Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	682	398	286	516
# contigs (>= 5000 bp)	45	147	15	65
# contigs (>= 10000 bp)	6	81	2	12
# contigs (>= 25000 bp)	0	28	0	0
# contigs (>= 50000 bp)	0	15	0	0
Total length (>= 1000 bp)	1485785	3379424	623770	1421670
Total length (>= 5000 bp)	378623	2826863	116444	548699
Total length (>= 10000 bp)	90695	2347941	26130	172626
Total length (>= 25000 bp)	0	1554492	0	0
Total length (>= 50000 bp)	0	1117588	0	0
# contigs	1713	615	733	1159
Largest contig	19022	156859	13112	20844
Total length	2197907	3529459	936044	1872872
Reference length	2153652	2153652	2153652	2153652
GC (%)	41.23	41.65	42.00	41.18
Reference GC (%)	41.72	41.72	41.72	41.72
N50	1449	17473	1549	2334
NG50	1475	51487	-	1800
N75	851	6880	846	1023
NG75	876	22388	-	755
L50	357	39	158	183
LG50	342	15	-	252
L75	859	117	372	500
LG75	821	31	-	740
# misassemblies	35	45	1	24
# misassembled contigs	33	34	1	23
Misassembled contigs length	43553	297020	1032	75643
# local misassemblies	41	51	32	23
# structural variations	11	5	2	8
# unaligned contigs	0 + 515 part	0 + 281 part	0 + 530 part	0 + 366 part
Unaligned length	811846	2347713	625289	579357
Genome fraction (%)	50.618	40.856	13.286	50.410
Duplication ratio	1.271	1.343	1.086	1.191
# N's per 100 kbp	0.59	687.78	9151.39	501.58
# mismatches per 100 kbp	3076.88	3580.11	2592.79	3170.34
# indels per 100 kbp	56.78	65.69	55.92	55.45
Largest alignment	9440	17580	8075	20729
NA50	596	-	-	791
NGA50	608	119	-	631
LA50	1005	-	-	516
LGA50	968	750	-	714

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

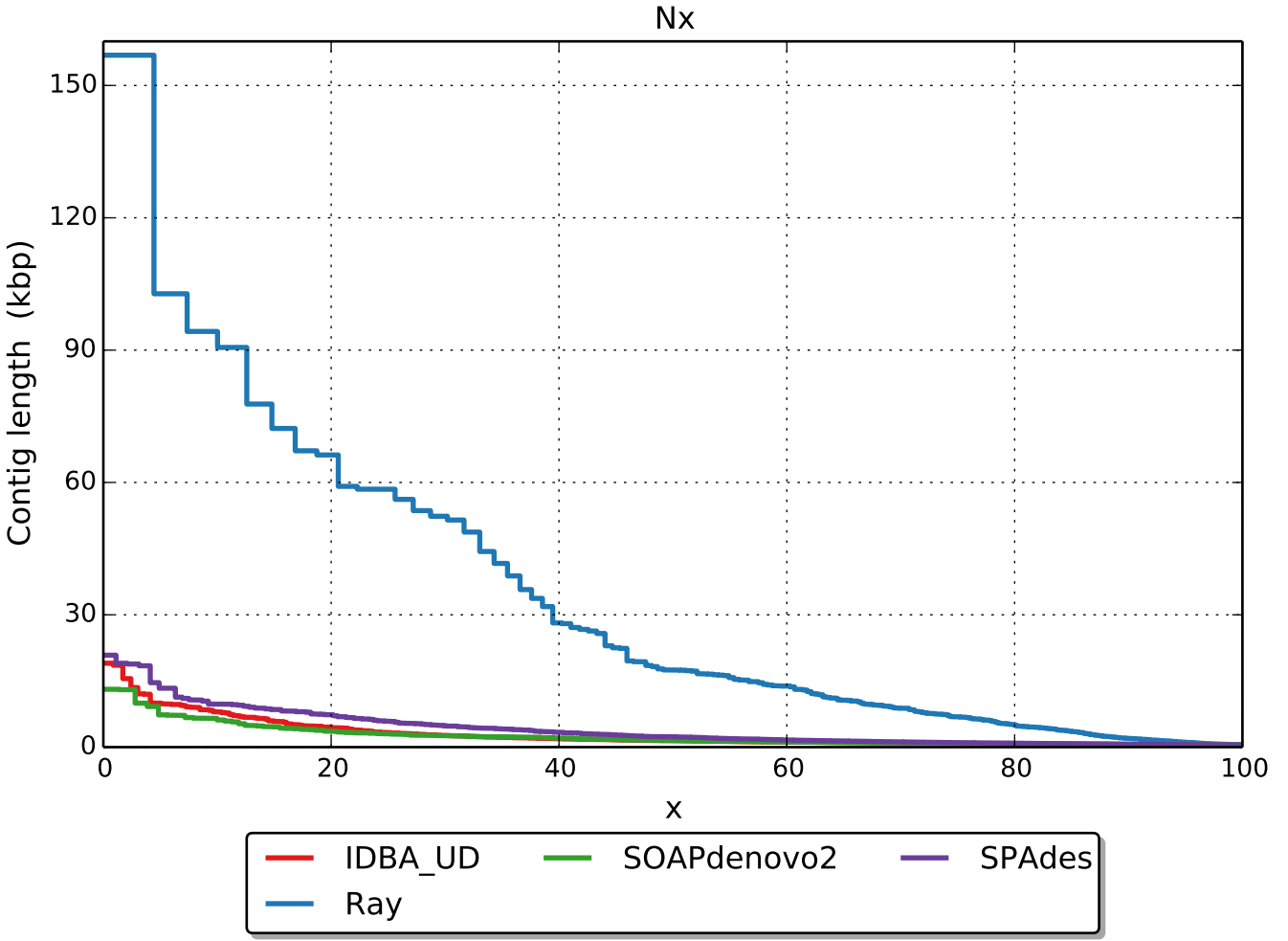
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	35	45	1	24
# relocations	35	45	1	24
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	81	166	44	85
# misassembled contigs	33	34	1	23
Misassembled contigs length	43553	297020	1032	75643
# local misassemblies	41	51	32	23
# structural variations	11	5	2	8
# mismatches	33542	31501	7419	34419
# indels	619	578	160	602
# short indels	558	556	123	570
# long indels	61	22	37	32
Indels length	2230	1048	1412	1403

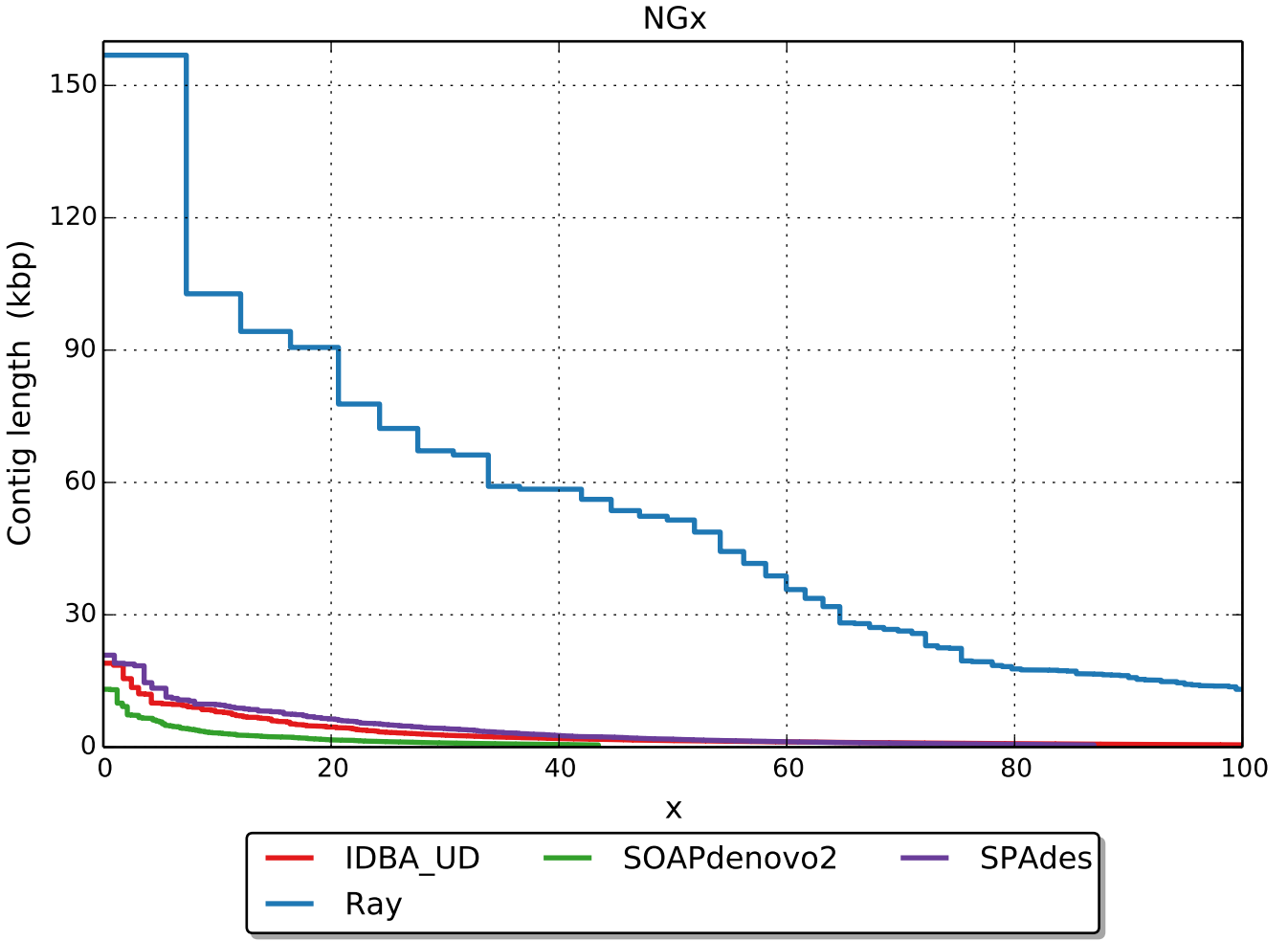
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

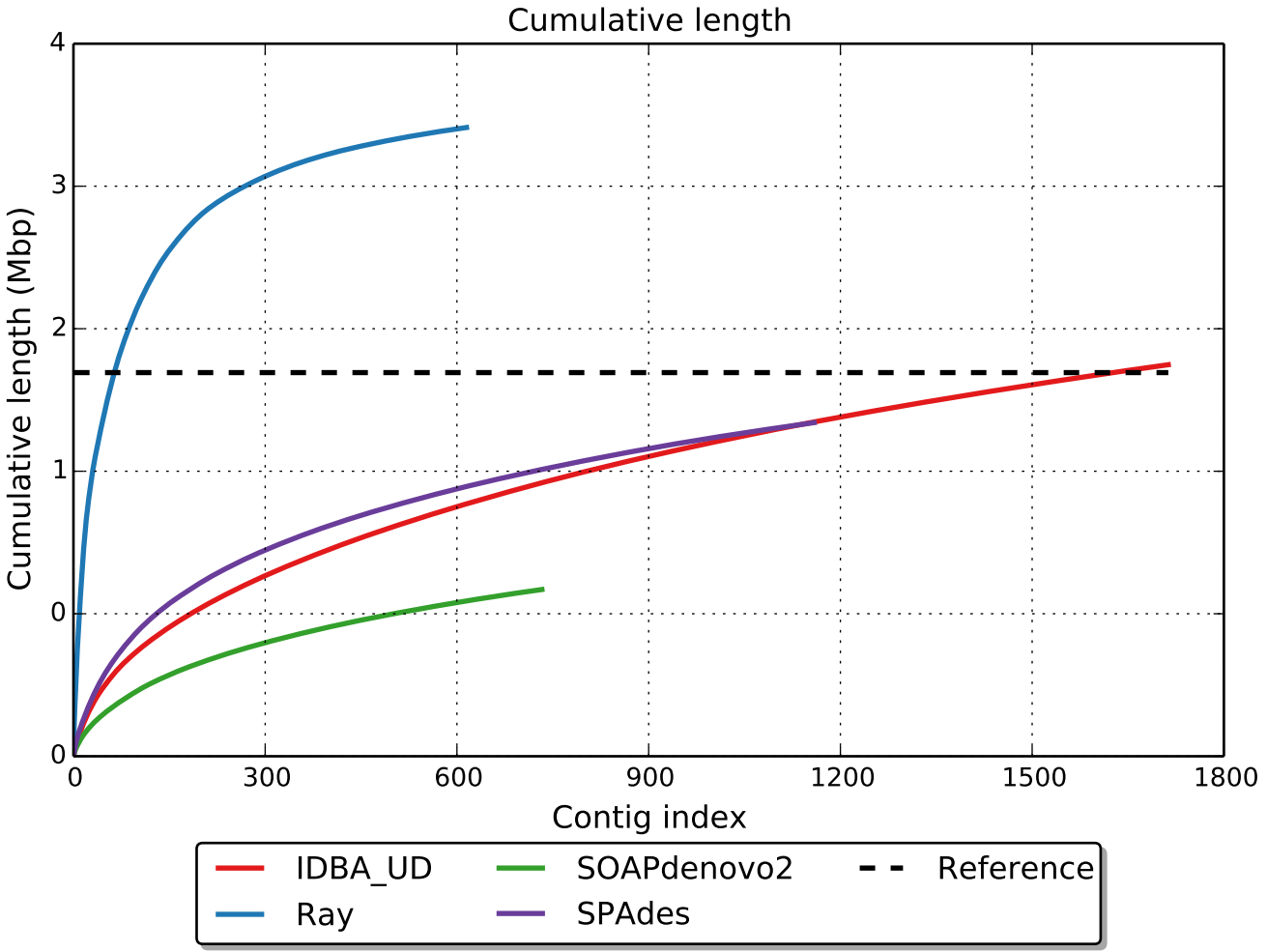
Unaligned report

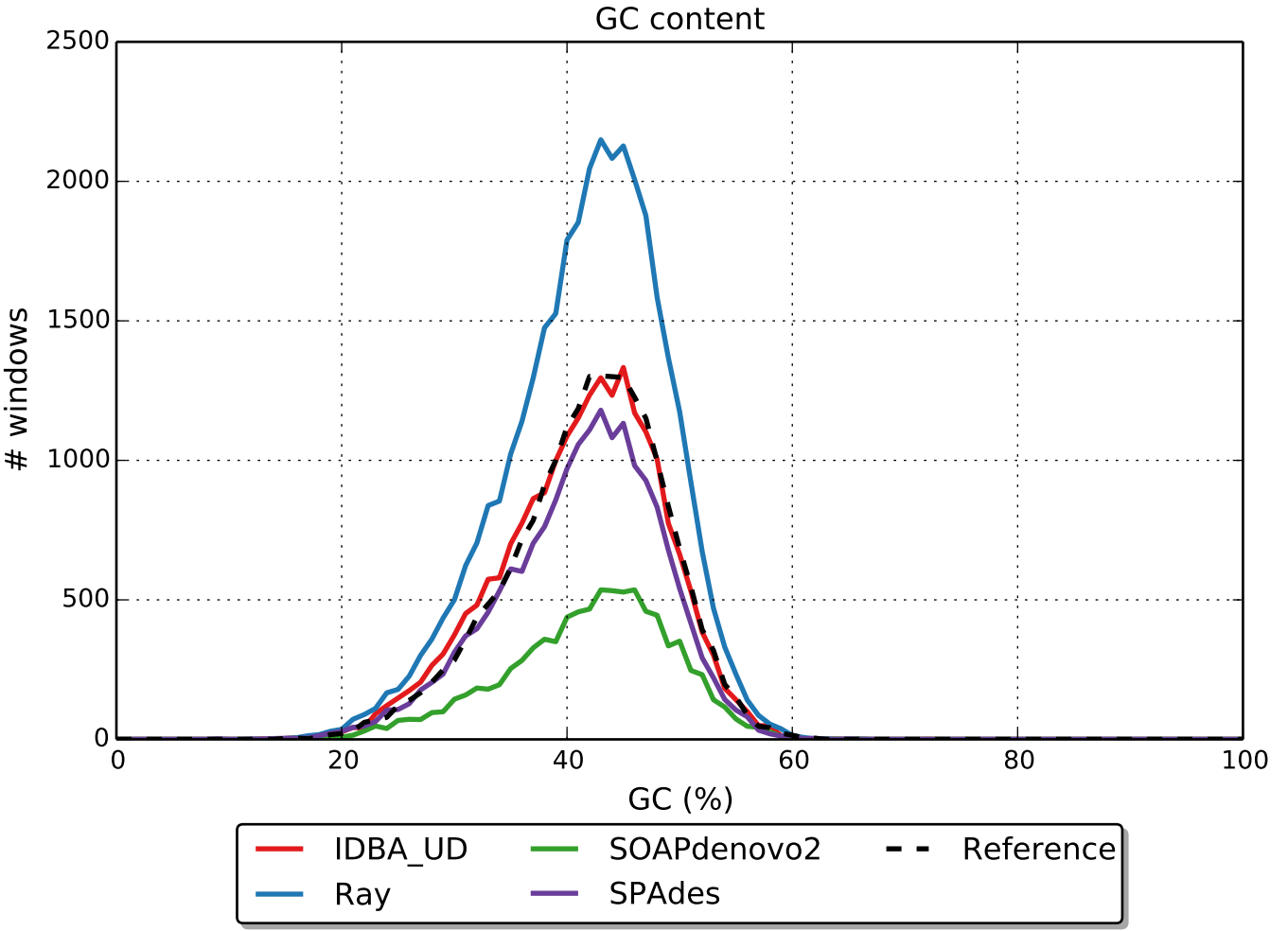
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	515	281	530	366
# with misassembly	35	67	69	20
# both parts are significant	71	130	38	73
Partially unaligned length	811846	2347713	625289	579357
# N's	13	24275	85661	9394

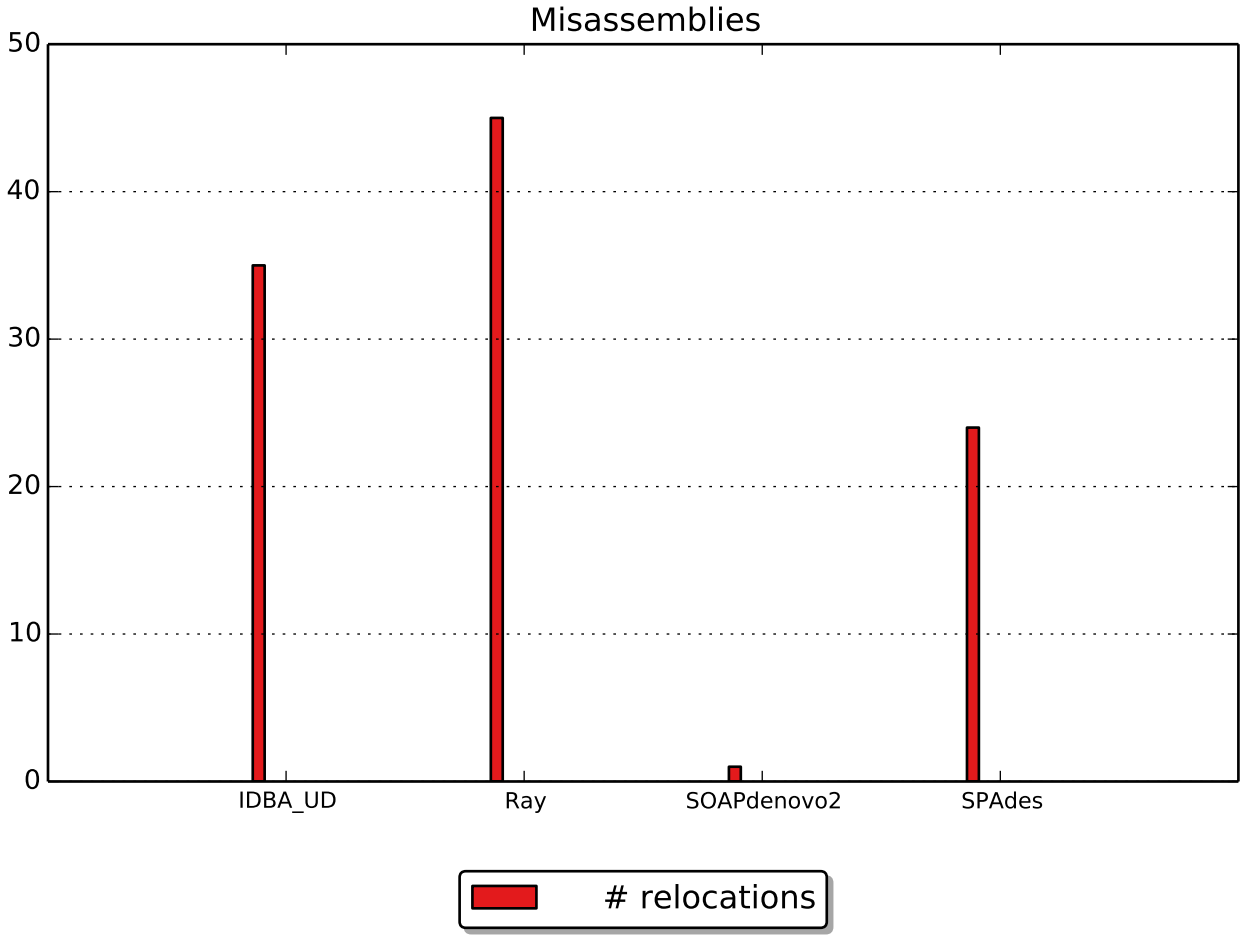
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

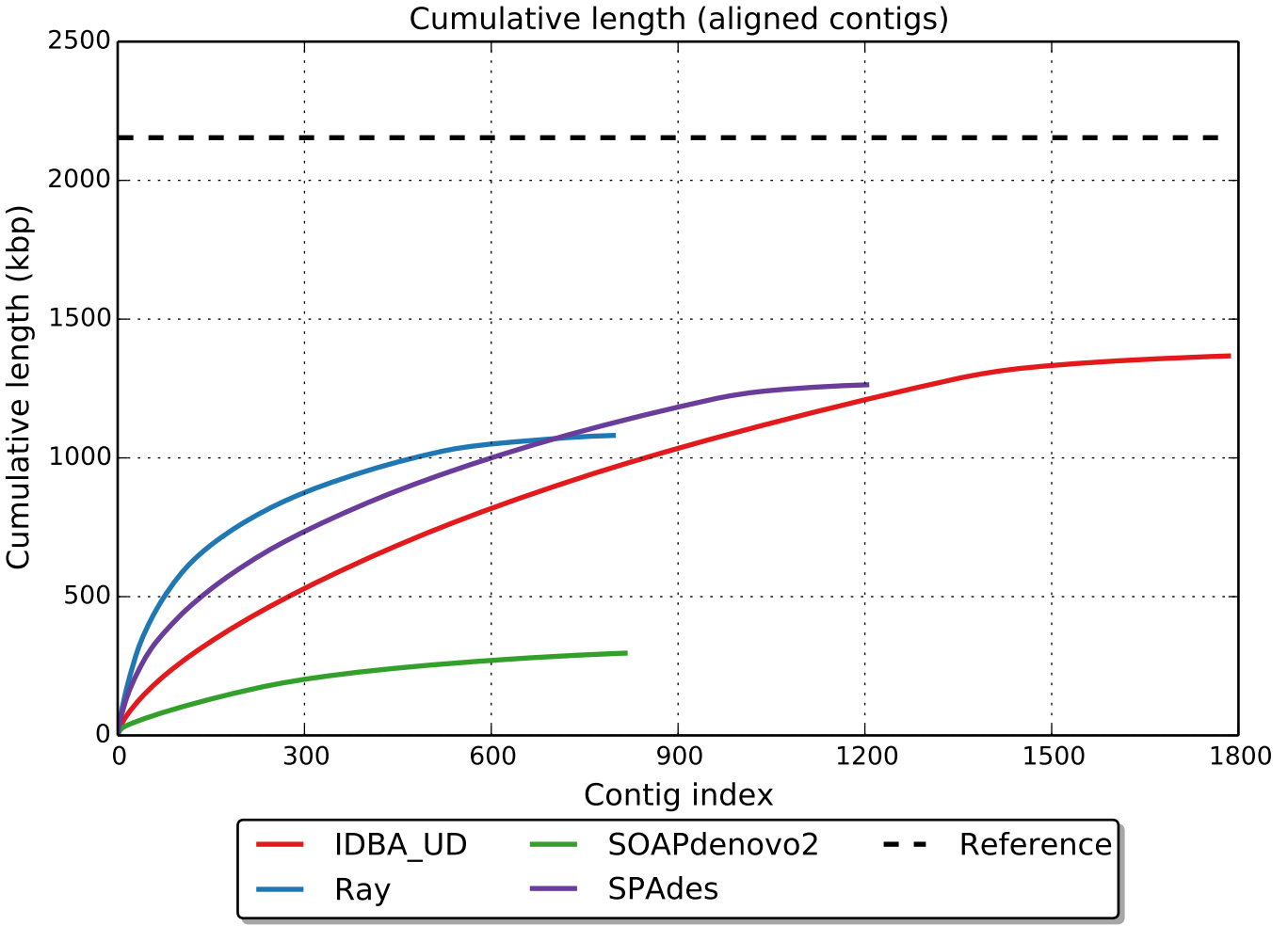

Nx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray

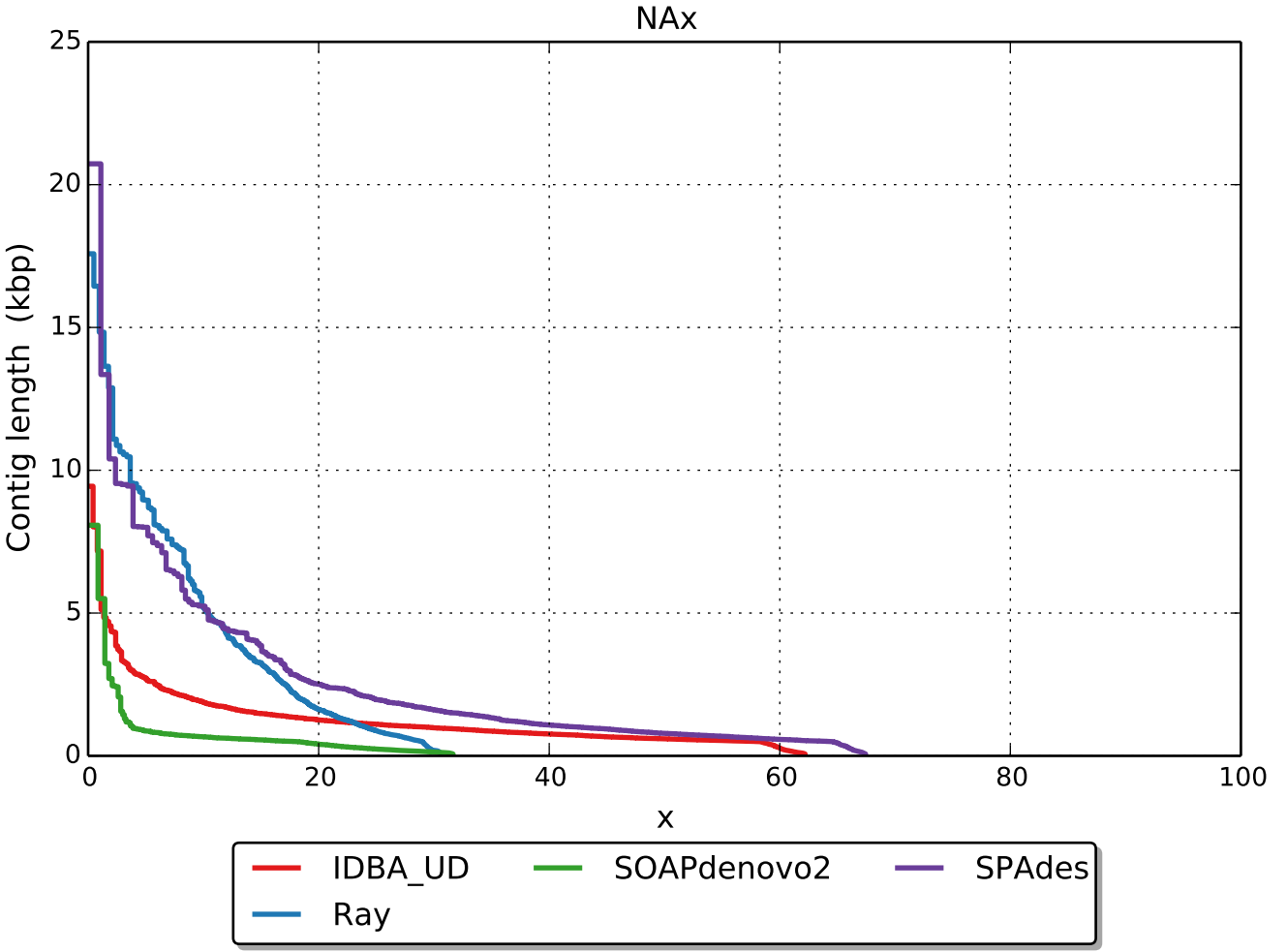

NGx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray

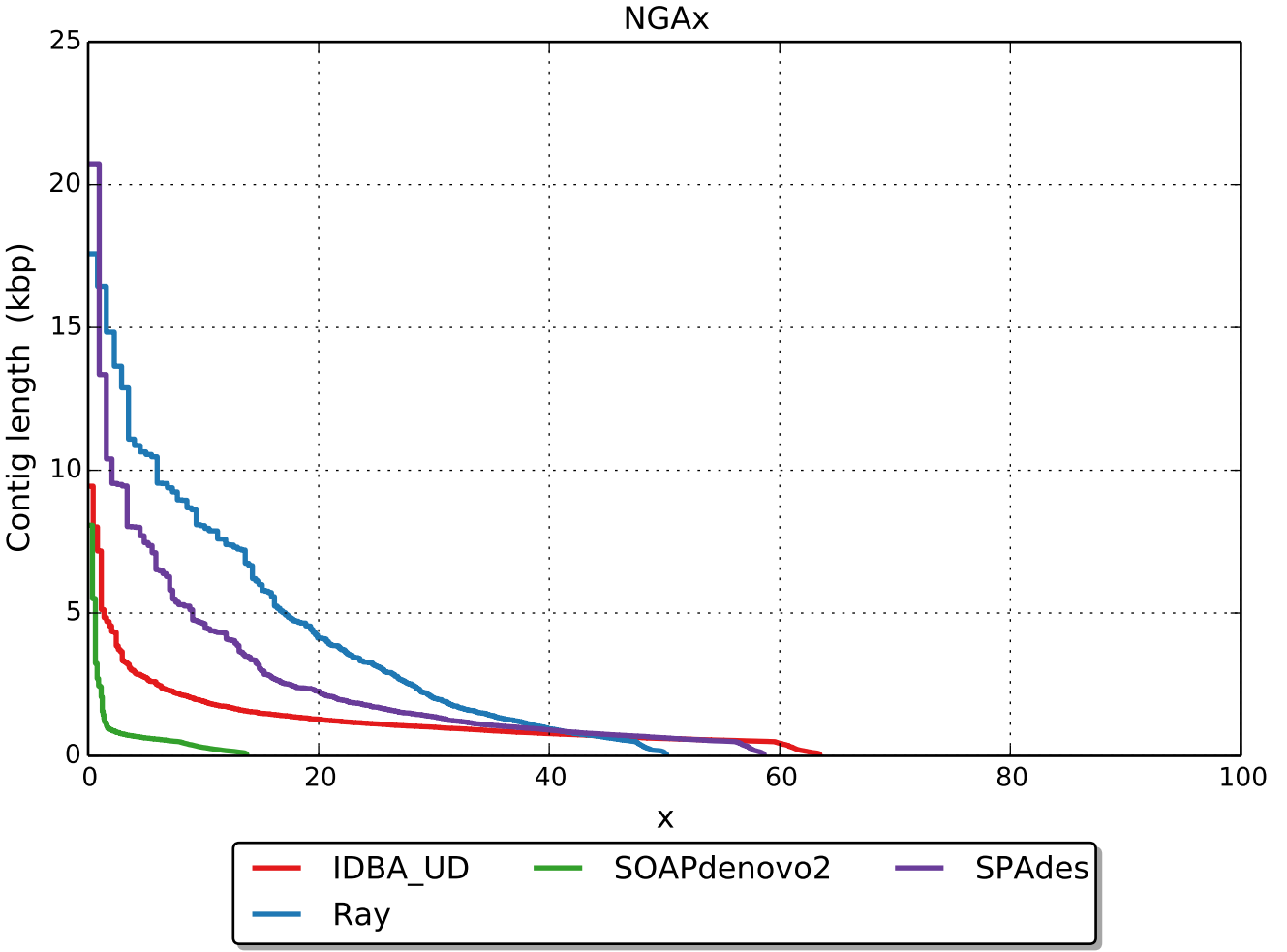

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
2
3
4
0
300
600
900
1200
1500
1800
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference

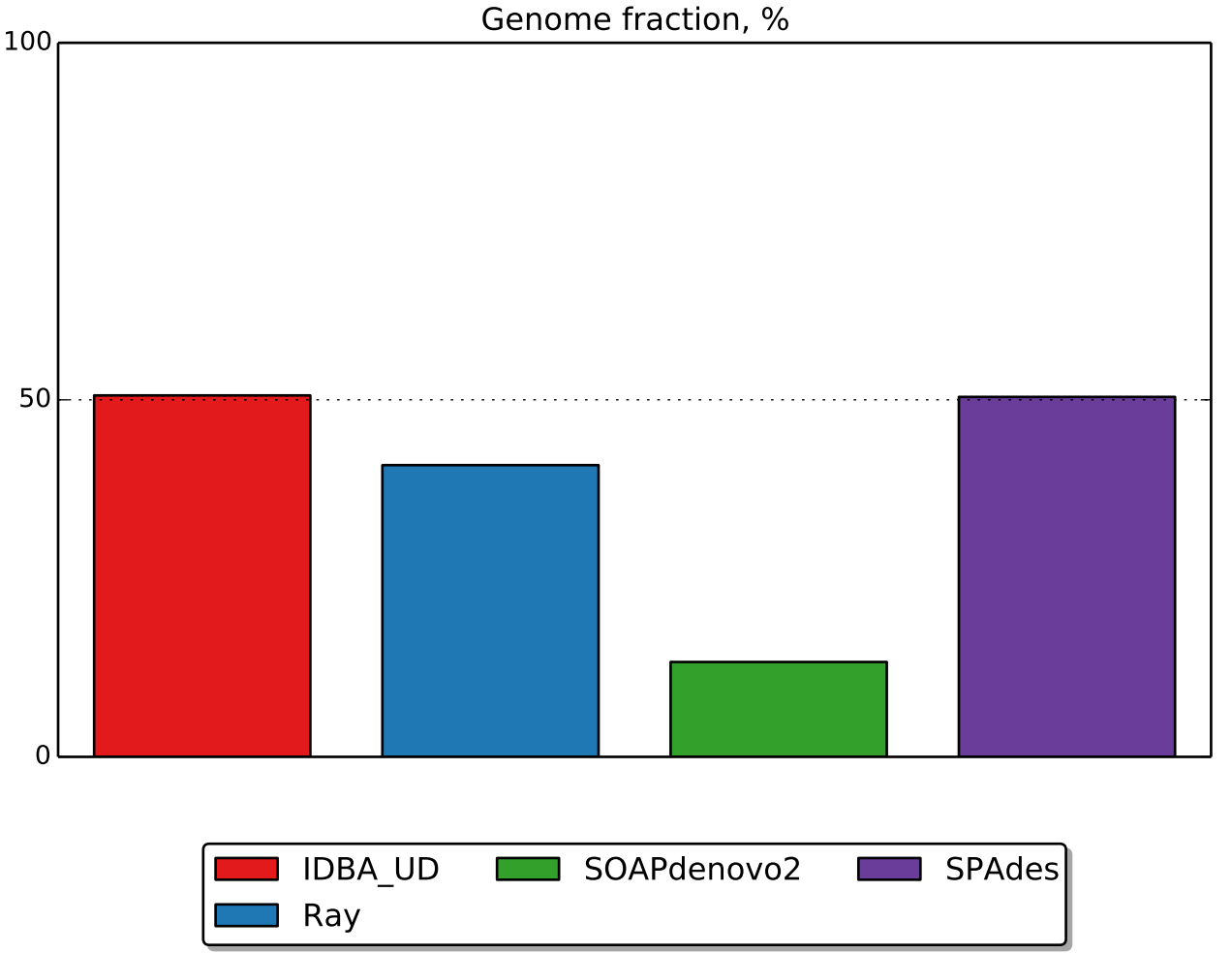

GC content
windows
GC (%)
0
500
1000
1500
2000
2500
0
20
40
60
80
100
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


Misassemblies
50
40
30
20
10
0
IDBA_UD
Ray
SOAPdenovo2
SPAdes
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
300
600
900
1200
1500
1800
Contig index
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


NAx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray


NGAx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray


Genome fraction, %
100
50
0
IDBA_UD
Ray
SOAPdenovo2
SPAdes