Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	265	50	144	173
# contigs (>= 5000 bp)	43	23	9	38
# contigs (>= 10000 bp)	20	17	1	21
# contigs (>= 25000 bp)	8	6	0	11
# contigs (>= 50000 bp)	4	2	0	4
Total length (>= 1000 bp)	1340562	568790	334871	1165608
Total length (>= 5000 bp)	882209	526135	66161	887099
Total length (>= 10000 bp)	723060	478123	10187	774400
Total length (>= 25000 bp)	550750	289570	0	602015
Total length (>= 50000 bp)	389651	124191	0	354482
# contigs	469	109	350	293
Largest contig	199153	64174	10187	144537
Total length	1492346	608173	477422	1248268
Reference length	4684745	4684745	4684745	4684745
GC (%)	42.49	42.82	40.97	41.54
Reference GC (%)	42.20	42.20	42.20	42.20
N50	8626	23624	1822	22813
N75	2299	11479	926	3911
L50	23	7	71	12
L75	115	15	168	50
# misassemblies	4	9	0	13
# misassembled contigs	4	6	0	9
Misassembled contigs length	157402	231469	0	430056
# local misassemblies	2	27	1	8
# structural variations	0	1	0	1
# unaligned contigs	0 + 19 part	0 + 14 part	0 + 4 part	0 + 21 part
Unaligned length	318651	174565	6834	178022
Genome fraction (%)	24.471	8.069	10.012	20.919
Duplication ratio	1.024	1.147	1.003	1.092
# N's per 100 kbp	81.88	773.79	33.72	173.04
# mismatches per 100 kbp	1188.21	2286.21	935.99	1844.78
# indels per 100 kbp	35.85	38.09	11.94	53.98
Largest alignment	39525	38783	10060	38744
NA50	2477	1891	1728	4875
NGA50	-	-	-	-
NA75	634	-	896	733
LA50	102	28	73	40
LA75	416	-	174	220

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

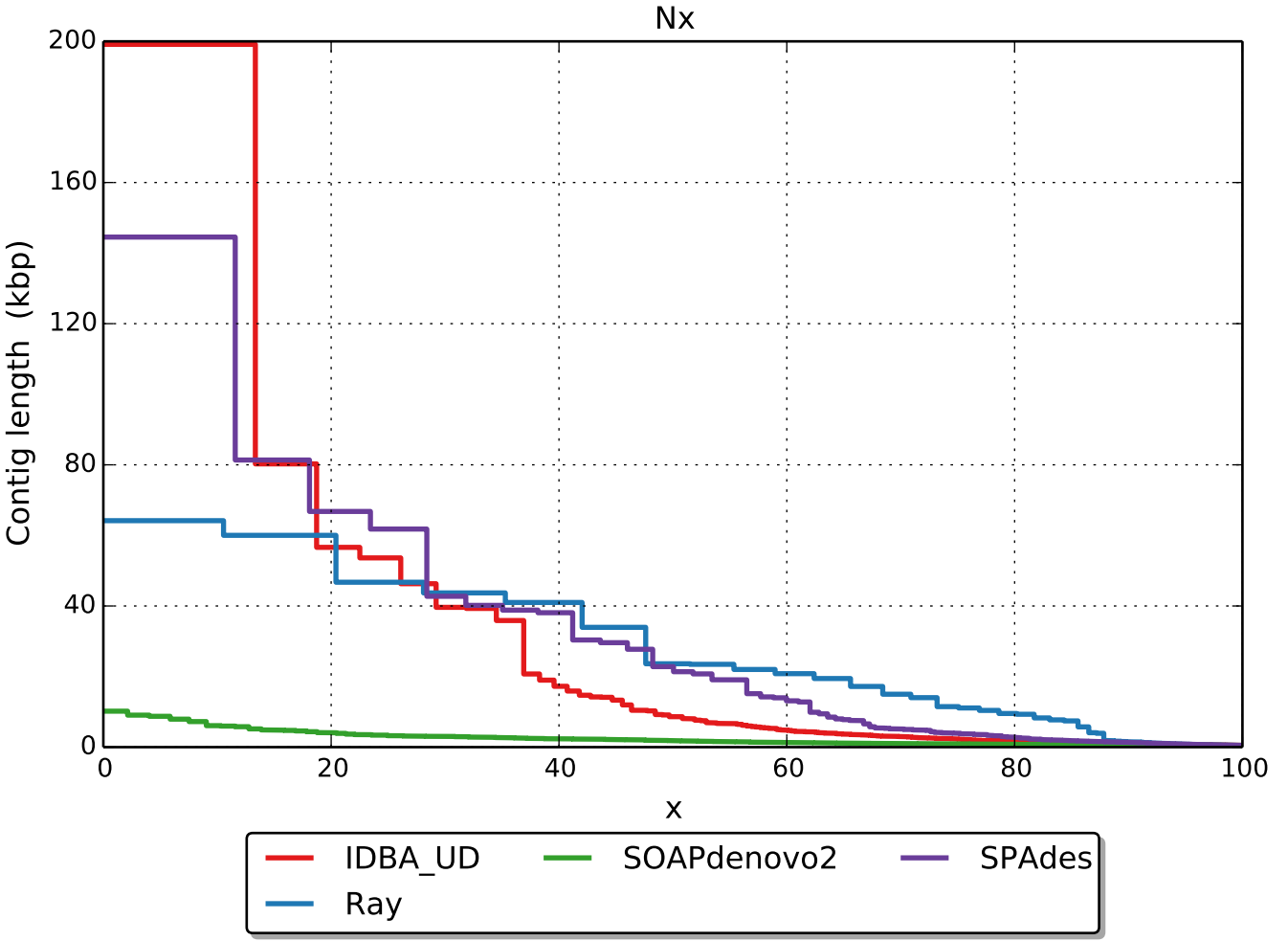
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	4	9	0	13
# relocations	4	9	0	12
# translocations	0	0	0	0
# inversions	0	0	0	1
# possibly misassembled contigs	10	18	1	24
# misassembled contigs	4	6	0	9
Misassembled contigs length	157402	231469	0	430056
# local misassemblies	2	27	1	8
# structural variations	0	1	0	1
# mismatches	13622	8642	4390	18079
# indels	411	144	56	529
# short indels	373	134	54	460
# long indels	38	10	2	69
Indels length	1000	328	80	1514

