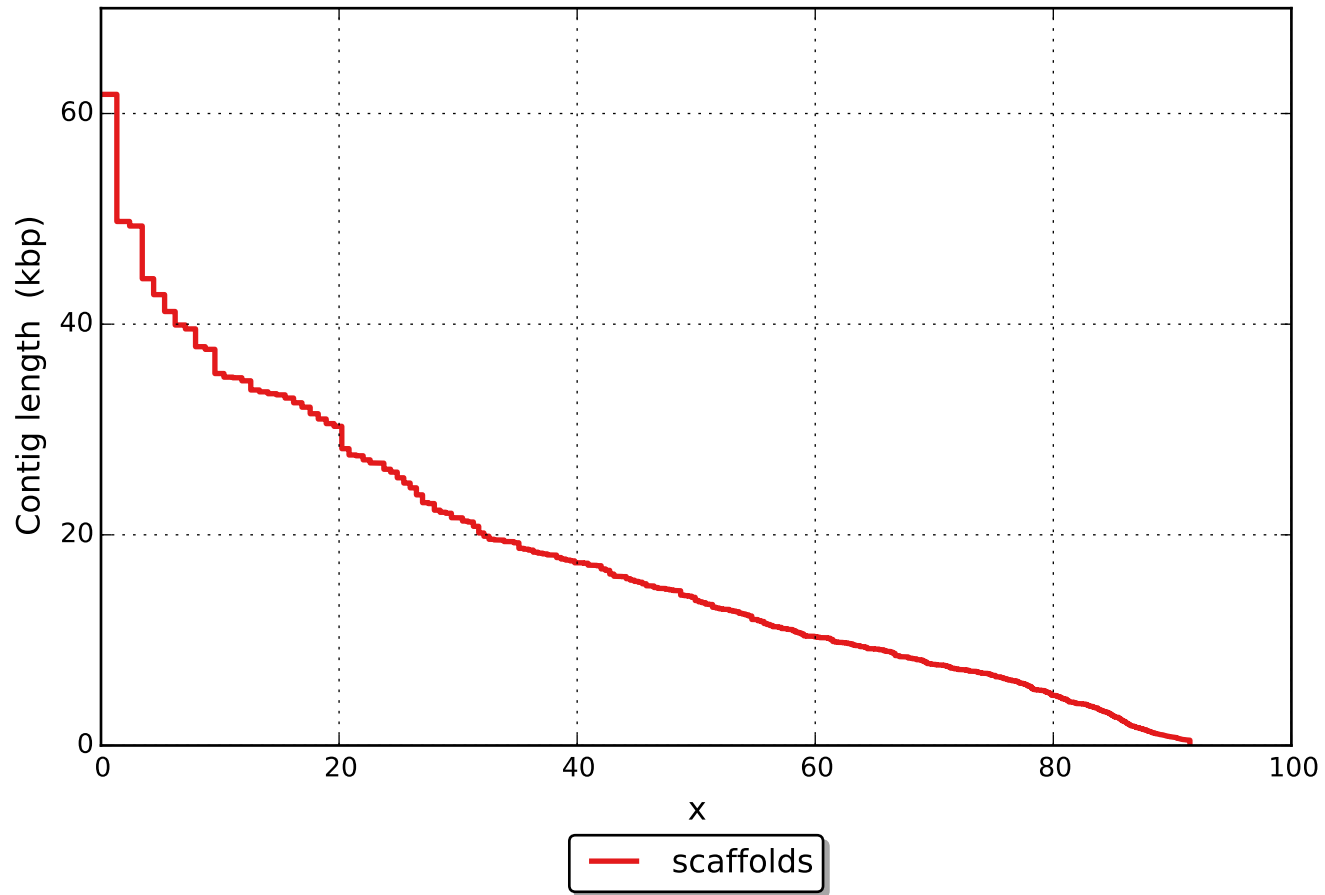
Misassemblies report

	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	99
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# mismatches	41617
# indels	411
# short indels	28
# long indels	383
Indels length	21086

