Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	64	21	36	54
# contigs (>= 5000 bp)	20	3	1	26
# contigs (>= 10000 bp)	12	2	0	14
# contigs (>= 25000 bp)	6	1	0	6
# contigs (>= 50000 bp)	4	0	0	2
Total length (>= 1000 bp)	795501	89070	61317	620156
Total length (>= 5000 bp)	691521	53501	6614	535864
Total length (>= 10000 bp)	636909	46938	0	443102
Total length (>= 25000 bp)	523615	34615	0	319462
Total length (>= 50000 bp)	449493	0	0	193695
# contigs	84	40	121	63
Largest contig	182993	34615	6614	120419
Total length	809887	102721	120596	627177
Reference length	2954616	2954616	2954616	2954616
GC (%)	43.42	41.97	45.09	42.45
Reference GC (%)	41.37	41.37	41.37	41.37
N50	77126	6563	1050	26166
N75	16670	2215	715	8905
L50	4	3	36	6
L75	11	12	71	17
# misassemblies	1	0	1	0
# misassembled contigs	1	0	1	0
Misassembled contigs length	7017	0	1165	0
# local misassemblies	2	5	62	3
# structural variations	0	0	0	0
# unaligned contigs	0 + 49 part	0 + 9 part	0 + 31 part	0 + 44 part
Unaligned length	632838	57004	18071	442375
Genome fraction (%)	5.713	1.426	3.303	5.847
Duplication ratio	1.049	1.085	1.051	1.070
# N's per 100 kbp	24.94	1763.03	4141.93	309.16
# mismatches per 100 kbp	1091.92	854.19	911.01	1220.11
# indels per 100 kbp	43.25	18.98	15.37	42.83
Largest alignment	19893	4456	3059	15302
NA50	-	-	751	-
NGA50	-	-	-	-
NA75	-	-	441	-
LA50	-	-	48	-
LA75	-	-	99	-

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

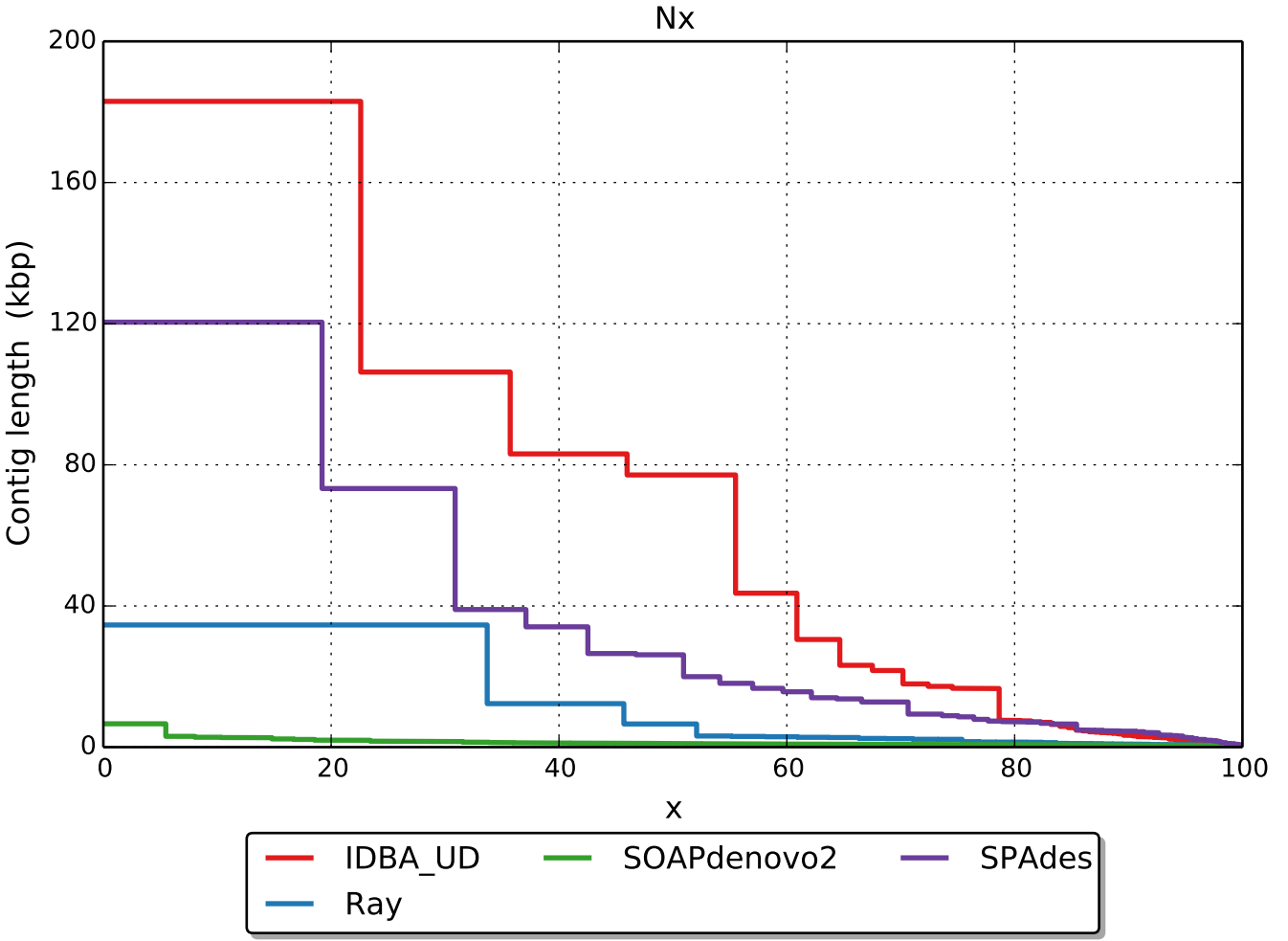
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	1	0	1	0
# relocations	0	0	1	0
# translocations	0	0	0	0
# inversions	1	0	0	0
# possibly misassembled contigs	11	4	3	20
# misassembled contigs	1	0	1	0
Misassembled contigs length	7017	0	1165	0
# local misassemblies	2	5	62	3
# structural variations	0	0	0	0
# mismatches	1843	360	889	2108
# indels	73	8	15	74
# short indels	66	8	14	63
# long indels	7	0	1	11
Indels length	233	8	24	217

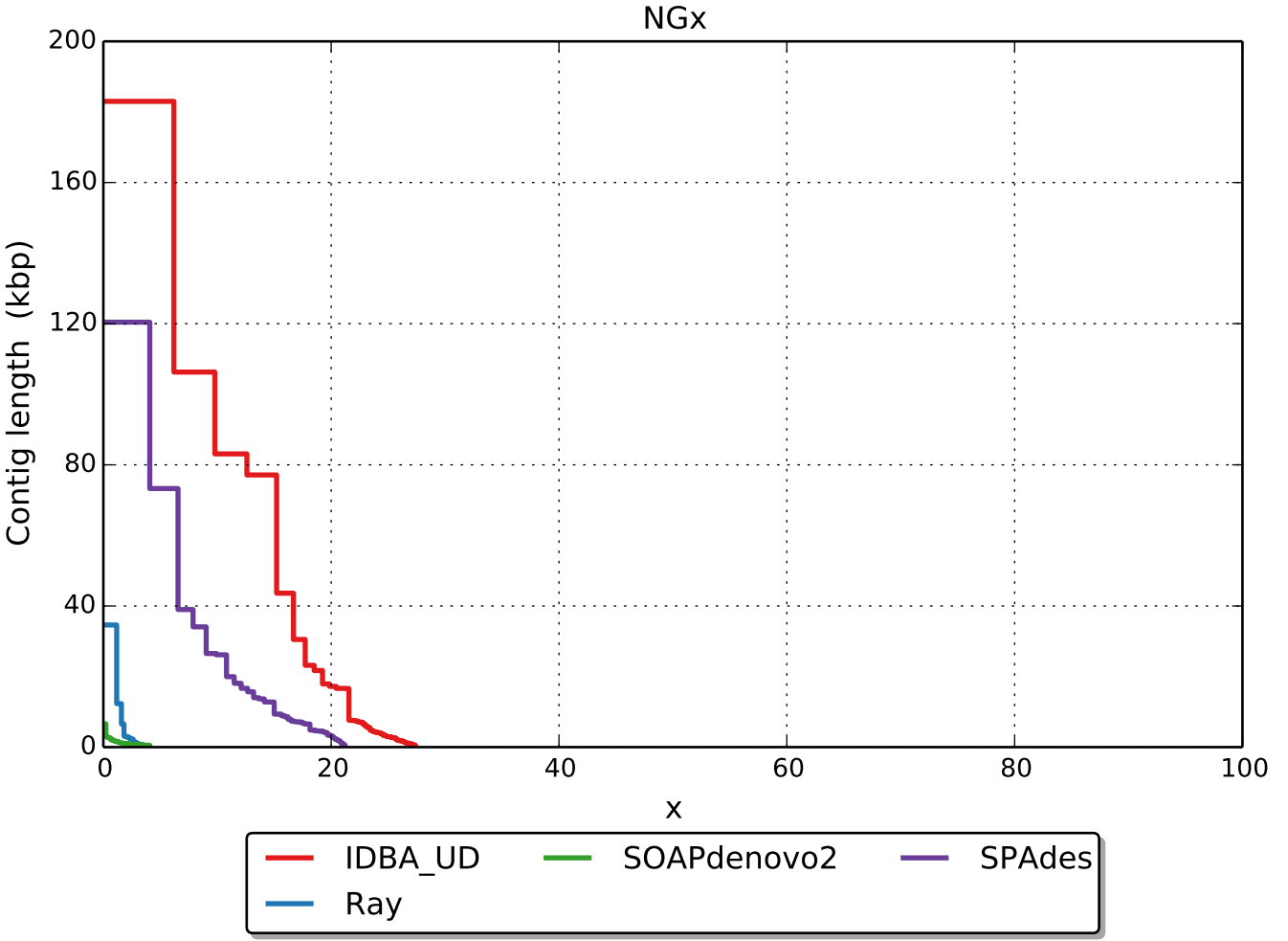
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

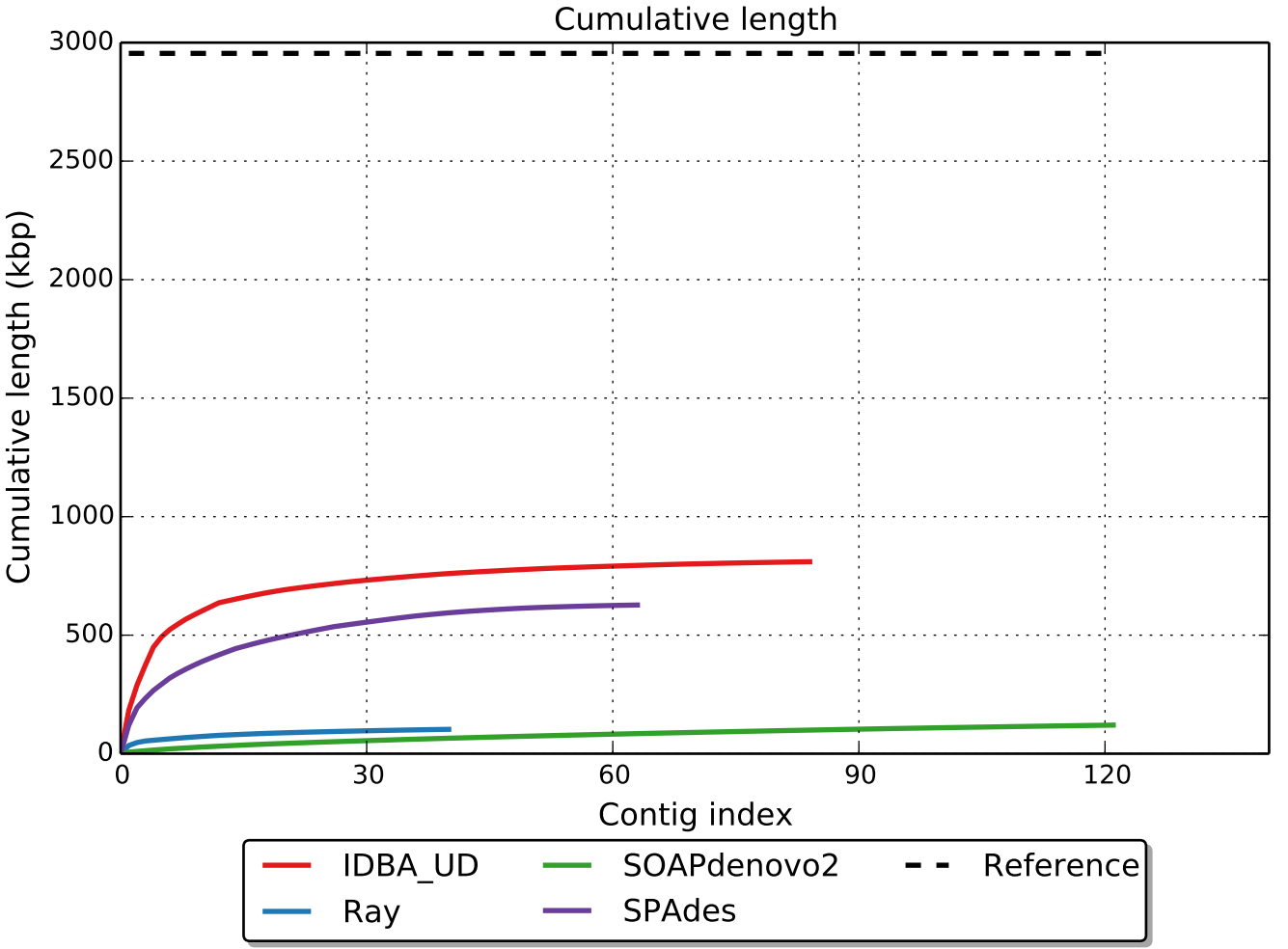
Unaligned report

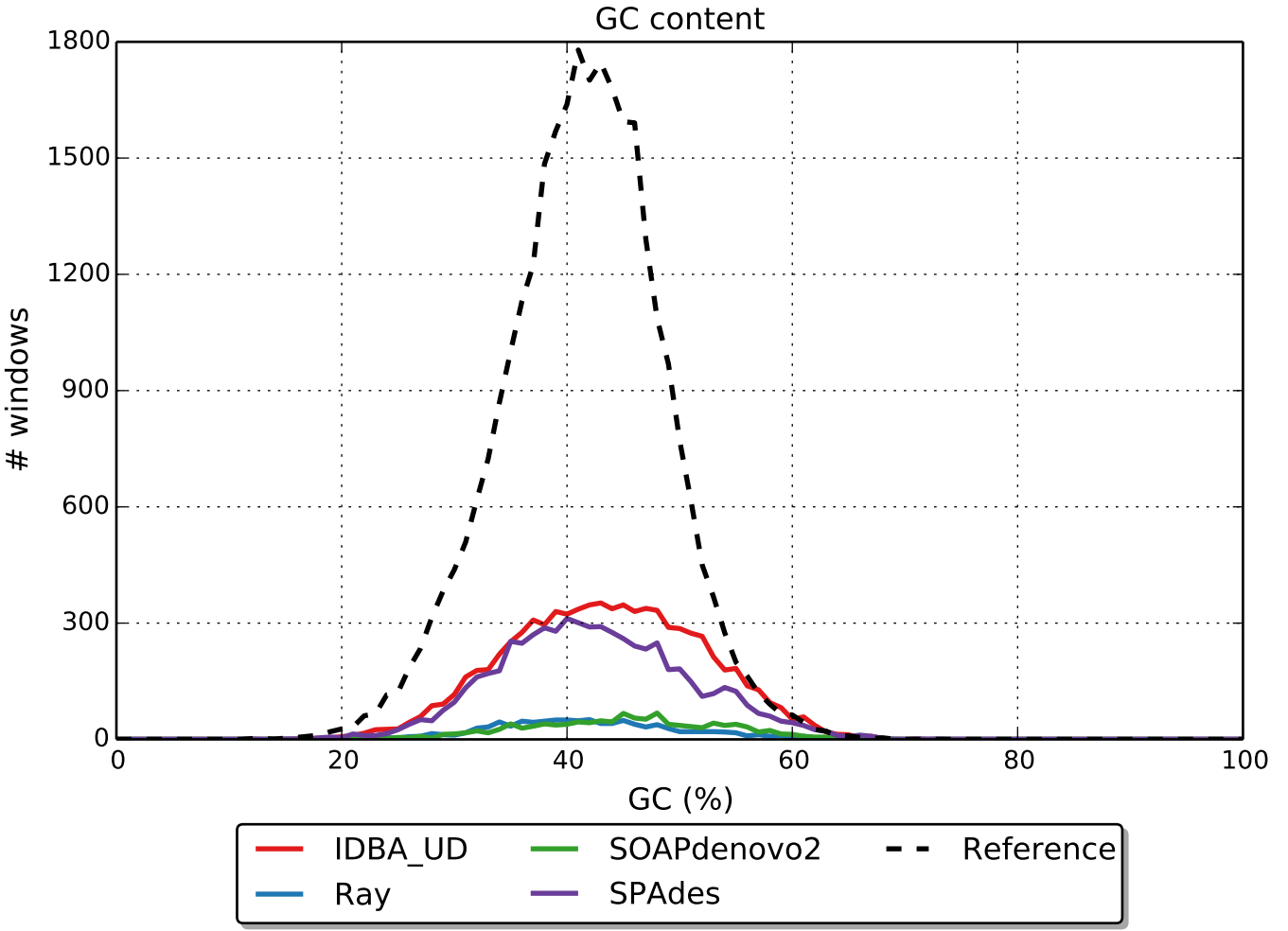
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	49	9	31	44
# with misassembly	1	0	5	0
# both parts are significant	10	3	3	19
Partially unaligned length	632838	57004	18071	442375
# N's	202	1811	4995	1939

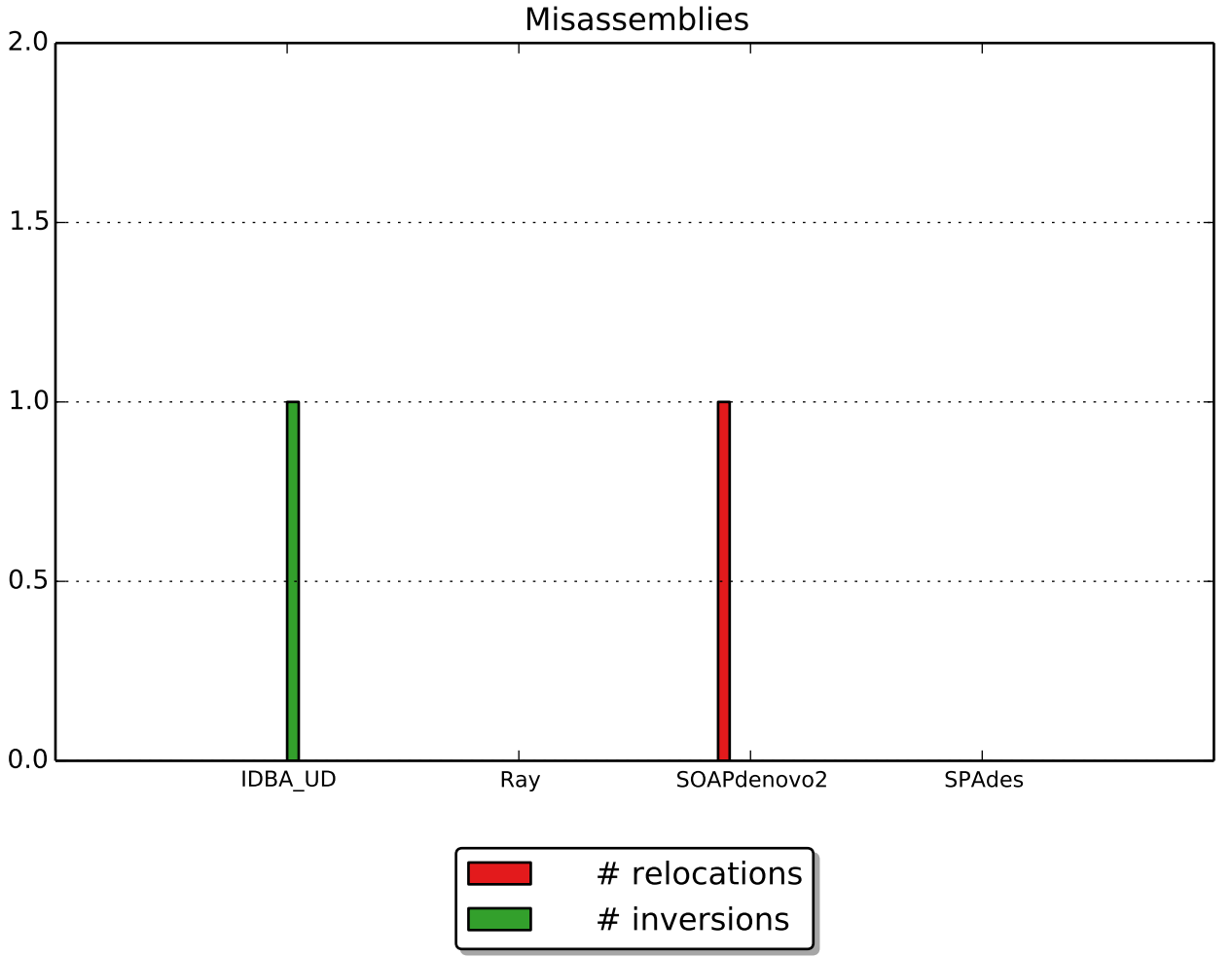
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

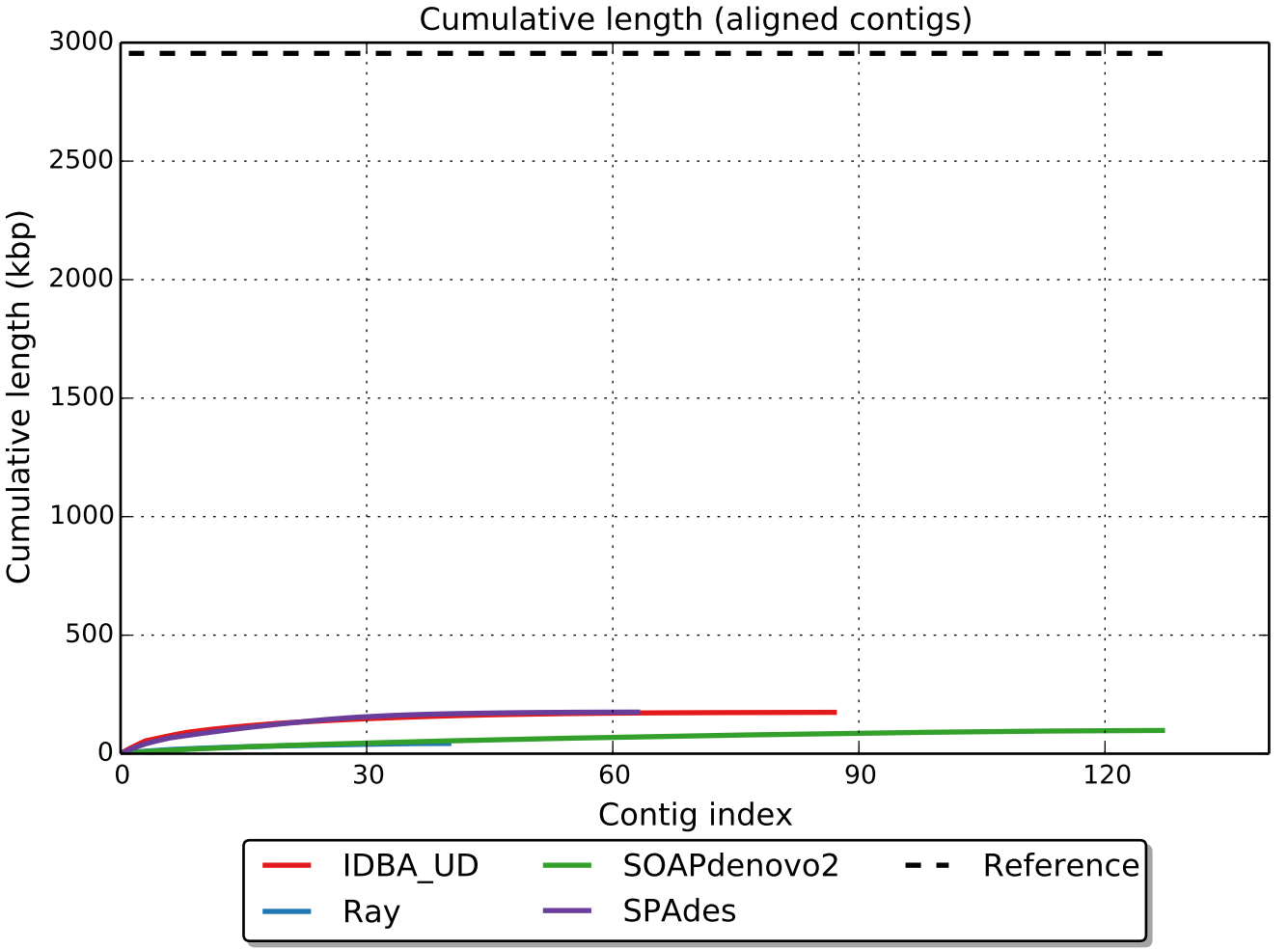

Nx
200
160
120
80
40
0
Contig length (kbp)
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray

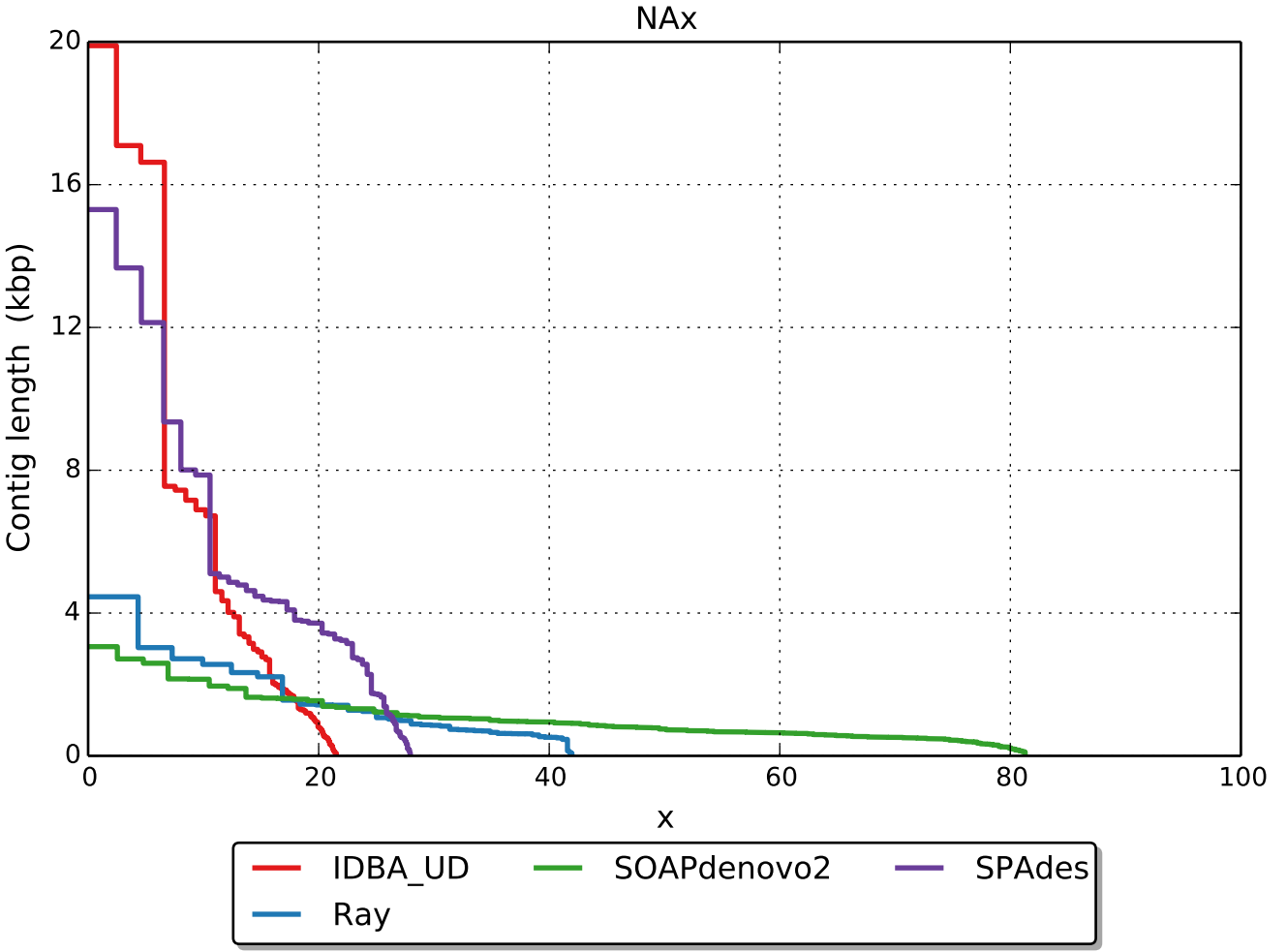

NGx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray

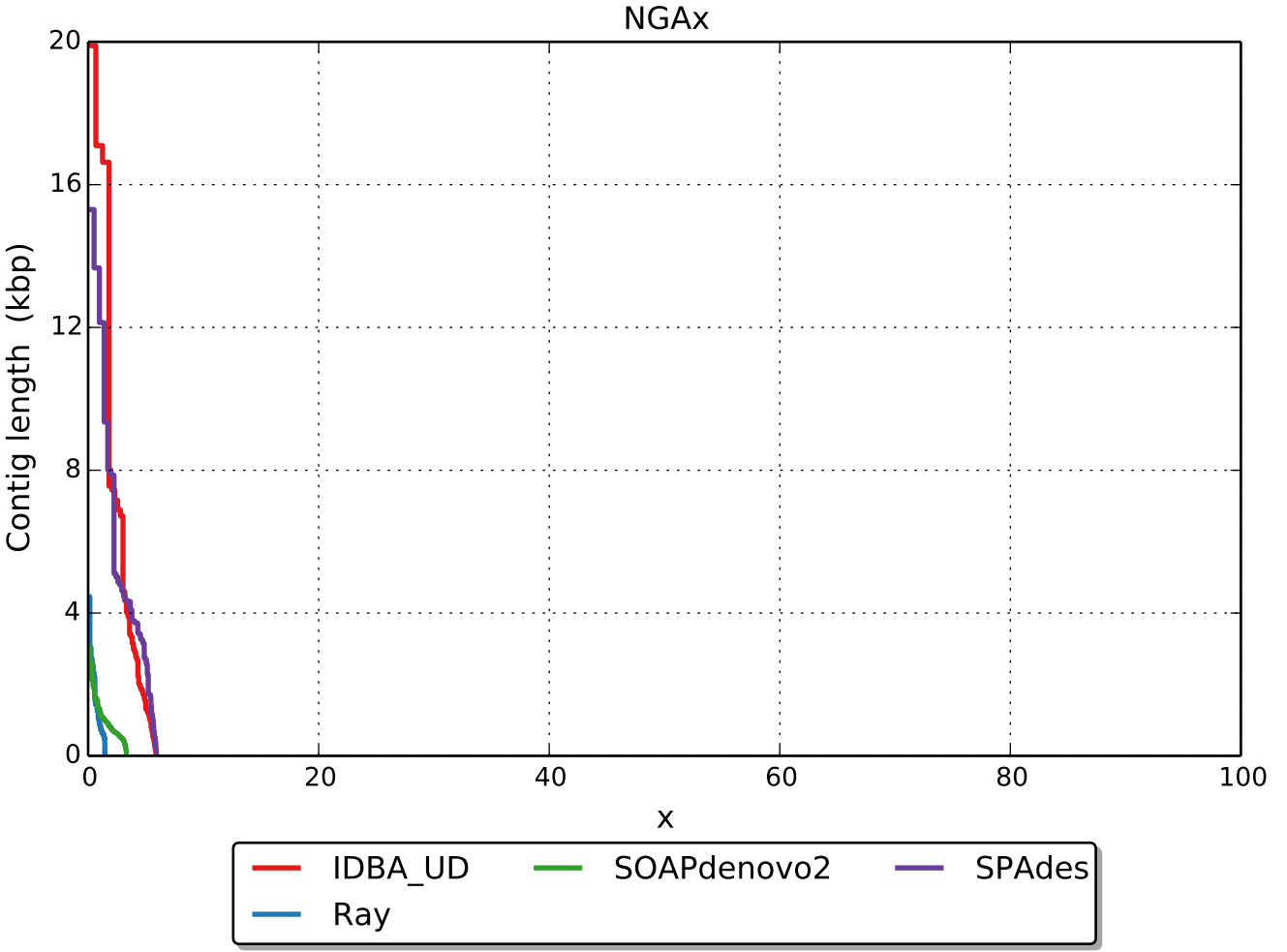

Cumulative length
Cumulative length (kbp)
3000
2500
2000
1500
1000
500
0
0
30
60
90
120
Contig index
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference

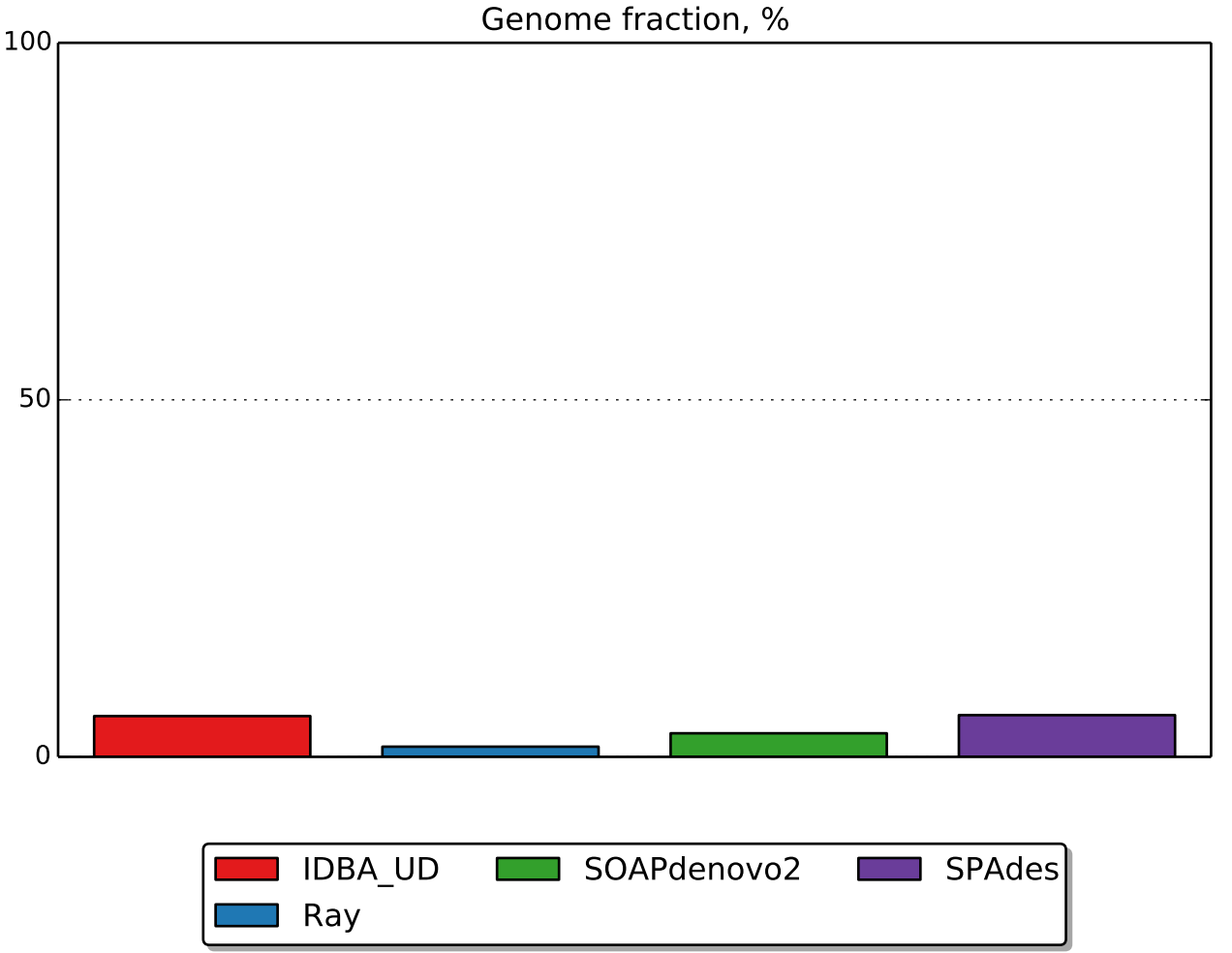

GC content
1800
1500
1200
900
600
300
0
windows
0
20
40
60
80
100
GC (%)
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


Misassemblies
2.0
1.5
1.0
0.5
0.0
IDBA_UD
Ray
SOAPdenovo2
SPAdes
relocations
inversions


Cumulative length (aligned contigs)
Cumulative length (kbp)
3000
2500
2000
1500
1000
500
0
0
30
60
90
120
Contig index
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


NAx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray


NGAx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray


Genome fraction, %
100
50
0
IDBA_UD
Ray
SOAPdenovo2
SPAdes