Report

	low_Assem_contigs	low_spadesoutput1_contigs	high_Assem_contigs	high_spadesout_contigs
# contigs (>= 0 bp)	305	128	16	1
# contigs (>= 1000 bp)	0	4	7	1
# contigs (>= 5000 bp)	0	0	7	1
# contigs (>= 10000 bp)	0	0	4	1
# contigs (>= 25000 bp)	0	0	1	1
# contigs (>= 50000 bp)	0	0	0	1
Total length (>= 0 bp)	56973	49818	100309	100000
Total length (>= 1000 bp)	0	5313	99584	100000
Total length (>= 5000 bp)	0	0	99584	100000
Total length (>= 10000 bp)	0	0	81134	100000
Total length (>= 25000 bp)	0	0	33235	100000
Total length (>= 50000 bp)	0	0	0	100000
# contigs	11	20	7	1
Largest contig	998	1737	33235	100000
Total length	7243	15922	99584	100000
Reference length	4639675	4639675	4639675	4639675
GC (%)	50.71	51.21	52.58	52.59
Reference GC (%)	50.79	50.79	50.79	50.79
N50	632	718	19911	100000
N75	542	635	13440	100000
L50	5	8	2	1
L75	8	13	4	1
# misassemblies	0	1	0	0
# misassembled contigs	0	1	0	0
Misassembled contigs length	0	1084	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 (%)	0.156	0.343	2.145	2.155
Duplication ratio	1.000	1.000	1.001	1.000
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	0.00	31.40	0.00	0.00
# indels per 100 kbp	0.00	0.00	0.00	0.00
Largest alignment	998	1737	33235	100000
Total aligned length	7243	15922	99584	100000
NA50	632	715	19911	100000
NGA50	-	-	-	-
NA75	542	587	13440	100000
LA50	5	8	2	1
LA75	8	14	4	1

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

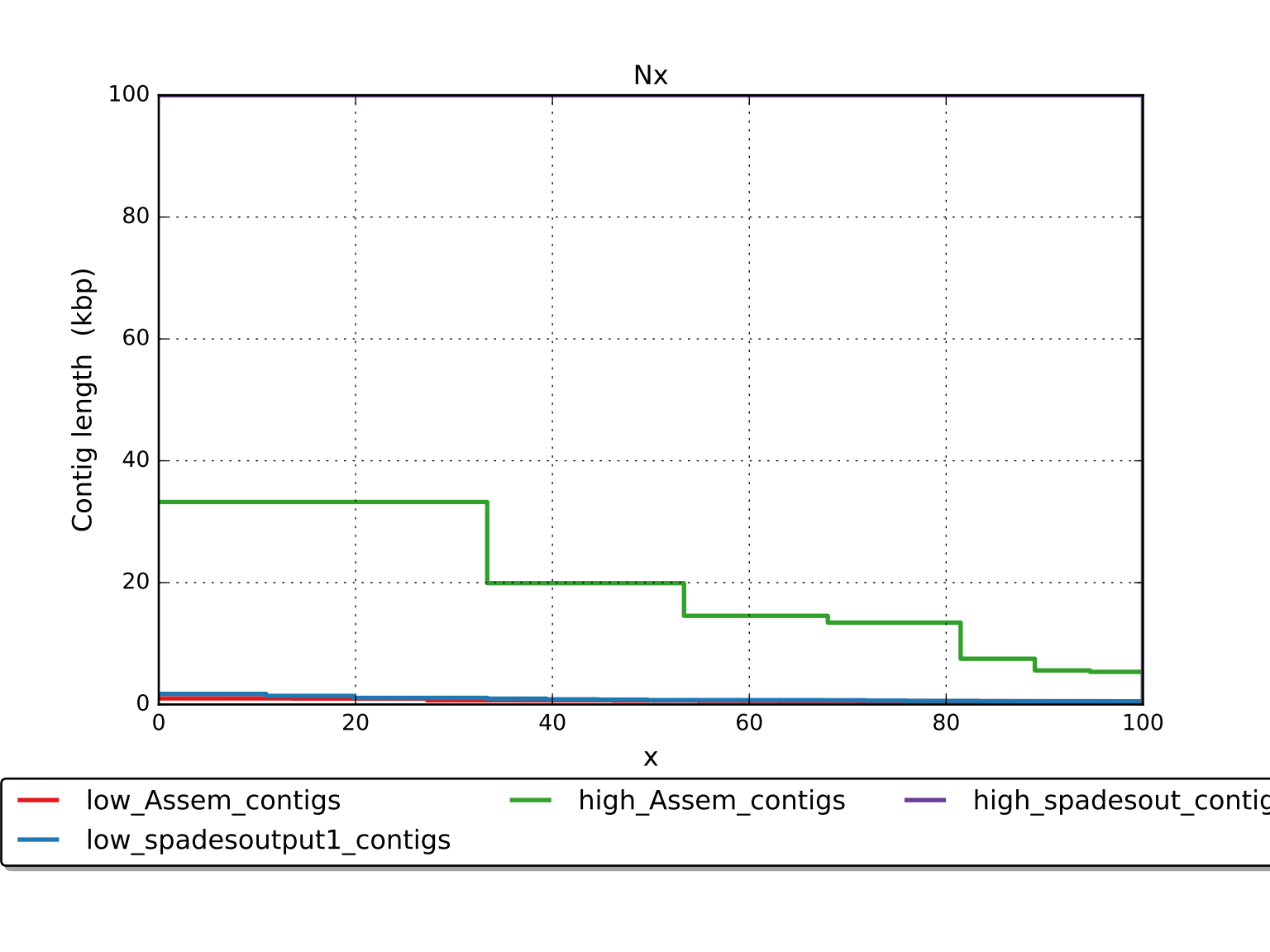
	low_Assem_contigs	low_spadesoutput1_contigs	high_Assem_contigs	high_spadesout_contigs
# misassemblies	0	1	0	0
# relocations	0	1	0	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# misassembled contigs	0	1	0	0
Misassembled contigs length	0	1084	0	0
# local misassemblies	0	0	0	0
# mismatches	0	5	0	0
# indels	0	0	0	0
# short indels	0	0	0	0
# long indels	0	0	0	0
Indels length	0	0	0	0

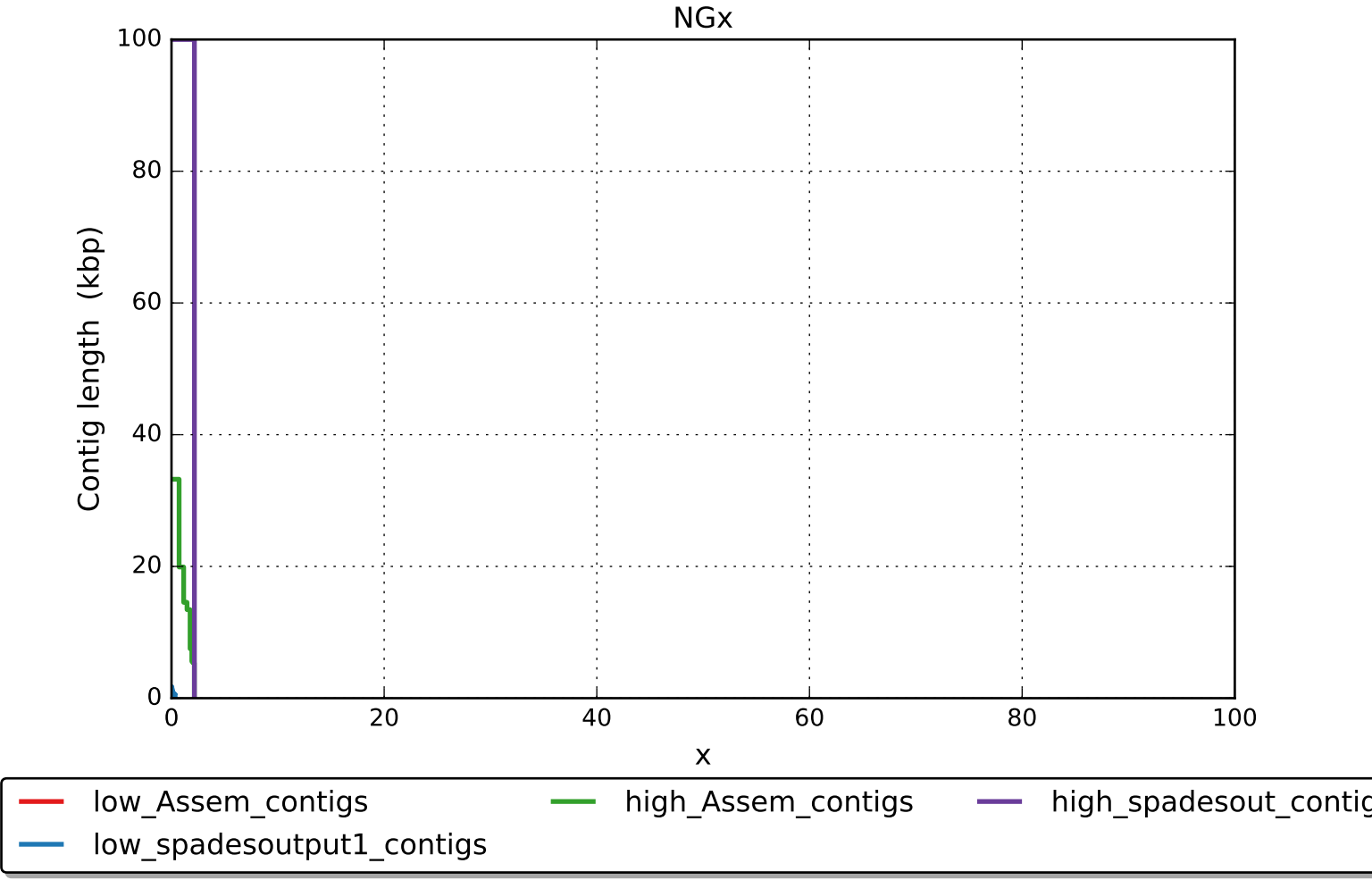
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

