Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	18	10	10	15
# contigs (>= 5000 bp)	6	2	1	7
# contigs (>= 10000 bp)	3	2	0	6
# contigs (>= 25000 bp)	2	0	0	2
# contigs (>= 50000 bp)	2	0	0	1
Total length (>= 1000 bp)	218290	57165	23750	177255
Total length (>= 5000 bp)	189586	39765	6369	157206
Total length (>= 10000 bp)	165868	39765	0	150470
Total length (>= 25000 bp)	154503	0	0	85524
Total length (>= 50000 bp)	154503	0	0	57182
# contigs	28	16	24	24
Largest contig	83095	23096	6369	57182
Total length	224712	61245	34087	183669
Reference length	3501911	3501911	3501911	3501911
GC (%)	44.38	46.10	44.84	42.05
Reference GC (%)	42.88	42.88	42.88	42.88
N50	71408	16669	1859	21719
N75	9600	3350	938	13198
L50	2	2	5	3
L75	4	4	12	6
# misassemblies	0	0	0	0
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	1	3	0
# structural variations	0	0	0	0
# unaligned contigs	0 + 14 part	0 + 3 part	0 + 6 part	0 + 15 part
Unaligned length	169535	28920	6328	147263
Genome fraction (%)	1.573	0.894	0.750	1.039
Duplication ratio	1.002	1.032	1.057	1.000
# N's per 100 kbp	38.27	1136.42	982.78	127.40
# mismatches per 100 kbp	1699.07	1893.84	1375.03	1945.64
# indels per 100 kbp	67.16	35.13	26.66	49.47
Largest alignment	8007	4119	4298	6152
NA50	-	509	969	-
NGA50	-	-	-	-
NA75	-	-	360	-
LA50	-	17	10	-
LA75	-	-	22	-

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

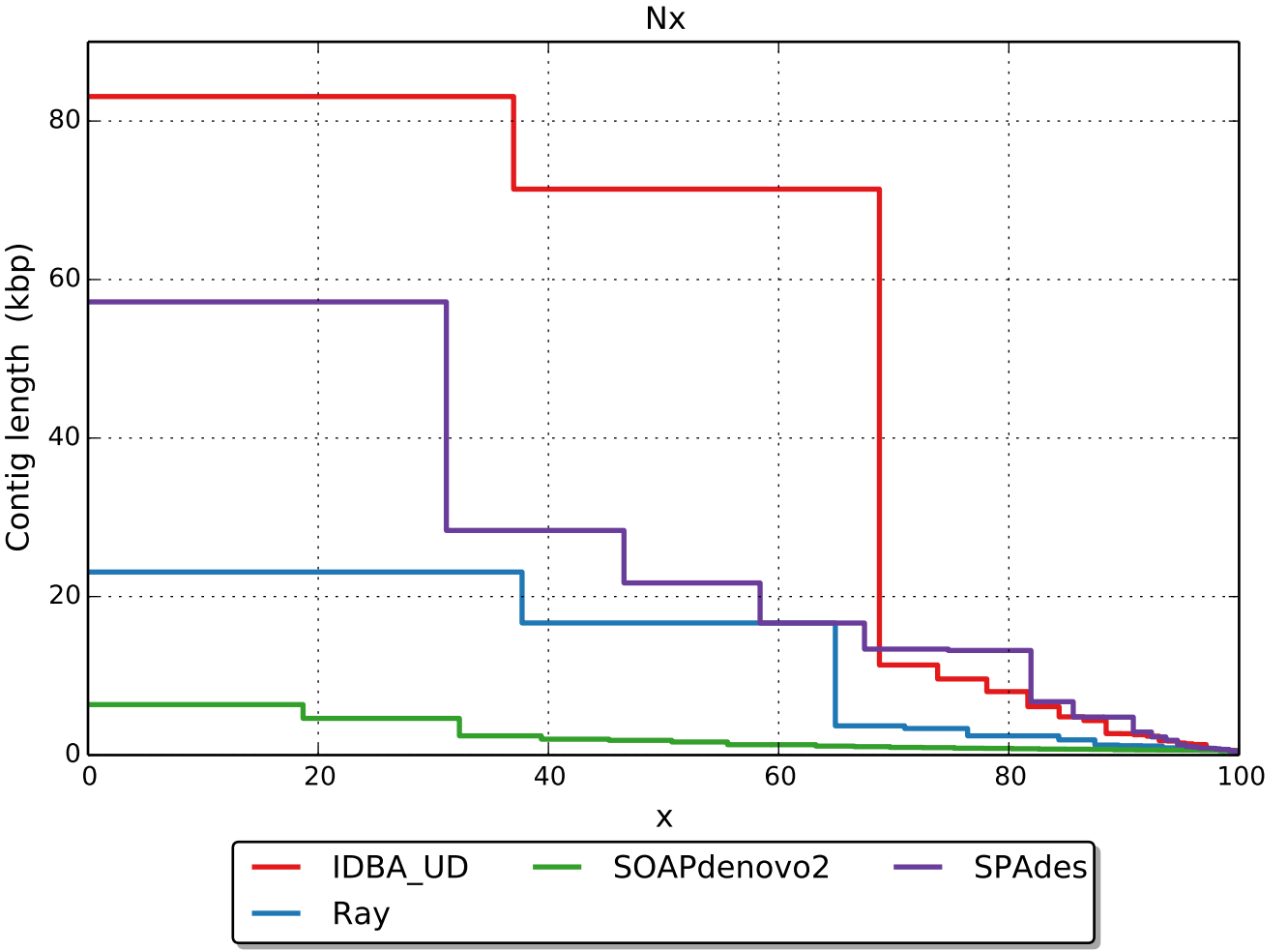
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	0	0	0
# relocations	0	0	0	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	6	3	2	6
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	1	3	0
# structural variations	0	0	0	0
# mismatches	936	593	361	708
# indels	37	11	7	18
# short indels	33	10	7	16
# long indels	4	1	0	2
Indels length	83	24	10	52

