Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	293	46	187	202
# contigs (>= 5000 bp)	42	12	9	41
# contigs (>= 10000 bp)	21	6	0	17
# contigs (>= 25000 bp)	8	4	0	8
# contigs (>= 50000 bp)	0	1	0	3
Total length (>= 1000 bp)	1104673	286072	410198	1084402
Total length (>= 5000 bp)	598213	227109	65002	762053
Total length (>= 10000 bp)	451205	184422	0	601035
Total length (>= 25000 bp)	273587	152469	0	469413
Total length (>= 50000 bp)	0	53450	0	298762
# contigs	541	110	480	357
Largest contig	44433	53450	9065	162985
Total length	1287925	328857	611581	1191257
Reference length	5622644	5622644	5622644	5622644
GC (%)	42.01	43.10	41.05	41.78
Reference GC (%)	42.33	42.33	42.33	42.33
N50	4318	17932	1559	10706
N75	1609	2616	847	2560
L50	52	5	102	17
L75	184	18	239	78
# misassemblies	8	2	0	6
# misassembled contigs	7	2	0	5
Misassembled contigs length	92801	90178	0	189136
# local misassemblies	3	23	136	4
# structural variations	0	0	0	0
# unaligned contigs	0 + 28 part	0 + 6 part	0 + 17 part	0 + 42 part
Unaligned length	94570	29511	6715	210254
Genome fraction (%)	20.601	4.703	10.583	16.908
Duplication ratio	1.030	1.132	1.016	1.032
# N's per 100 kbp	111.81	1150.04	1163.54	335.61
# mismatches per 100 kbp	1082.41	1865.37	967.64	1327.61
# indels per 100 kbp	39.45	46.13	14.96	51.86
Largest alignment	39202	28223	9065	51687
NA50	2887	3925	1516	3584
NGA50	-	-	-	-
NA75	1056	660	800	706
LA50	85	13	104	59
LA75	275	80	248	262

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

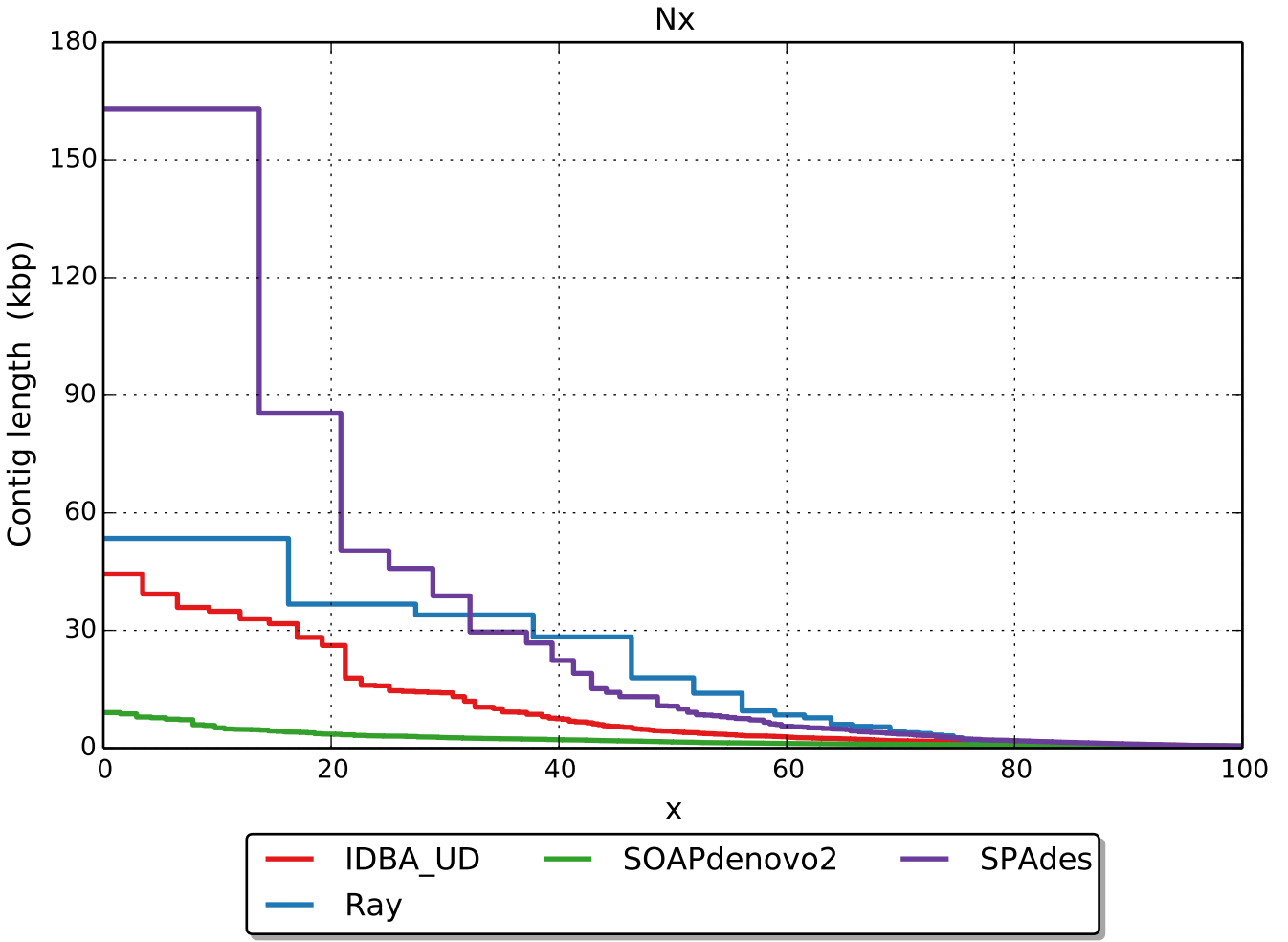
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	8	2	0	6
# relocations	7	1	0	5
# translocations	1	1	0	1
# inversions	0	0	0	0
# possibly misassembled contigs	13	7	2	24
# misassembled contigs	7	2	0	5
Misassembled contigs length	92801	90178	0	189136
# local misassemblies	3	23	136	4
# structural variations	0	0	0	0
# mismatches	12538	4933	5758	12621
# indels	457	122	89	493
# short indels	407	112	85	412
# long indels	50	10	4	81
Indels length	1224	297	139	1566

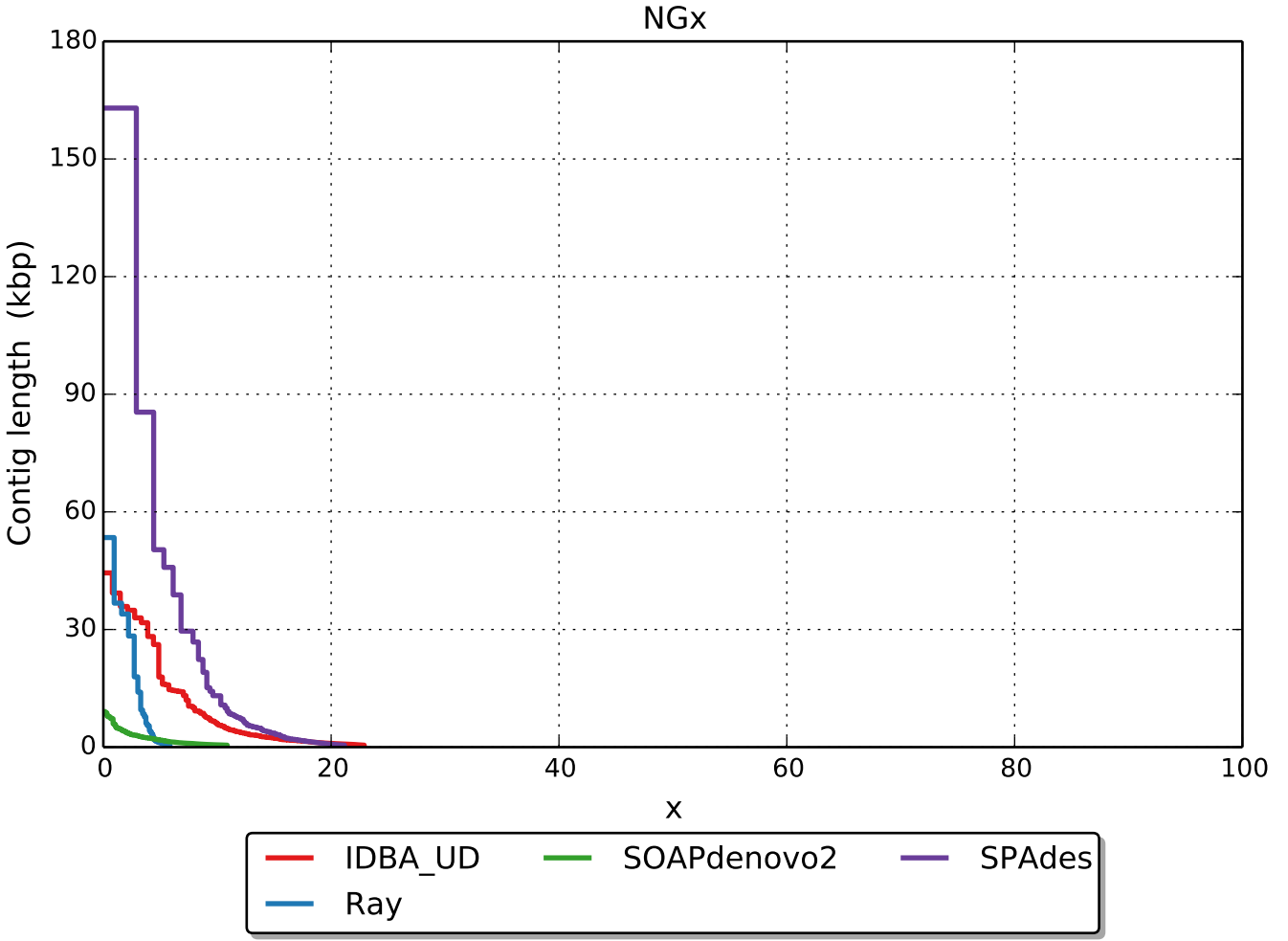
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

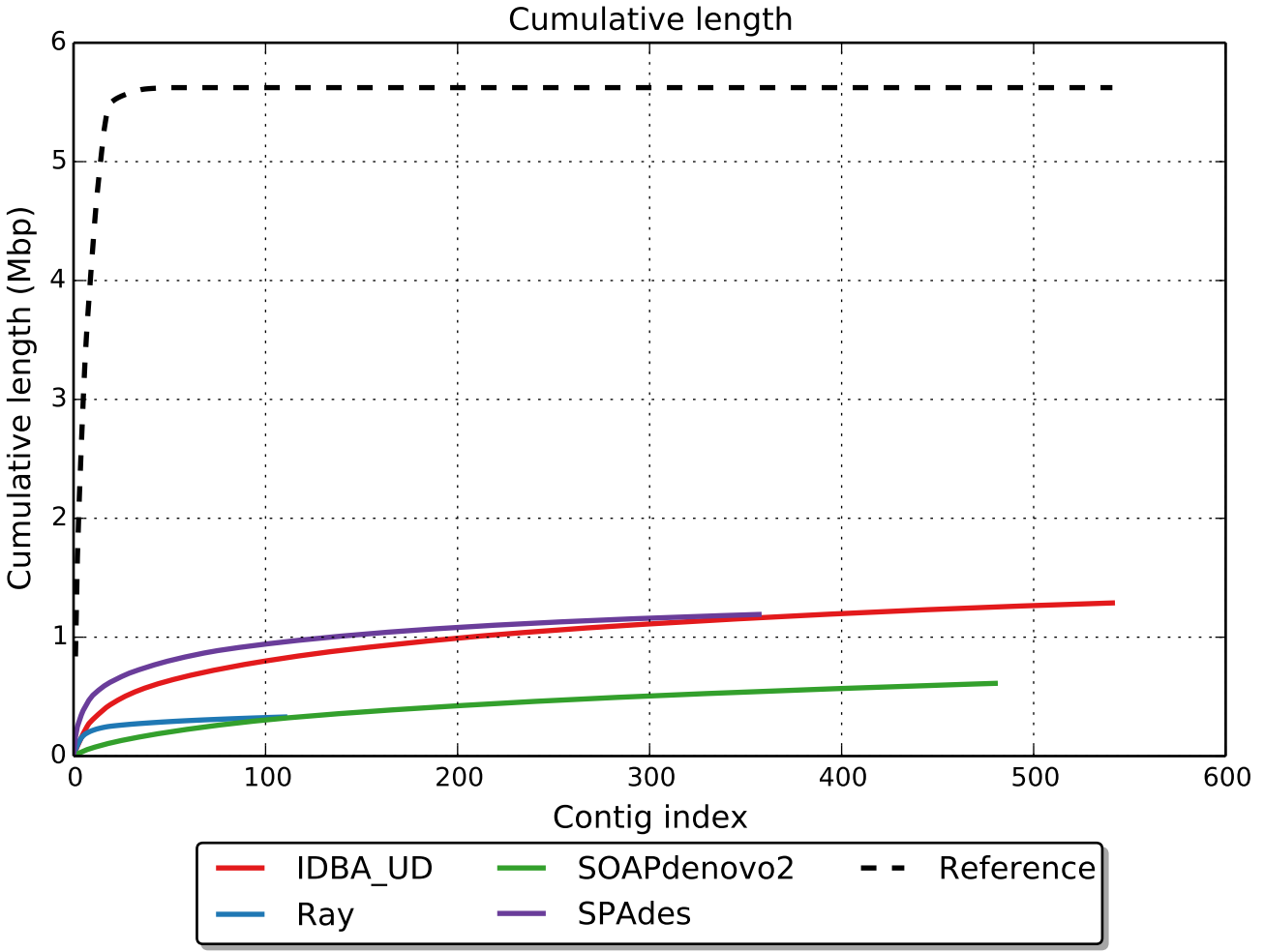
Unaligned report

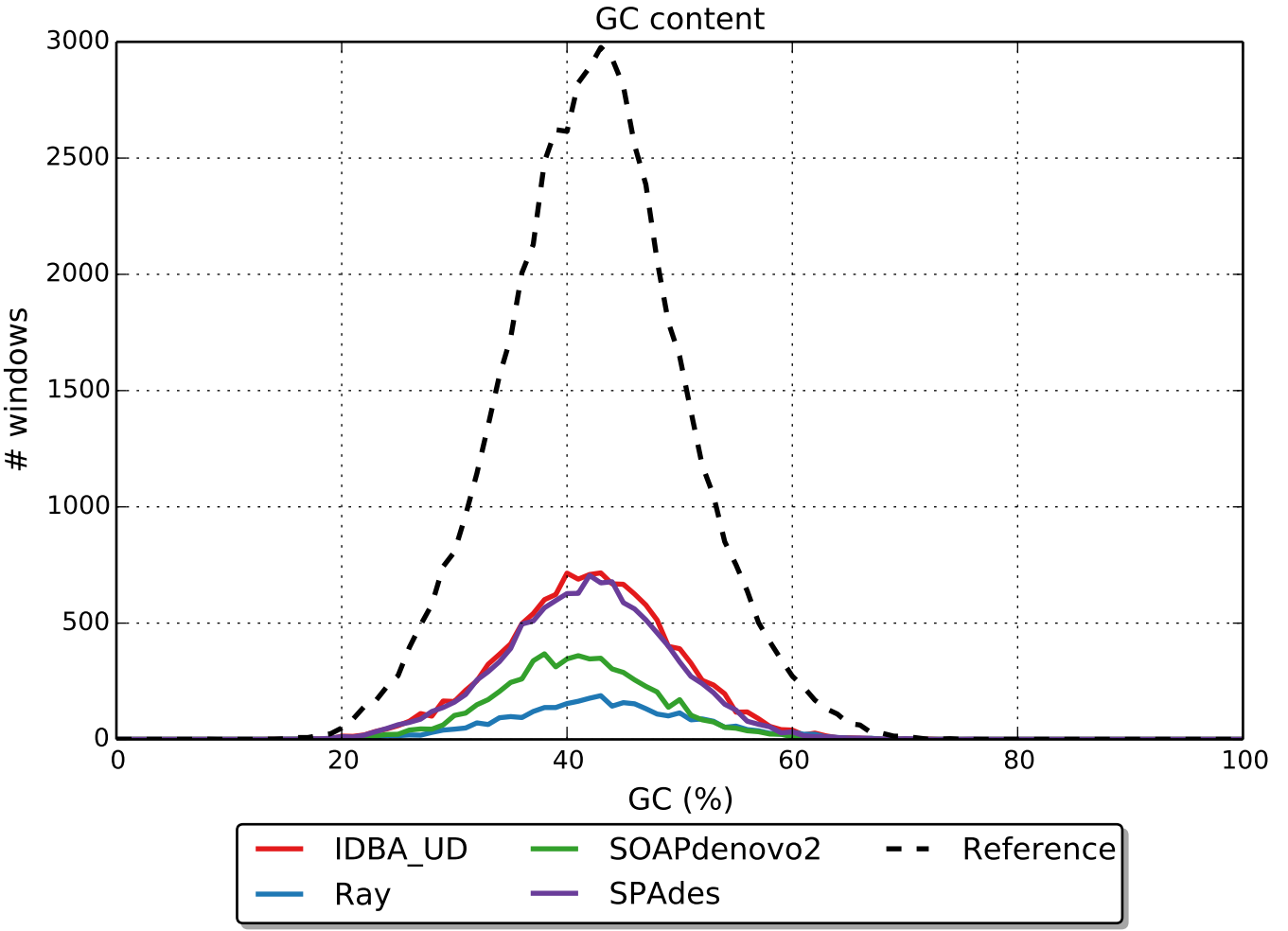
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	28	6	17	42
# with misassembly	1	3	3	4
# both parts are significant	9	4	2	19
Partially unaligned length	94570	29511	6715	210254
# N's	1440	3782	7116	3998

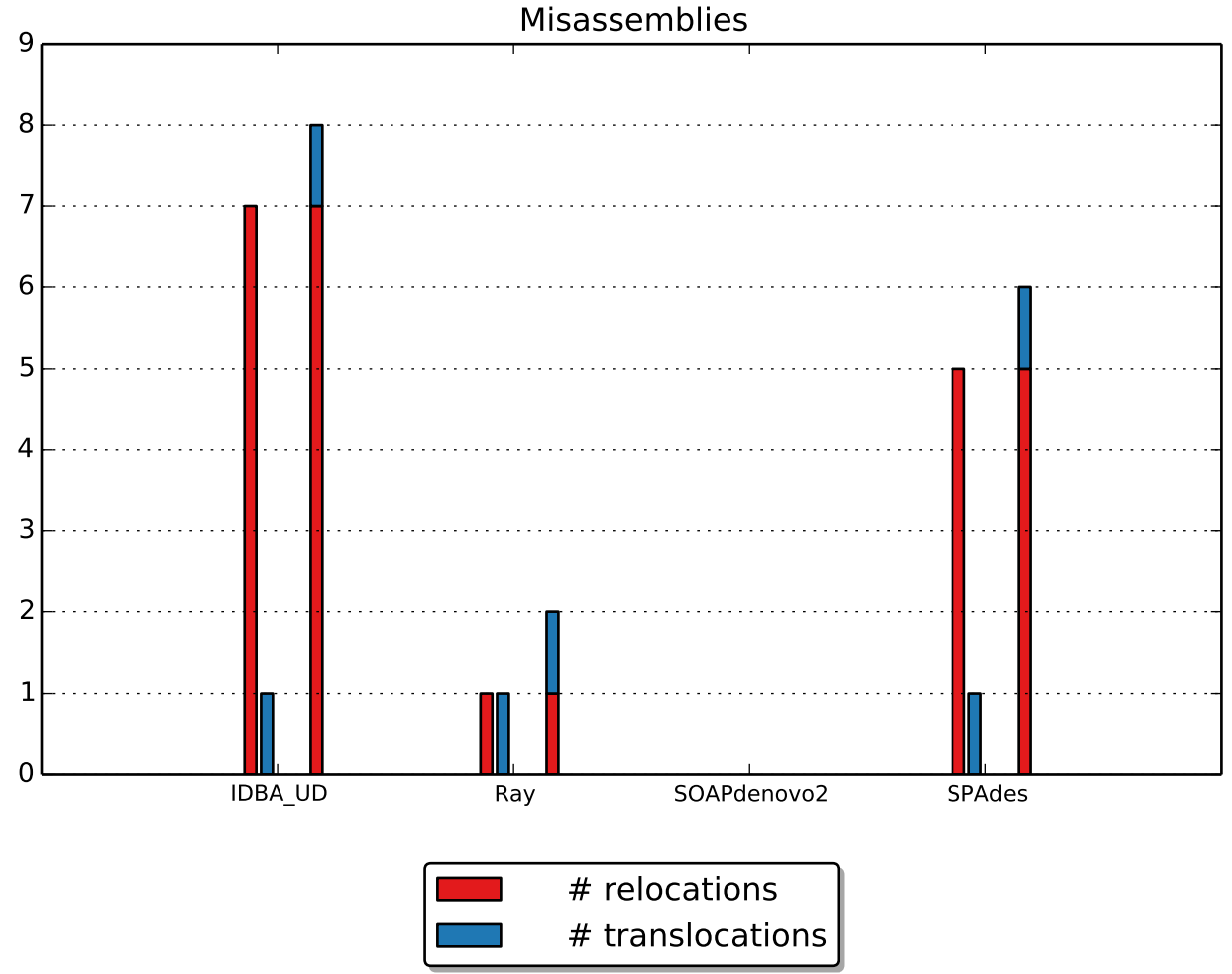
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

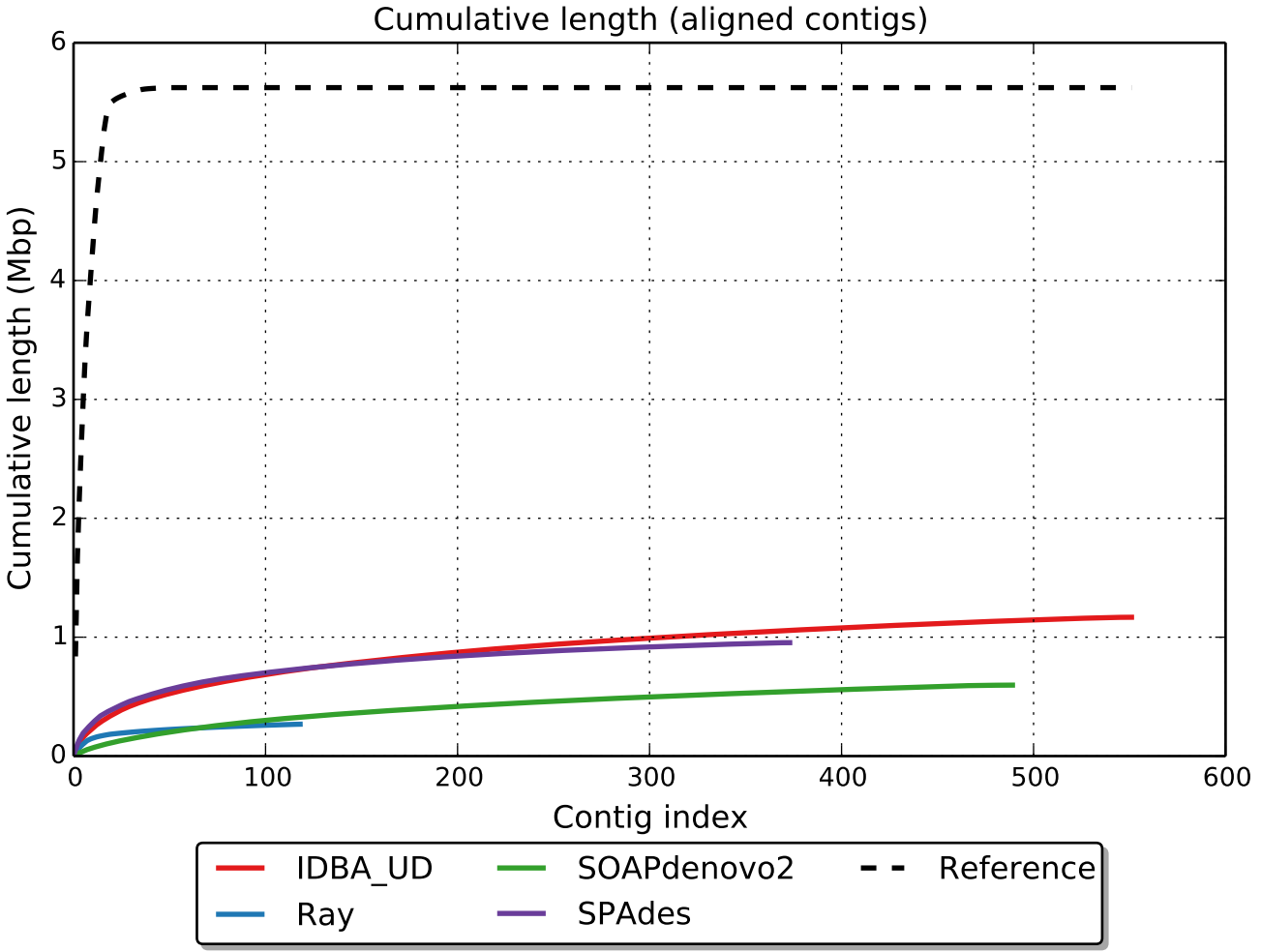

Nx
180
150
120
90
60
30
0
Contig length (kbp)
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray

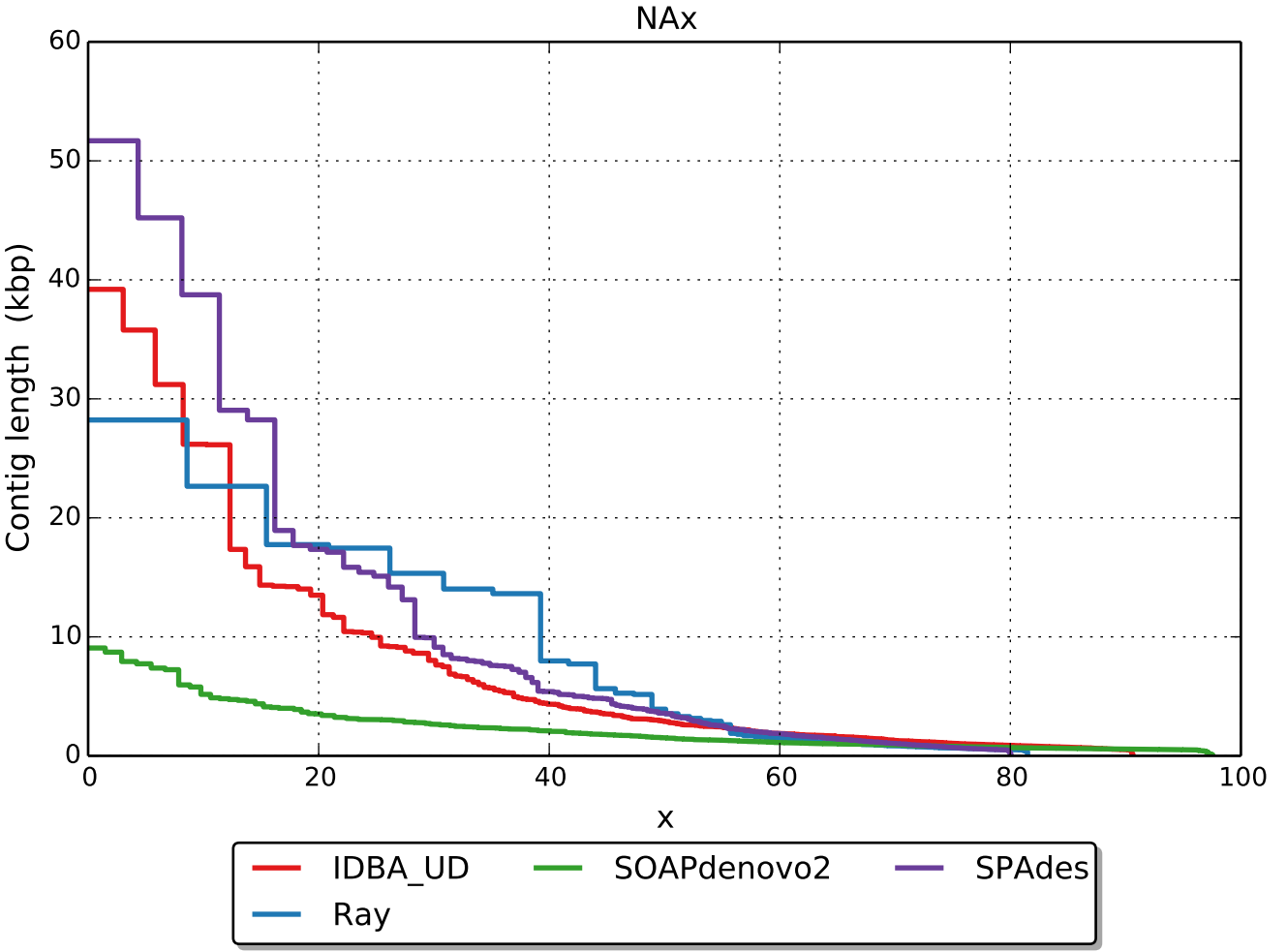

NGx
Contig length (kbp)
180
150
120
90
60
30
0
0
20
40
60
80
100
x
IDBA_UD
SOAPdenovo2
SPAdes
Ray

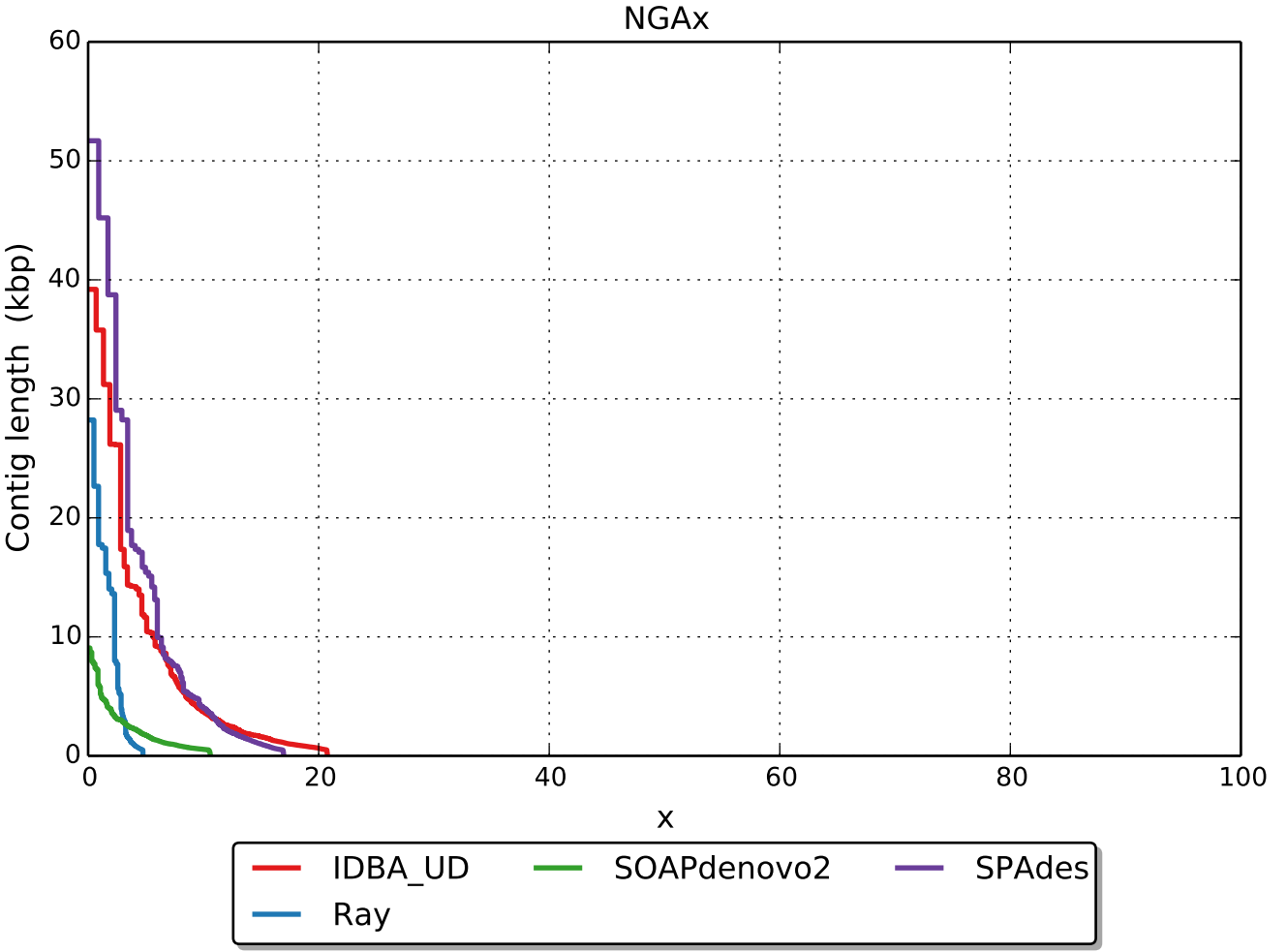

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
6
0
100
200
300
400
500
600
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference

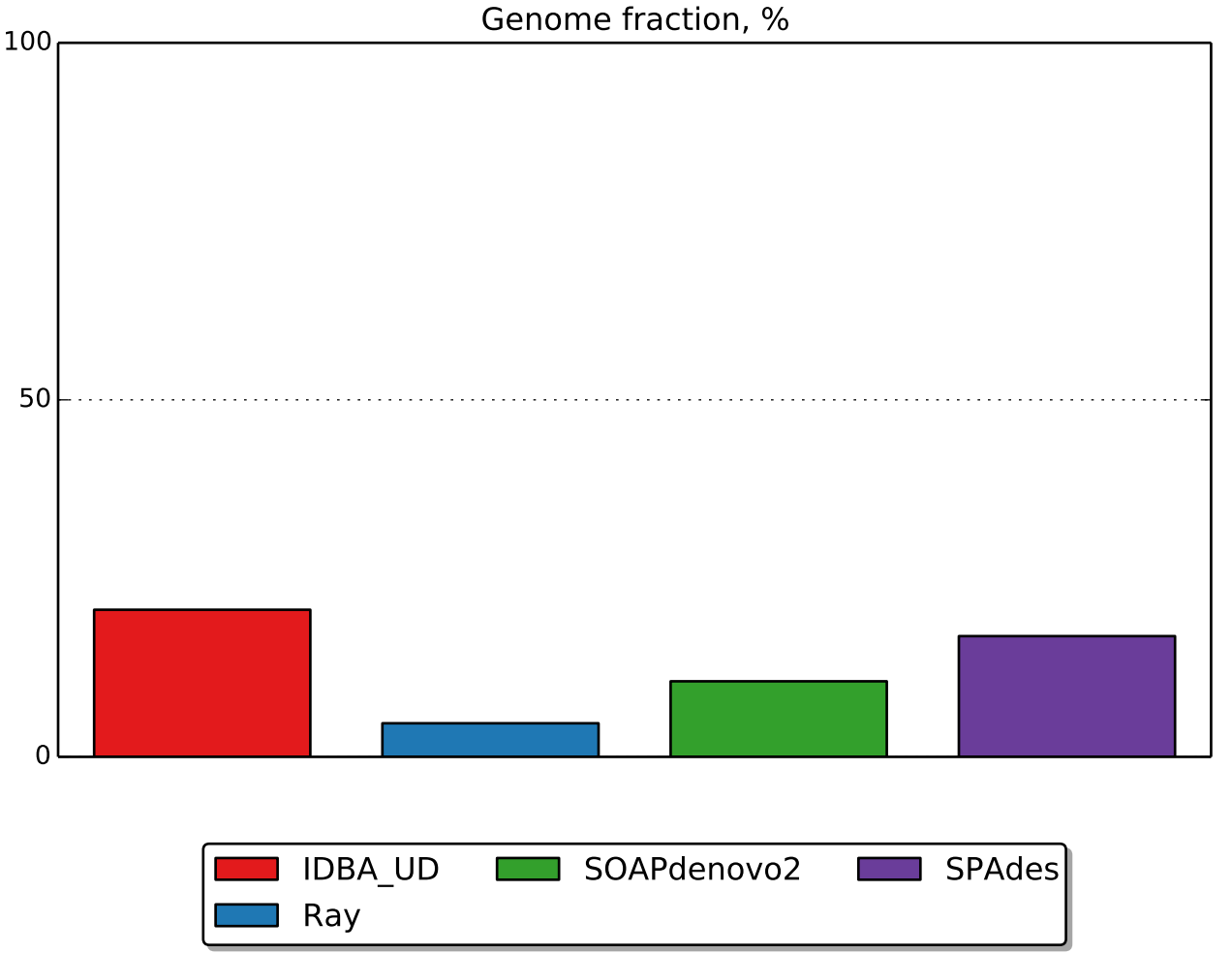

GC content
windows
GC (%)
0
500
1000
1500
2000
2500
3000
0
20
40
60
80
100
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


Misassemblies
9
8
7
6
5
4
3
2
1
0
IDBA_UD
Ray
SOAPdenovo2
SPAdes
relocations
translocations


Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
6
0
100
200
300
400
500
600
IDBA_UD
Ray
SOAPdenovo2
SPAdes
Reference


NAx
Contig length (kbp)
x
0
10
20
30
40
50
60
0
20
40
60
80
100
IDBA_UD
SOAPdenovo2
SPAdes
Ray


NGAx
Contig length (kbp)
x
0
10
20
30
40
50
60
0
20
40
60
80
100
IDBA_UD
Ray
SOAPdenovo2
SPAdes


Genome fraction, %
100
50
0
IDBA_UD
Ray
SOAPdenovo2
SPAdes