Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	380	89	292	162
# contigs (>= 5000 bp)	121	31	4	78
# contigs (>= 10000 bp)	53	26	0	62
# contigs (>= 25000 bp)	2	19	0	21
# contigs (>= 50000 bp)	0	15	0	8
Total length (>= 1000 bp)	1872889	2454628	481458	1946091
Total length (>= 5000 bp)	1302167	2327678	28048	1770068
Total length (>= 10000 bp)	807589	2291677	0	1656119
Total length (>= 25000 bp)	52609	2162387	0	987199
Total length (>= 50000 bp)	0	2023993	0	552099
# contigs	796	217	986	374
Largest contig	27493	431523	9794	108978
Total length	2154562	2543606	953949	2096621
Reference length	2264603	2264603	2264603	2264603
GC (%)	59.31	59.37	59.64	59.39
Reference GC (%)	59.62	59.62	59.62	59.62
N50	7025	112466	1003	23860
NG50	6682	141171	-	21476
N75	2422	64462	688	11848
NG75	1868	80268	-	7365
L50	85	7	288	24
LG50	93	5	-	28
L75	210	14	578	55
LG75	249	11	-	67
# misassemblies	6	32	0	15
# misassembled contigs	5	14	0	14
Misassembled contigs length	48637	1592707	0	465360
# local misassemblies	88	69	14	67
# structural variations	0	3	0	1
# unaligned contigs	0 + 359 part	0 + 78 part	0 + 234 part	0 + 142 part
Unaligned length	1014666	527548	146346	527969
Genome fraction (%)	42.018	56.473	35.179	59.702
Duplication ratio	1.198	1.576	1.014	1.160
# N's per 100 kbp	0.00	270.21	1799.47	411.90
# mismatches per 100 kbp	2417.01	3077.69	2071.24	2984.57
# indels per 100 kbp	130.52	196.11	58.37	170.41
Largest alignment	17013	140615	9794	59694
NA50	-	834	787	5203
NGA50	-	5629	-	2824
NA75	-	-	536	-
LA50	-	122	361	67
LGA50	-	48	-	90
LA75	-	-	735	-

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

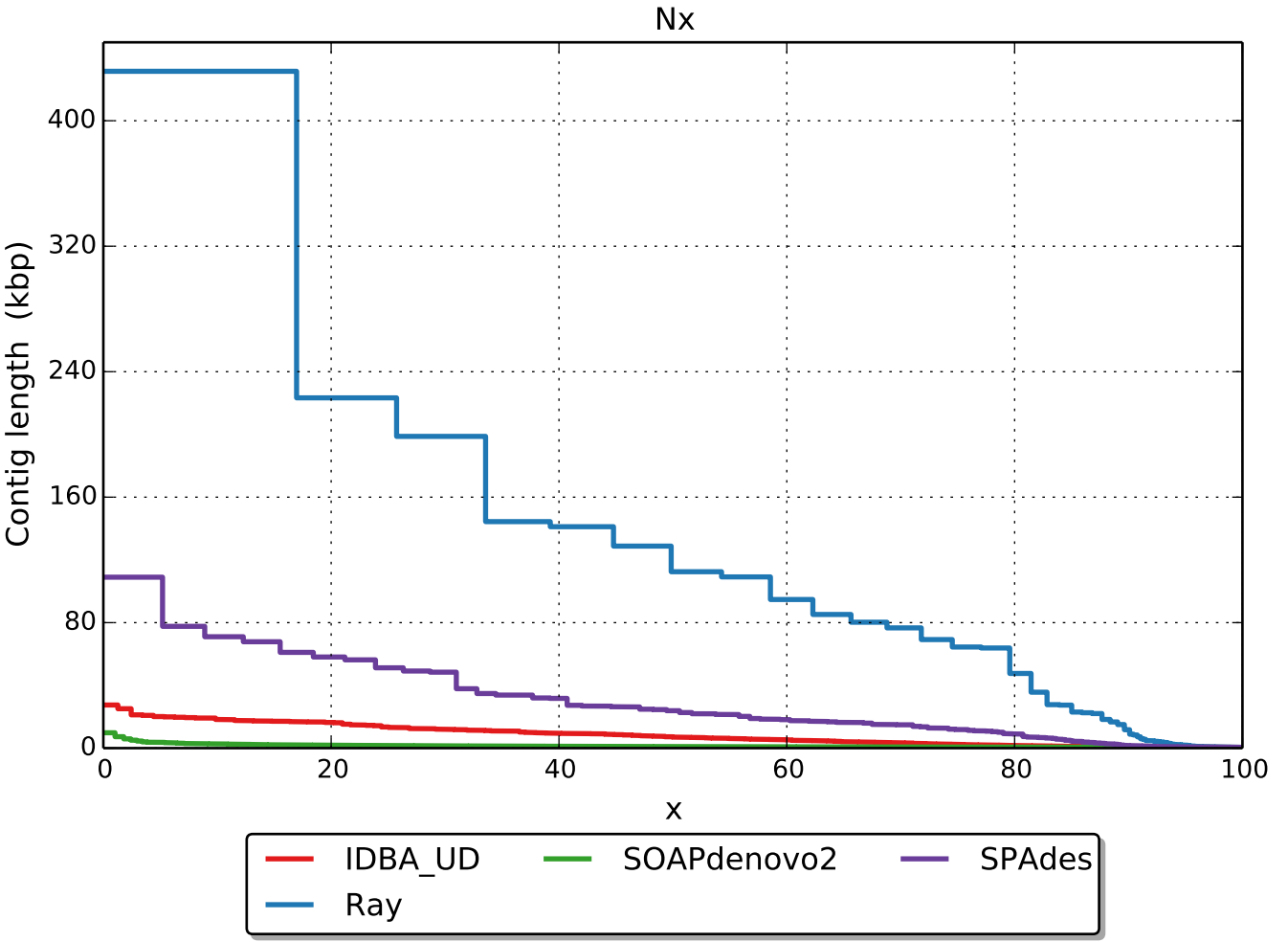
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	6	32	0	15
# relocations	6	31	0	15
# translocations	0	0	0	0
# inversions	0	1	0	0
# possibly misassembled contigs	161	35	19	65
# misassembled contigs	5	14	0	14
Misassembled contigs length	48637	1592707	0	465360
# local misassemblies	88	69	14	67
# structural variations	0	3	0	1
# mismatches	22999	39360	16501	40352
# indels	1242	2508	465	2304
# short indels	951	2133	411	1954
# long indels	291	375	54	350
Indels length	8348	7842	1579	7541

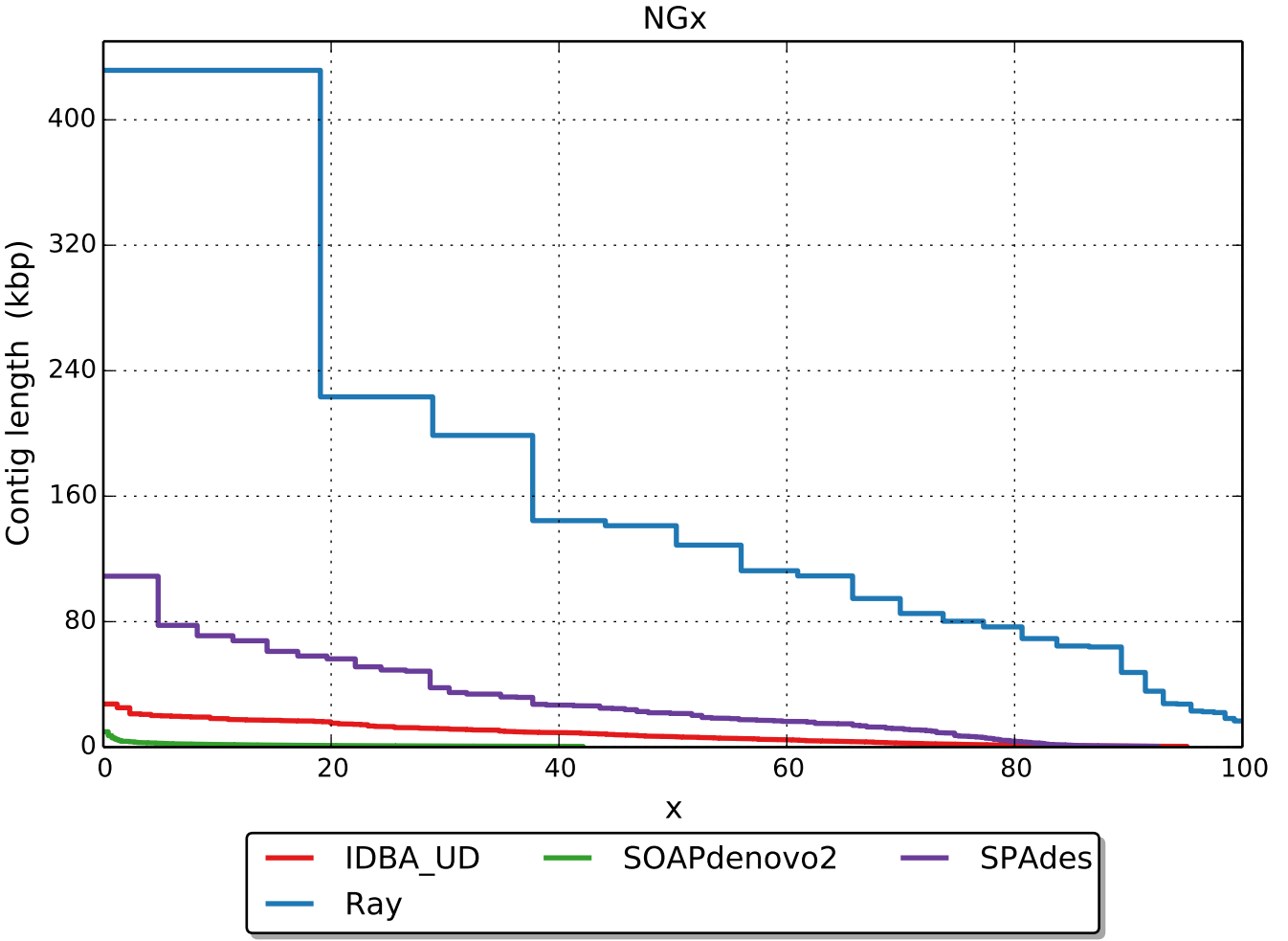
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

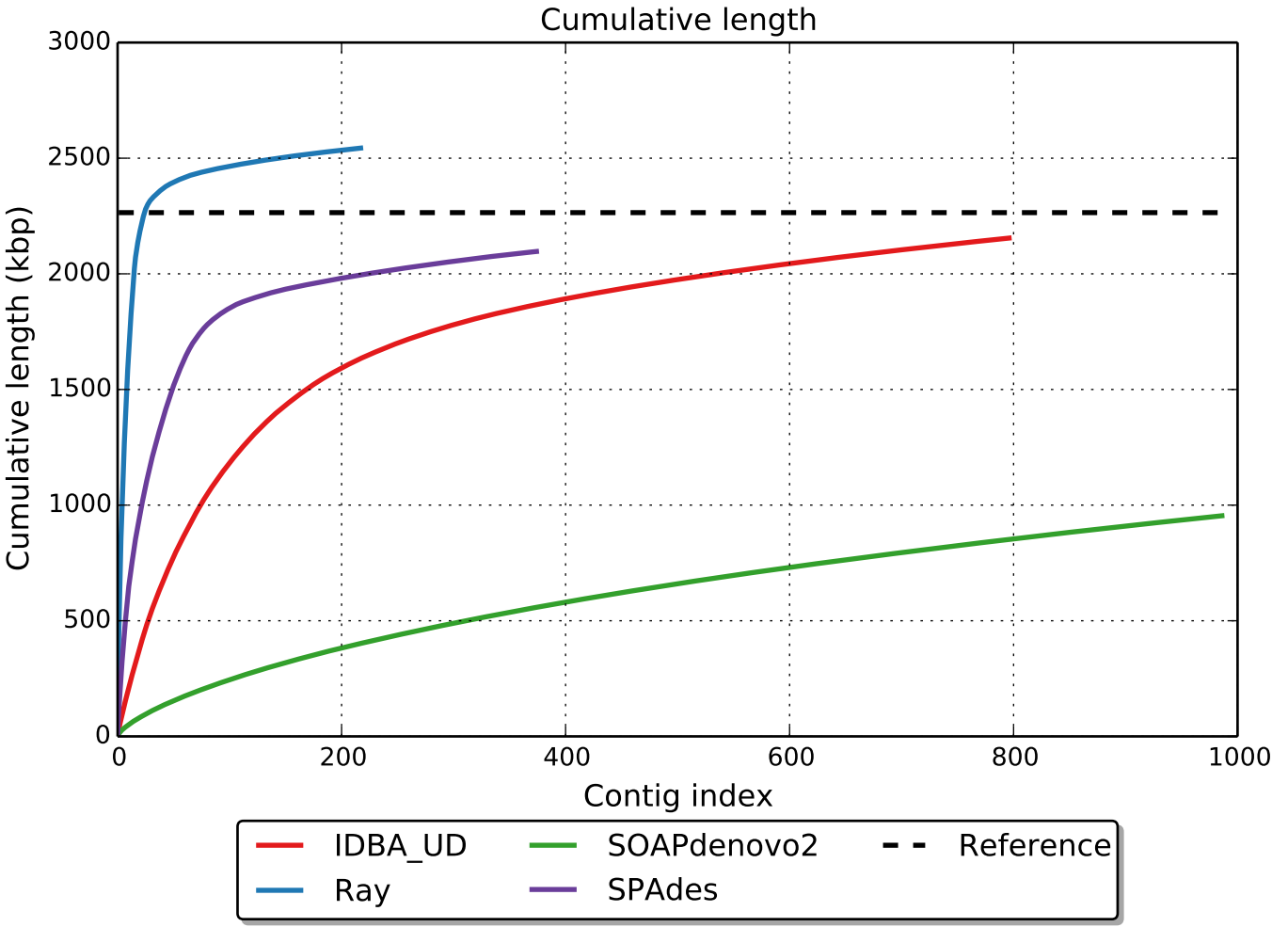
Unaligned report

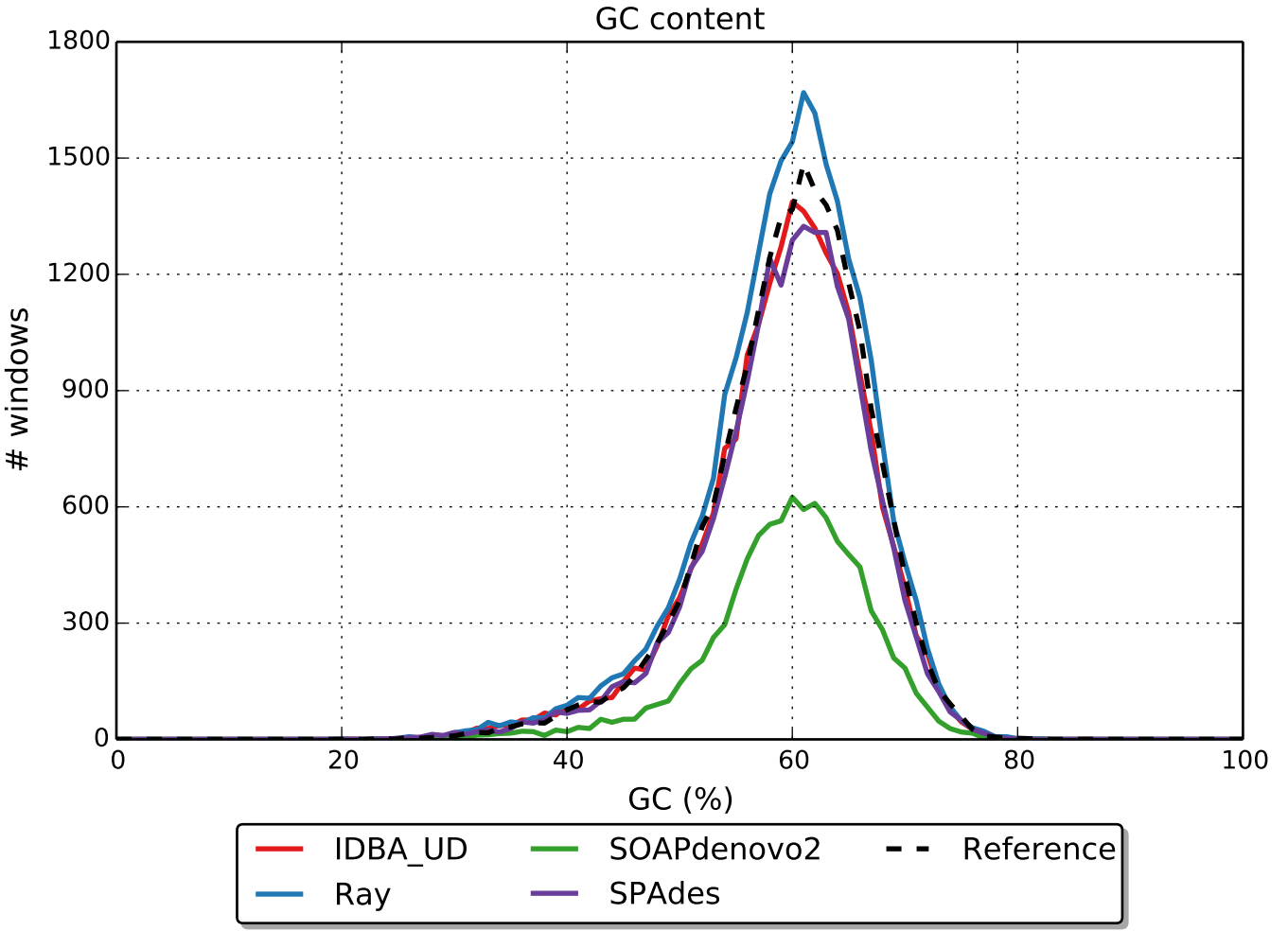
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	359	78	234	142
# with misassembly	67	16	17	22
# both parts are significant	130	19	18	42
Partially unaligned length	1014666	527548	146346	527969
# N's	0	6873	17166	8636

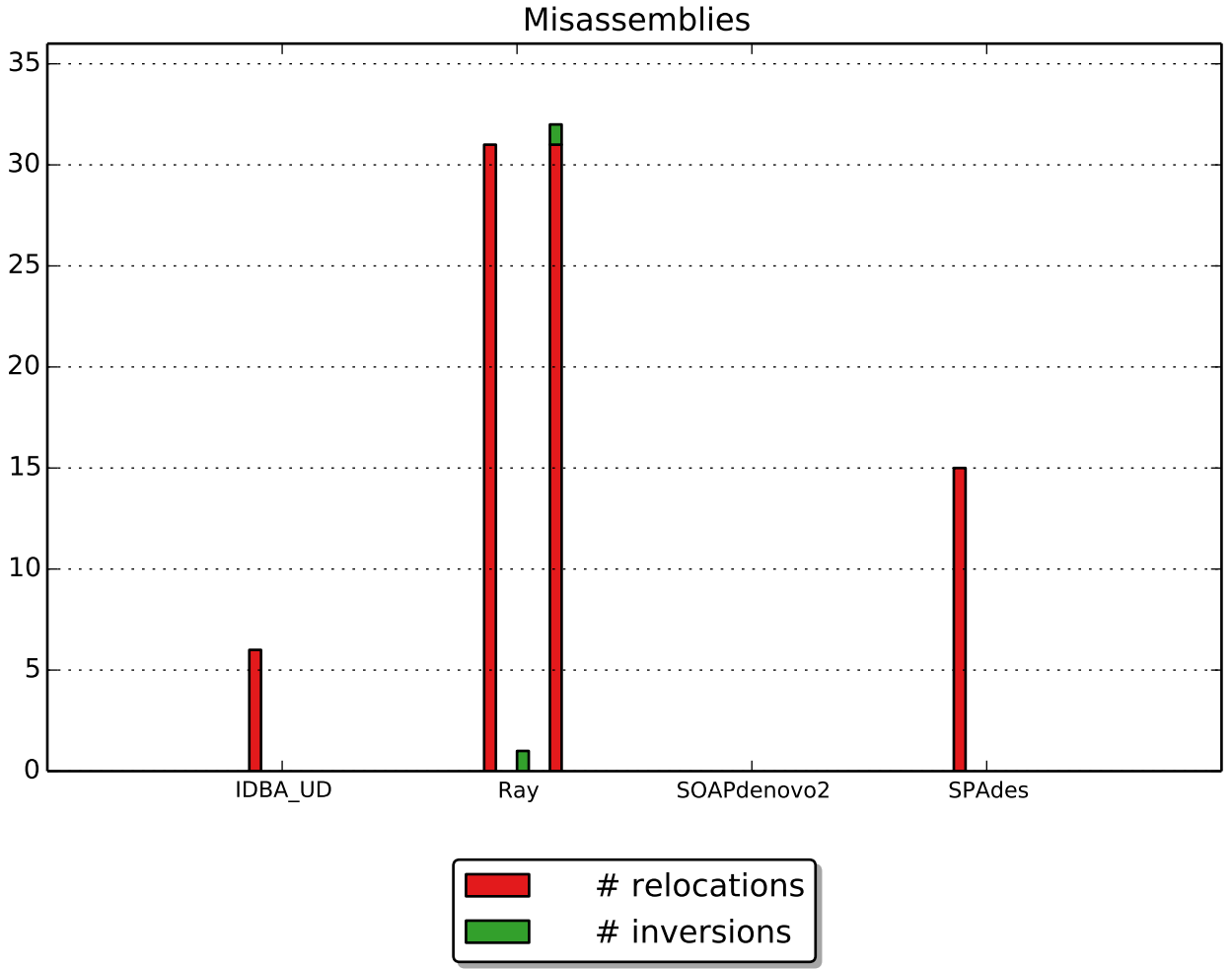
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

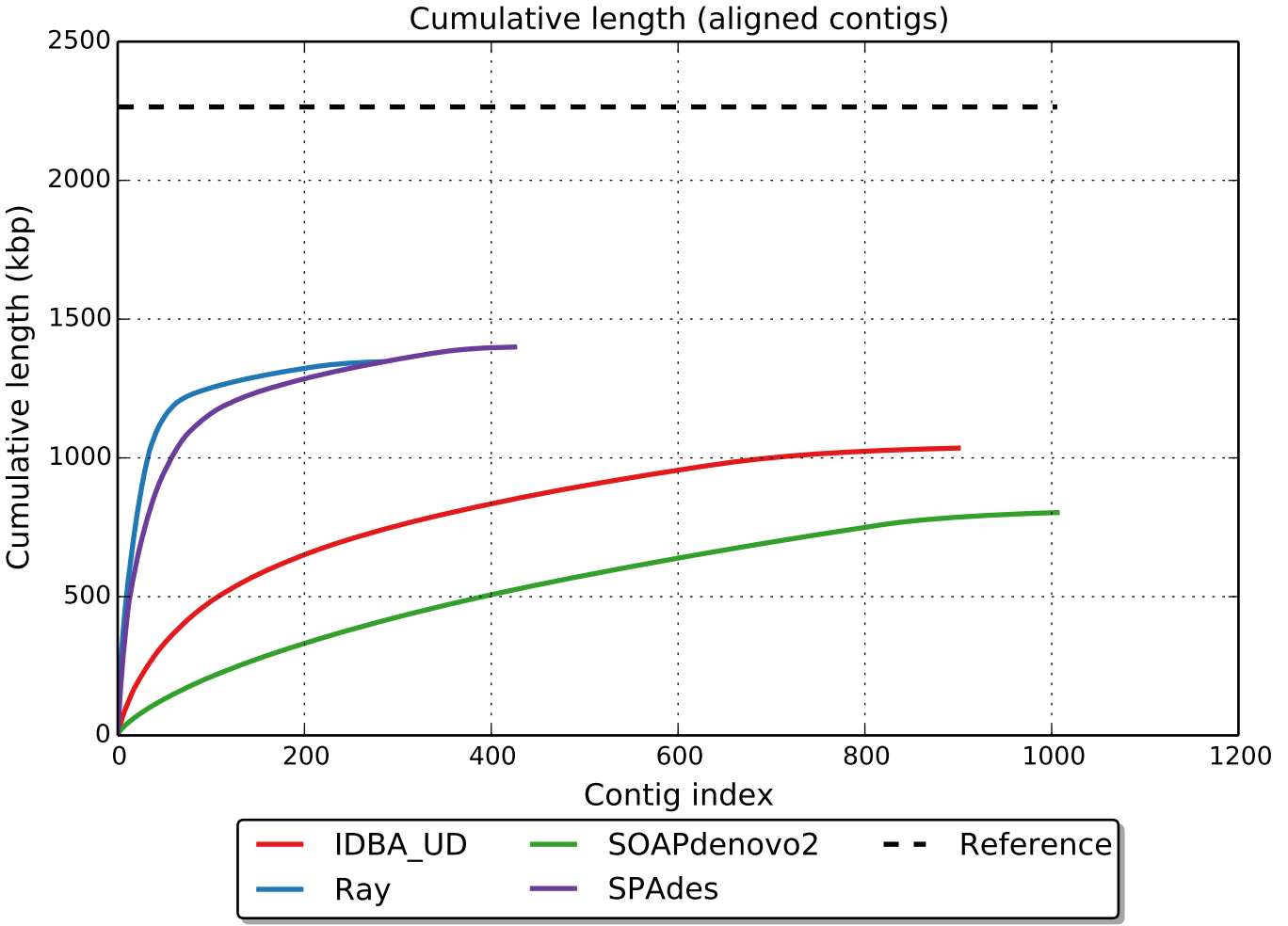

Nx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray

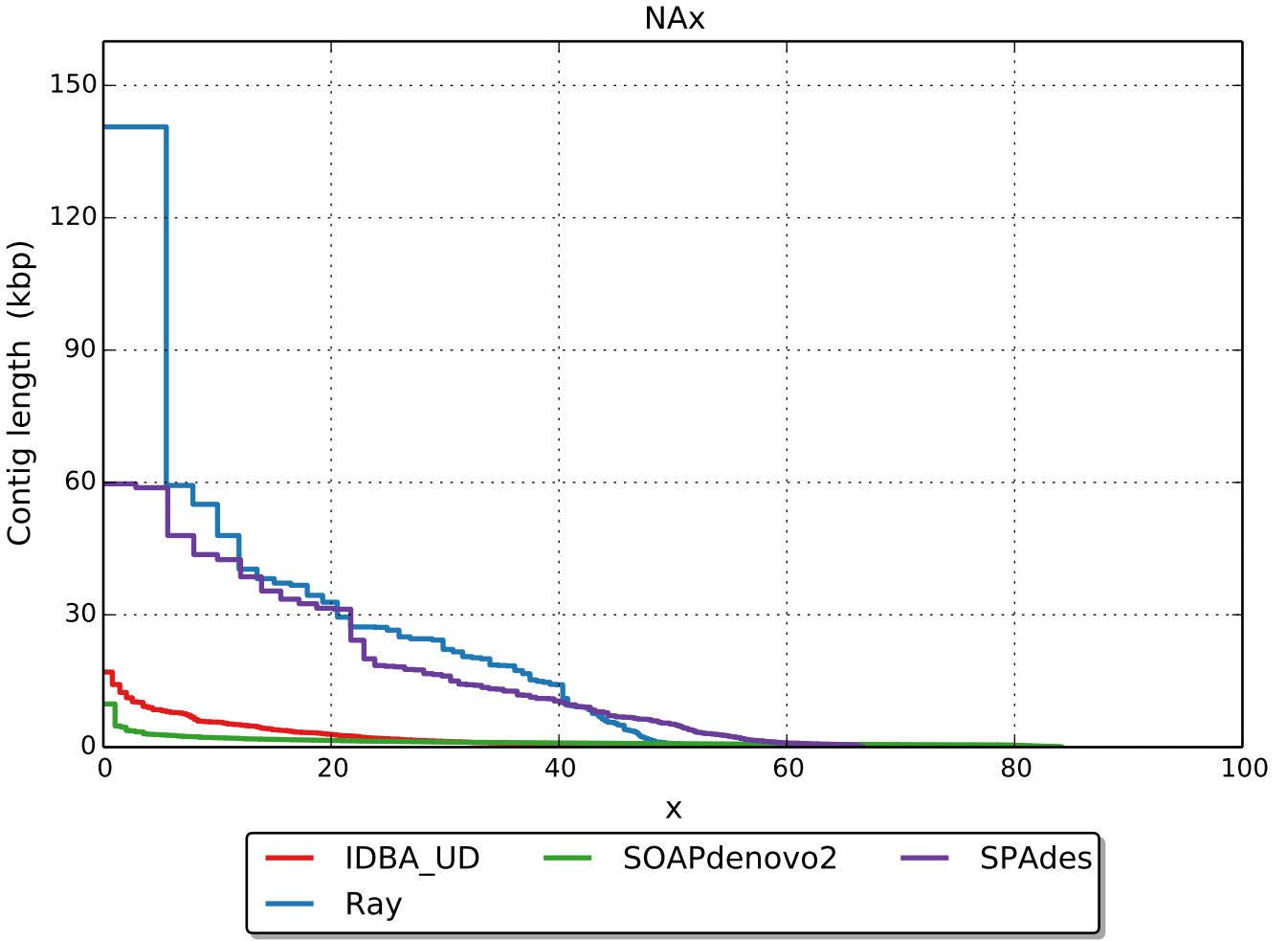

NGx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray

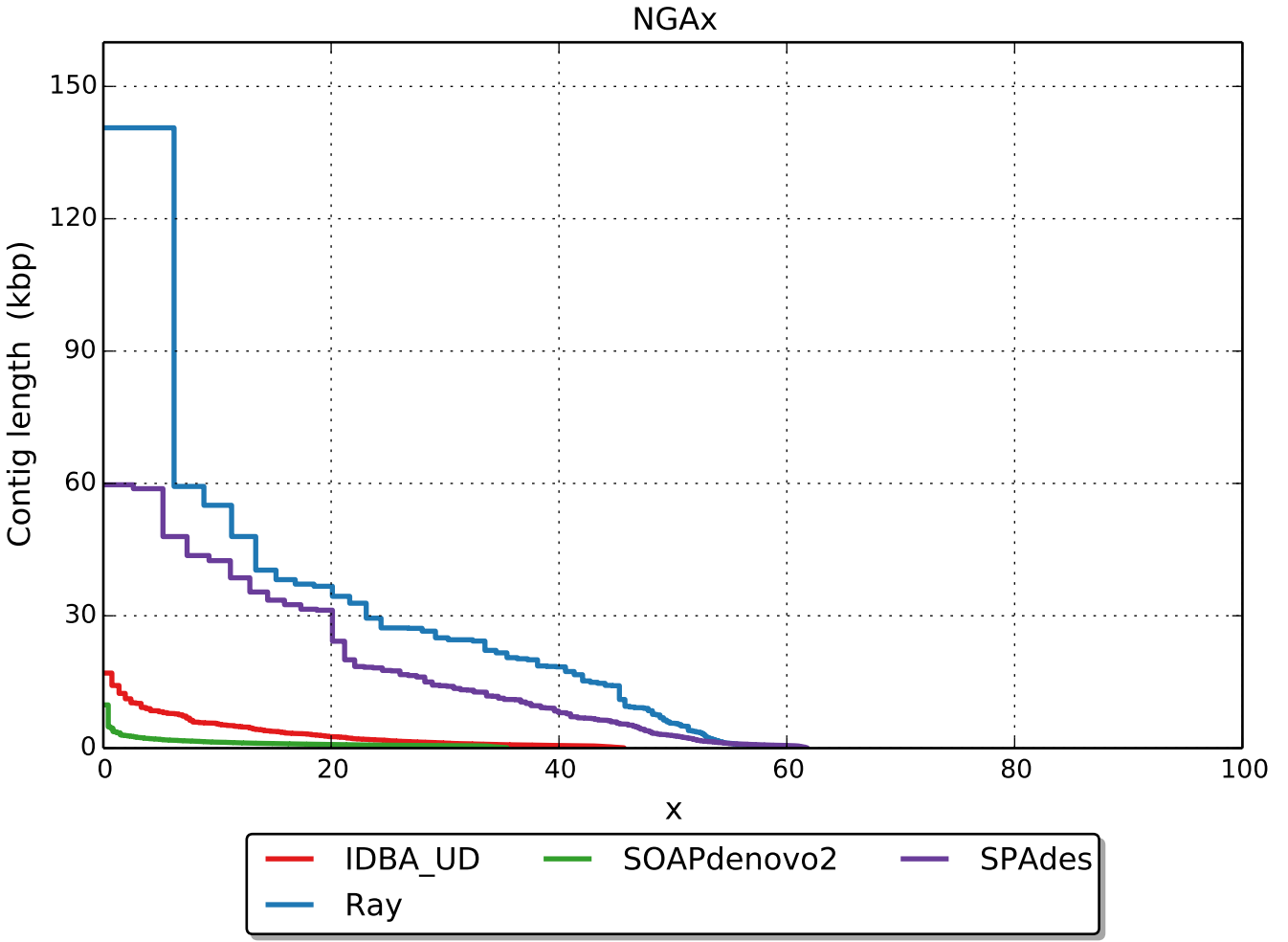

Cumulative length
Cumulative length (kbp)
Contig index
0
500
1000
1500
2000
2500
3000
0
200
400
600
800
1000
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference

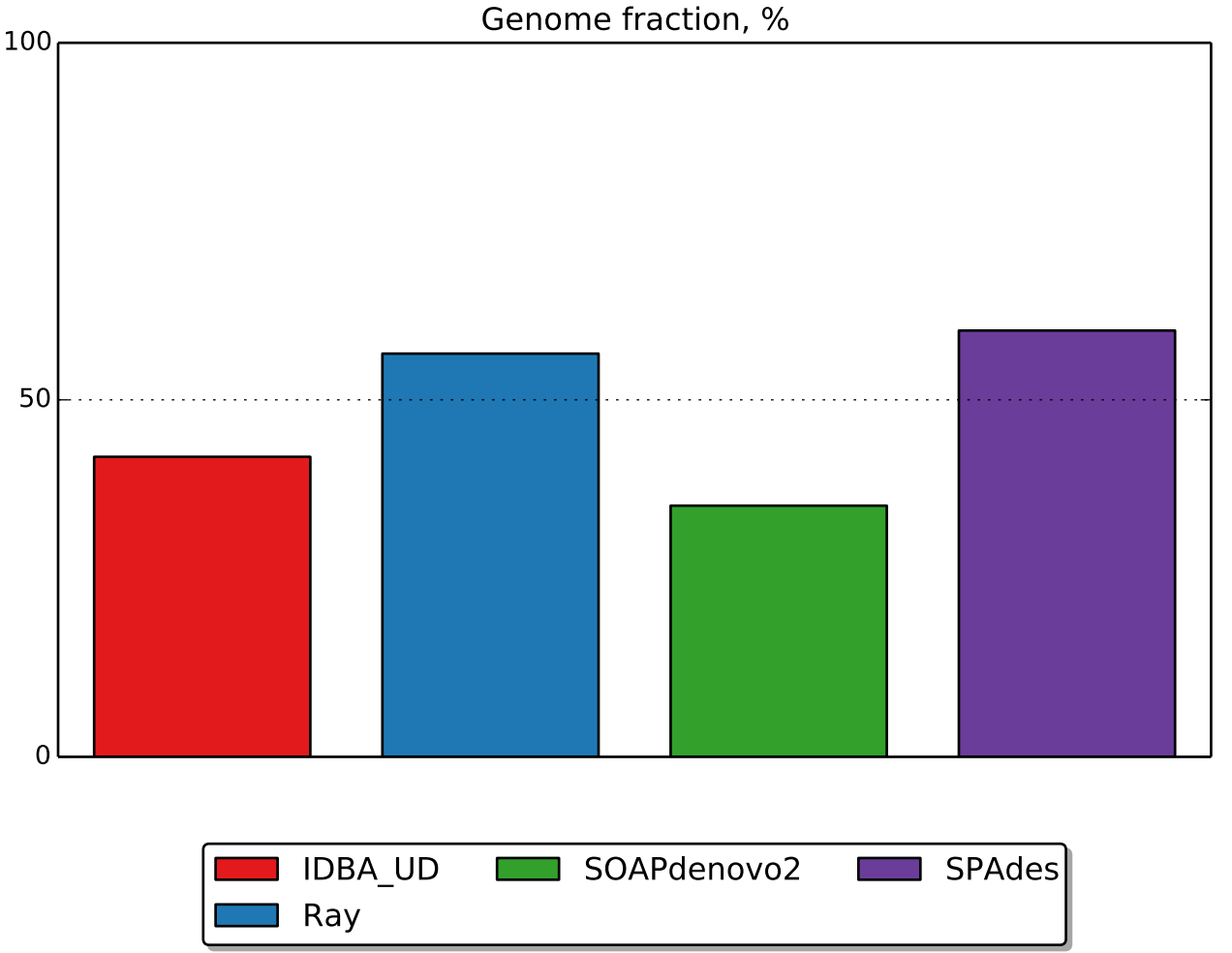

GC content
windows
GC (%)
0
300
600
900
1200
1500
1800
0
20
40
60
80
100
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


Misassemblies
35
30
25
20
15
10
5
0
IDBA_UD
Ray
SOAPdenovo2
SPAdes
relocations
inversions


Cumulative length (aligned contigs)
Cumulative length (kbp)
Contig index
0
500
1000
1500
2000
2500
0
200
400
600
800
1000
1200
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


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


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


Genome fraction, %
100
50
0
IDBA_UD
Ray
SOAPdenovo2
SPAdes