Report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	40	46	749	346	50
# contigs (>= 5000 bp)	29	34	175	193	34
# contigs (>= 10000 bp)	22	25	20	106	27
# contigs (>= 25000 bp)	20	22	0	15	25
# contigs (>= 50000 bp)	19	19	0	1	18
Total length (>= 1000 bp)	3050805	3040675	2779237	3001846	3030044
Total length (>= 5000 bp)	3025413	3013246	1302167	2579509	2994791
Total length (>= 10000 bp)	2974649	2949590	270793	1940843	2947523
Total length (>= 25000 bp)	2944333	2898386	0	538501	2919247
Total length (>= 50000 bp)	2908839	2791119	0	61821	2669127
# contigs	43	55	857	387	69
Largest contig	901072	552496	22803	61821	506133
Total length	3053013	3047484	2861002	3032419	3043661
Reference length	3055484	3055484	3055484	3055484	3055484
GC (%)	35.37	35.36	35.34	35.35	35.35
Reference GC (%)	35.37	35.37	35.37	35.37	35.37
N50	164828	164828	4677	13588	146375
NG50	164828	164828	4298	13359	146375
N75	103670	75273	2743	7472	106768
NG75	103670	75273	2461	7407	106768
L50	5	6	202	70	7
LG50	5	6	224	71	7
L75	11	12	403	145	13
LG75	11	12	460	147	13
# misassemblies	0	13	2	4	14
# misassembled contigs	0	10	2	4	9
Misassembled contigs length	0	979518	6388	14824	782785
# local misassemblies	0	3	9	1	4
# structural variations	0	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 0 part	0 + 1 part	0 + 3 part	0 + 2 part
Unaligned length	0	0	84	171	714
Genome fraction (%)	99.919	99.725	91.338	99.125	99.536
Duplication ratio	1.000	1.000	1.025	1.001	1.001
# N's per 100 kbp	0.00	0.00	31.14	12.17	12.75
# mismatches per 100 kbp	0.00	3.35	1.04	23.01	32.85
# indels per 100 kbp	0.00	0.07	0.11	3.90	0.66
Largest alignment	901072	552496	22803	61821	505955
NA50	164828	125833	4674	13588	129815
NGA50	164828	125833	4298	13359	129815
NA75	103670	69524	2743	7472	74927
NGA75	103670	69524	2461	7407	74927
LA50	5	7	202	70	8
LGA50	5	7	224	71	8
LA75	11	15	404	145	15
LGA75	11	15	460	147	15

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

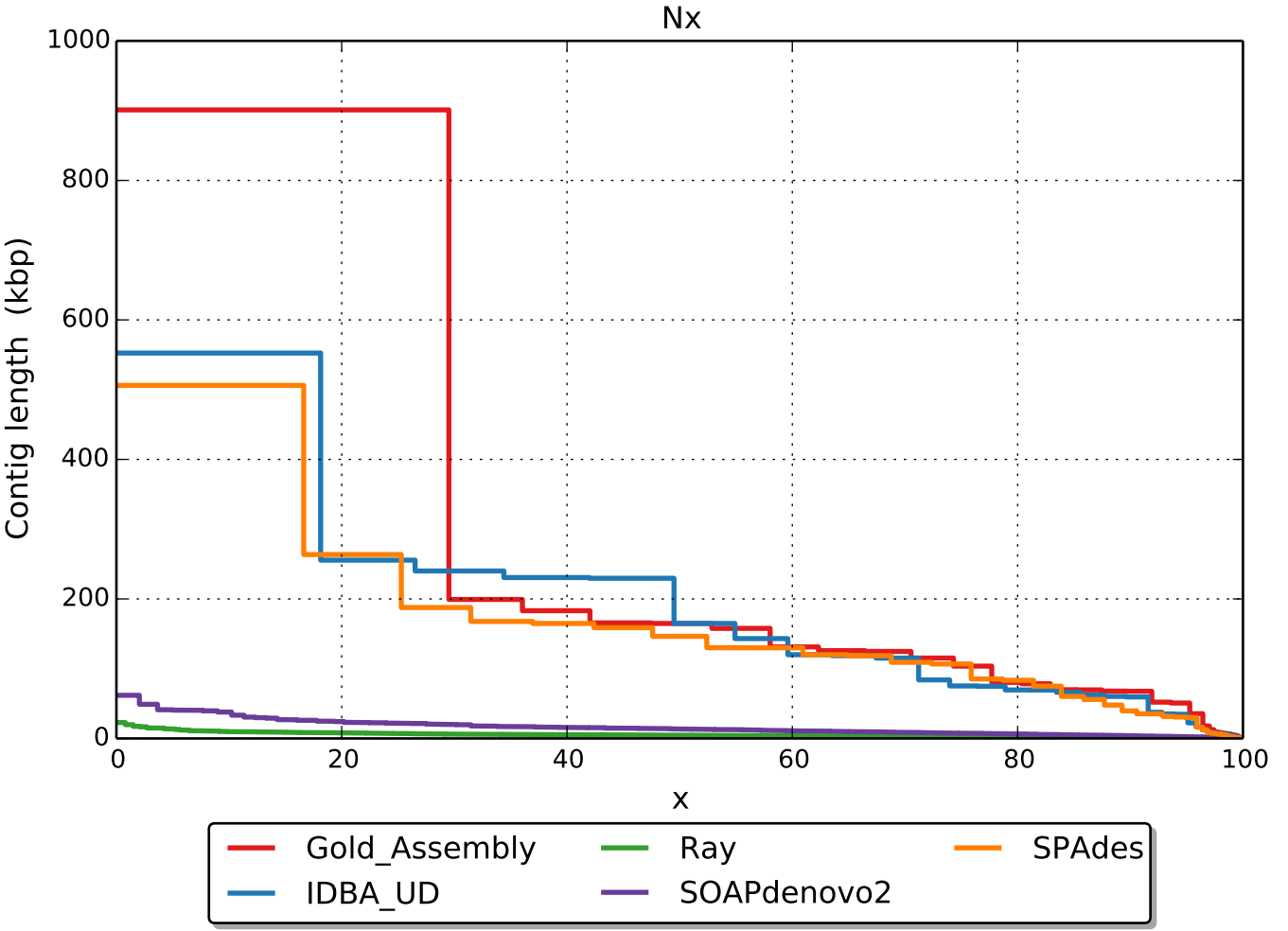
	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	13	2	4	14
# relocations	0	0	0	0	1
# translocations	0	13	2	4	13
# inversions	0	0	0	0	0
# possibly misassembled contigs	0	0	0	0	0
# misassembled contigs	0	10	2	4	9
Misassembled contigs length	0	979518	6388	14824	782785
# local misassemblies	0	3	9	1	4
# structural variations	0	0	0	0	0
# mismatches	0	102	29	697	999
# indels	0	2	3	118	20
# short indels	0	2	0	56	14
# long indels	0	0	3	62	6
Indels length	0	5	154	841	207