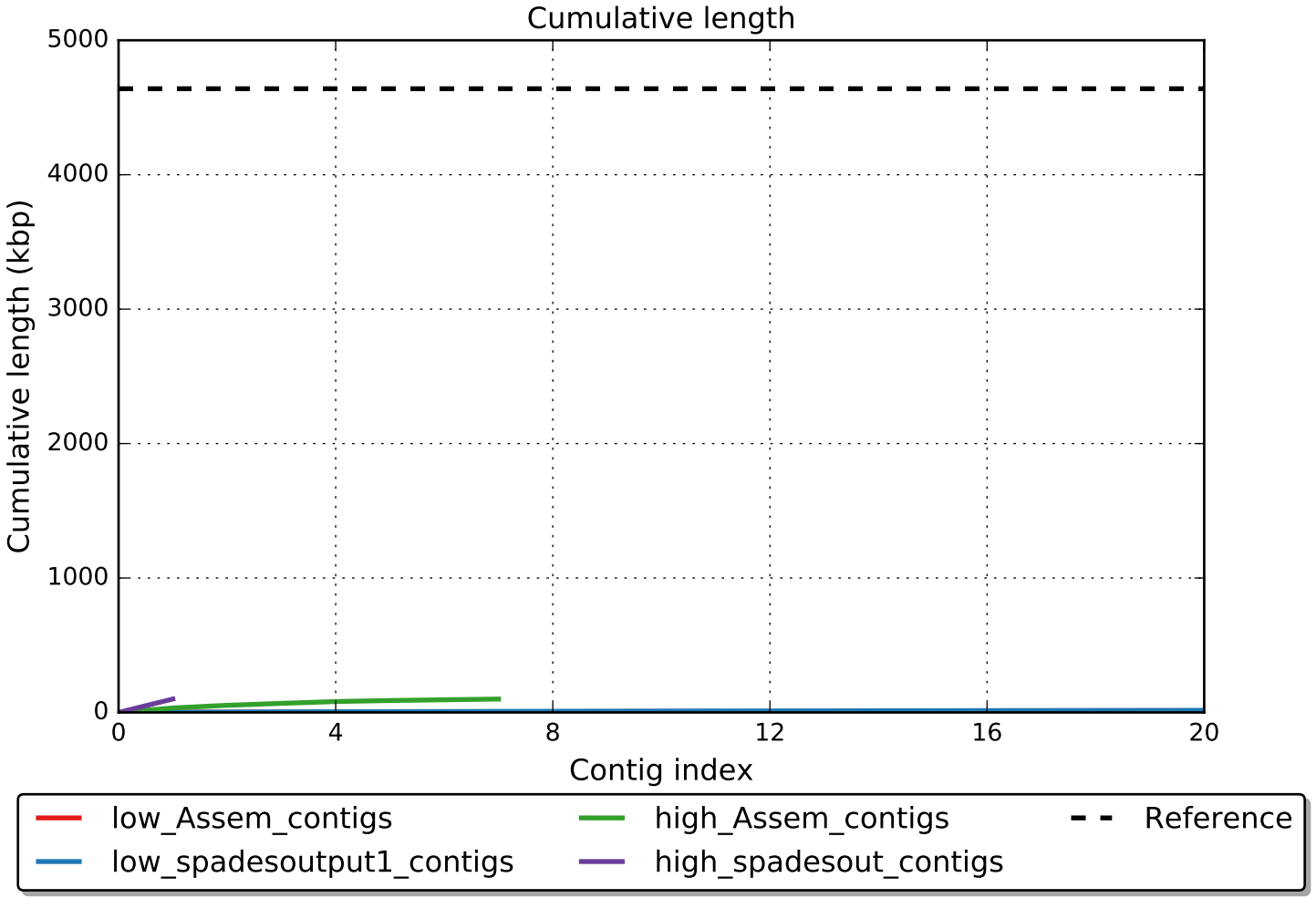
Unaligned report

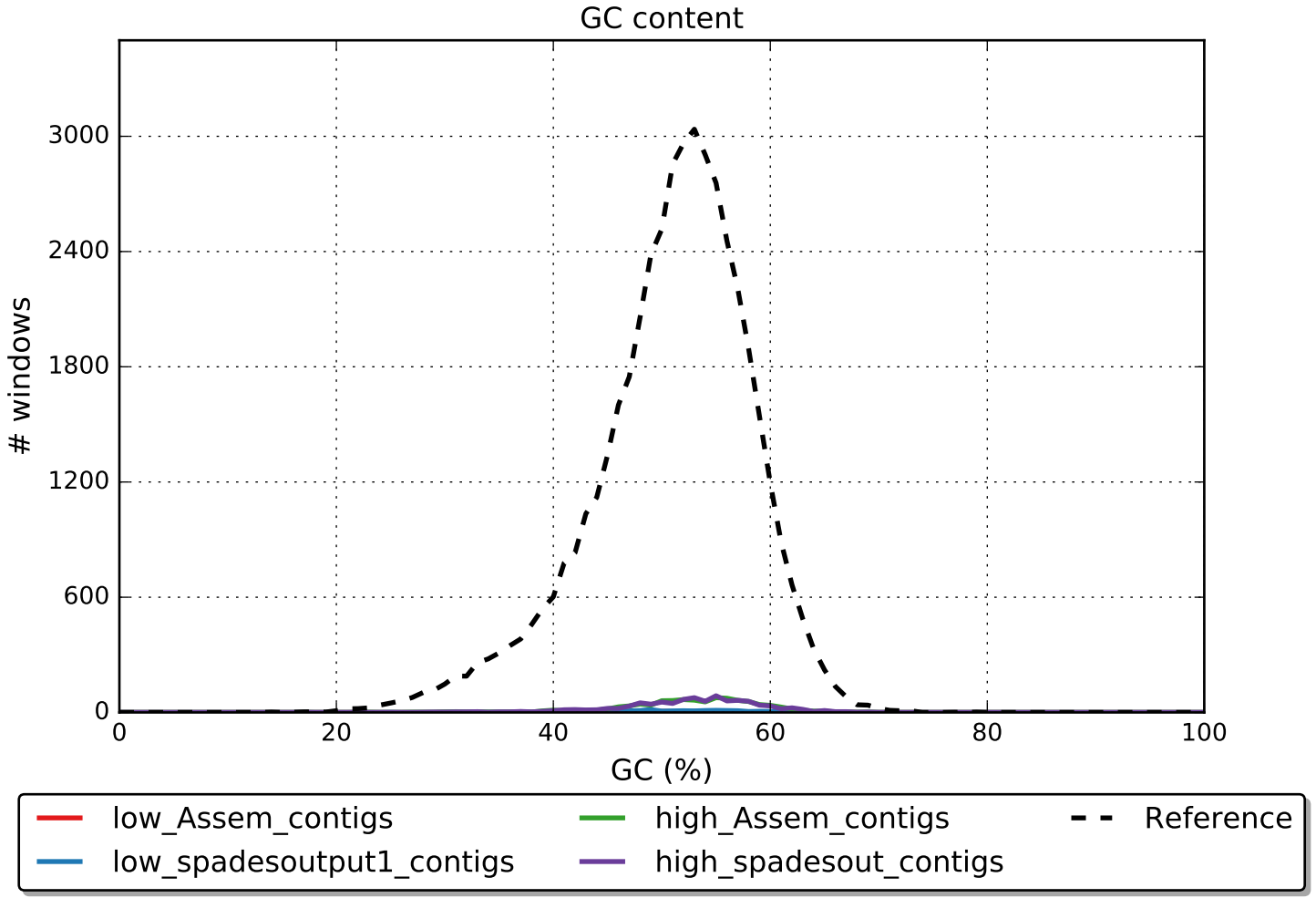
	low_Assem_contigs	low_spadesoutput1_contigs	high_Assem_contigs	high_spadesout_contigs
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	0	0	0	0
# with misassembly	0	0	0	0
# both parts are significant	0	0	0	0
Partially unaligned length	0	0	0	0
# N's	0	0	0	0

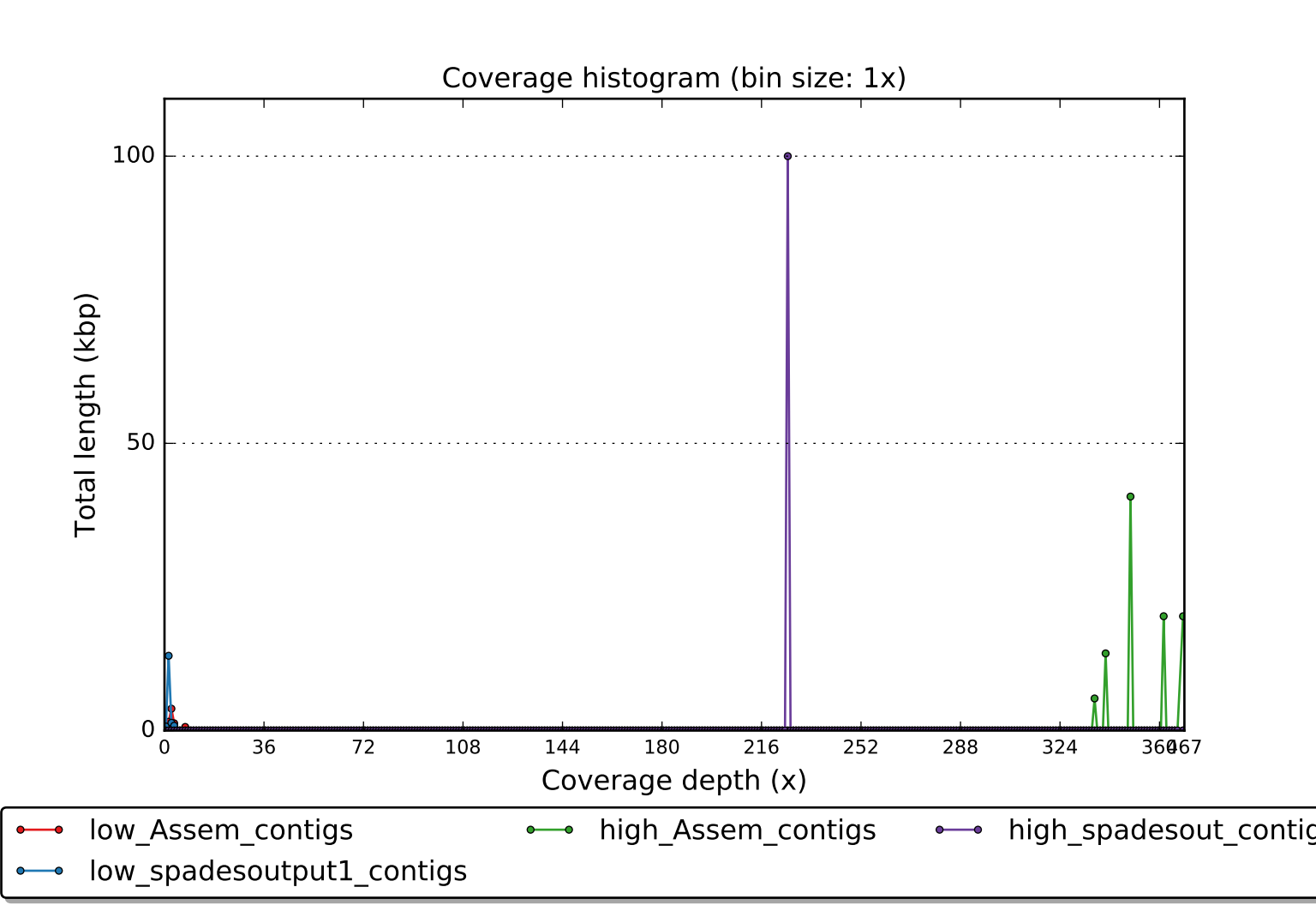
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

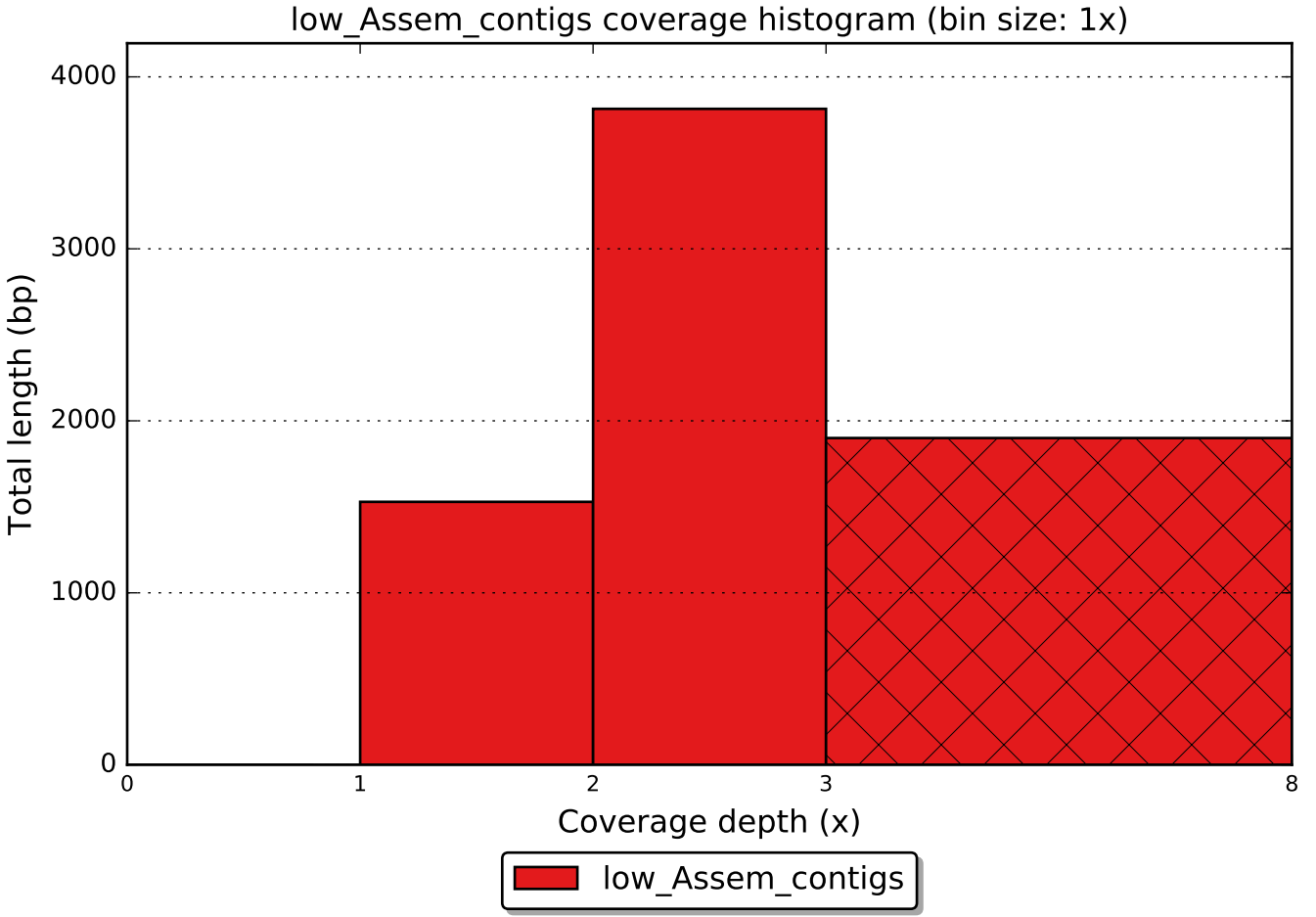

Nx
Contig length (kbp)
x
0
20
40
60
80
100
low_Assem_contigs
high_Assem_contigs
high_spadesout_contig
low_spadesoutput1_contigs

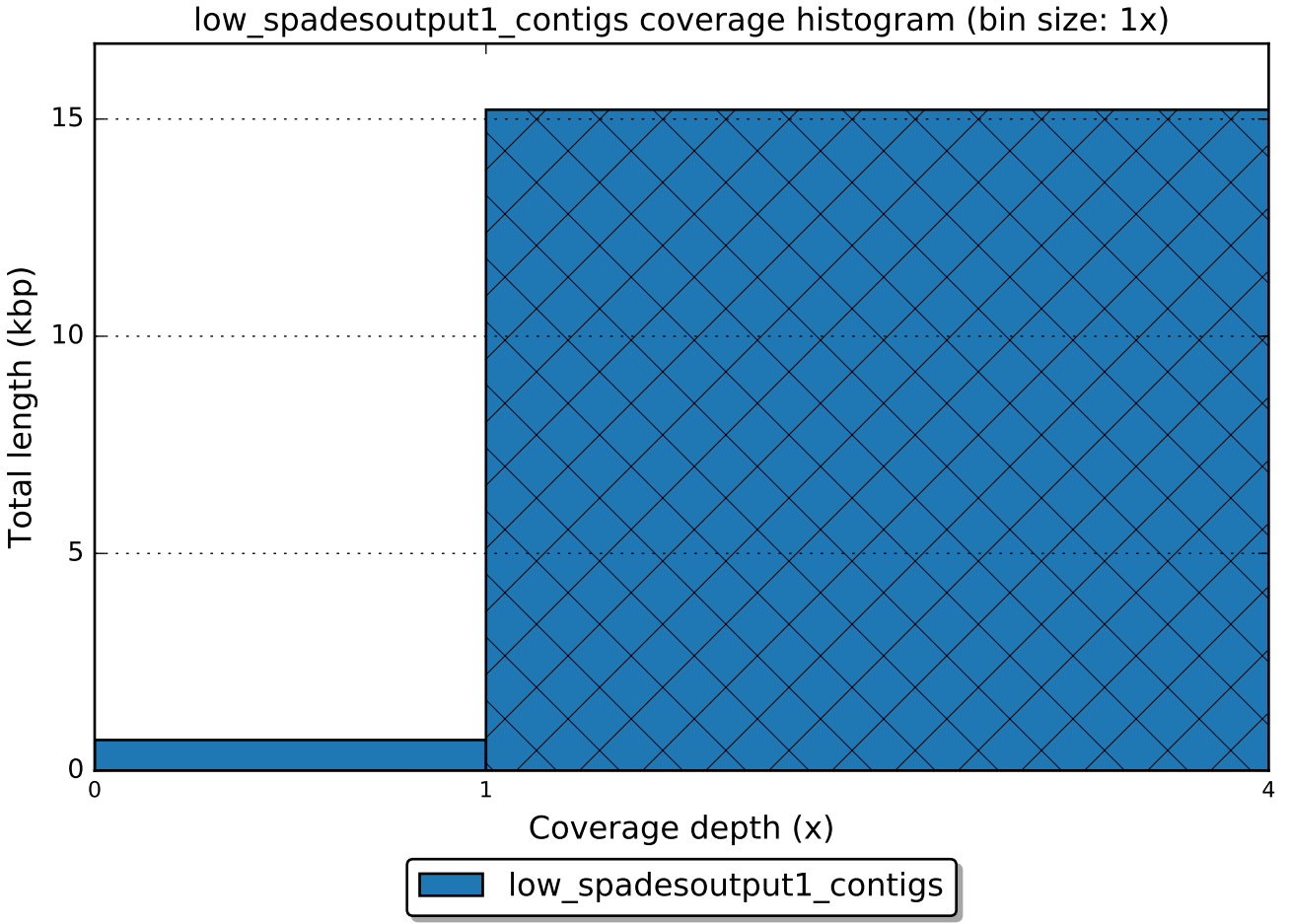

NGx
Contig length (kbp)
x
0
20
40
60
80
100
low_Assem_contigs
high_Assem_contigs
high_spadesout_contig
low_spadesoutput1_contigs

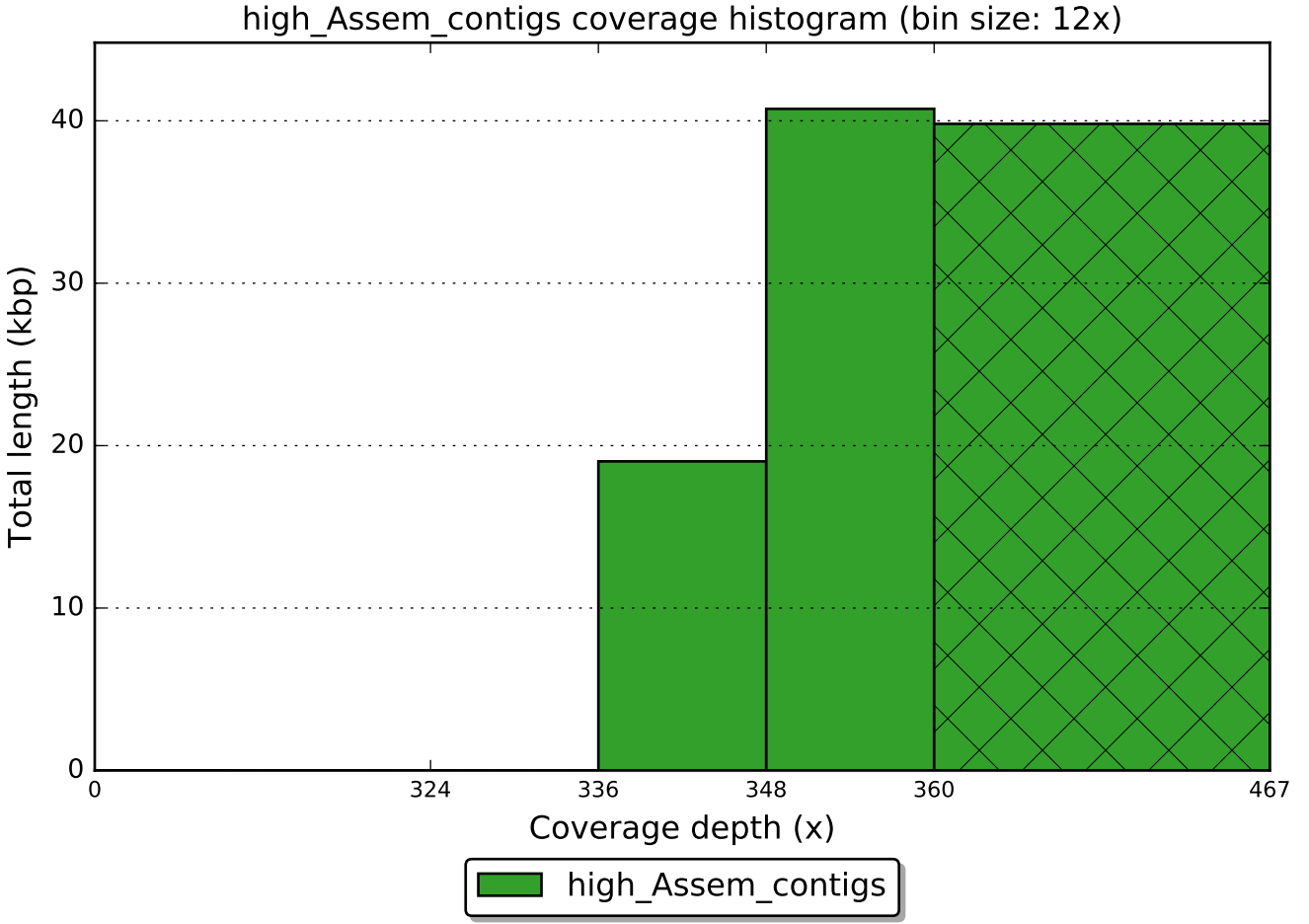

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
4
8
12
16
20
Contig index
low_Assem_contigs
high_Assem_contigs
Reference
low_spadesoutput1_contigs
high_spadesout_contigs

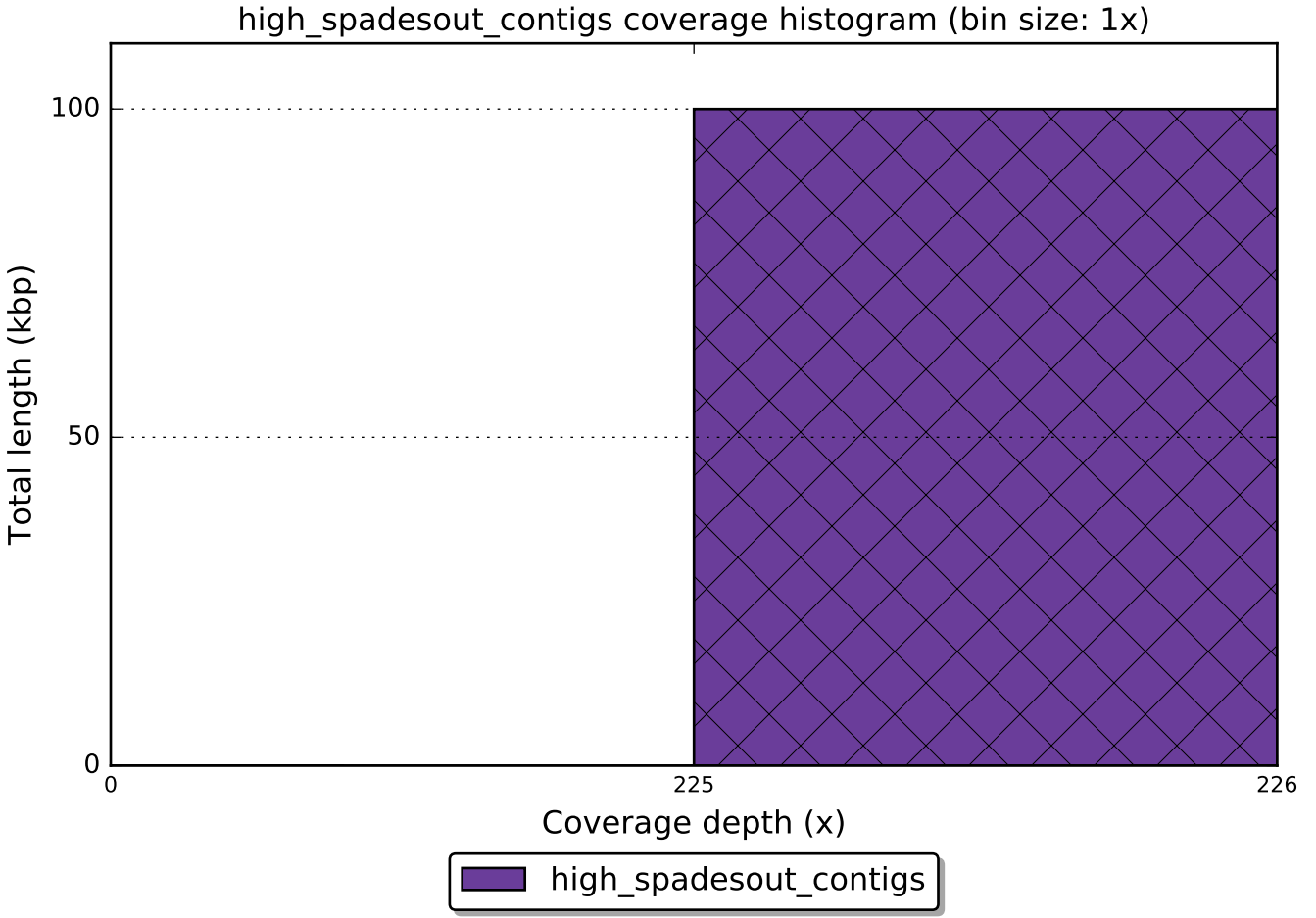

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
low_Assem_contigs
low_spadesoutput1_contigs
high_Assem_contigs
high_spadesout_contigs
Reference

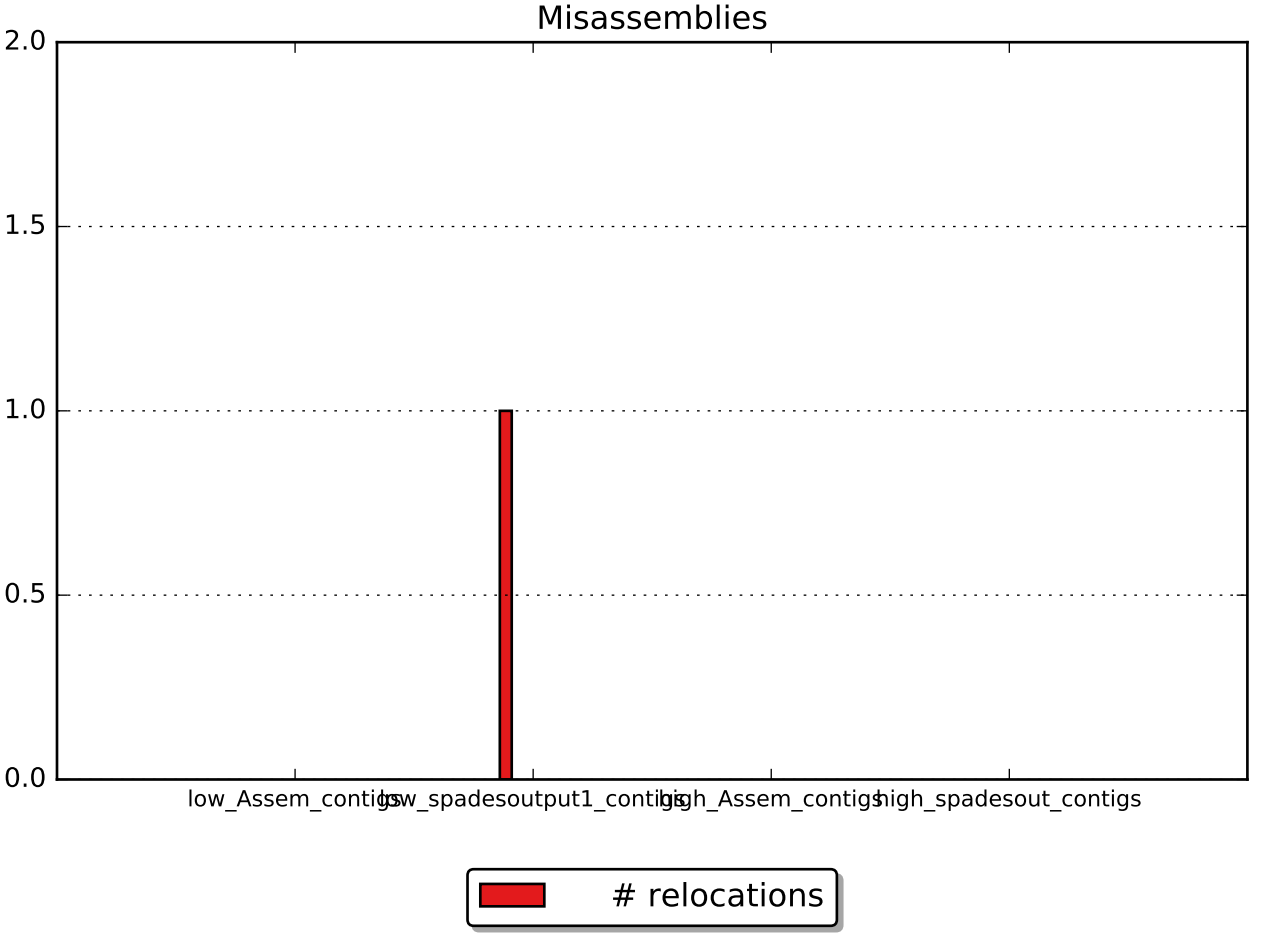

Coverage histogram (bin size: 1x)
Total length (kbp)
100
50
0
0
36
72
108
144
180
216
252
288
324
360
367
Coverage depth (x)
low_Assem_contigs
low_spadesoutput1_contigs
high_Assem_contigs
high_spadesout_contig

