Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	82	373	161	139
# contigs (>= 5000 bp)	59	47	69	90
# contigs (>= 10000 bp)	50	11	29	50
# contigs (>= 25000 bp)	23	1	2	14
# contigs (>= 50000 bp)	11	0	0	2
Total length (>= 1000 bp)	1766377	1101963	977638	1583135
Total length (>= 5000 bp)	1711922	382394	749066	1444523
Total length (>= 10000 bp)	1636246	148038	470191	1143619
Total length (>= 25000 bp)	1157478	26575	64918	523174
Total length (>= 50000 bp)	742266	0	0	153129
# contigs	112	565	213	164
Largest contig	95558	26575	38379	92179
Total length	1787272	1244137	1014875	1600763
Reference length	2052007	2052007	2052007	2052007
GC (%)	39.69	39.41	39.38	39.47
Reference GC (%)	39.43	39.43	39.43	39.43
N50	36115	3310	9142	19129
NG50	34534	1267	-	14467
N75	21984	1649	4662	9024
NG75	13658	-	-	2923
L50	15	106	33	27
LG50	19	306	-	41
L75	31	241	72	57
LG75	42	-	-	115
# misassemblies	27	10	1	14
# misassembled contigs	19	10	1	10
Misassembled contigs length	548245	35101	11761	273552
# local misassemblies	33	76	19	18
# structural variations	5	2	3	6
# unaligned contigs	0 + 44 part	0 + 73 part	0 + 93 part	0 + 67 part
Unaligned length	266930	158084	368557	261469
Genome fraction (%)	63.783	49.175	29.227	59.931
Duplication ratio	1.162	1.076	1.078	1.089
# N's per 100 kbp	0.00	1665.97	1728.59	42.23
# mismatches per 100 kbp	3986.78	3422.82	3327.43	3916.04
# indels per 100 kbp	85.65	56.19	82.87	80.01
Largest alignment	74809	19128	20955	36776
NA50	15662	1946	1632	9415
NGA50	11348	575	-	5753
NA75	-	882	-	1881
LA50	27	161	102	42
LGA50	37	522	-	72
LA75	-	394	-	122

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

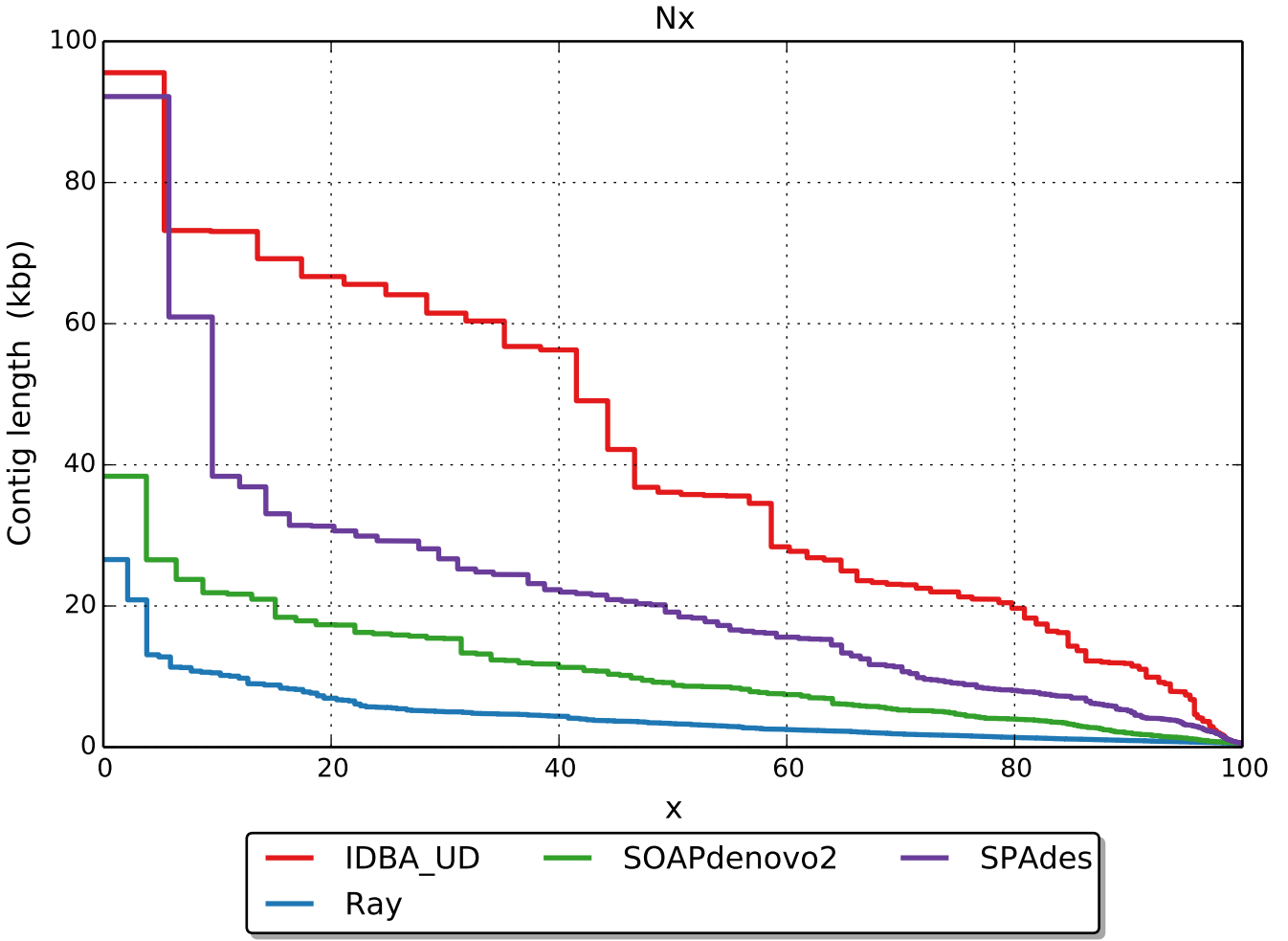
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	27	10	1	14
# relocations	27	10	1	14
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	51	63	60	55
# misassembled contigs	19	10	1	10
Misassembled contigs length	548245	35101	11761	273552
# local misassemblies	33	76	19	18
# structural variations	5	2	3	6
# mismatches	52180	34539	19956	48159
# indels	1121	567	497	984
# short indels	1066	546	338	913
# long indels	55	21	159	71
Indels length	2111	950	4049	2339

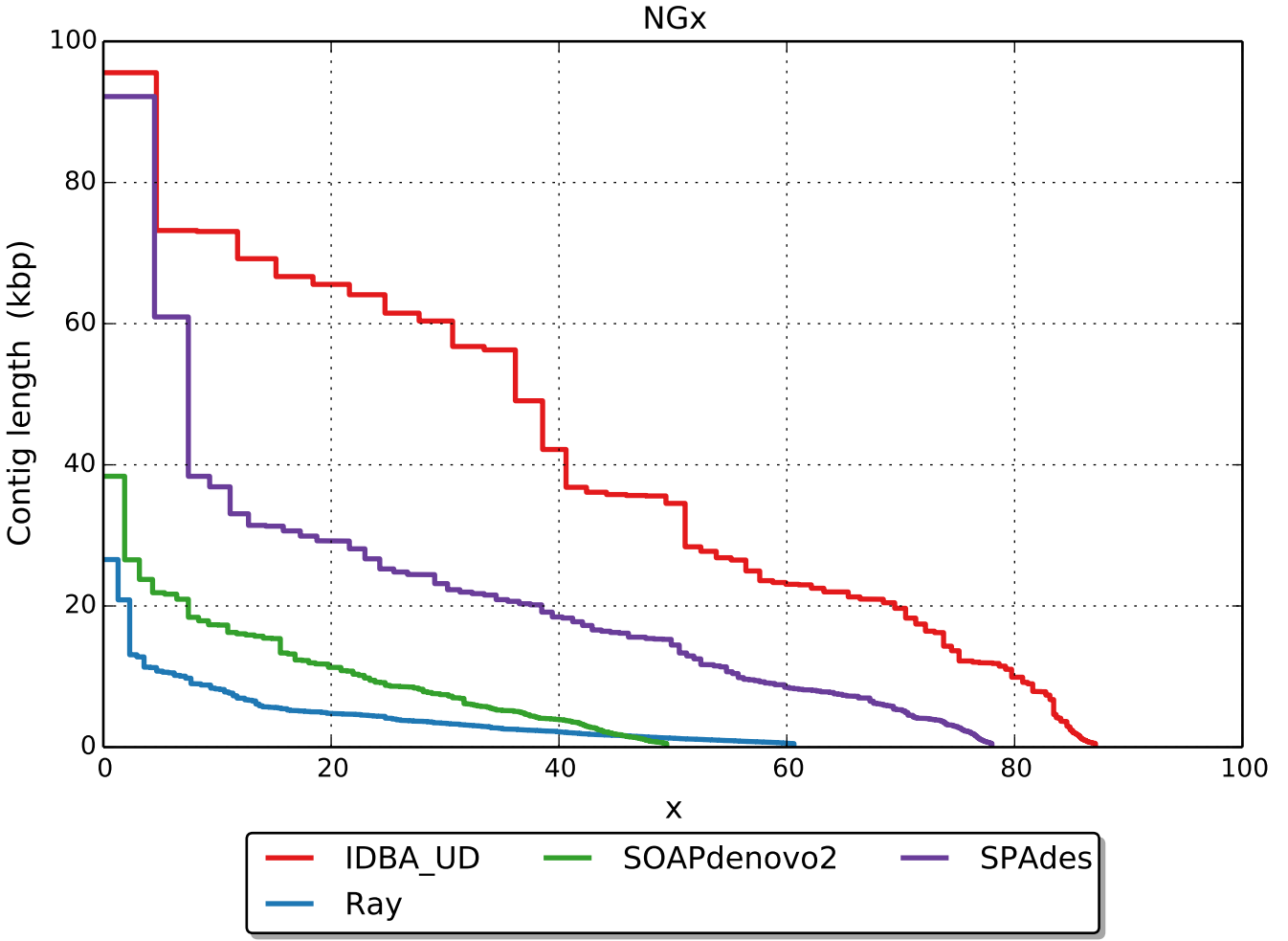
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

