Report

	EF.contigs	contigs
# contigs (>= 0 bp)	12	189
# contigs (>= 1000 bp)	12	49
# contigs (>= 5000 bp)	10	32
# contigs (>= 10000 bp)	8	23
# contigs (>= 25000 bp)	5	17
# contigs (>= 50000 bp)	2	16
Total length (>= 0 bp)	3153250	3098278
Total length (>= 1000 bp)	3153250	3073892
Total length (>= 5000 bp)	3144227	3025806
Total length (>= 10000 bp)	3124517	2961855
Total length (>= 25000 bp)	3086414	2867451
Total length (>= 50000 bp)	2991823	2831946
# contigs	12	53
Largest contig	2772839	542117
Total length	3153250	3076511
Reference length	3168410	3168410
GC (%)	37.76	37.63
Reference GC (%)	37.70	37.70
N50	2772839	179830
NG50	2772839	179830
N75	2772839	132475
NG75	2772839	125623
L50	1	5
LG50	1	5
L75	1	10
LG75	1	11
# misassemblies	5	1
# misassembled contigs	4	1
Misassembled contigs length	287004	19277
# local misassemblies	1	0
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 0 part	1 + 1 part
Unaligned length	0	6126
Genome fraction (%)	98.189	96.797
Duplication ratio	1.014	1.001
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	1.96	10.73
# indels per 100 kbp	15.72	4.53
Largest alignment	2772839	542117
Total aligned length	3153250	3070385
NA50	2772839	179830
NGA50	2772839	179830
NA75	2772839	132475
NGA75	2772839	125623
LA50	1	5
LGA50	1	5
LA75	1	10
LGA75	1	11

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

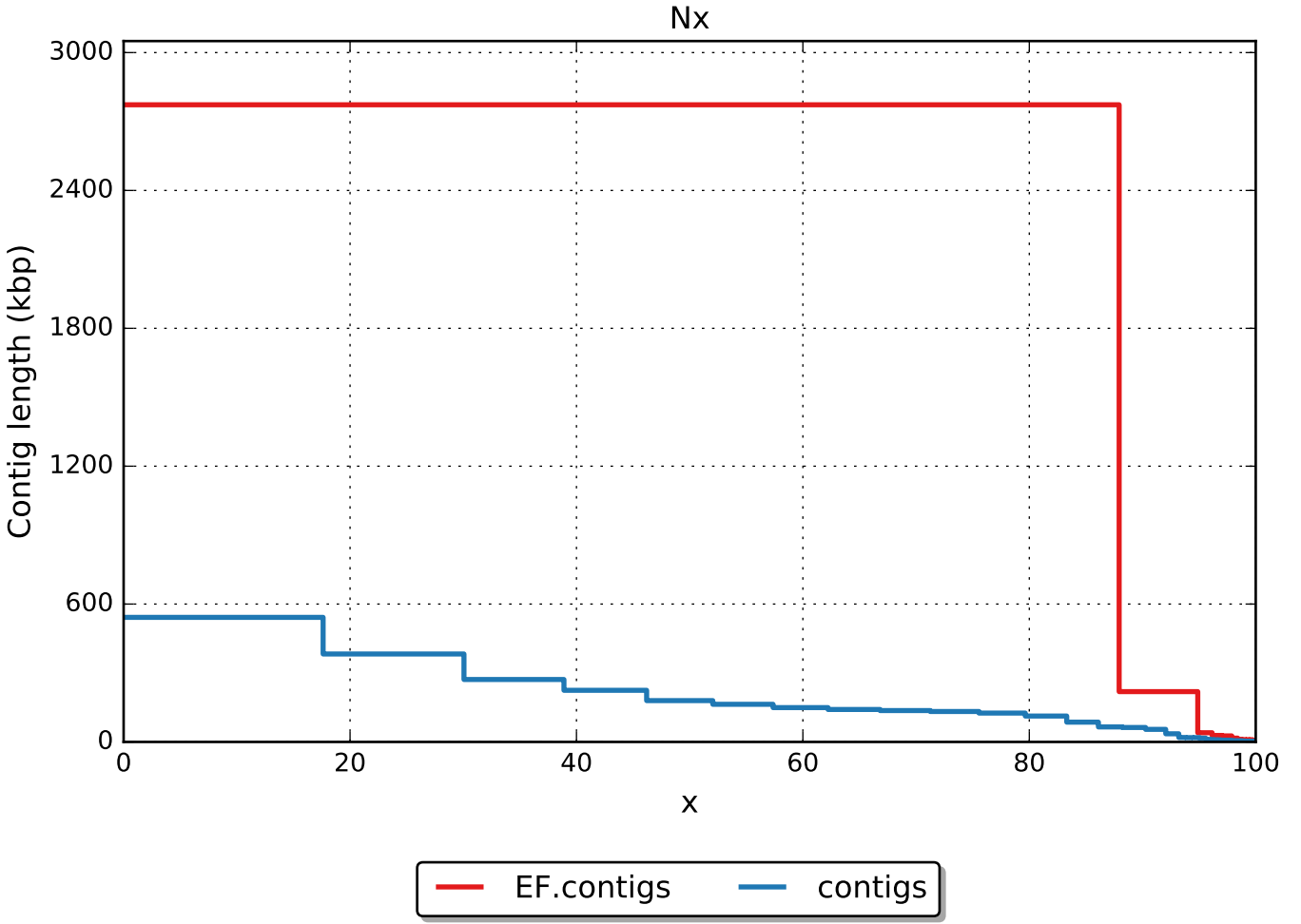
	EF.contigs	contigs
# misassemblies	5	1
# relocations	3	0
# translocations	2	1
# inversions	0	0
# misassembled contigs	4	1
Misassembled contigs length	287004	19277
# local misassemblies	1	0
# unaligned mis. contigs	0	0
# mismatches	61	329
# indels	489	139
# indels (<= 5 bp)	481	131
# indels (> 5 bp)	8	8
Indels length	636	268

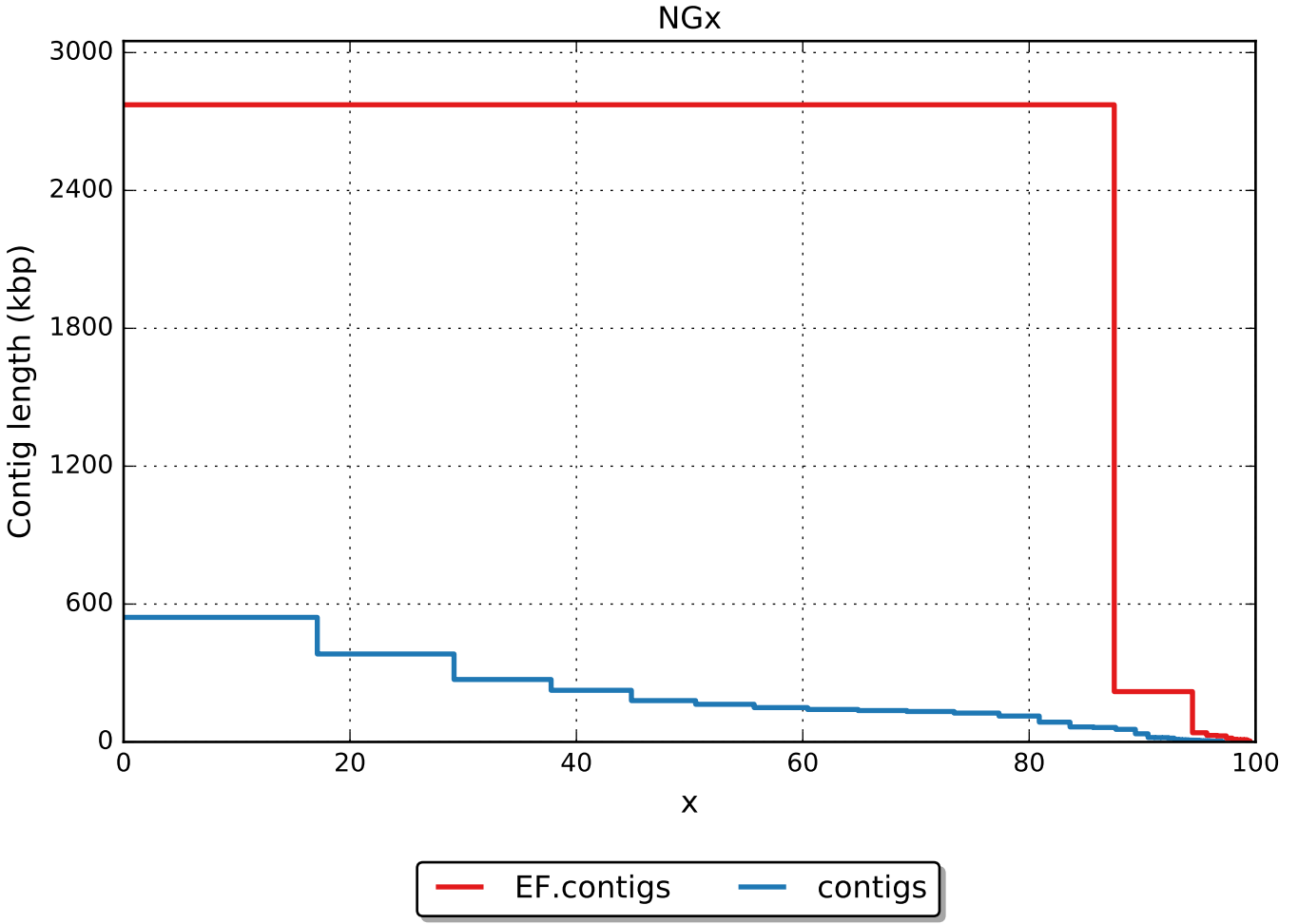
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

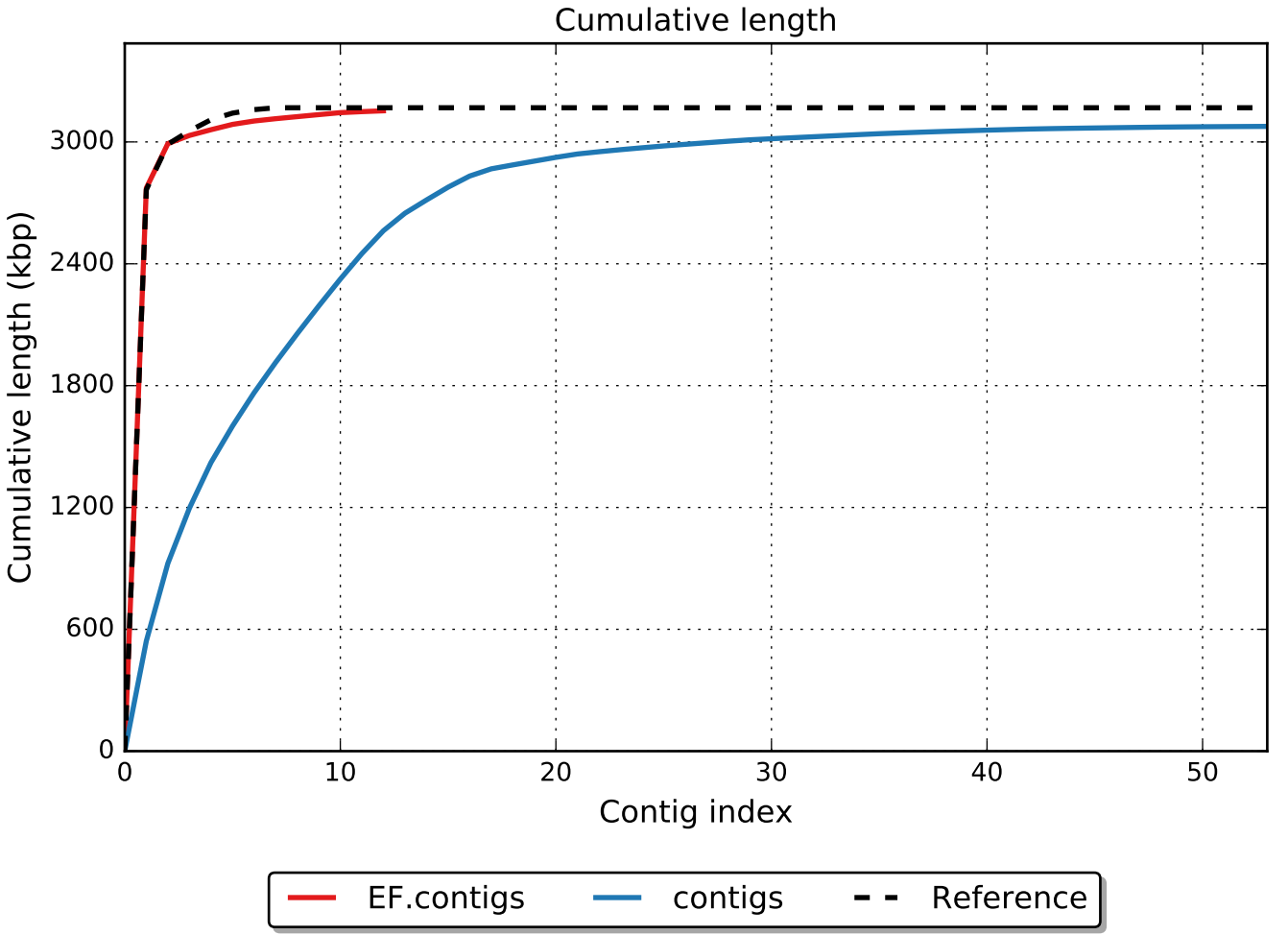
Unaligned report

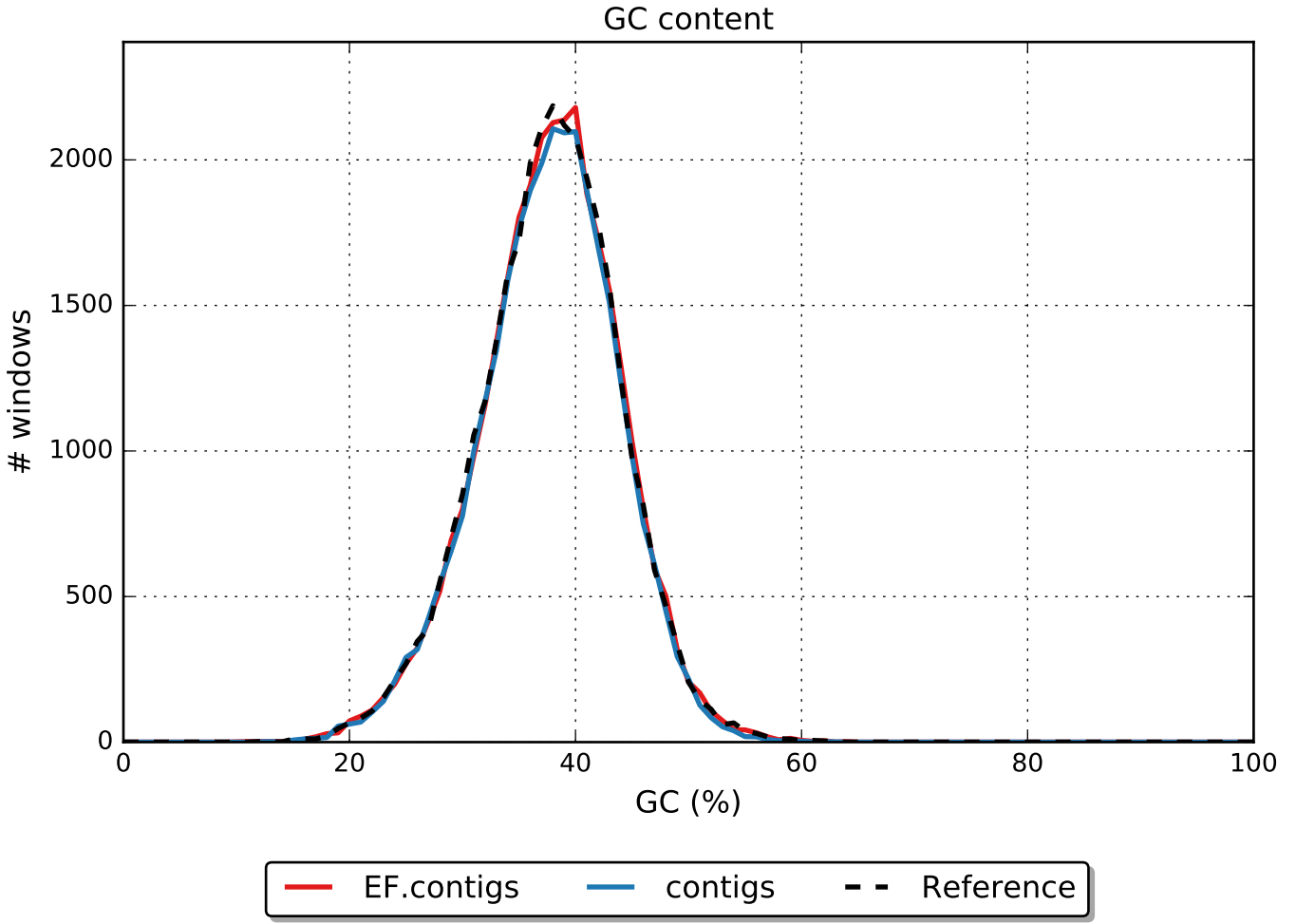
	EF.contigs	contigs
# fully unaligned contigs	0	1
Fully unaligned length	0	3214
# partially unaligned contigs	0	1
Partially unaligned length	0	2912
# N's	0	0

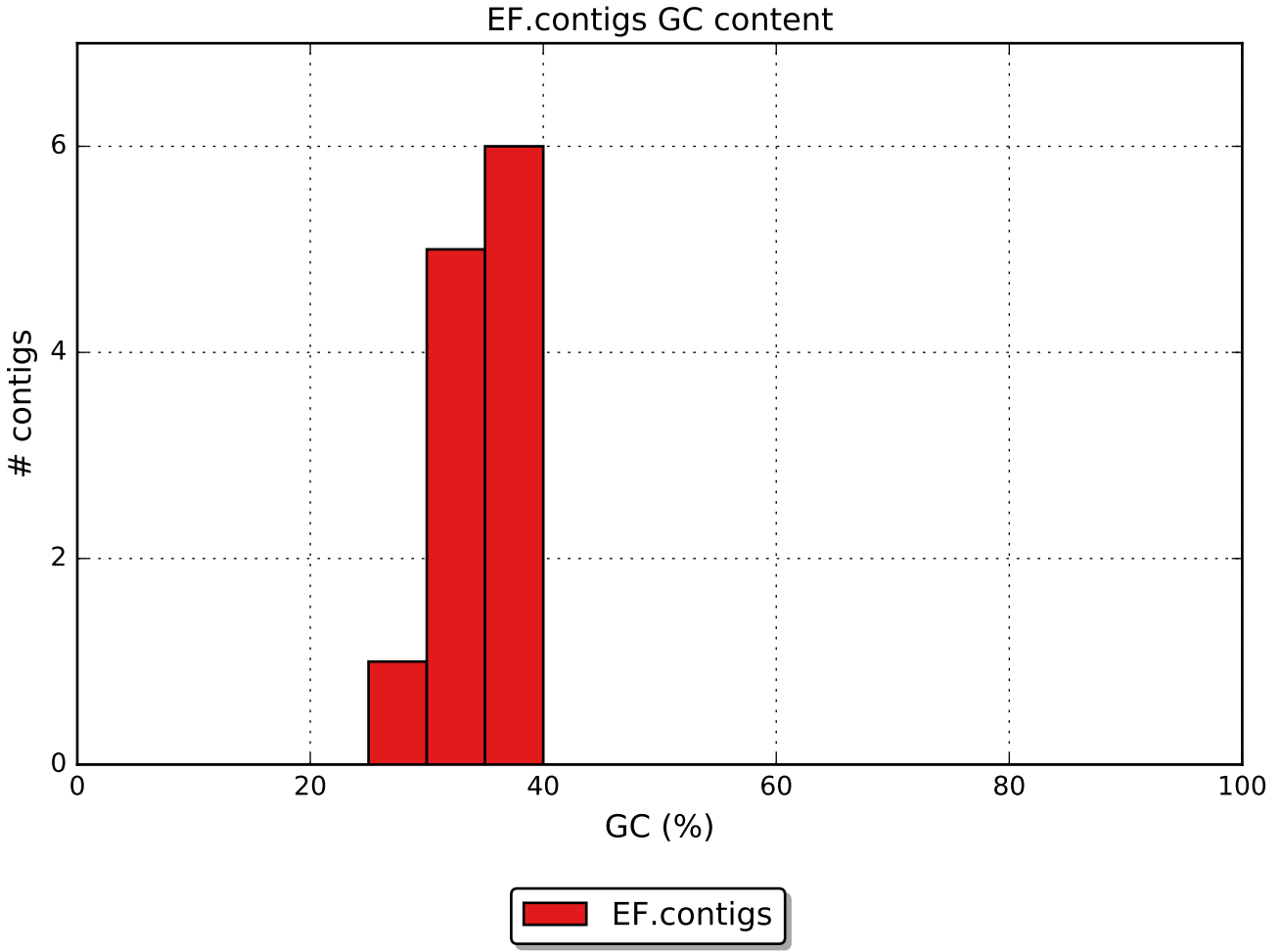
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

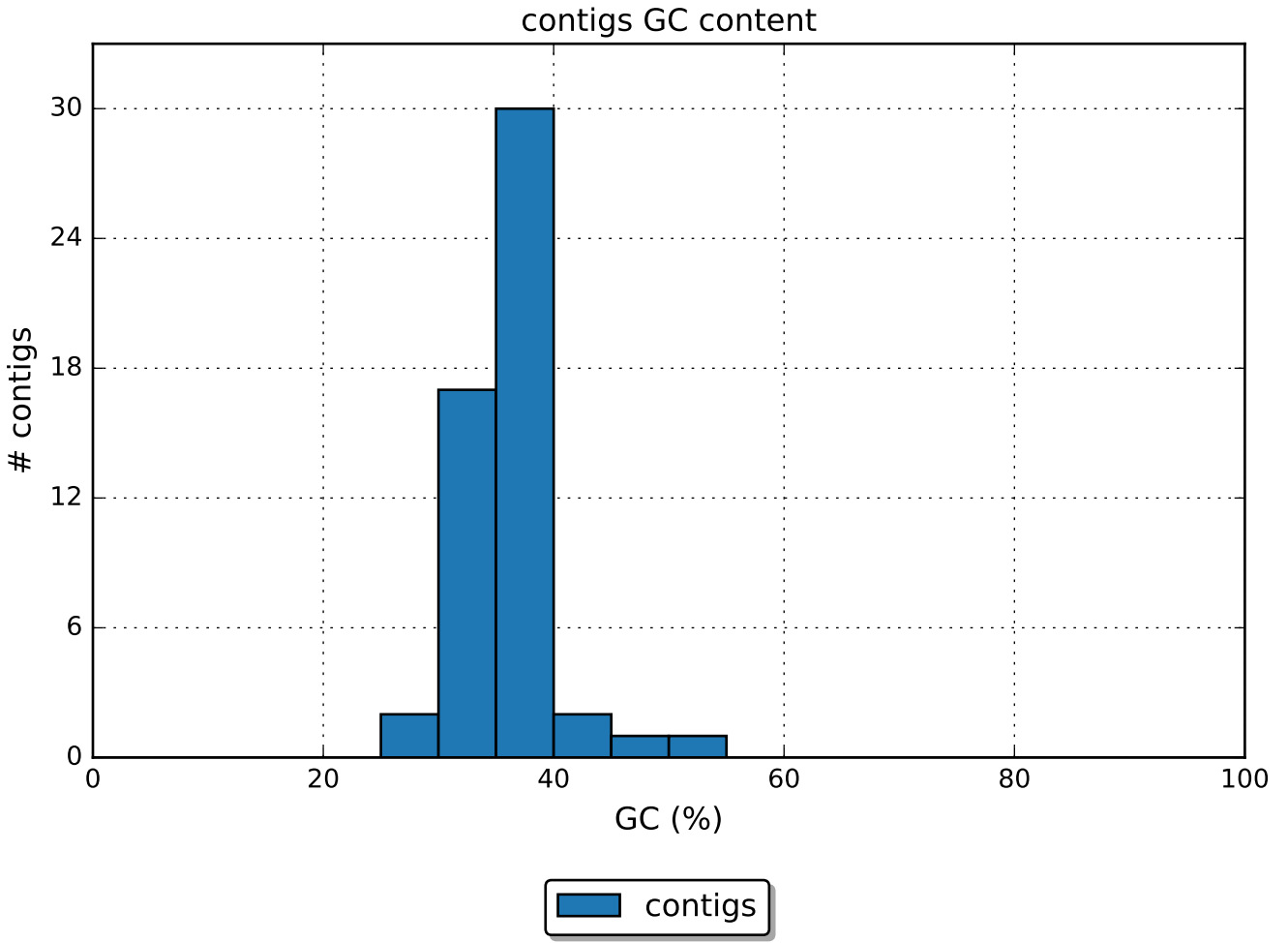

Nx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
EF.contigs
contigs

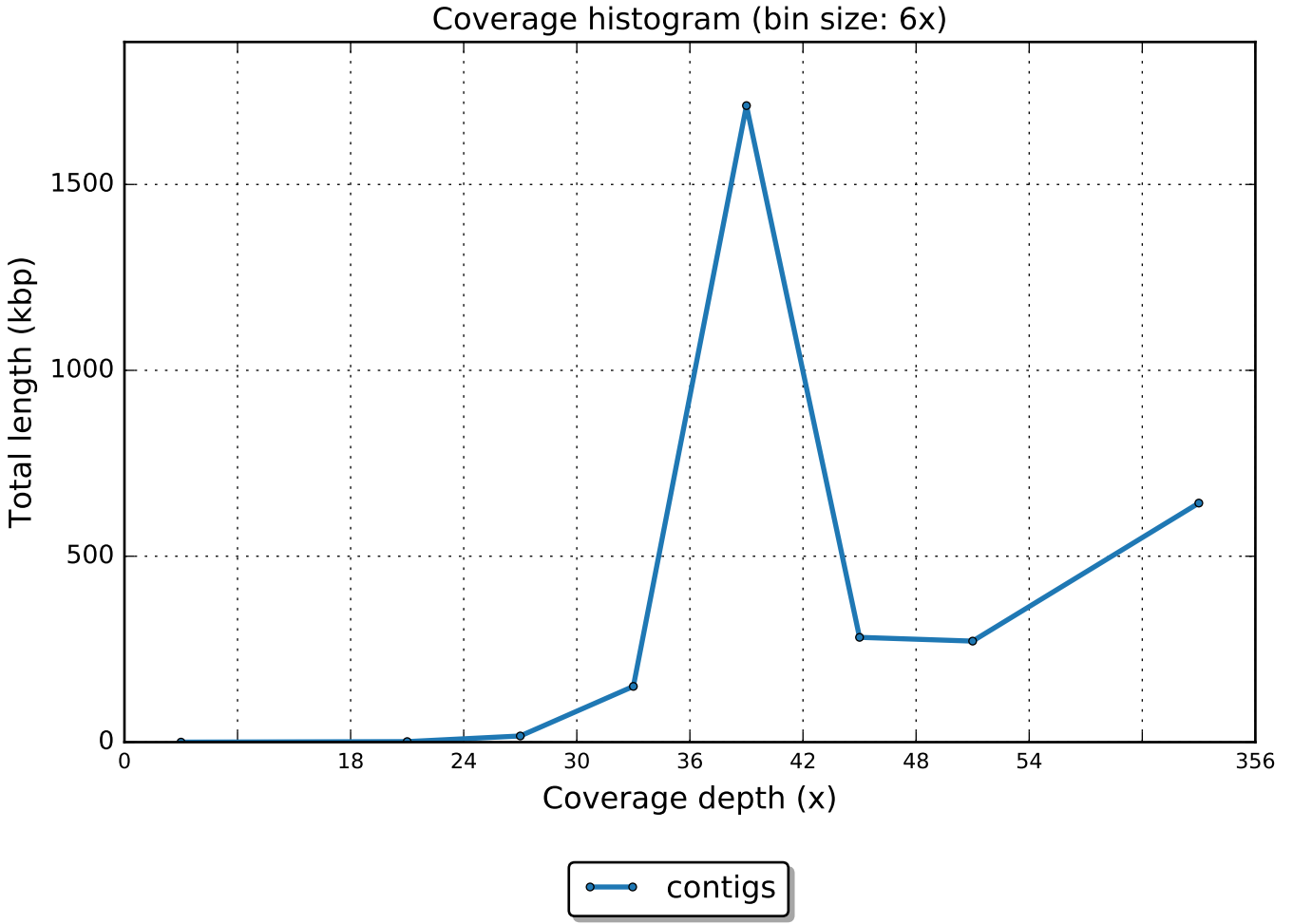

NGx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
EF.contigs
contigs

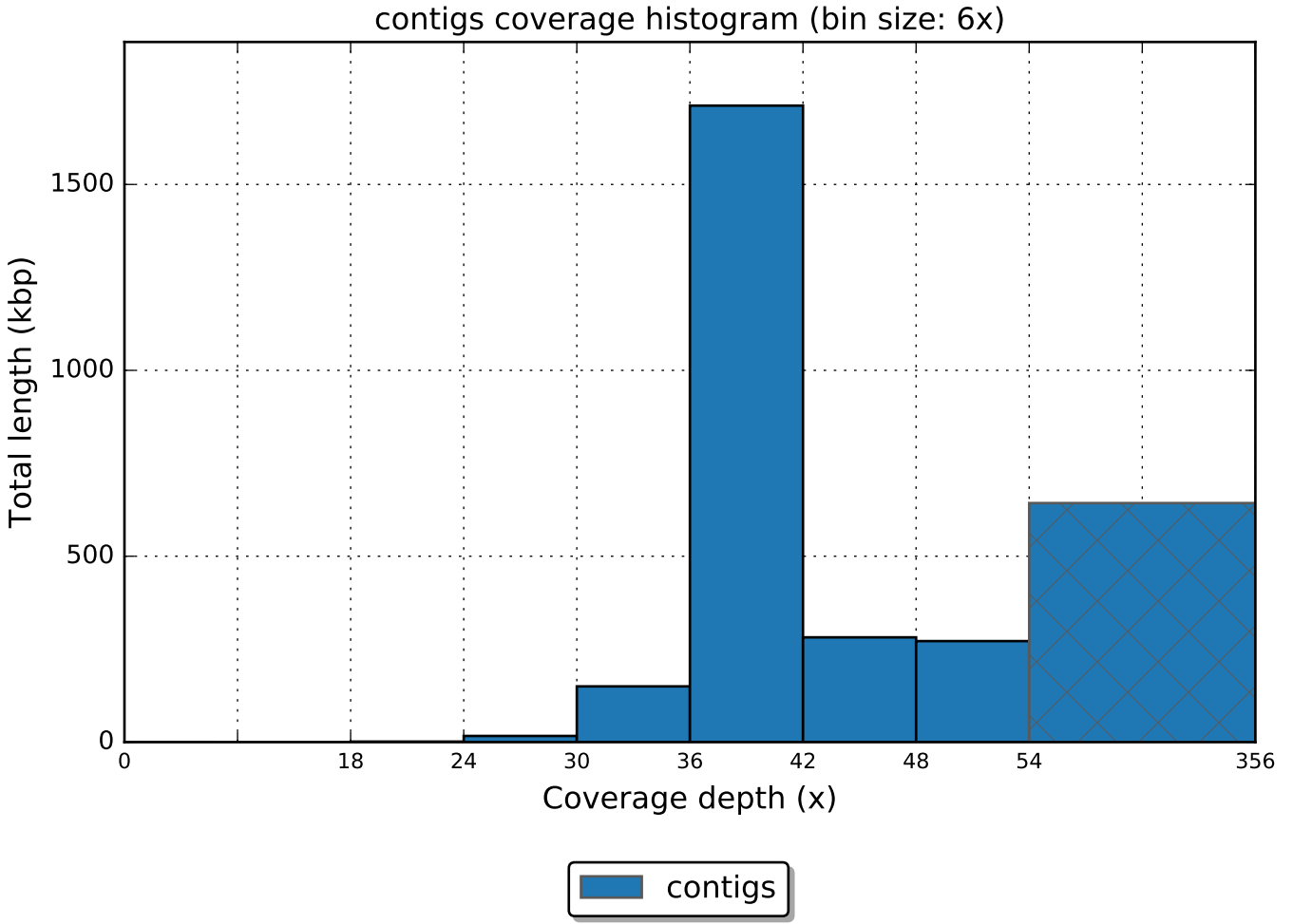

Cumulative length
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
10
20
30
40
50
Contig index
EF.contigs
contigs
Reference

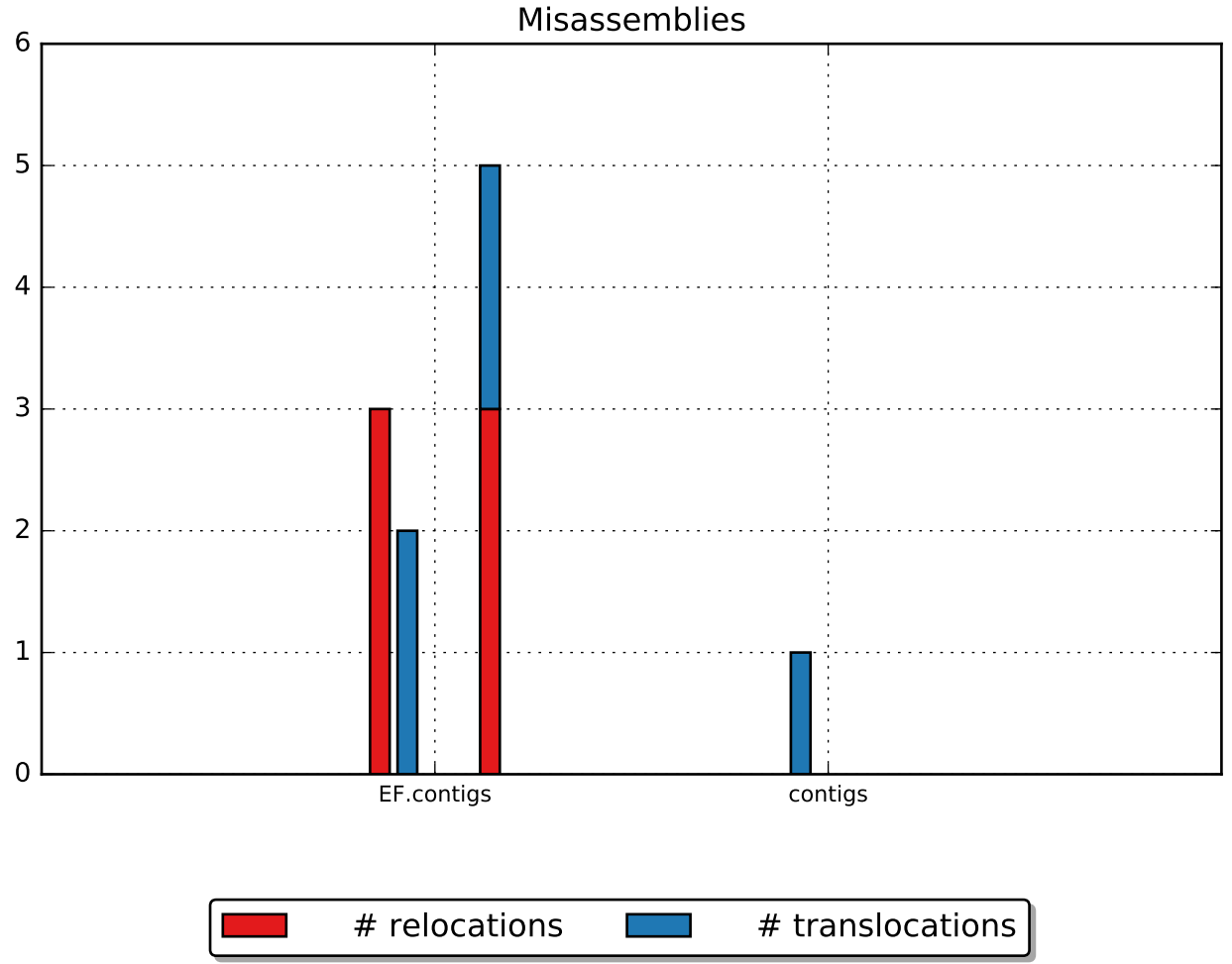

GC content
windows
GC (%)
0
500
1000
1500
2000
0
20
40
60
80
100
EF.contigs
contigs
Reference

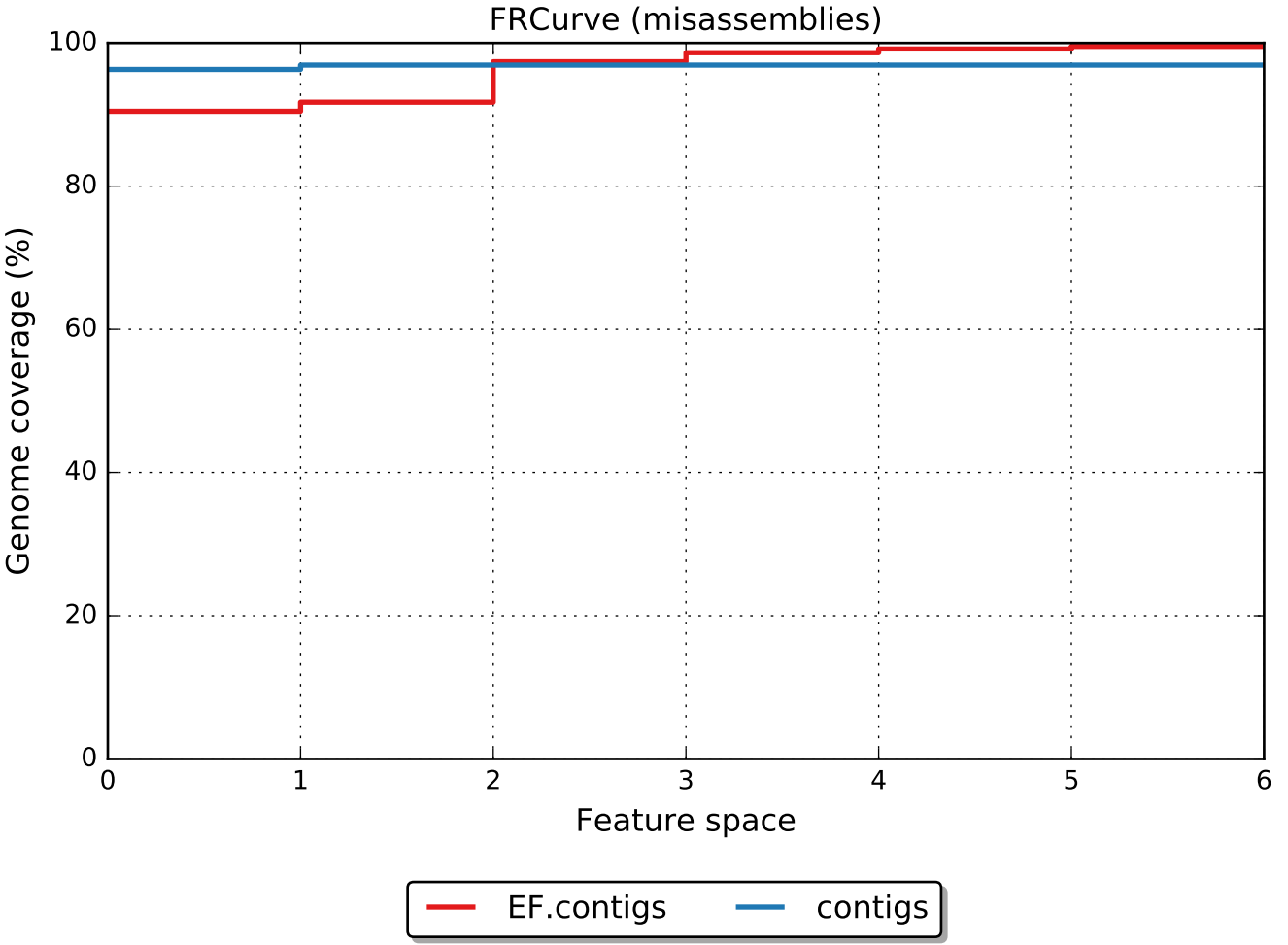

EF.contigs GC content
contigs
GC (%)
0
2
4
6
0
20
40
60
80
100
EF.contigs

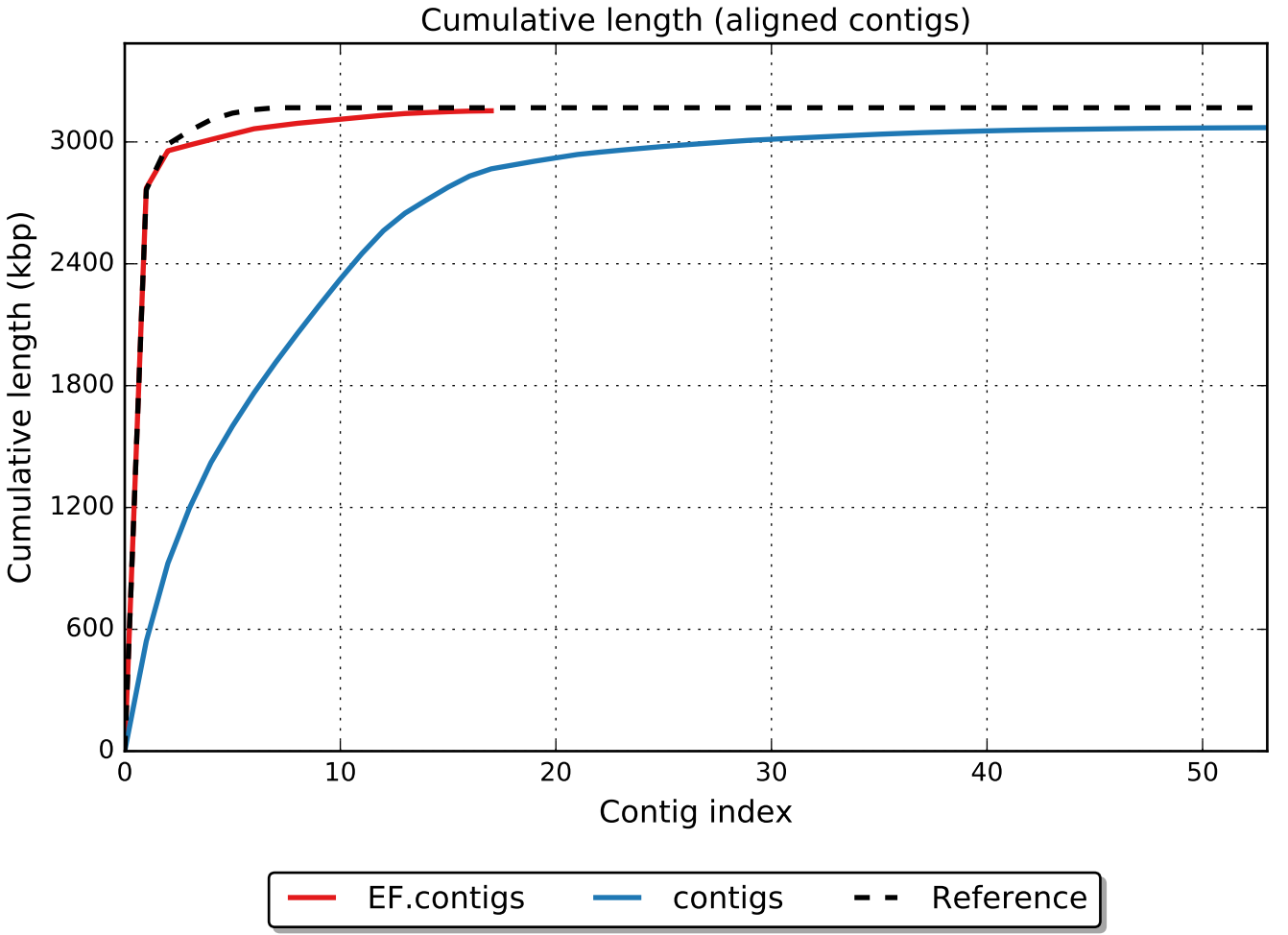

contigs GC content
contigs
GC (%)
0
6
12
18
24
30
0
20
40
60
80
100
contigs

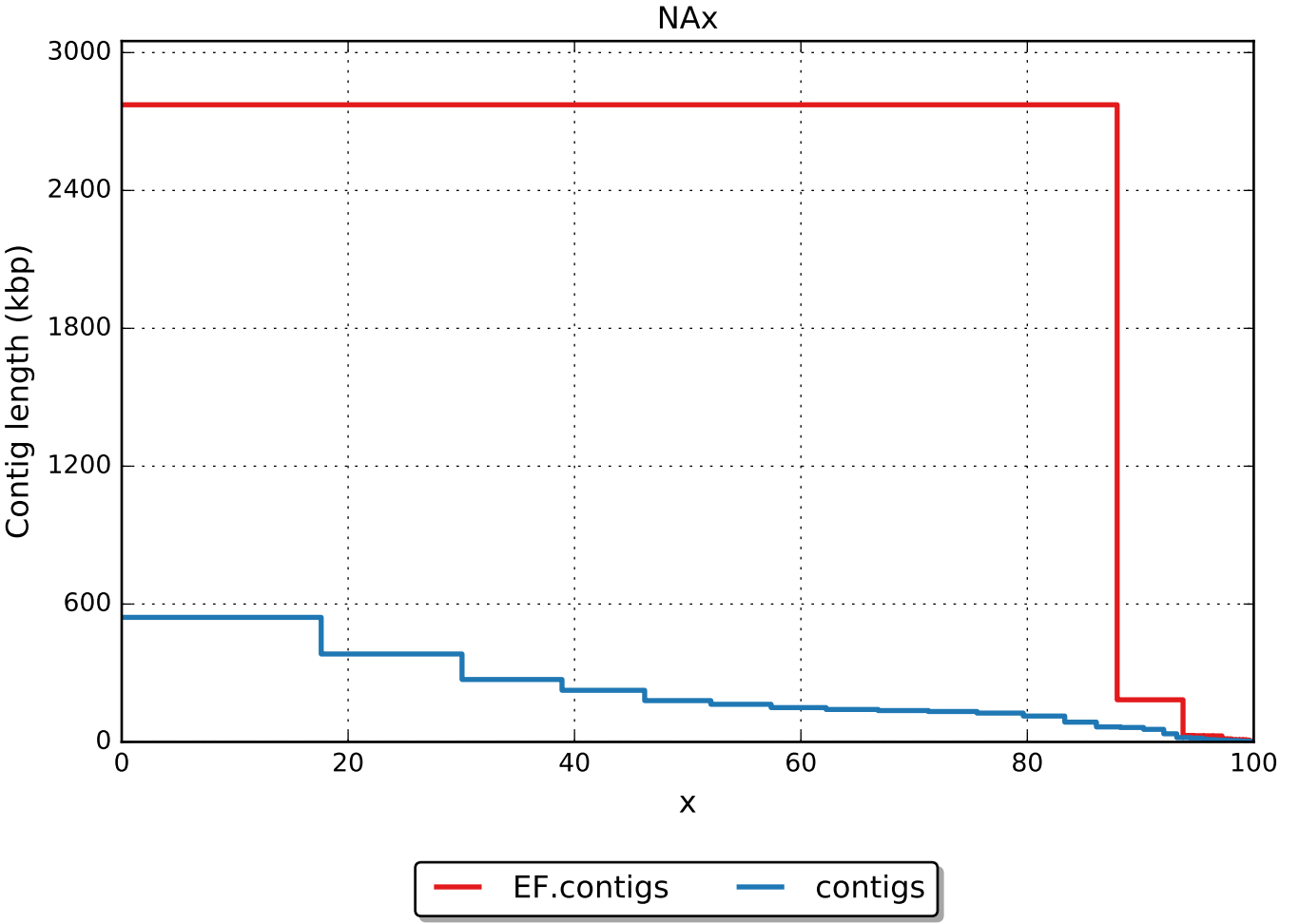

Coverage histogram (bin size: 6x)
Total length (kbp)
0
500
1000
1500
0
18
24
30
36
42
48
54
356
Coverage depth (x)
contigs

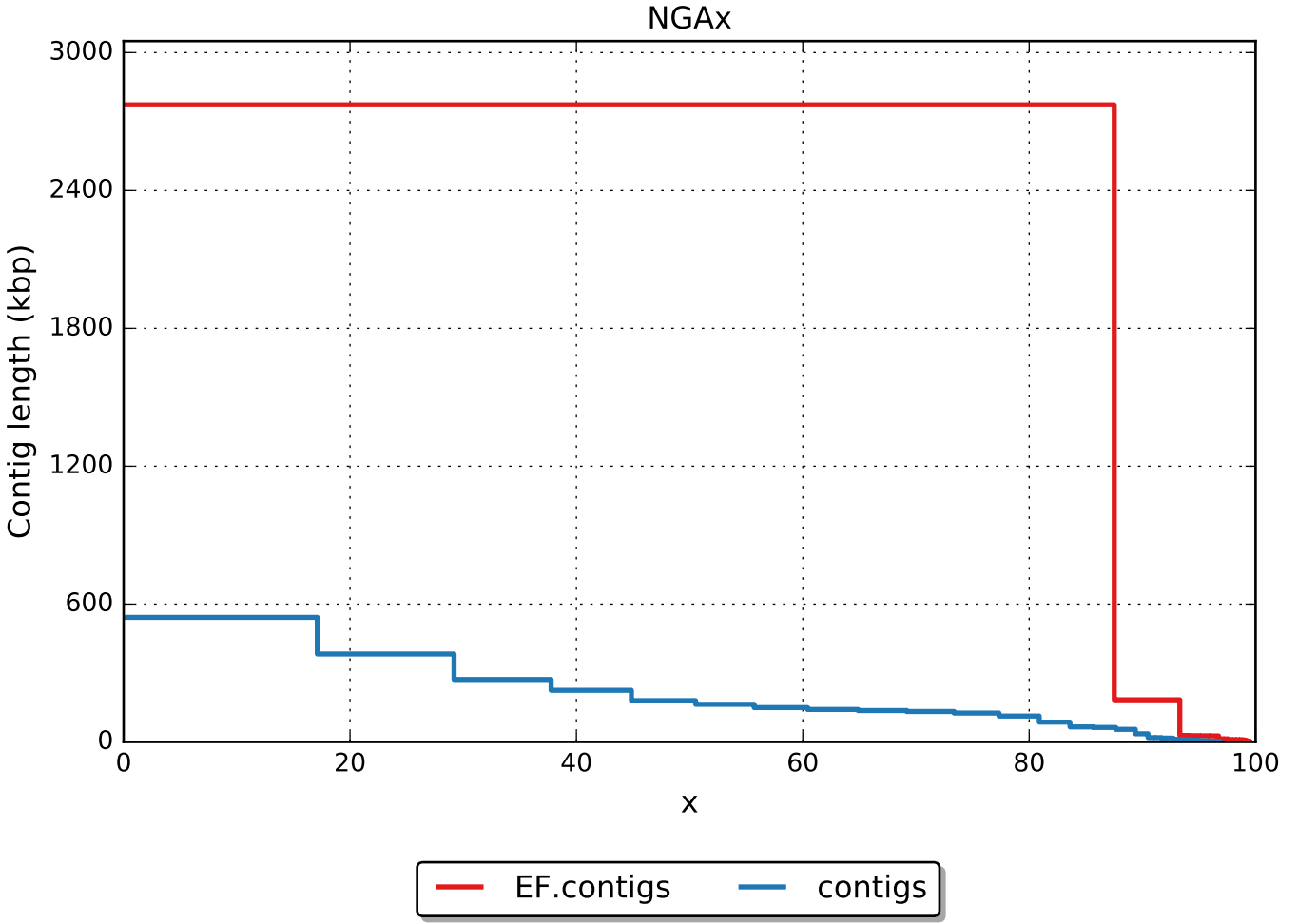

contigs coverage histogram (bin size: 6x)
Total length (kbp)
0
500
1000
1500
0
18
24
30
36
42
48
54
356
Coverage depth (x)
contigs

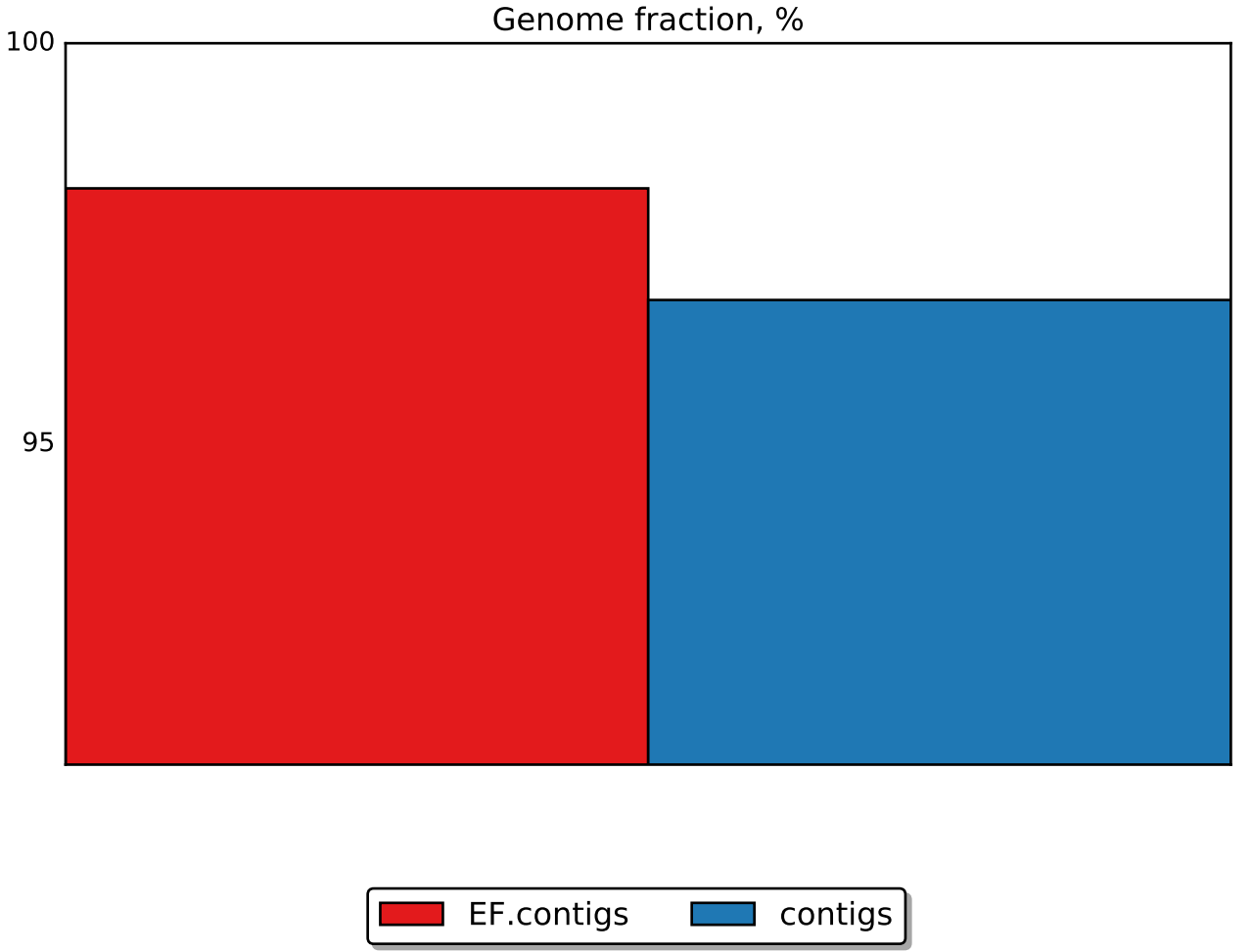

Misassemblies
6
5
4
3
2
1
0
EF.contigs
contigs
relocations
translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
3
4
5
6
Feature space
EF.contigs
contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
600
1200
1800
2400
3000
0
10
20
30
40
50
Contig index
EF.contigs
contigs
Reference


NAx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
EF.contigs
contigs


NGAx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
EF.contigs
contigs


Genome fraction, %
100
95
EF.contigs
contigs