Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	83	15	3	138
# contigs (>= 5000 bp)	13	8	1	6
# contigs (>= 10000 bp)	9	7	0	4
# contigs (>= 25000 bp)	6	5	0	4
# contigs (>= 50000 bp)	5	2	0	2
Total length (>= 1000 bp)	788609	308196	13441	437631
Total length (>= 5000 bp)	692632	291777	6841	246558
Total length (>= 10000 bp)	660126	284189	0	234061
Total length (>= 25000 bp)	601183	246461	0	234061
Total length (>= 50000 bp)	553075	139054	0	149890
# contigs	499	15	27	691
Largest contig	199153	79037	6841	83103
Total length	1072464	308196	28268	806483
Reference length	4811379	4811379	4811379	4811379
GC (%)	44.88	44.34	40.15	44.21
Reference GC (%)	45.06	45.06	45.06	45.06
N50	56705	48365	844	1126
N75	934	27618	642	690
L50	5	3	4	106
L75	100	5	14	344
# misassemblies	1	0	0	2
# misassembled contigs	1	0	0	2
Misassembled contigs length	748	0	0	2675
# local misassemblies	0	0	45	3
# structural variations	0	0	0	0
# unaligned contigs	0 + 35 part	0 + 14 part	0 + 6 part	0 + 67 part
Unaligned length	706958	284623	9372	281784
Genome fraction (%)	7.578	0.434	0.320	10.754
Duplication ratio	1.003	1.128	1.226	1.014
# N's per 100 kbp	55.01	675.87	12303.66	1230.65
# mismatches per 100 kbp	788.01	2057.71	1504.83	967.49
# indels per 100 kbp	30.17	52.64	12.97	71.70
Largest alignment	2911	4420	2911	2911
NA50	-	-	293	578
NGA50	-	-	-	-
LA50	-	-	23	460

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

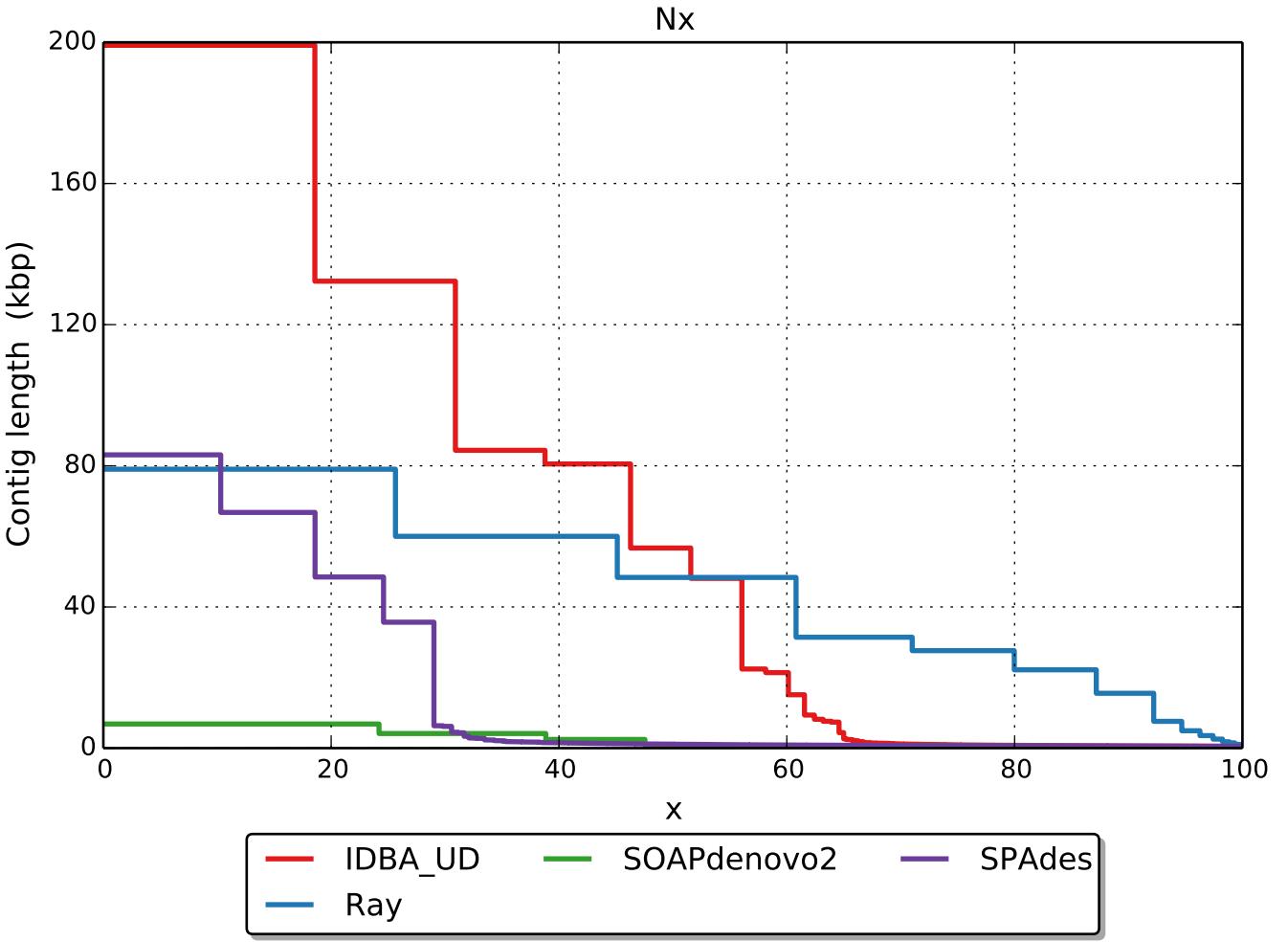
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	1	0	0	2
# relocations	1	0	0	2
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	3	3	3	16
# misassembled contigs	1	0	0	2
Misassembled contigs length	748	0	0	2675
# local misassemblies	0	0	45	3
# structural variations	0	0	0	0
# mismatches	2873	430	232	5006
# indels	110	11	2	371
# short indels	96	9	2	249
# long indels	14	2	0	122
Indels length	276	23	2	1965

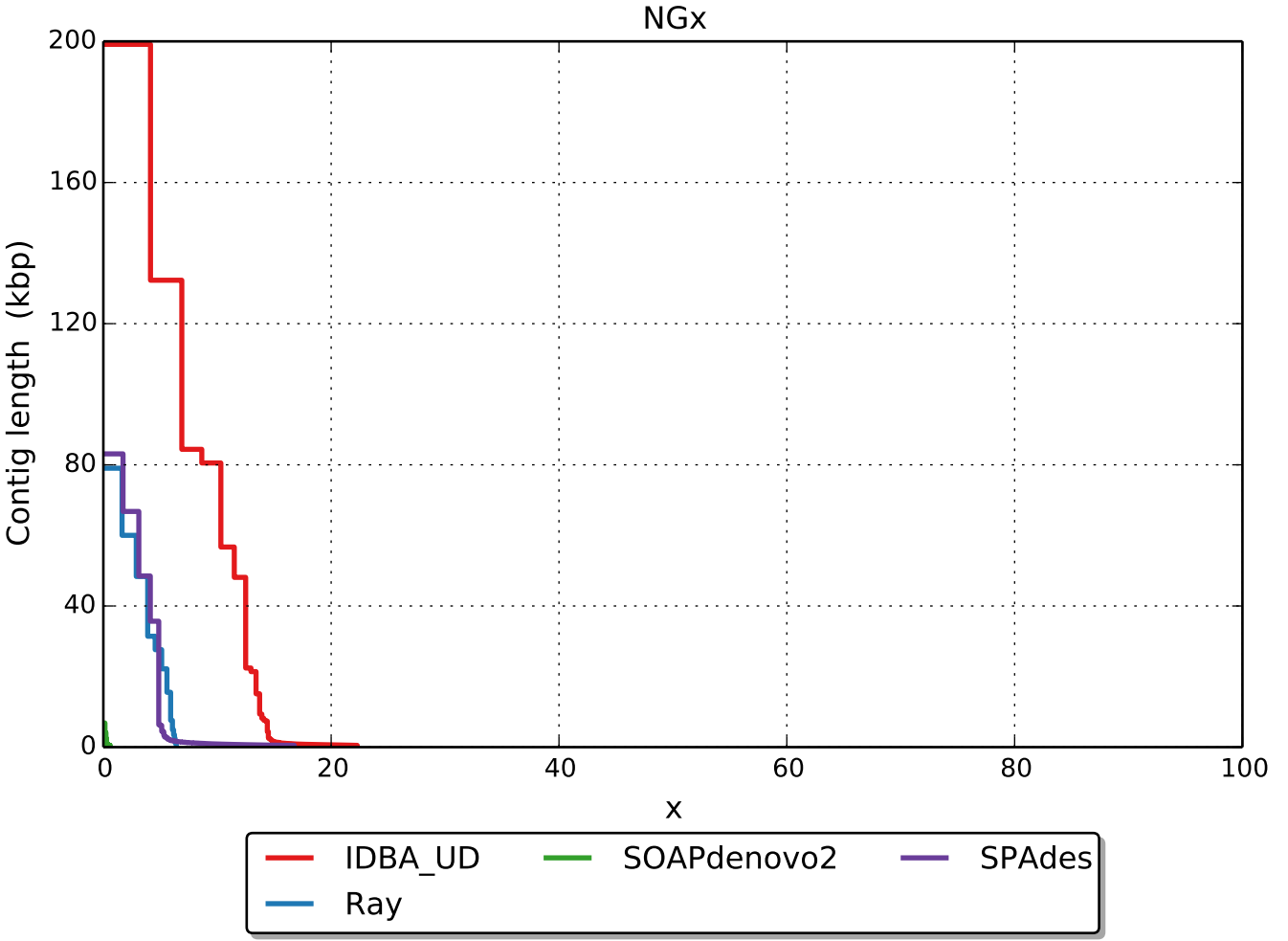
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

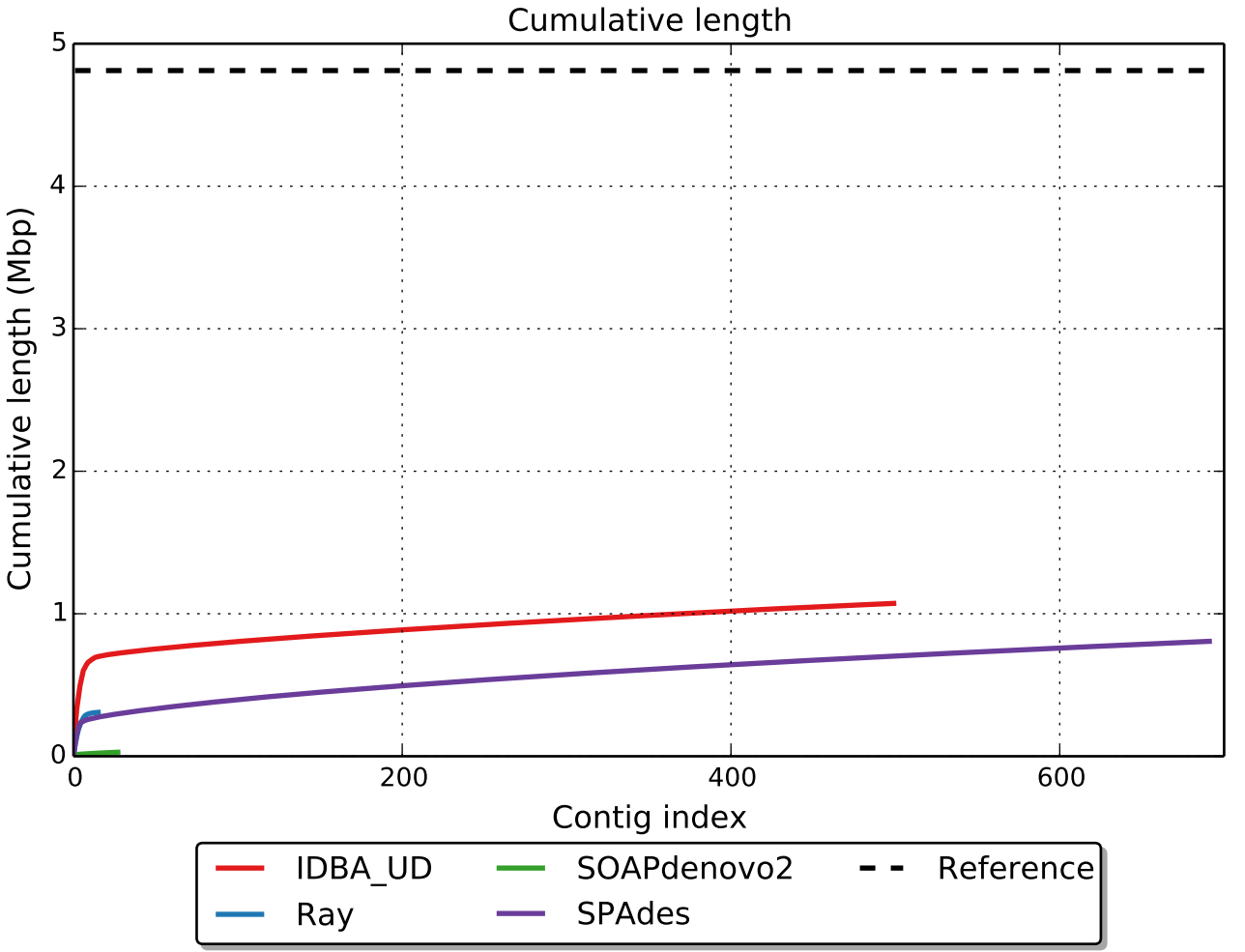
Unaligned report

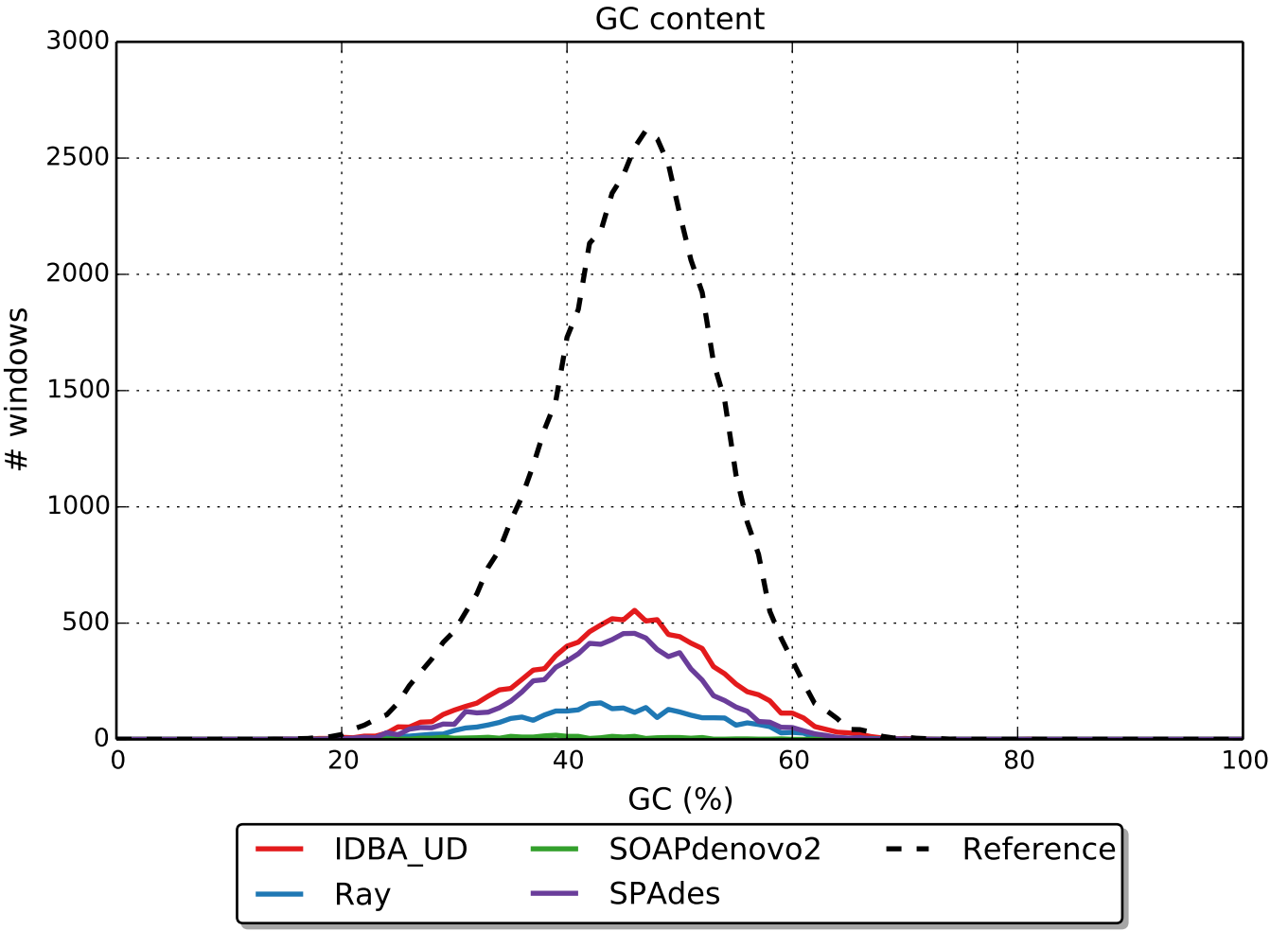
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	35	14	6	67
# with misassembly	2	3	2	6
# both parts are significant	3	3	3	16
Partially unaligned length	706958	284623	9372	281784
# N's	590	2083	3478	9925

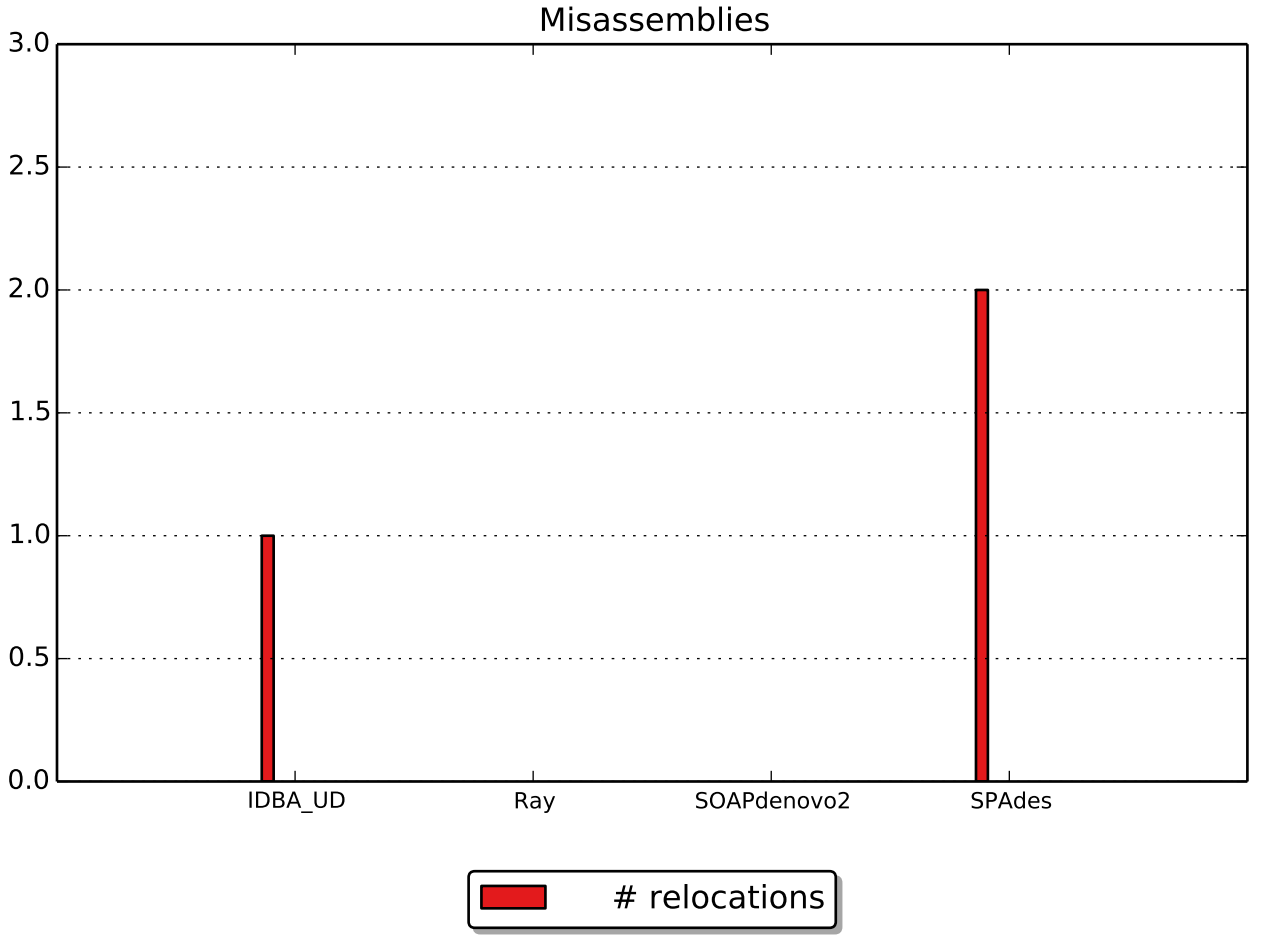
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

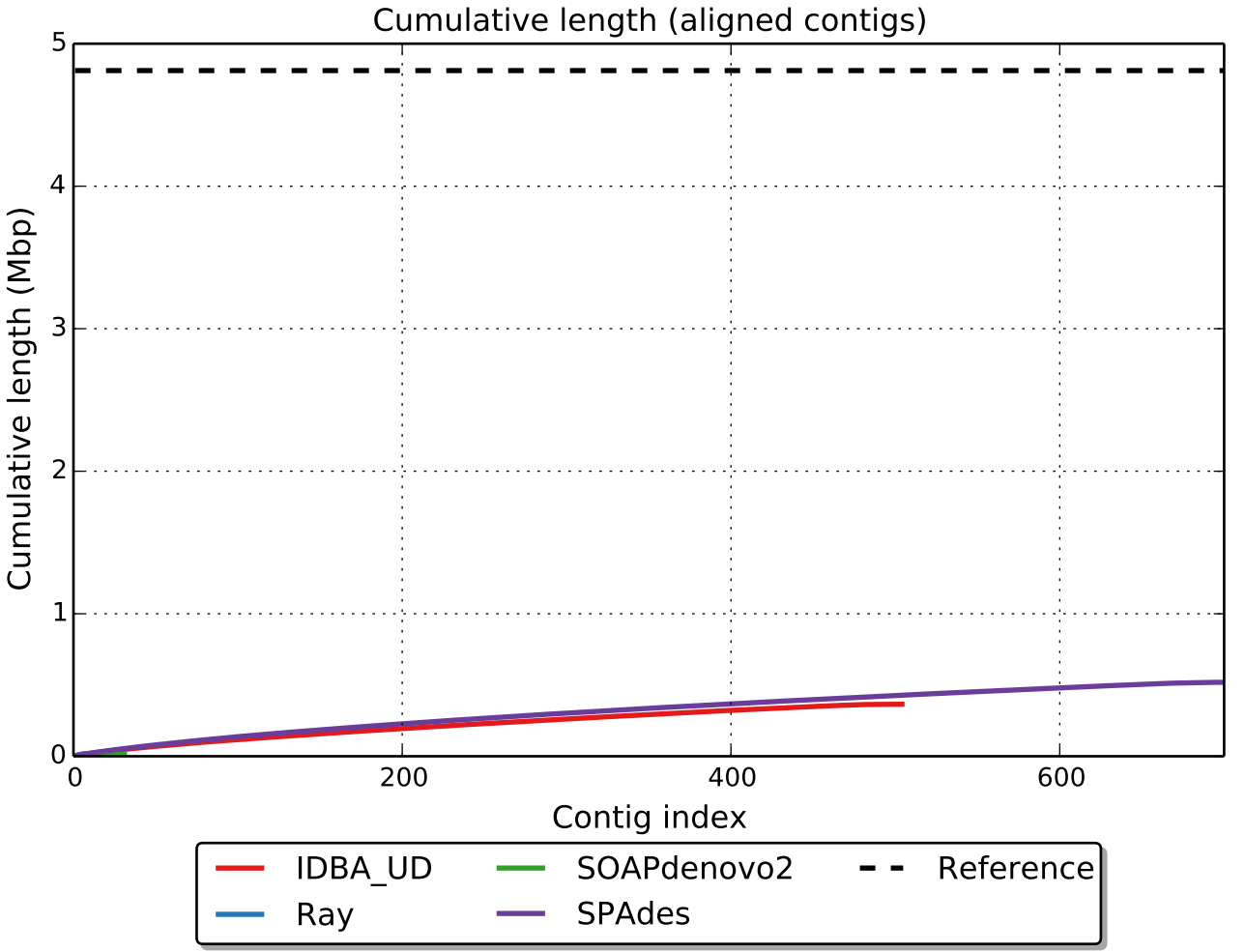

Nx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray

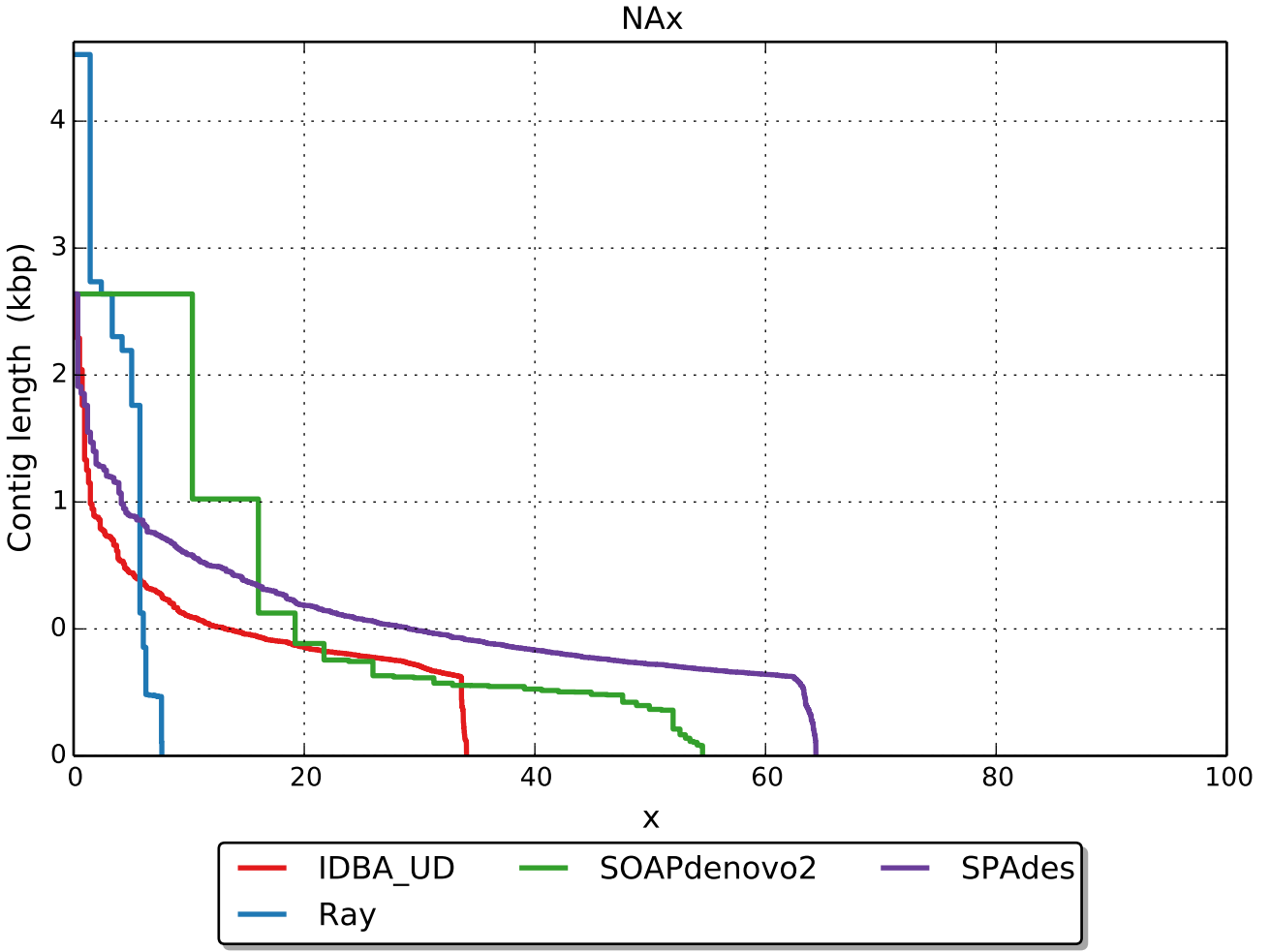

NGx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
IDBA_UD
Ray
SOAPdenovo2
SPAdes

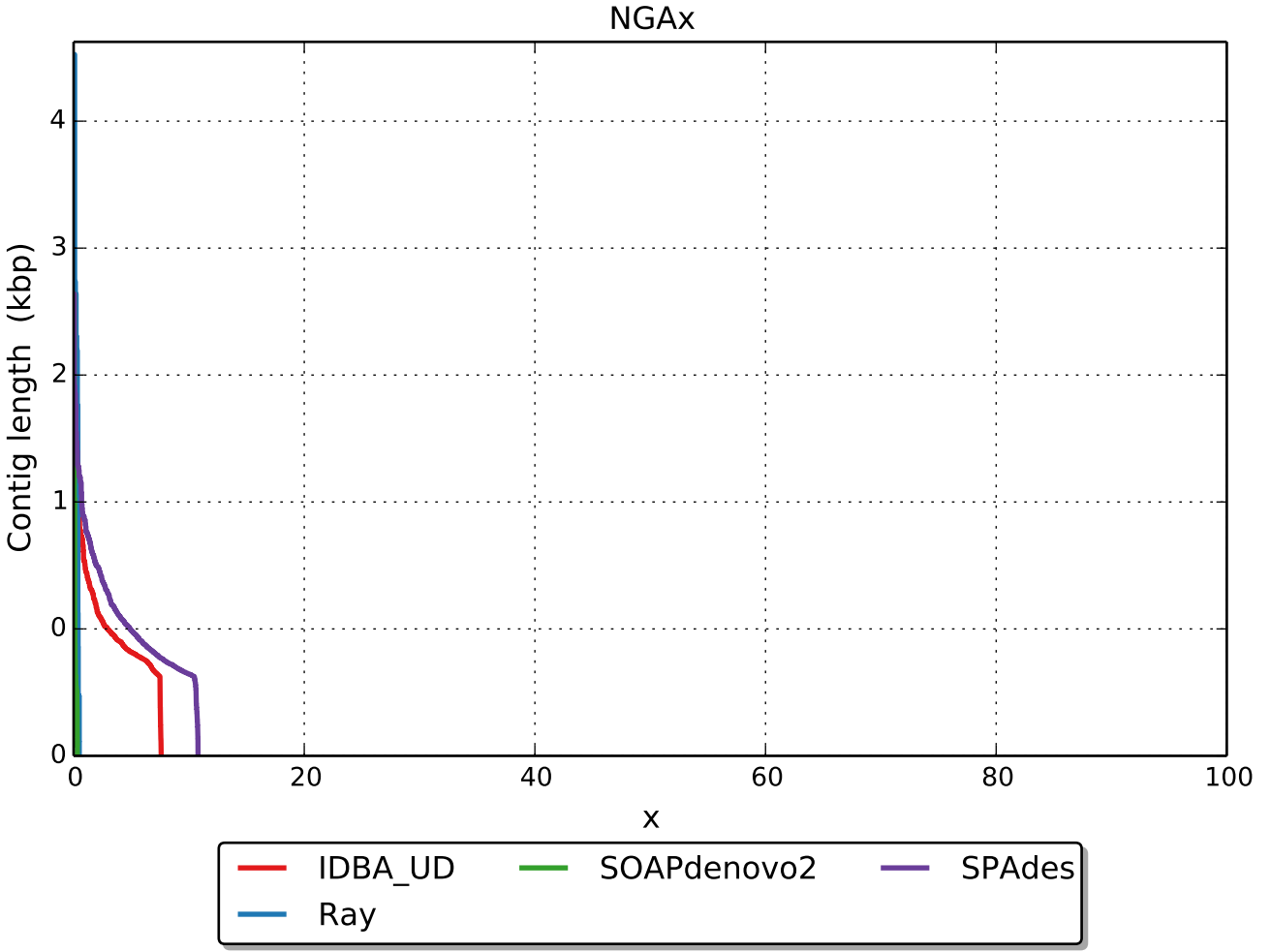

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
0
200
400
600
Contig index
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference

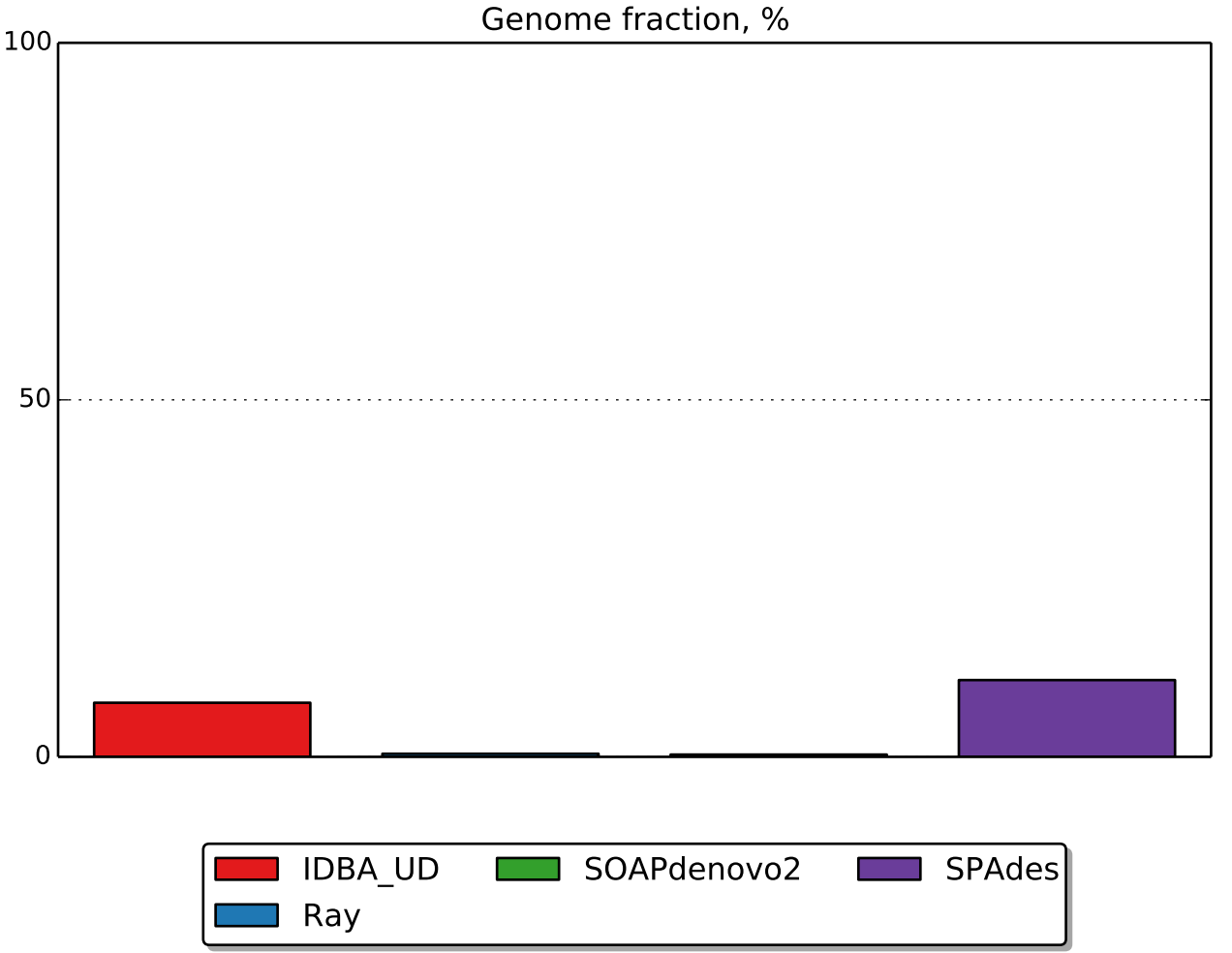

GC content
3000
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


Misassemblies
3.0
2.5
2.0
1.5
1.0
0.5
0.0
IDBA_UD
Ray
SOAPdenovo2
SPAdes
relocations


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
0
200
400
600
Contig index
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


NAx
Contig length (kbp)
0
1
2
3
4
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray


NGAx
Contig length (kbp)
0
1
2
3
4
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray


Genome fraction, %
100
50
0
IDBA_UD
SOAPdenovo2
SPAdes
Ray