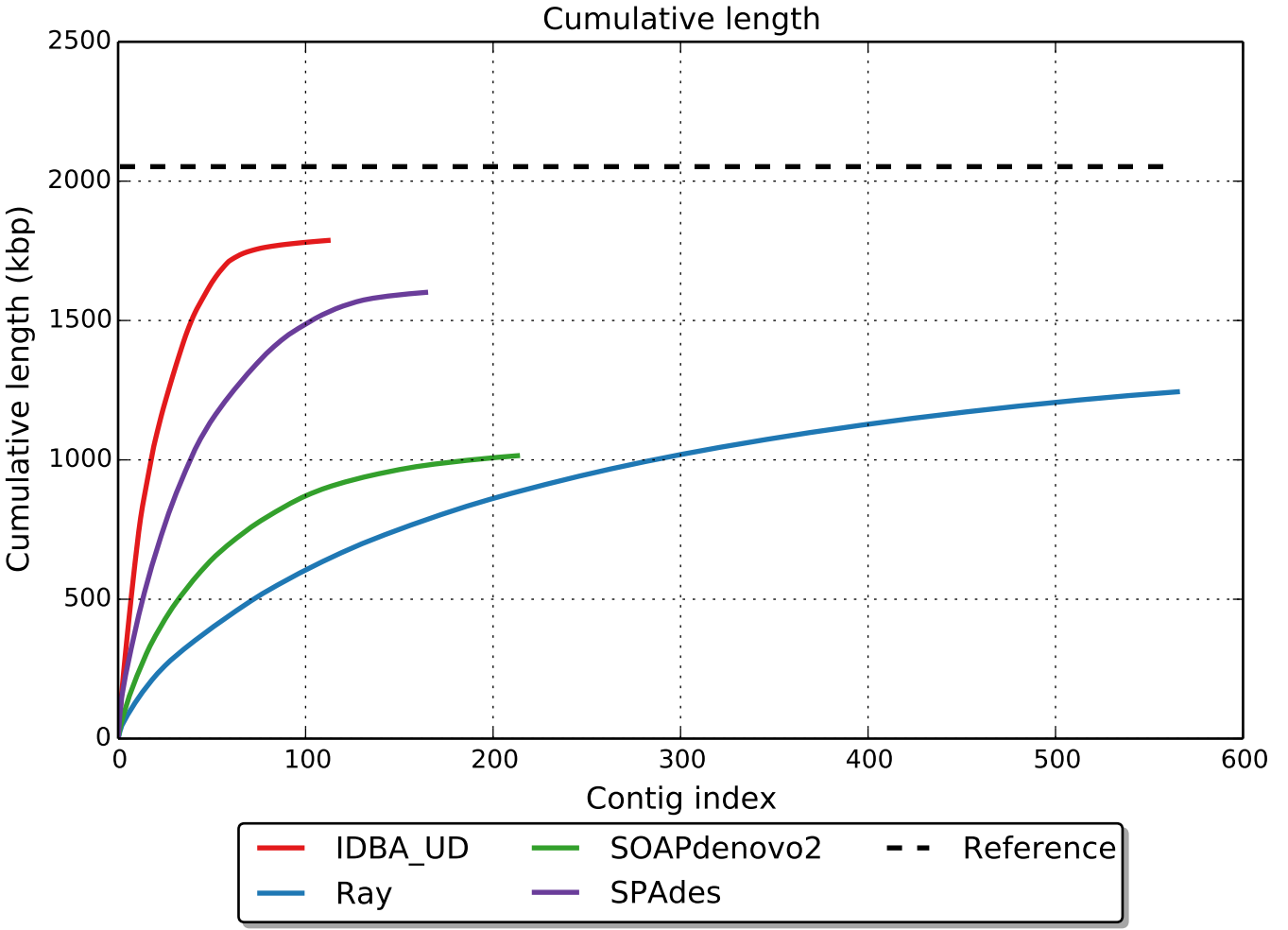
Unaligned report

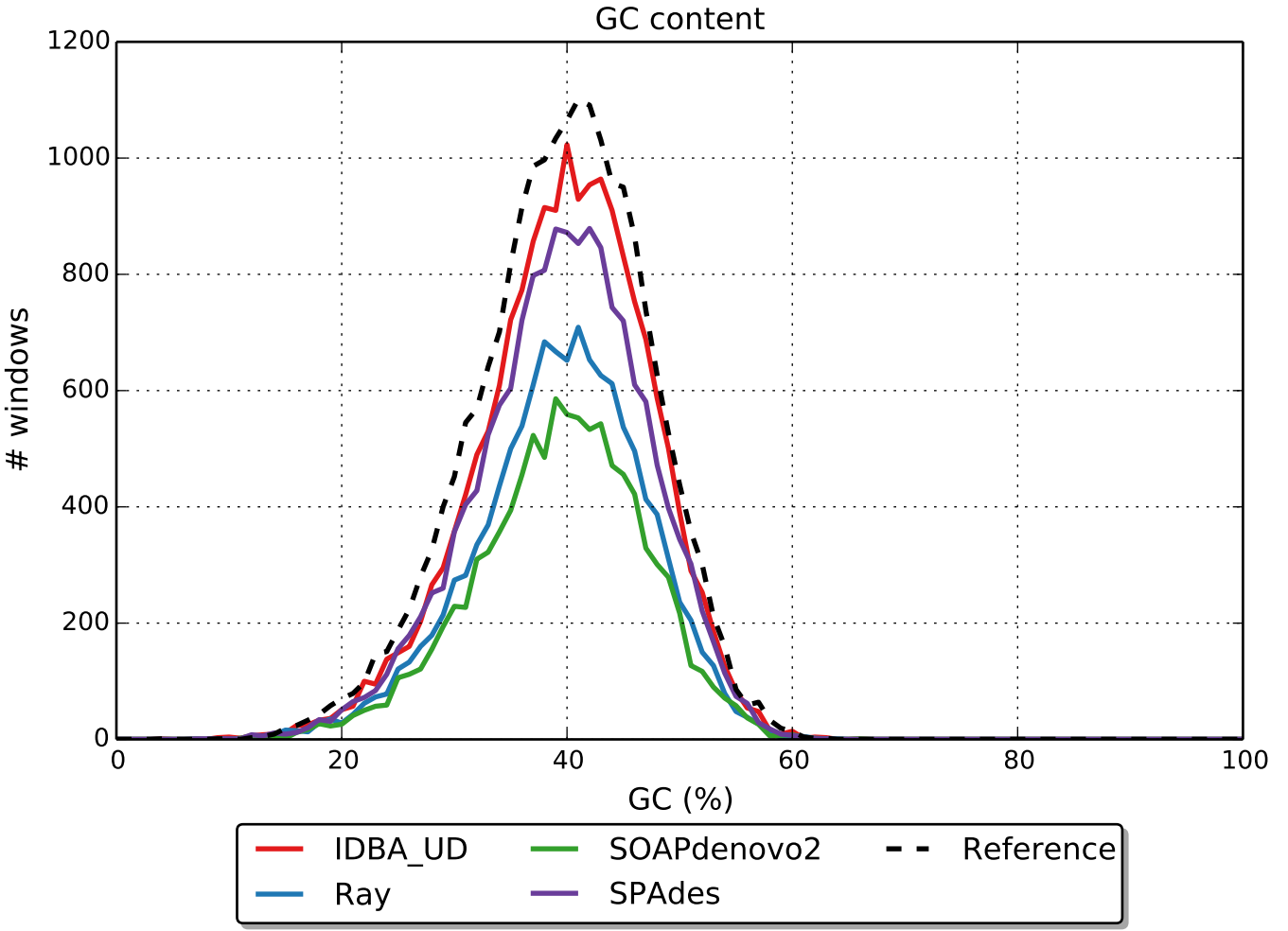
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	44	73	93	67
# with misassembly	5	11	10	4
# both parts are significant	22	45	48	35
Partially unaligned length	266930	158084	368557	261469
# N's	0	20727	17543	676

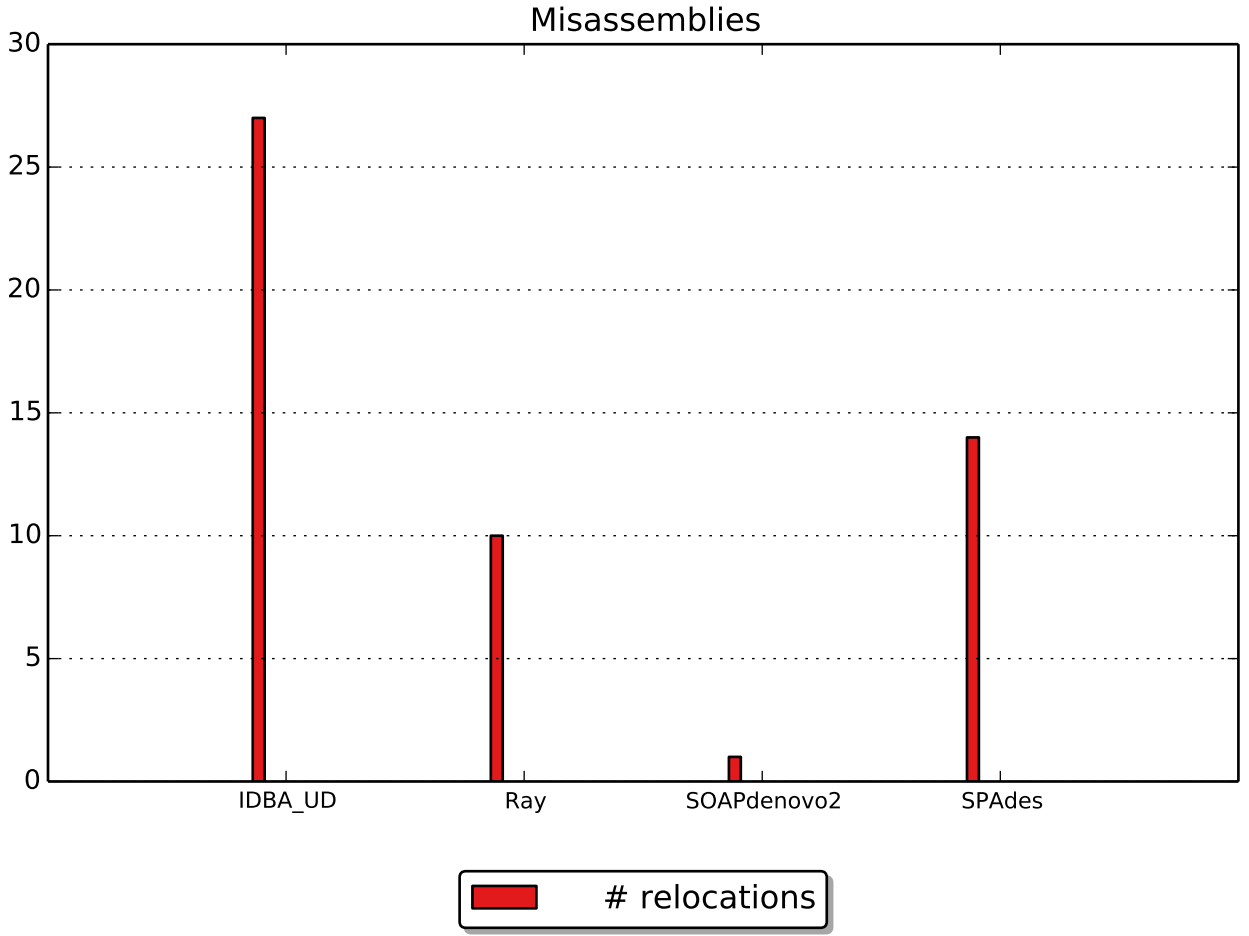
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

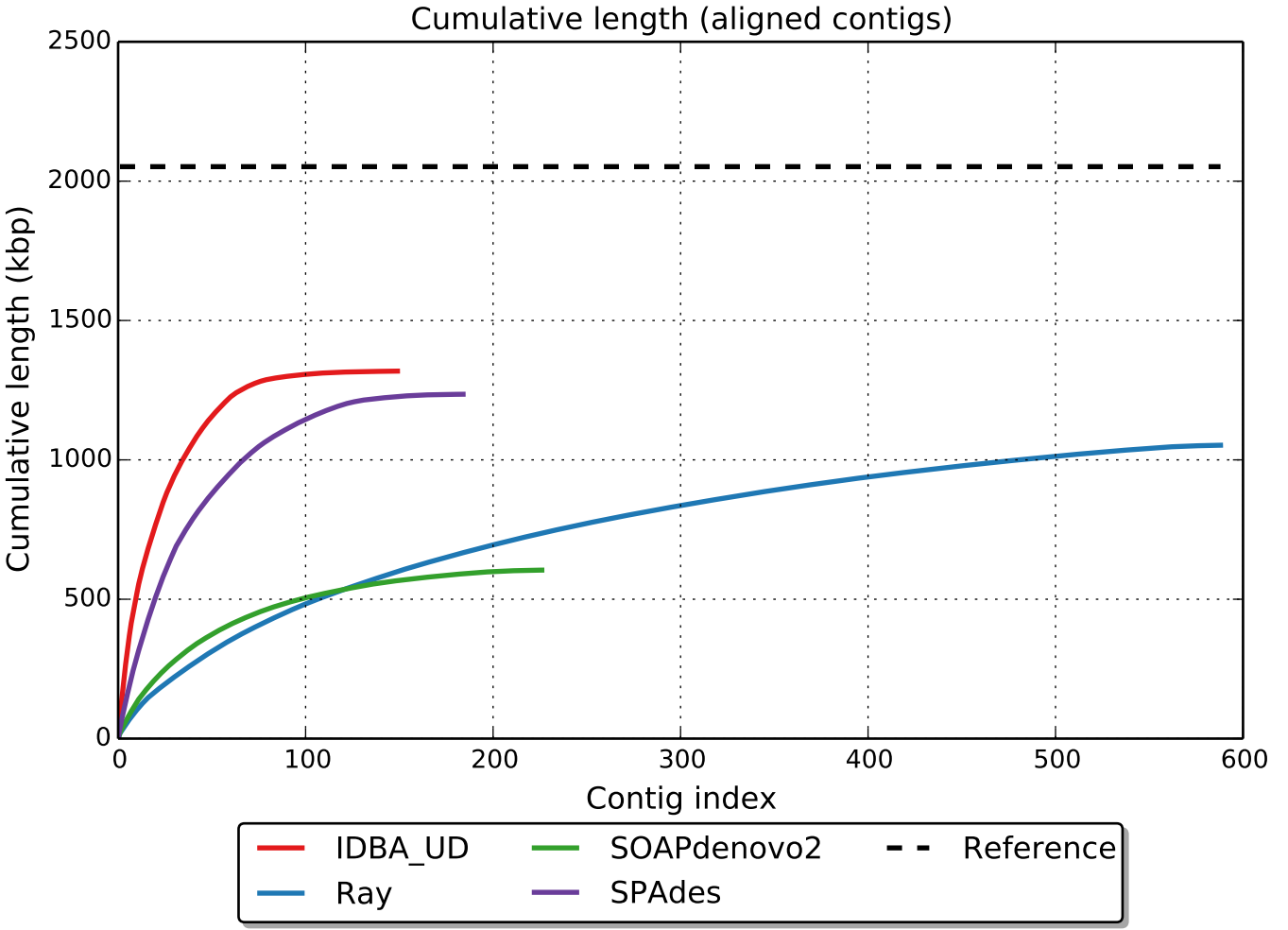

Nx
Contig length (kbp)
x
0
20
40
60
80
100
IDBA_UD
SOAPdenovo2
SPAdes
Ray

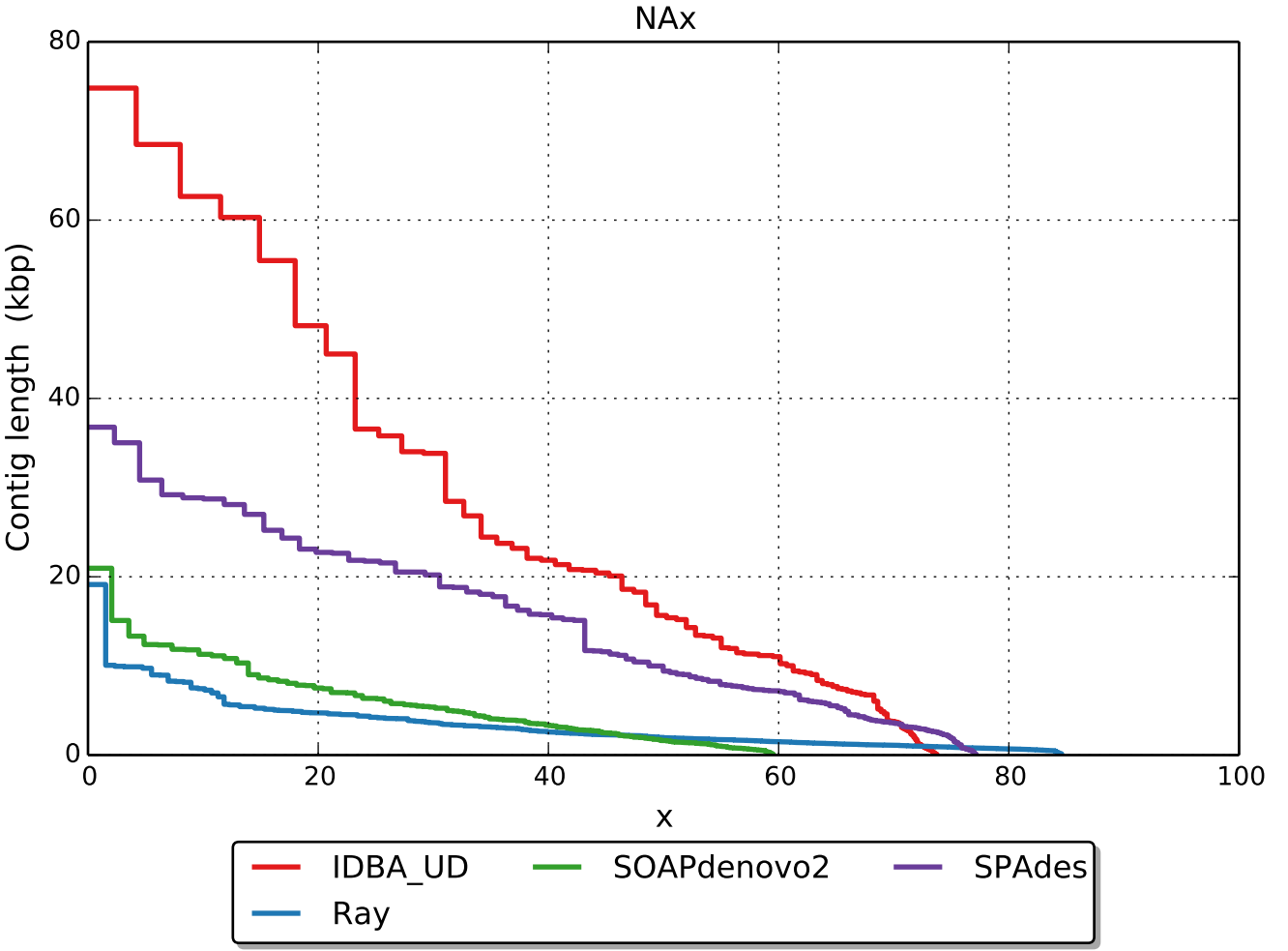

NGx
Contig length (kbp)
x
0
20
40
60
80
100
IDBA_UD
SOAPdenovo2
SPAdes
Ray

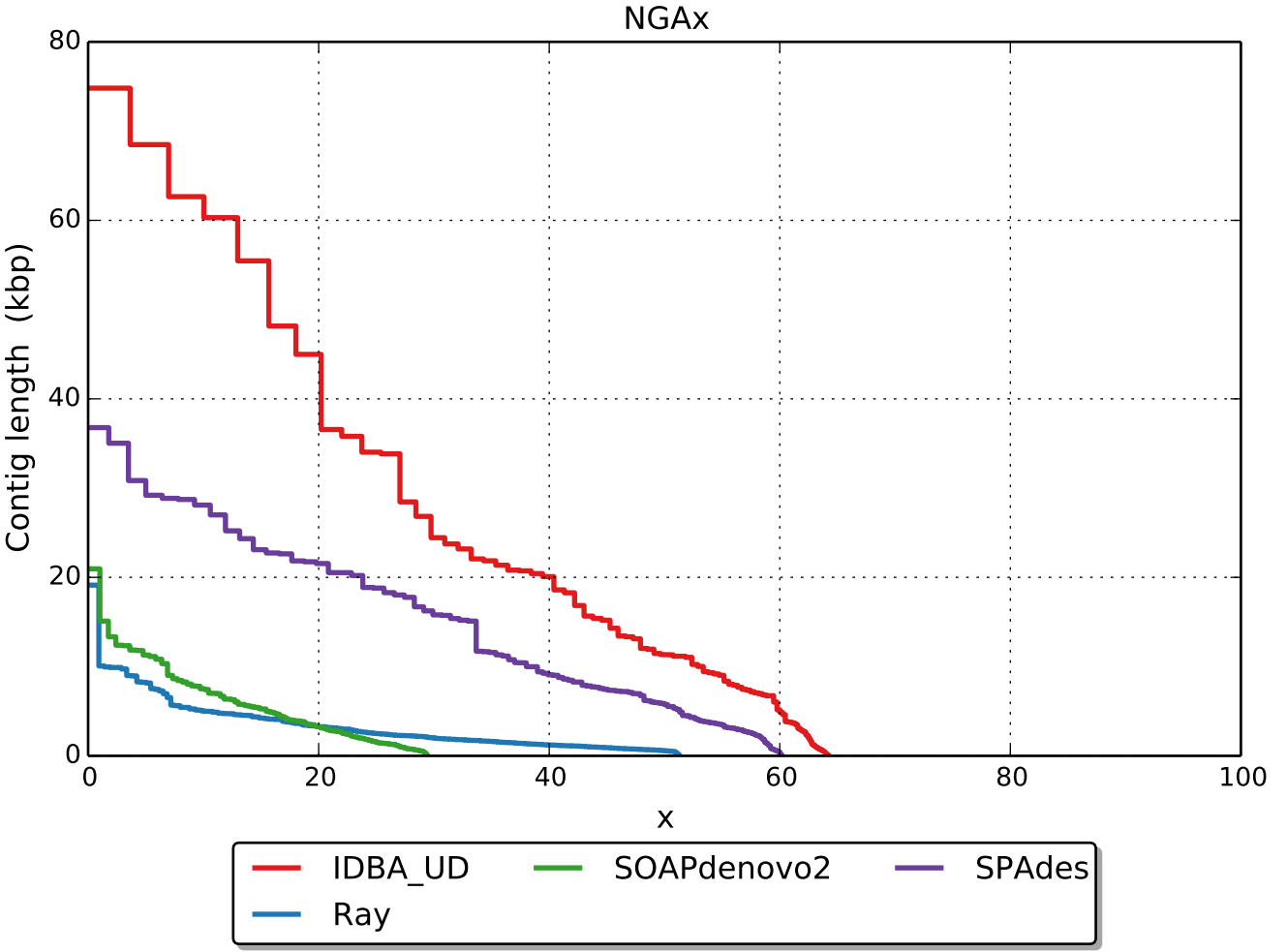

Cumulative length
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
100
200
300
400
500
600
Contig index
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference

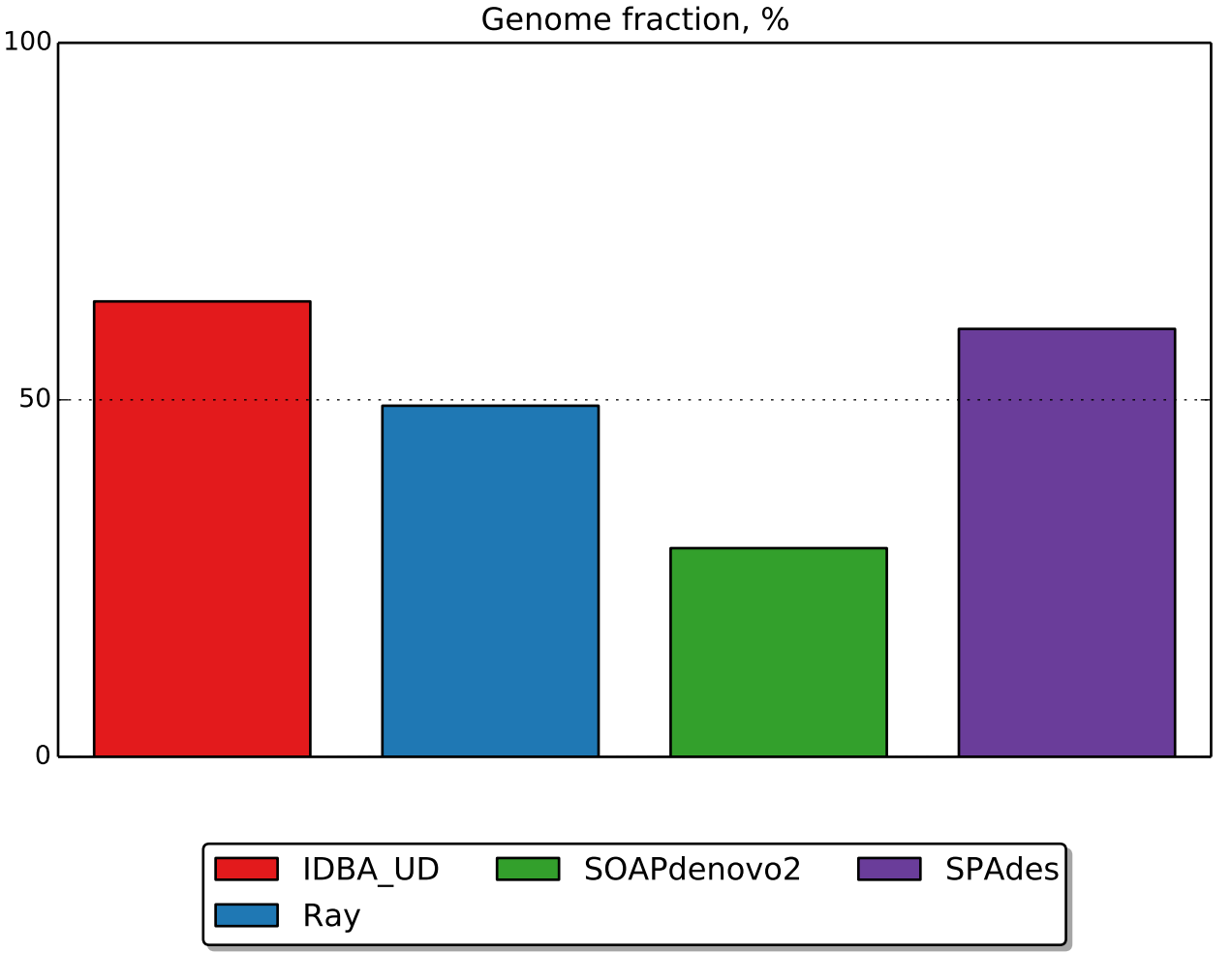

GC content
windows
GC (%)
0
200
400
600
800
1000
1200
0
20
40
60
80
100
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


Misassemblies
30
25
20
15
10
5
0
IDBA_UD
Ray
SOAPdenovo2
SPAdes
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
100
200
300
400
500
600
Contig index
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


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


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


Genome fraction, %
100
50
0
IDBA_UD
Ray
SOAPdenovo2
SPAdes