Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	44	19	19	36
# contigs (>= 5000 bp)	18	3	1	25
# contigs (>= 10000 bp)	12	1	0	16
# contigs (>= 25000 bp)	8	0	0	4
# contigs (>= 50000 bp)	7	0	0	0
Total length (>= 1000 bp)	933488	59363	37842	405429
Total length (>= 5000 bp)	880489	26511	8799	382629
Total length (>= 10000 bp)	837112	12214	0	313909
Total length (>= 25000 bp)	767455	0	0	144319
Total length (>= 50000 bp)	740124	0	0	0
# contigs	59	34	37	40
Largest contig	215617	12214	8799	49825
Total length	943382	70434	50141	408526
Reference length	2249085	2249085	2249085	2249085
GC (%)	42.94	42.99	43.28	41.95
Reference GC (%)	41.39	41.39	41.39	41.39
N50	125915	2723	1475	14741
N75	51158	1818	1019	10139
L50	3	6	8	8
L75	7	14	19	16
# misassemblies	1	1	2	0
# misassembled contigs	1	1	2	0
Misassembled contigs length	1571	12214	3919	0
# local misassemblies	0	6	12	0
# structural variations	0	0	0	0
# unaligned contigs	0 + 32 part	0 + 12 part	0 + 14 part	0 + 31 part
Unaligned length	861788	25058	12314	335675
Genome fraction (%)	3.457	1.694	1.524	3.235
Duplication ratio	1.049	1.191	1.104	1.001
# N's per 100 kbp	54.70	4098.87	3589.88	126.80
# mismatches per 100 kbp	2272.67	1858.27	2039.86	2388.97
# indels per 100 kbp	77.17	41.99	72.96	107.22
Largest alignment	8987	3620	7706	14642
NA50	-	625	812	-
NGA50	-	-	-	-
LA50	-	25	17	-

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

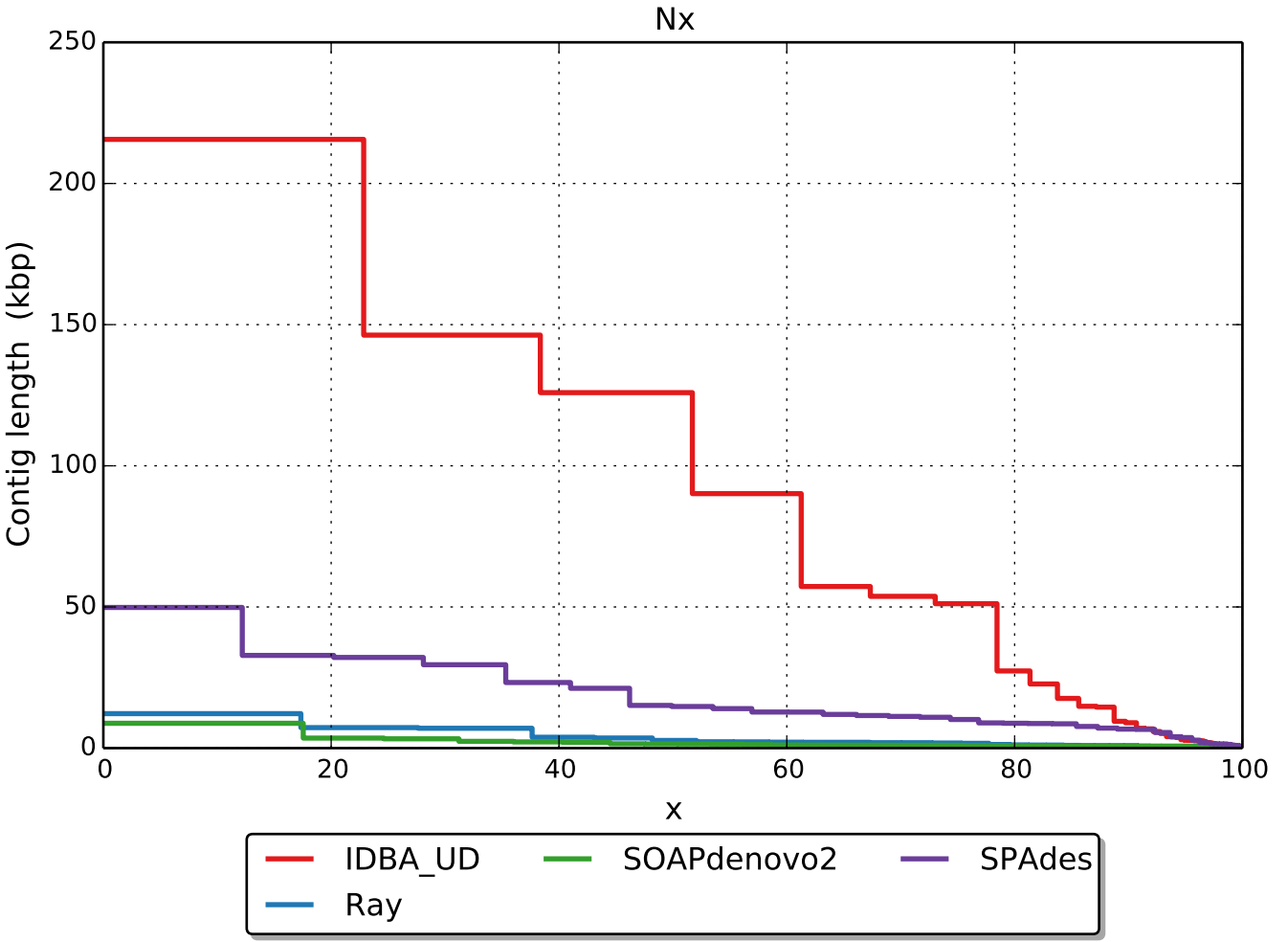
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	1	1	2	0
# relocations	1	1	2	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	8	6	4	13
# misassembled contigs	1	1	2	0
Misassembled contigs length	1571	12214	3919	0
# local misassemblies	0	6	12	0
# structural variations	0	0	0	0
# mismatches	1767	708	699	1738
# indels	60	16	25	78
# short indels	60	16	25	75
# long indels	0	0	0	3
Indels length	93	22	31	145

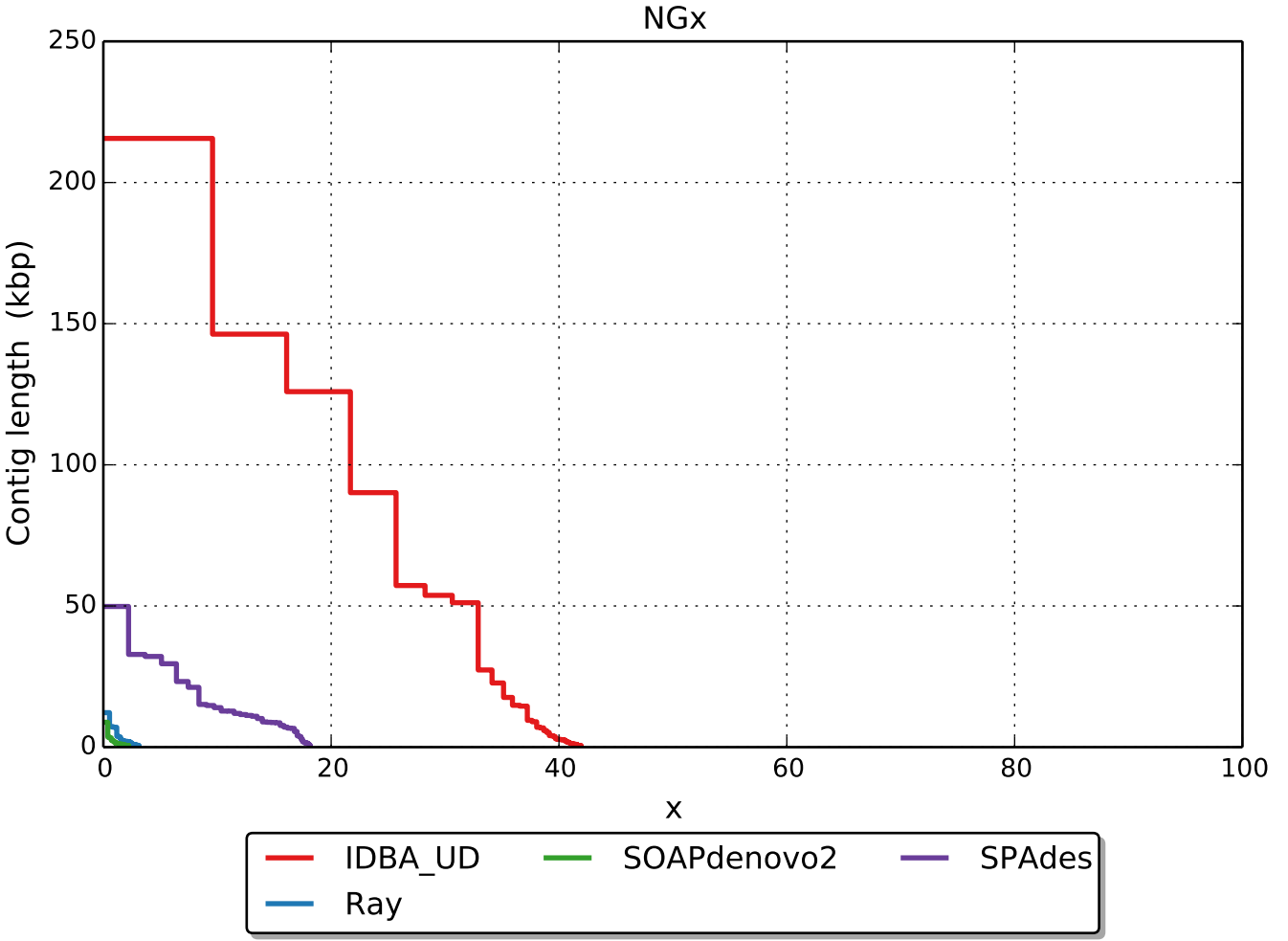
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

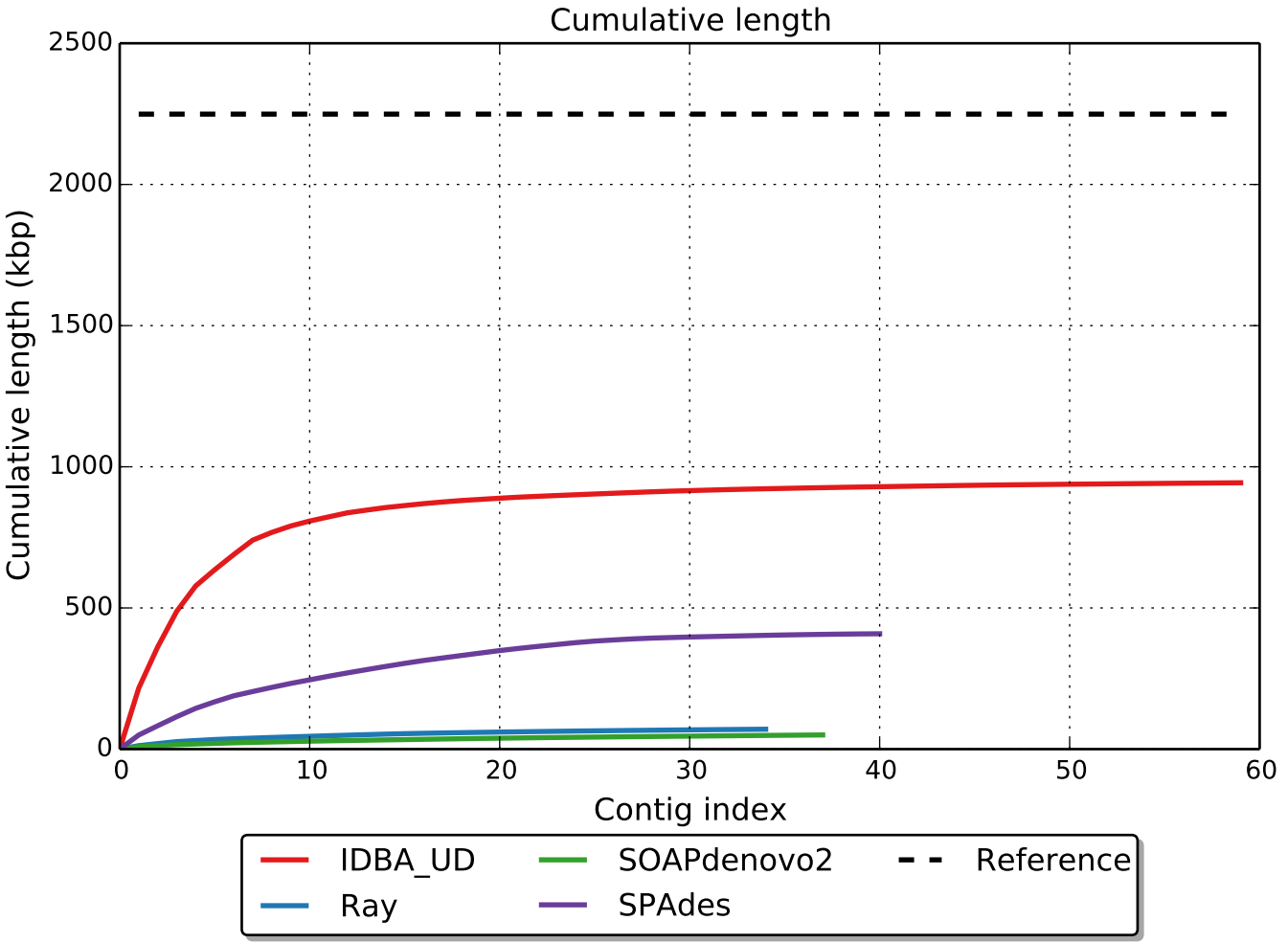
Unaligned report

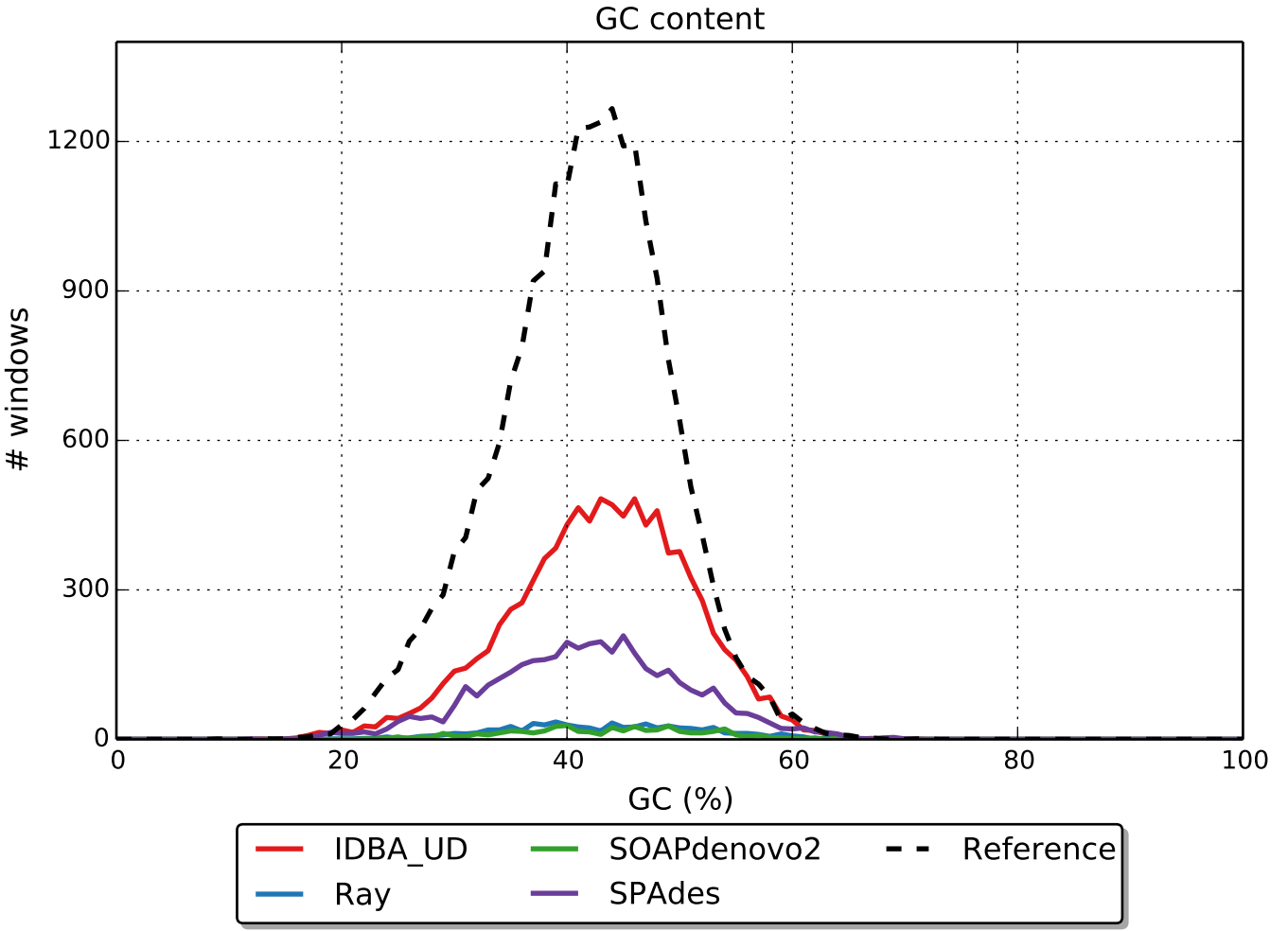
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	32	12	14	31
# with misassembly	4	0	3	1
# both parts are significant	8	5	2	13
Partially unaligned length	861788	25058	12314	335675
# N's	516	2887	1800	518

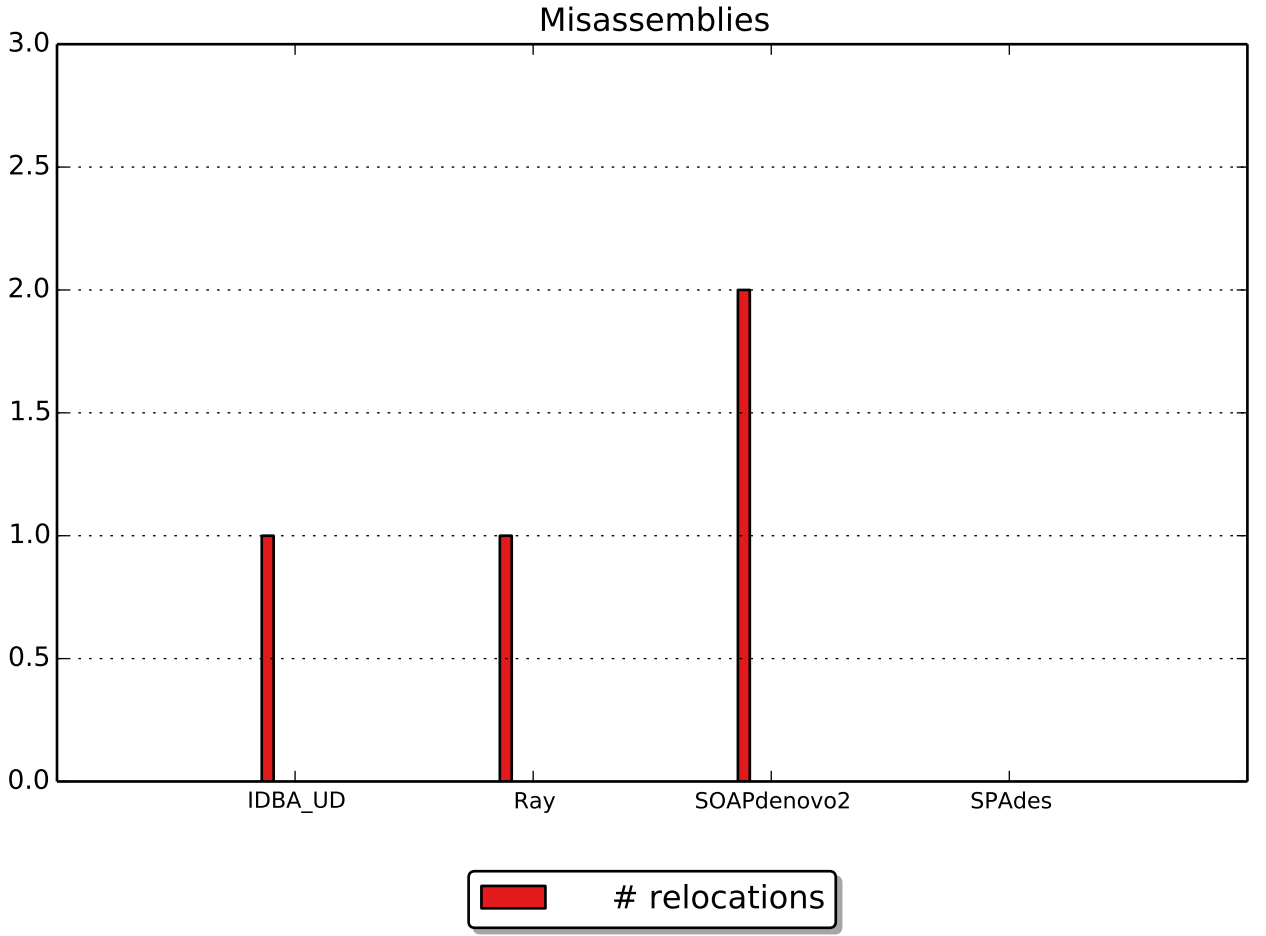
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

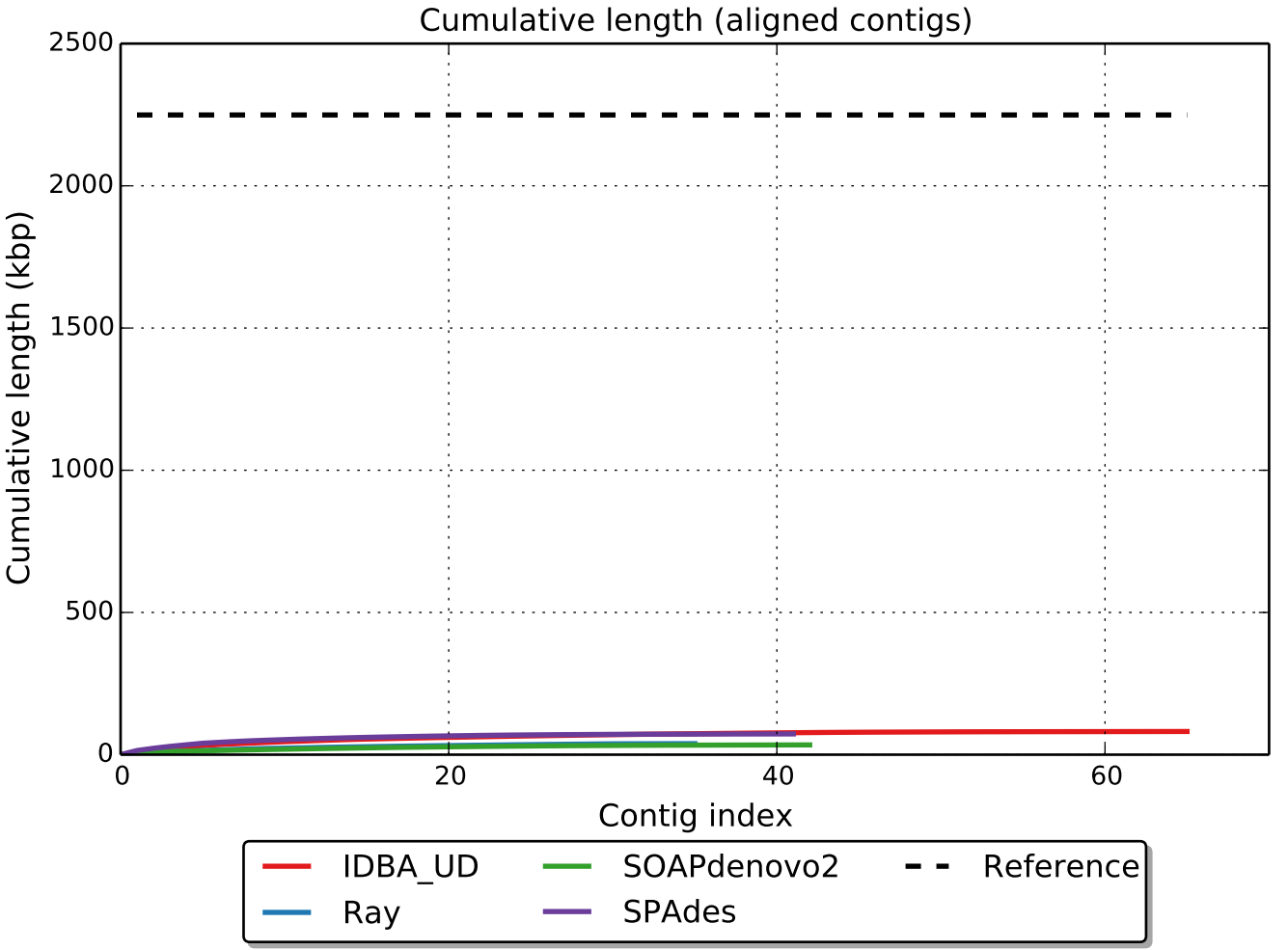

Nx
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray

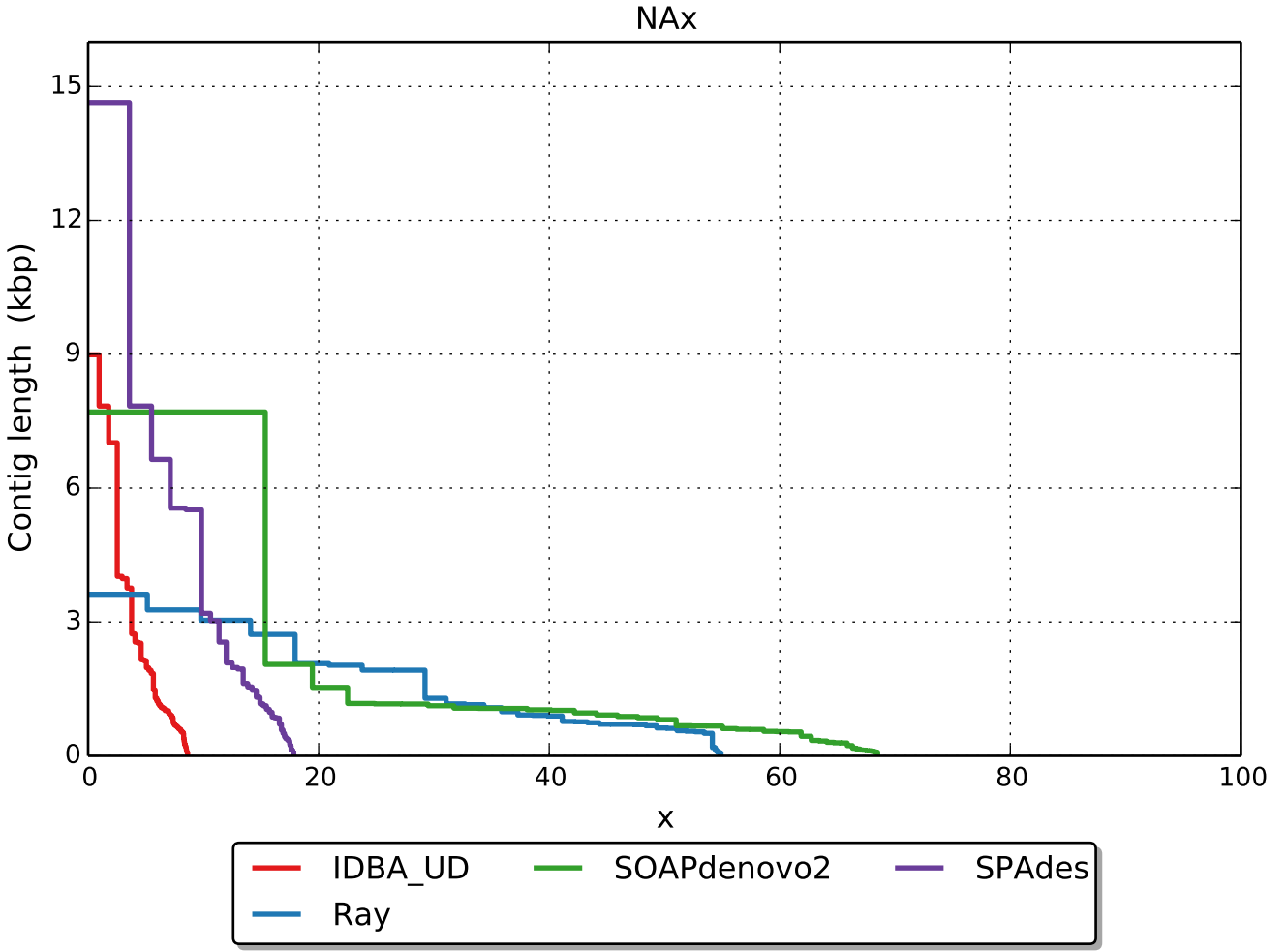

NGx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray

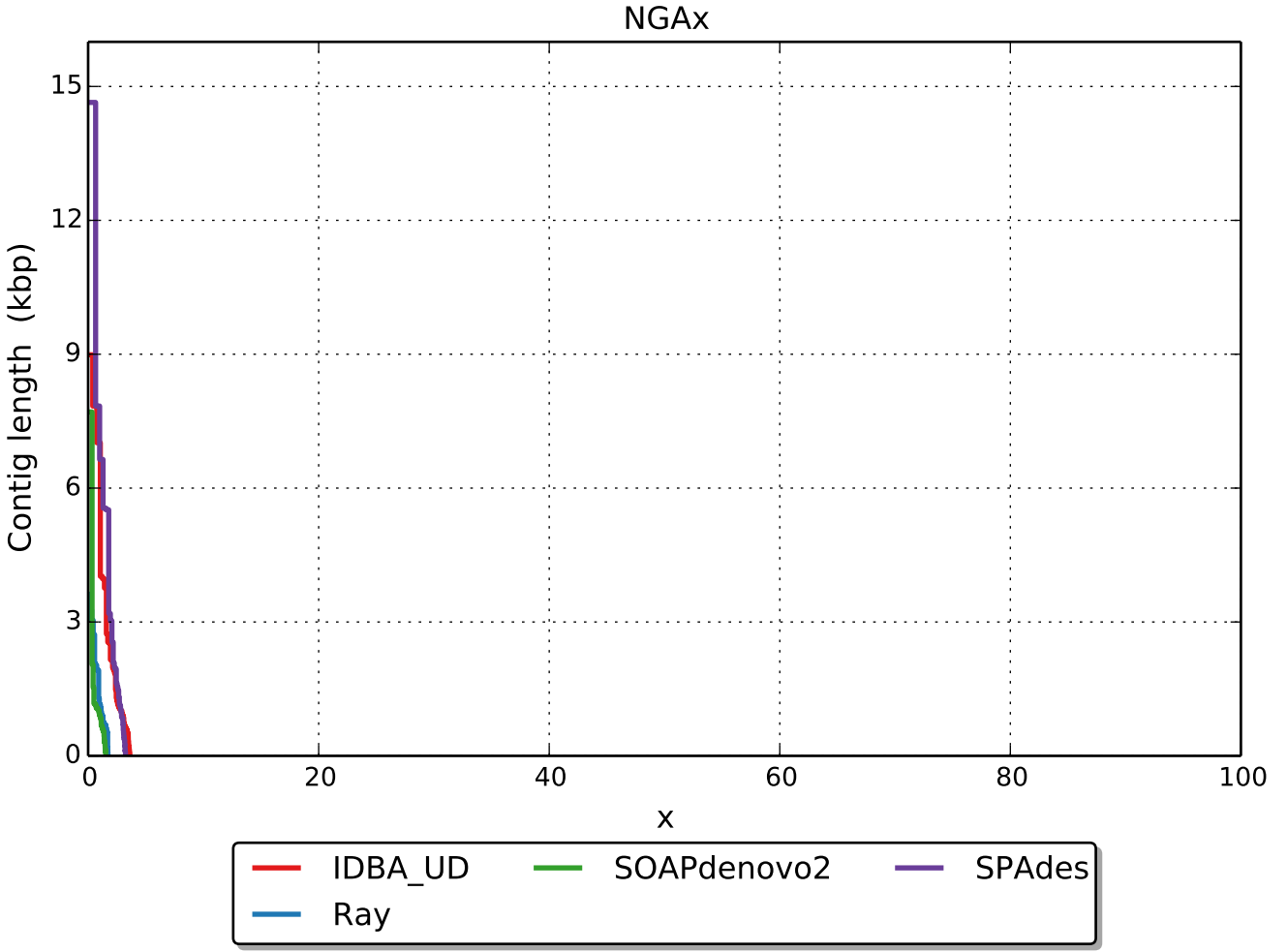

Cumulative length
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
10
20
30
40
50
60
Contig index
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference

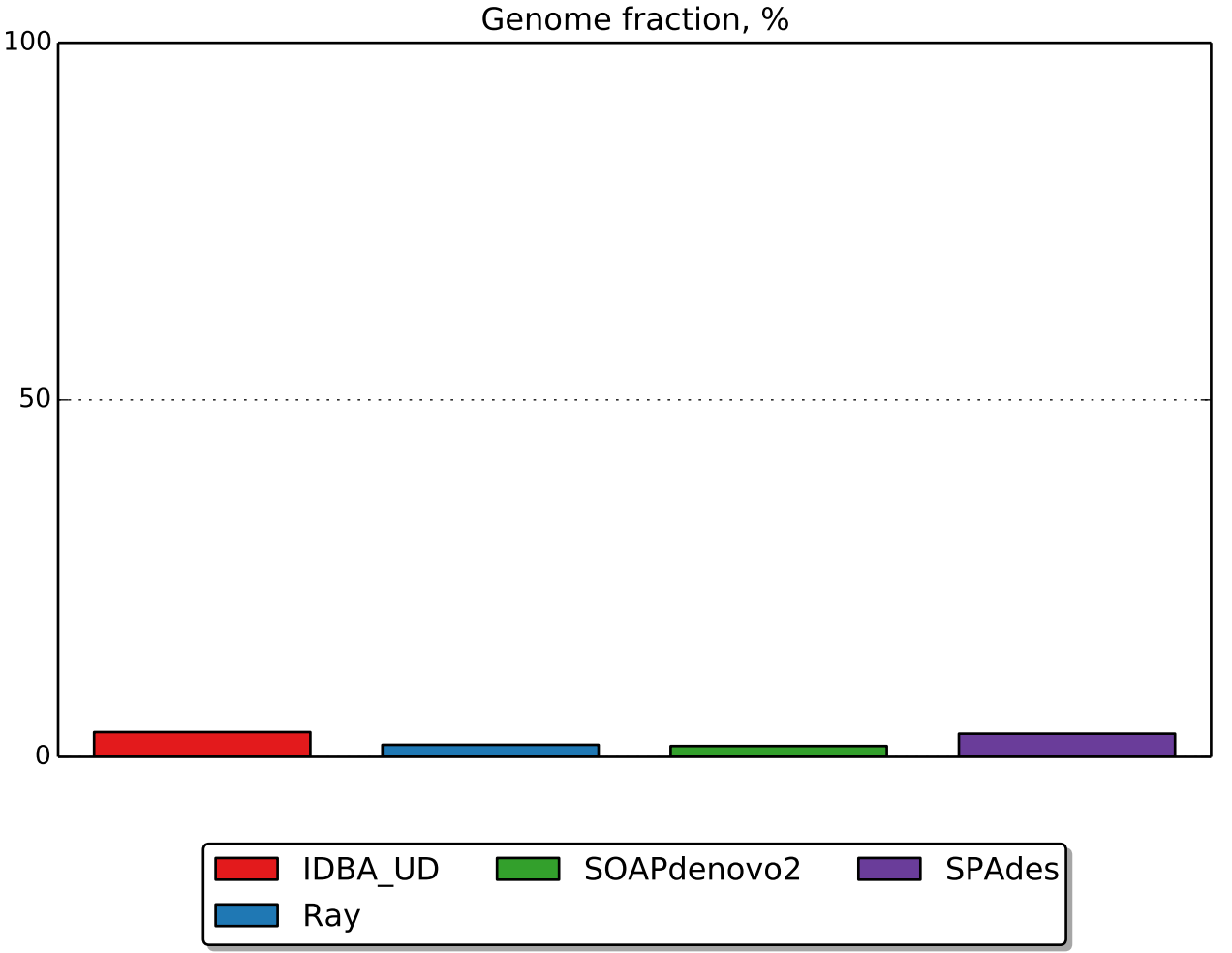

GC content
windows
GC (%)
0
300
600
900
1200
0
20
40
60
80
100
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


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


Cumulative length (aligned contigs)
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
Contig index
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


NAx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray


NGAx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray


Genome fraction, %
100
50
0
IDBA_UD
Ray
SOAPdenovo2
SPAdes