

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	31	12	25	45
# contigs (>= 5000 bp)	3	5	2	5
# contigs (>= 10000 bp)	2	1	0	2
# contigs (>= 25000 bp)	0	0	0	1
# contigs (>= 50000 bp)	0	0	0	0
Total length (>= 1000 bp)	82930	48368	60394	133673
Total length (>= 5000 bp)	37309	40198	11764	66540
Total length (>= 10000 bp)	31333	14202	0	44010
Total length (>= 25000 bp)	0	0	0	33368
Total length (>= 50000 bp)	0	0	0	0
# contigs	201	17	53	290
Largest contig	17131	14202	6297	33368
Total length	193771	52073	79197	292390
Reference length	5277274	5277274	5277274	5277274
GC (%)	43.79	44.54	45.00	44.07
Reference GC (%)	43.27	43.27	43.27	43.27
N50	819	6731	1939	896
N75	636	5447	1015	618
L50	47	3	11	59
L75	116	5	25	159
# misassemblies	0	0	0	3
# misassembled contigs	0	0	0	3
Misassembled contigs length	0	0	0	3319
# local misassemblies	0	0	7	0
# structural variations	0	0	0	0
# unaligned contigs	0 + 19 part	0 + 3 part	0 + 1 part	0 + 31 part
Unaligned length	27201	18630	257	64395
Genome fraction (%)	3.150	0.623	1.478	4.292
Duplication ratio	1.002	1.017	1.012	1.007
# N's per 100 kbp	85.15	647.17	382.59	1335.20
# mismatches per 100 kbp	771.82	246.24	331.97	916.18
# indels per 100 kbp	15.64	6.08	7.69	65.35
Largest alignment	17131	14187	6297	33330
NA50	679	1033	1939	618
NGA50	-	-	-	-
NA75	542	-	1015	473
LA50	75	8	11	134
LA75	154	-	25	266

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

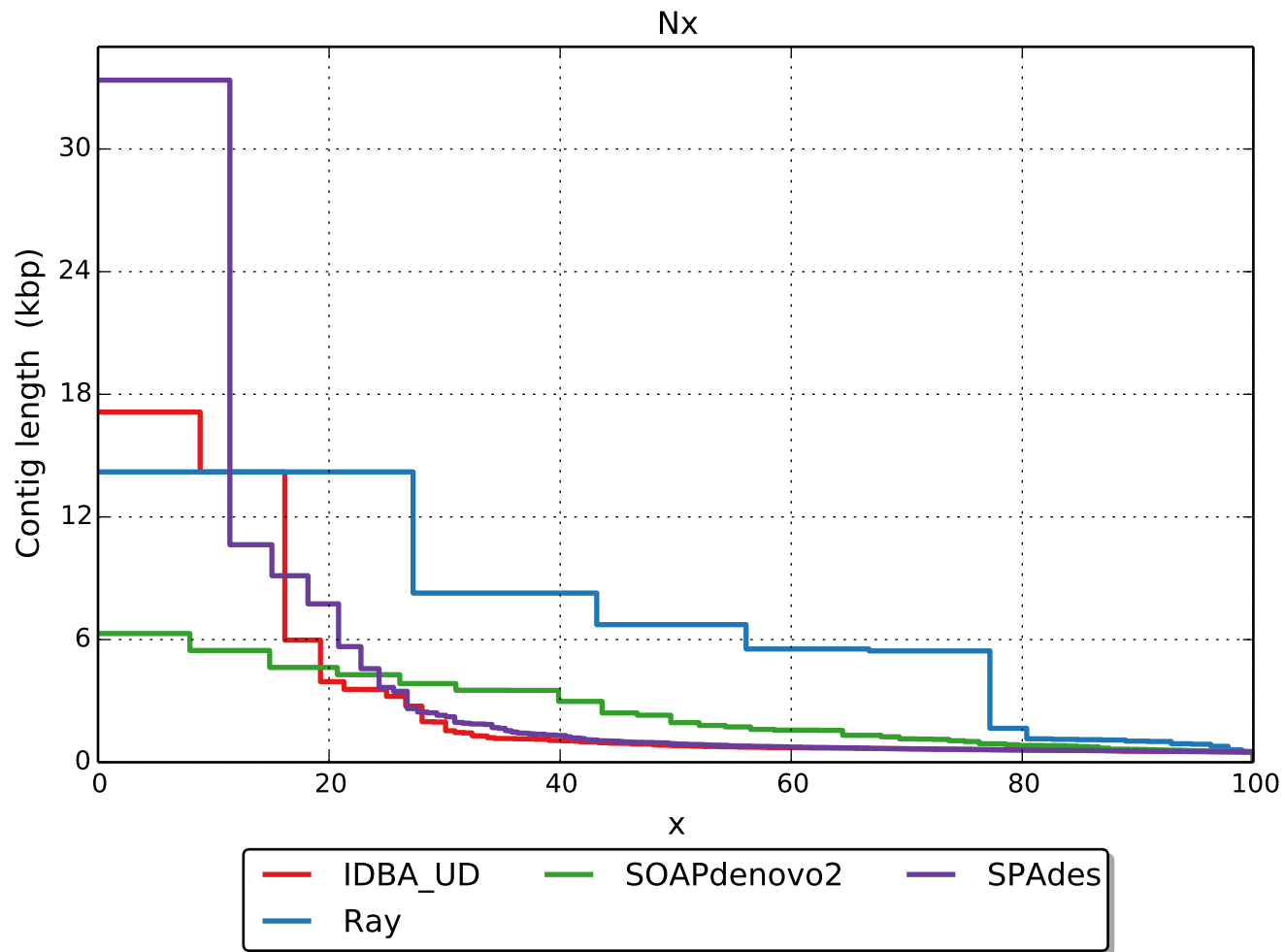
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	0	0	3
# relocations	0	0	0	3
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	1	1	0	3
# misassembled contigs	0	0	0	3
Misassembled contigs length	0	0	0	3319
# local misassemblies	0	0	7	0
# structural variations	0	0	0	0
# mismatches	1283	81	259	2075
# indels	26	2	6	148
# short indels	23	2	6	110
# long indels	3	0	0	38
Indels length	74	3	6	687

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).

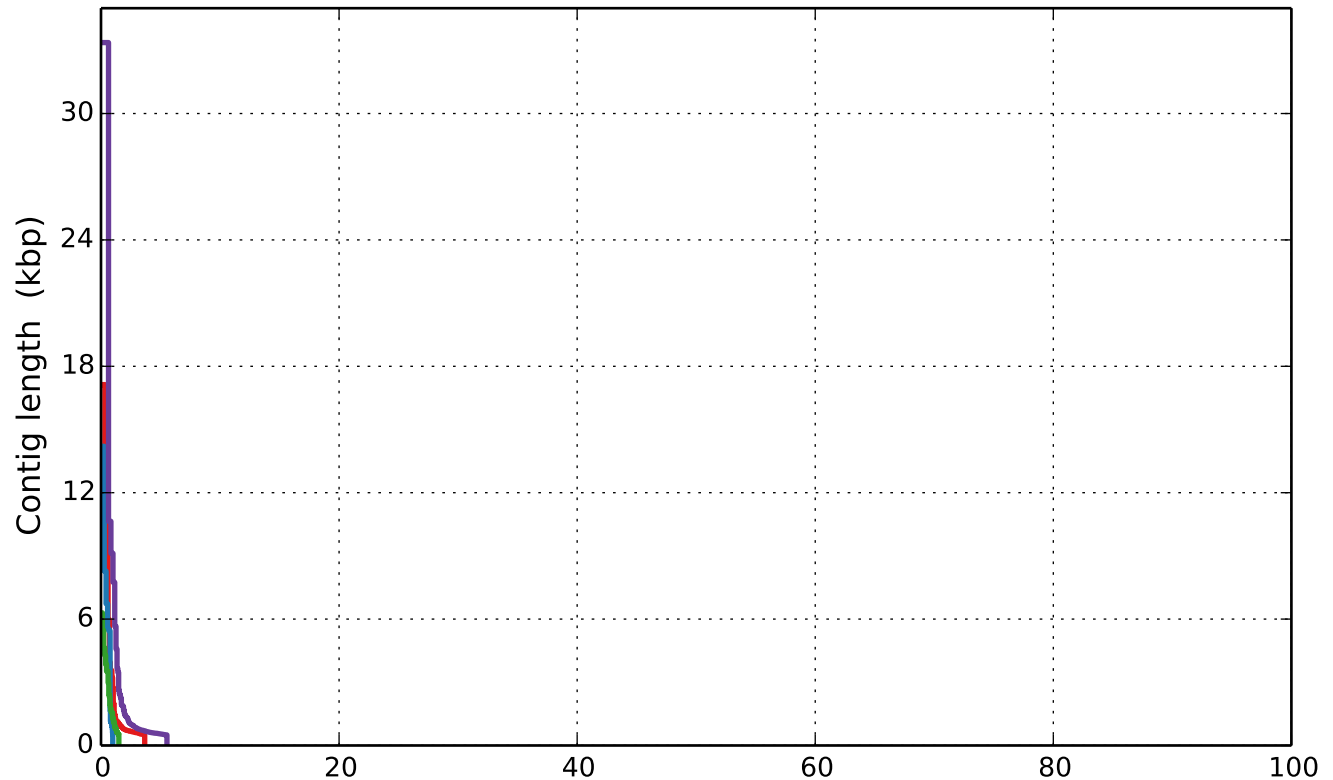
Unaligned report

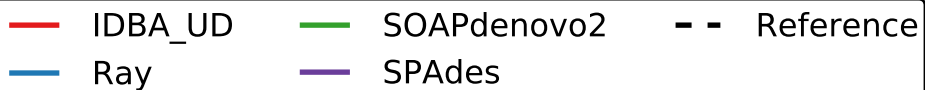
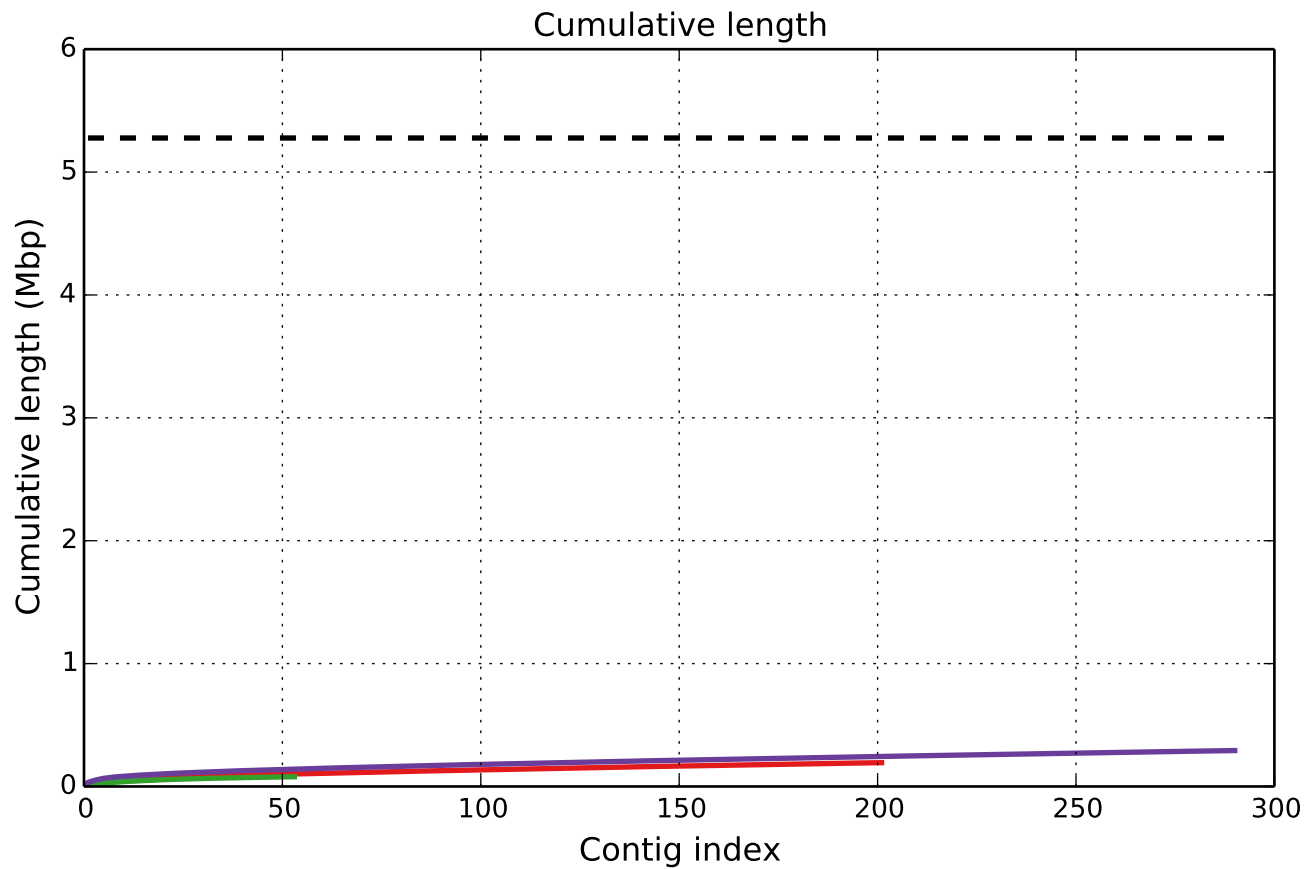
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	19	3	1	31
# with misassembly	0	1	0	1
# both parts are significant	1	1	0	2
Partially unaligned length	27201	18630	257	64395
# N's	165	337	303	3904

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).

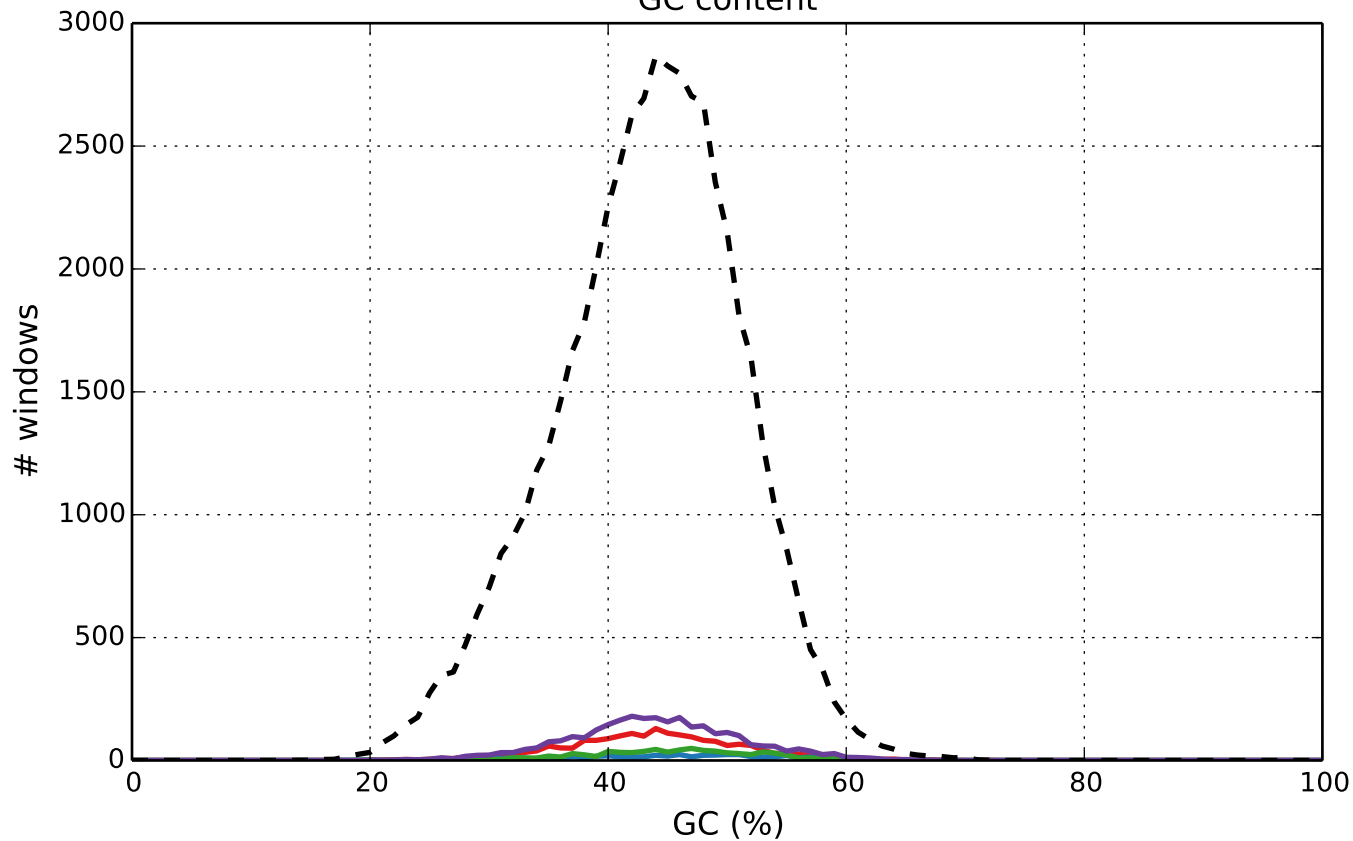


NGx

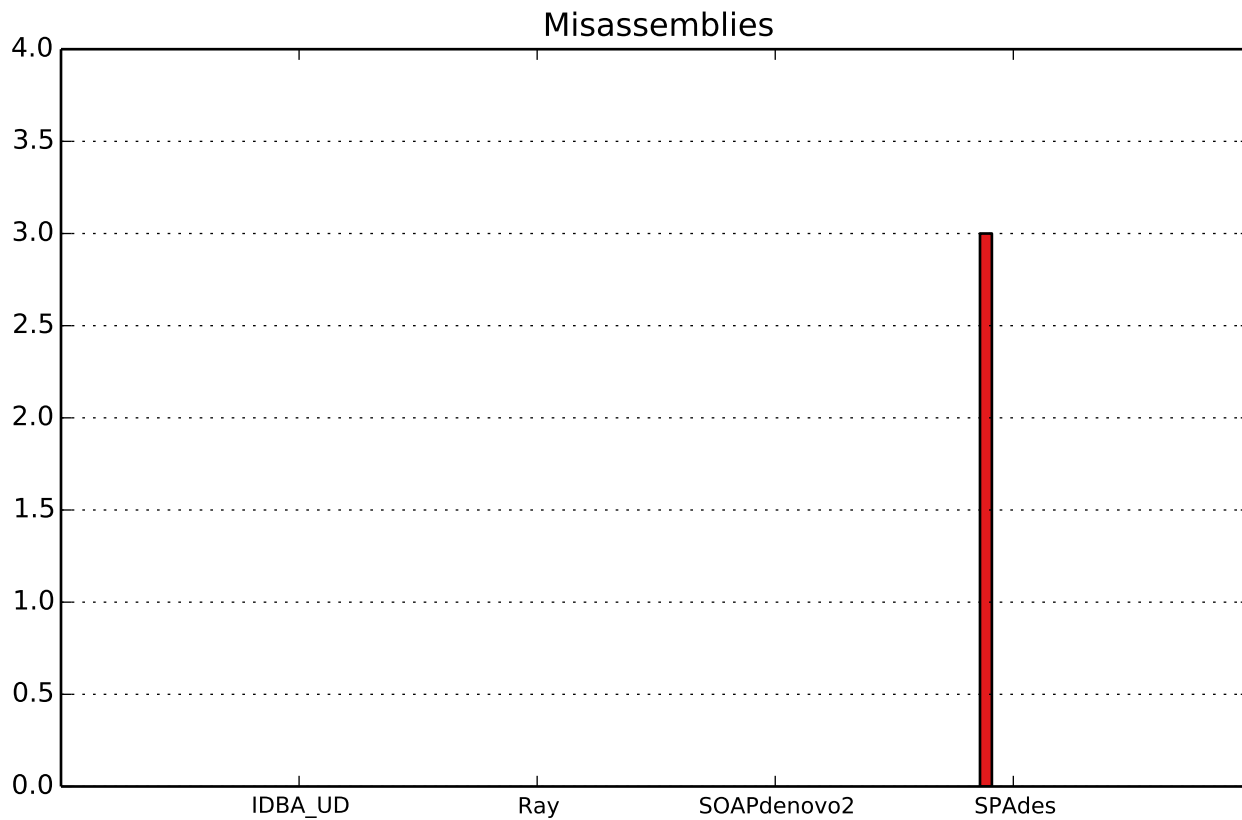




