Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	16	11	18	9
# contigs (>= 5000 bp)	5	4	3	4
# contigs (>= 10000 bp)	4	3	0	4
# contigs (>= 25000 bp)	3	2	0	3
# contigs (>= 50000 bp)	2	2	0	1
Total length (>= 1000 bp)	500159	169951	51222	192181
Total length (>= 5000 bp)	478942	161306	20130	184202
Total length (>= 10000 bp)	471153	155859	0	184202
Total length (>= 25000 bp)	454022	145509	0	169995
Total length (>= 50000 bp)	409921	145509	0	92873
# contigs	19	17	34	15
Largest contig	210768	79037	8648	92873
Total length	502466	174182	62138	196130
Reference length	4458741	4458741	4458741	4458741
GC (%)	43.92	44.87	43.97	44.30
Reference GC (%)	45.25	45.25	45.25	45.25
N50	199153	66472	3524	43754
N75	199153	66472	1303	33368
L50	2	2	6	2
L75	2	2	14	3
# misassemblies	0	0	0	0
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	0	0	0
# structural variations	0	0	0	0
# unaligned contigs	0 + 3 part	0 + 3 part	0 + 4 part	0 + 6 part
Unaligned length	415237	116577	11912	115249
Genome fraction (%)	1.951	1.267	1.121	1.813
Duplication ratio	1.003	1.020	1.005	1.001
# N's per 100 kbp	11.34	761.85	0.00	26.51
# mismatches per 100 kbp	575.82	423.01	336.11	541.82
# indels per 100 kbp	26.43	21.24	8.00	22.27
Largest alignment	25330	12950	8648	33330
NA50	-	-	1545	-
NGA50	-	-	-	-
NA75	-	-	604	-
LA50	-	-	9	-
LA75	-	-	26	-

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

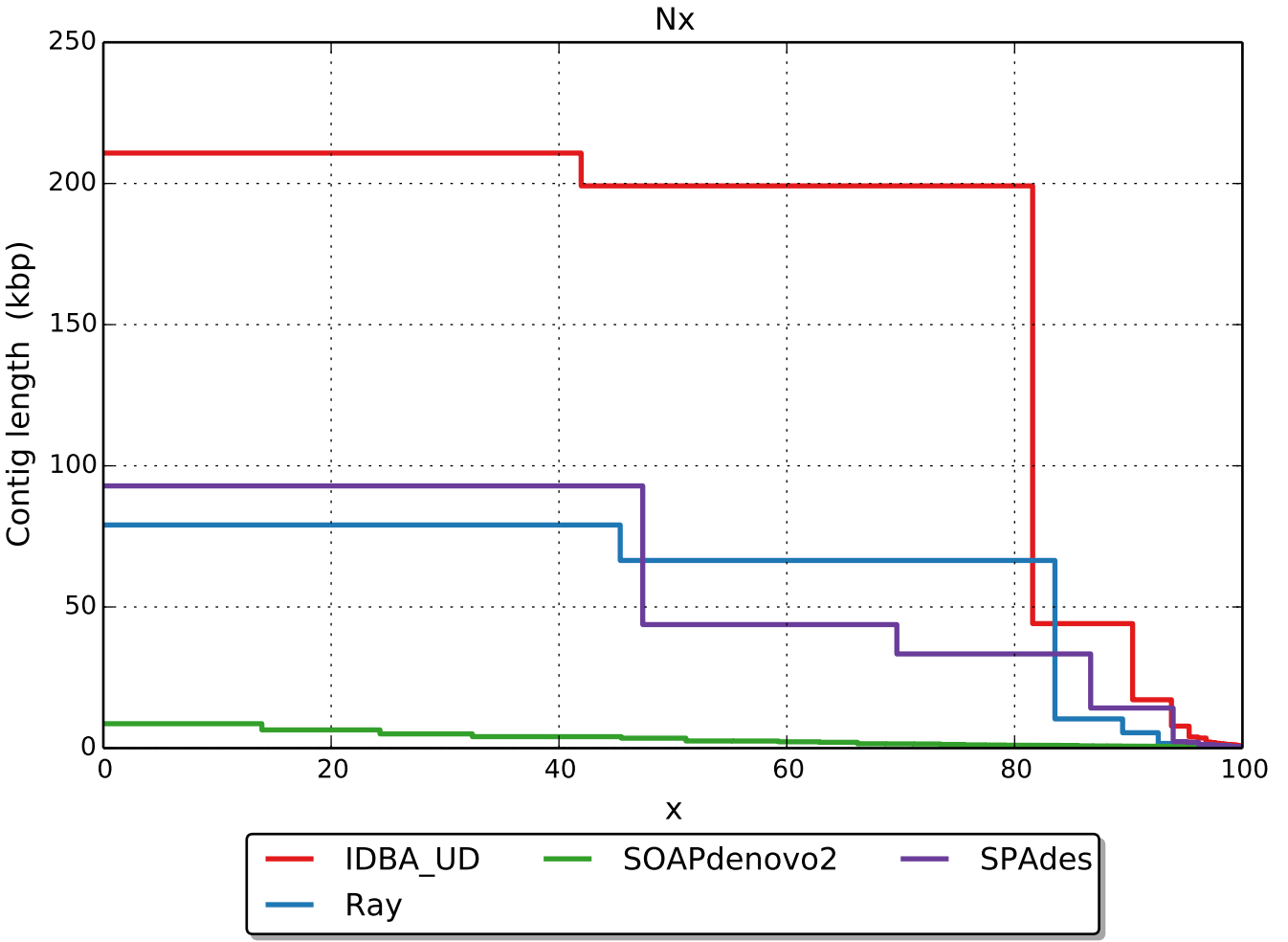
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	0	0	0
# relocations	0	0	0	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	2	2	1	2
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	0	0	0
# structural variations	0	0	0	0
# mismatches	501	239	168	438
# indels	23	12	4	18
# short indels	20	12	4	18
# long indels	3	0	0	0
Indels length	64	21	7	31

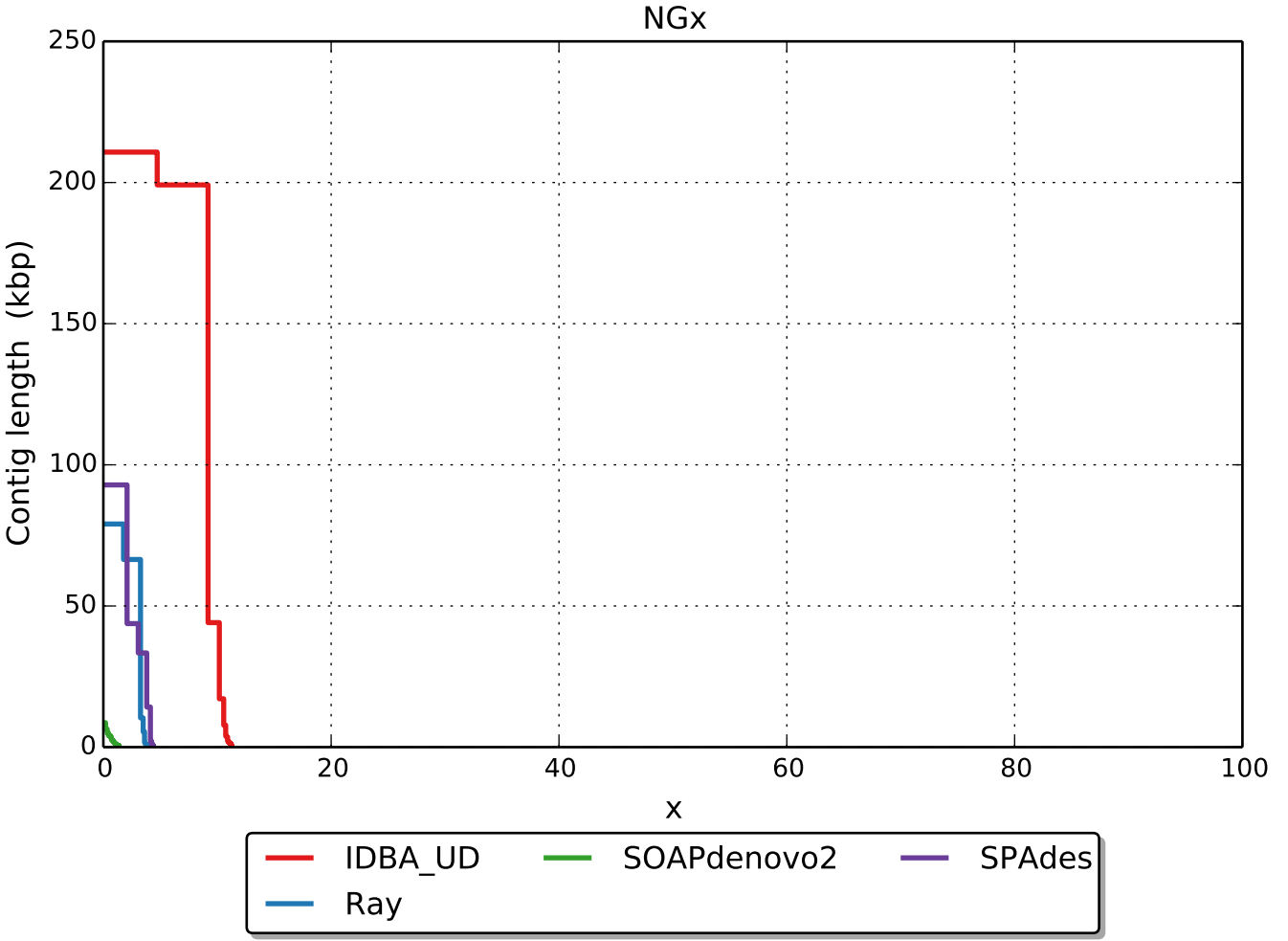
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

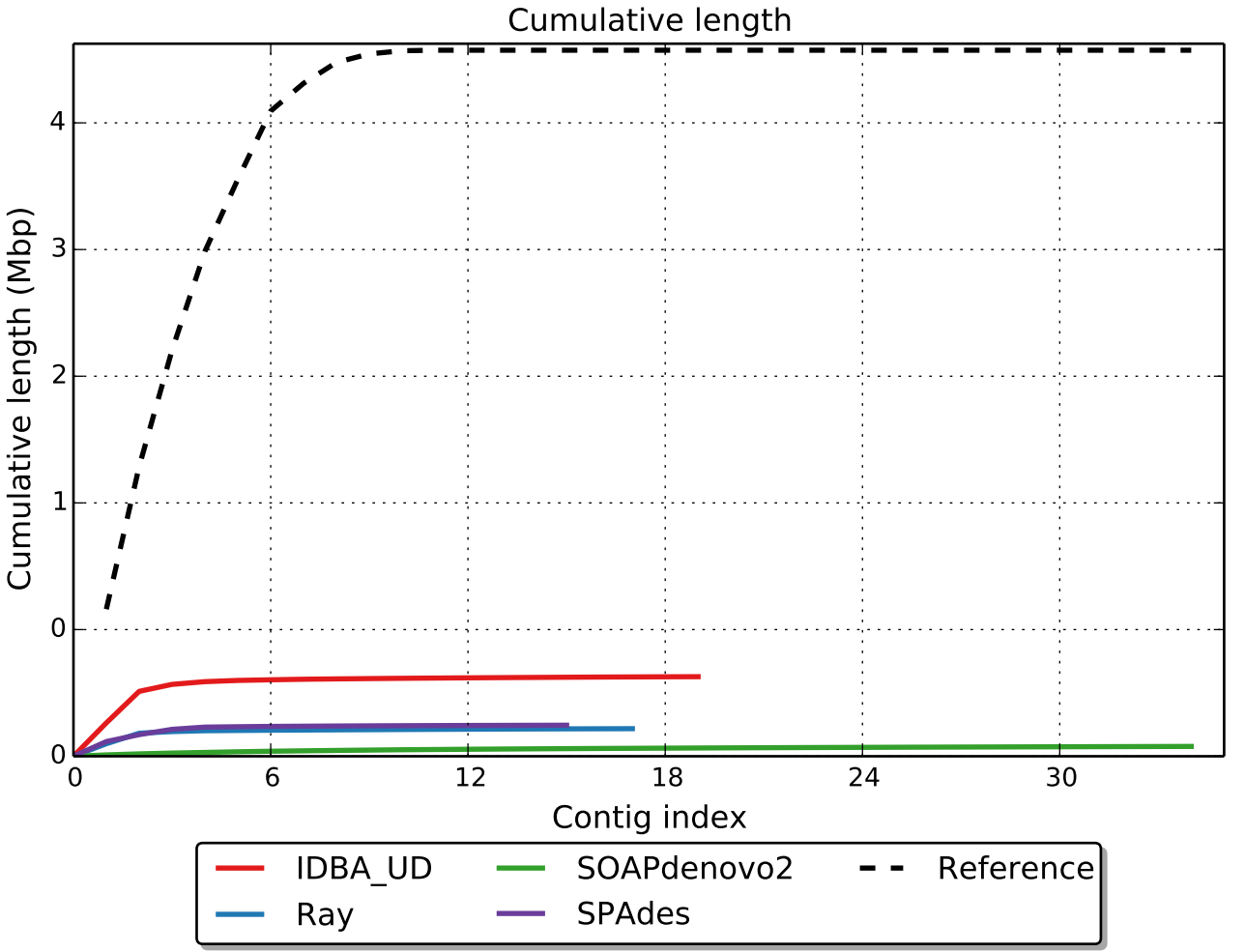
Unaligned report

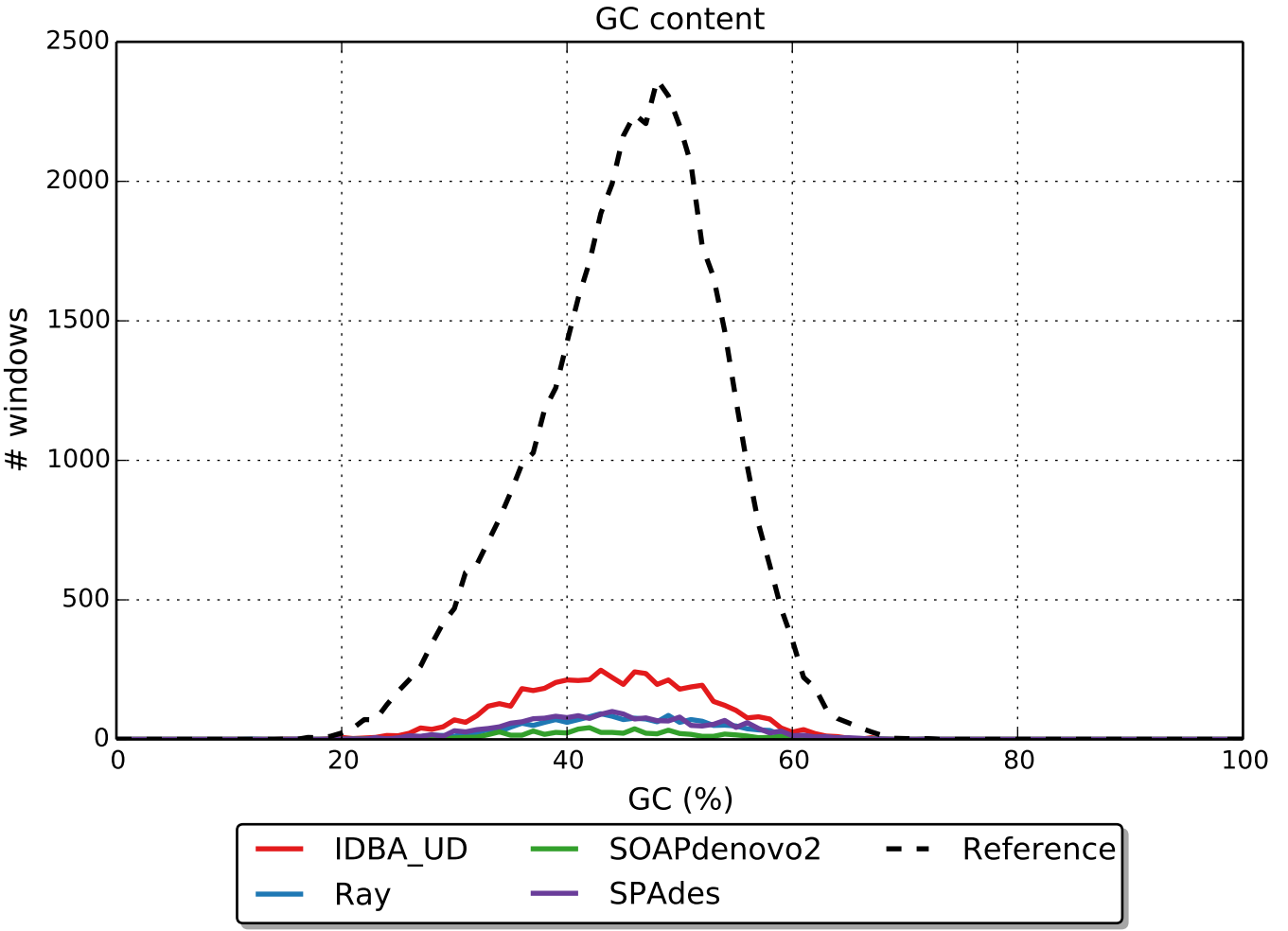
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	3	3	4	6
# with misassembly	2	3	0	1
# both parts are significant	2	2	1	2
Partially unaligned length	415237	116577	11912	115249
# N's	57	1327	0	52

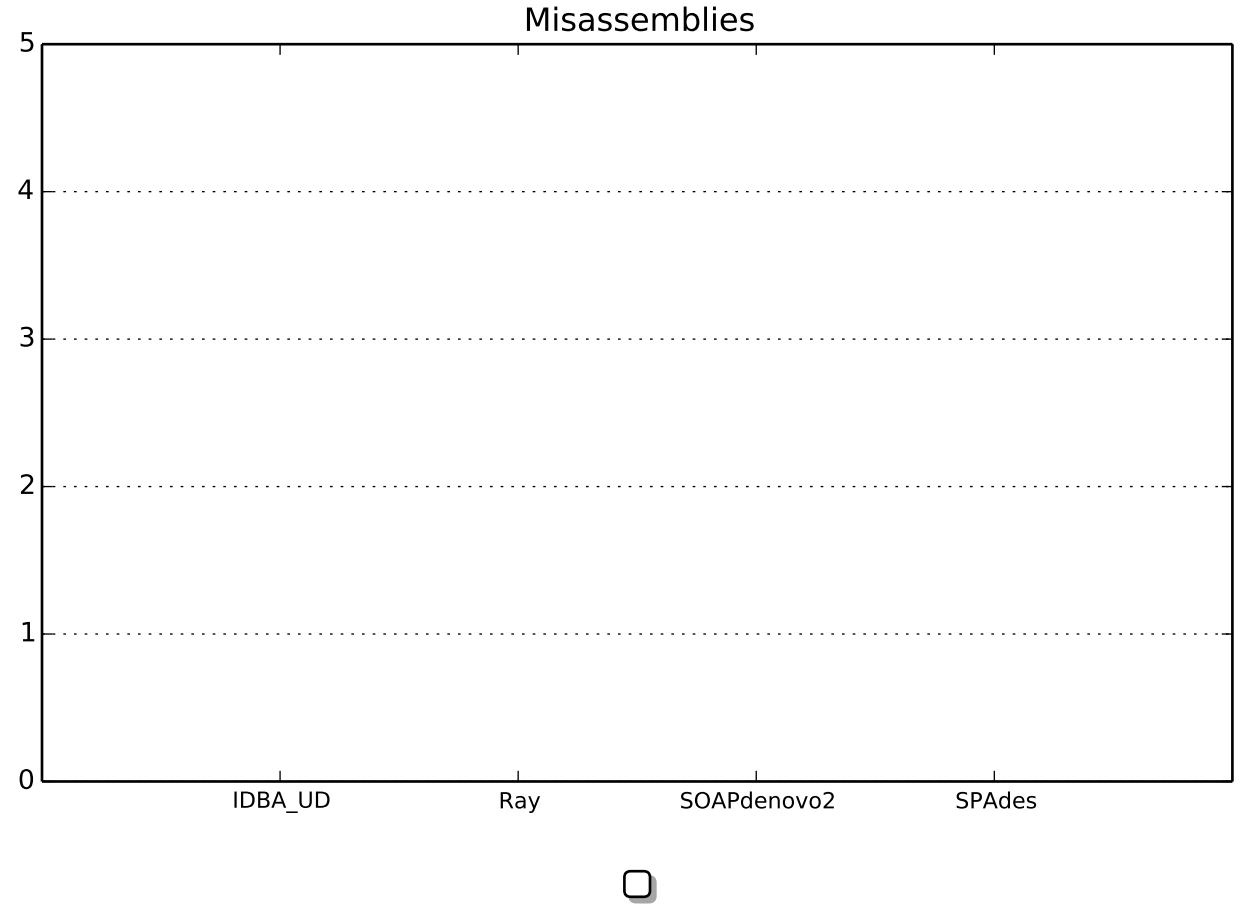
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

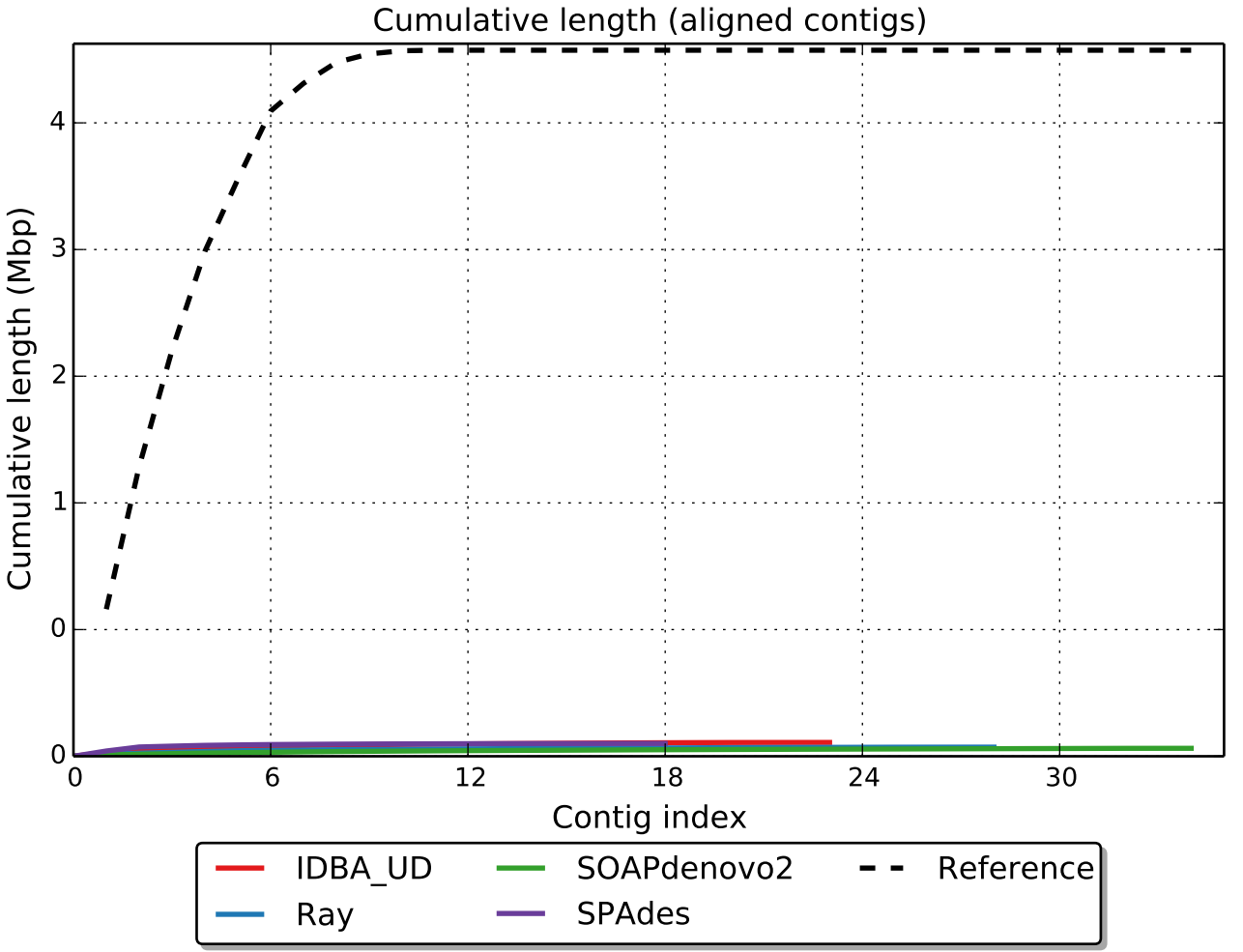

Nx
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray

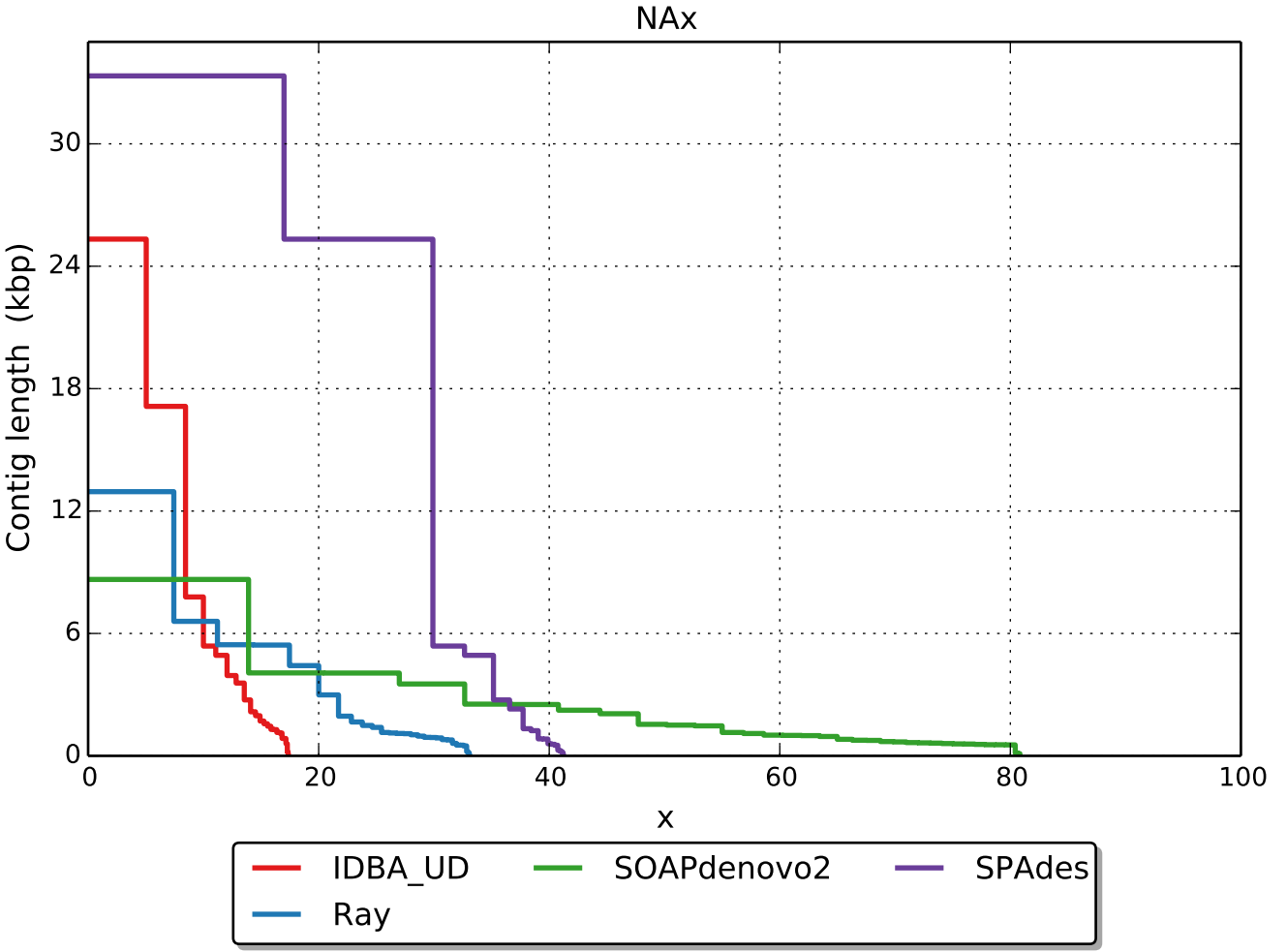

NGx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray

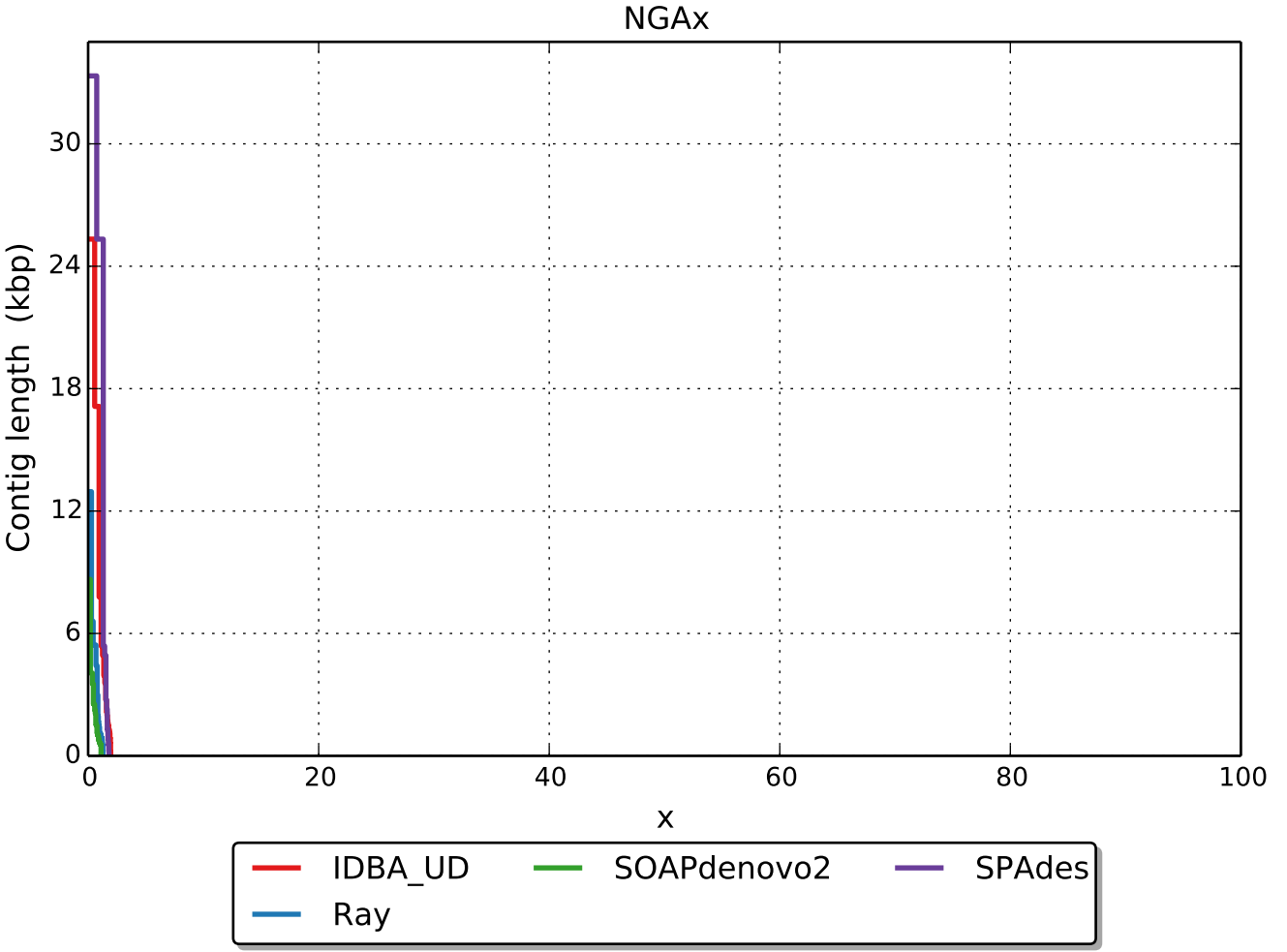

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
0
6
12
18
24
30
Contig index
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference

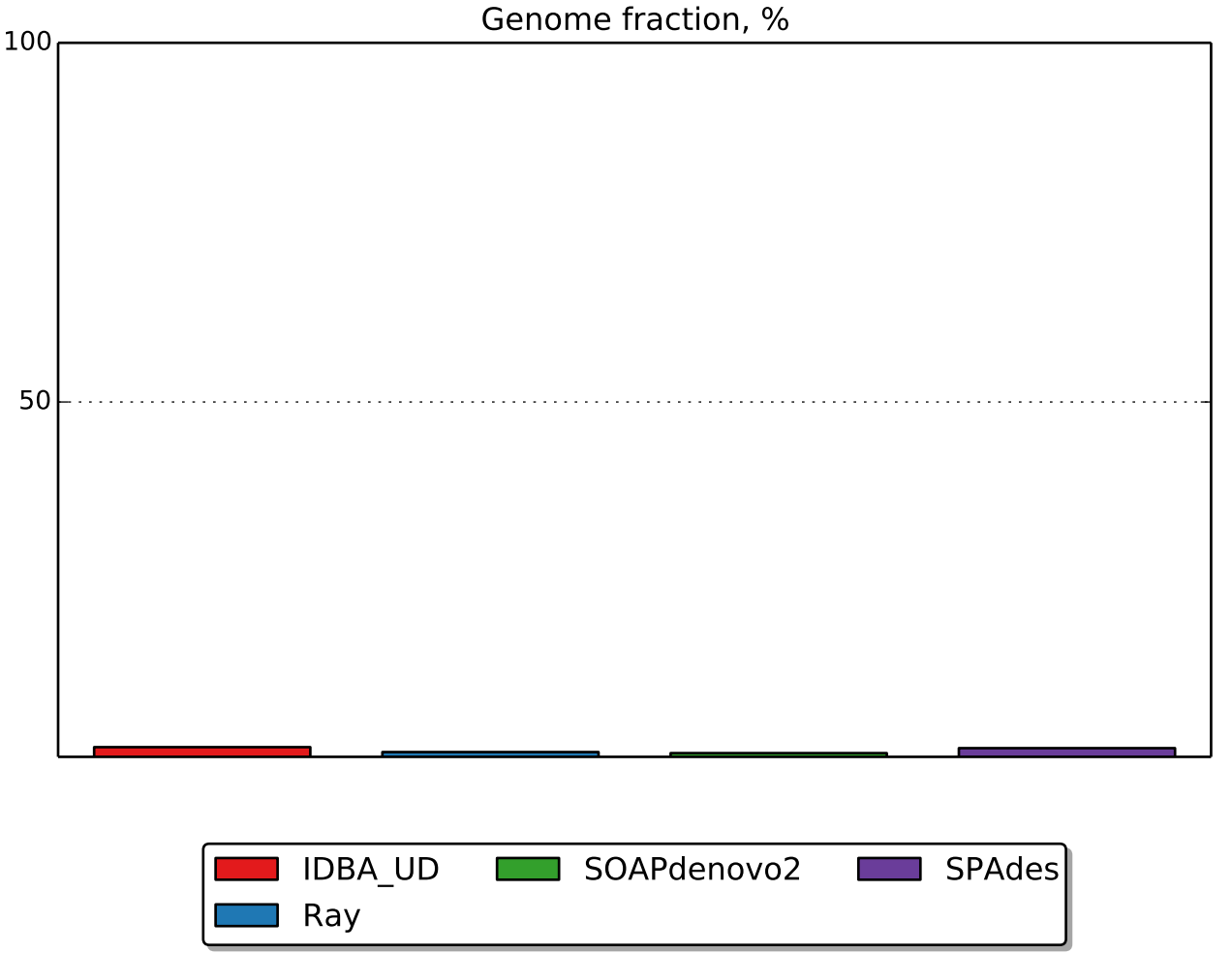

GC content
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


Misassemblies
5
4
3
2
1
0
IDBA_UD
Ray
SOAPdenovo2
SPAdes


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
0
6
12
18
24
30
Contig index
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


NAx
Contig length (kbp)
0
6
12
18
24
30
0
20
40
60
80
100
x
IDBA_UD
Ray
SOAPdenovo2
SPAdes


NGAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
IDBA_UD
Ray
SOAPdenovo2
SPAdes


Genome fraction, %
100
50
IDBA_UD
Ray
SOAPdenovo2
SPAdes