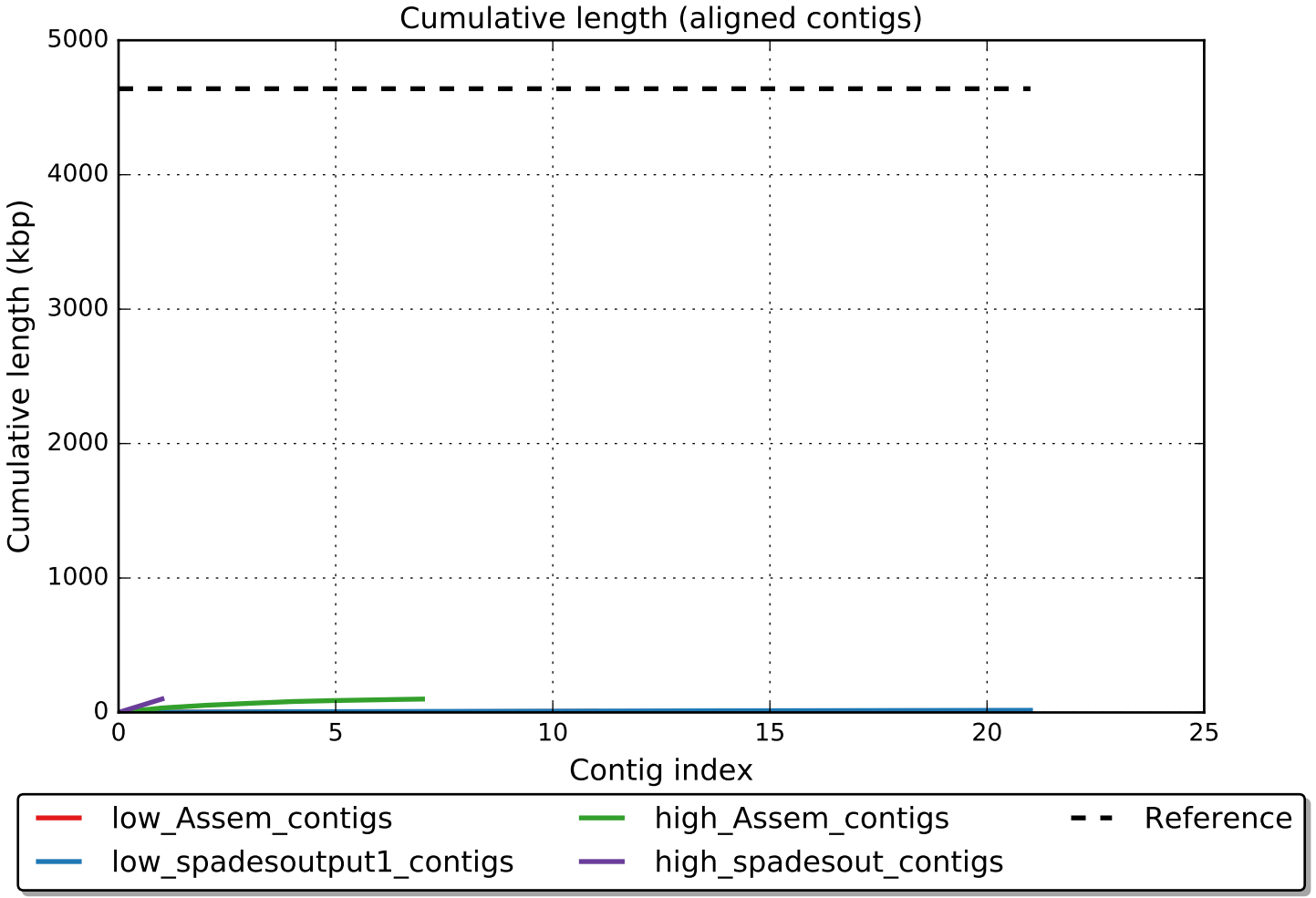

low_Assem_contigs coverage histogram (bin size: 1x)
Total length (bp)
4000
3000
2000
1000
0
0
1
2
3
8
Coverage depth (x)
low_Assem_contigs

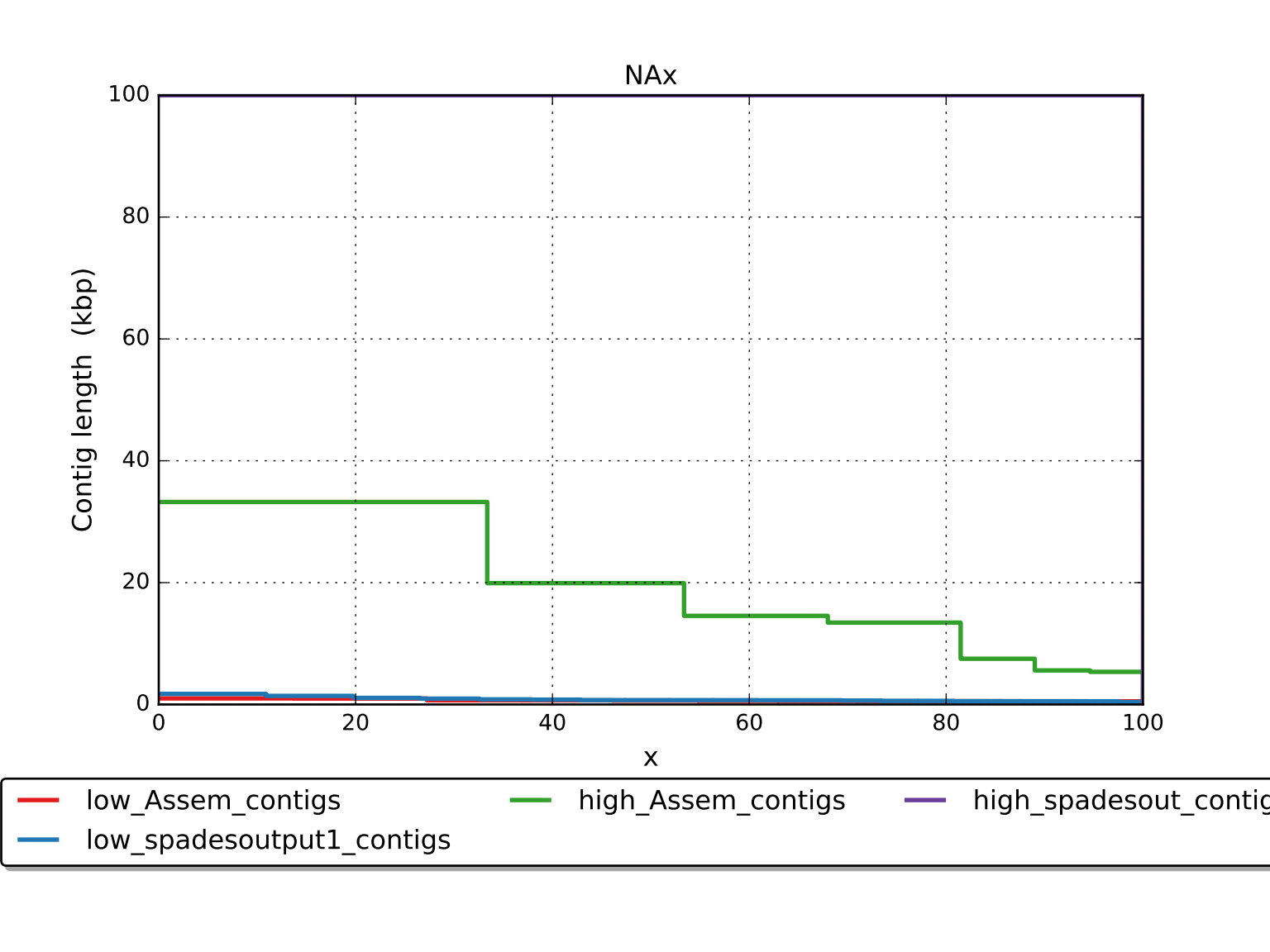

low_spadesoutput1_contigs coverage histogram (bin size: 1x)
Total length (kbp)
15
10
5
0
0
1
4
Coverage depth (x)
low_spadesoutput1_contigs

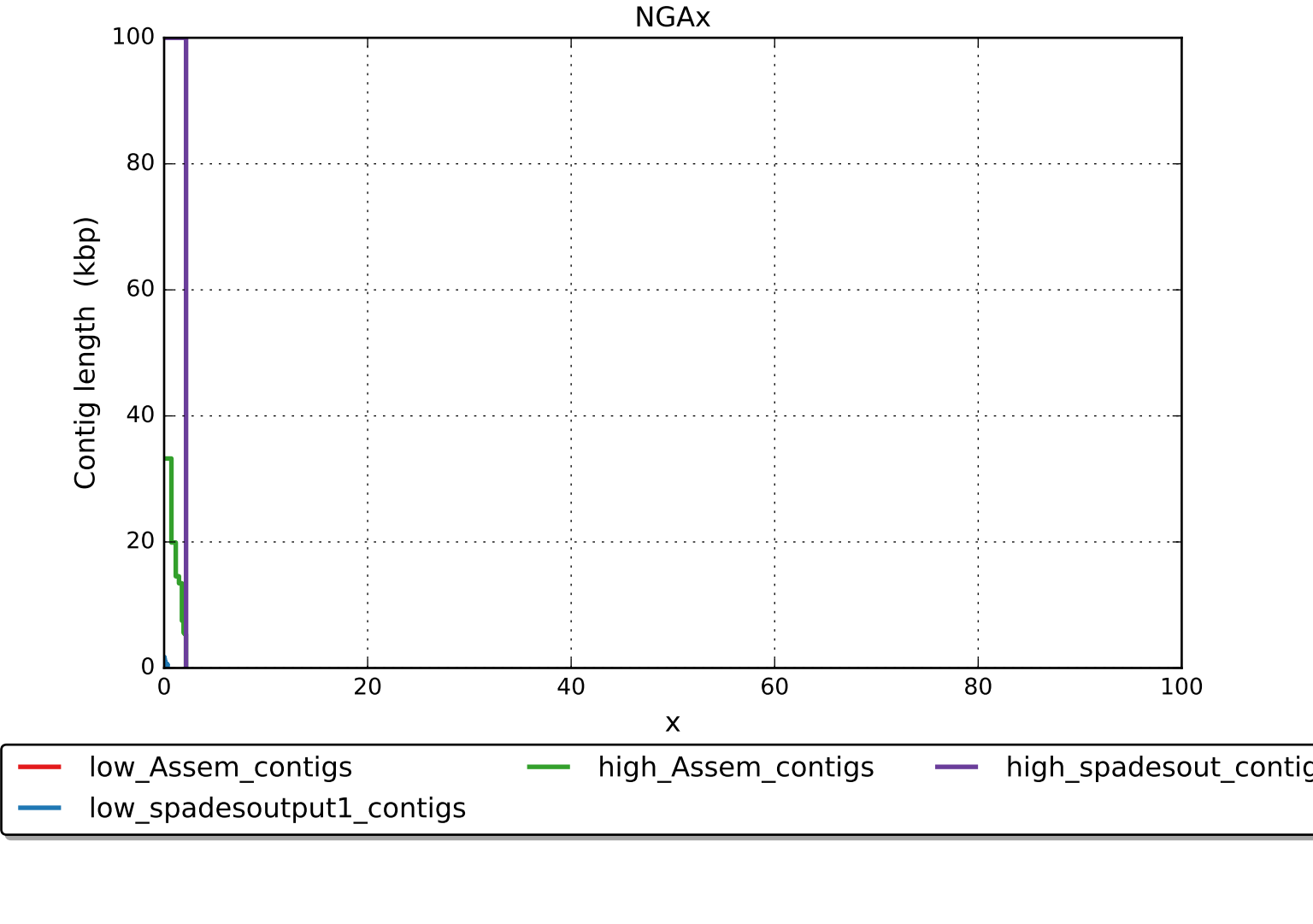

high_Assem_contigs coverage histogram (bin size: 12x)
Total length (kbp)
0
10
20
30
40
0
324
336
348
360
467
Coverage depth (x)
high_Assem_contigs

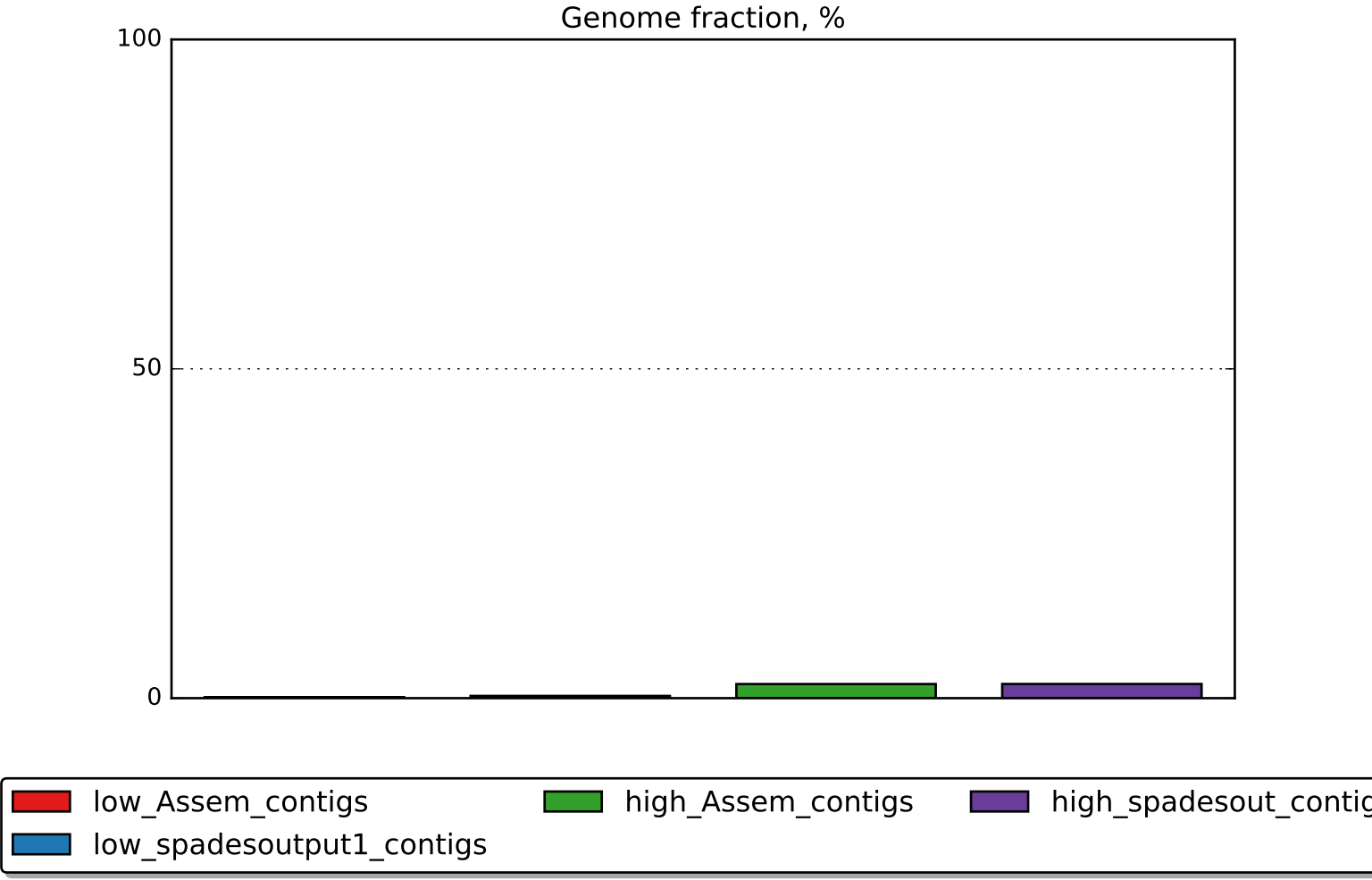

high_spadesout_contigs coverage histogram (bin size: 1x)
Total length (kbp)
100
50
0
0
225
226
Coverage depth (x)
high_spadesout_contigs


Misassemblies
2.0
1.5
1.0
0.5
0.0
low_Assem_contigs
low_spadesoutput1_contigs
high_Assem_contigs
high_spadesout_contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
5
10
15
20
25
Contig index
low_Assem_contigs
high_Assem_contigs
Reference
low_spadesoutput1_contigs
high_spadesout_contigs


NAx
Contig length (kbp)
x
0
20
40
60
80
100
low_Assem_contigs
high_Assem_contigs
high_spadesout_contig
low_spadesoutput1_contigs


NGAx
Contig length (kbp)
x
0
20
40
60
80
100
low_Assem_contigs
high_Assem_contigs
high_spadesout_contig
low_spadesoutput1_contigs


Genome fraction, %
100
50
0
low_Assem_contigs
high_Assem_contigs
high_spadesout_contig
low_spadesoutput1_contigs