Report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	59	31	40	307	23
# contigs (>= 5000 bp)	49	24	30	2	20
# contigs (>= 10000 bp)	46	24	29	0	20
# contigs (>= 25000 bp)	40	22	26	0	19
# contigs (>= 50000 bp)	23	18	22	0	14
Total length (>= 1000 bp)	6155820	3105721	3114933	417724	3088772
Total length (>= 5000 bp)	6133385	3092963	3092166	11050	3083339
Total length (>= 10000 bp)	6110609	3092963	3087159	0	3083339
Total length (>= 25000 bp)	5982633	3047653	3017223	0	3062156
Total length (>= 50000 bp)	5328956	2881317	2867634	0	2866756
# contigs	65	37	41	1560	25
Largest contig	679003	489962	490164	5668	514709
Total length	6159994	3109793	3115823	1271809	3090222
Reference length	3571452	3571452	3571452	3571452	3571452
GC (%)	38.13	38.14	38.11	37.88	38.12
Reference GC (%)	37.89	37.89	37.89	37.89	37.89
N50	322981	174114	151837	816	220876
NG50	361481	162333	119086	-	187831
N75	162689	119232	77824	636	163851
NG75	338777	66123	58396	-	111153
L50	7	6	7	550	5
LG50	4	8	9	-	7
L75	15	11	14	998	10
LG75	6	15	19	-	12
# misassemblies	109	50	51	2	48
# misassembled contigs	31	19	21	2	16
Misassembled contigs length	5529524	2881316	2727347	2283	2811363
# local misassemblies	44	23	22	2	25
# structural variations	84	45	43	15	41
# unaligned contigs	0 + 10 part	0 + 5 part	0 + 9 part	0 + 47 part	0 + 1 part
Unaligned length	116960	72382	101445	12943	36207
Genome fraction (%)	73.752	71.879	71.943	35.150	71.943
Duplication ratio	2.294	1.183	1.173	1.003	1.189
# N's per 100 kbp	0.00	0.00	1.19	0.00	0.00
# mismatches per 100 kbp	1329.15	1296.55	1302.90	1125.64	1307.62
# indels per 100 kbp	46.24	44.29	44.10	28.04	44.37
Largest alignment	326383	324197	324197	5668	323982
NA50	48880	50141	48880	804	50738
NGA50	101492	43382	40791	-	42313
NA75	18318	18318	17973	629	21128
NGA75	58772	-	-	-	-
LA50	31	14	18	561	14
LGA50	11	19	23	-	19
LA75	84	39	44	1015	38
LGA75	23	-	-	-	-

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

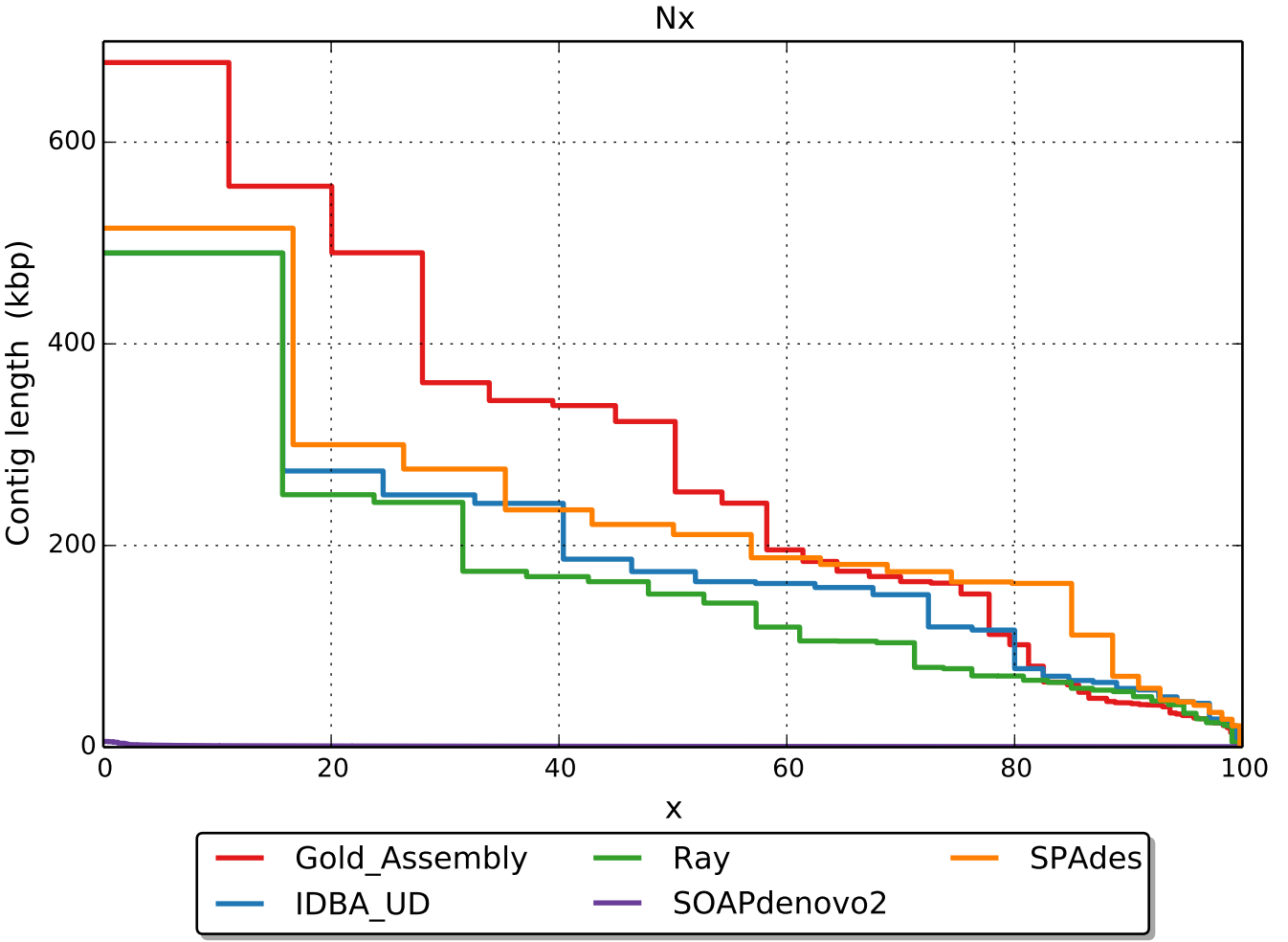
	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	109	50	51	2	48
# relocations	81	39	39	2	40
# translocations	26	11	12	0	6
# inversions	2	0	0	0	2
# possibly misassembled contigs	36	23	27	4	19
# misassembled contigs	31	19	21	2	16
Misassembled contigs length	5529524	2881316	2727347	2283	2811363
# local misassemblies	44	23	22	2	25
# structural variations	84	45	43	15	41
# mismatches	35010	33284	33477	14131	33598
# indels	1218	1137	1133	352	1140
# short indels	1080	1009	1006	329	1012
# long indels	138	128	127	23	128
Indels length	4017	3523	3500	757	3520

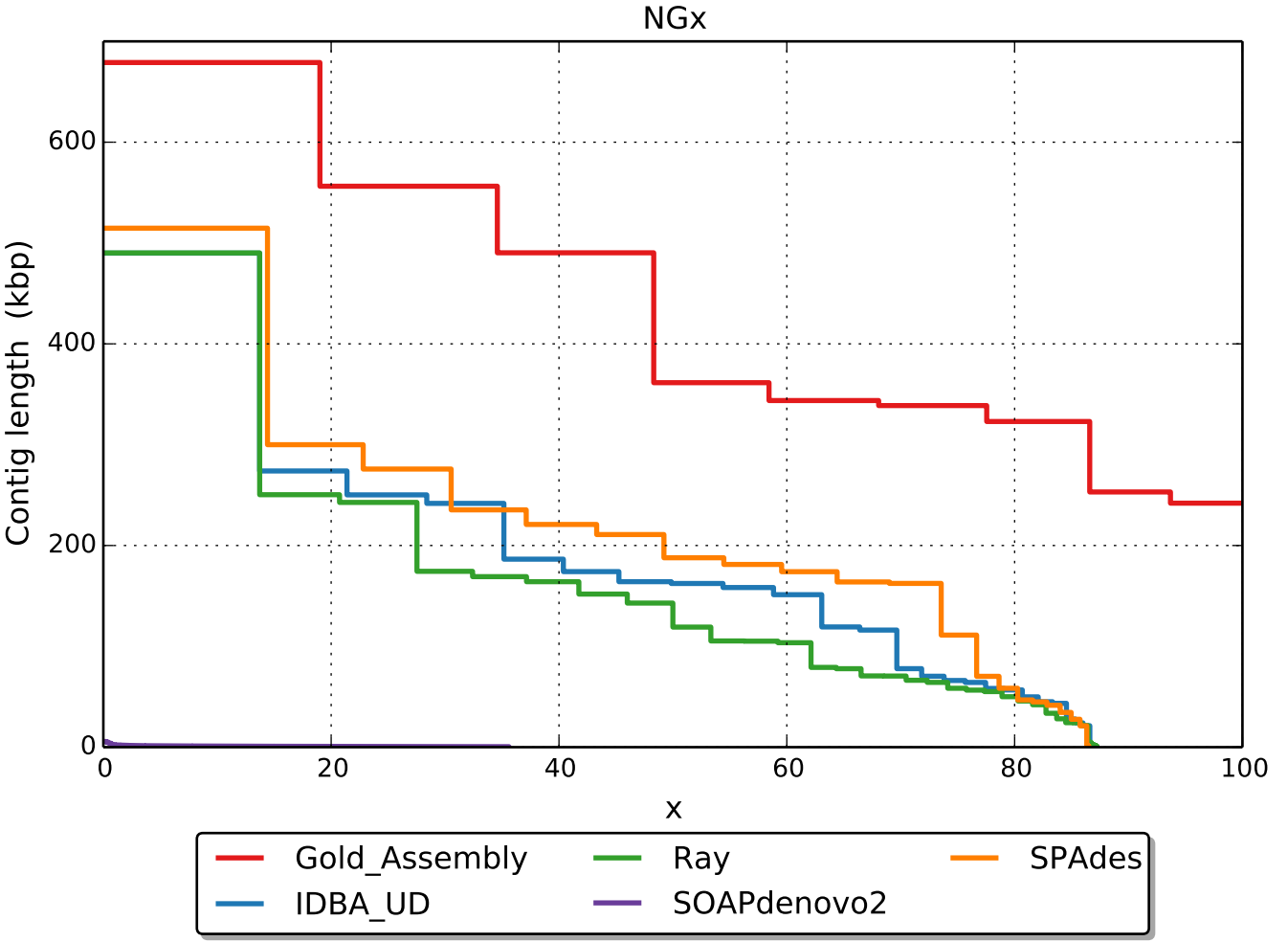
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

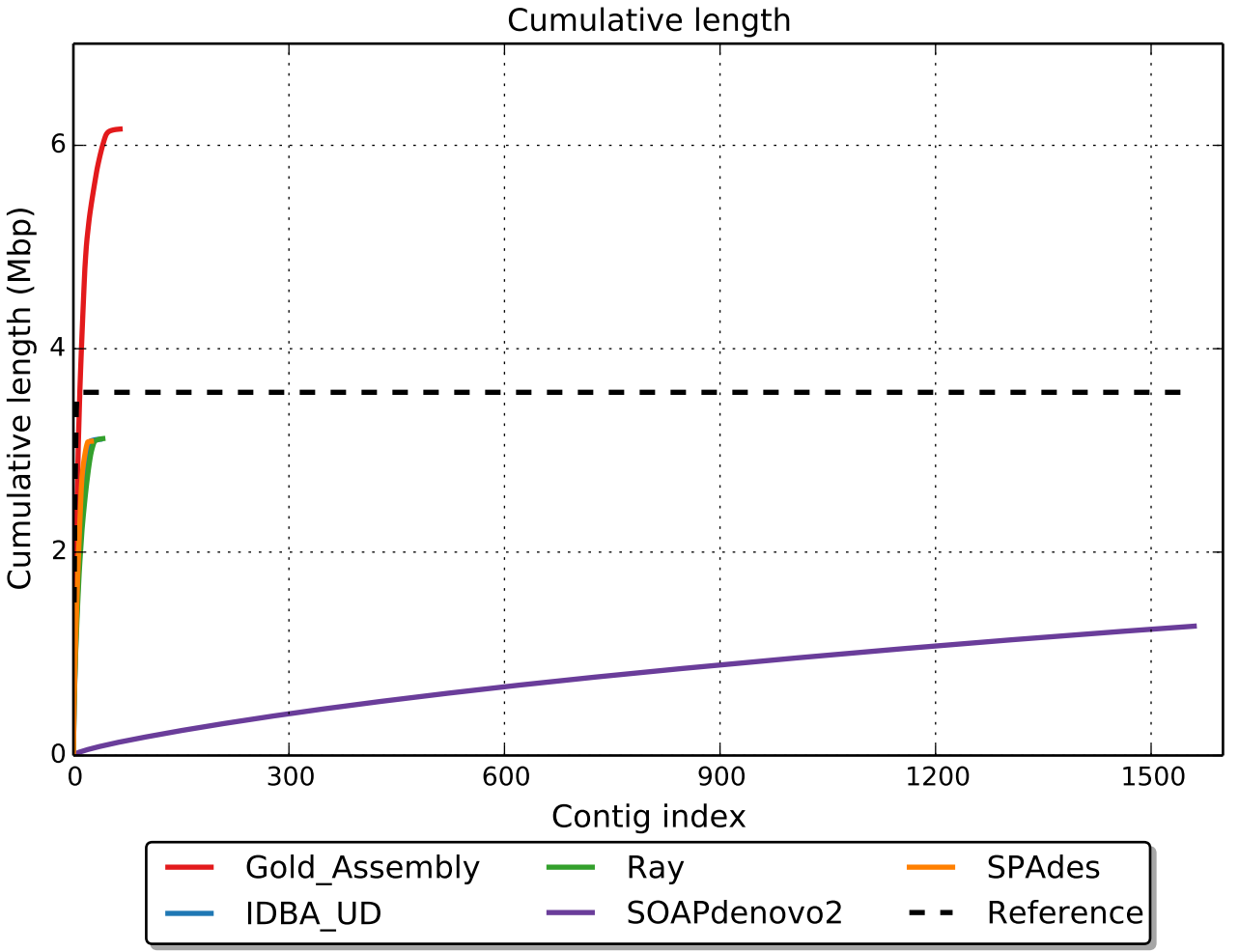
Unaligned report

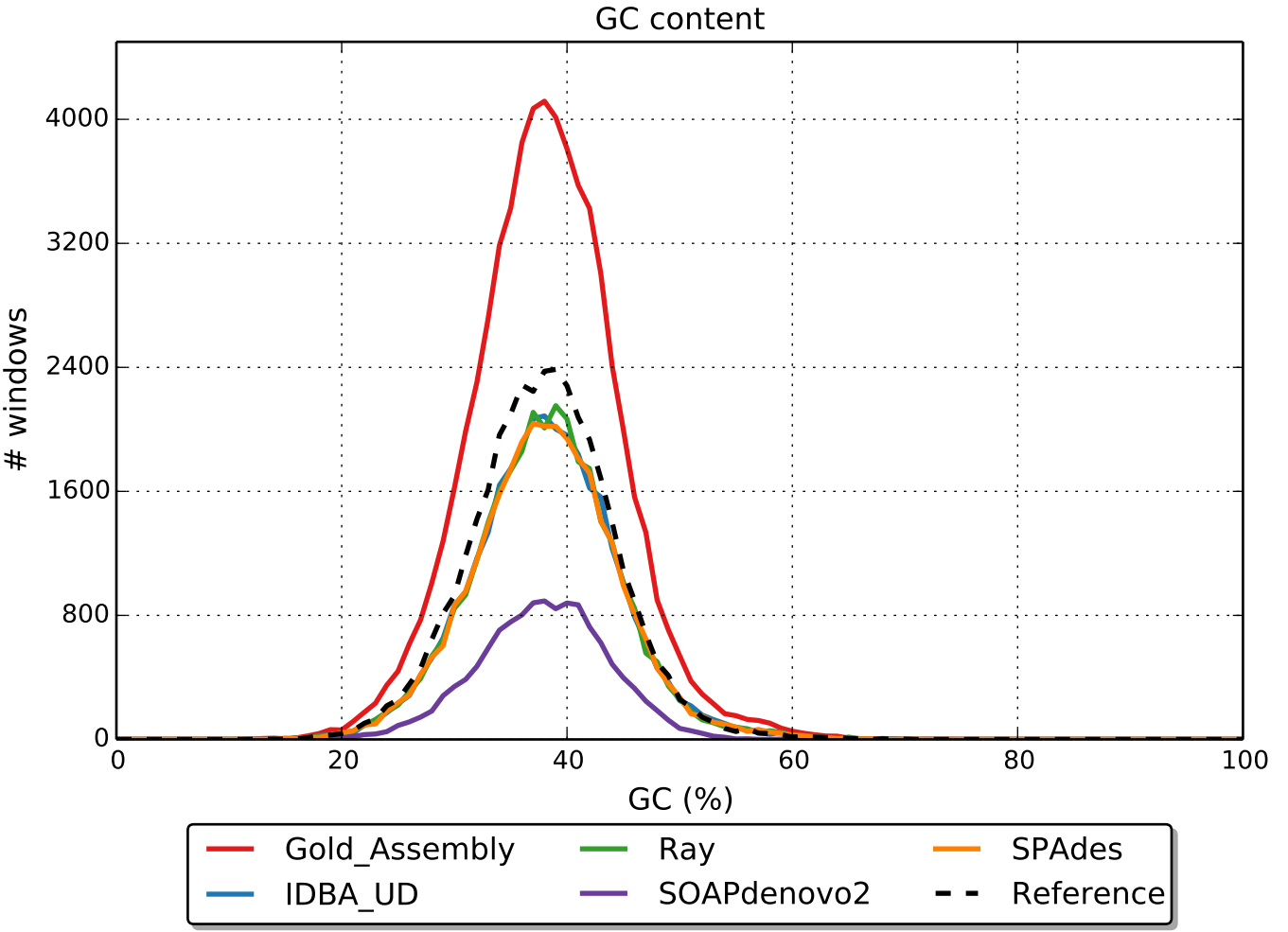
	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0	0
Fully unaligned length	0	0	0	0	0
# partially unaligned contigs	10	5	9	47	1
# with misassembly	2	1	2	1	0
# both parts are significant	4	3	5	3	1
Partially unaligned length	116960	72382	101445	12943	36207
# N's	0	0	37	0	0

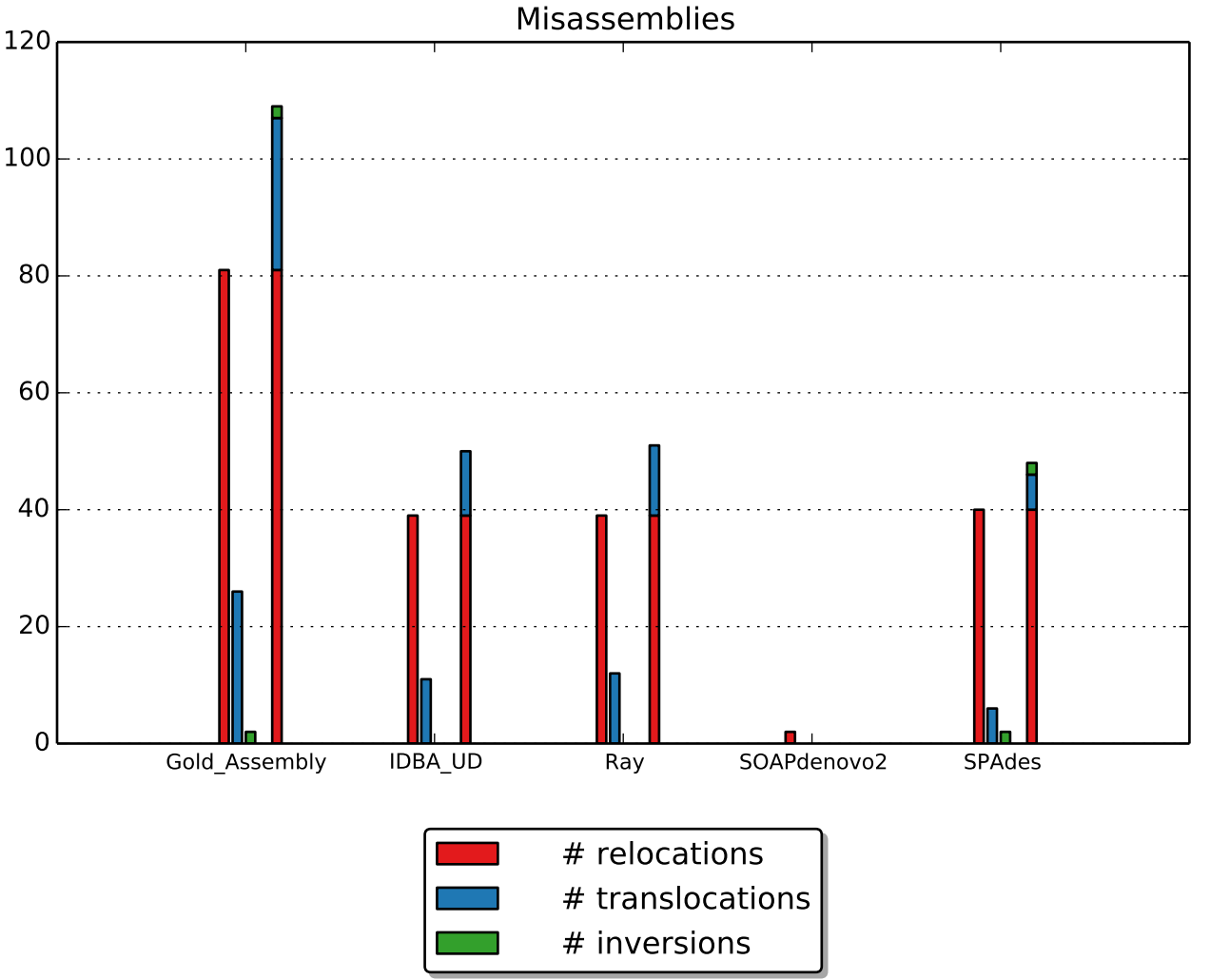
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

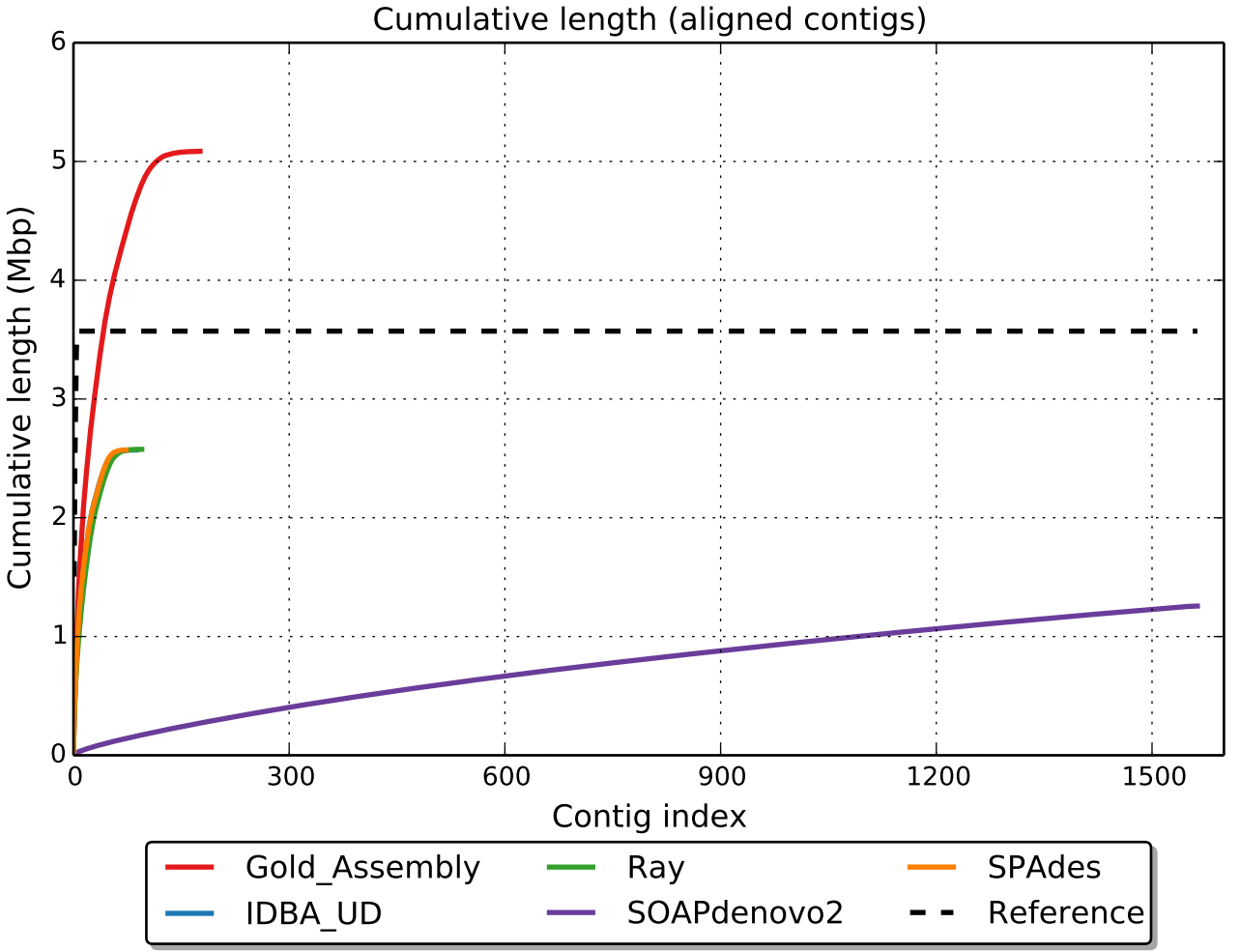

Nx
Contig length (kbp)
600
400
200
0
0
20
40
60
80
100
x
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes

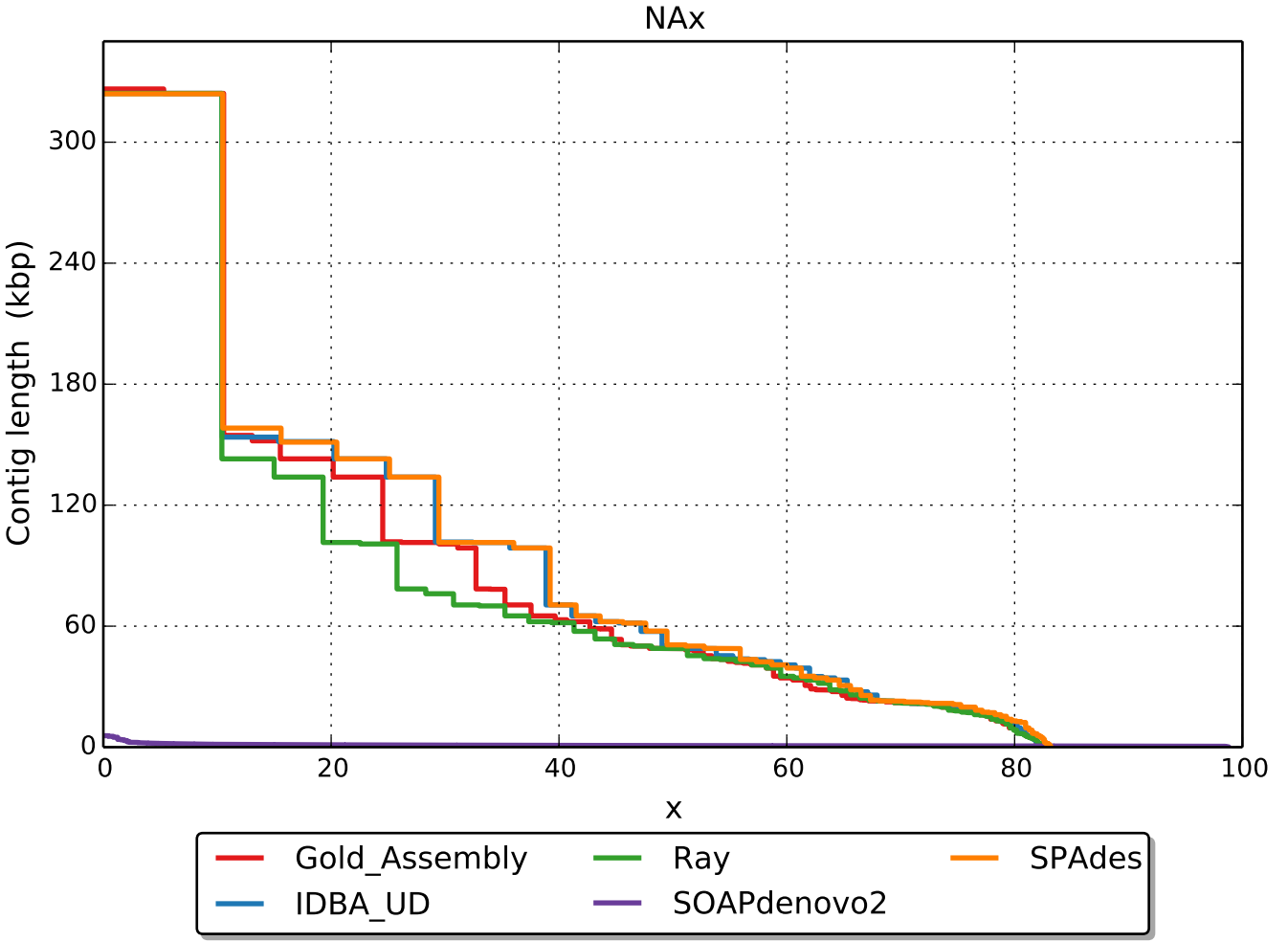

NGx
Contig length (kbp)
600
400
200
0
0
20
40
60
80
100
x
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes

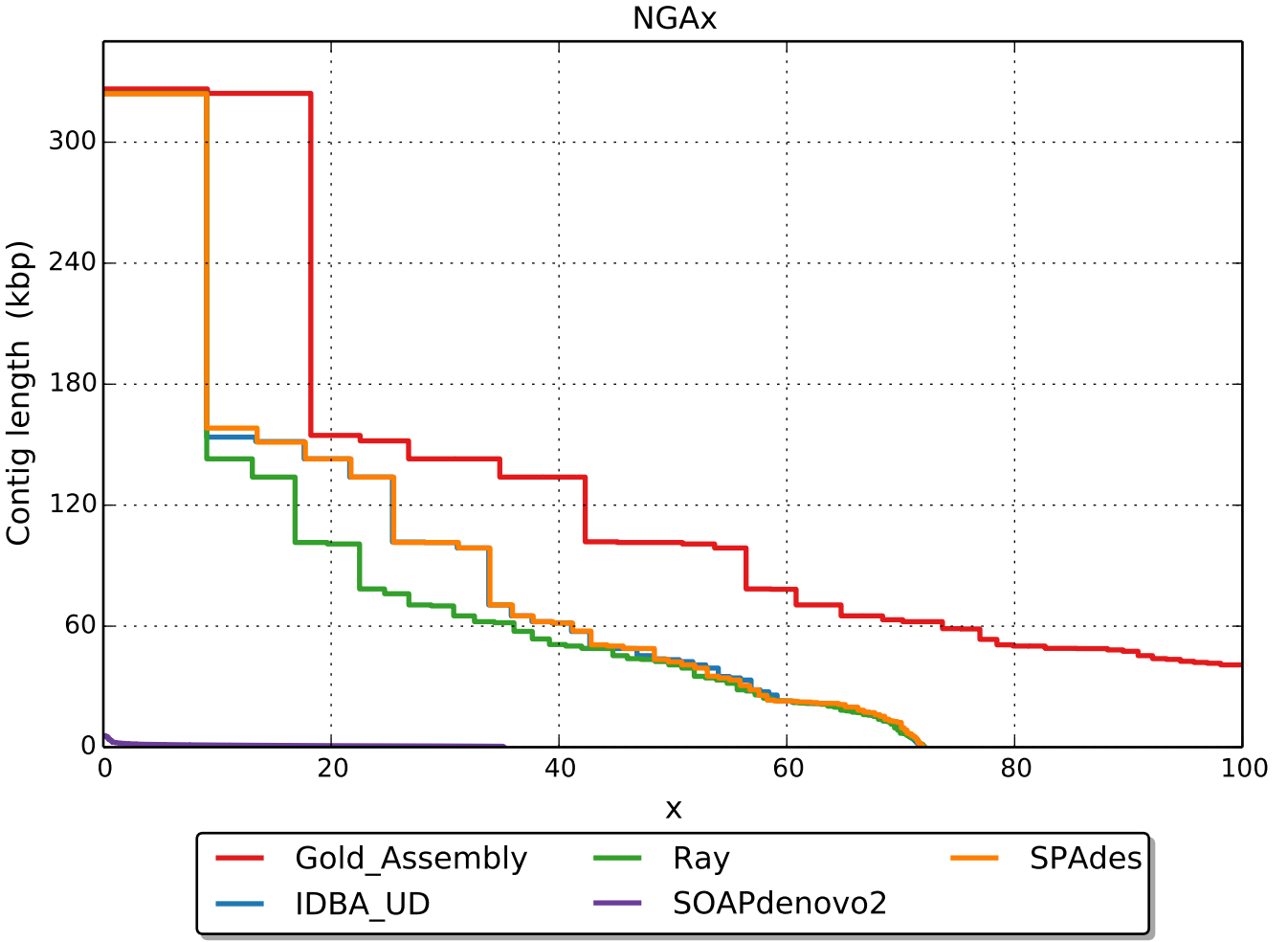

Cumulative length
Cumulative length (Mbp)
0
2
4
6
0
300
600
900
1200
1500
Contig index
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference

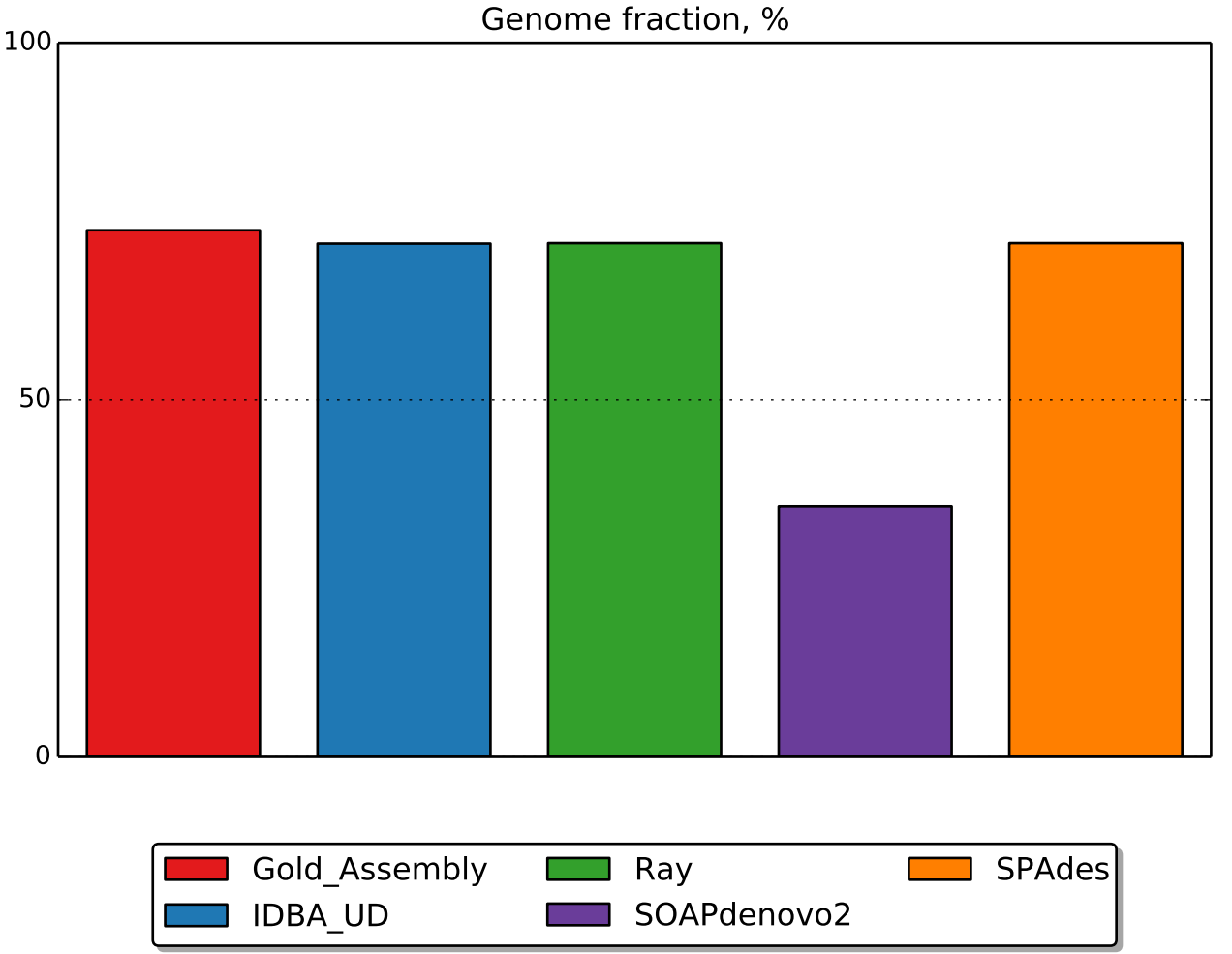

GC content
windows
GC (%)
0
800
1600
2400
3200
4000
0
20
40
60
80
100
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


Misassemblies
120
100
80
60
40
20
0
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes
relocations
translocations
inversions


Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
6
0
300
600
900
1200
1500
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


NAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes


NGAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes


Genome fraction, %
100
50
0
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes