Report

	low_contigs	high_contigs	low_contigs 1	high_contigs 1
# contigs (>= 0 bp)	128	1	305	16
# contigs (>= 1000 bp)	4	1	0	7
# contigs (>= 5000 bp)	0	1	0	7
# contigs (>= 10000 bp)	0	1	0	4
# contigs (>= 25000 bp)	0	1	0	1
# contigs (>= 50000 bp)	0	1	0	0
Total length (>= 0 bp)	49818	100000	56973	100309
Total length (>= 1000 bp)	5313	100000	0	99584
Total length (>= 5000 bp)	0	100000	0	99584
Total length (>= 10000 bp)	0	100000	0	81134
Total length (>= 25000 bp)	0	100000	0	33235
Total length (>= 50000 bp)	0	100000	0	0
# contigs	20	1	11	7
Largest contig	1737	100000	998	33235
Total length	15922	100000	7243	99584
Reference length	4639675	4639675	4639675	4639675
GC (%)	51.21	52.59	50.71	52.58
Reference GC (%)	50.79	50.79	50.79	50.79
N50	718	100000	632	19911
N75	635	100000	542	13440
L50	8	1	5	2
L75	13	1	8	4
# misassemblies	1	0	0	0
# misassembled contigs	1	0	0	0
Misassembled contigs length	1084	0	0	0
# local misassemblies	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part
Unaligned length	0	0	0	0
Genome fraction (%)	0.343	2.155	0.156	2.145
Duplication ratio	1.000	1.000	1.000	1.001
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	31.40	0.00	0.00	0.00
# indels per 100 kbp	0.00	0.00	0.00	0.00
Largest alignment	1737	100000	998	33235
Total aligned length	15922	100000	7243	99584
NA50	715	100000	632	19911
NGA50	-	-	-	-
NA75	587	100000	542	13440
LA50	8	1	5	2
LA75	14	1	8	4

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

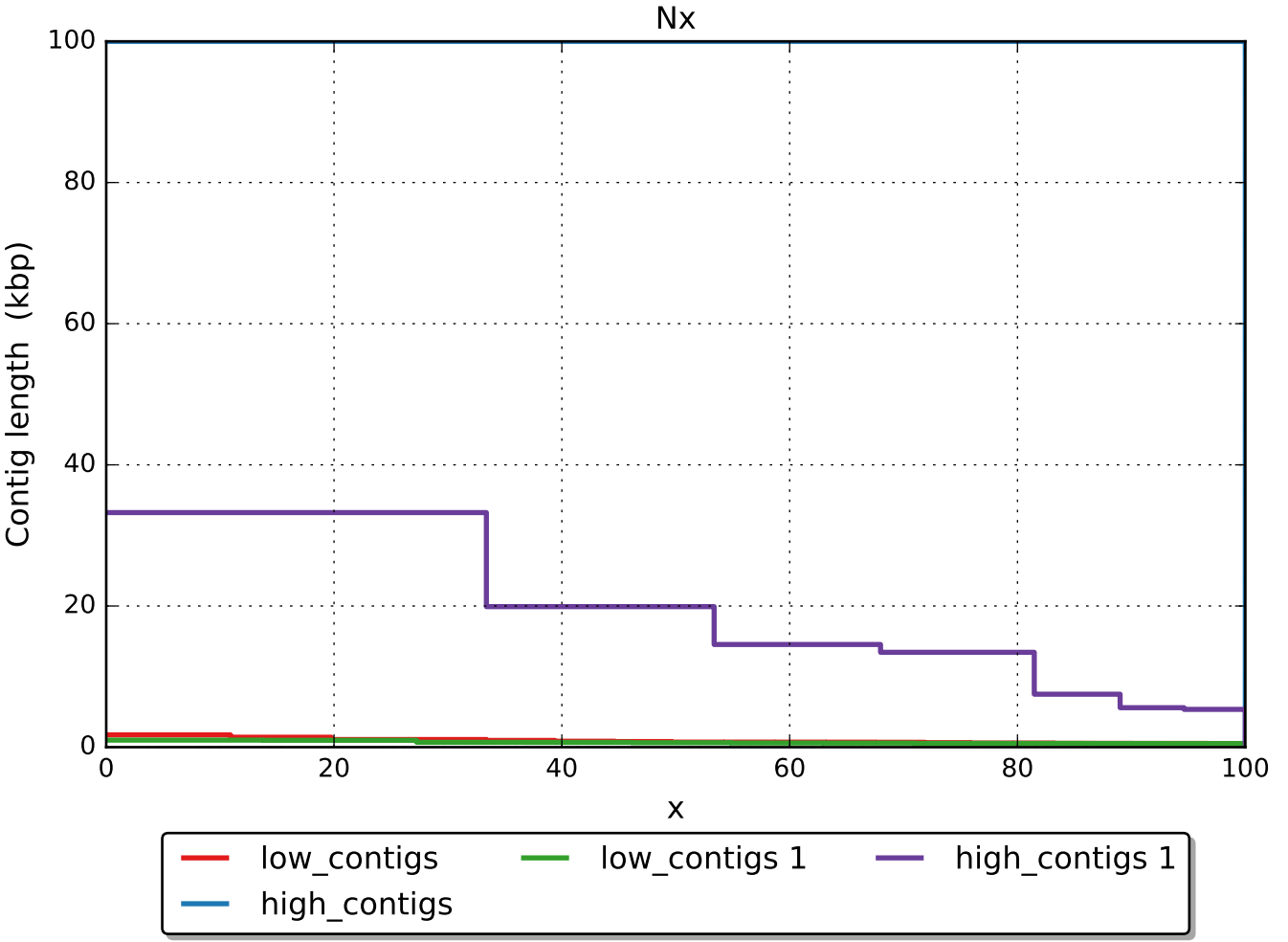
	low_contigs	high_contigs	low_contigs 1	high_contigs 1
# misassemblies	1	0	0	0
# relocations	1	0	0	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# misassembled contigs	1	0	0	0
Misassembled contigs length	1084	0	0	0
# local misassemblies	0	0	0	0
# mismatches	5	0	0	0
# indels	0	0	0	0
# short indels	0	0	0	0
# long indels	0	0	0	0
Indels length	0	0	0	0