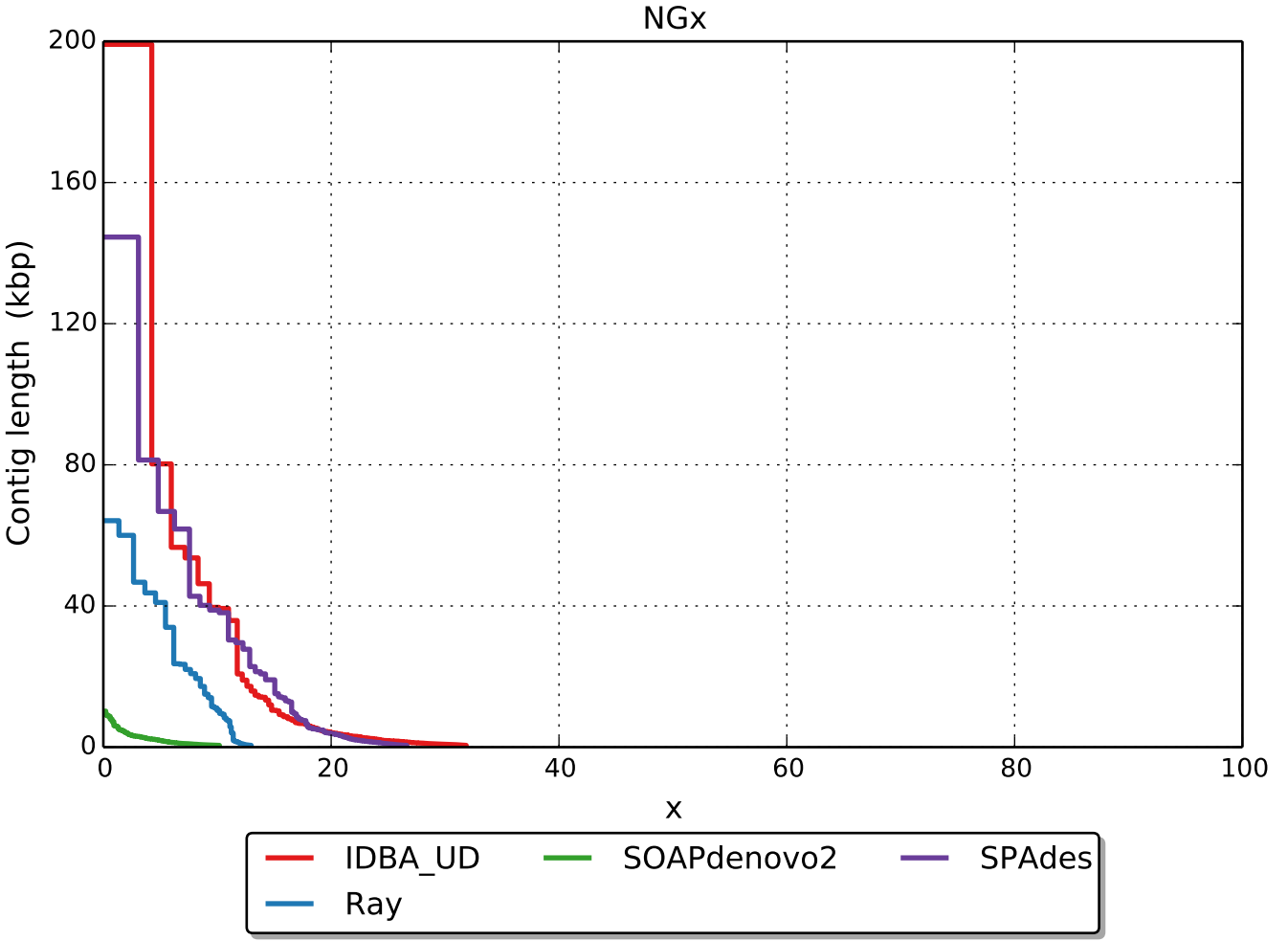
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

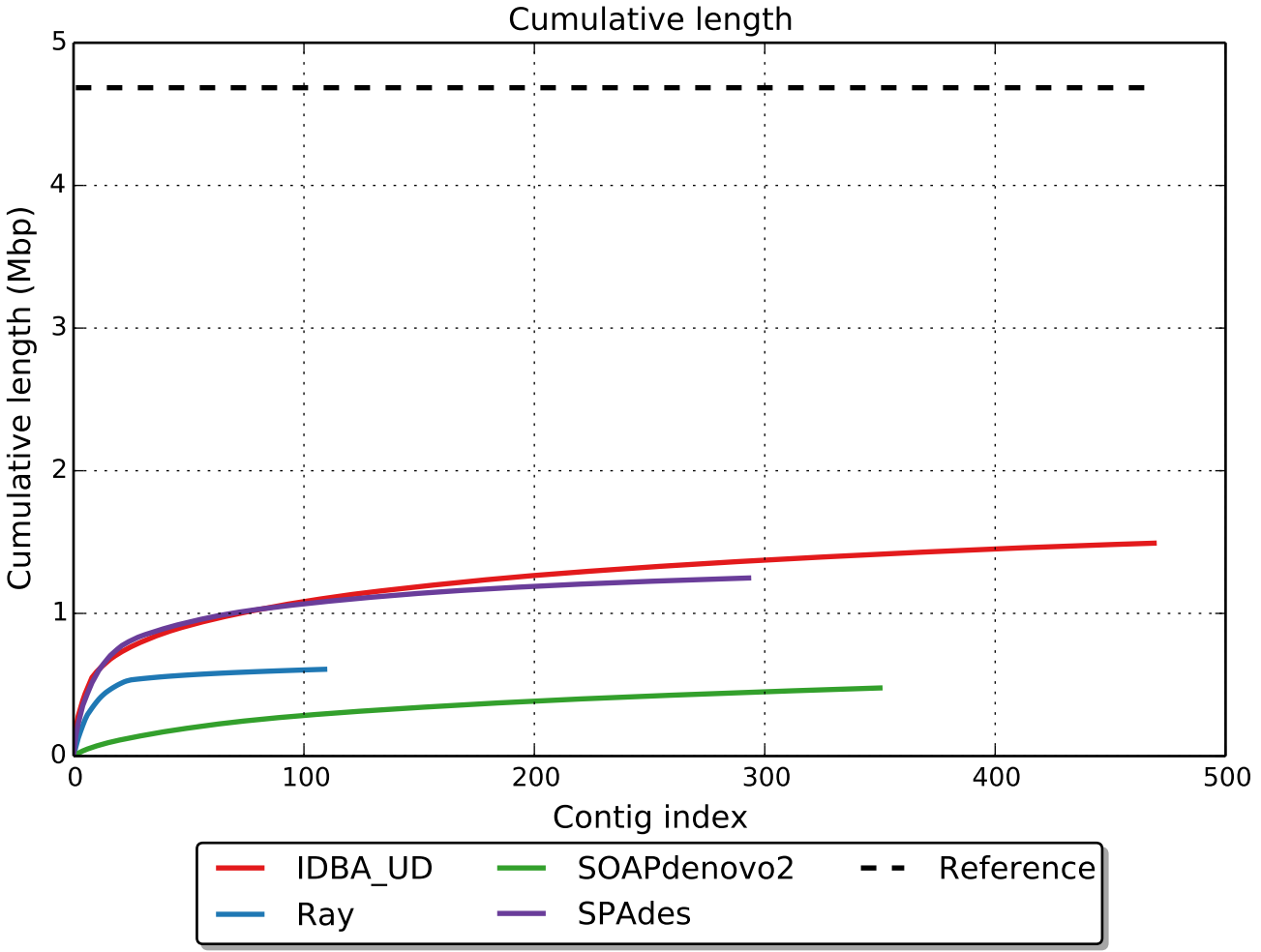
Unaligned report

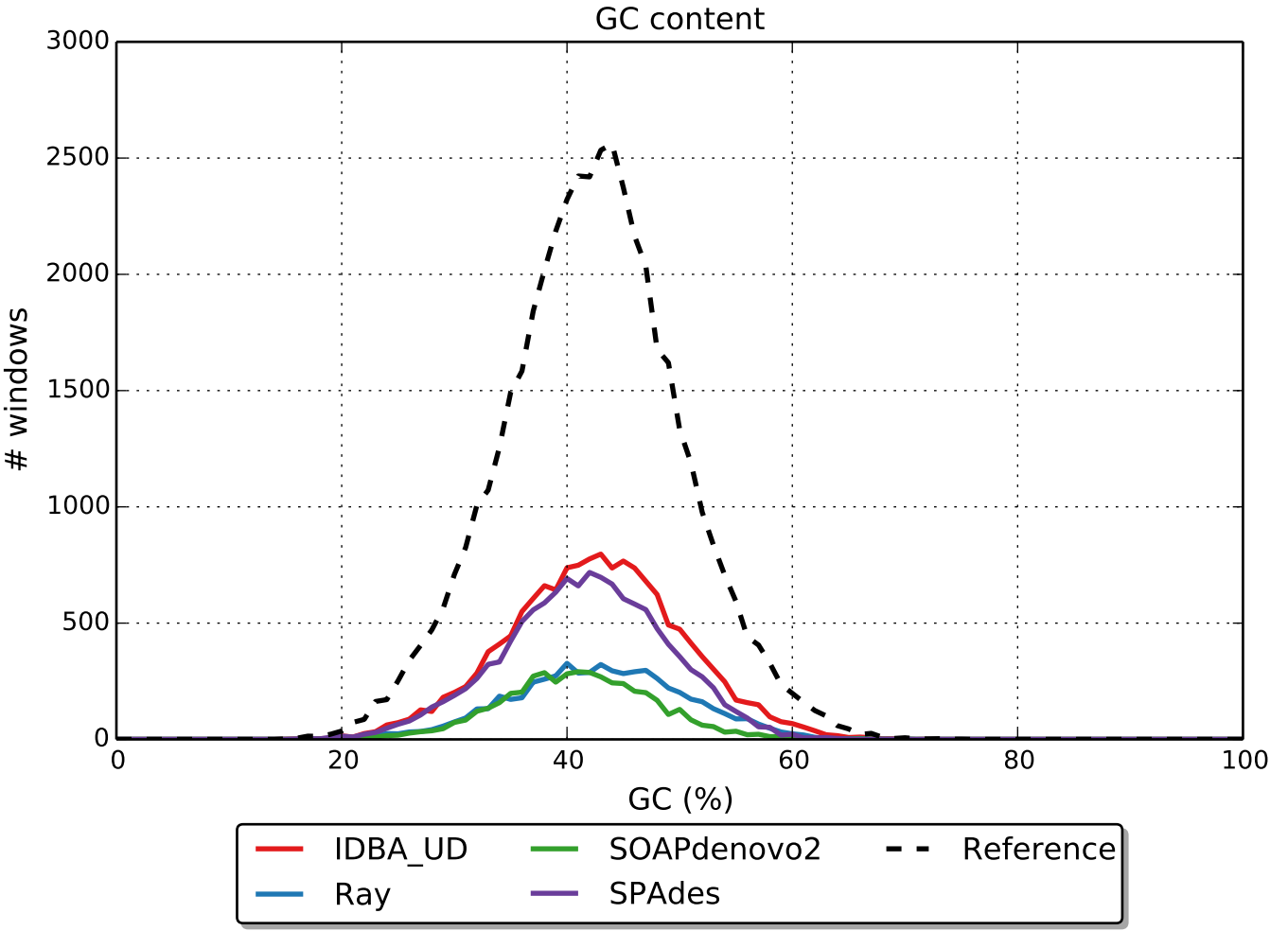
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	19	14	4	21
# with misassembly	3	3	0	2
# both parts are significant	7	9	1	13
Partially unaligned length	318651	174565	6834	178022
# N's	1222	4706	161	2160

