Report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	48	361	1032	1433	437
# contigs (>= 5000 bp)	43	256	0	157	275
# contigs (>= 10000 bp)	40	170	0	10	177
# contigs (>= 25000 bp)	38	50	0	0	35
# contigs (>= 50000 bp)	33	4	0	0	4
Total length (>= 1000 bp)	4607095	4592978	1457547	4038065	4640644
Total length (>= 5000 bp)	4595910	4304854	0	1108719	4204101
Total length (>= 10000 bp)	4571097	3648048	0	128133	3510558
Total length (>= 25000 bp)	4533326	1743396	0	0	1264094
Total length (>= 50000 bp)	4380795	244980	0	0	242573
# contigs	52	389	3358	1942	472
Largest contig	365371	71692	3457	15914	71456
Total length	4610012	4613330	3085333	4413644	4667505
Reference length	4616889	4616889	4616889	4616889	4616889
GC (%)	54.84	54.84	54.85	54.82	55.05
Reference GC (%)	54.83	54.83	54.83	54.83	54.83
N50	165311	19216	968	3137	16687
NG50	165311	19216	706	3018	16718
N75	88540	11486	705	1785	10014
NG75	88540	11486	-	1627	10096
L50	11	76	1119	439	87
LG50	11	76	2051	472	86
L75	21	153	2059	902	177
LG75	21	153	-	991	173
# misassemblies	0	8	2	2	12
# misassembled contigs	0	7	2	2	9
Misassembled contigs length	0	98895	1476	4271	110688
# local misassemblies	0	11	14	1	6
# structural variations	0	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 13 part	0 + 4 part	0 + 6 part	0 + 23 part
Unaligned length	0	18620	3861	261	78031
Genome fraction (%)	99.851	99.191	65.686	95.303	99.057
Duplication ratio	1.000	1.003	1.016	1.003	1.004
# N's per 100 kbp	0.00	0.00	16.27	48.15	42.12
# mismatches per 100 kbp	0.00	25.00	2.04	102.66	125.75
# indels per 100 kbp	0.00	0.41	0.03	20.30	0.68
Largest alignment	365371	71692	3457	15914	71456
NA50	165311	18739	966	3136	15961
NGA50	165311	18739	705	3002	16179
NA75	88540	11323	703	1785	9051
NGA75	88540	11323	-	1627	9316
LA50	11	78	1122	439	92
LGA50	11	78	2056	472	90
LA75	21	156	2064	902	186
LGA75	21	156	-	992	182

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

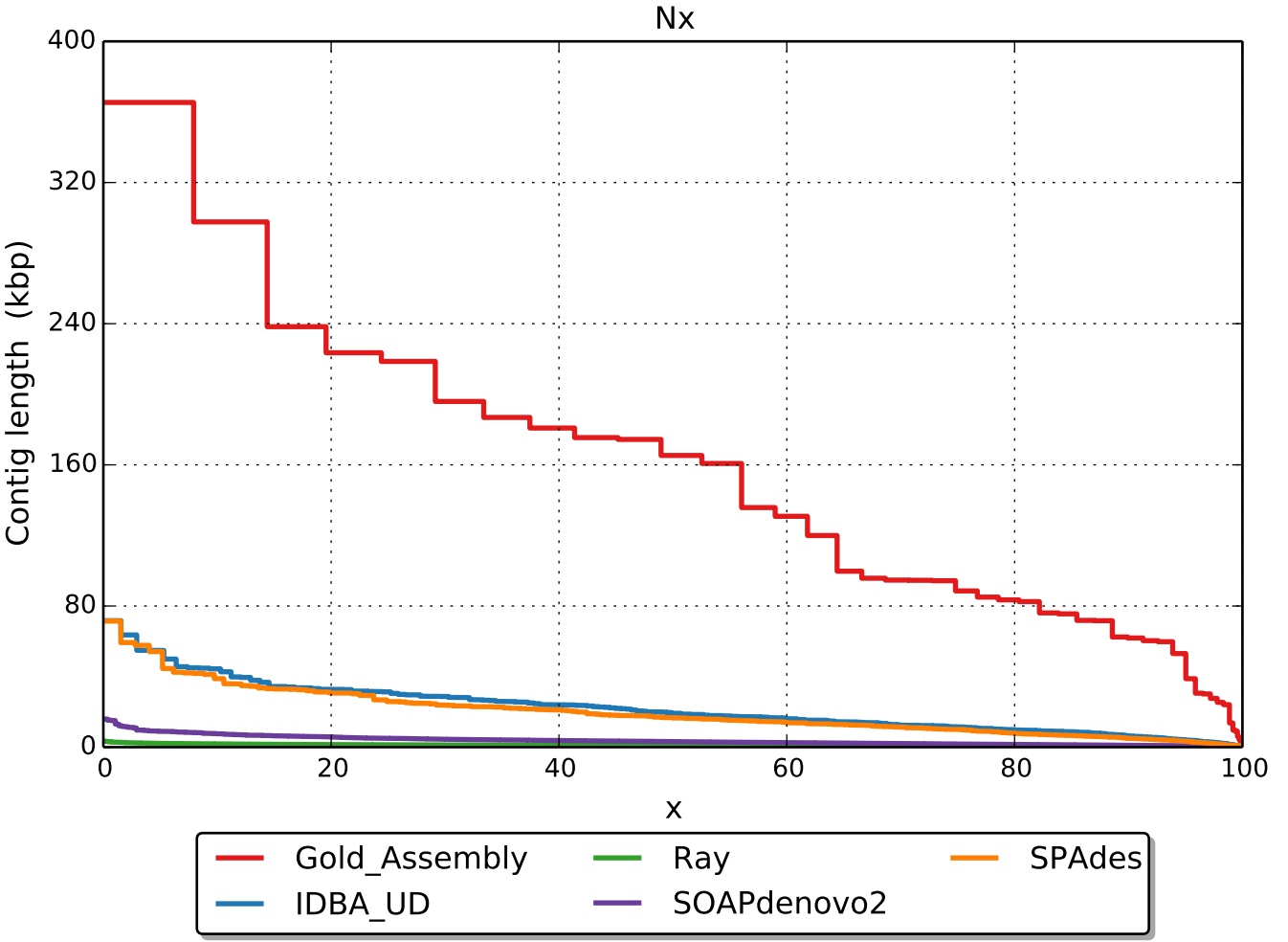
	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	8	2	2	12
# relocations	0	2	0	0	7
# translocations	0	6	2	2	5
# inversions	0	0	0	0	0
# possibly misassembled contigs	0	7	0	0	9
# misassembled contigs	0	7	2	2	9
Misassembled contigs length	0	98895	1476	4271	110688
# local misassemblies	0	11	14	1	6
# structural variations	0	0	0	0	0
# mismatches	0	1145	62	4517	5751
# indels	0	19	1	893	31
# short indels	0	15	1	411	20
# long indels	0	4	0	482	11
Indels length	0	107	1	6546	389

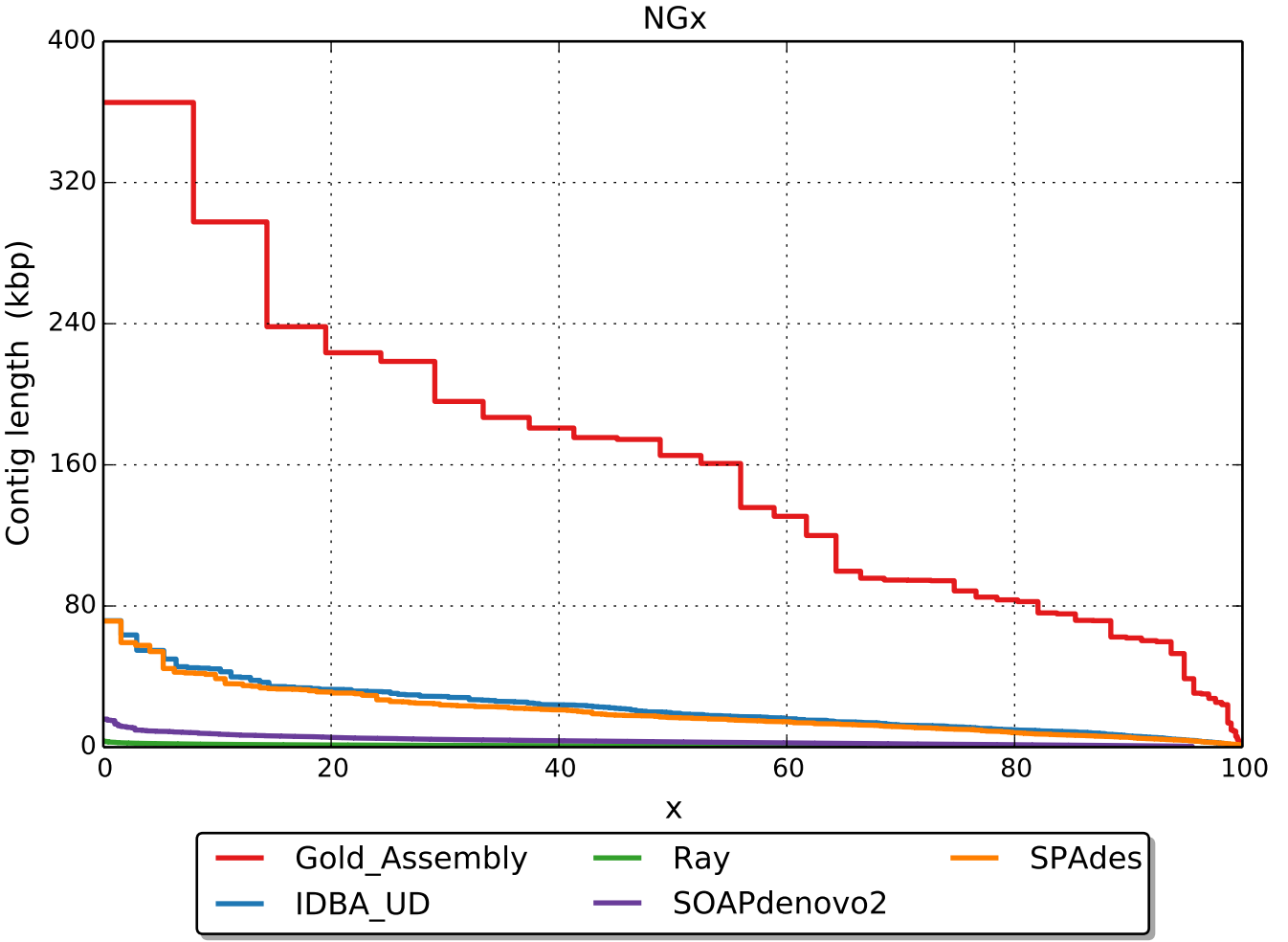
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

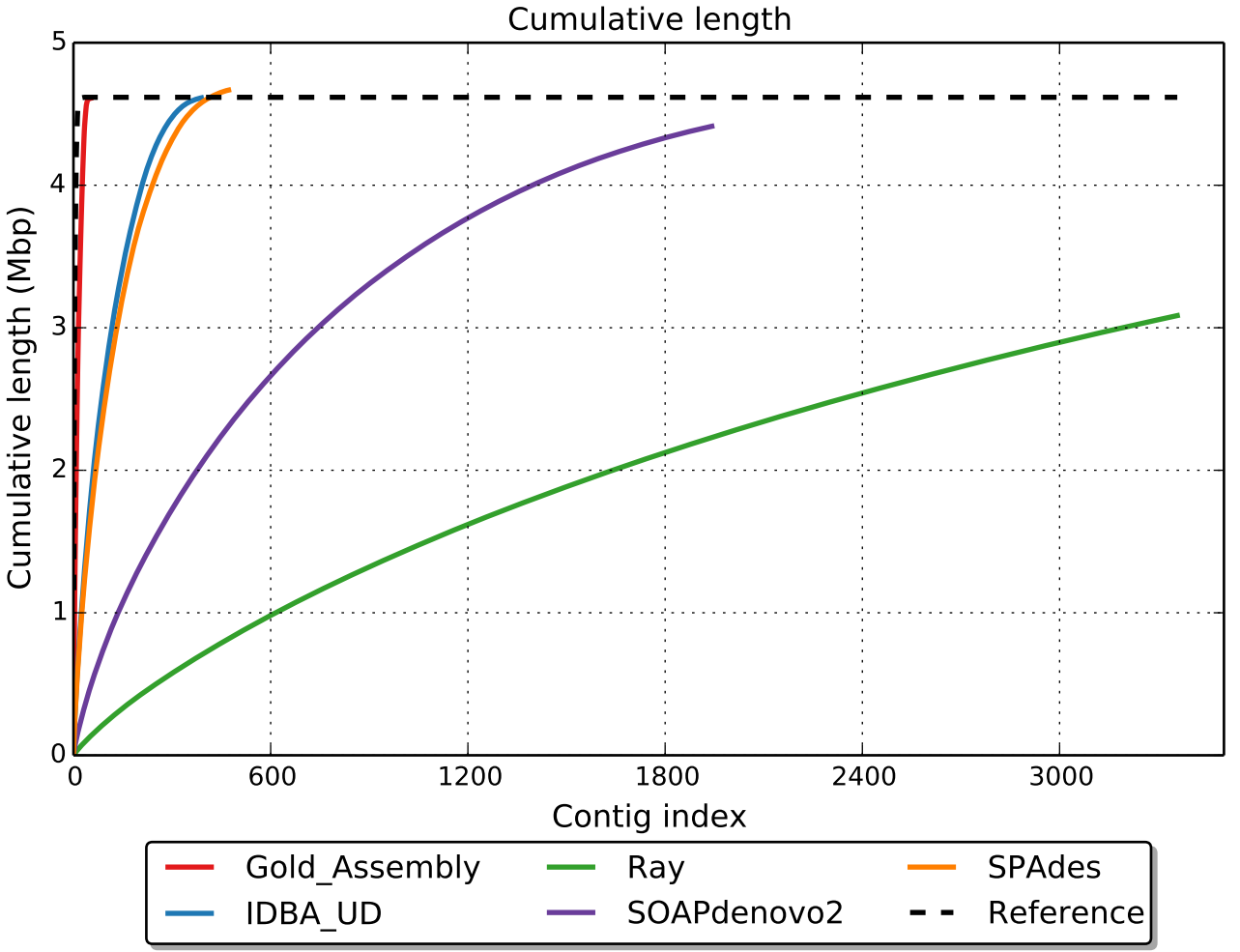
Unaligned report

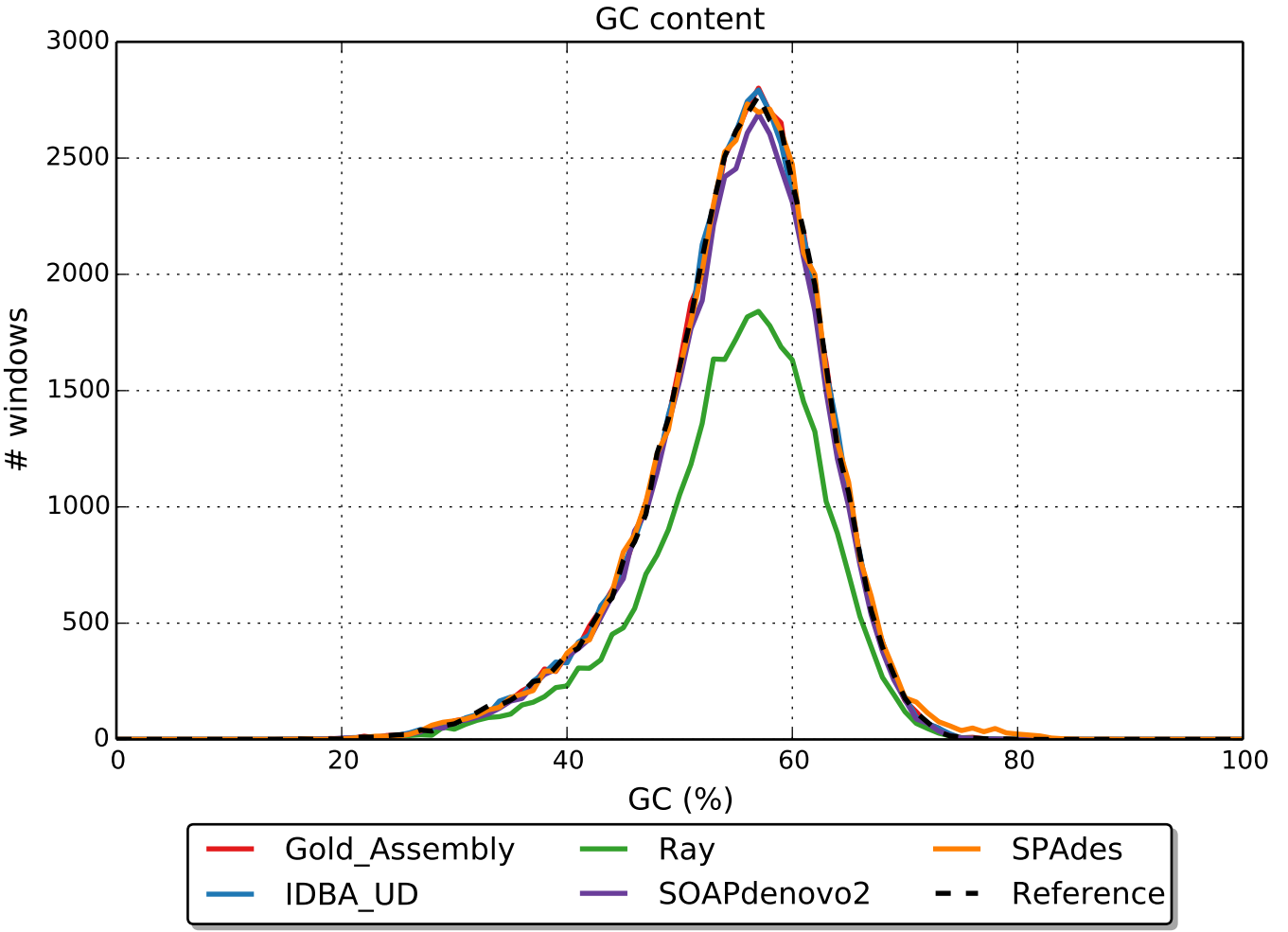
	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0	0
Fully unaligned length	0	0	0	0	0
# partially unaligned contigs	0	13	4	6	23
# with misassembly	0	0	0	0	0
# both parts are significant	0	6	0	0	8
Partially unaligned length	0	18620	3861	261	78031
# N's	0	0	502	2125	1966

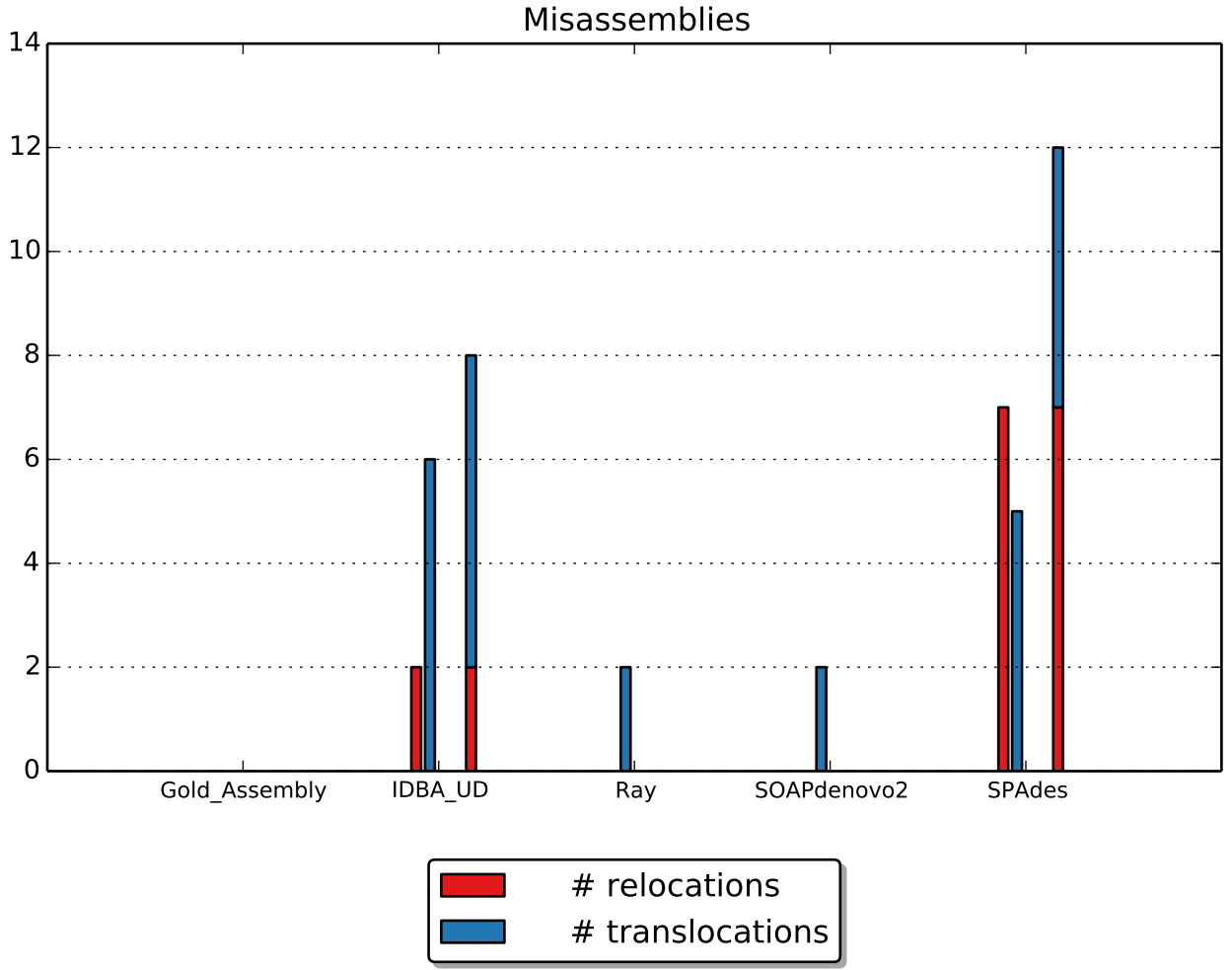
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

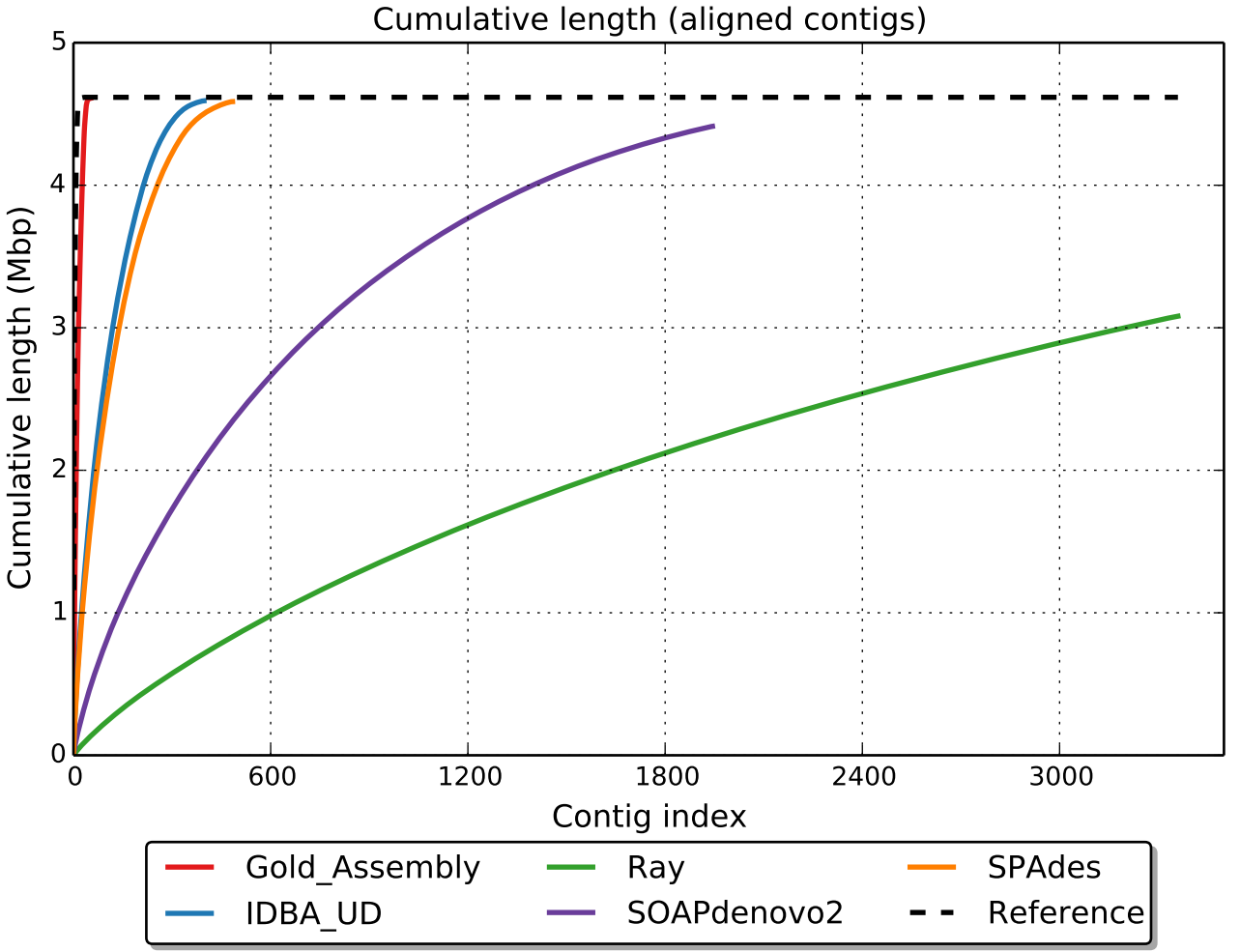

Nx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes

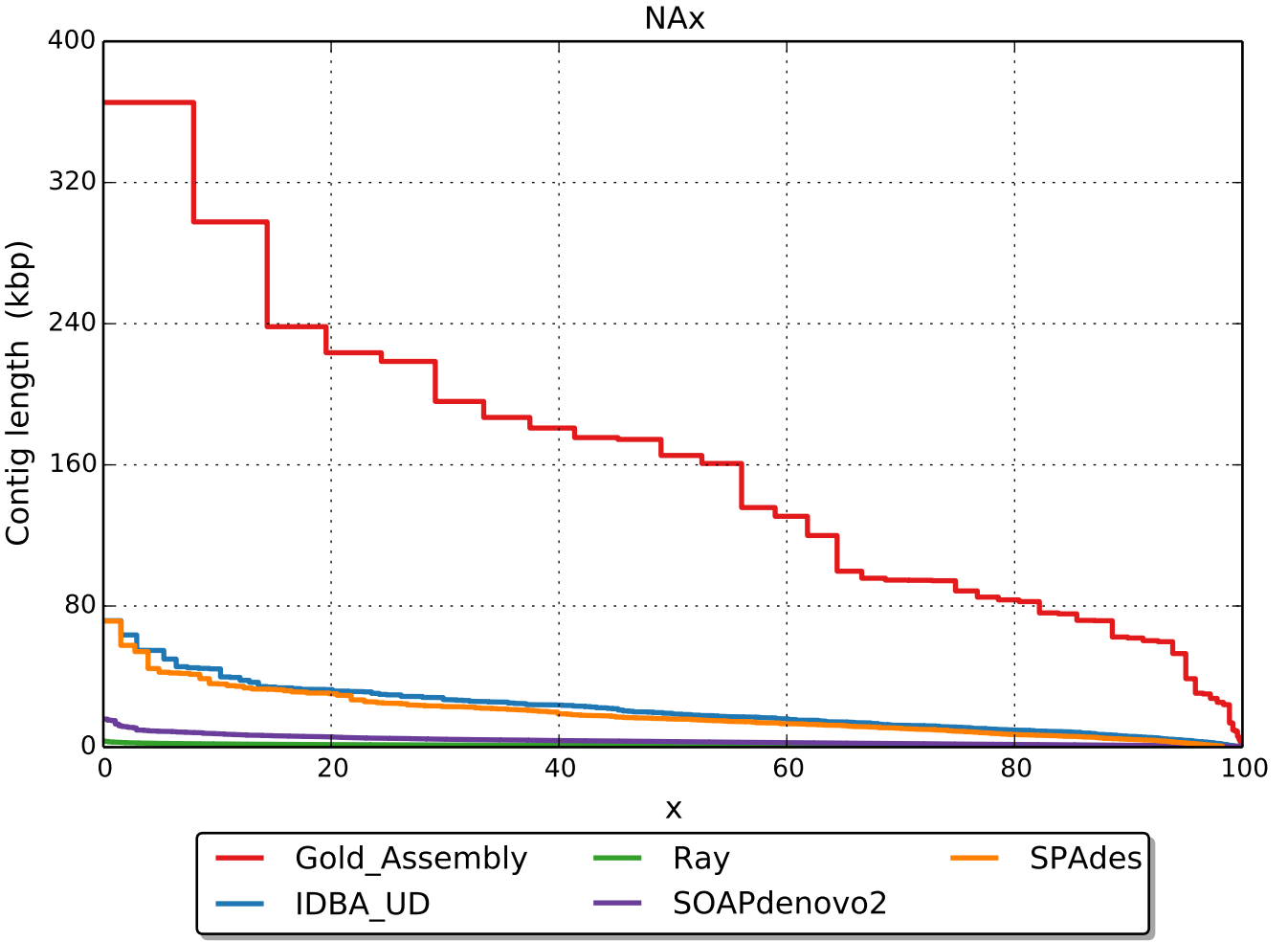

NGx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes

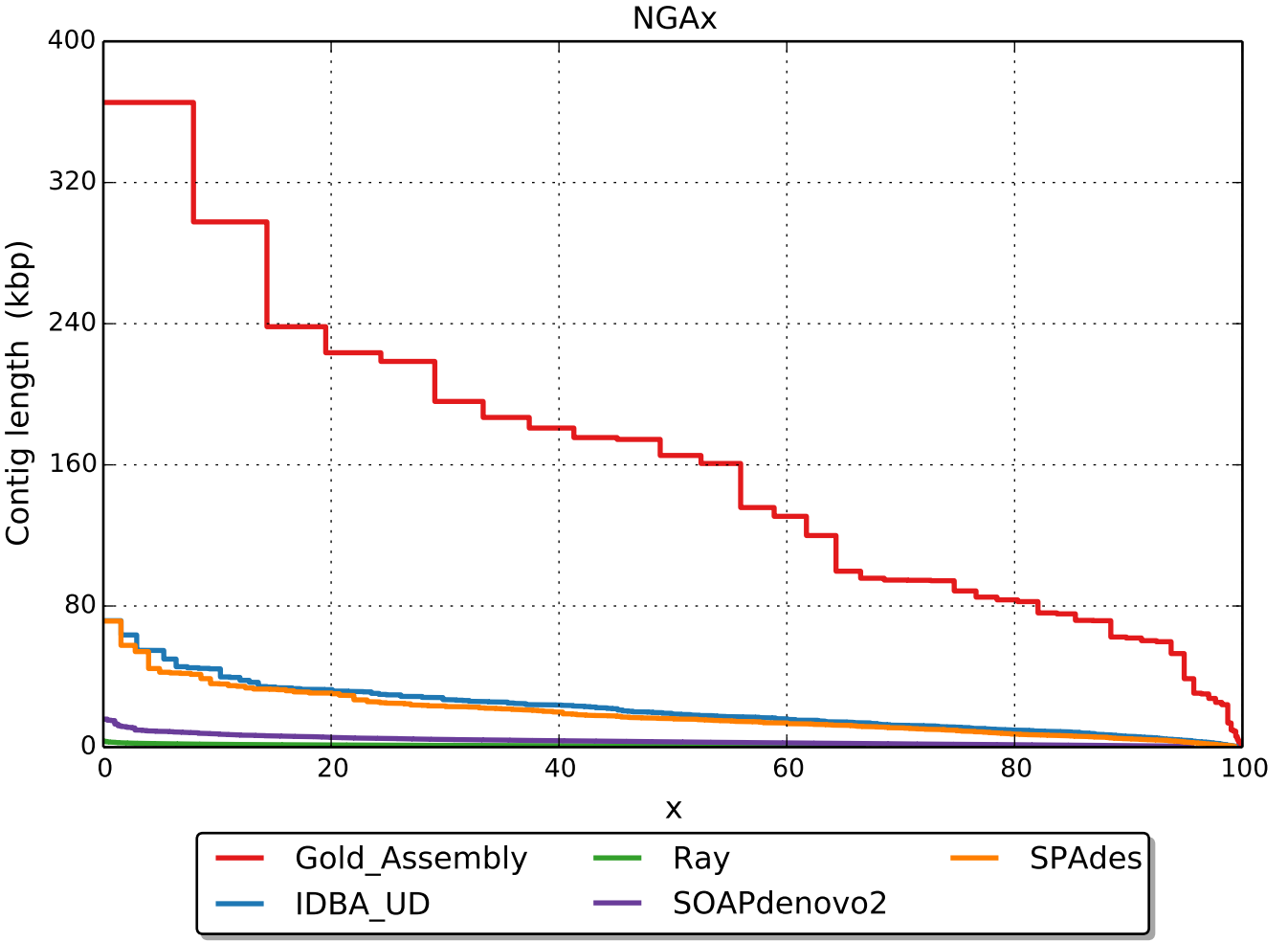

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
0
600
1200
1800
2400
3000
Contig index
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference

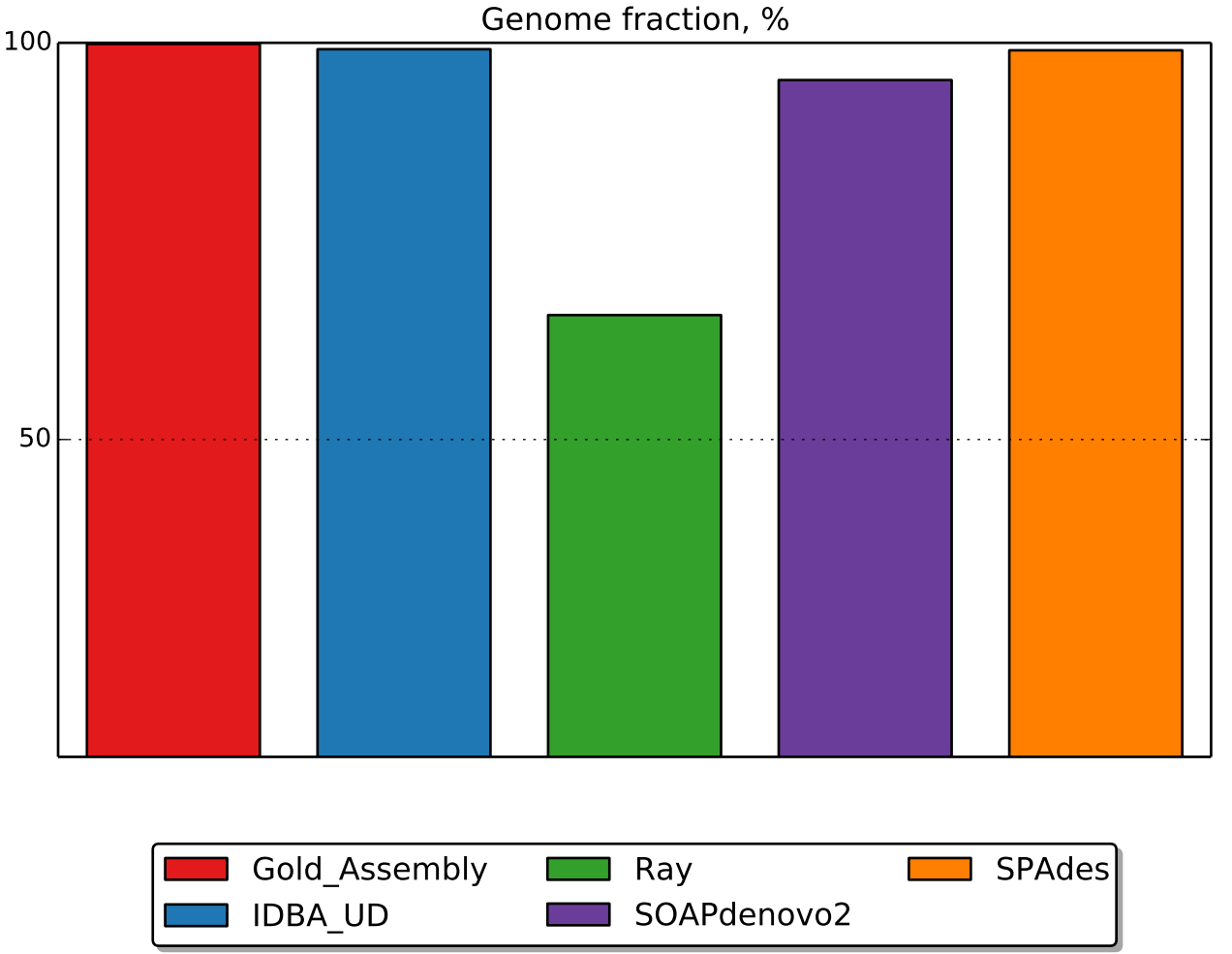

GC content
windows
GC (%)
0
500
1000
1500
2000
2500
3000
0
20
40
60
80
100
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


Misassemblies
14
12
10
8
6
4
2
0
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes
relocations
translocations


Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
0
600
1200
1800
2400
3000
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


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


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


Genome fraction, %
100
50
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes