Report

	pb.asm	pb.asm.nextpolish1	pb.asm.racon1	ont.asm	ont.asm.nextpolish1	ont.asm.racon1
# contigs (>= 0 bp)	557	557	556	329	329	329
# contigs (>= 1000 bp)	557	557	556	329	329	329
# contigs (>= 5000 bp)	557	557	556	327	327	327
# contigs (>= 10000 bp)	543	537	534	316	317	317
# contigs (>= 25000 bp)	173	164	165	222	217	222
# contigs (>= 50000 bp)	87	86	86	130	131	133
Total length (>= 0 bp)	238893883	229392481	231583305	221739507	231851442	231932961
Total length (>= 1000 bp)	238893883	229392481	231583305	221739507	231851442	231932961
Total length (>= 5000 bp)	238893883	229392481	231583305	221732577	231844290	231925923
Total length (>= 10000 bp)	238762938	229204877	231377347	221643884	231764517	231846997
Total length (>= 25000 bp)	232922978	223330286	225555245	219896651	229903727	230076329
Total length (>= 50000 bp)	230064559	220740664	222921080	216592676	226762435	226872099
# contigs	557	557	556	329	329	329
Largest contig	26592668	25515591	25771587	30803648	32268337	32271759
Total length	238893883	229392481	231583305	221739507	231851442	231932961
Reference length	248956422	248956422	248956422	248956422	248956422	248956422
GC (%)	42.27	41.72	41.64	42.62	41.98	41.98
Reference GC (%)	41.72	41.72	41.72	41.72	41.72	41.72
N50	9667702	9276286	9366075	13737048	14388056	14389820
NG50	7443273	6715613	7209582	9733330	14388056	14389820
N75	4287682	3802336	4156603	5228706	5474595	5475483
NG75	3858118	3047287	3390954	3632744	4120162	4120691
L50	8	8	8	6	6	6
LG50	9	10	9	7	6	6
L75	18	19	18	12	12	12
LG75	20	23	22	17	15	15
# misassemblies	46	28	41	16	33	23
# misassembled contigs	40	26	39	15	21	18
Misassembled contigs length	12313140	9494196	9760101	28851842	31011501	30619976
# local misassemblies	39	4	10	3	4	11
# scaffold gap ext. mis.	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0
# possible TEs	0	0	0	0	6	4
# unaligned mis. contigs	1	0	0	29	28	8
# unaligned contigs	34 + 86 part	17 + 48 part	2 + 51 part	80 + 124 part	96 + 106 part	158 + 44 part
Unaligned length	1002739	307941	70526	6235359	6163688	6431927
Genome fraction (%)	97.097	97.301	97.291	97.087	97.077	97.106
Duplication ratio	1.063	1.022	1.032	0.963	1.009	1.008
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	5425.25	165.25	115.42	4973.49	30.79	34.63
# indels per 100 kbp	7127.93	631.97	1233.12	4126.88	43.39	83.87
Largest alignment	26588612	25515573	25771470	30803348	32268337	32271759
Total aligned length	237783372	228993014	231409104	215462315	225627614	225432606
NA50	9667701	9276285	9366075	11752532	12307661	12308656
NGA50	7441138	6715605	7209261	9733330	12307661	12308656
NA75	3853317	3700553	3738159	5128326	5371256	5372053
NGA75	3498735	3047038	3327669	3509012	4085906	4086453
LA50	8	8	8	6	6	6
LGA50	9	10	9	7	6	6
LA75	19	19	19	13	13	13
LGA75	21	23	22	18	16	16

All statistics are based on contigs of size >= 3000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

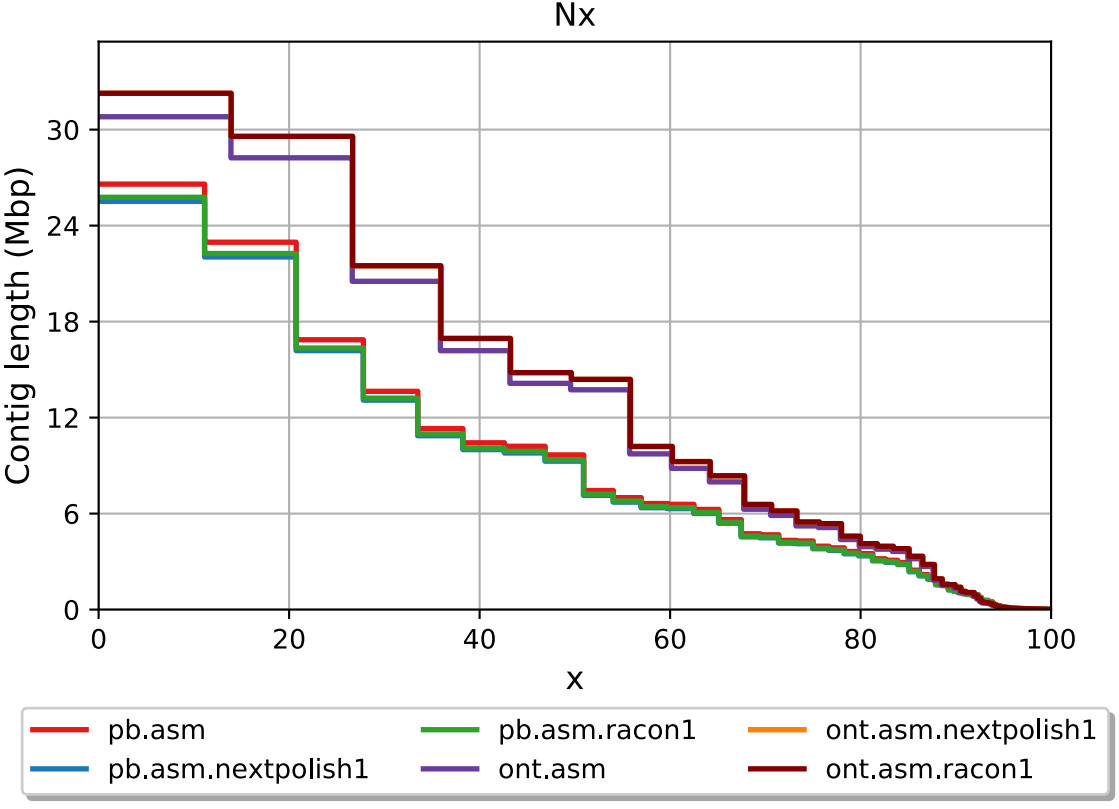
	pb.asm	pb.asm.nextpolish1	pb.asm.racon1	ont.asm	ont.asm.nextpolish1	ont.asm.racon1
# misassemblies	46	28	41	16	33	23
# contig misassemblies	46	28	41	16	33	23
# c. relocations	45	27	40	16	33	23
# c. translocations	0	0	0	0	0	0
# c. inversions	1	1	1	0	0	0
# scaffold misassemblies	0	0	0	0	0	0
# s. relocations	0	0	0	0	0	0
# s. translocations	0	0	0	0	0	0
# s. inversions	0	0	0	0	0	0
# misassembled contigs	40	26	39	15	21	18
Misassembled contigs length	12313140	9494196	9760101	28851842	31011501	30619976
# local misassemblies	39	4	10	3	4	11
# scaffold gap ext. mis.	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0
# possible TEs	0	0	0	0	6	4
# unaligned mis. contigs	1	0	0	29	28	8
# mismatches	12141134	370583	258809	11129037	68890	77504
# indels	15951531	1417256	2765093	9234603	97088	187713
# indels (<= 5 bp)	15895341	1414471	2762347	8837260	94588	185693
# indels (> 5 bp)	56190	2785	2746	397343	2500	2020
Indels length	21136384	1649660	3420105	18639535	208875	316913

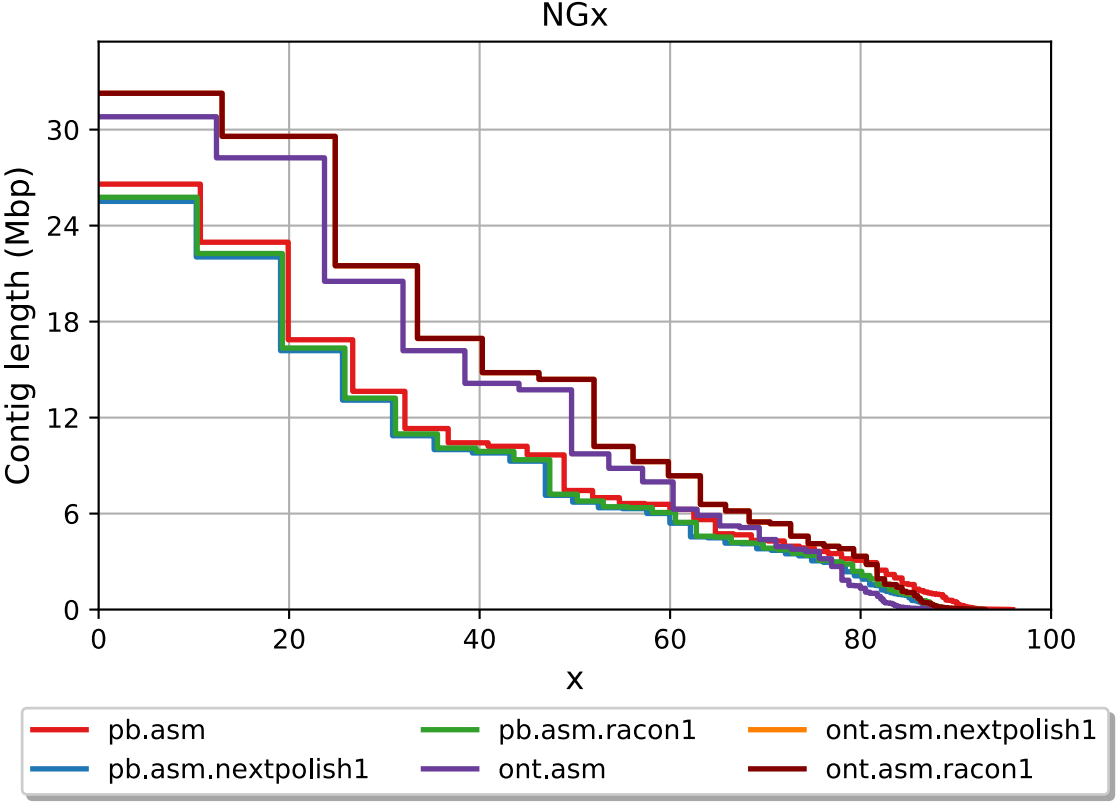
All statistics are based on contigs of size >= 3000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

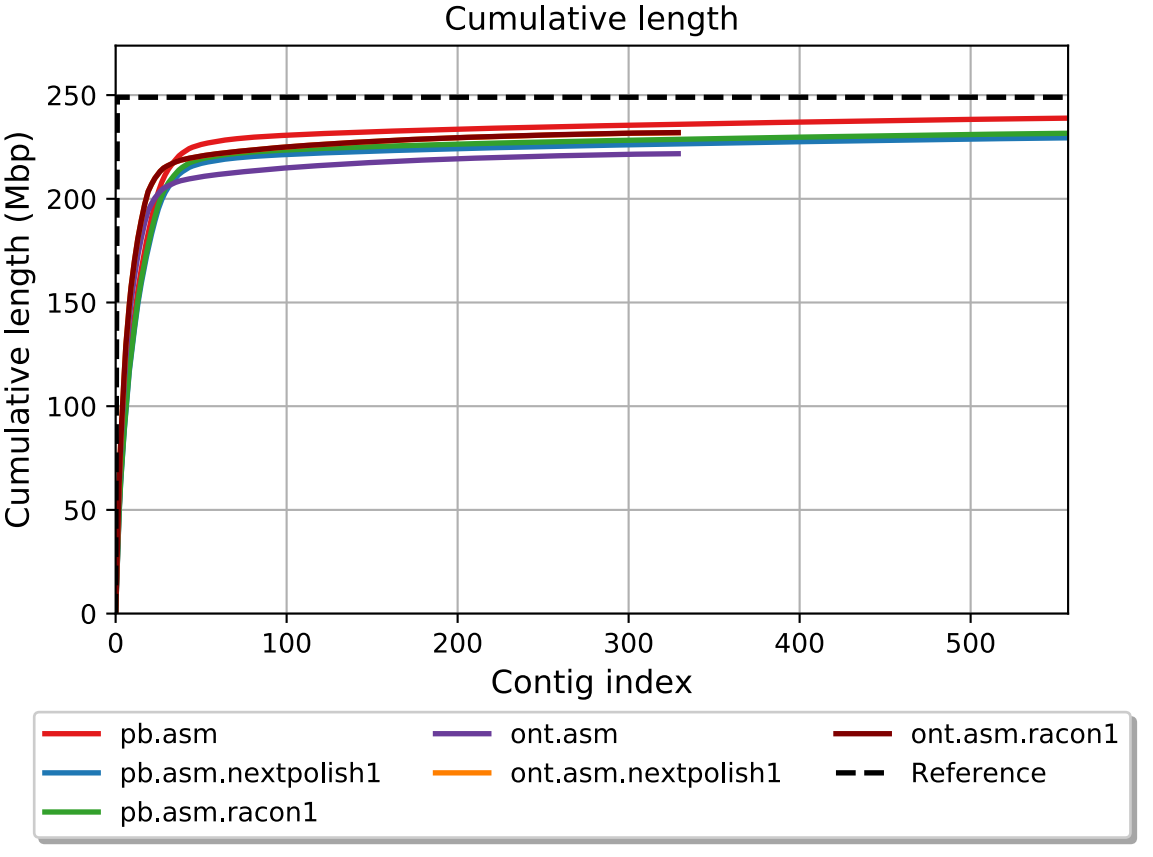
Unaligned report

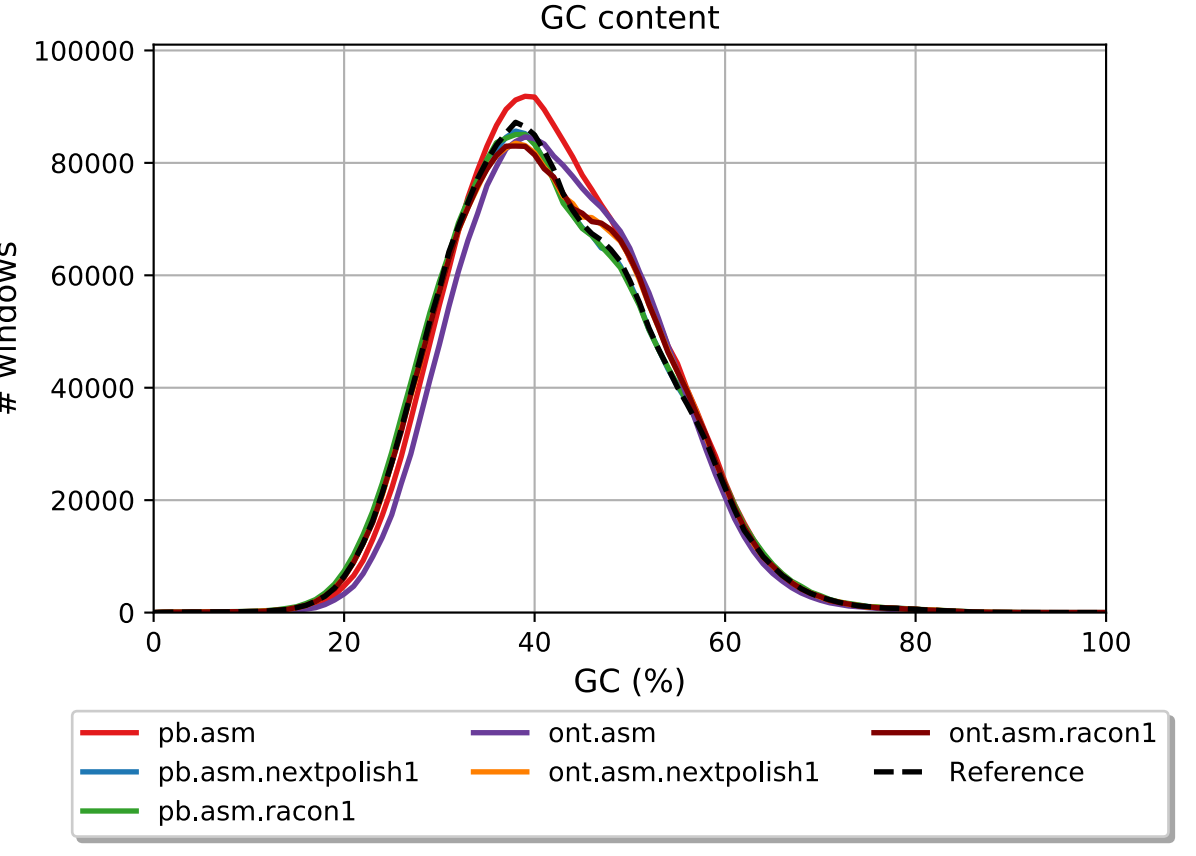
	pb.asm	pb.asm.nextpolish1	pb.asm.racon1	ont.asm	ont.asm.nextpolish1	ont.asm.racon1
# fully unaligned contigs	34	17	2	80	96	158
Fully unaligned length	691006	249325	25698	2839270	3128915	5436487
# partially unaligned contigs	86	48	51	124	106	44
Partially unaligned length	311733	58616	44828	3396089	3034773	995440
# N's	0	0	0	0	0	0

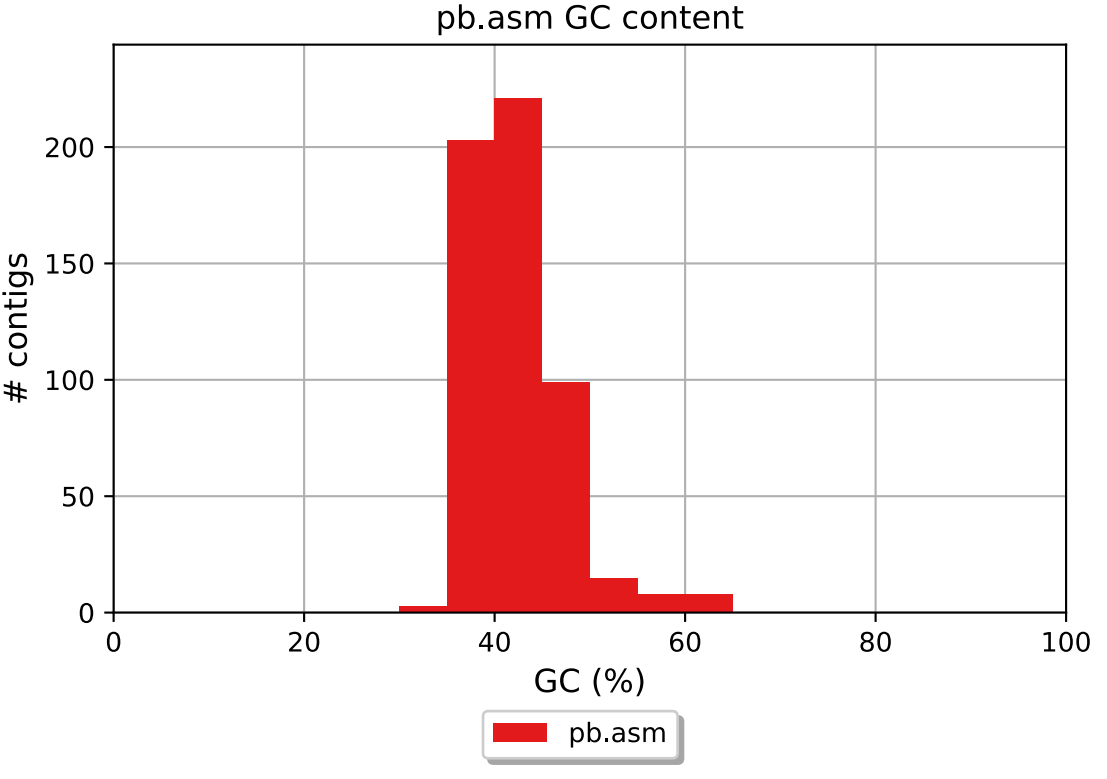
All statistics are based on contigs of size >= 3000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

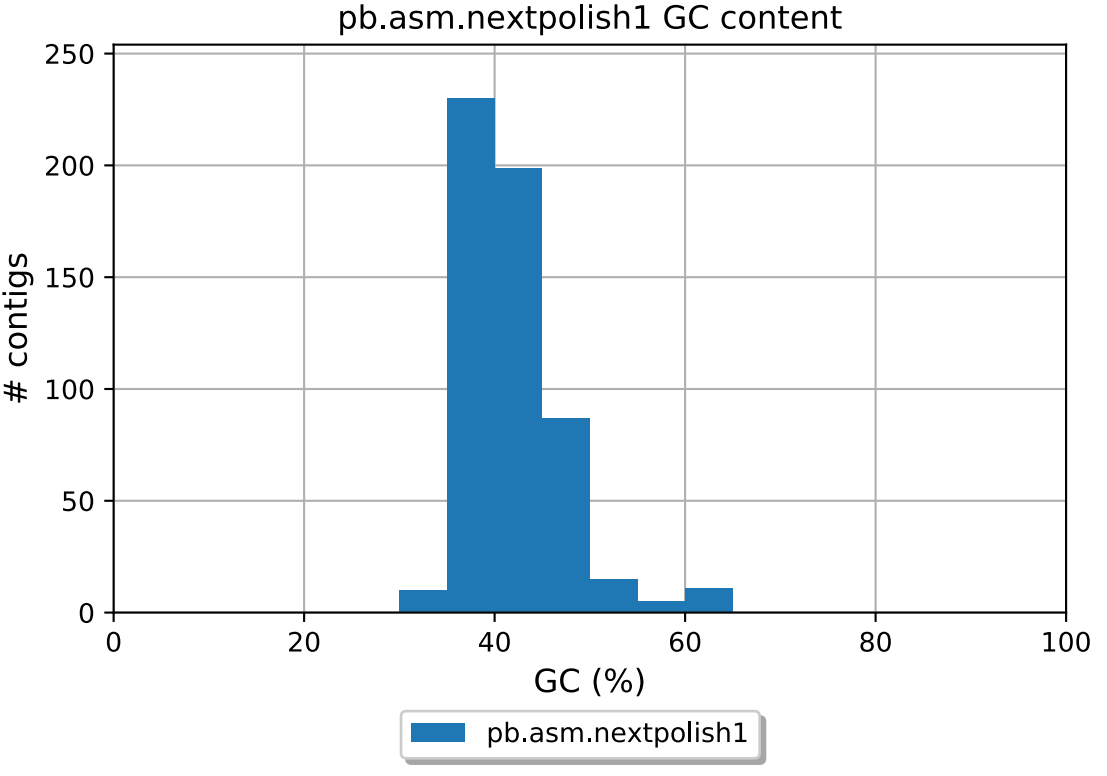

Nx
Contig length (Mbp)
0
6
12
18
24
30
0
20
40
60
80
100
x
pb.asm
pb.asm.nextpolish1
pb.asm.racon1
ont.asm
ont.asm.nextpolish1
ont.asm.racon1

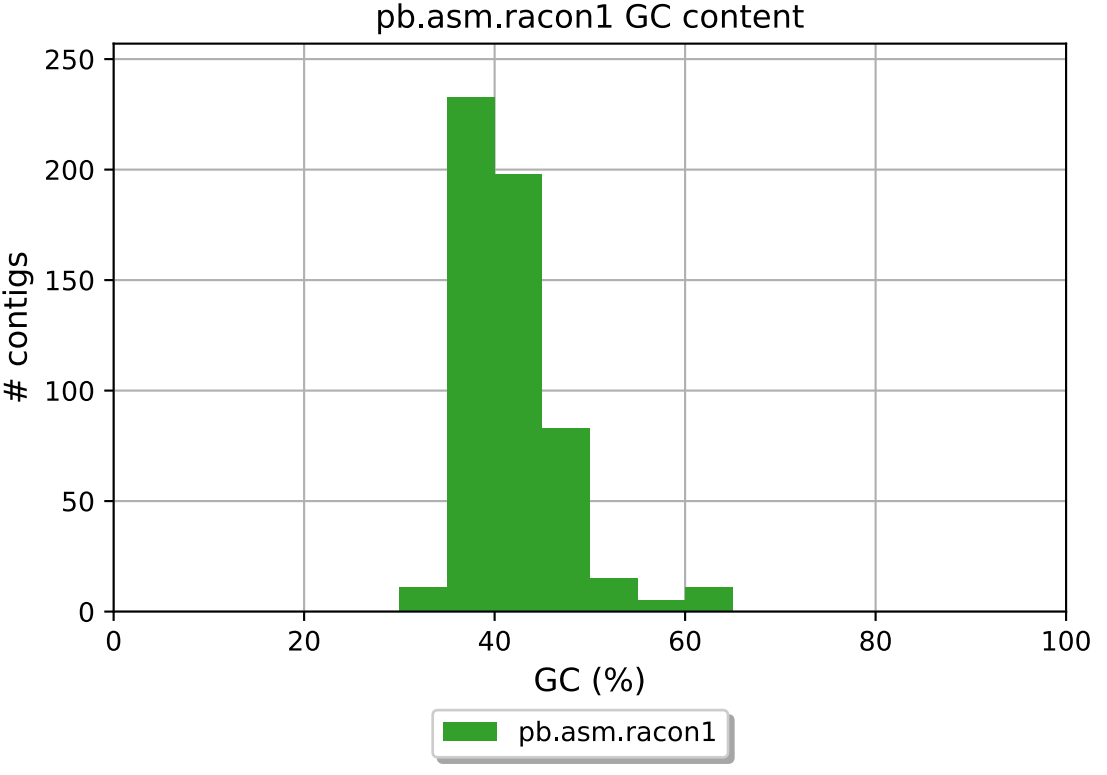

NGx
Contig length (Mbp)
0
6
12
18
24
30
0
20
40
60
80
100
x
pb.asm
pb.asm.nextpolish1
pb.asm.racon1
ont.asm
ont.asm.nextpolish1
ont.asm.racon1

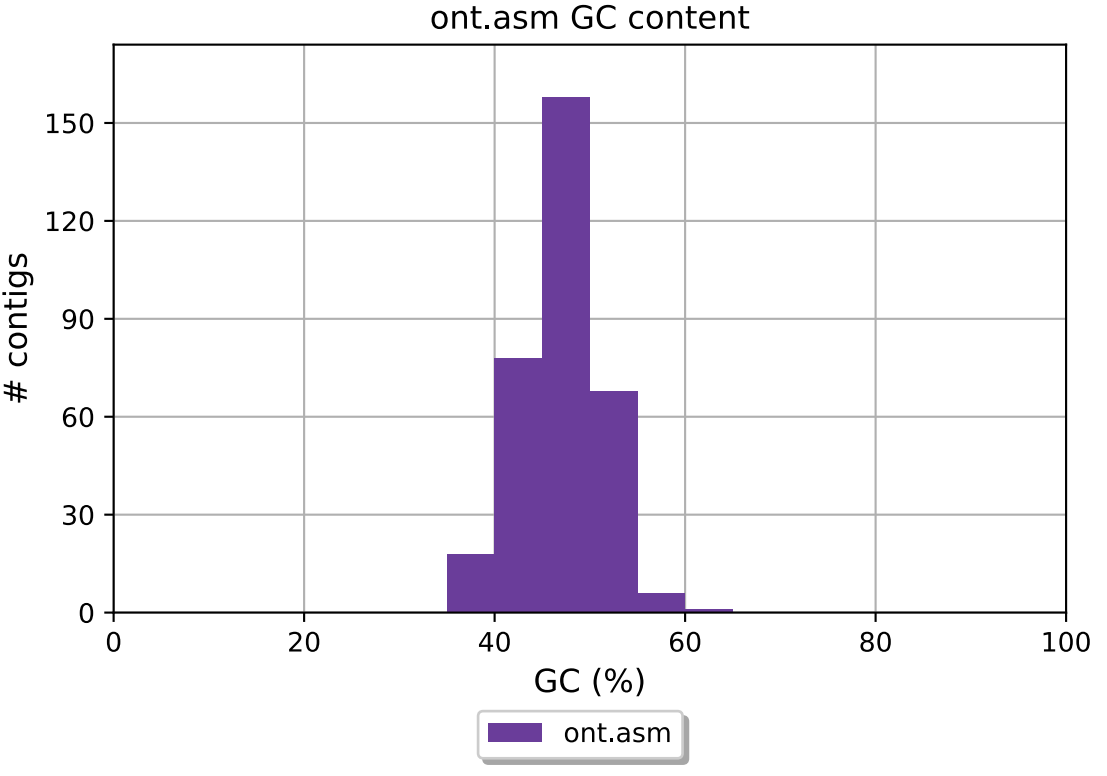

Cumulative length
Cumulative length (Mbp)
250
200
150
100
50
0
0
100
200
300
400
500
Contig index
pb.asm
pb.asm.nextpolish1
pb.asm.racon1
ont.asm
ont.asm.nextpolish1
ont.asm.racon1
Reference

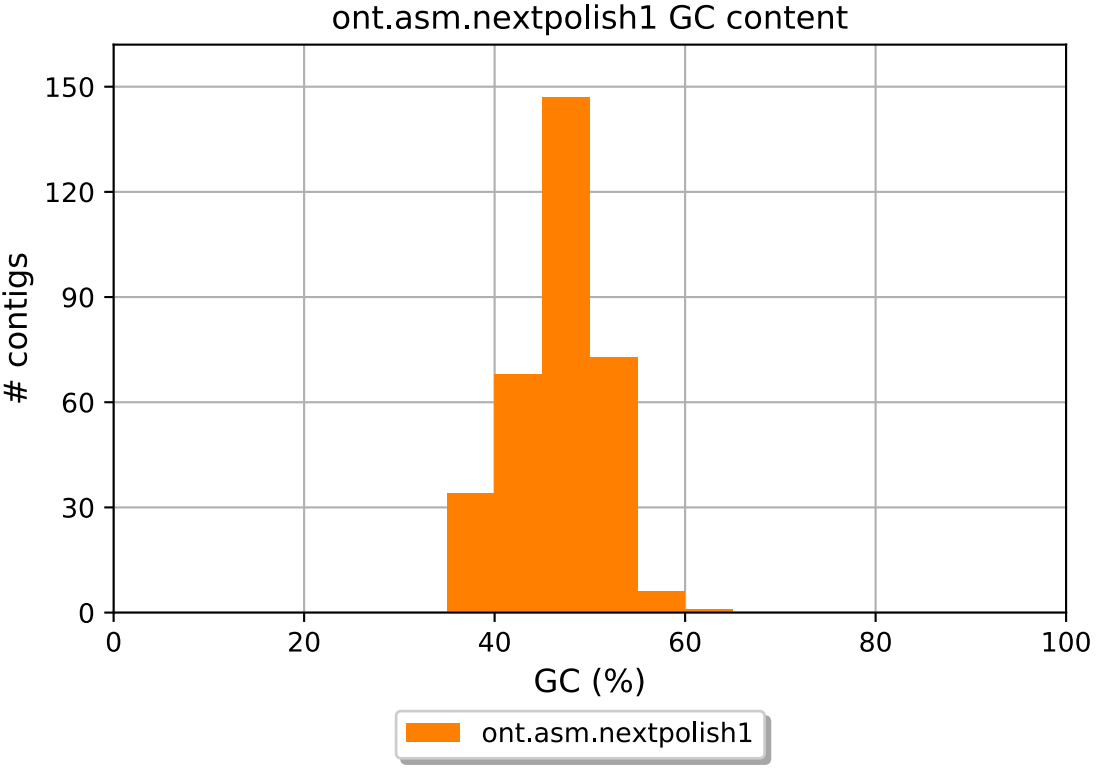

GC content
100000
80000
60000
40000
20000
0
windows
0
20
40
60
80
100
GC (%)
pb.asm
pb.asm.nextpolish1
pb.asm.racon1
ont.asm
ont.asm.nextpolish1
ont.asm.racon1
Reference

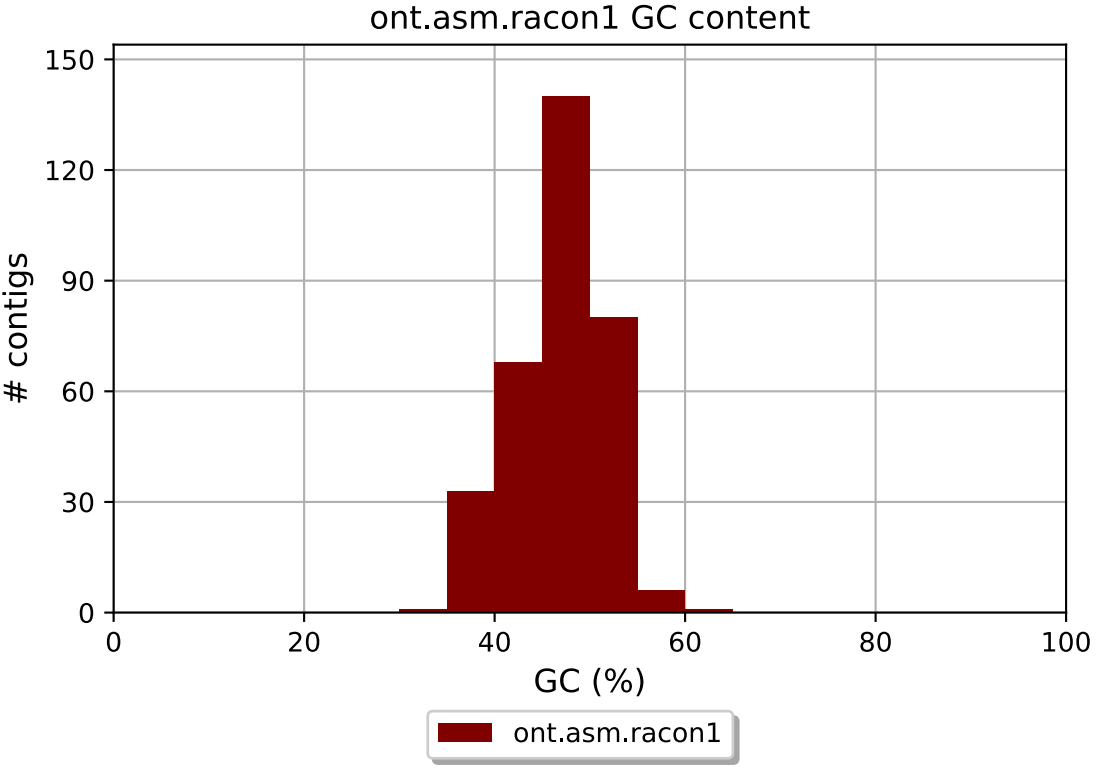

pb.asm GC content
contigs
0
50
100
150
200
0
20
40
60
80
100
GC (%)
pb.asm


pb.asm.nextpolish1 GC content
contigs
GC (%)
0
50
100
150
200
250
0
20
40
60
80
100
pb.asm.nextpolish1

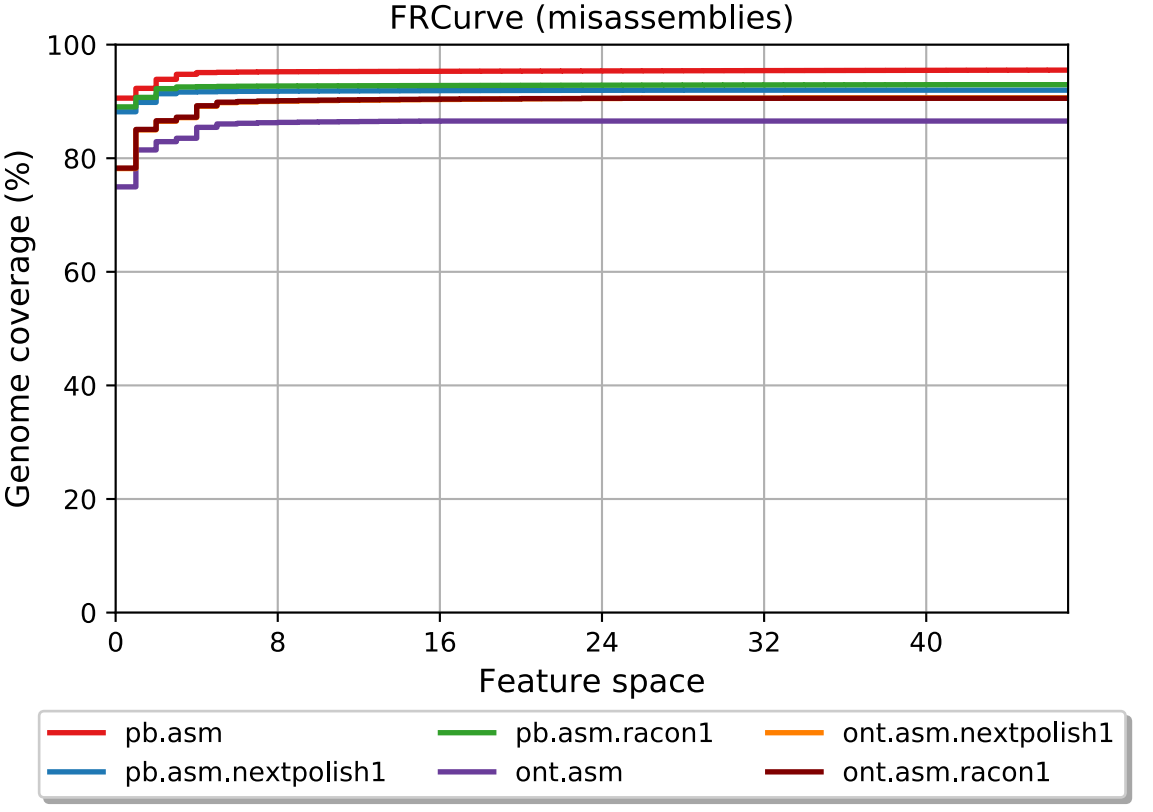

pb.asm.racon1 GC content
contigs
GC (%)
0
50
100
150
200
250
0
20
40
60
80
100
pb.asm.racon1

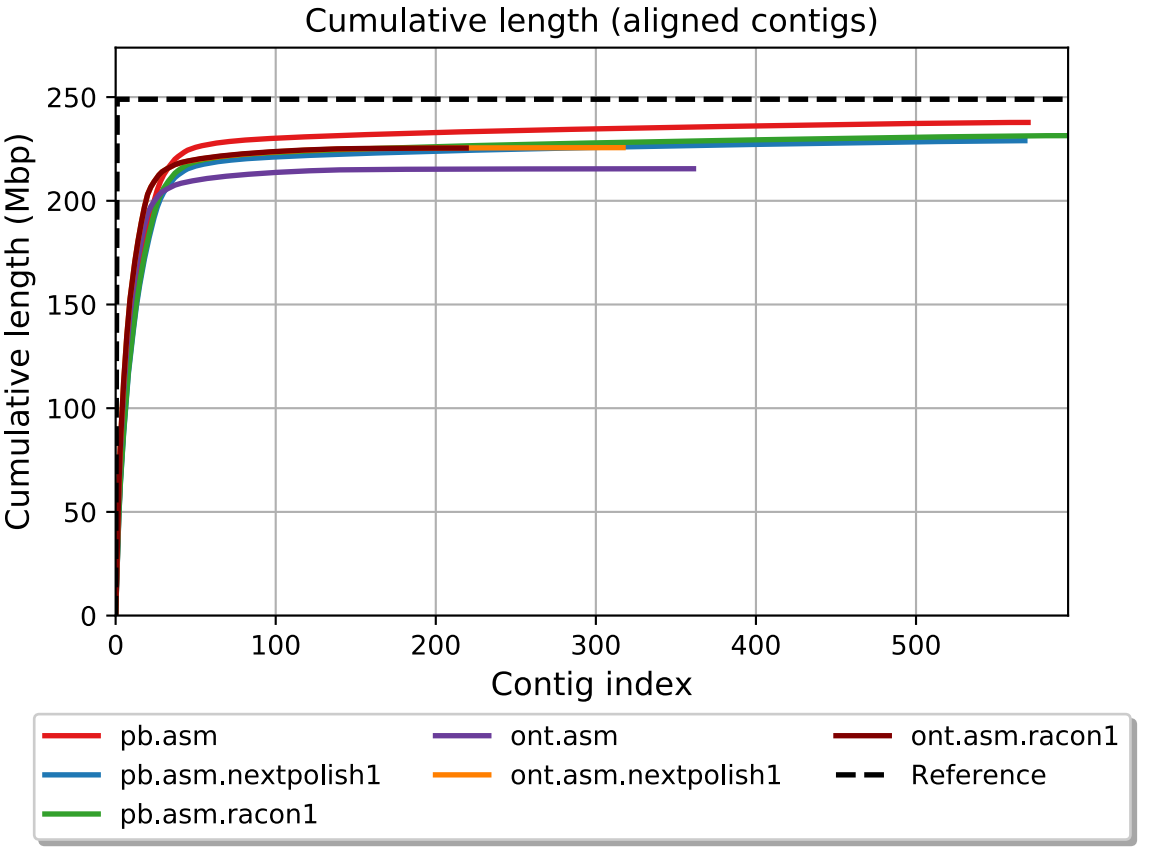

ont.asm GC content
contigs
150
120
90
60
30
0
0
20
40
60
80
100
GC (%)
ont.asm

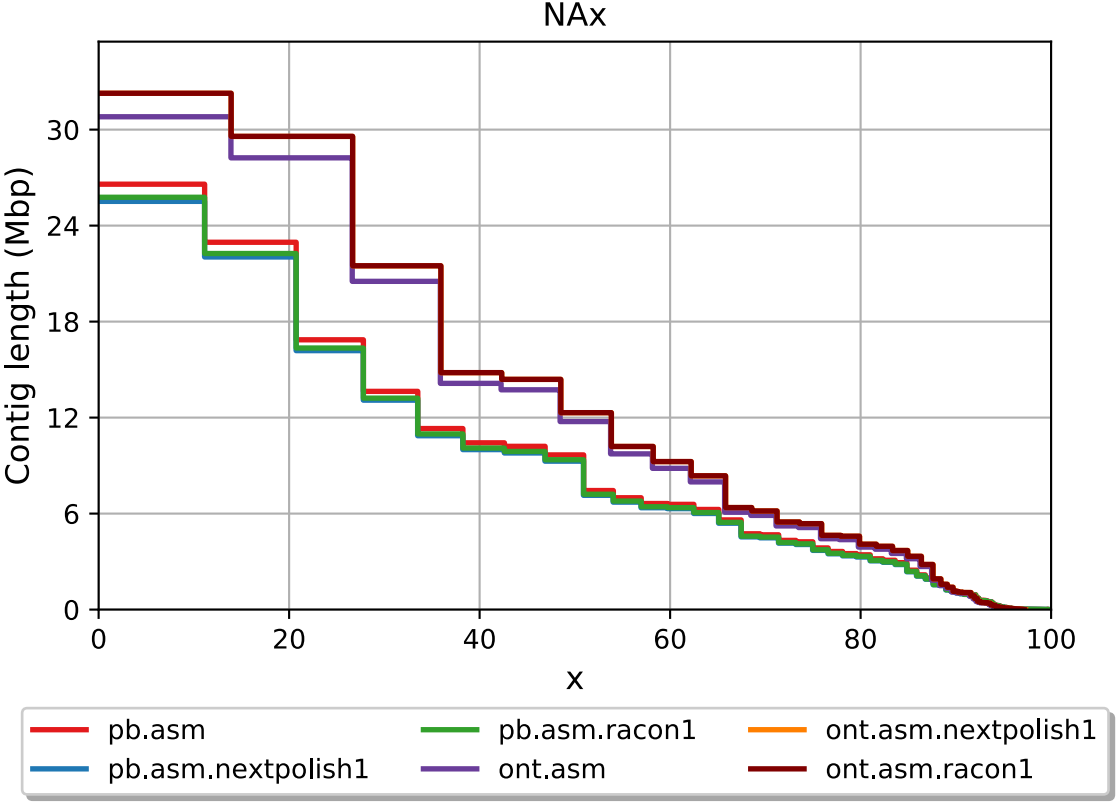

ont.asm.nextpolish1 GC content
contigs
150
120
90
60
30
0
0
20
40
60
80
100
GC (%)
ont.asm.nextpolish1

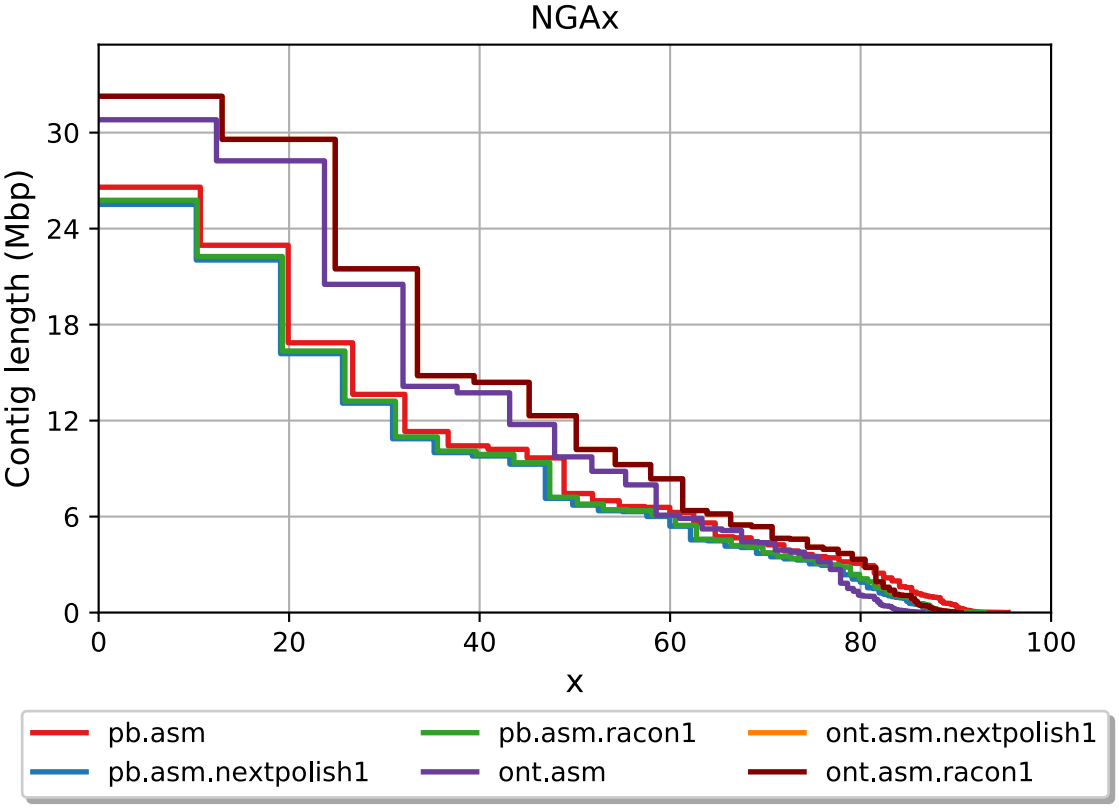

ont.asm.racon1 GC content
contigs
GC (%)
0
30
60
90
120
150
0
20
40
60
80
100
ont.asm.racon1

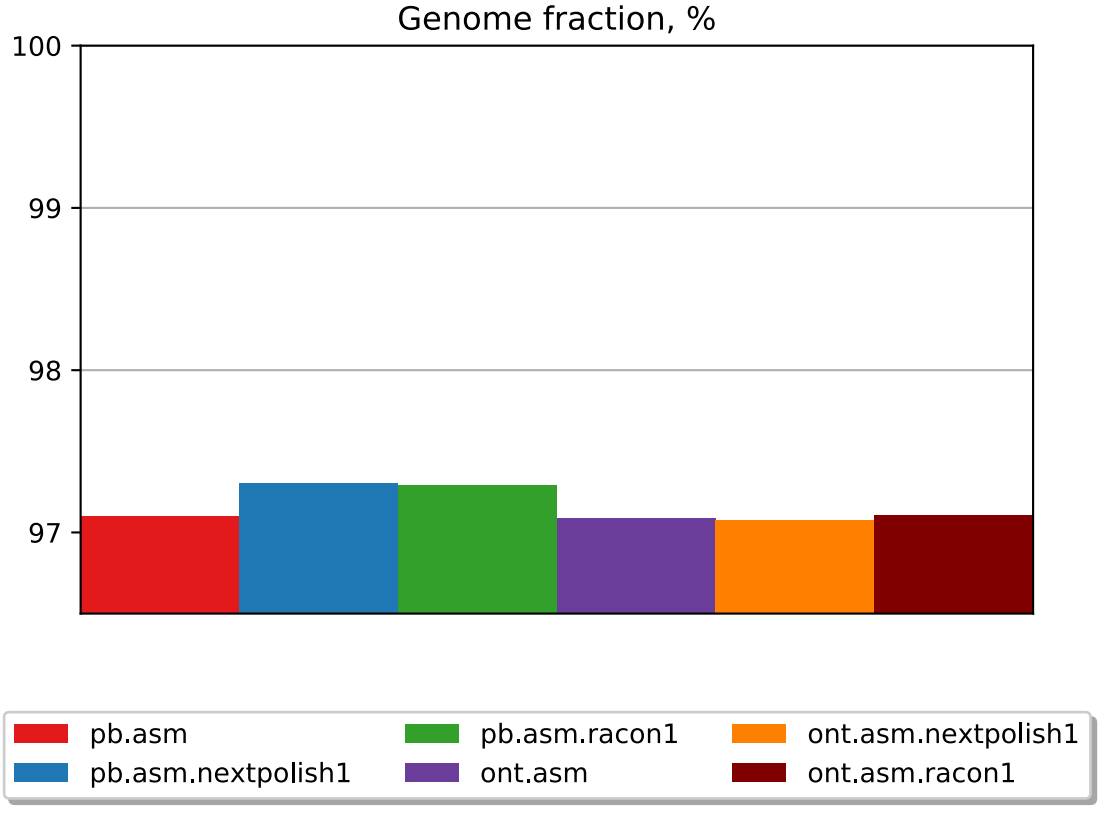
Misassemblies
50
40
30
20
10
0
pb.asm
pb.asm.nextpolish1
pb.asm.racon1
ont.asm
ont.asm.nextpolish1
ont.asm.racon1
relocations
inversions


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
8
16
24
32
40
Feature space
pb.asm
pb.asm.racon1
ont.asm.nextpolish1
pb.asm.nextpolish1
ont.asm
ont.asm.racon1


Cumulative length (aligned contigs)
Cumulative length (Mbp)
250
200
150
100
50
0
0
100
200
300
400
500
Contig index
pb.asm
pb.asm.nextpolish1
pb.asm.racon1
ont.asm
ont.asm.nextpolish1
ont.asm.racon1
Reference


NAx
Contig length (Mbp)
0
6
12
18
24
30
0
20
40
60
80
100
x
pb.asm
pb.asm.nextpolish1
pb.asm.racon1
ont.asm
ont.asm.nextpolish1
ont.asm.racon1


NGAx
Contig length (Mbp)
0
6
12
18
24
30
0
20
40
60
80
100
x
pb.asm
pb.asm.nextpolish1
pb.asm.racon1
ont.asm
ont.asm.nextpolish1
ont.asm.racon1


Genome fraction, %
100
99
98
97
pb.asm
pb.asm.nextpolish1
pb.asm.racon1
ont.asm
ont.asm.nextpolish1
ont.asm.racon1