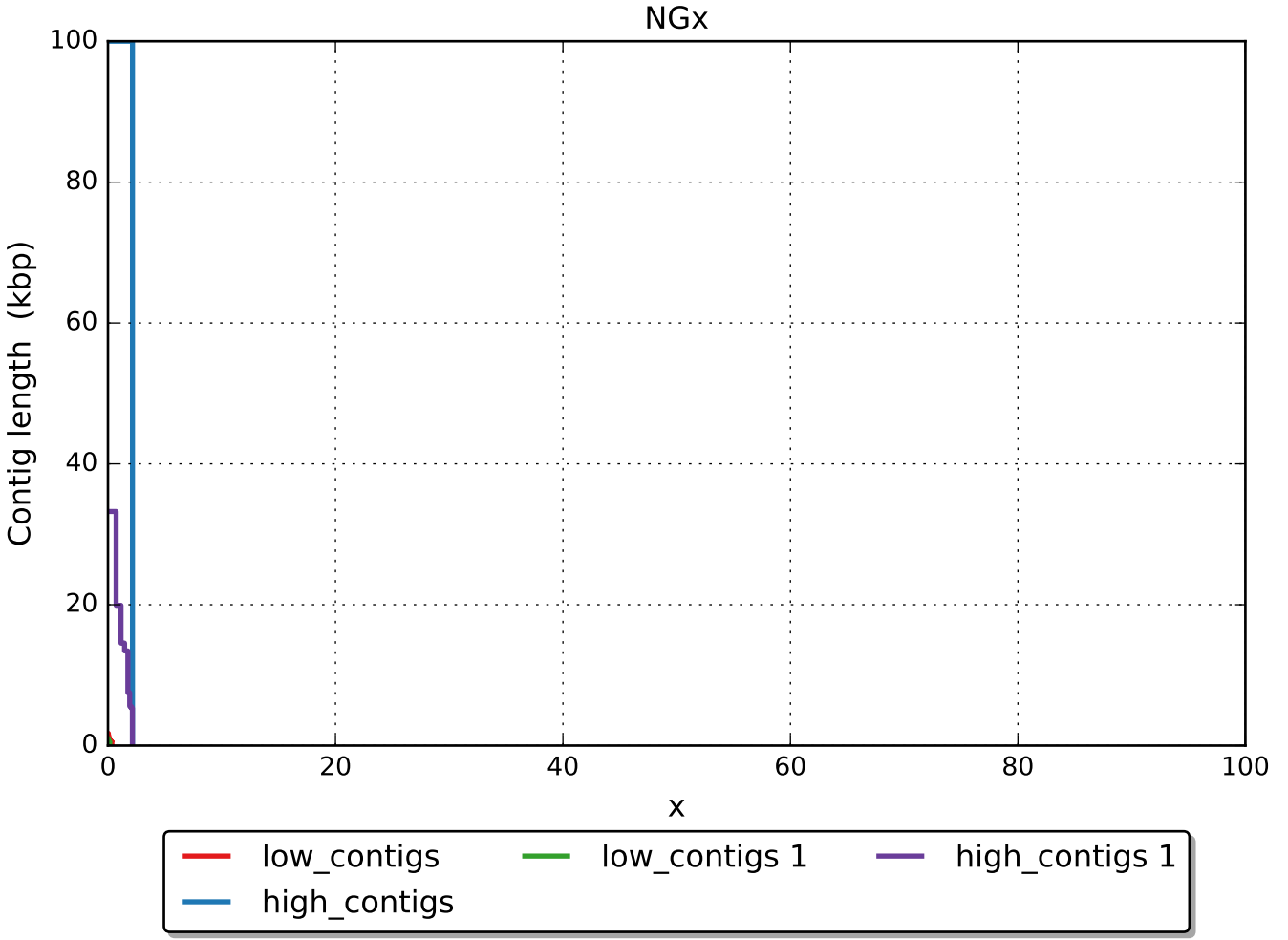
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

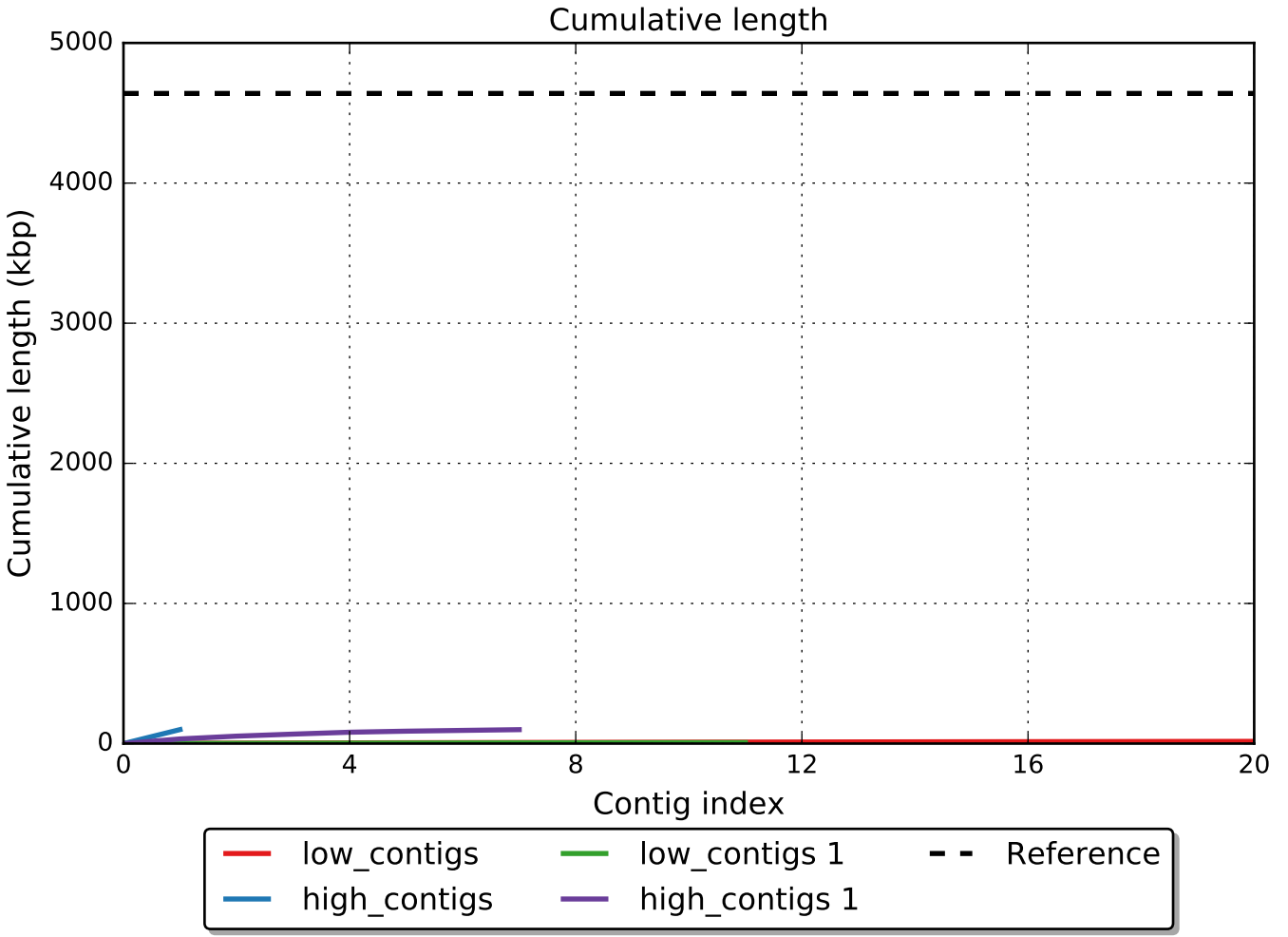
Unaligned report

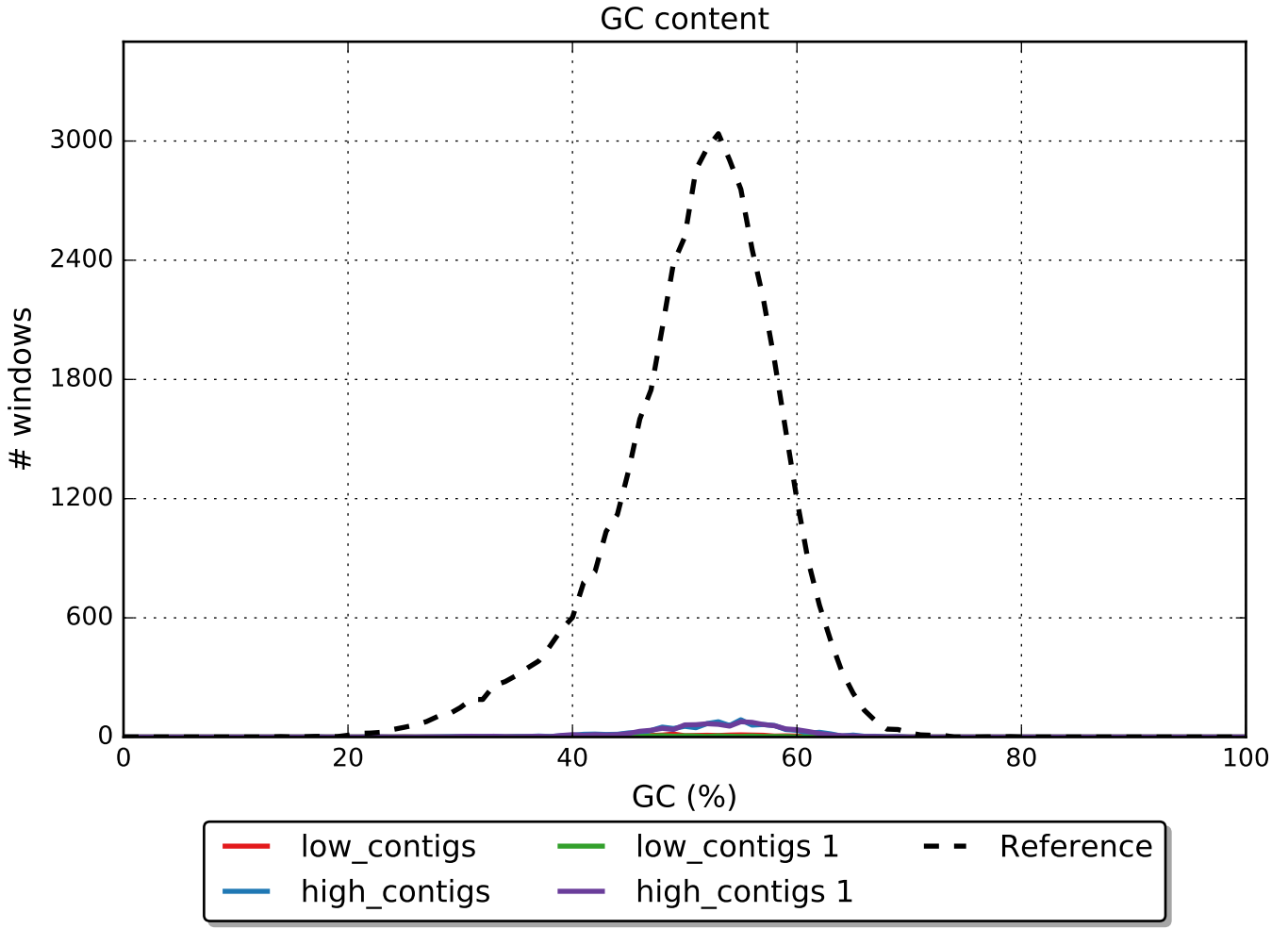
	low_contigs	high_contigs	low_contigs 1	high_contigs 1
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	0	0	0	0
# with misassembly	0	0	0	0
# both parts are significant	0	0	0	0
Partially unaligned length	0	0	0	0
# N's	0	0	0	0

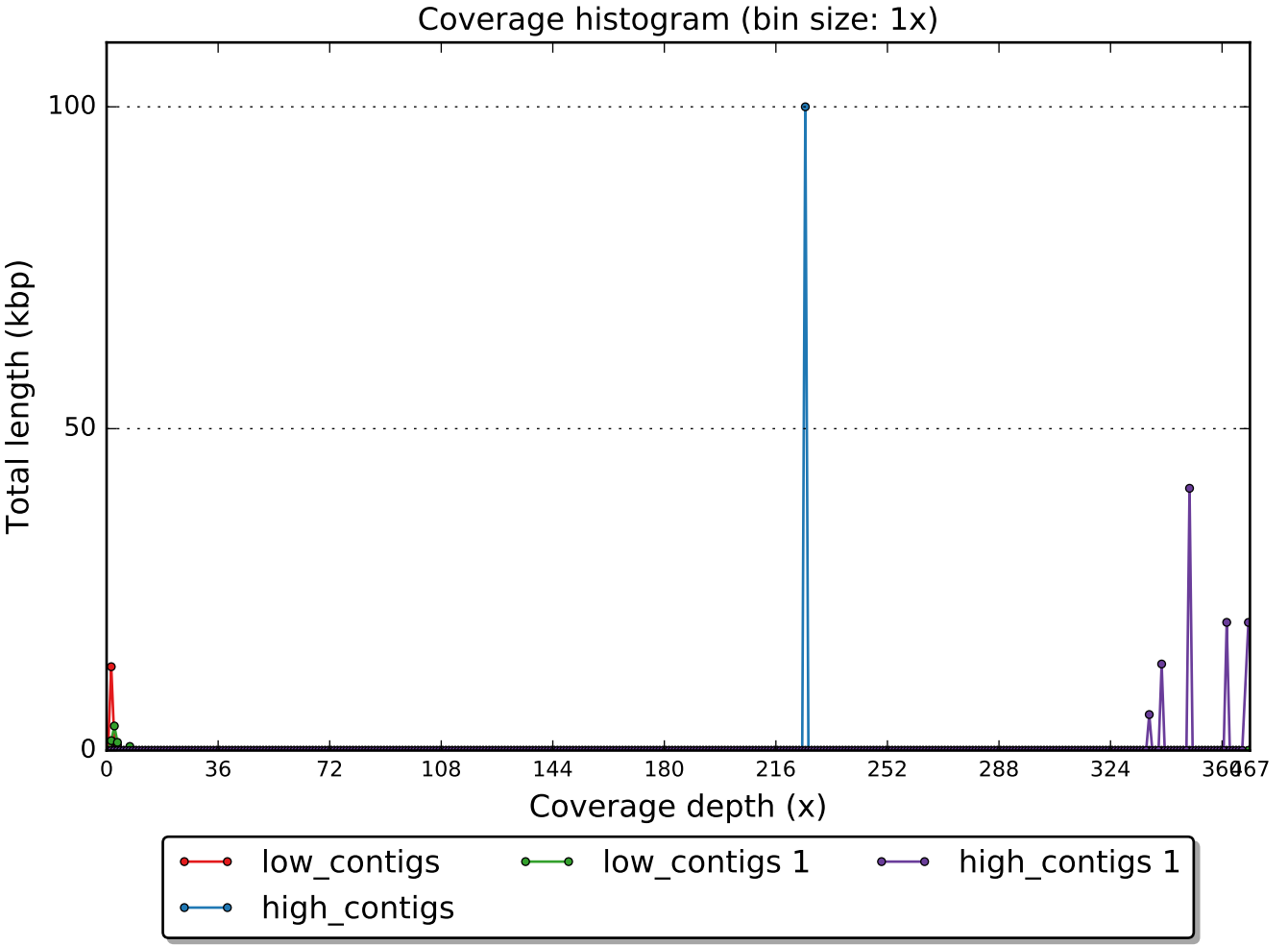
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

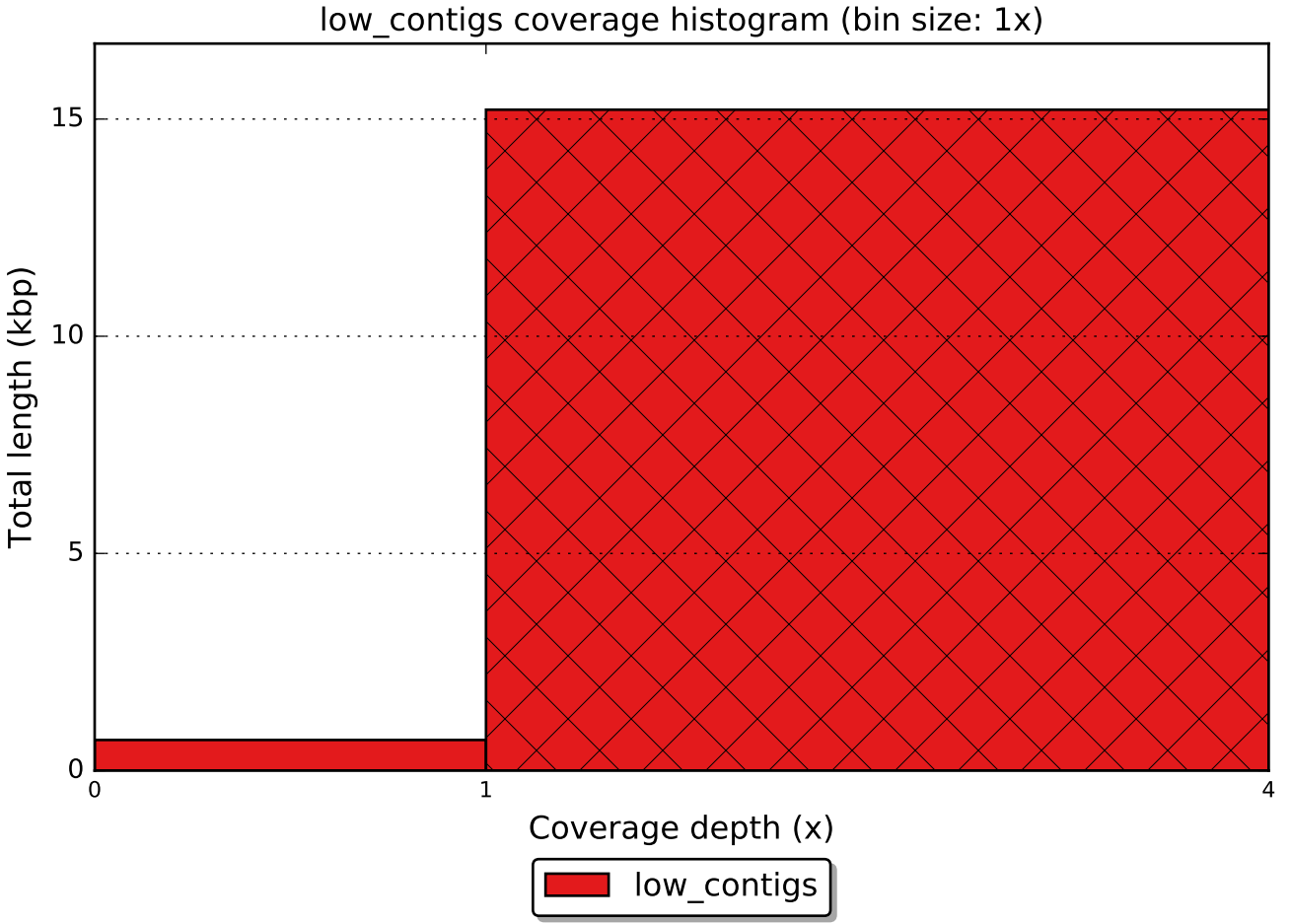

Nx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
low_contigs
high_contigs
low_contigs 1
high_contigs 1

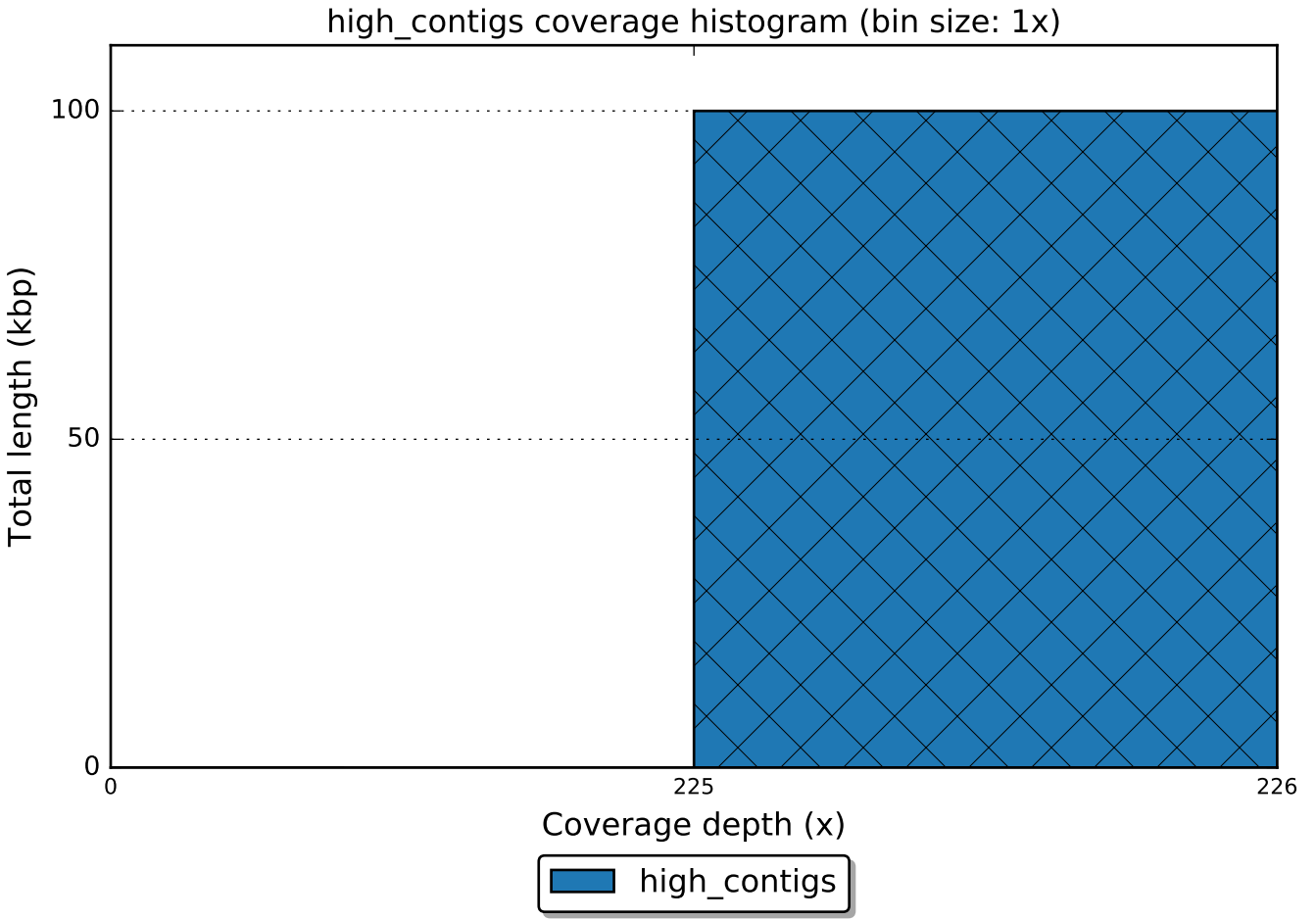

NGx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
low_contigs
high_contigs
low_contigs 1
high_contigs 1

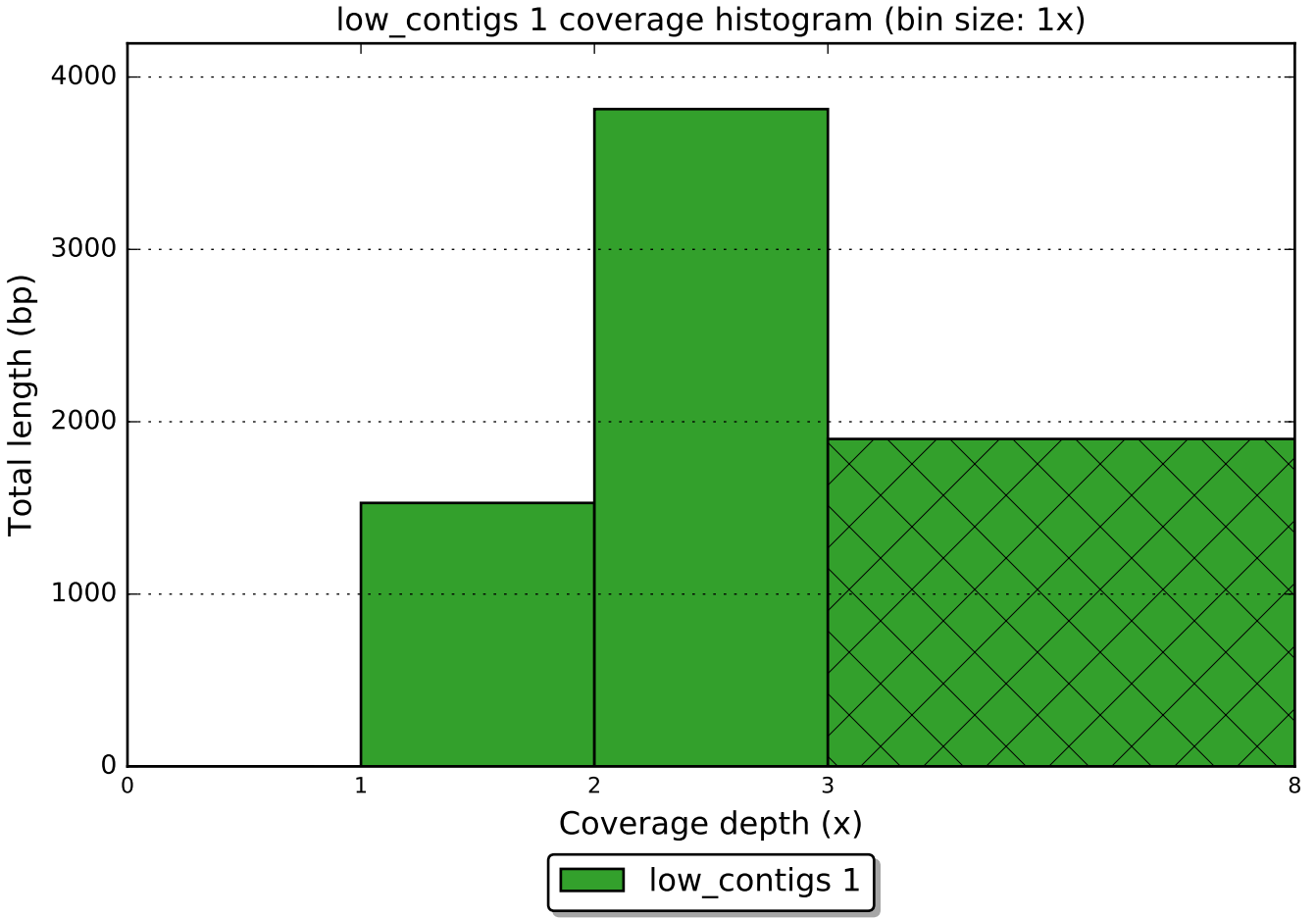

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
4
8
12
16
20
Contig index
low_contigs
high_contigs
low_contigs 1
high_contigs 1
Reference

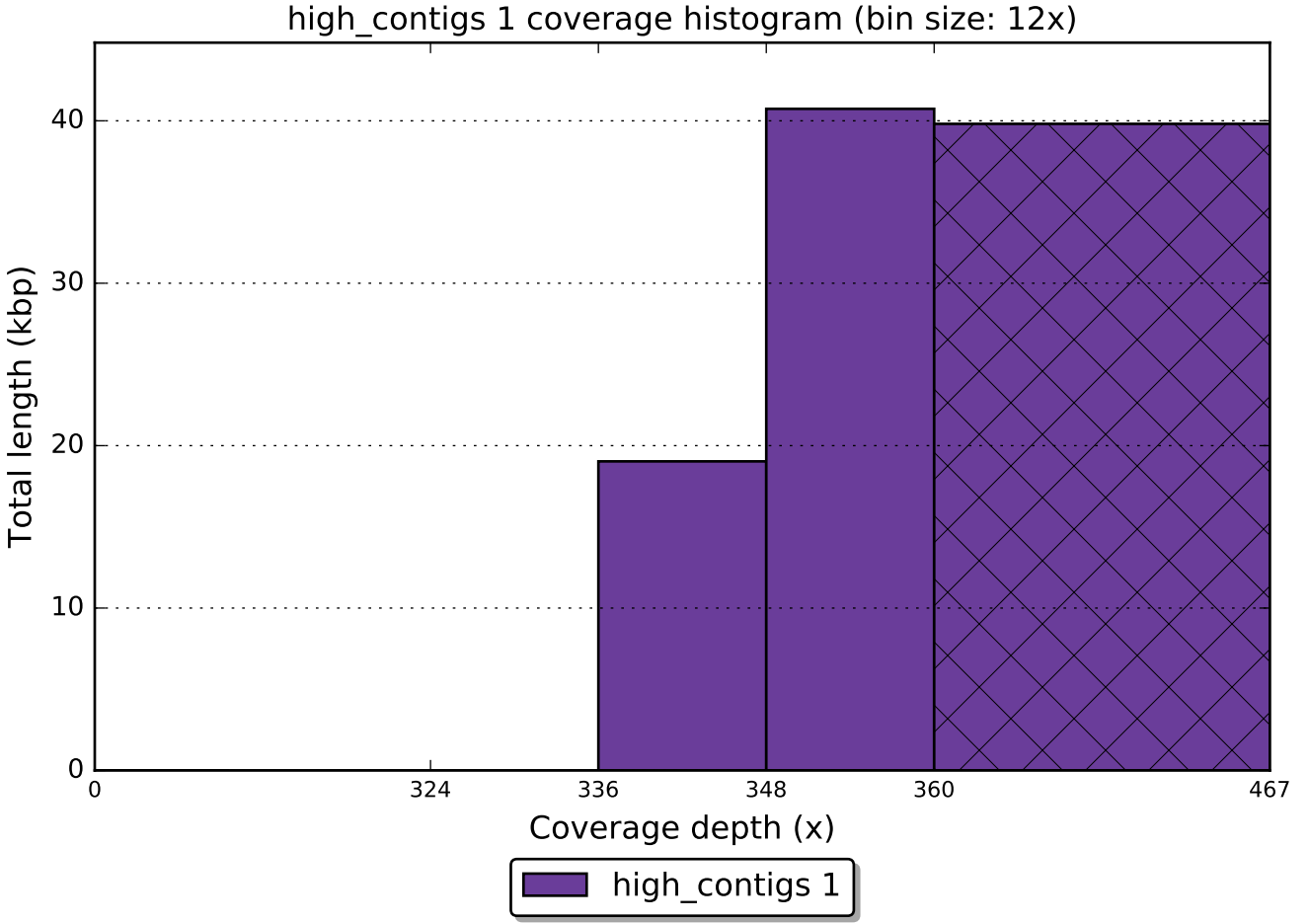

GC content
windows
GC (%)
0
600
1200
1800
2400
3000
0
20
40
60
80
100
low_contigs
high_contigs
low_contigs 1
high_contigs 1
Reference

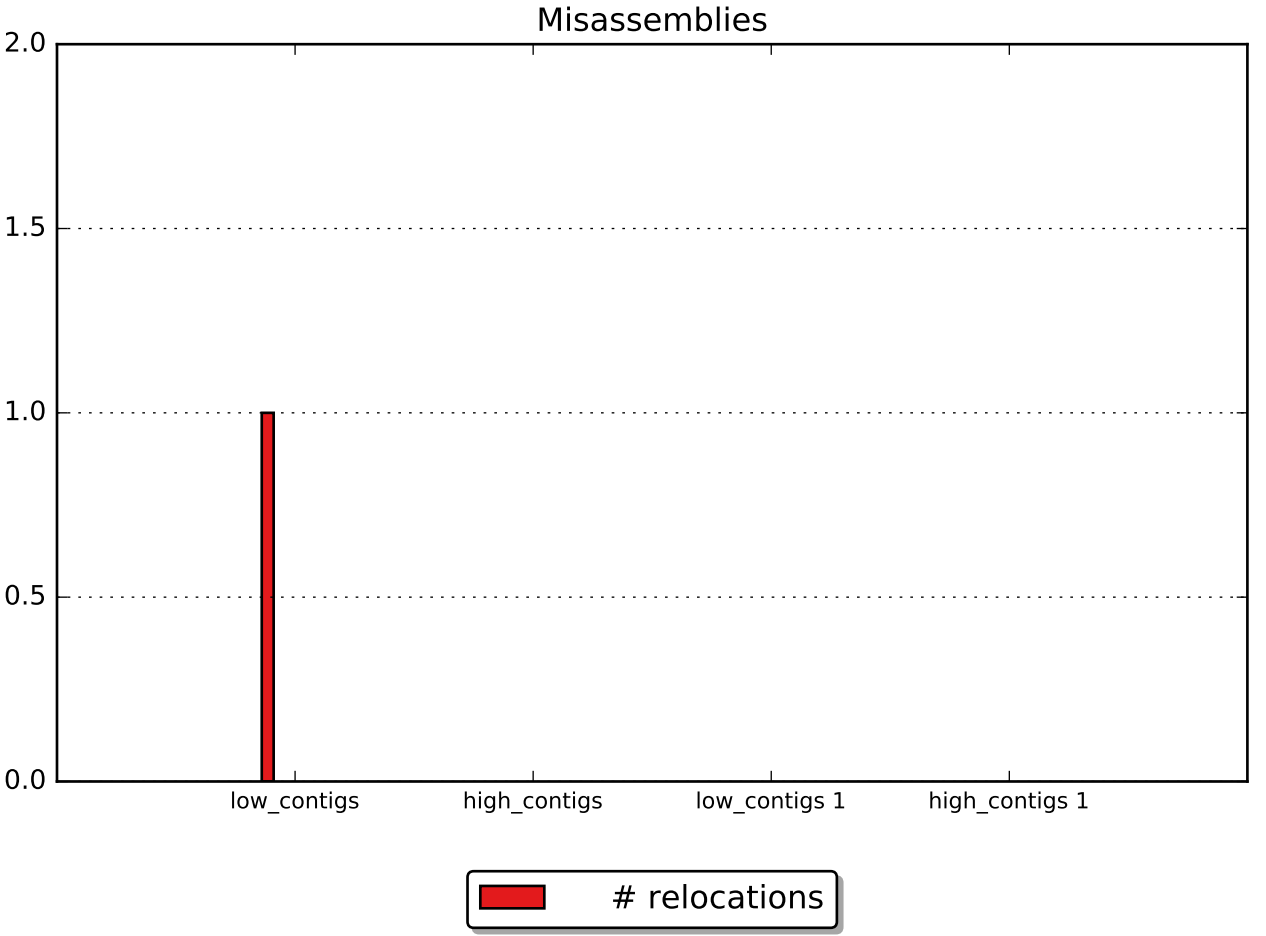

Coverage histogram (bin size: 1x)
Total length (kbp)
100
50
0
0
36
72
108
144
180
216
252
288
324
360
367
Coverage depth (x)
low_contigs
low_contigs 1
high_contigs 1
high_contigs

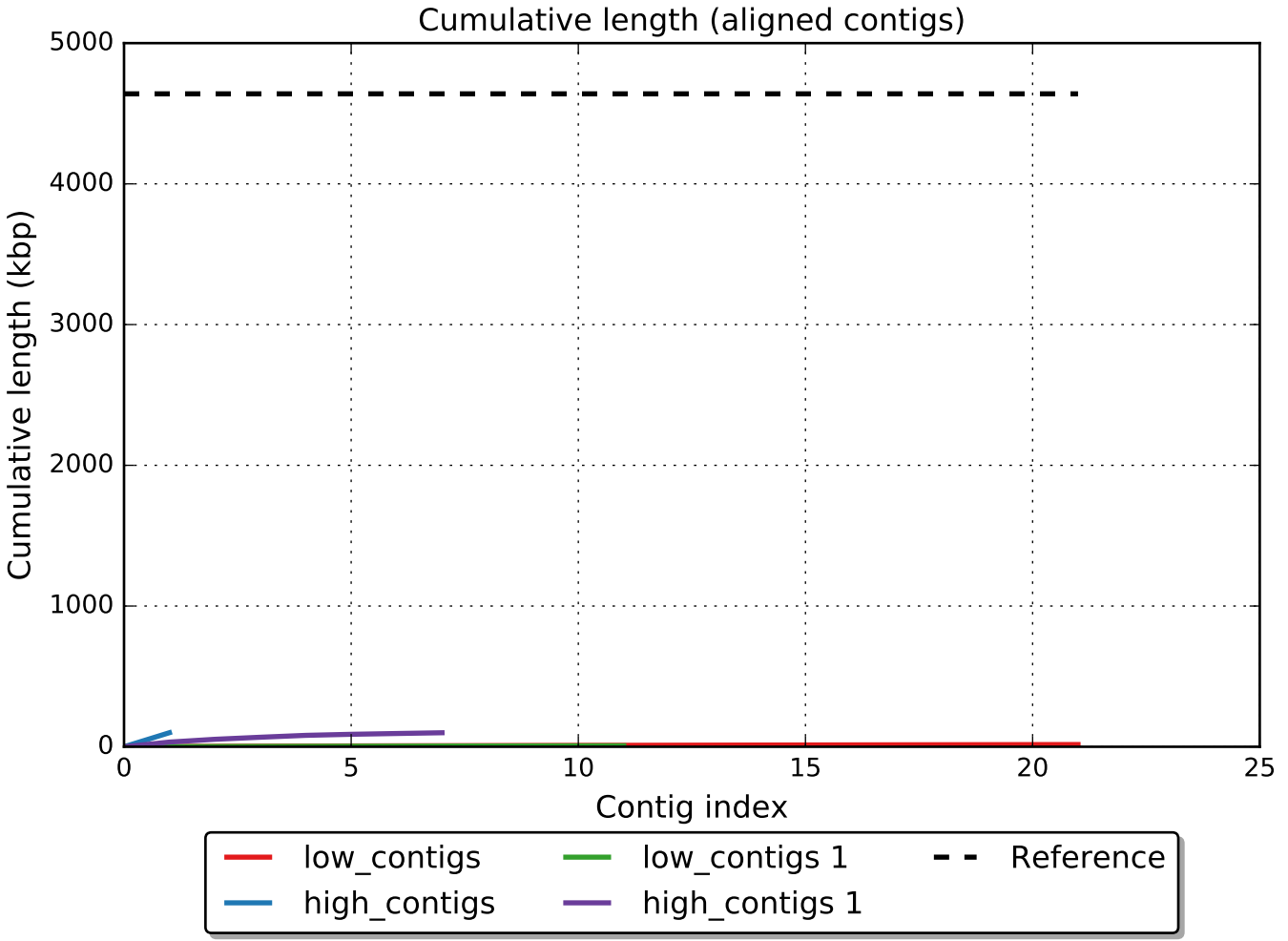

low_contigs coverage histogram (bin size: 1x)
Total length (kbp)
15
10
5
0
0
1
4
Coverage depth (x)
low_contigs

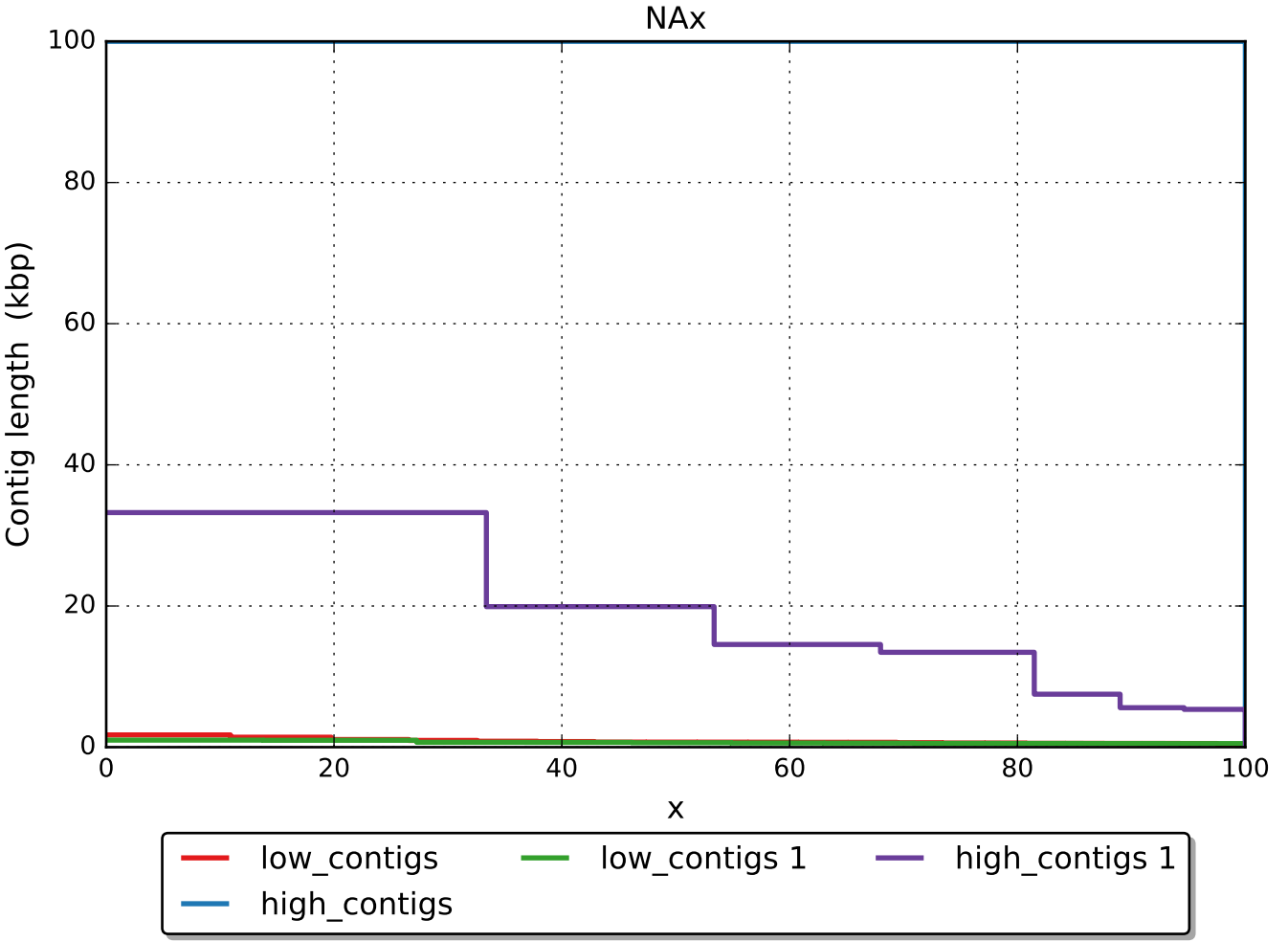

high_contigs coverage histogram (bin size: 1x)
Total length (kbp)
100
50
0
0
225
226
Coverage depth (x)
high_contigs

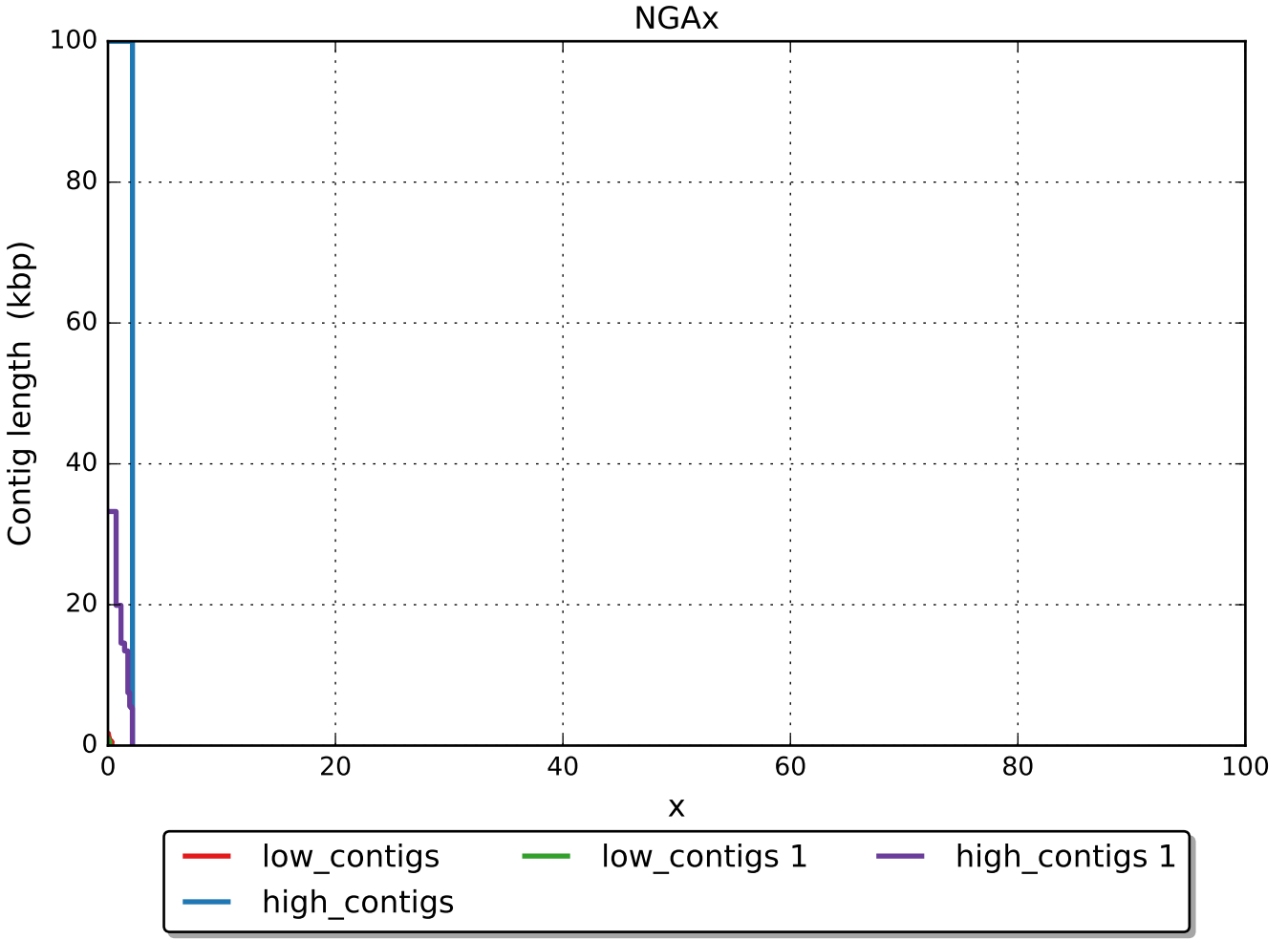

low_contigs 1 coverage histogram (bin size: 1x)
Total length (bp)
4000
3000
2000
1000
0
0
1
2
3
8
Coverage depth (x)
low_contigs 1

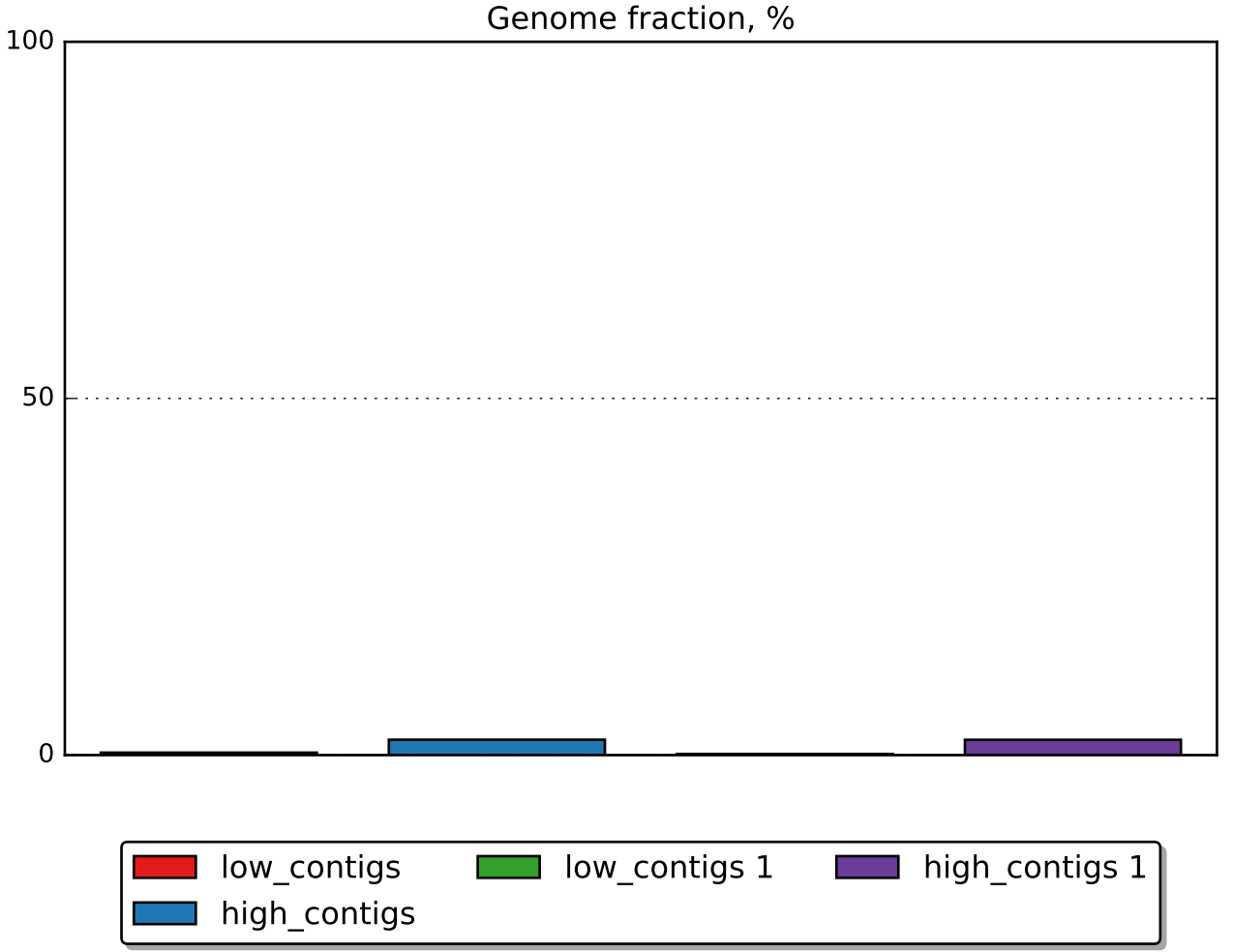

high_contigs 1 coverage histogram (bin size: 12x)
Total length (kbp)
0
10
20
30
40
0
324
336
348
360
467
Coverage depth (x)
high_contigs 1


Misassemblies
2.0
1.5
1.0
0.5
0.0
low_contigs
high_contigs
low_contigs 1
high_contigs 1
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
5
10
15
20
25
Contig index
low_contigs
high_contigs
low_contigs 1
high_contigs 1
Reference


NAx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
low_contigs
high_contigs
low_contigs 1
high_contigs 1


NGAx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
low_contigs
high_contigs
low_contigs 1
high_contigs 1


Genome fraction, %
100
50
0
low_contigs
low_contigs 1
high_contigs 1
high_contigs