Report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	32	35	35	578	82
# contigs (>= 5000 bp)	25	29	32	306	68
# contigs (>= 10000 bp)	25	25	31	146	61
# contigs (>= 25000 bp)	23	22	27	18	45
# contigs (>= 50000 bp)	18	19	22	0	30
Total length (>= 1000 bp)	4470204	4460700	4707201	4337822	4449038
Total length (>= 5000 bp)	4453430	4444438	4697503	3585221	4410284
Total length (>= 10000 bp)	4453430	4412826	4692354	2455598	4359269
Total length (>= 25000 bp)	4424403	4372530	4624303	554301	4100299
Total length (>= 50000 bp)	4227911	4257734	4442678	0	3529558
# contigs	32	38	40	641	92
Largest contig	888872	800397	560953	40778	311540
Total length	4470204	4462277	4711213	4383923	4456754
Reference length	4470560	4470560	4470560	4470560	4470560
GC (%)	74.44	74.45	74.47	74.49	74.46
Reference GC (%)	74.43	74.43	74.43	74.43	74.43
N50	279499	275977	239755	11173	104980
NG50	279499	275977	289952	11104	104980
N75	167790	154751	139215	6173	53904
NG75	167790	154751	162391	5974	53904
L50	5	5	7	122	12
LG50	5	5	6	126	12
L75	10	10	13	253	27
LG75	10	10	12	264	27
# misassemblies	0	11	12	2	10
# misassembled contigs	0	9	9	2	10
Misassembled contigs length	0	2164416	1520106	28461	1147192
# local misassemblies	0	0	1	0	0
# structural variations	0	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 0 part	0 + 3 part	0 + 8 part	0 + 8 part
Unaligned length	0	0	5351	399	5972
Genome fraction (%)	99.992	99.785	99.781	97.783	99.490
Duplication ratio	1.000	1.000	1.055	1.003	1.001
# N's per 100 kbp	0.00	0.00	3.40	14.23	1.37
# mismatches per 100 kbp	0.00	0.20	0.13	11.23	20.53
# indels per 100 kbp	0.00	0.02	0.20	10.34	0.43
Largest alignment	888872	800397	560953	40778	311540
NA50	279499	191116	196728	11139	83639
NGA50	279499	191116	222617	11046	83639
NA75	167790	93438	106956	6169	49274
NGA75	167790	93438	129052	5851	49274
LA50	5	6	8	122	14
LGA50	5	6	7	126	14
LA75	10	14	15	255	32
LGA75	10	14	14	266	32

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

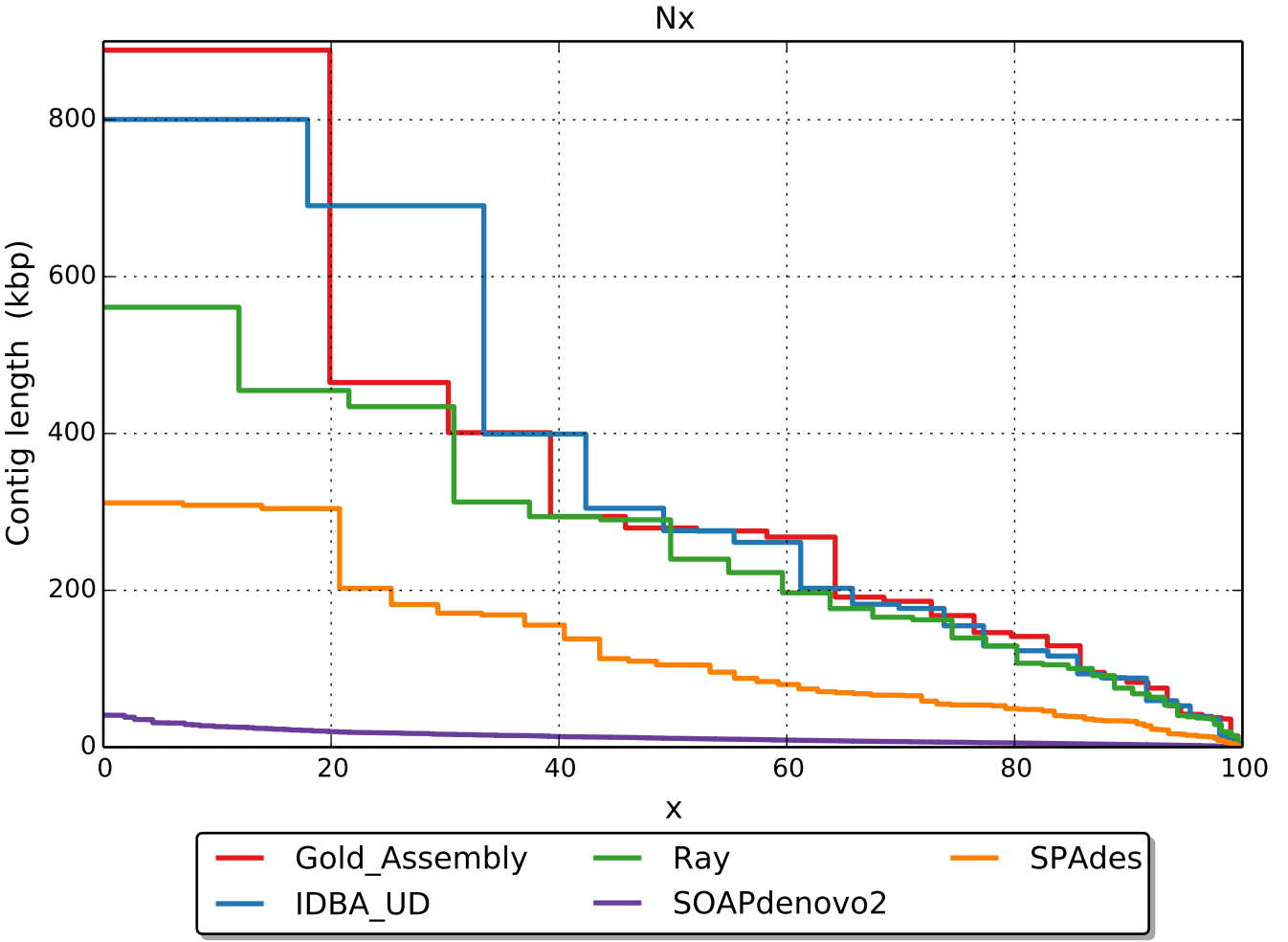
	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	11	12	2	10
# relocations	0	0	0	0	0
# translocations	0	11	12	2	10
# inversions	0	0	0	0	0
# possibly misassembled contigs	0	0	3	0	3
# misassembled contigs	0	9	9	2	10
Misassembled contigs length	0	2164416	1520106	28461	1147192
# local misassemblies	0	0	1	0	0
# structural variations	0	0	0	0	0
# mismatches	0	9	6	491	913
# indels	0	1	9	452	19
# short indels	0	0	3	174	17
# long indels	0	1	6	278	2
Indels length	0	9	122	9953	91

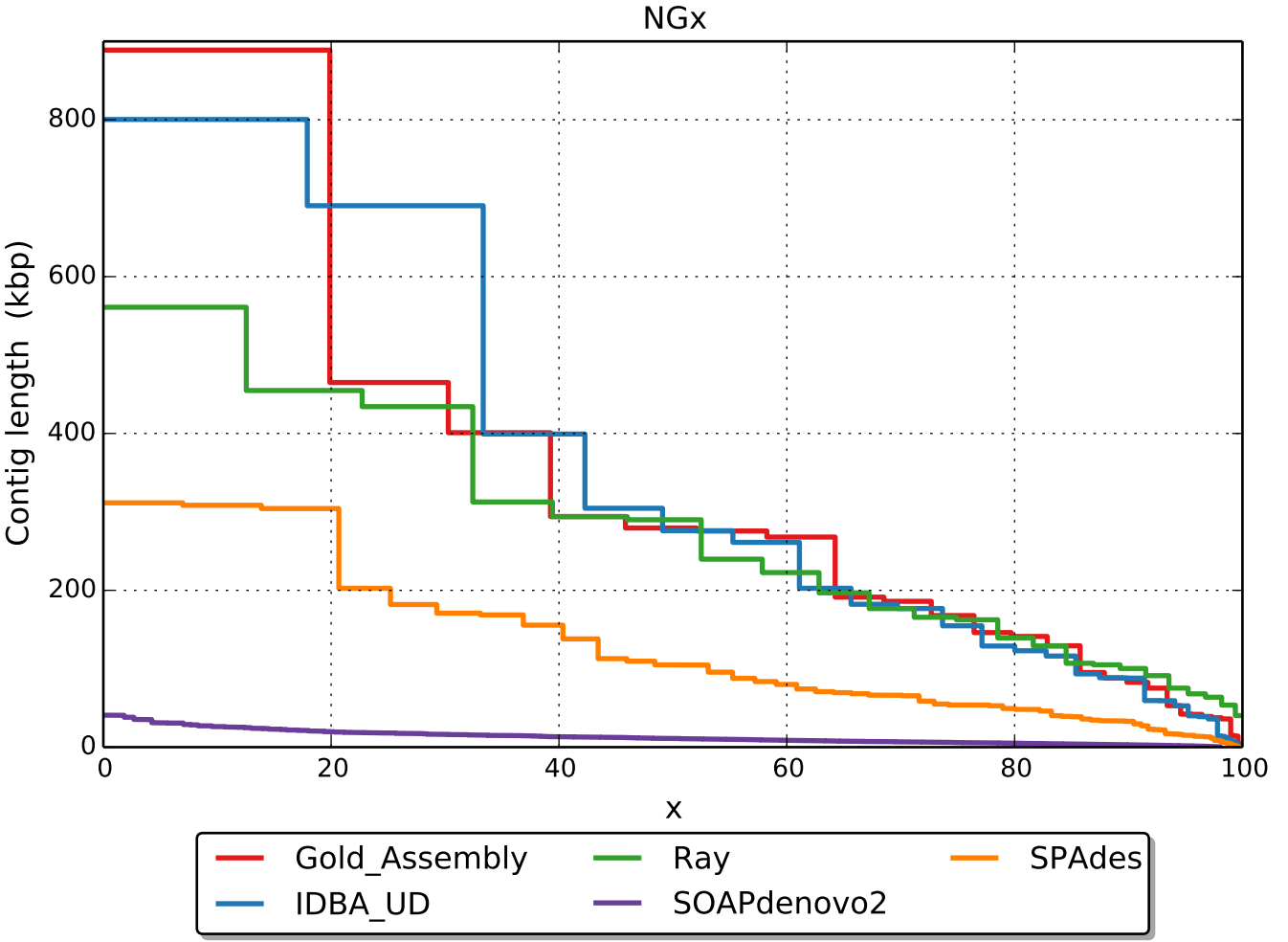
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

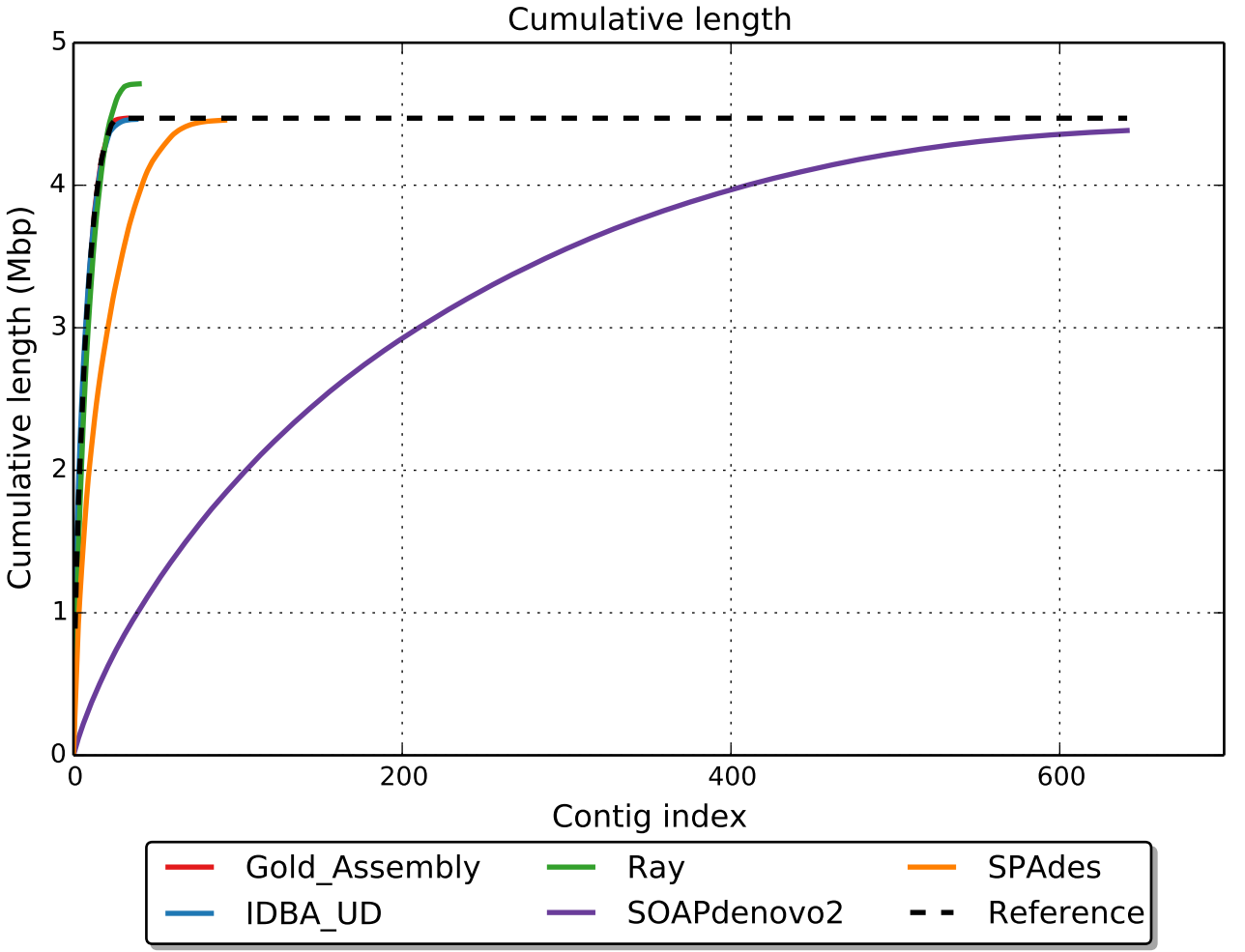
Unaligned report

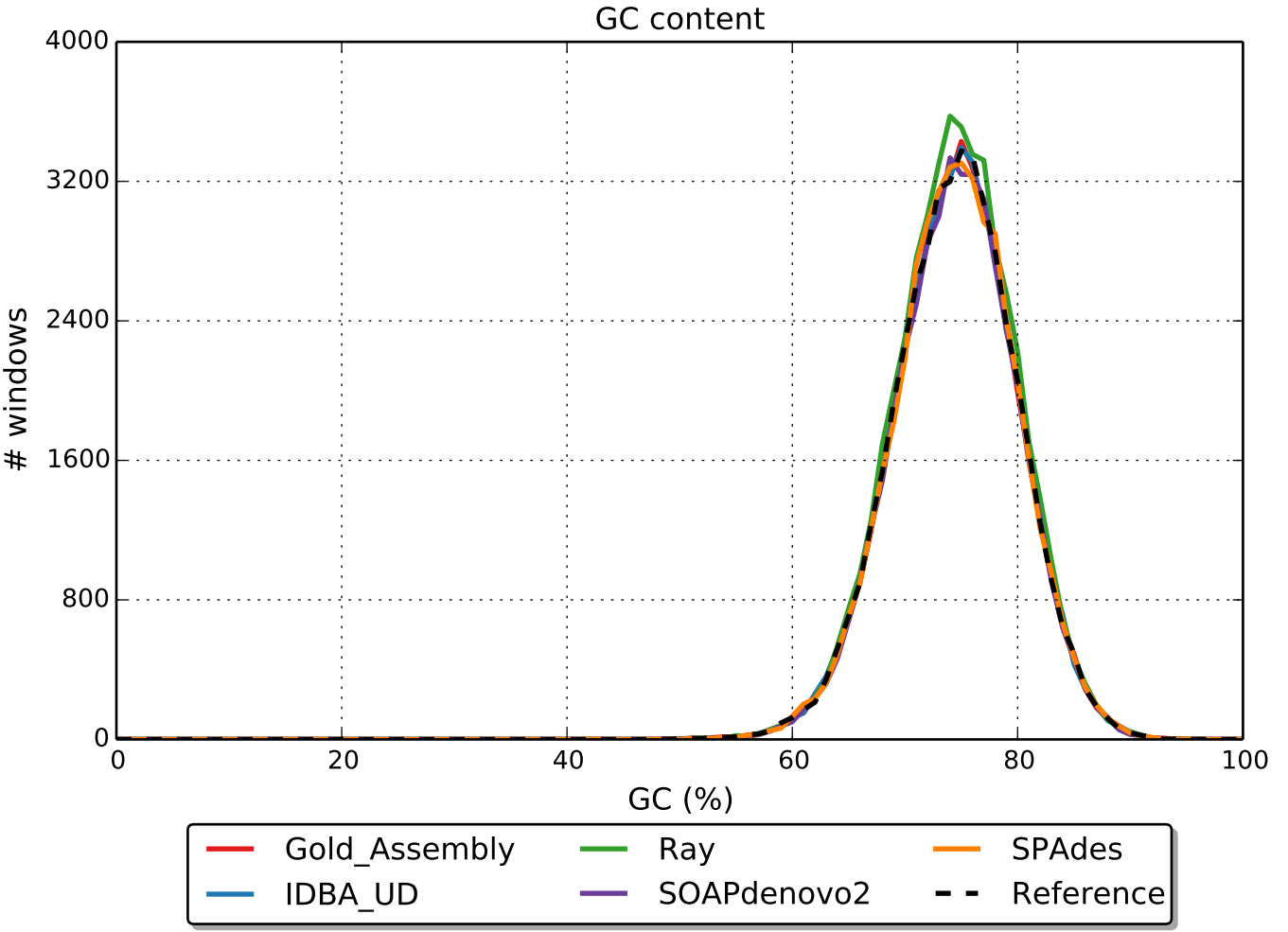
	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0	0
Fully unaligned length	0	0	0	0	0
# partially unaligned contigs	0	0	3	8	8
# with misassembly	0	0	0	0	0
# both parts are significant	0	0	2	0	3
Partially unaligned length	0	0	5351	399	5972
# N's	0	0	160	624	61

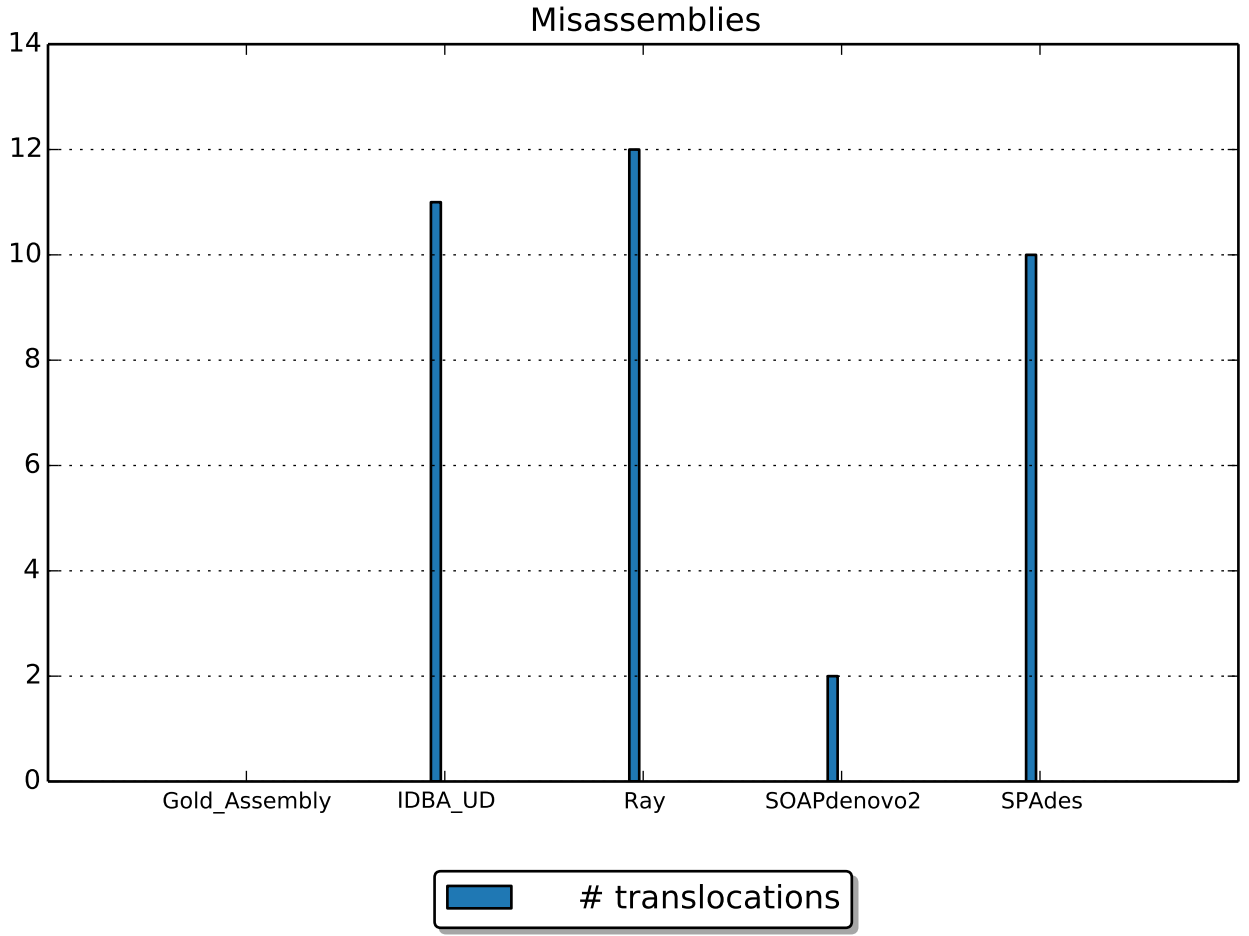
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

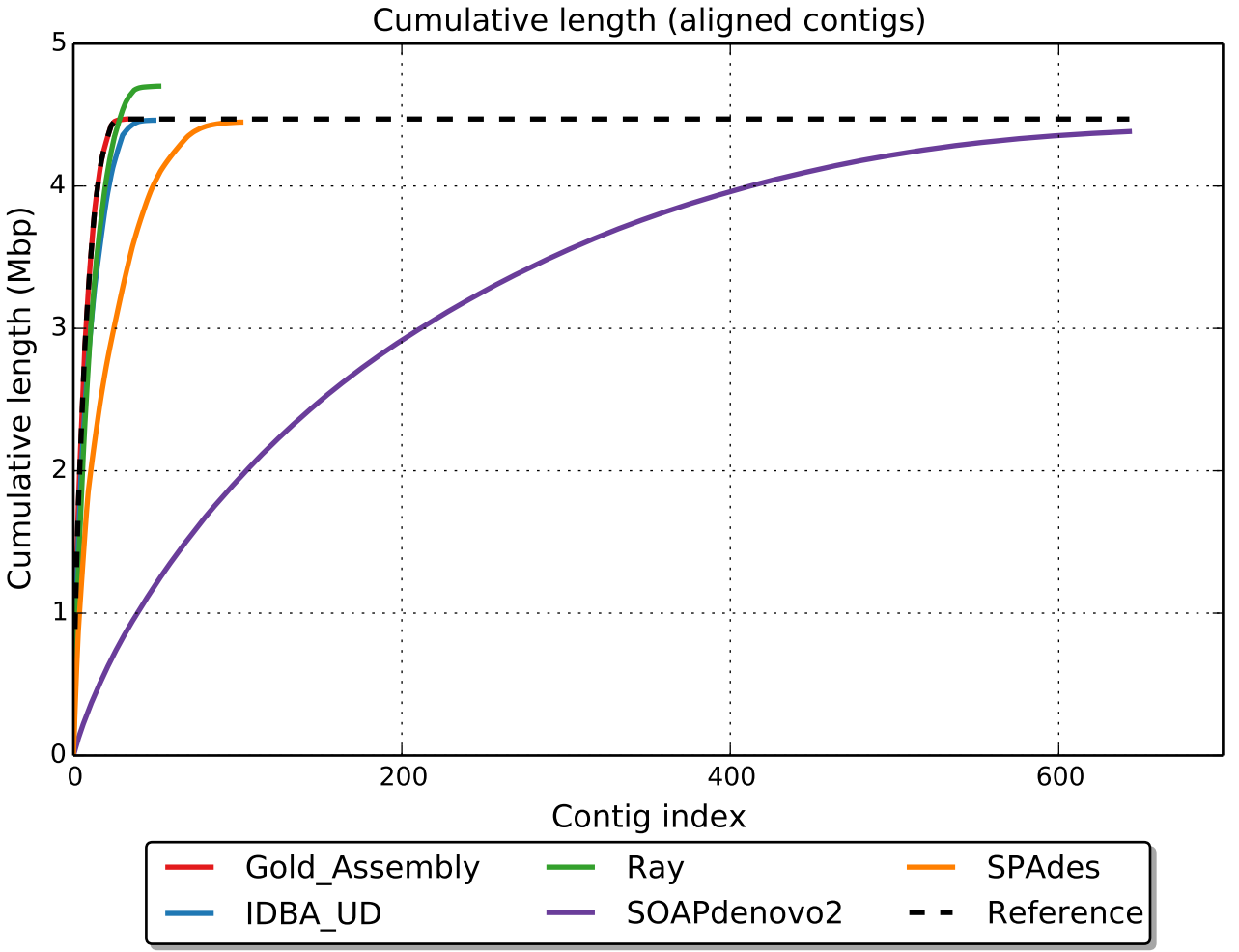

Nx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes

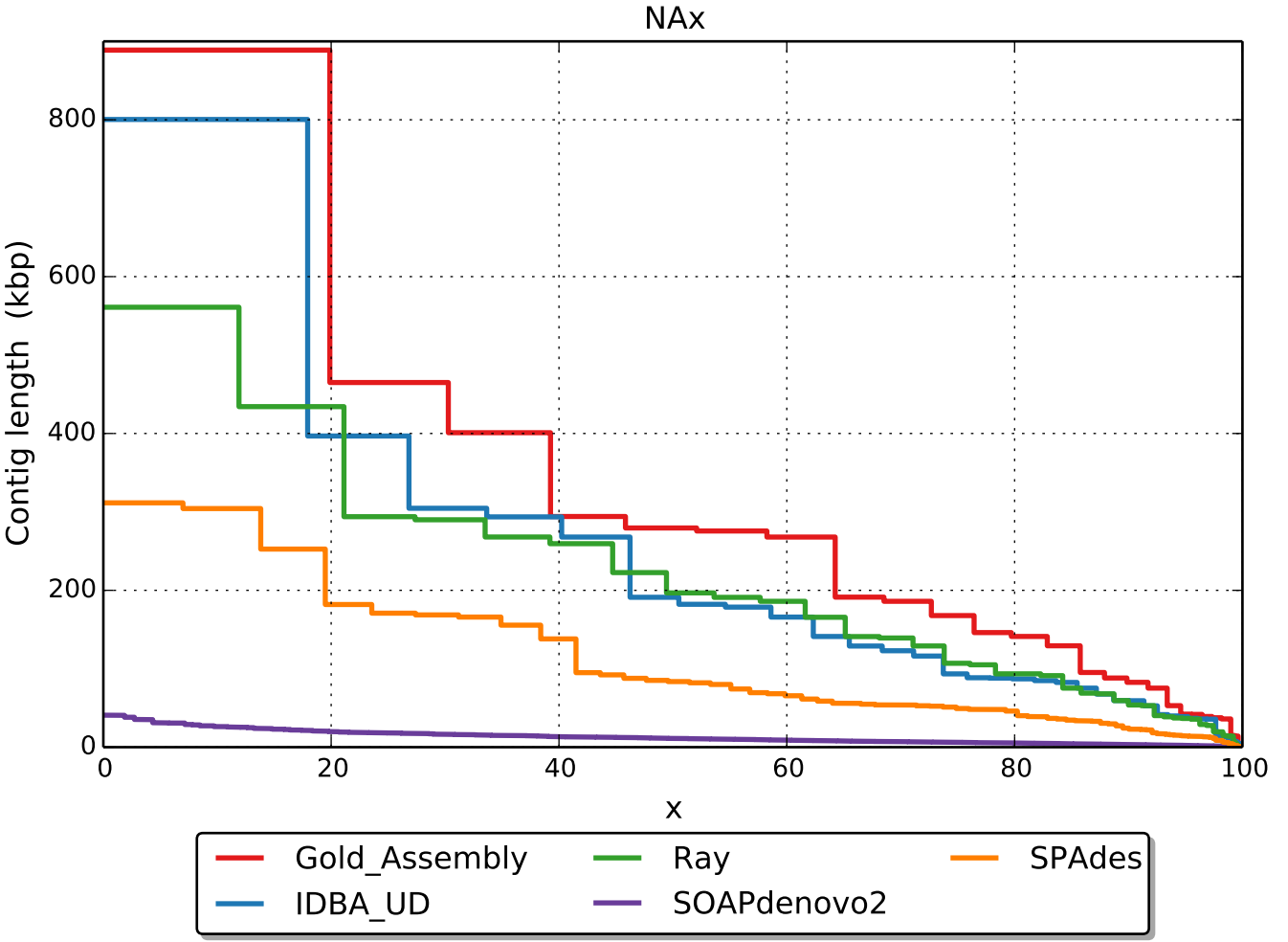

NGx
Contig length (kbp)
0
200
400
600
800
0
20
40
60
80
100
x
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes

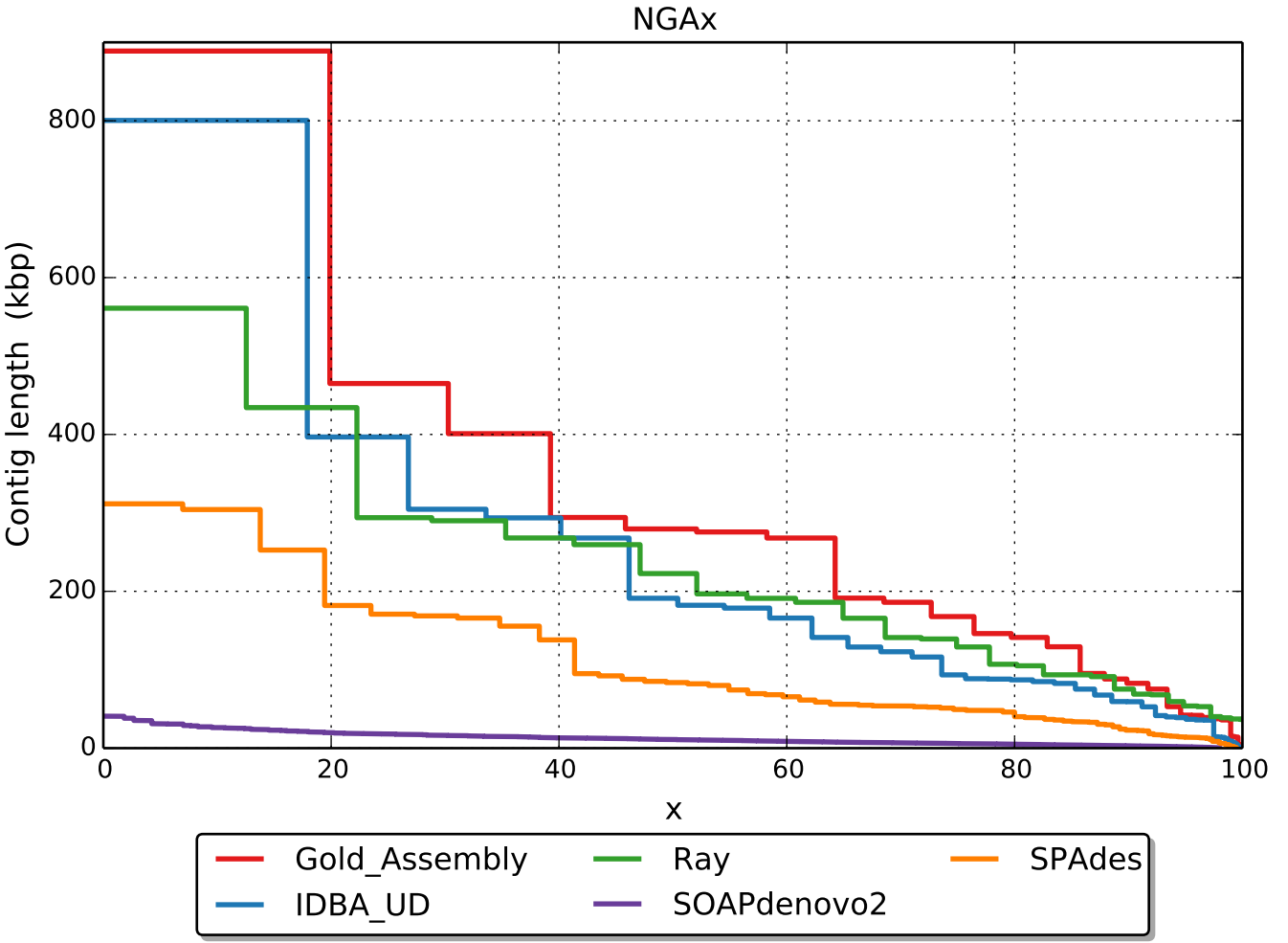

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
0
200
400
600
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference

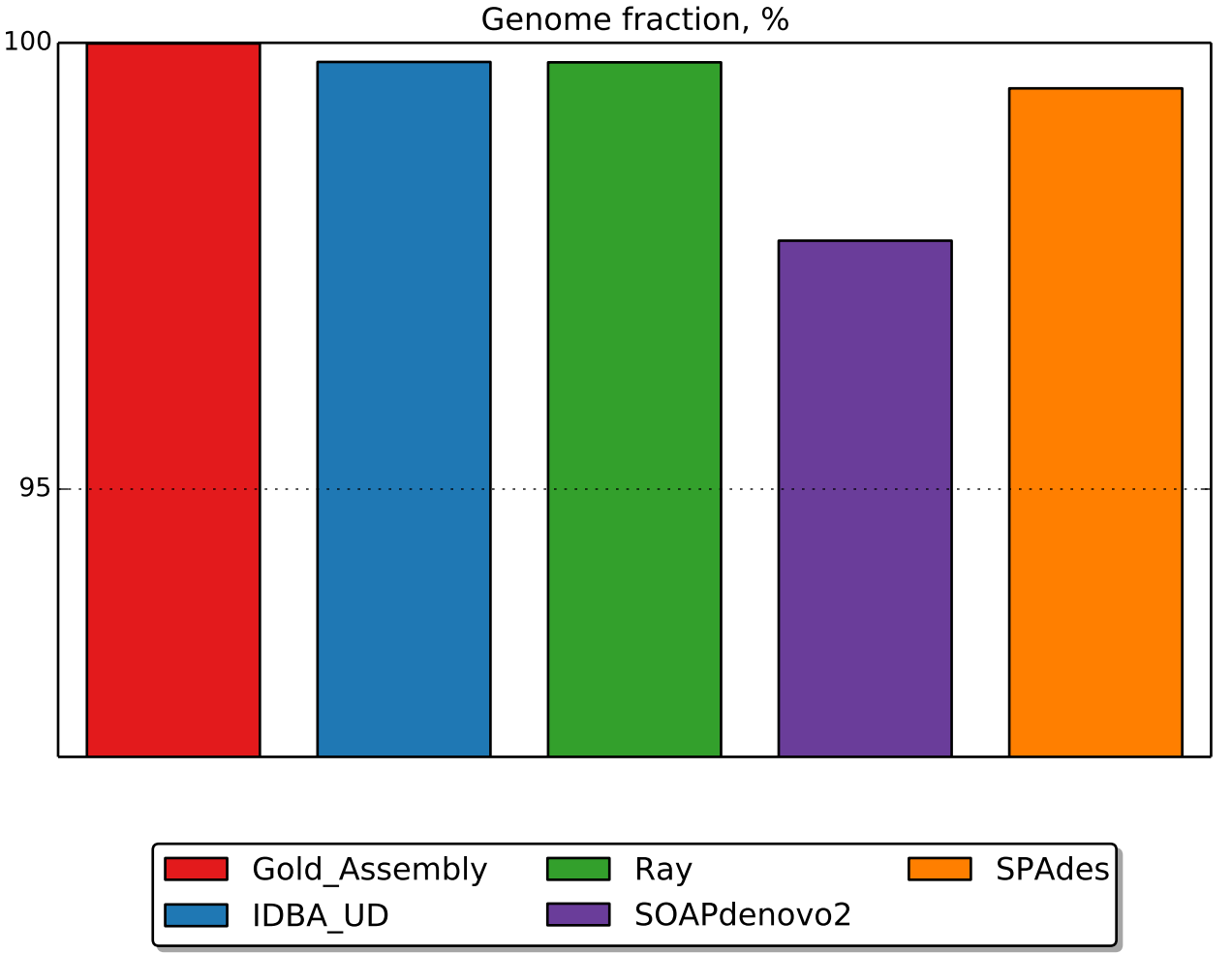

GC content
4000
3200
2400
1600
800
0
windows
0
20
40
60
80
100
GC (%)
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


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


Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
0
200
400
600
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


NAx
Contig length (kbp)
0
200
400
600
800
0
20
40
60
80
100
x
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes


NGAx
Contig length (kbp)
0
200
400
600
800
0
20
40
60
80
100
x
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes


Genome fraction, %
100
95
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes