Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	53	7	18	90
# contigs (>= 5000 bp)	9	4	1	10
# contigs (>= 10000 bp)	8	0	0	5
# contigs (>= 25000 bp)	3	0	0	3
# contigs (>= 50000 bp)	1	0	0	2
Total length (>= 1000 bp)	390441	37401	35845	436886
Total length (>= 5000 bp)	313033	29693	8370	289261
Total length (>= 10000 bp)	306305	0	0	252427
Total length (>= 25000 bp)	239519	0	0	220730
Total length (>= 50000 bp)	182993	0	0	192449
# contigs	141	15	48	220
Largest contig	182993	8080	8370	131559
Total length	452997	42442	55919	525309
Reference length	3545606	3545606	3545606	3545606
GC (%)	44.15	39.73	39.42	40.64
Reference GC (%)	44.19	44.19	44.19	44.19
N50	27793	7669	1238	8401
N75	2374	2807	761	1384
L50	3	3	11	7
L75	18	5	26	54
# misassemblies	2	1	1	1
# misassembled contigs	2	1	1	1
Misassembled contigs length	3040	564	860	2325
# local misassemblies	3	4	17	3
# structural variations	0	0	0	0
# unaligned contigs	0 + 63 part	0 + 4 part	0 + 18 part	0 + 134 part
Unaligned length	333445	19826	19709	380541
Genome fraction (%)	3.210	0.539	0.968	3.954
Duplication ratio	1.051	1.184	1.055	1.033
# N's per 100 kbp	88.96	1069.70	4647.79	935.07
# mismatches per 100 kbp	1627.46	953.03	1276.37	1661.94
# indels per 100 kbp	92.27	68.07	52.45	113.41
Largest alignment	9029	5104	2413	5105
NA50	-	-	553	-
NGA50	-	-	-	-
LA50	-	-	29	-

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

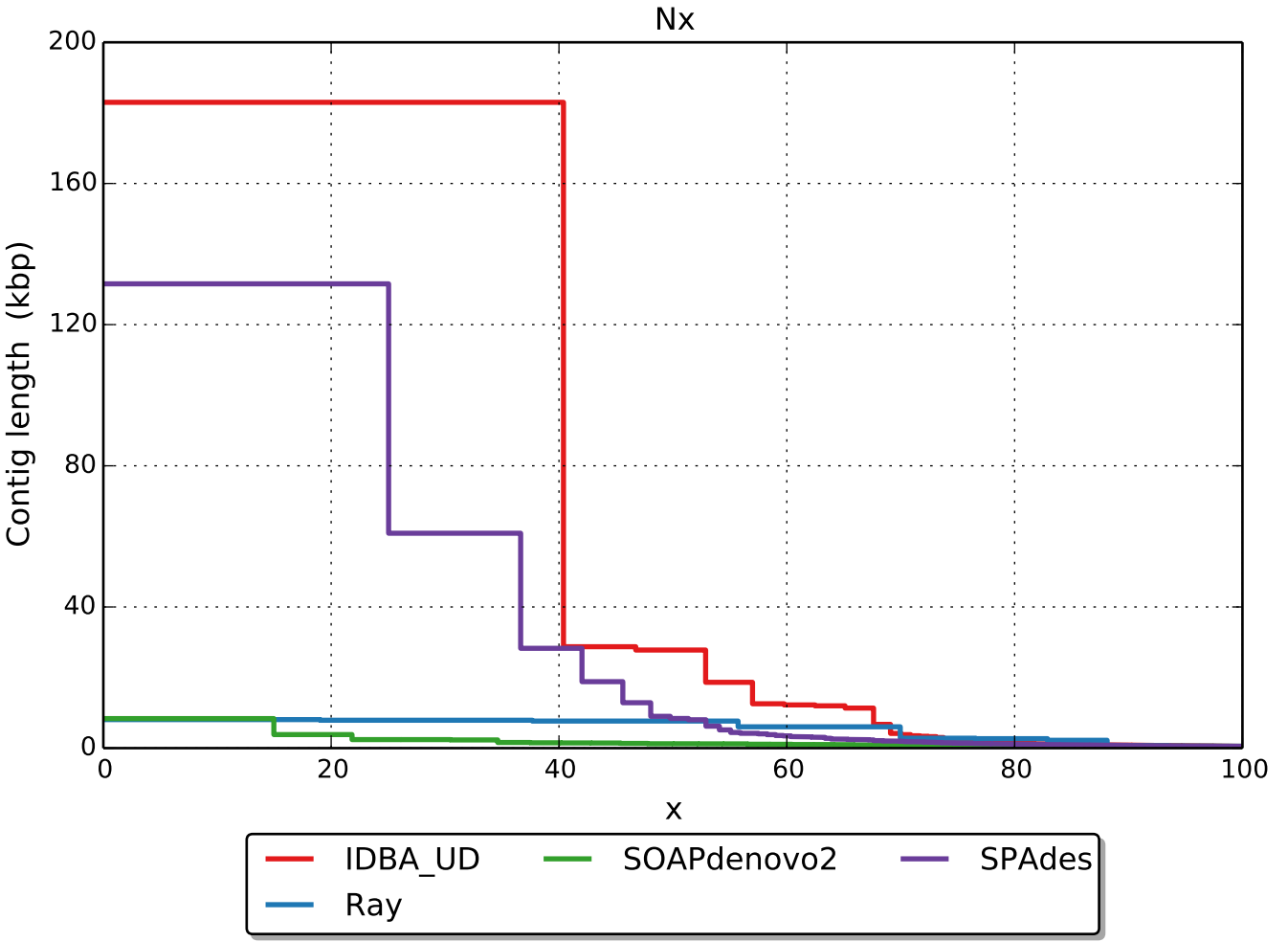
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	2	1	1	1
# relocations	1	1	1	1
# translocations	0	0	0	0
# inversions	1	0	0	0
# possibly misassembled contigs	9	4	4	16
# misassembled contigs	2	1	1	1
Misassembled contigs length	3040	564	860	2325
# local misassemblies	3	4	17	3
# structural variations	0	0	0	0
# mismatches	1852	182	438	2330
# indels	105	13	18	159
# short indels	101	13	17	133
# long indels	4	0	1	26
Indels length	160	14	28	467

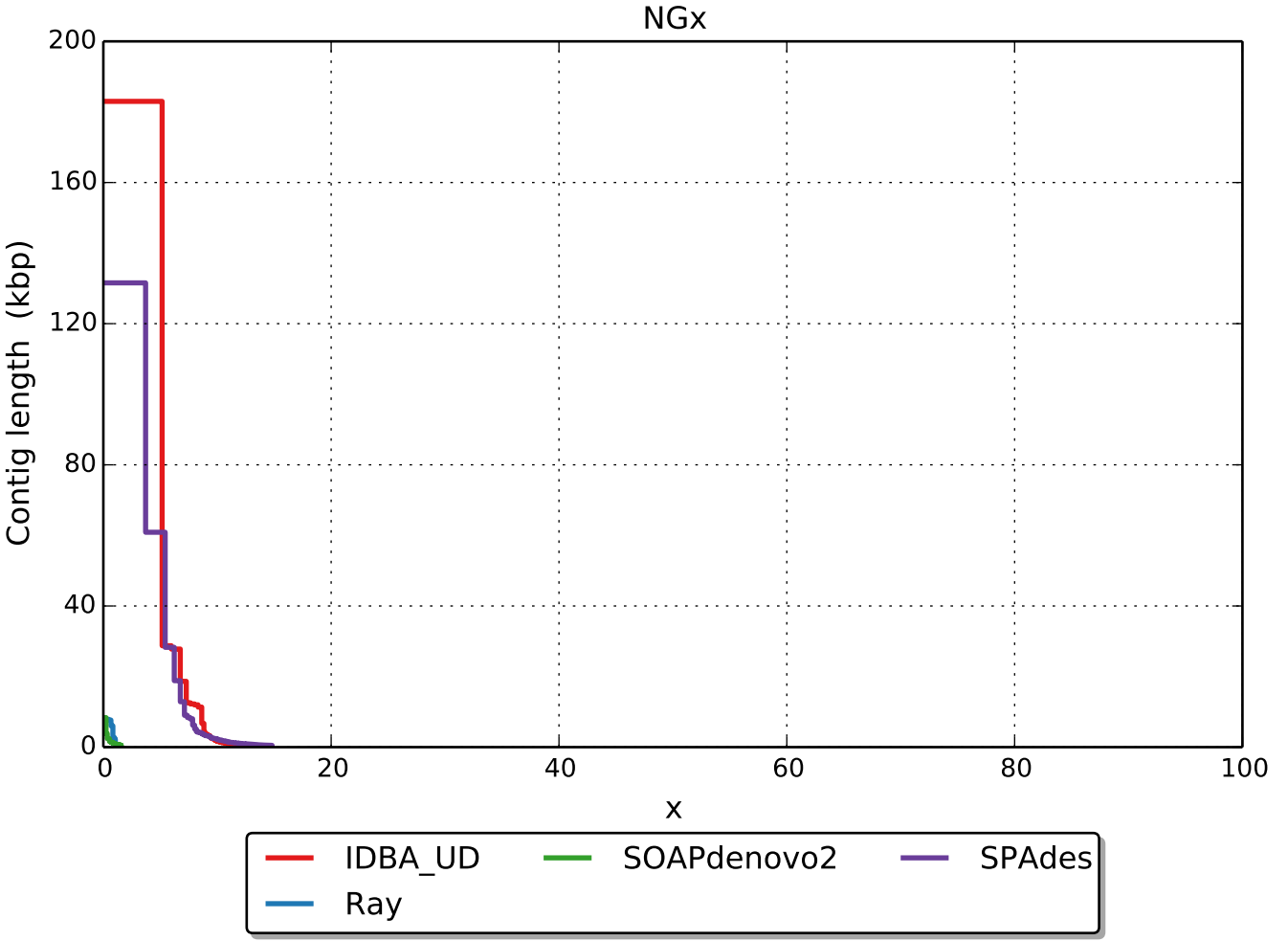
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

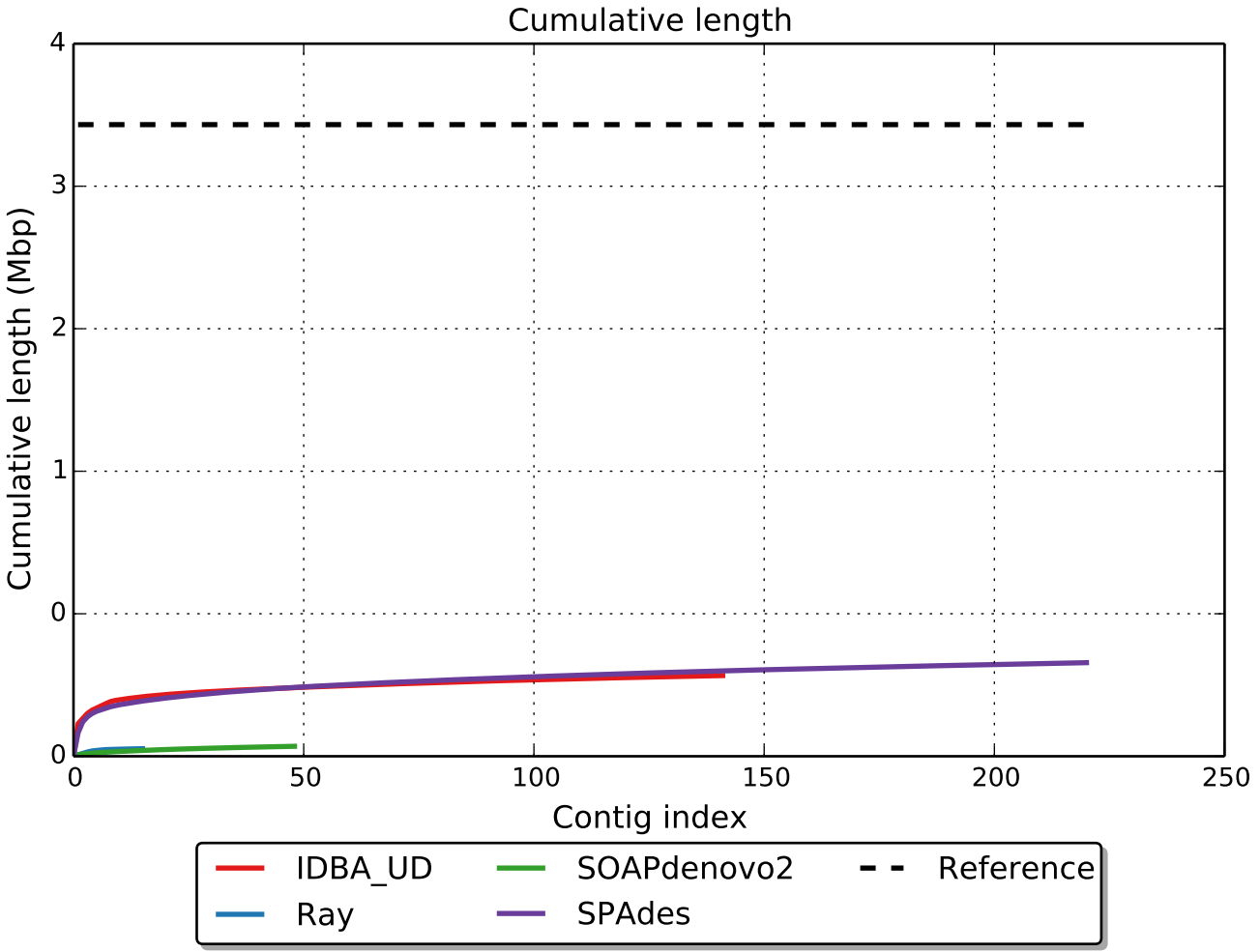
Unaligned report

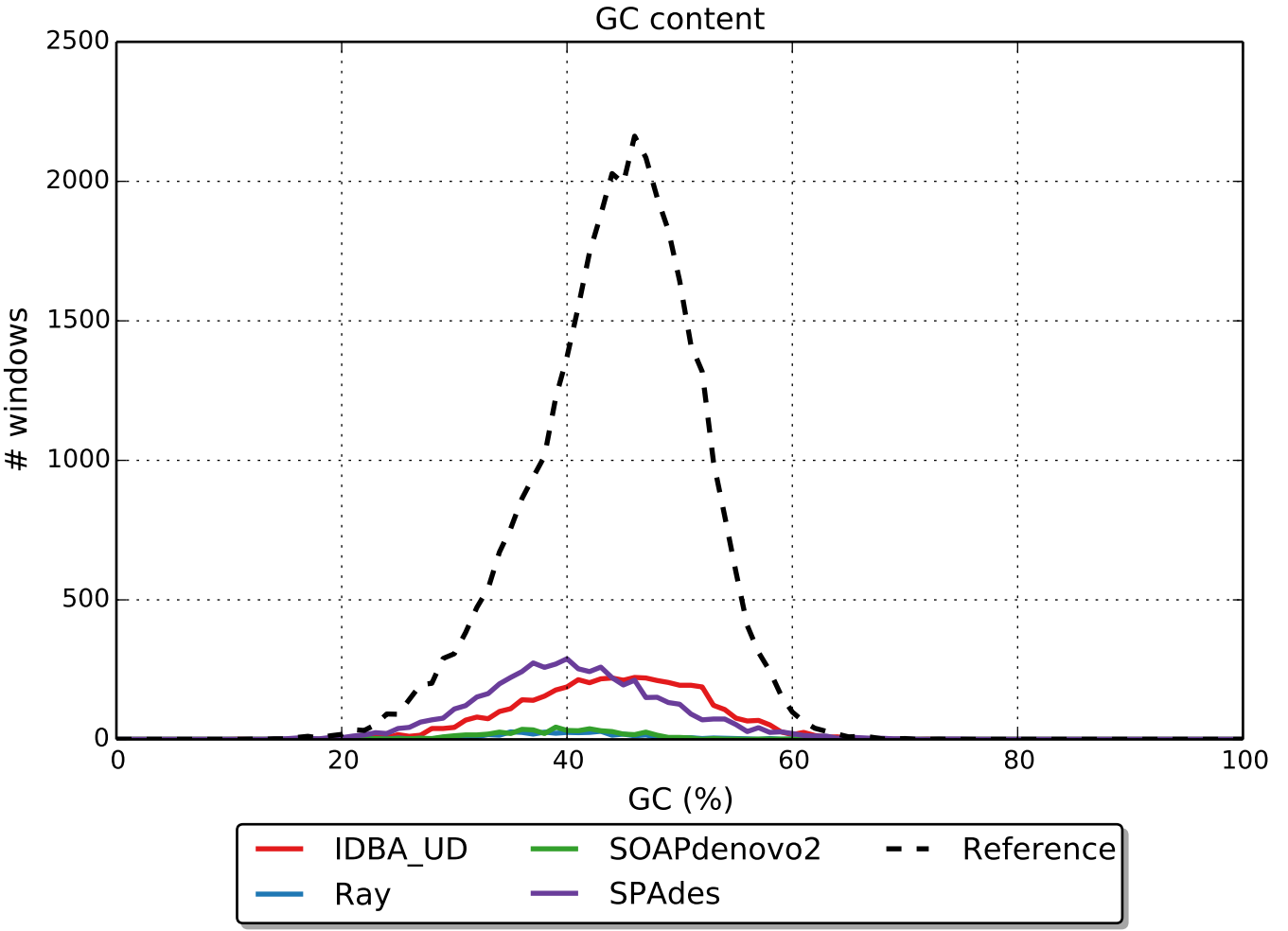
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	63	4	18	134
# with misassembly	1	1	4	4
# both parts are significant	7	3	3	14
Partially unaligned length	333445	19826	19709	380541
# N's	403	454	2599	4912

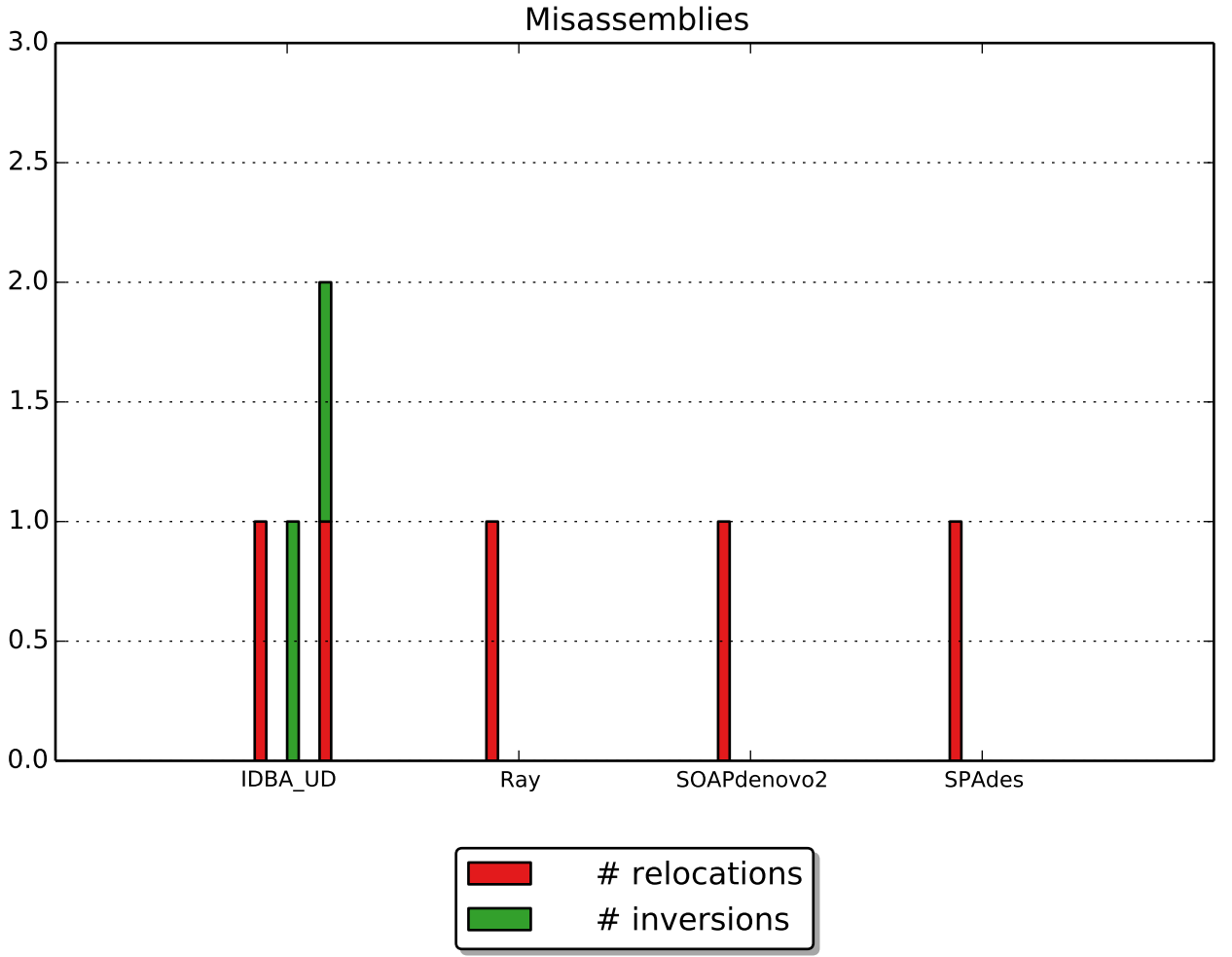
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

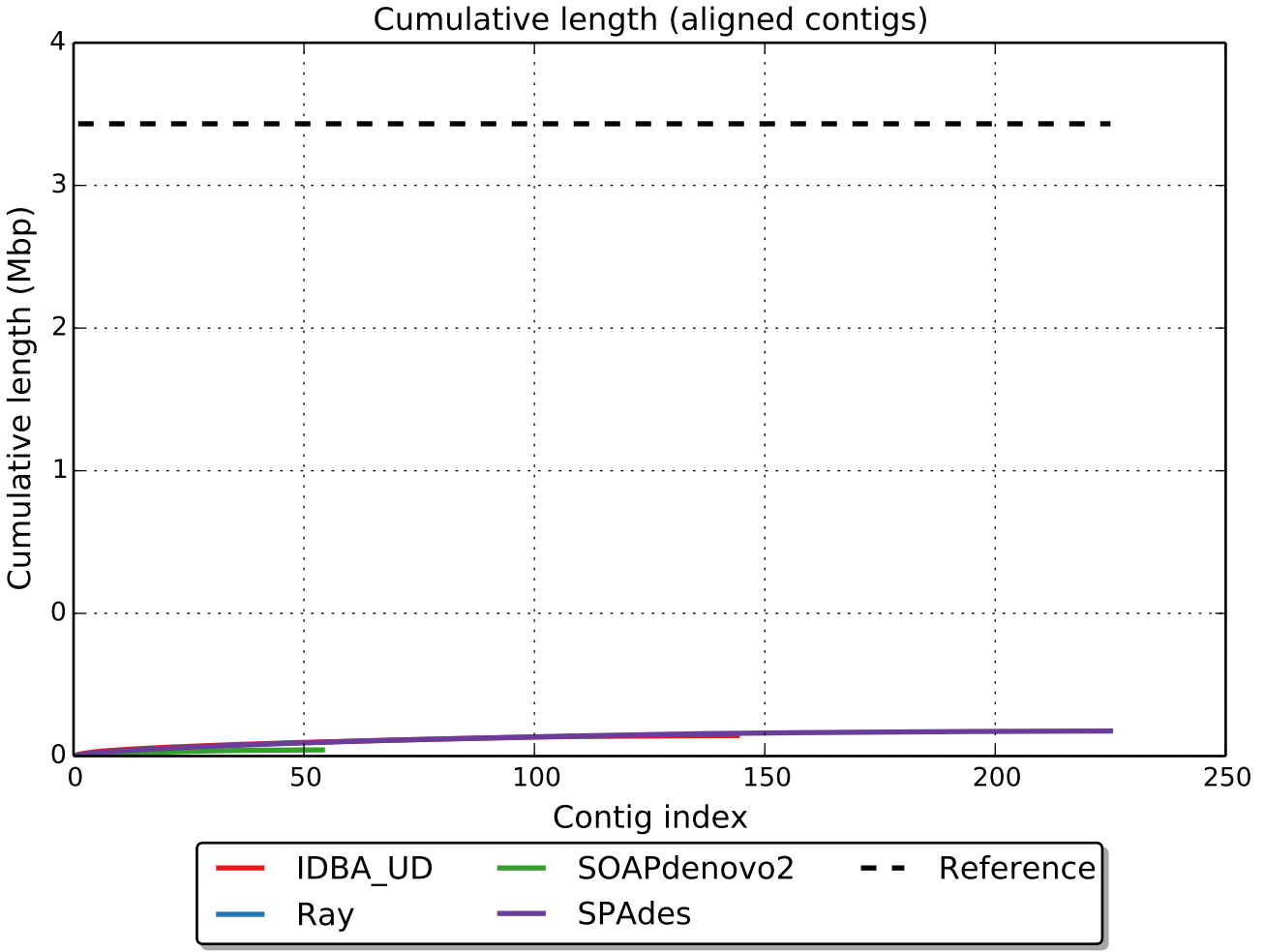

Nx
200
160
120
80
40
0
Contig length (kbp)
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray

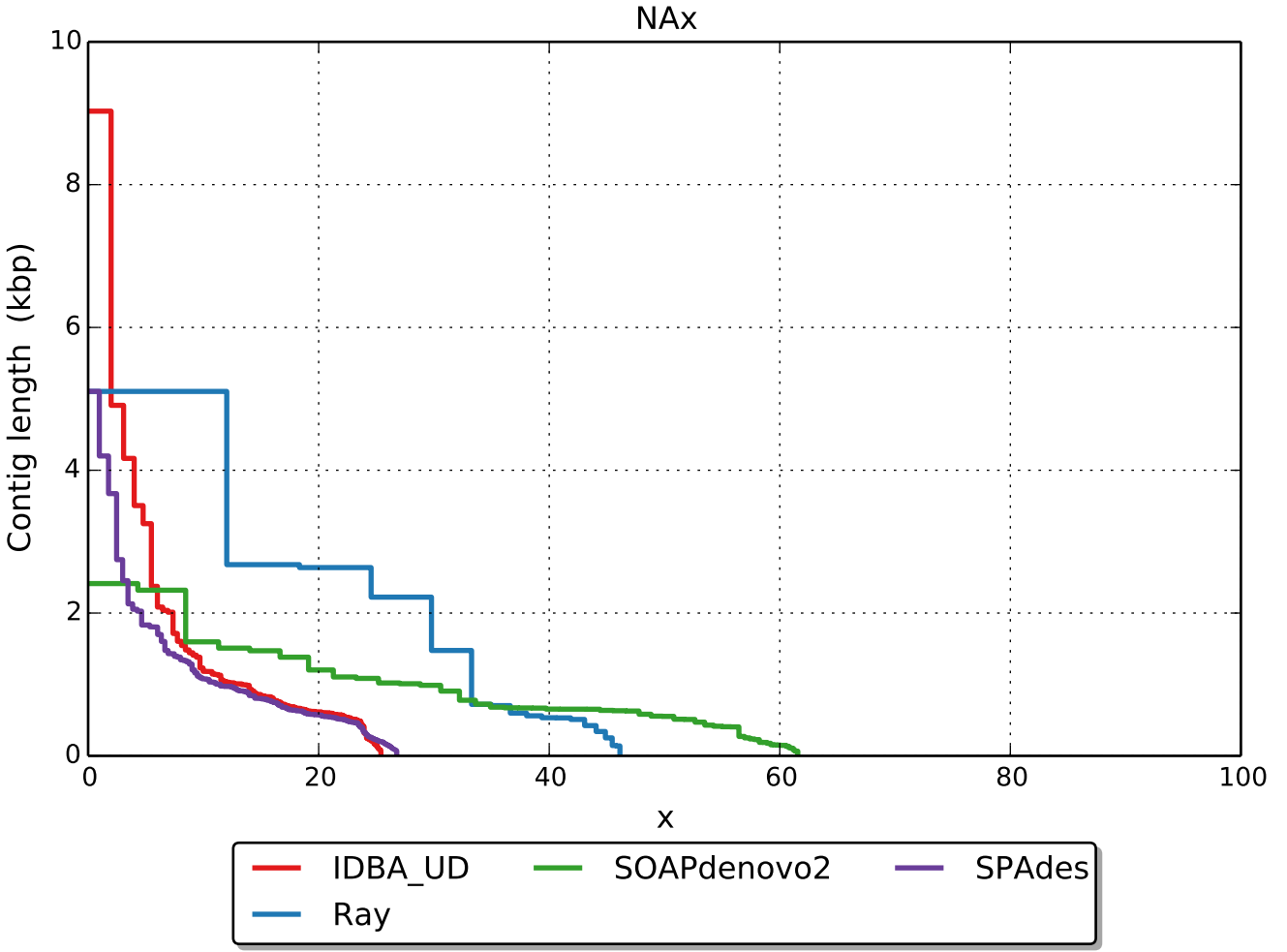

NGx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray

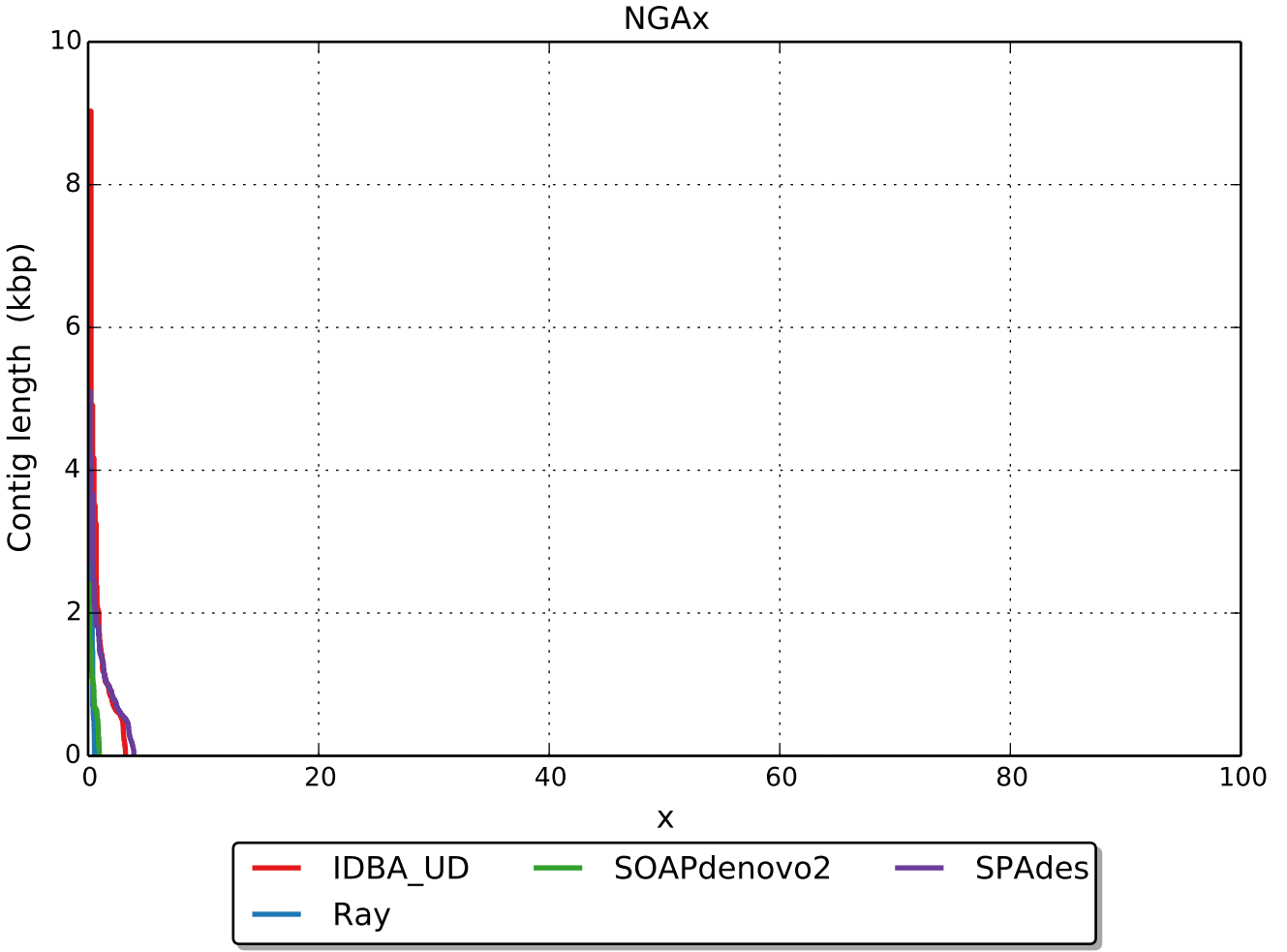

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
2
3
4
0
50
100
150
200
250
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference

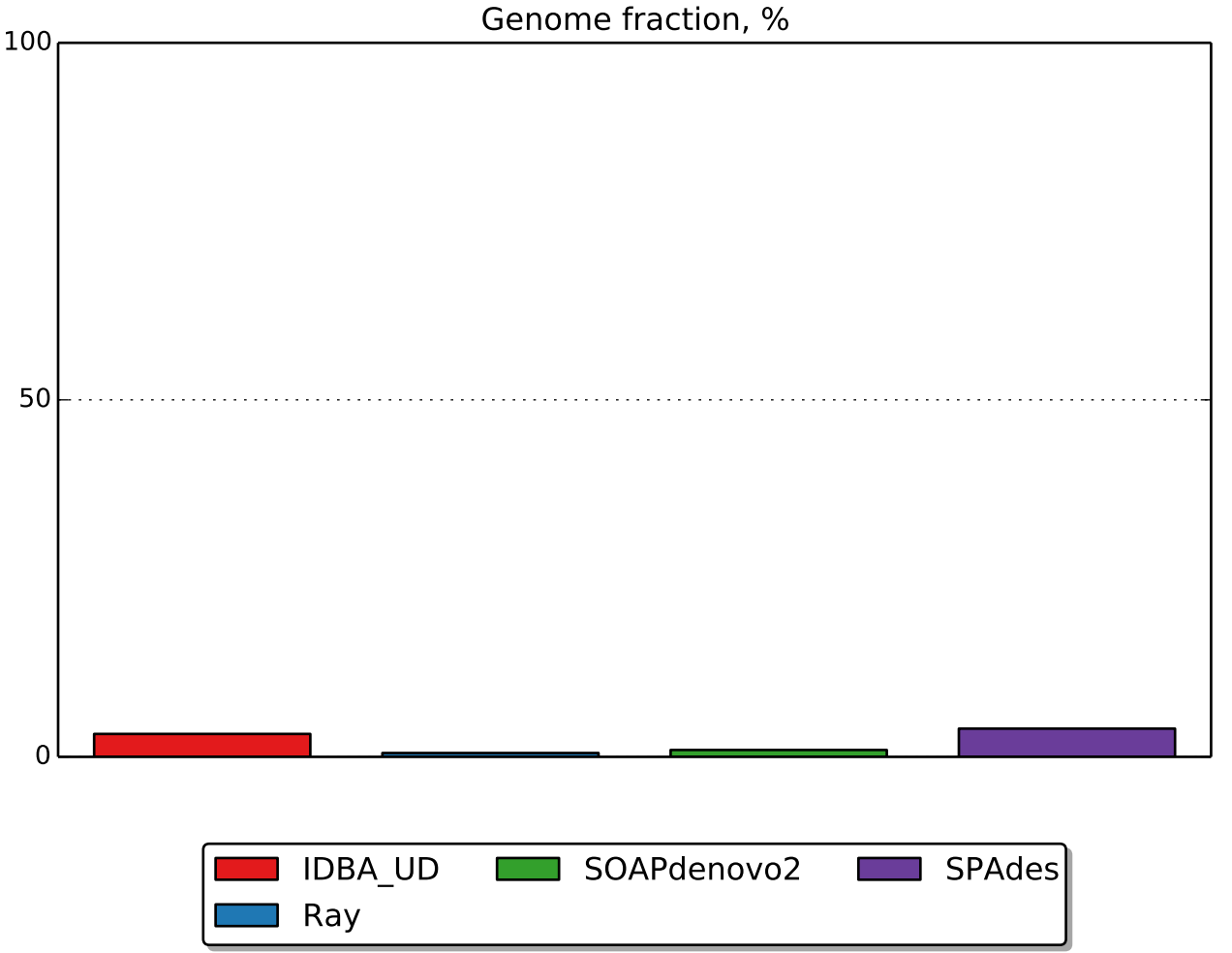

GC content
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


Misassemblies
3.0
2.5
2.0
1.5
1.0
0.5
0.0
IDBA_UD
Ray
SOAPdenovo2
SPAdes
relocations
inversions


Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
0
50
100
150
200
250
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


NAx
Contig length (kbp)
x
0
2
4
6
8
10
0
20
40
60
80
100
IDBA_UD
SOAPdenovo2
SPAdes
Ray


NGAx
Contig length (kbp)
10
8
6
4
2
0
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray


Genome fraction, %
100
50
0
IDBA_UD
Ray
SOAPdenovo2
SPAdes