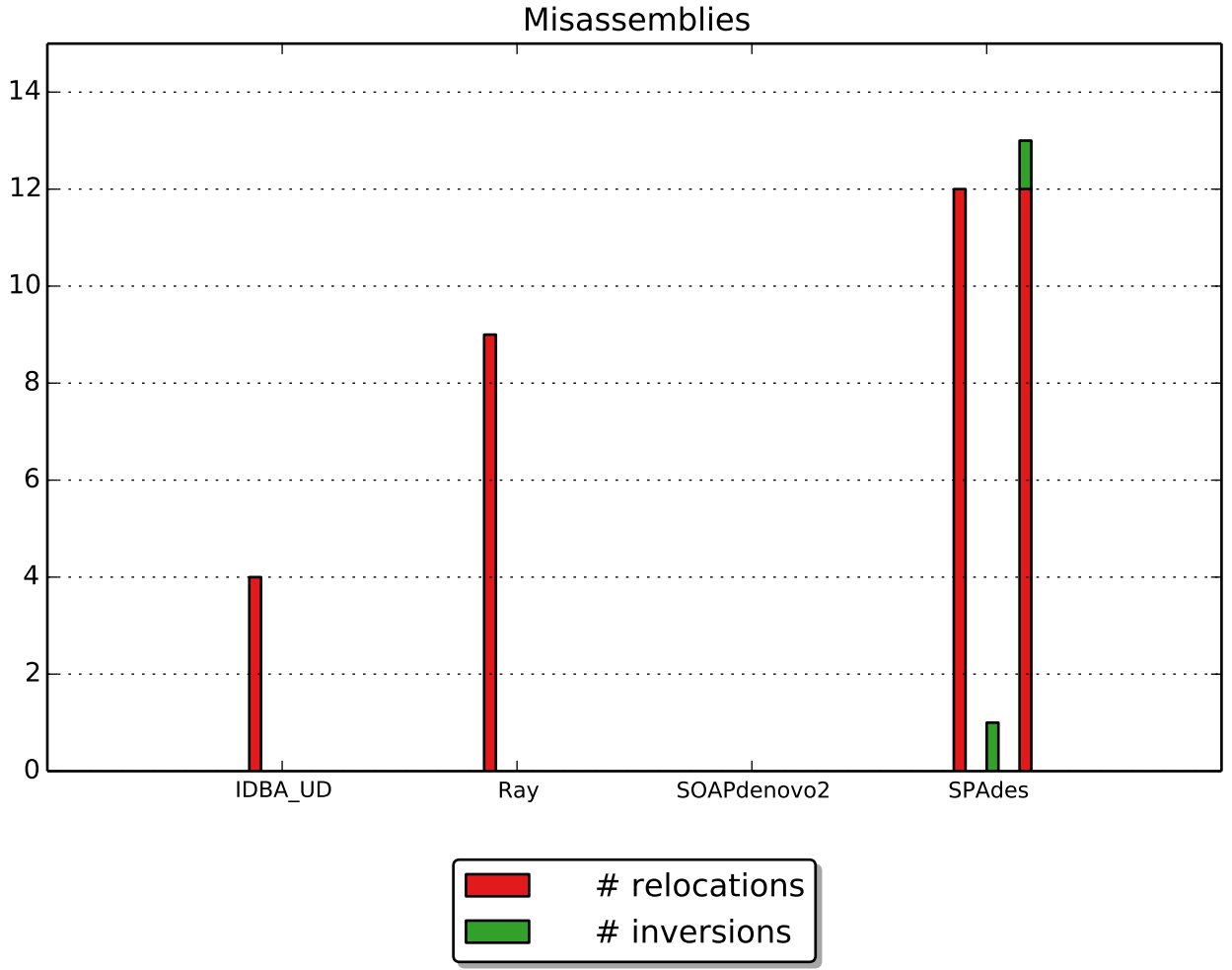
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

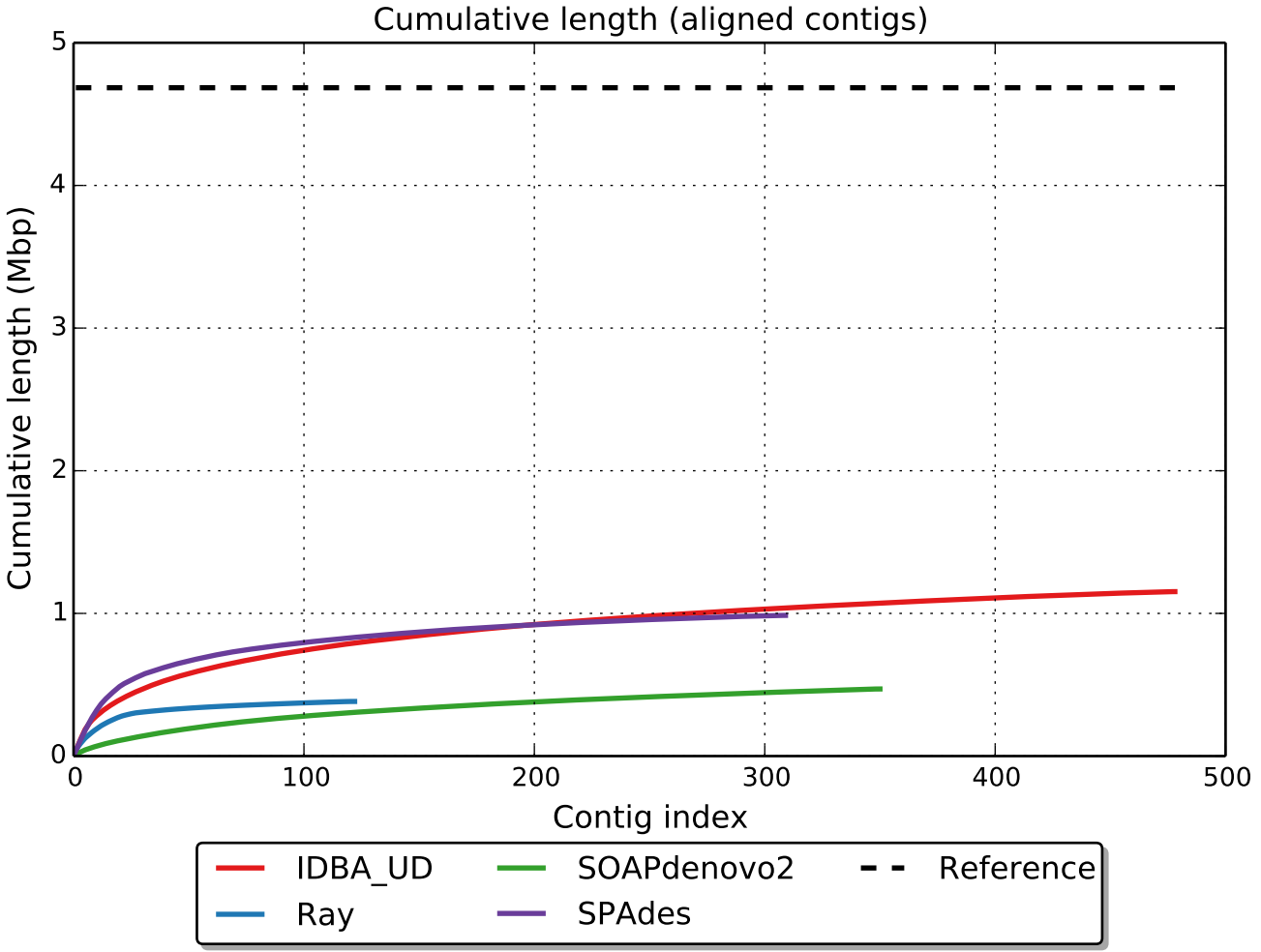

Nx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray

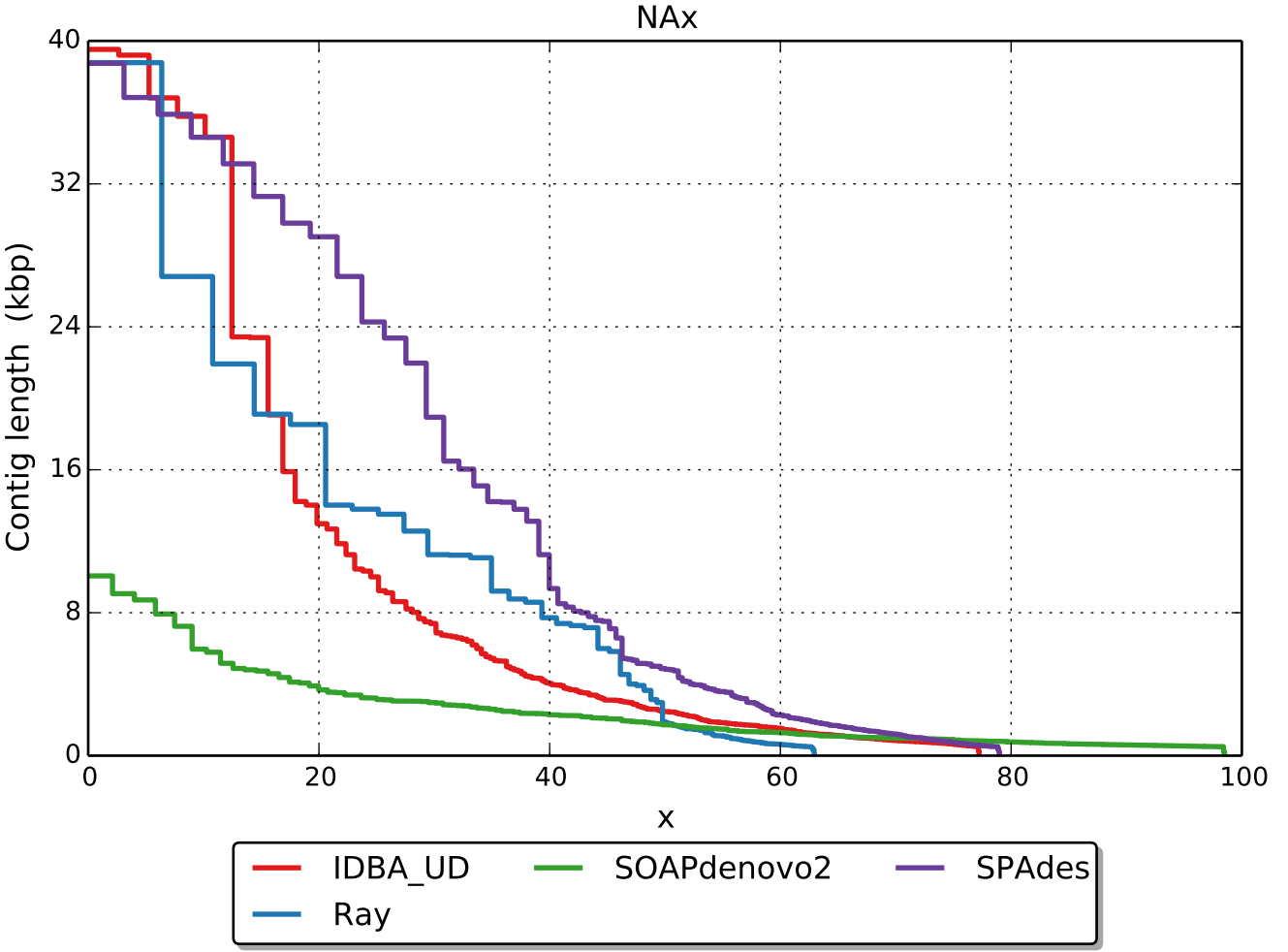

NGx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray

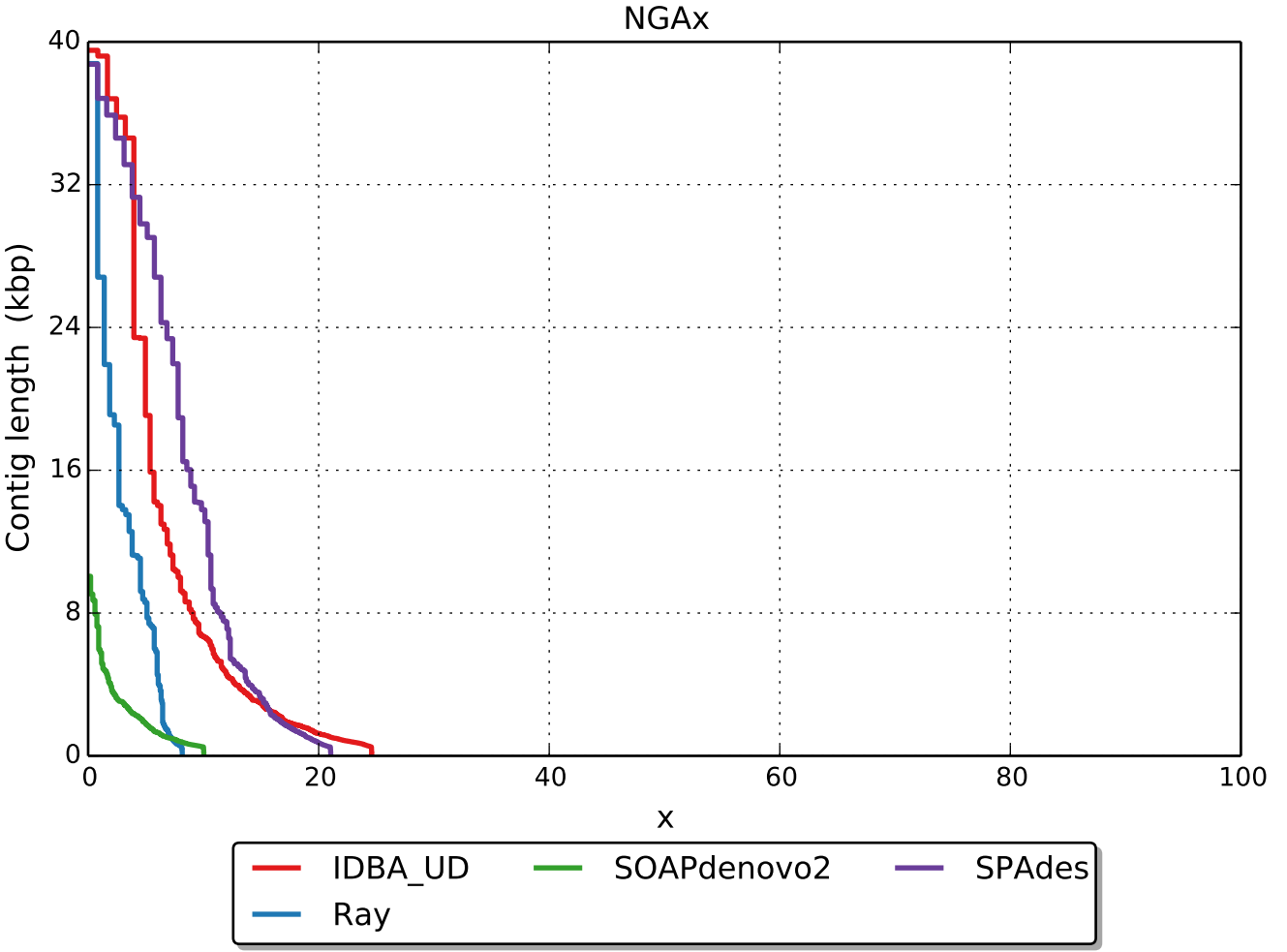

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
0
100
200
300
400
500
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference

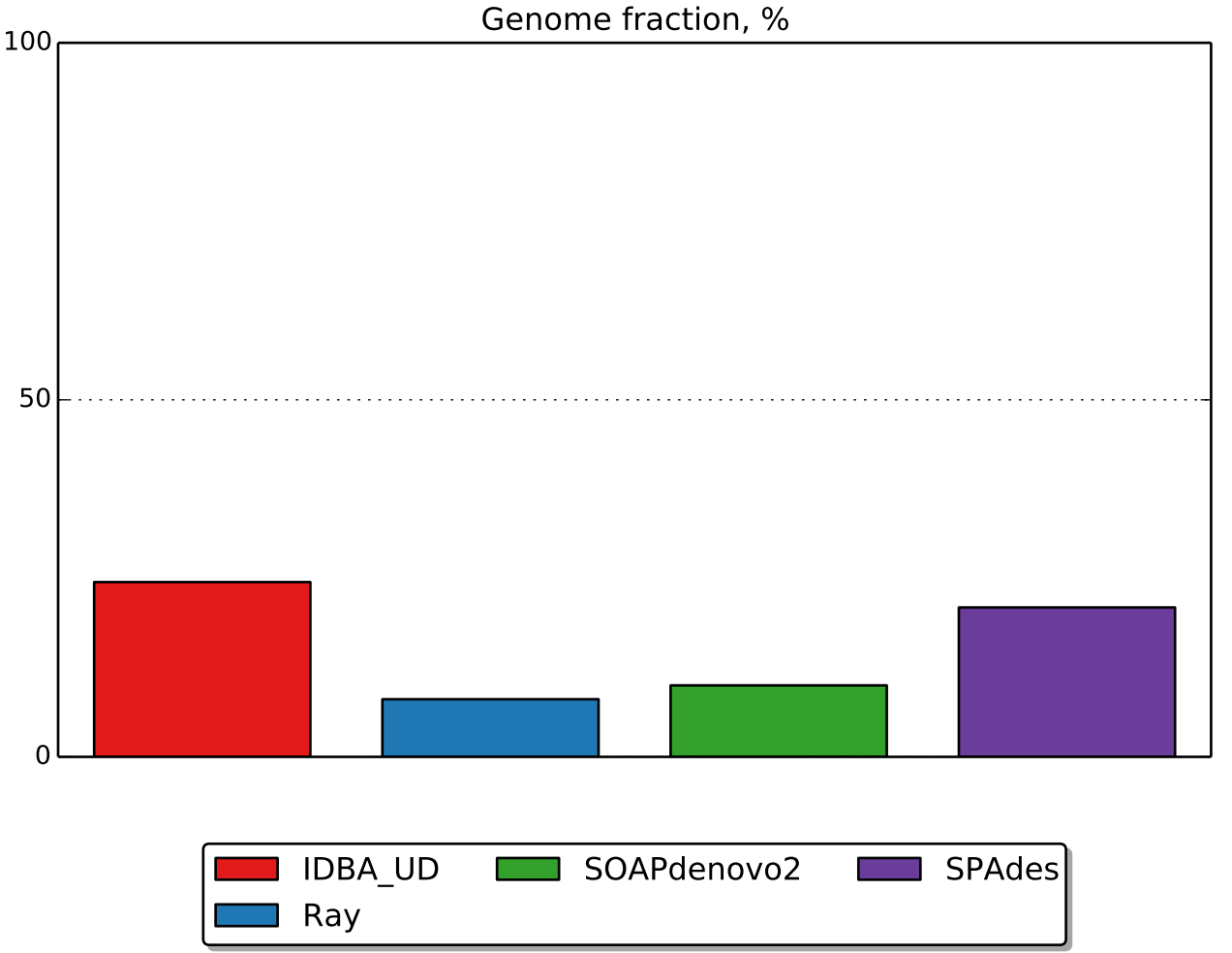

GC content
3000
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


Misassemblies
14
12
10
8
6
4
2
0
IDBA_UD
Ray
SOAPdenovo2
SPAdes
relocations
inversions


Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
0
100
200
300
400
500
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


NAx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray


NGAx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray


Genome fraction, %
100
50
0
IDBA_UD
Ray
SOAPdenovo2
SPAdes