Report

	contigs
# contigs (>= 0 bp)	4117
# contigs (>= 1000 bp)	1574
# contigs (>= 5000 bp)	15
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4252614
Total length (>= 1000 bp)	2850746
Total length (>= 5000 bp)	89652
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2916
Largest contig	9678
Total length	3827178
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	1518
NG50	1284
N75	991
NG75	682
L50	813
LG50	1104
L75	1594
LG75	2331
# misassemblies	40
# misassembled contigs	39
Misassembled contigs length	114373
# local misassemblies	8
# unaligned contigs	0 + 3 part
Unaligned length	60
Genome fraction (%)	81.862
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	936.62
# indels per 100 kbp	1.76
Largest alignment	9678
NA50	1500
NGA50	1268
NA75	984
NGA75	679
LA50	830
LGA50	1125
LA75	1620
LGA75	2362

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).
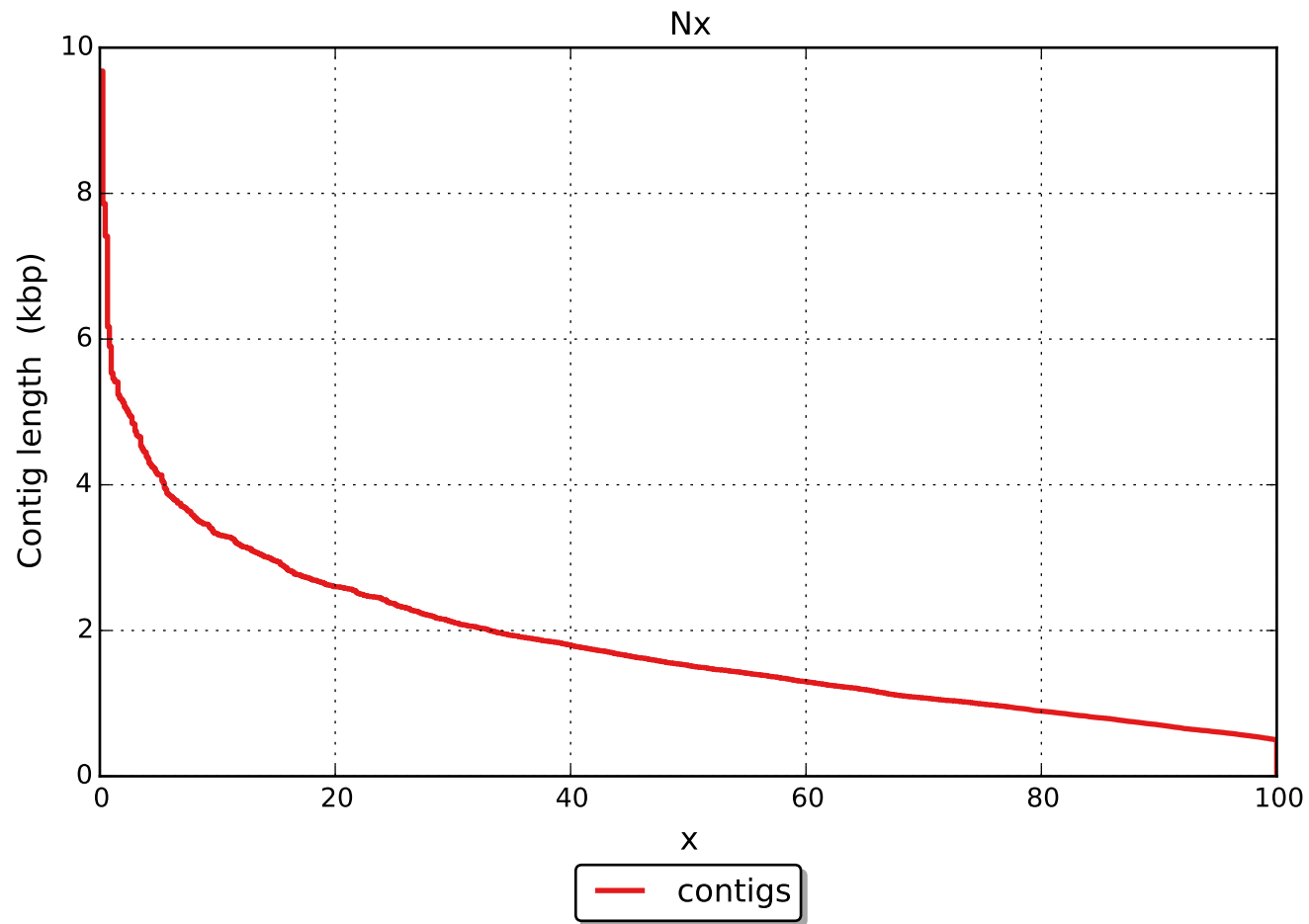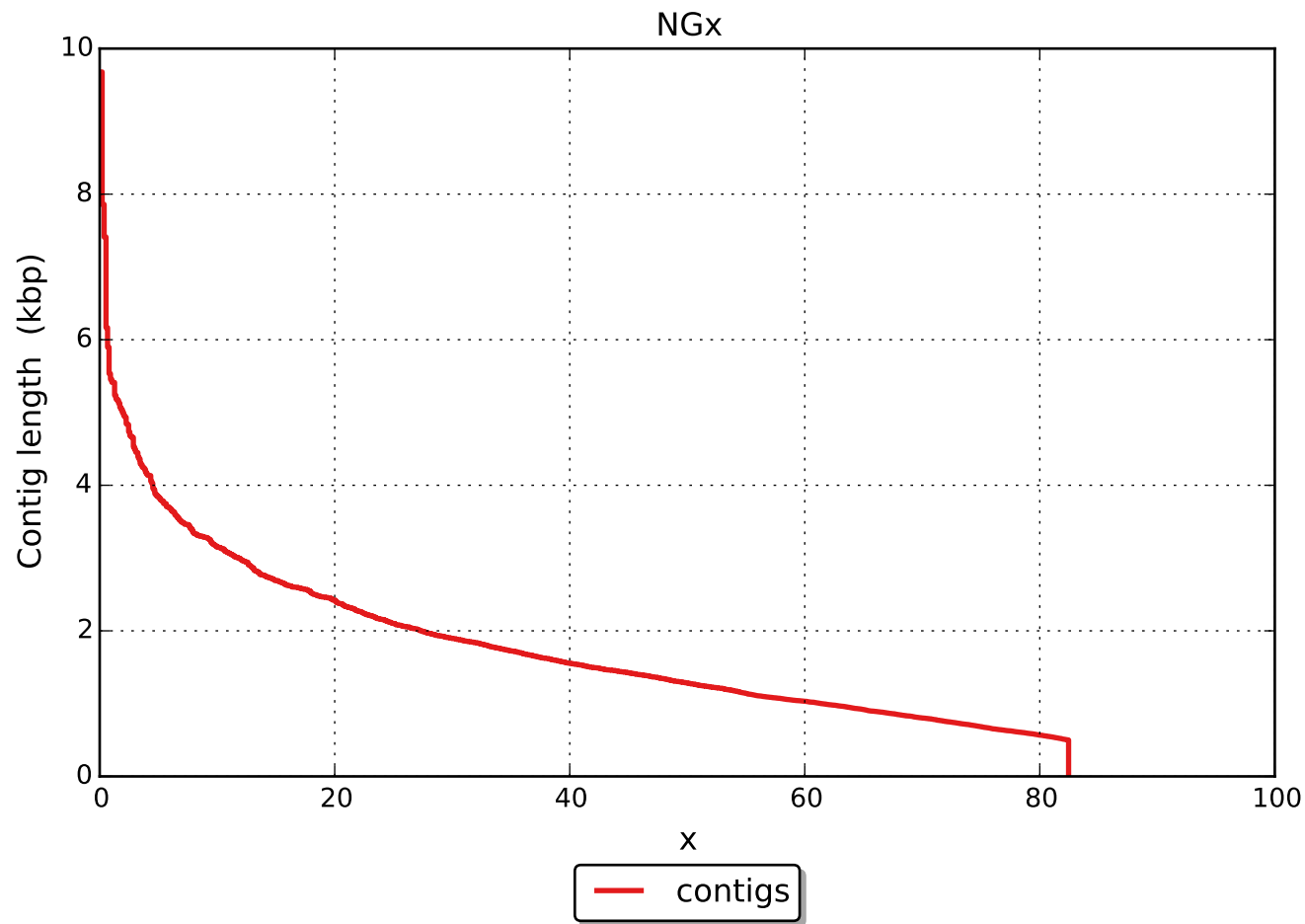
Misassemblies report

	contigs
# misassemblies	40
# relocations	39
# translocations	0
# inversions	1
# misassembled contigs	39
Misassembled contigs length	114373
# local misassemblies	8
# mismatches	35589
# indels	67
# short indels	65
# long indels	2
Indels length	169

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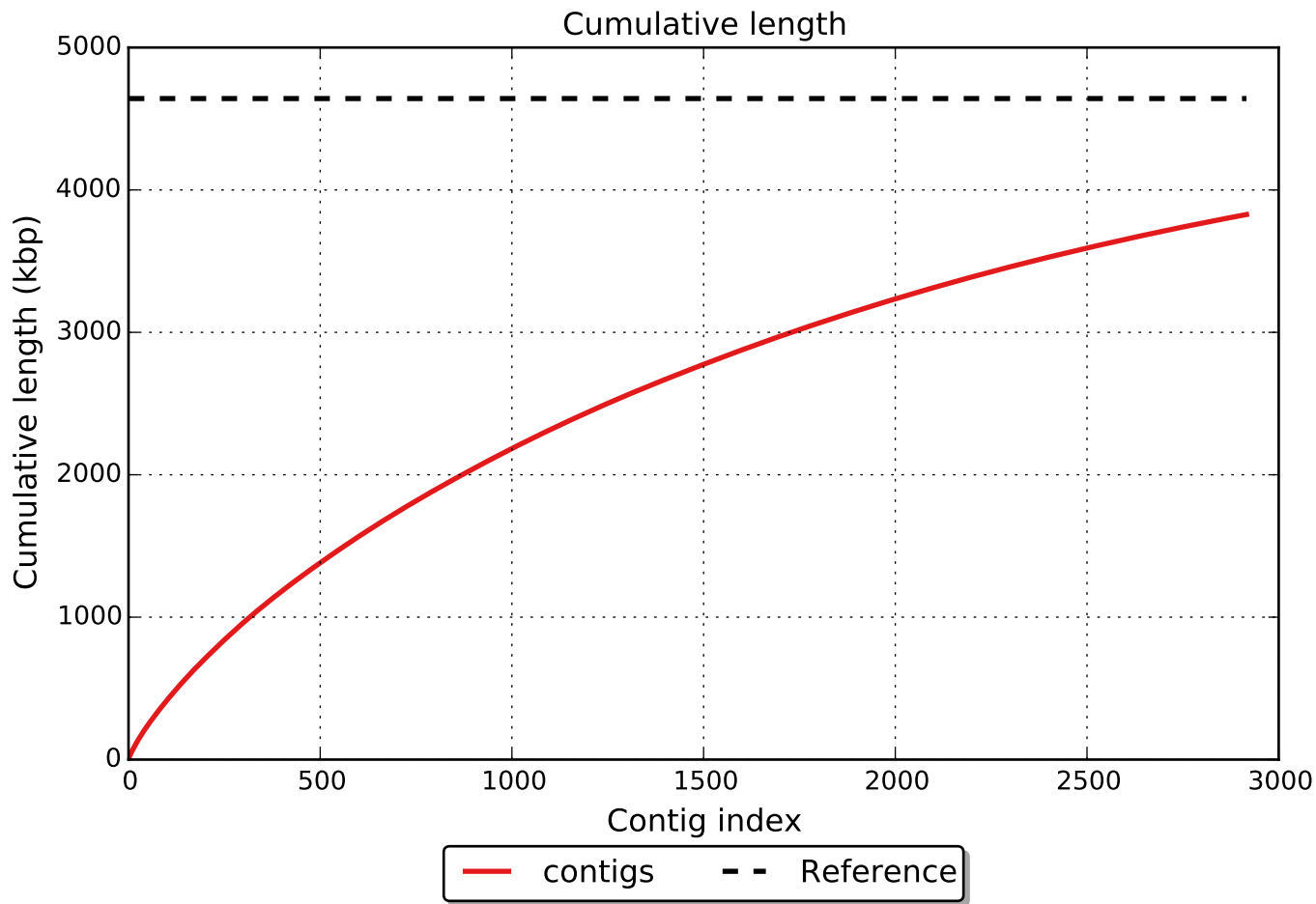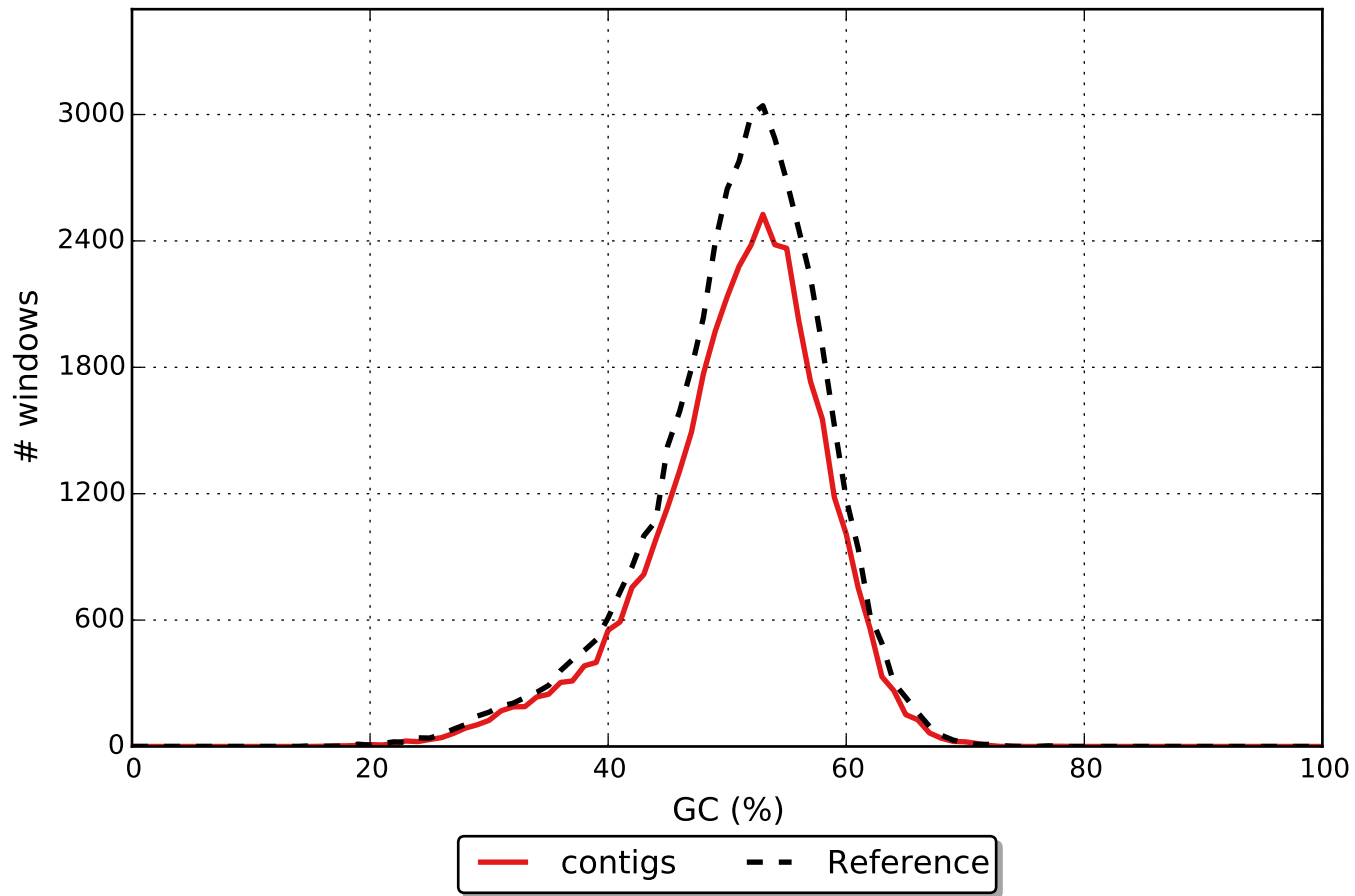(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	0
Partially unaligned length	60
# 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).
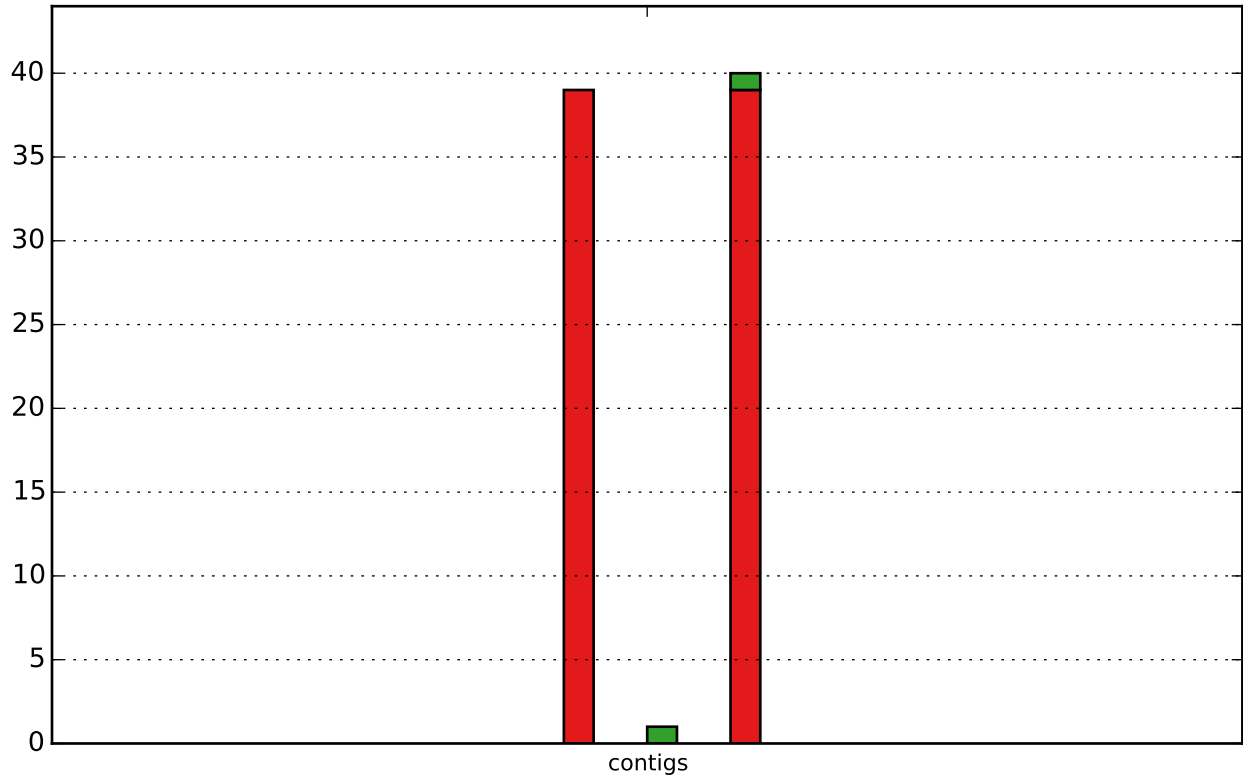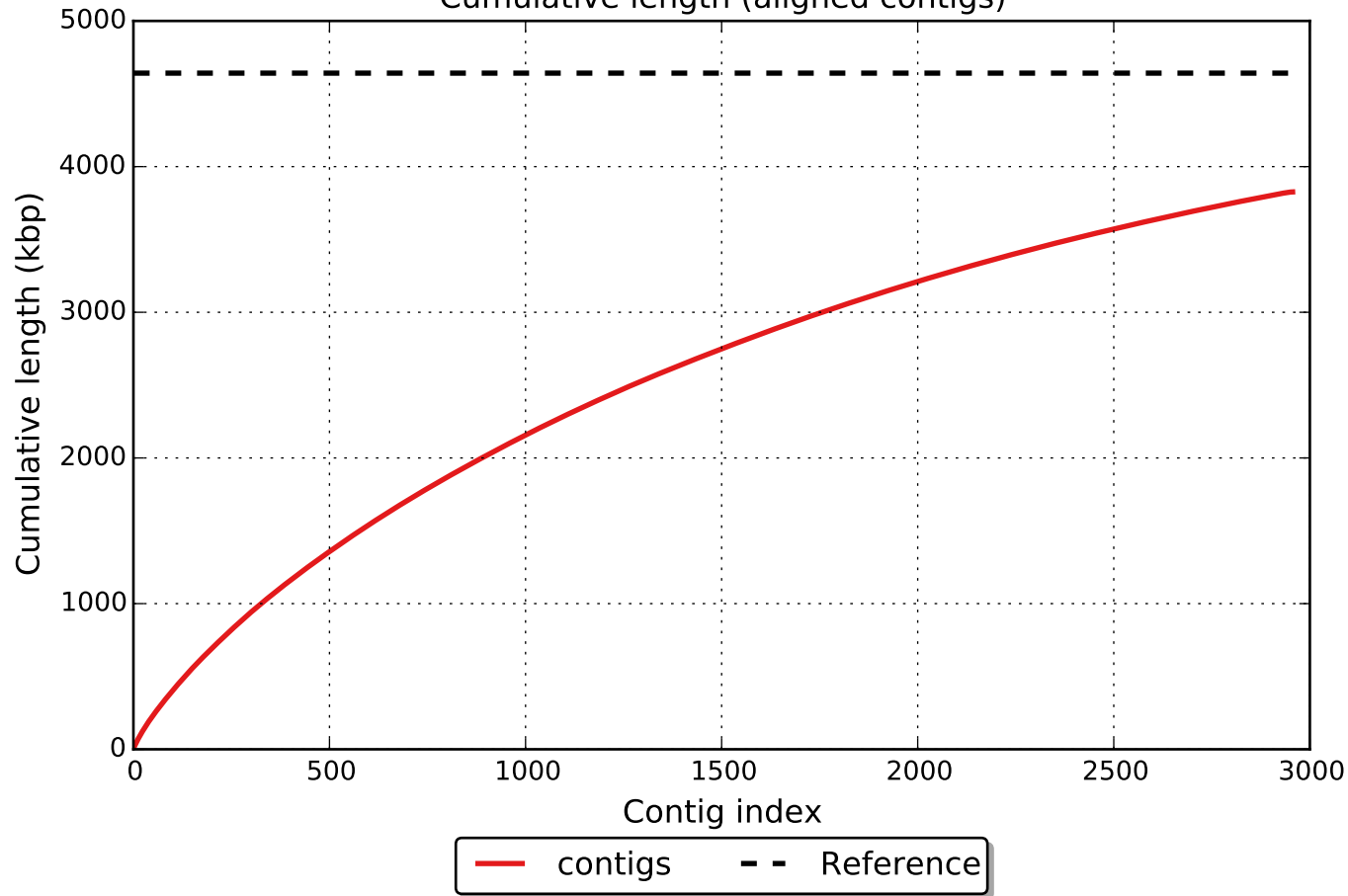
Nx

Contig length (kbp) vs x

contigs

NGx

Cumulative length

GC content

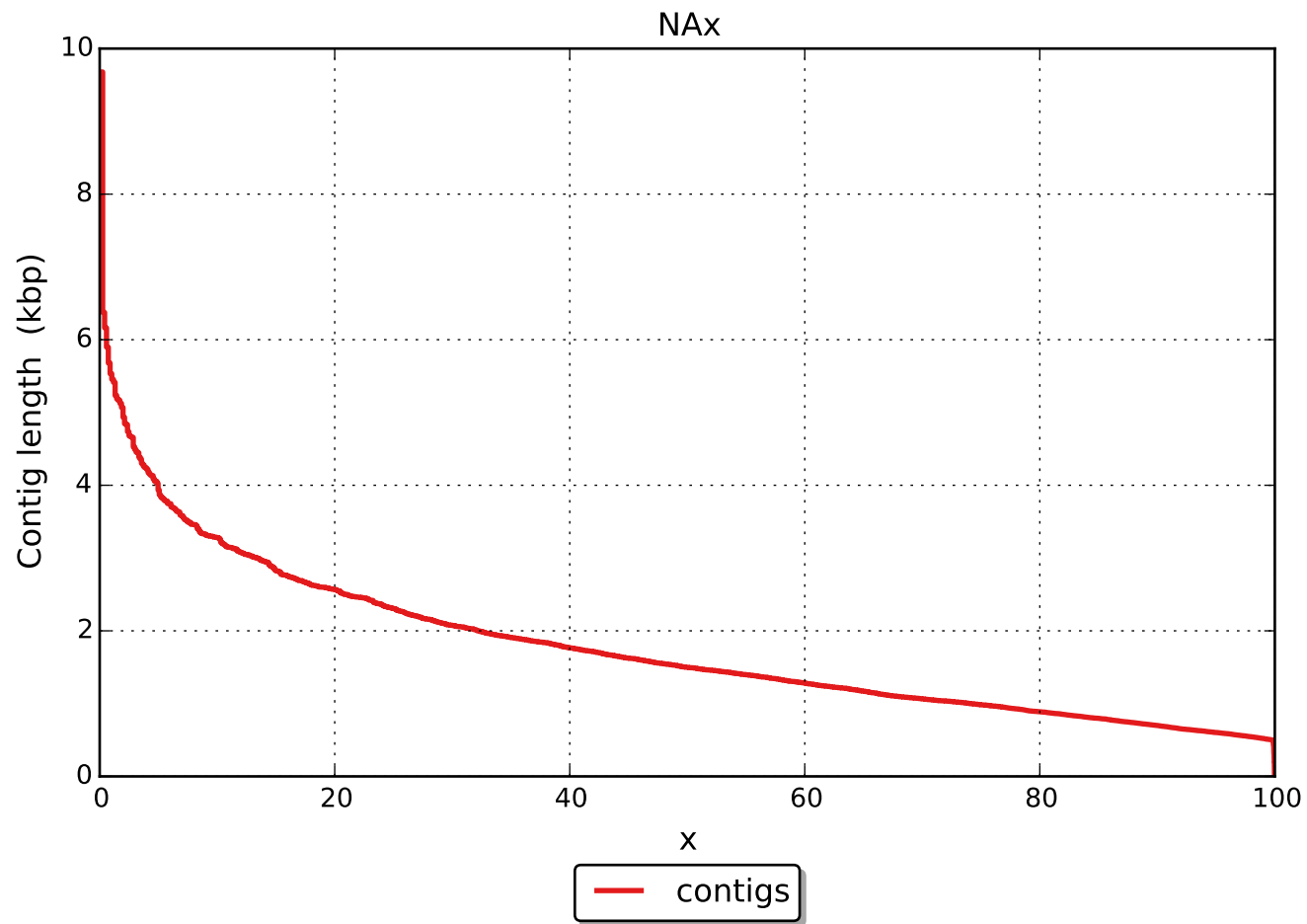# windows vs GC (%)

Legend: contigs (red solid line), Reference (black dashed line)

Misassemblies

Cumulative length (aligned contigs)

NAx

Contig length (kbp)

x

contigs