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).
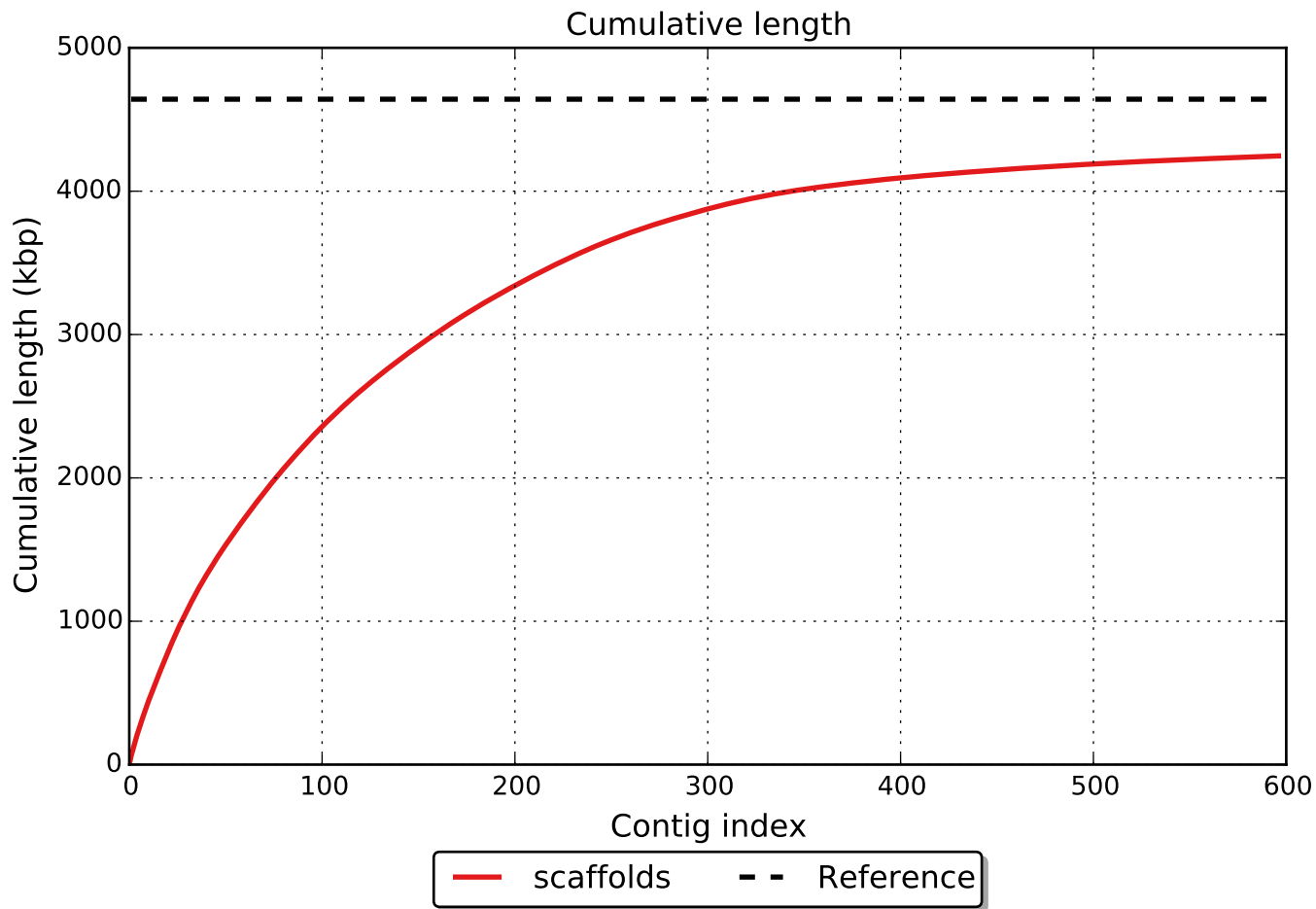
Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	145213

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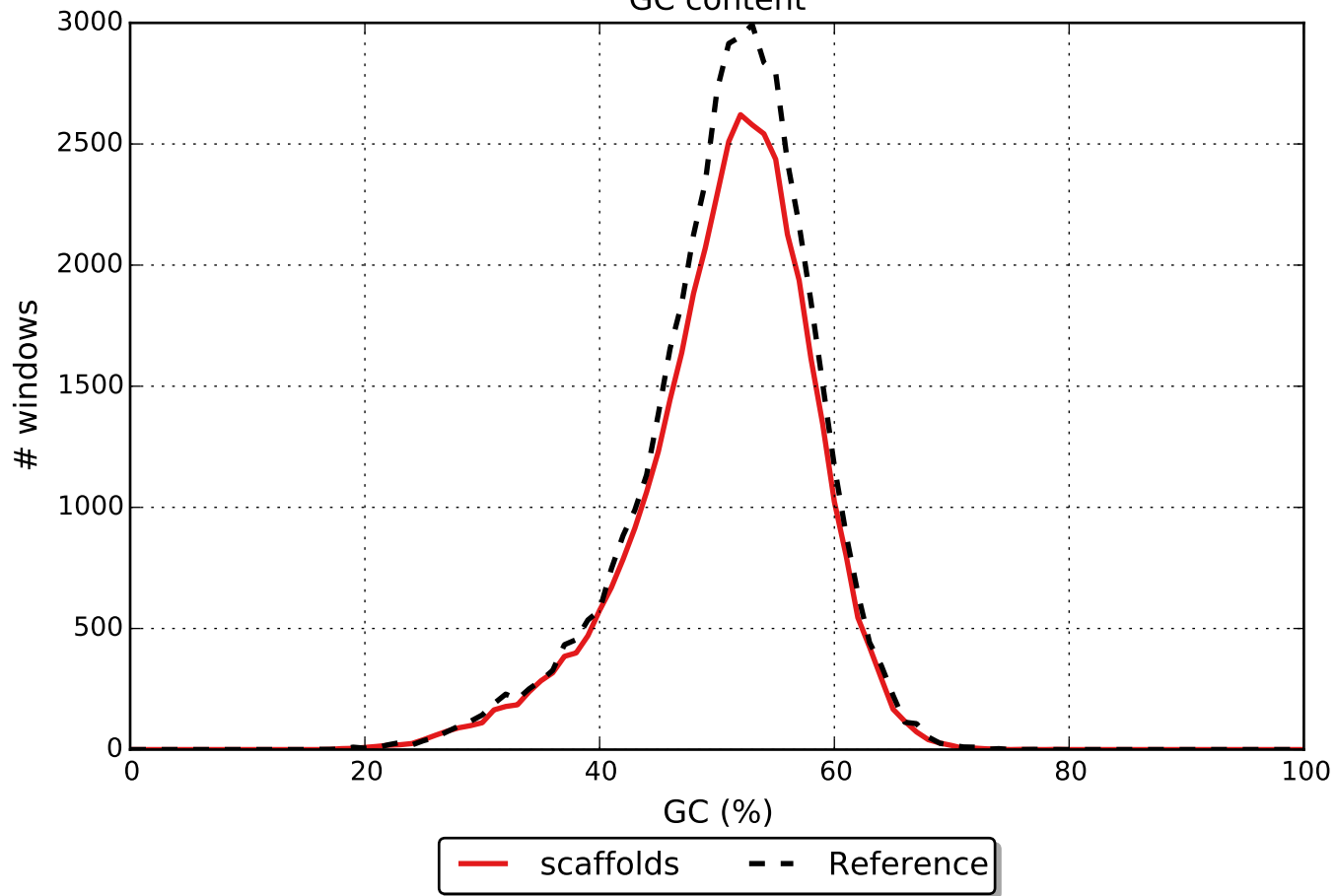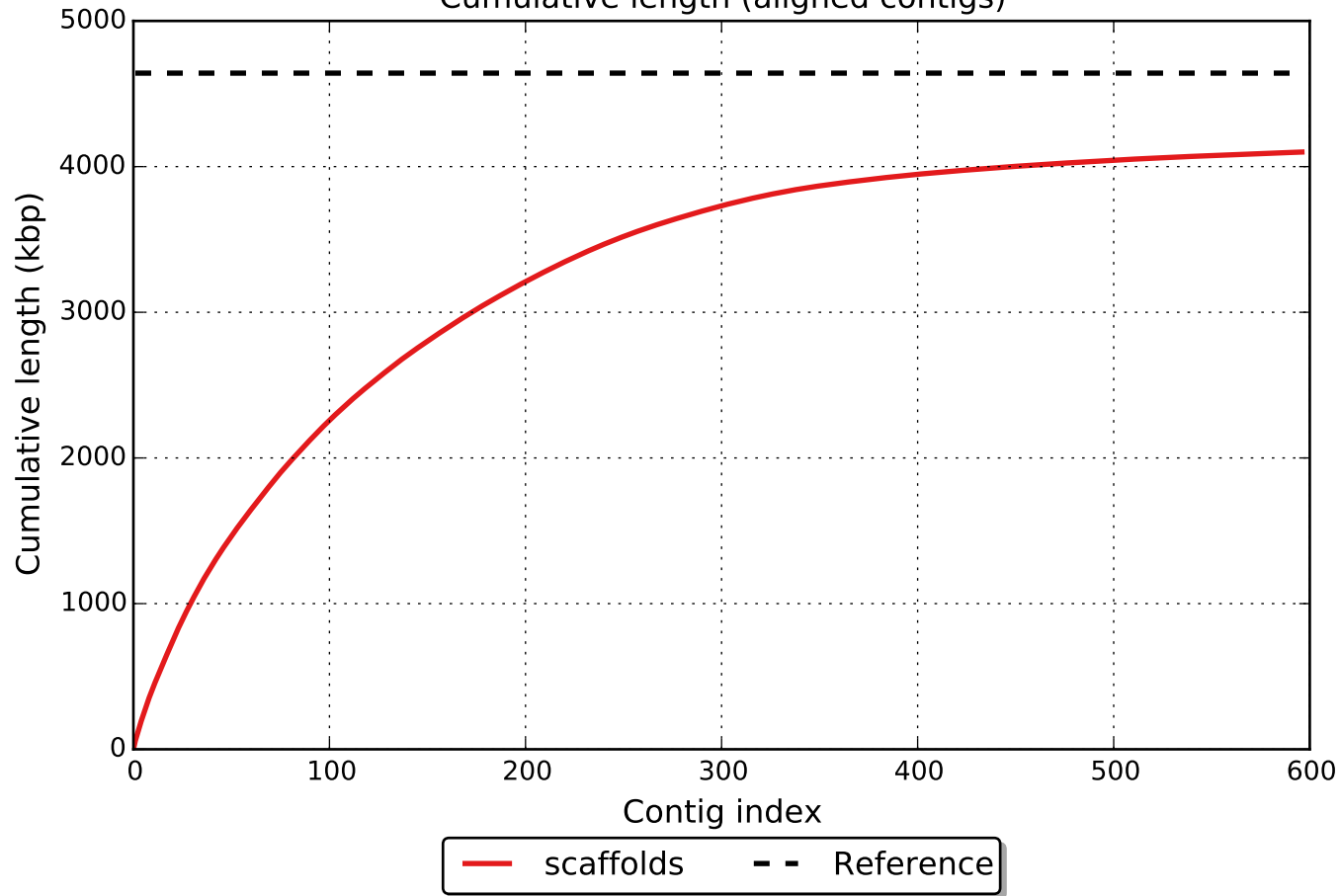(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

NGx

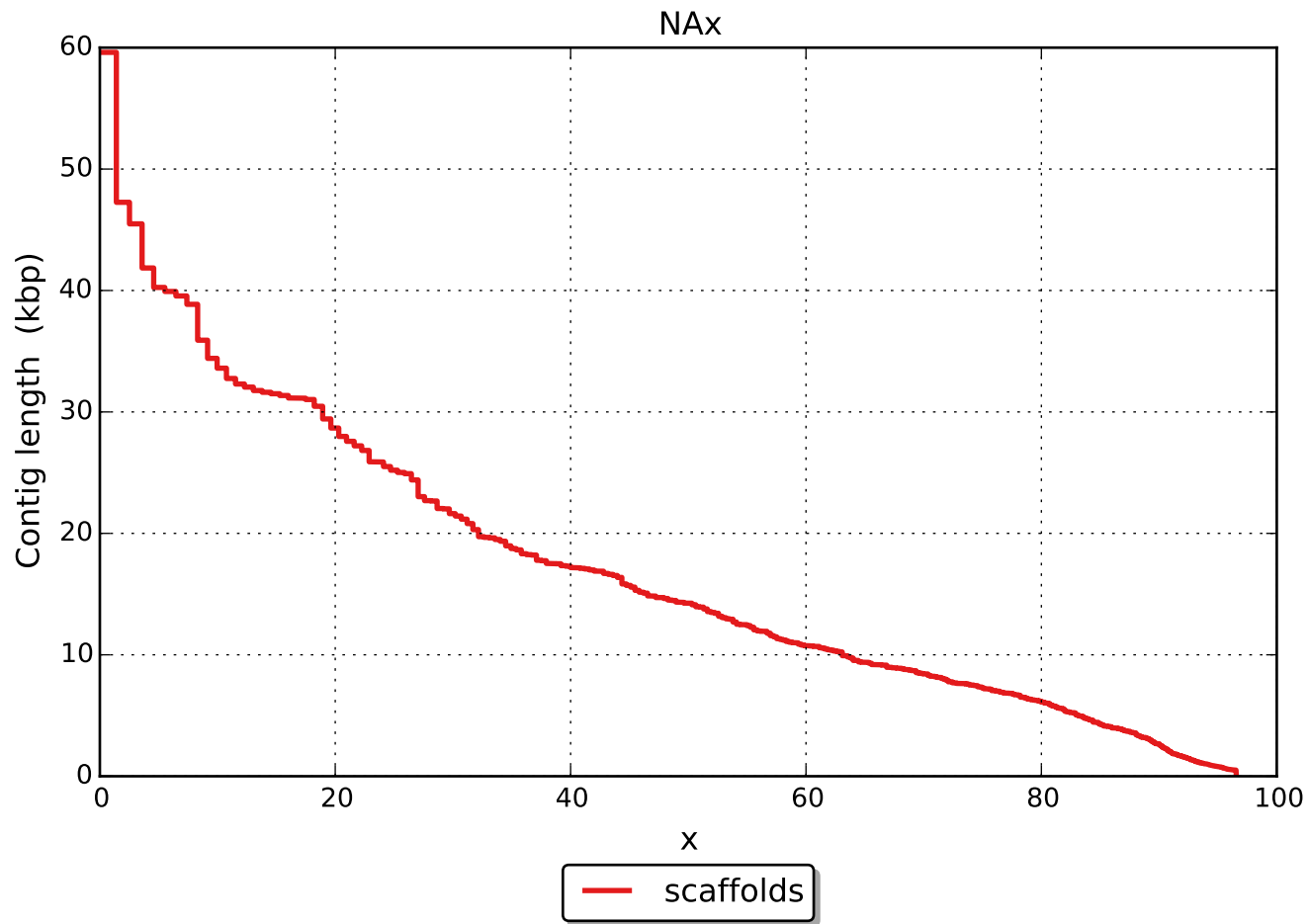Cumulative length

GC content

Misassemblies

scaffolds

Cumulative length (aligned contigs)