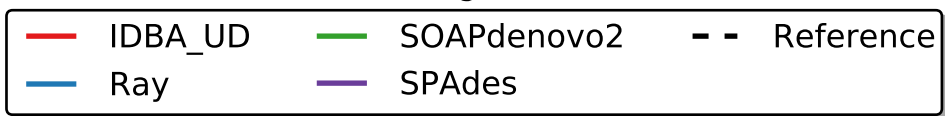
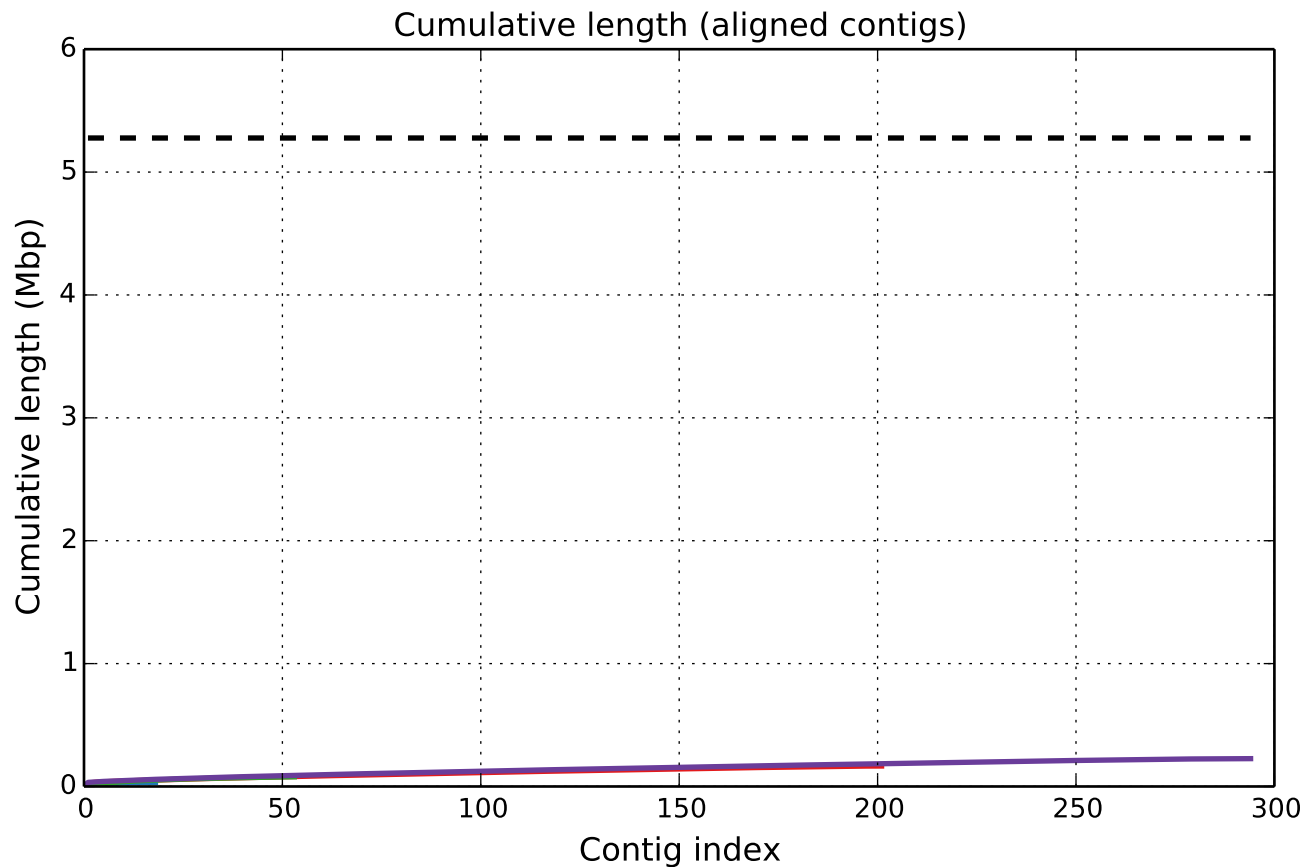
GC content



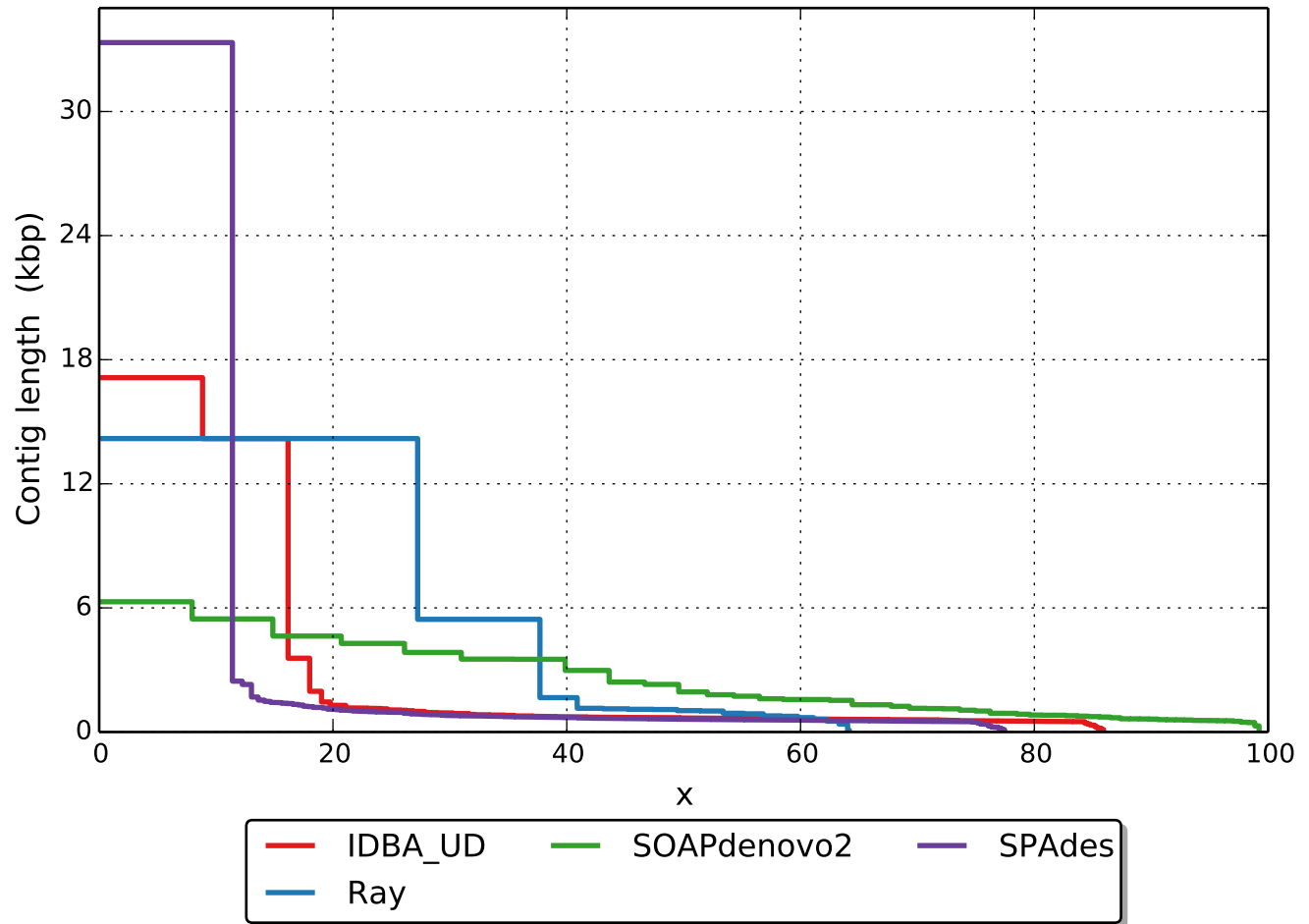
— IDBA_UD — SOAPdenovo2 - - Reference
— Ray — SPAdes



 # relocations



NAx



NGAx