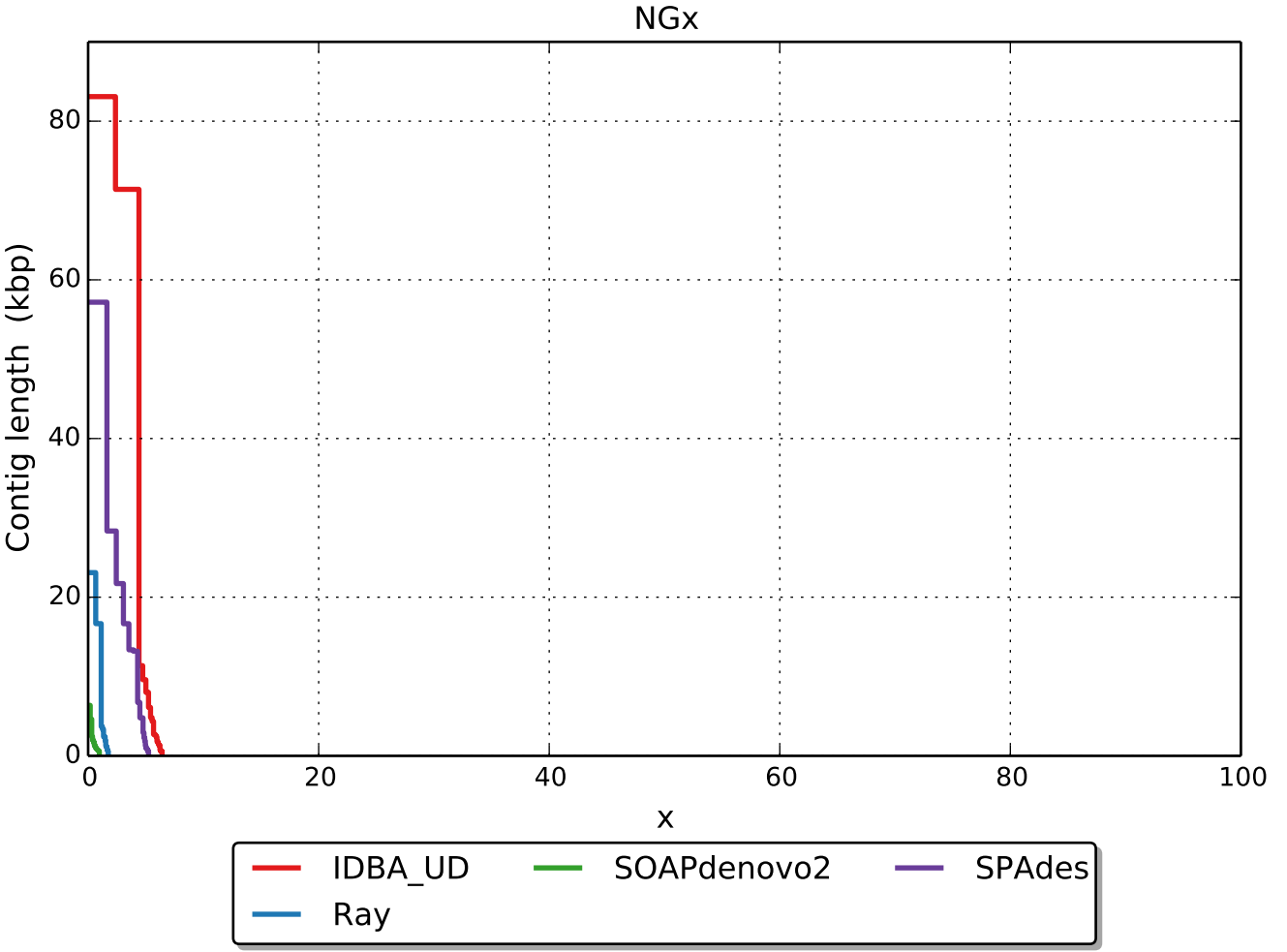
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

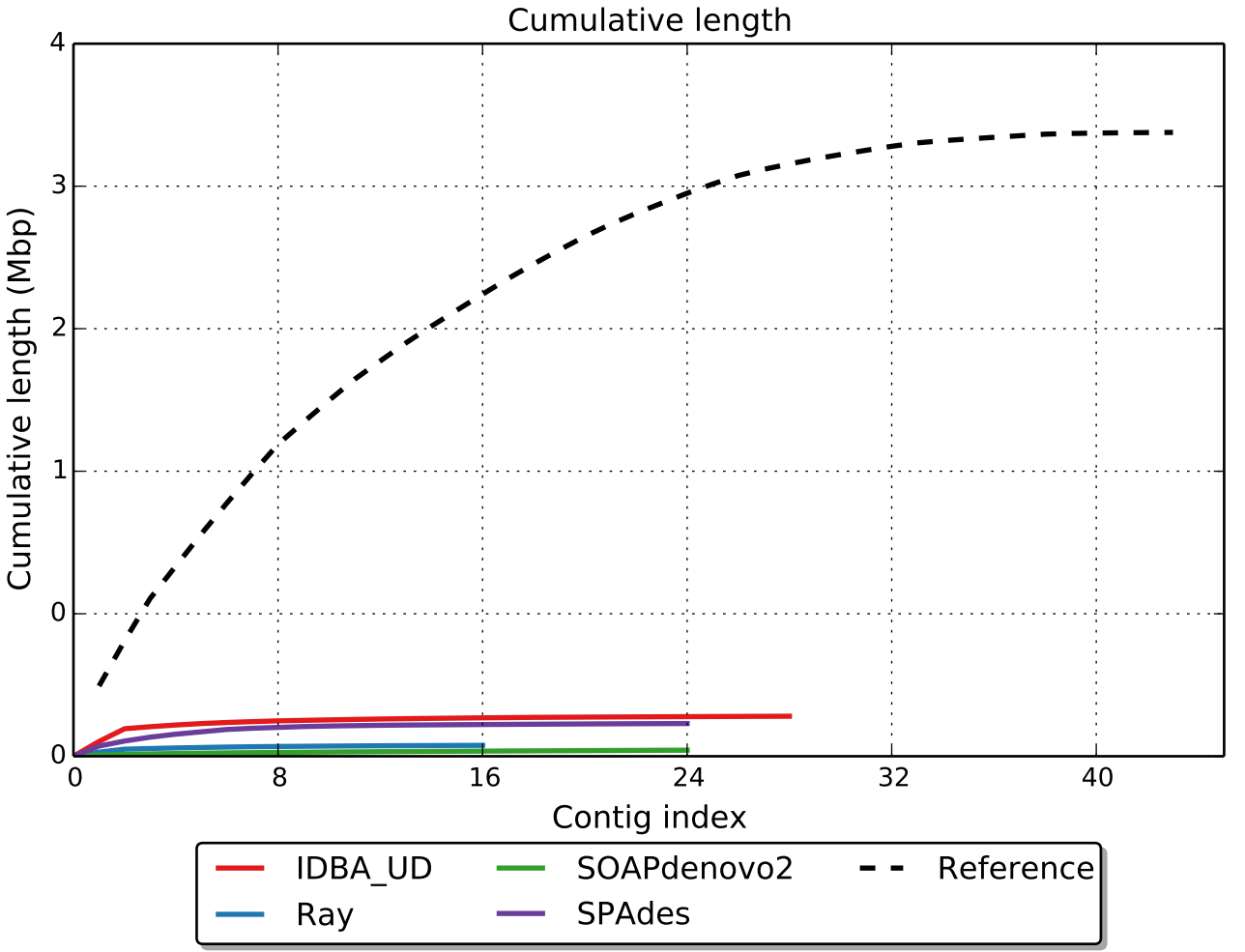
Unaligned report

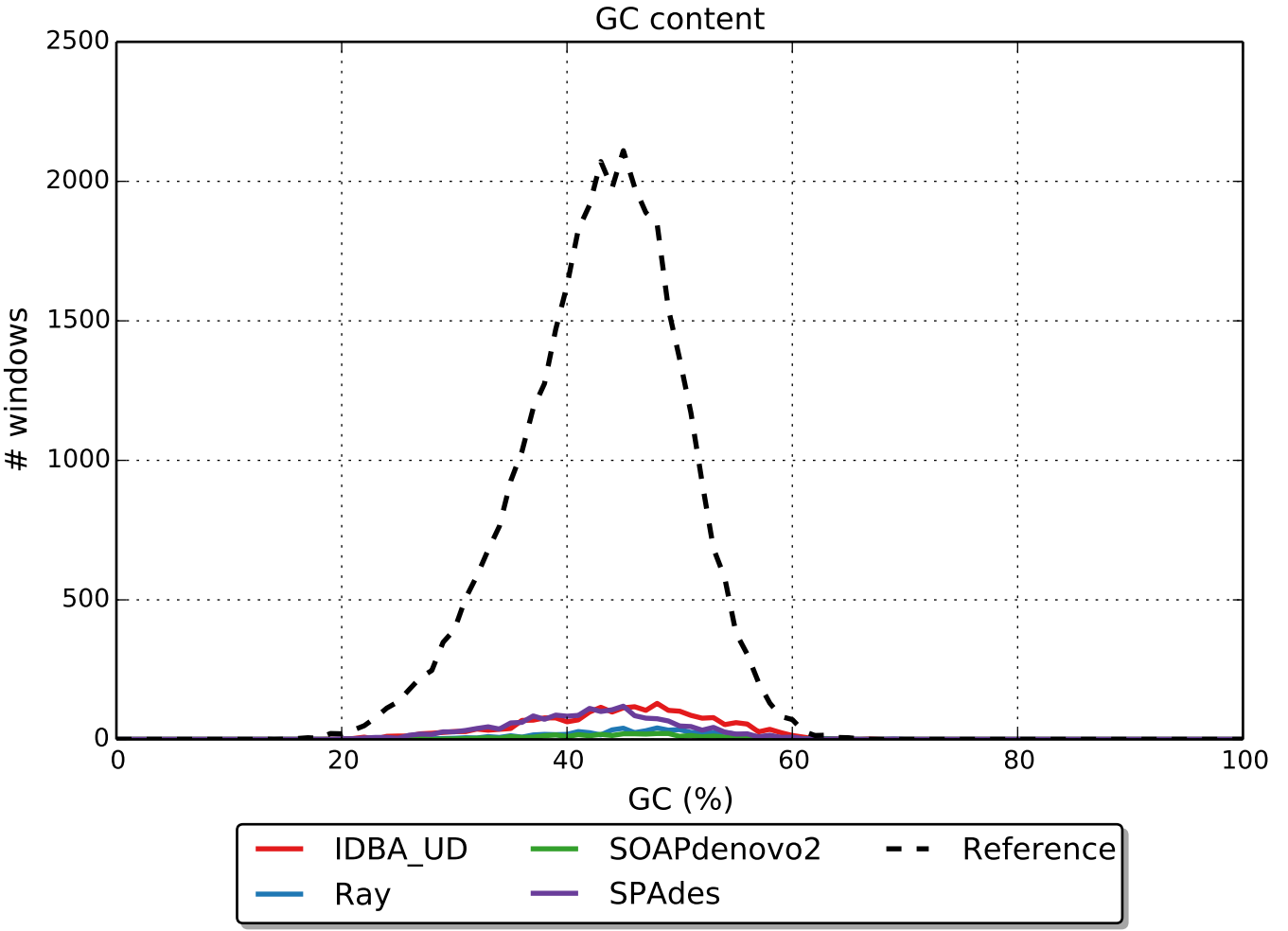
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	14	3	6	15
# with misassembly	2	1	0	2
# both parts are significant	6	2	1	6
Partially unaligned length	169535	28920	6328	147263
# N's	86	696	335	234

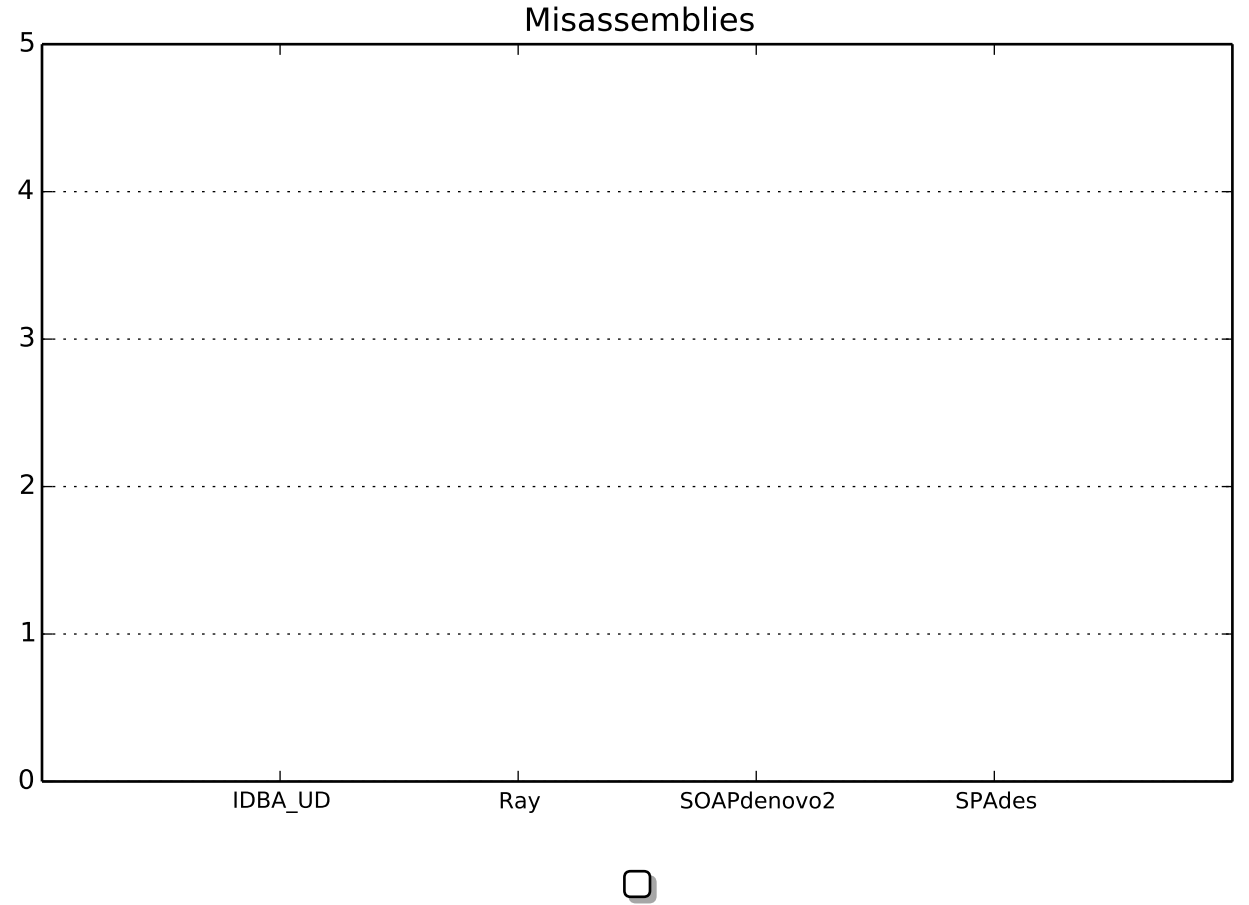
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

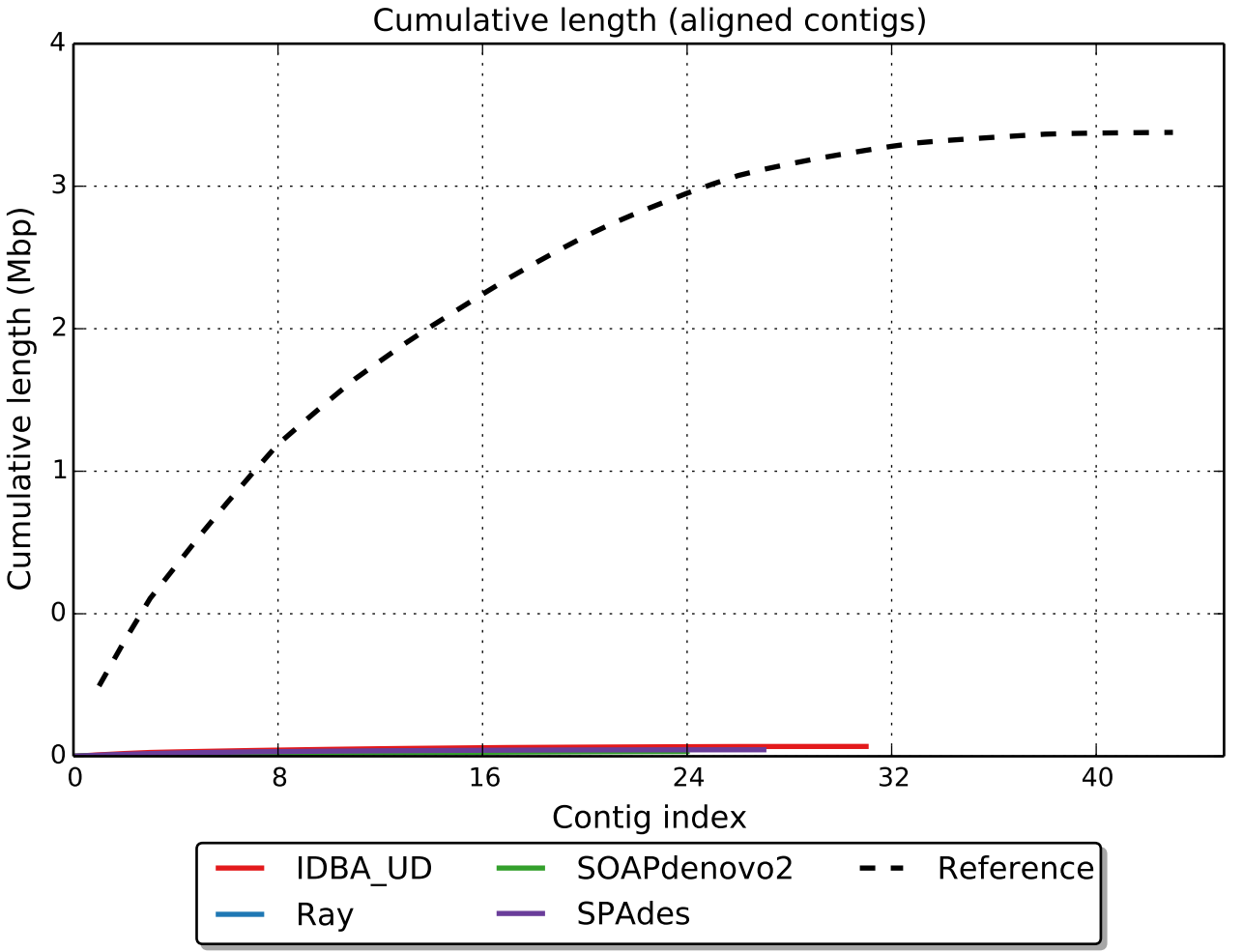

Nx
Contig length (kbp)
0
20
40
60
80
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray

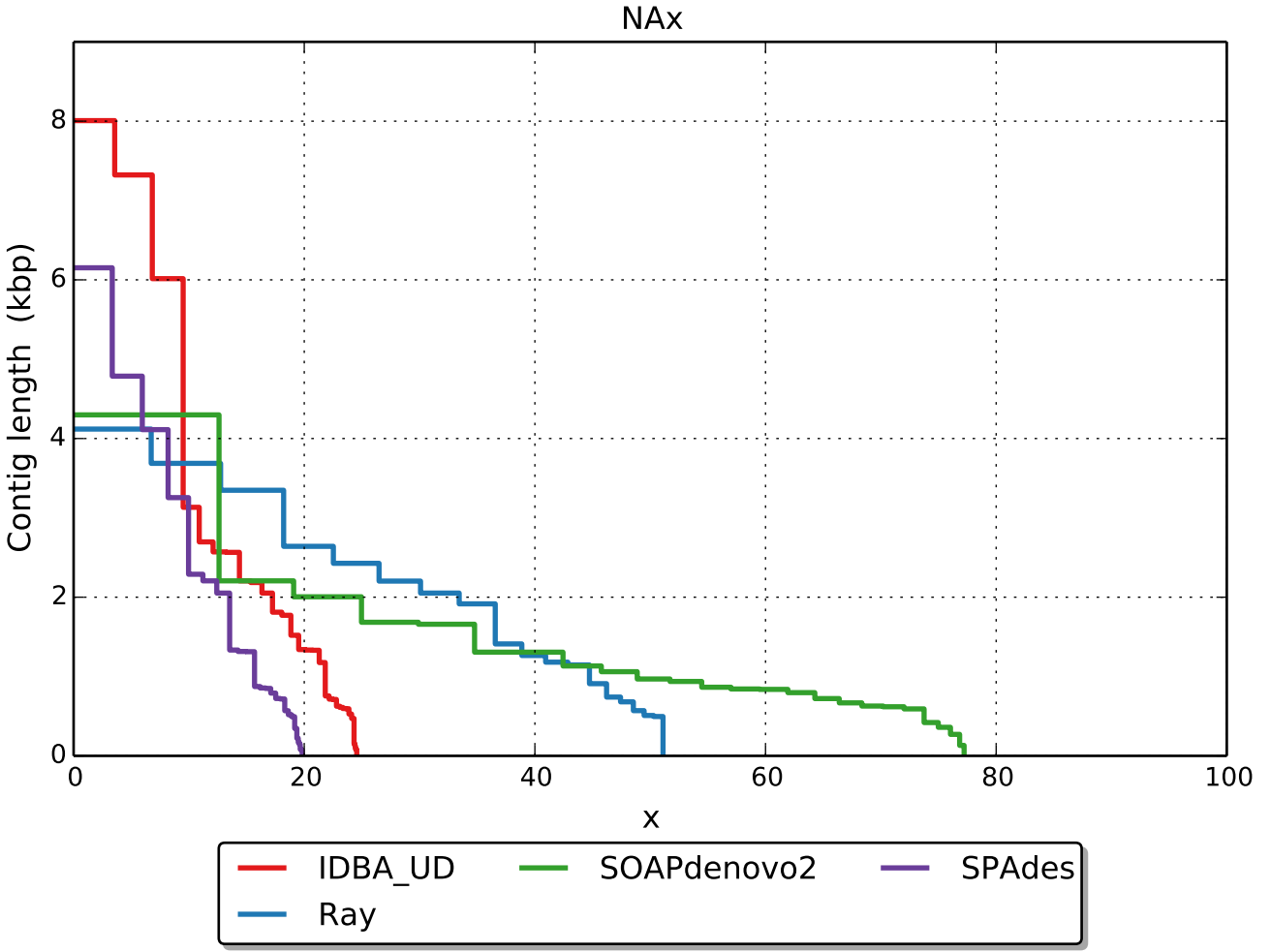

NGx
Contig length (kbp)
0
20
40
60
80
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray

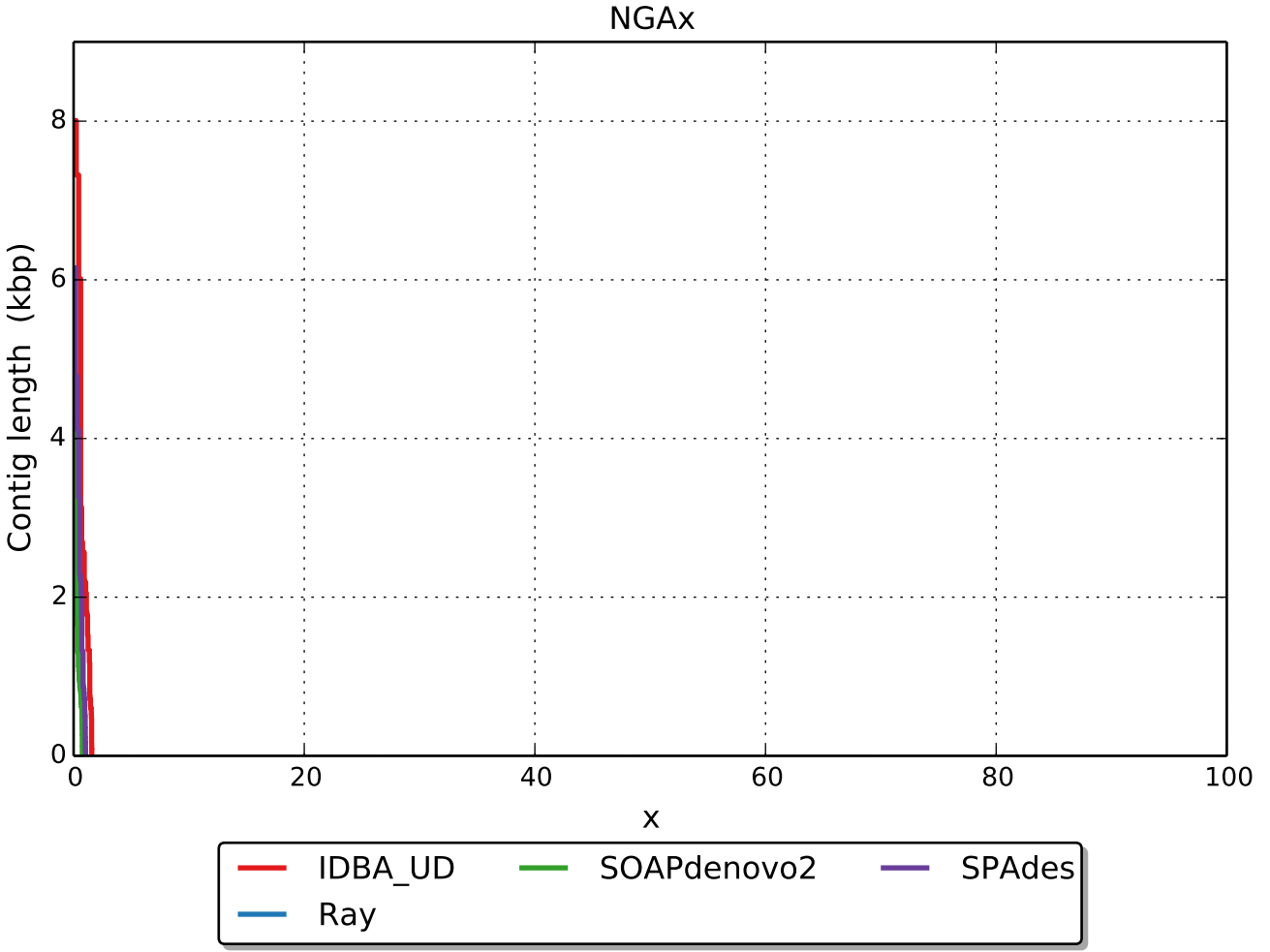

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
2
3
4
0
8
16
24
32
40
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference

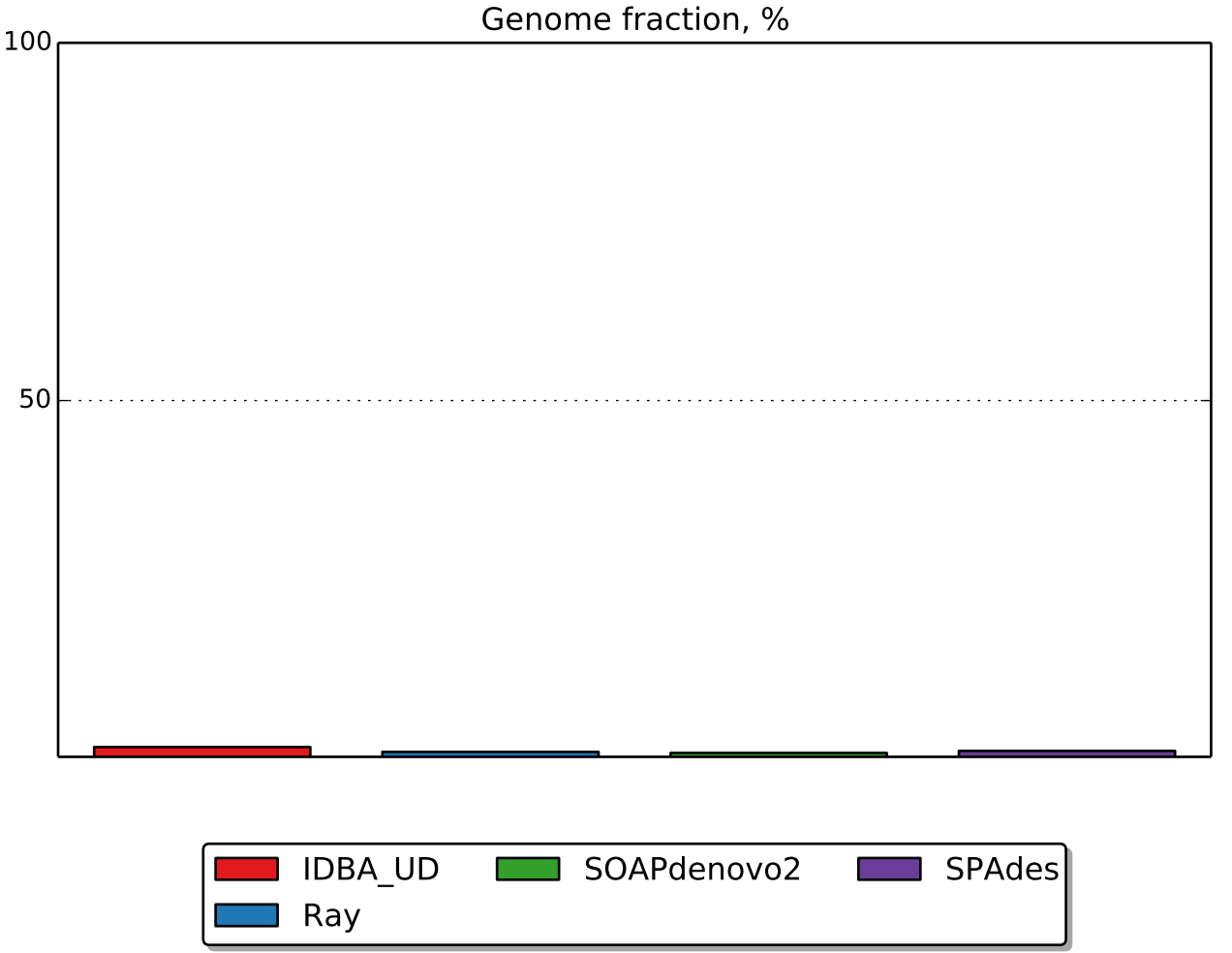

GC content
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


Misassemblies
5
4
3
2
1
0
IDBA_UD
Ray
SOAPdenovo2
SPAdes


Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
0
8
16
24
32
40
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


NAx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray


NGAx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray


Genome fraction, %
100
50
IDBA_UD
Ray
SOAPdenovo2
SPAdes