

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	19	9	33	27
# contigs (>= 5000 bp)	5	3	2	6
# contigs (>= 10000 bp)	5	2	1	2
# contigs (>= 25000 bp)	0	1	0	1
# contigs (>= 50000 bp)	0	0	0	0
Total length (>= 1000 bp)	119844	60251	88438	118033
Total length (>= 5000 bp)	93417	47464	26077	79523
Total length (>= 10000 bp)	93417	38151	19780	49646
Total length (>= 25000 bp)	0	27618	0	35679
Total length (>= 50000 bp)	0	0	0	0
# contigs	55	12	61	106
Largest contig	24854	27618	19780	35679
Total length	143852	62642	107586	171434
Reference length	4102660	4102660	4102660	4102660
GC (%)	43.20	41.58	43.69	44.00
Reference GC (%)	45.93	45.93	45.93	45.93
N50	13308	10533	2375	3387
N75	1707	9313	1318	891
L50	4	2	11	8
L75	11	3	26	39
# misassemblies	1	0	0	0
# misassembled contigs	1	0	0	0
Misassembled contigs length	663	0	0	0
# local misassemblies	0	0	12	0
# structural variations	0	0	0	0
# unaligned contigs	0 + 28 part	0 + 8 part	0 + 12 part	0 + 53 part
Unaligned length	109716	53426	28352	110613
Genome fraction (%)	0.828	0.225	1.886	1.430
Duplication ratio	1.005	1.000	1.024	1.037
# N's per 100 kbp	91.07	2357.84	1820.87	2407.92
# mismatches per 100 kbp	1519.52	2365.71	747.07	2197.15
# indels per 100 kbp	41.23	43.41	19.39	85.23
Largest alignment	3936	2113	6297	8684
NA50	-	-	1318	-
NGA50	-	-	-	-
LA50	-	-	22	-

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

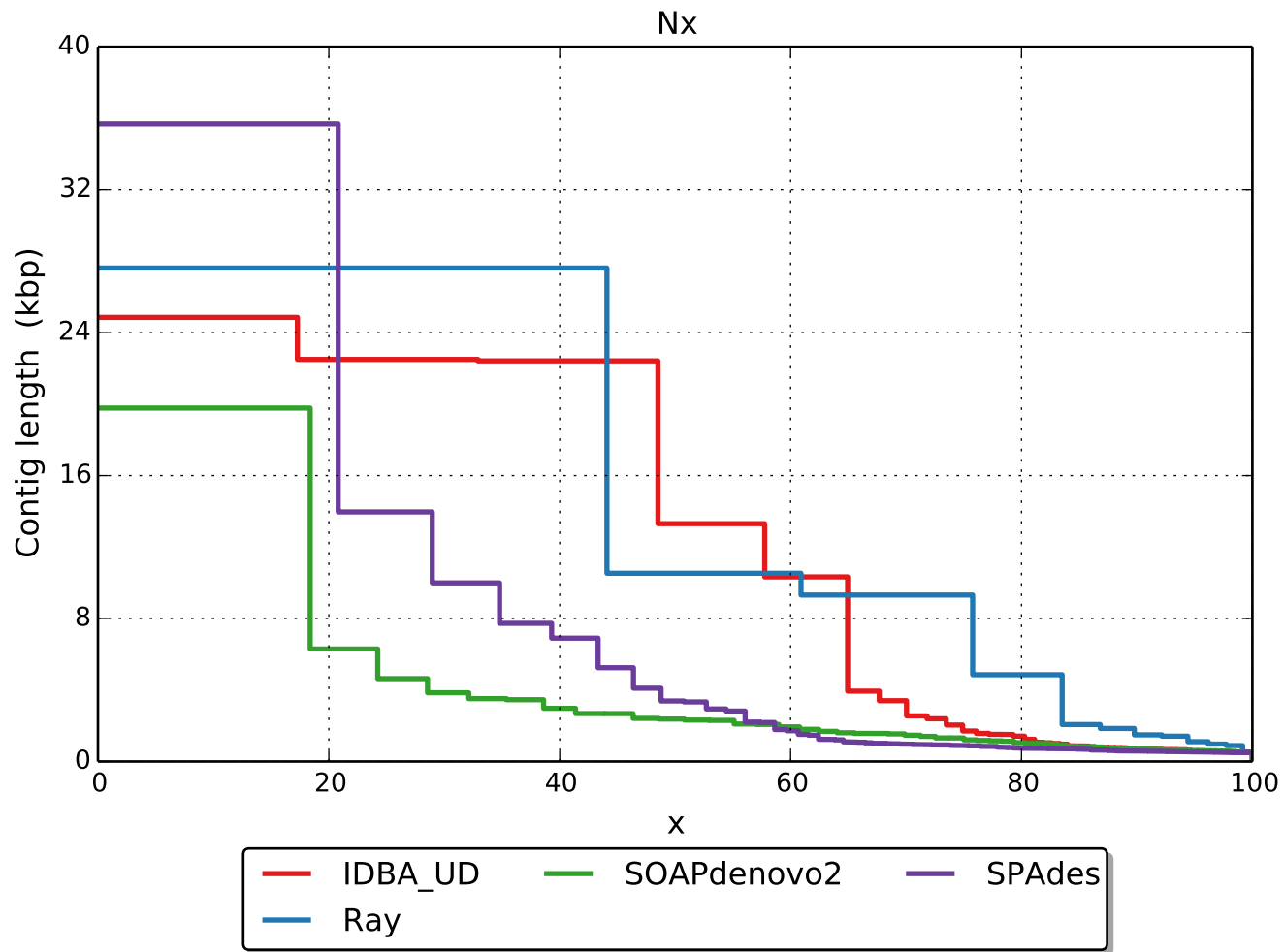
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	1	0	0	0
# relocations	1	0	0	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	2	1	3	4
# misassembled contigs	1	0	0	0
Misassembled contigs length	663	0	0	0
# local misassemblies	0	0	12	0
# structural variations	0	0	0	0
# mismatches	516	218	578	1289
# indels	14	4	15	50
# short indels	14	4	15	41
# long indels	0	0	0	9
Indels length	23	4	24	183

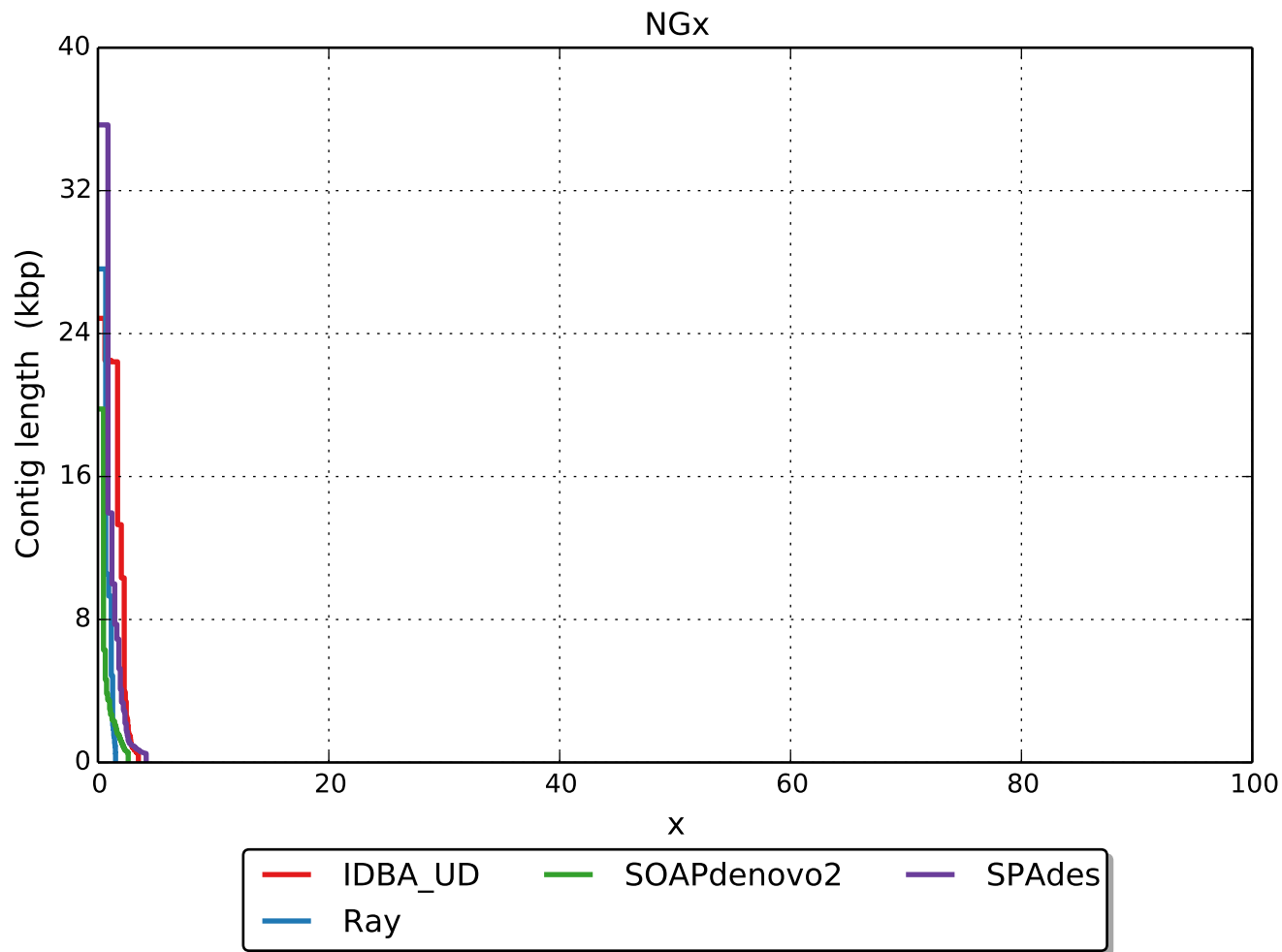
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

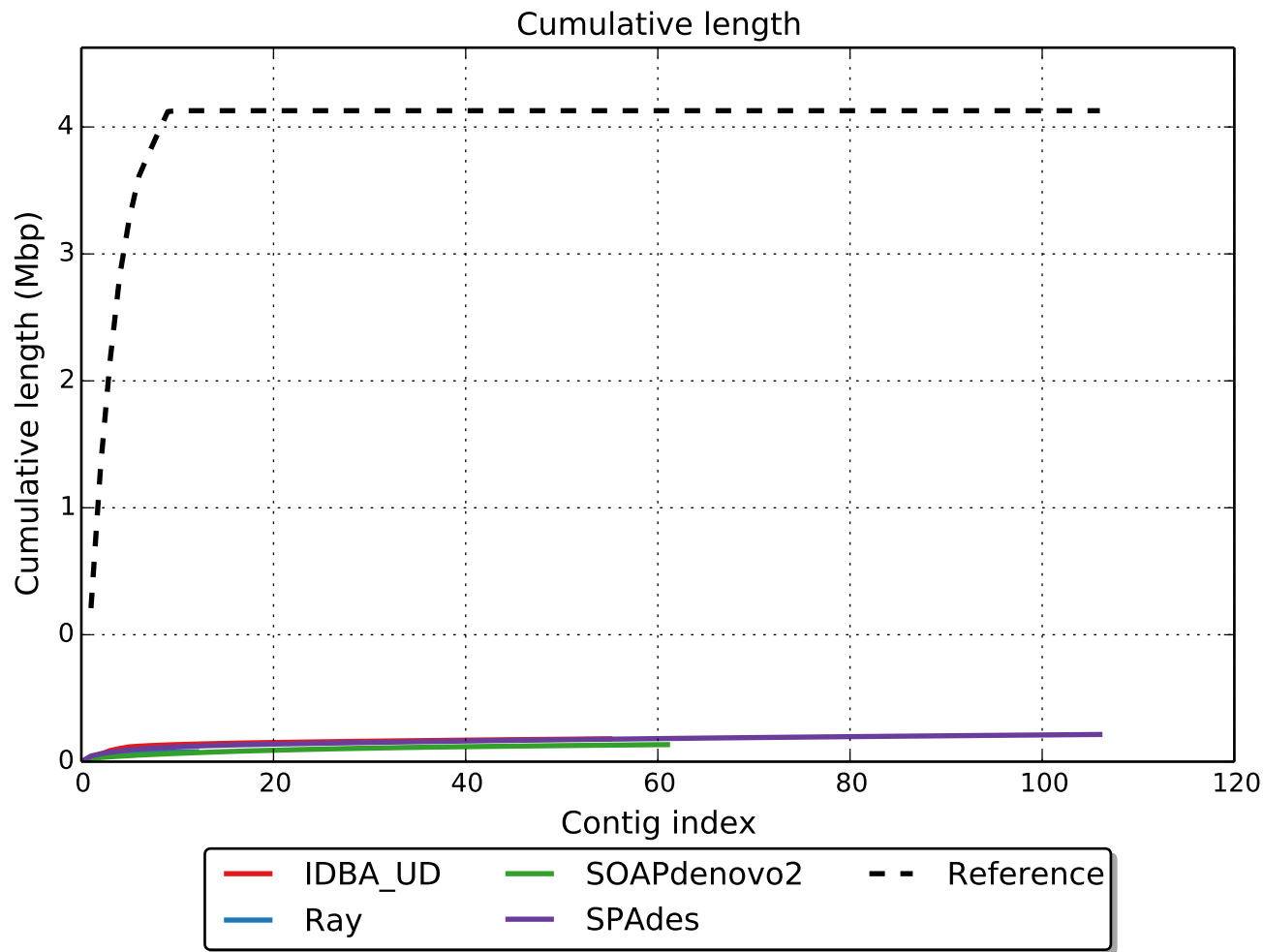
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	28	8	12	53
# with misassembly	1	1	2	3
# both parts are significant	2	1	2	4
Partially unaligned length	109716	53426	28352	110613
# N's	131	1477	1959	4128

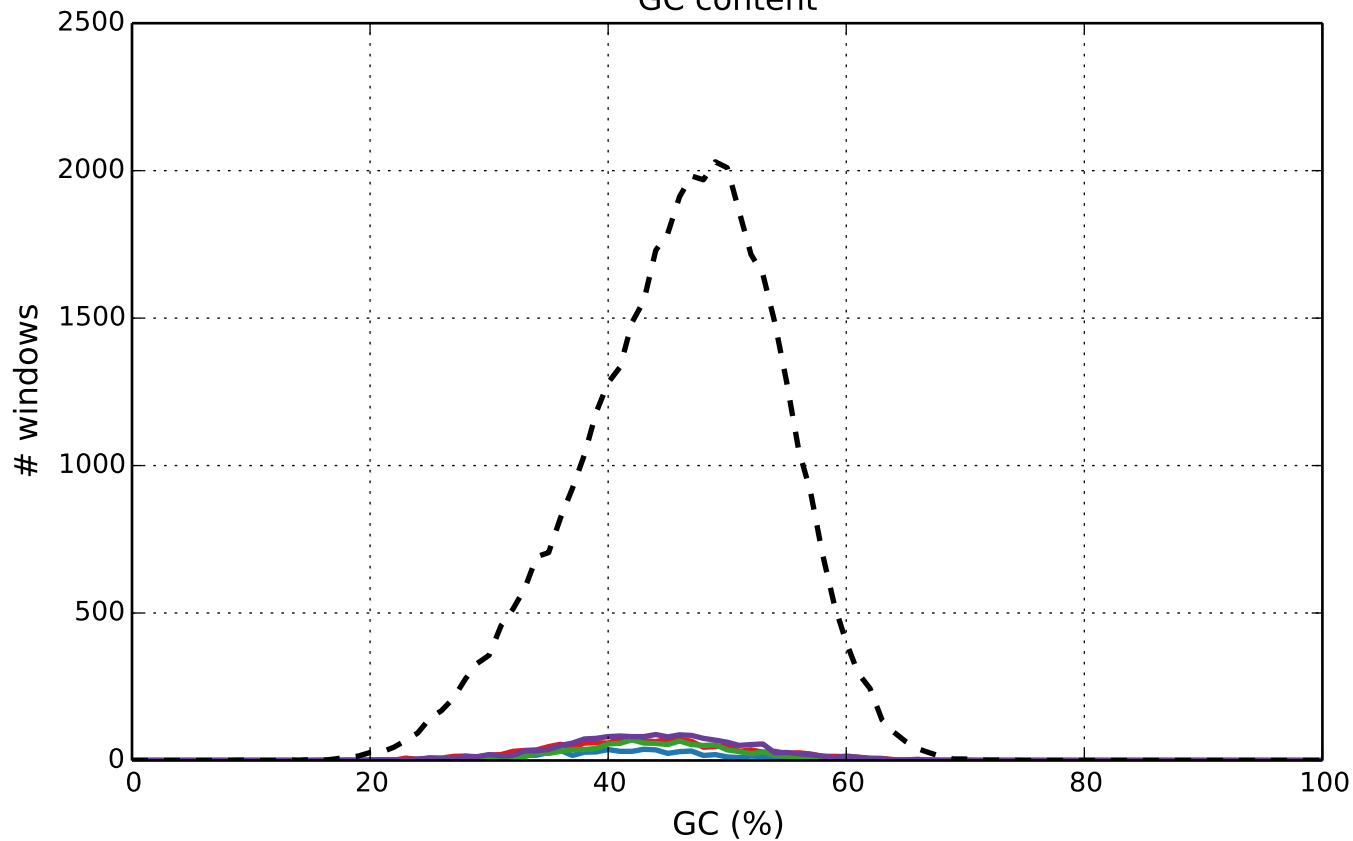
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



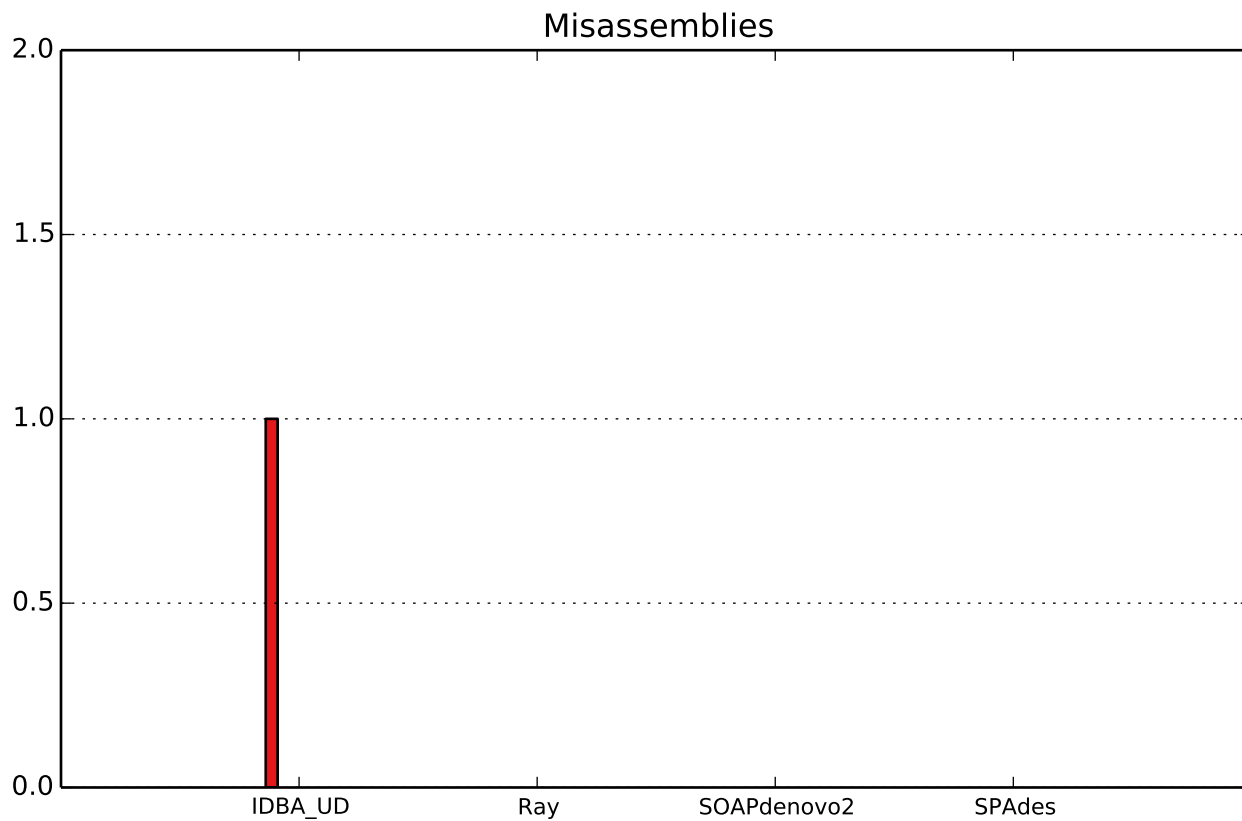




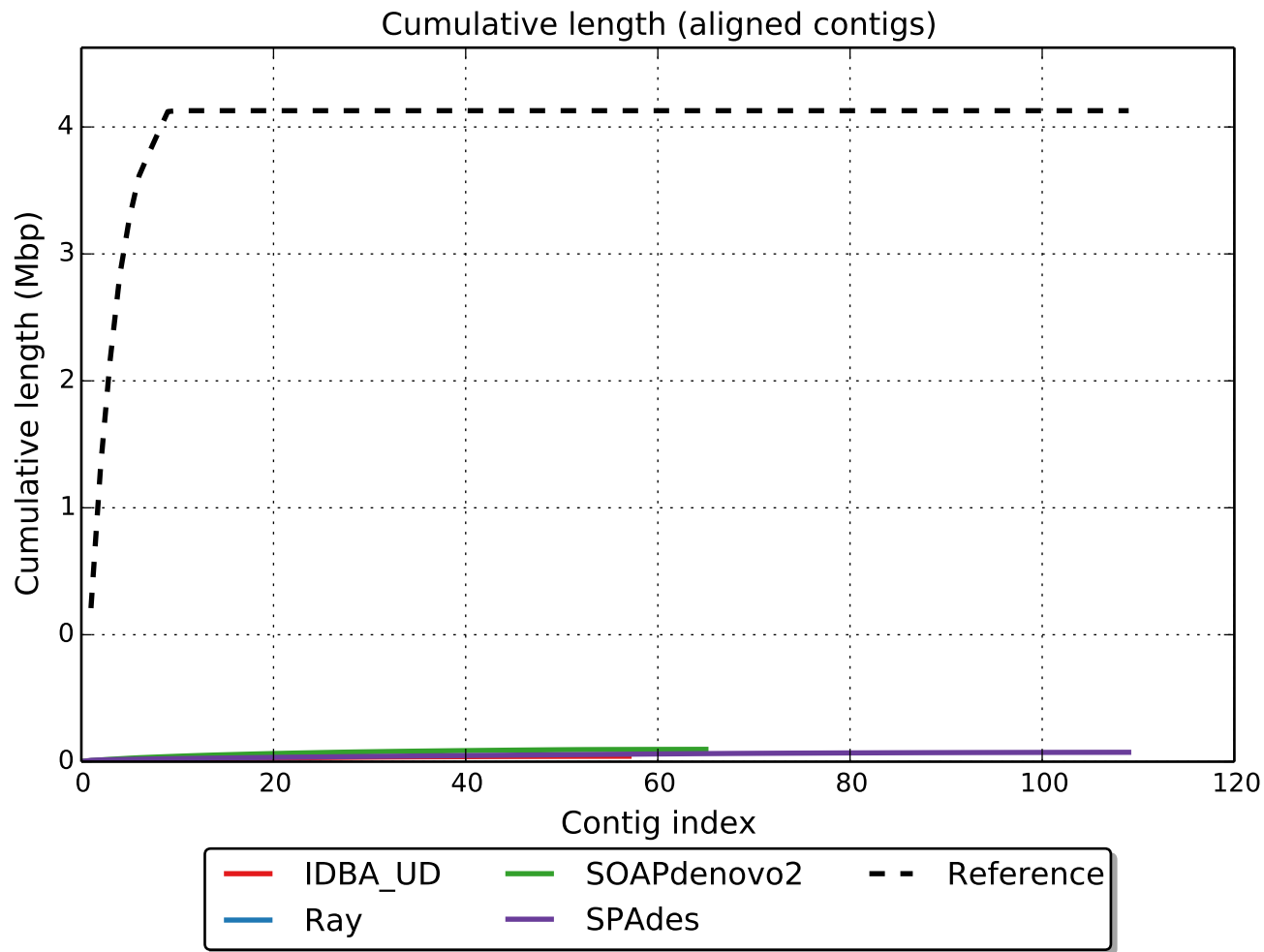
GC content



— IDBA_UD — SOAPdenovo2 - - Reference
— Ray — SPAdes



 # relocations



NAx