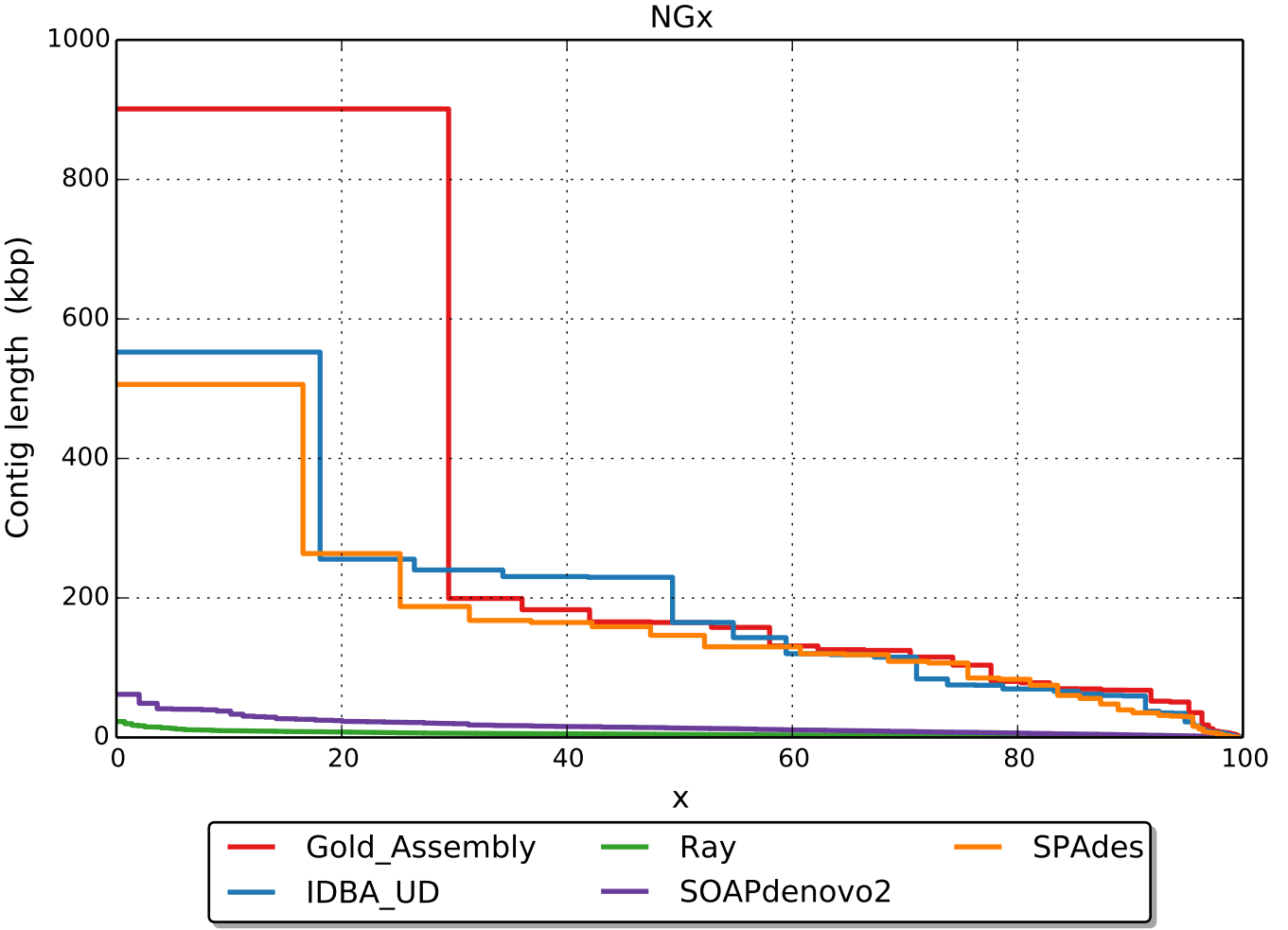
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

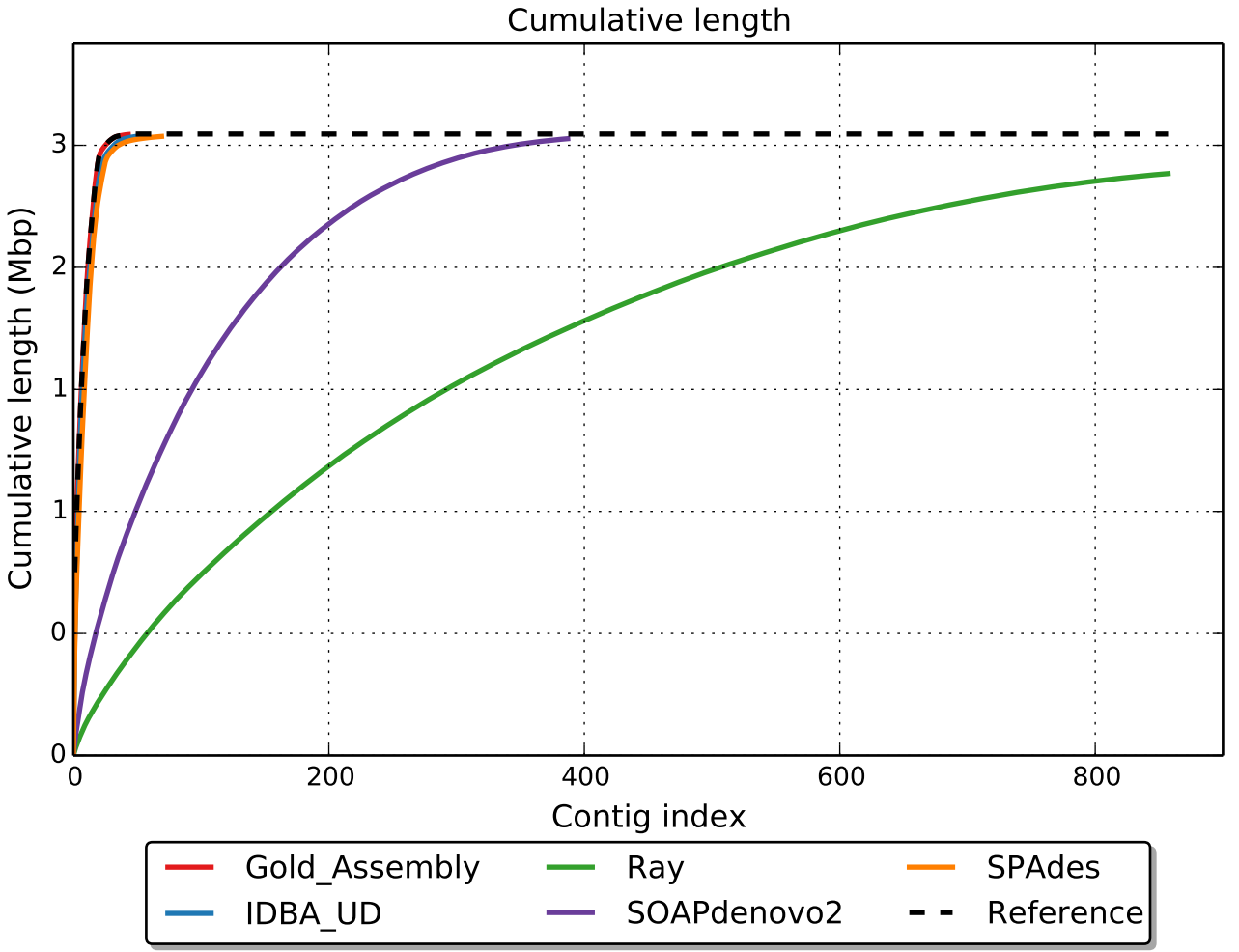
Unaligned report

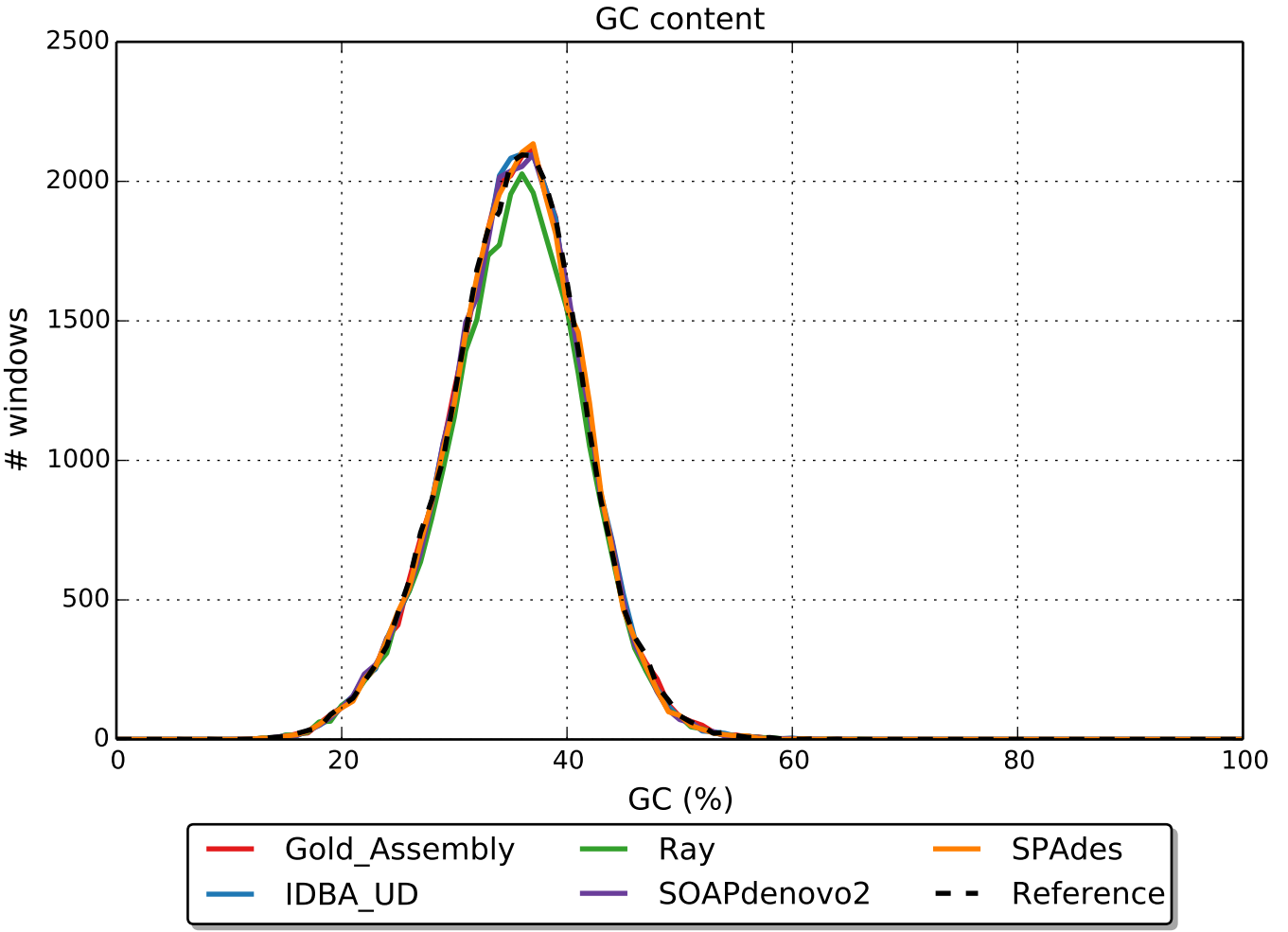
	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0	0
Fully unaligned length	0	0	0	0	0
# partially unaligned contigs	0	0	1	3	2
# with misassembly	0	0	0	0	0
# both parts are significant	0	0	0	0	0
Partially unaligned length	0	0	84	171	714
# N's	0	0	891	369	388

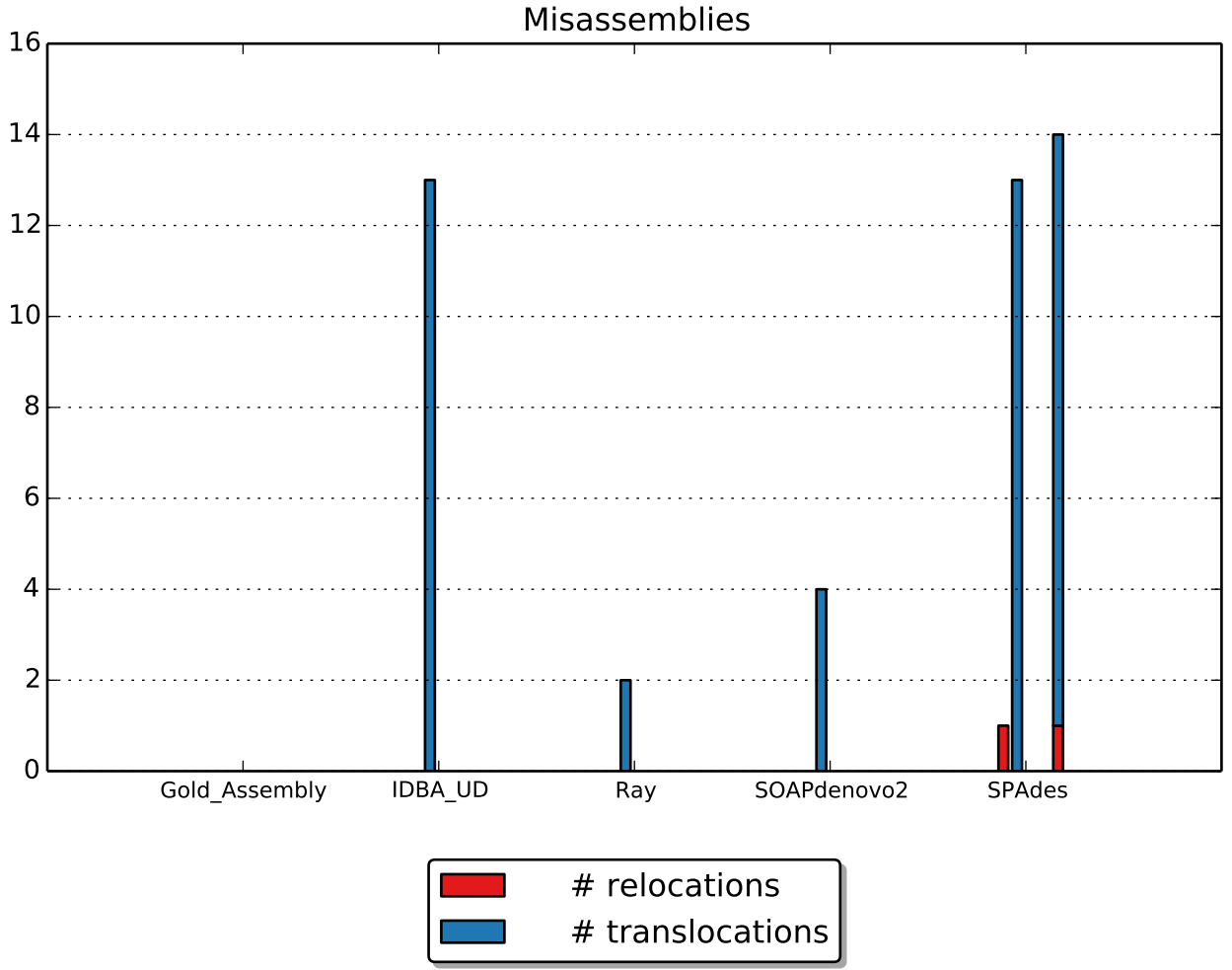
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

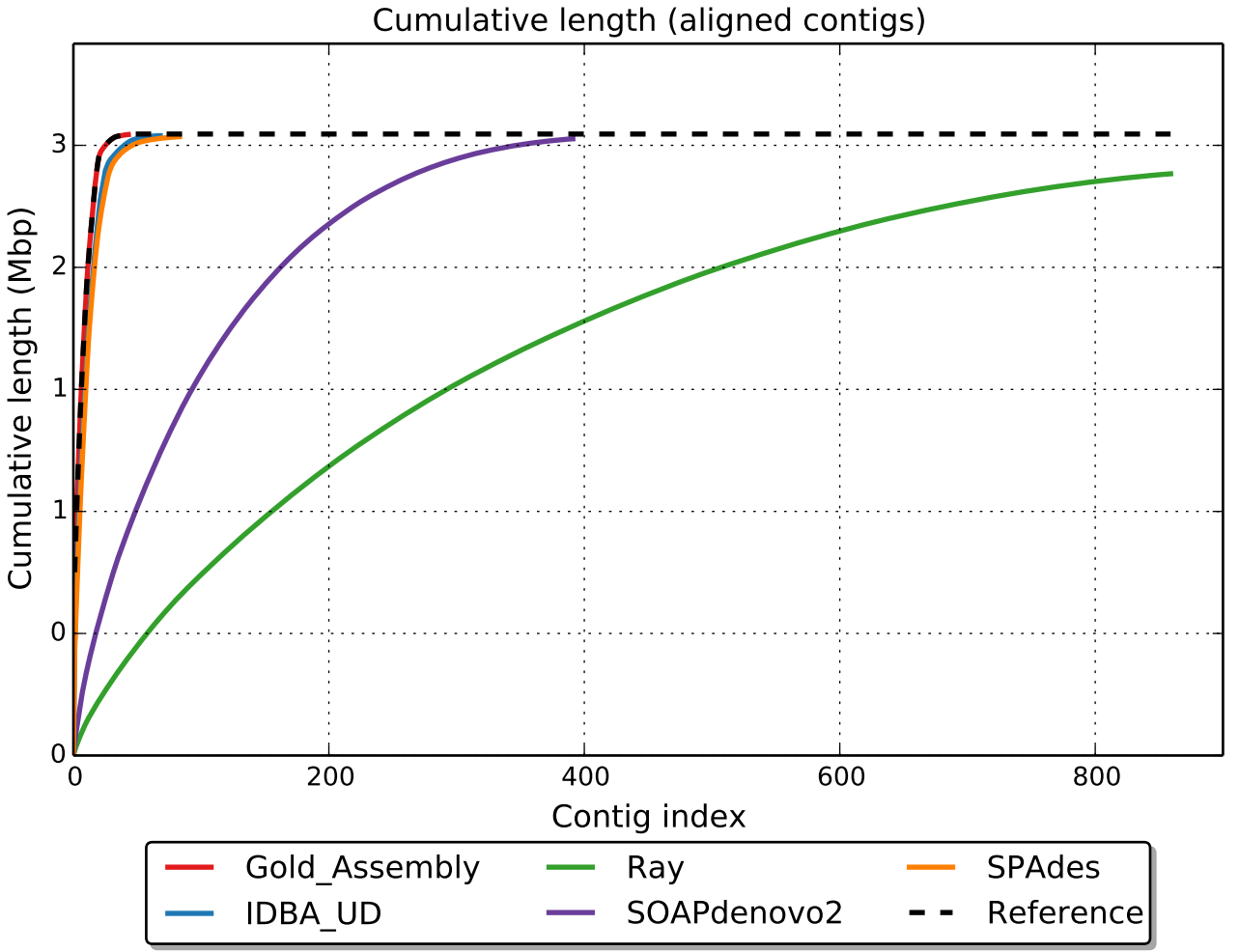

Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes

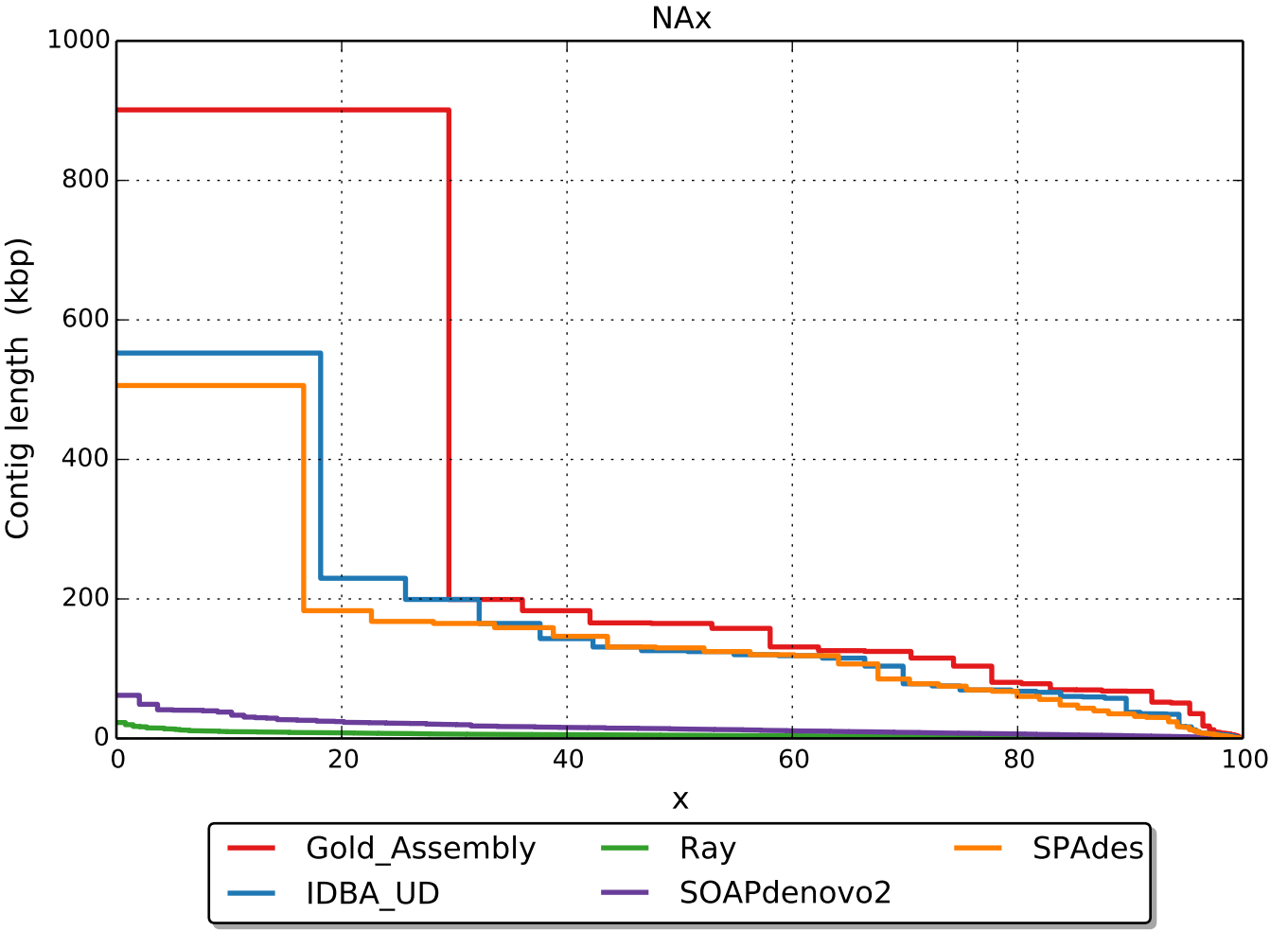

NGx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes

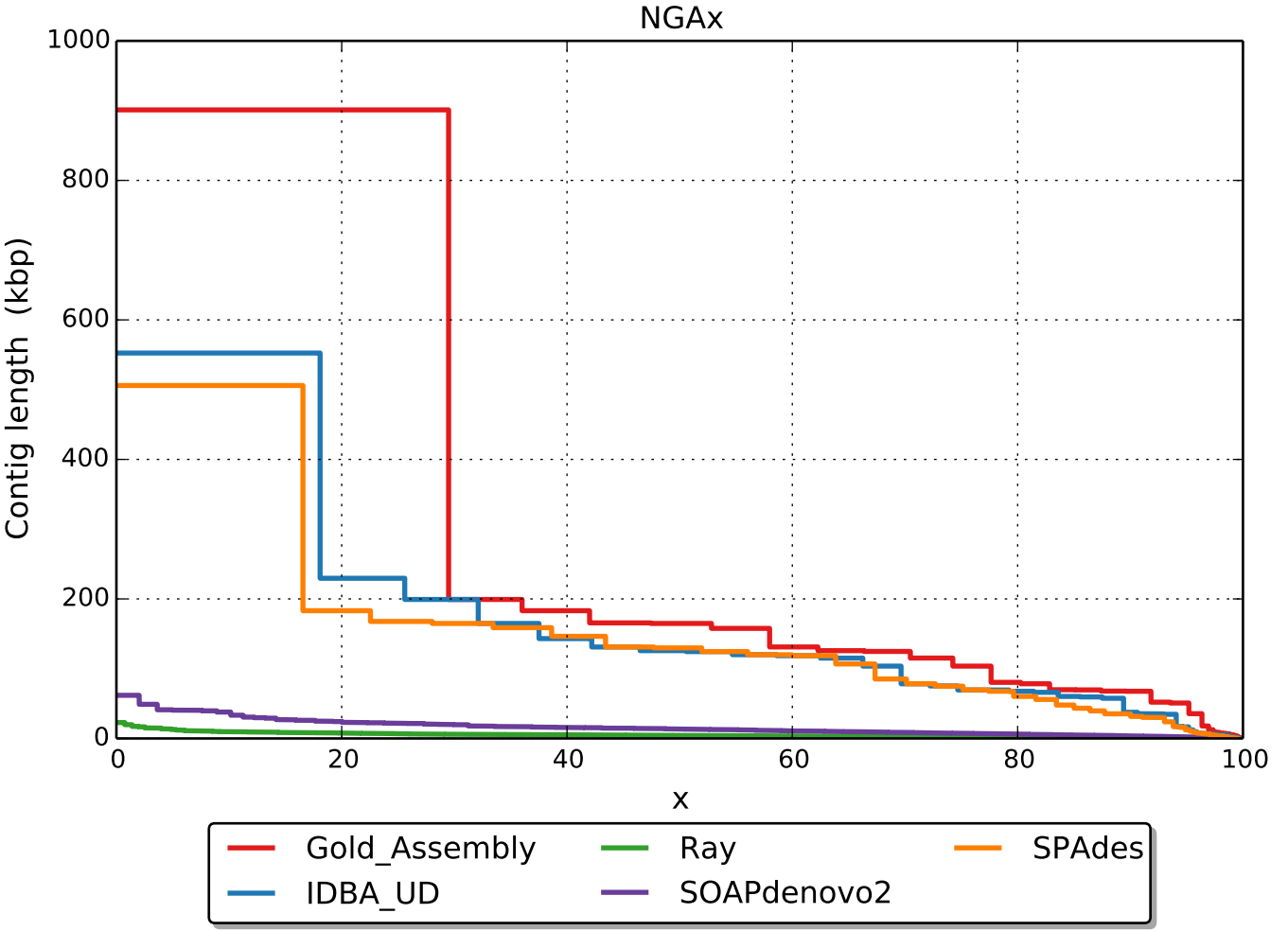

Cumulative length
Cumulative length (Mbp)
0
1
1
2
3
0
200
400
600
800
Contig index
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference

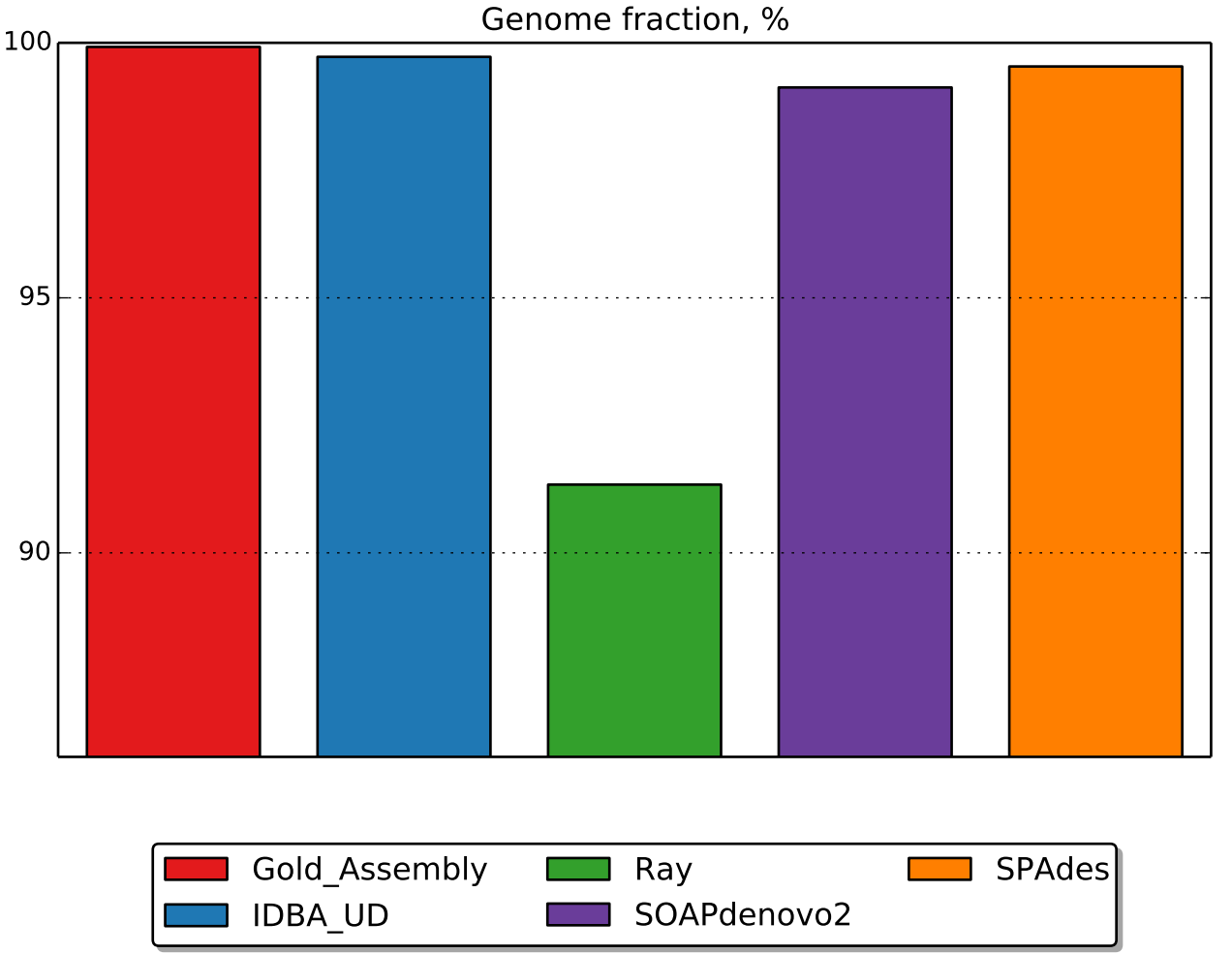

GC content
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


Misassemblies
16
14
12
10
8
6
4
2
0
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes
relocations
translocations


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
1
2
3
0
200
400
600
800
Contig index
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


NAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes


NGAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes


Genome fraction, %
100
95
90
Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes