

Report

	IDBA_UD	Ray	SPAdes
# contigs (>= 1000 bp)	2	1	2
# contigs (>= 5000 bp)	1	0	1
# contigs (>= 10000 bp)	0	0	0
# contigs (>= 25000 bp)	0	0	0
# contigs (>= 50000 bp)	0	0	0
Total length (>= 1000 bp)	11858	3415	10486
Total length (>= 5000 bp)	8932	0	9349
Total length (>= 10000 bp)	0	0	0
Total length (>= 25000 bp)	0	0	0
Total length (>= 50000 bp)	0	0	0
# contigs	5	1	2
Largest contig	8932	3415	9349
Total length	14047	3415	10486
Reference length	2313752	2313752	2313752
GC (%)	37.84	38.92	41.47
Reference GC (%)	56.38	56.38	56.38
N50	8932	3415	9349
N75	2926	3415	9349
L50	1	1	1
L75	2	1	1
# misassemblies	0	0	0
# misassembled contigs	0	0	0
Misassembled contigs length	0	0	0
# local misassemblies	0	0	0
# structural variations	0	0	0
# unaligned contigs	0 + 5 part	0 + 1 part	0 + 2 part
Unaligned length	13017	3186	10176
Genome fraction (%)	0.031	0.010	0.008
Duplication ratio	1.429	1.000	1.598
# N's per 100 kbp	263.40	0.00	0.00
# mismatches per 100 kbp	1386.96	3056.77	2061.86
# indels per 100 kbp	277.39	0.00	0.00
Largest alignment	373	229	194
NGA50	-	-	-

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

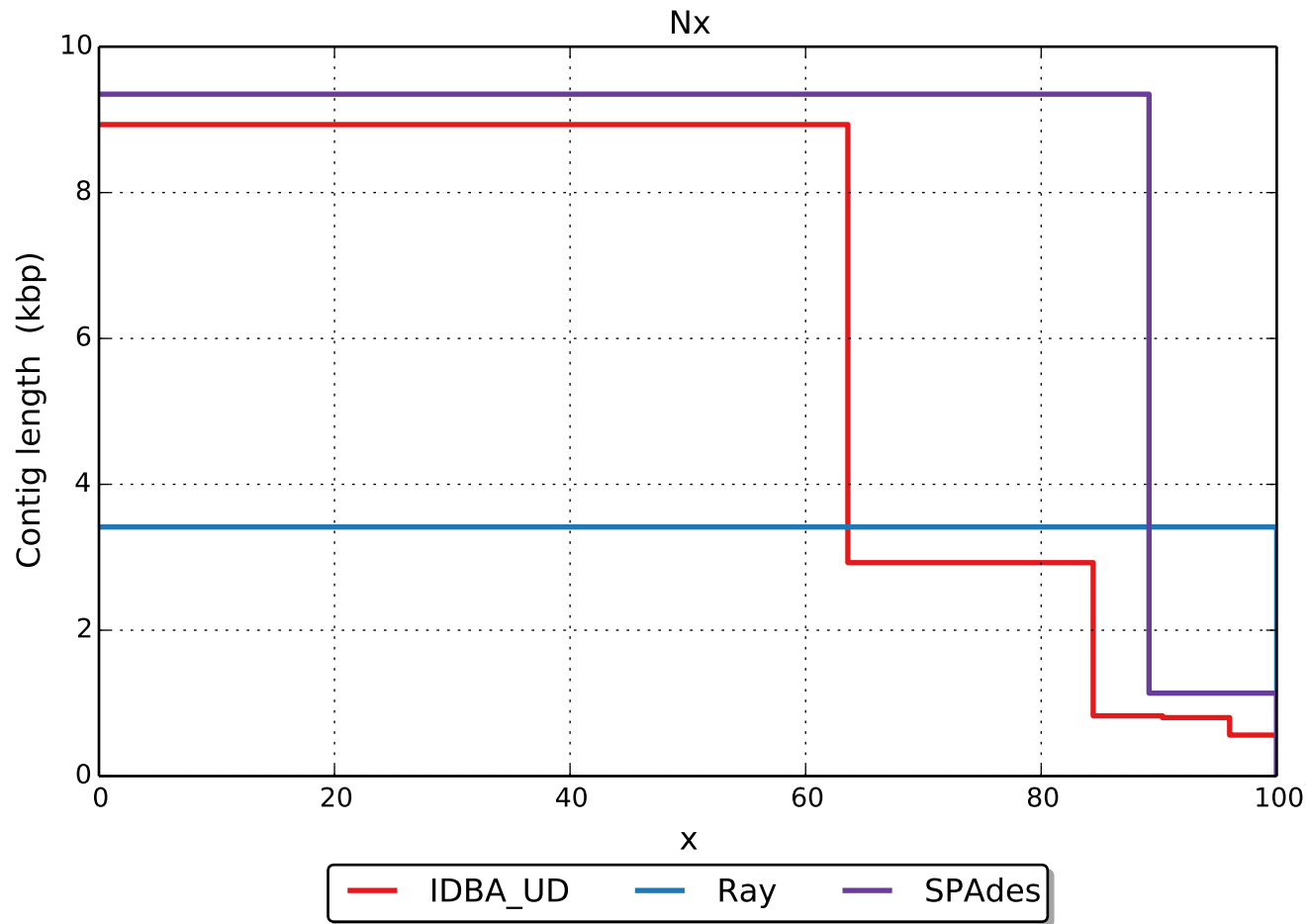
	IDBA_UD	Ray	SPAdes
# misassemblies	0	0	0
# relocations	0	0	0
# translocations	0	0	0
# inversions	0	0	0
# possibly misassembled contigs	0	0	0
# misassembled contigs	0	0	0
Misassembled contigs length	0	0	0
# local misassemblies	0	0	0
# structural variations	0	0	0
# mismatches	10	7	4
# indels	2	0	0
# short indels	2	0	0
# long indels	0	0	0
Indels length	7	0	0

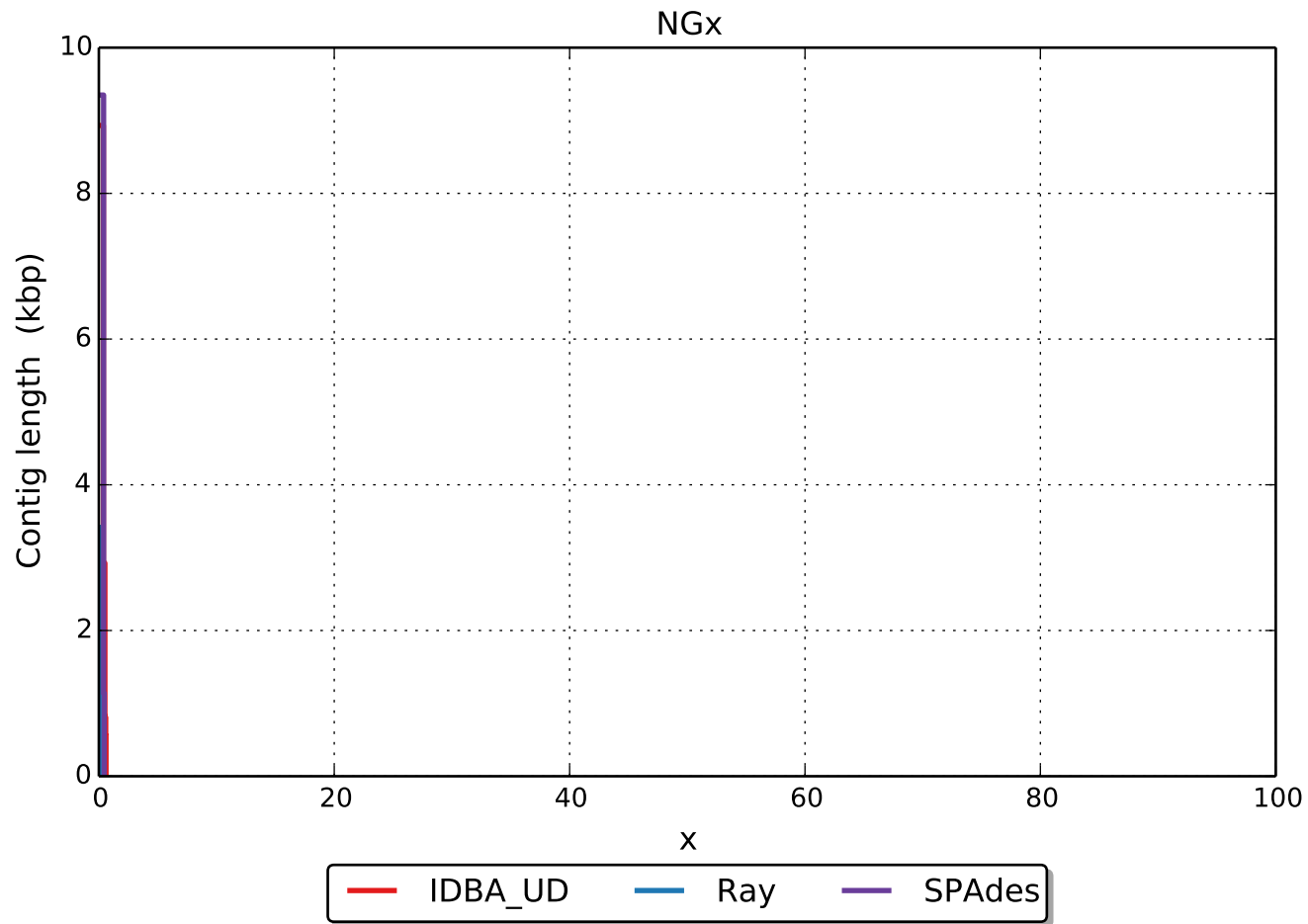
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

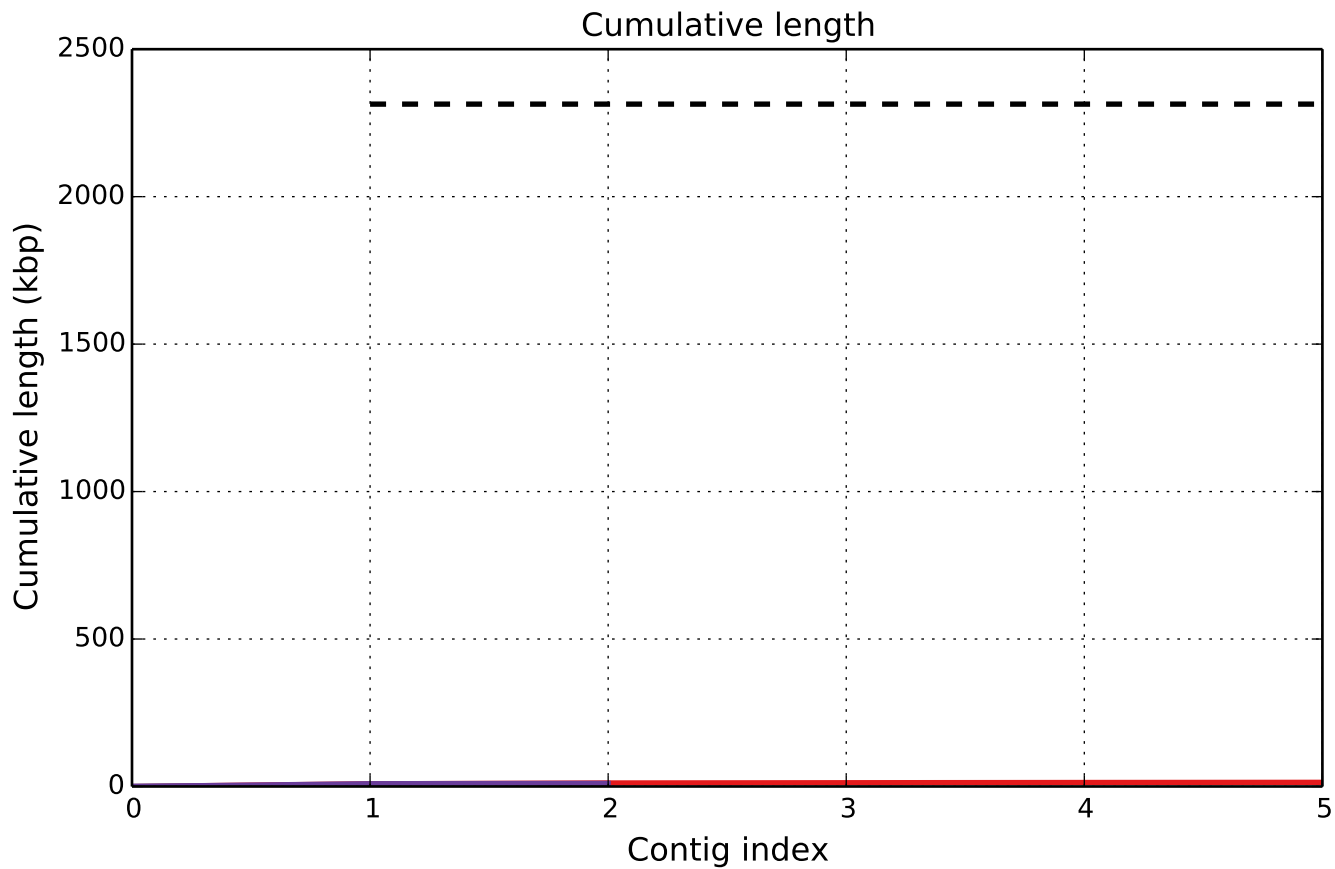
Unaligned report

	IDBA_UD	Ray	SPAdes
# fully unaligned contigs	0	0	0
Fully unaligned length	0	0	0
# partially unaligned contigs	5	1	2
# with misassembly	0	0	0
# both parts are significant	0	0	0
Partially unaligned length	13017	3186	10176
# N's	37	0	0

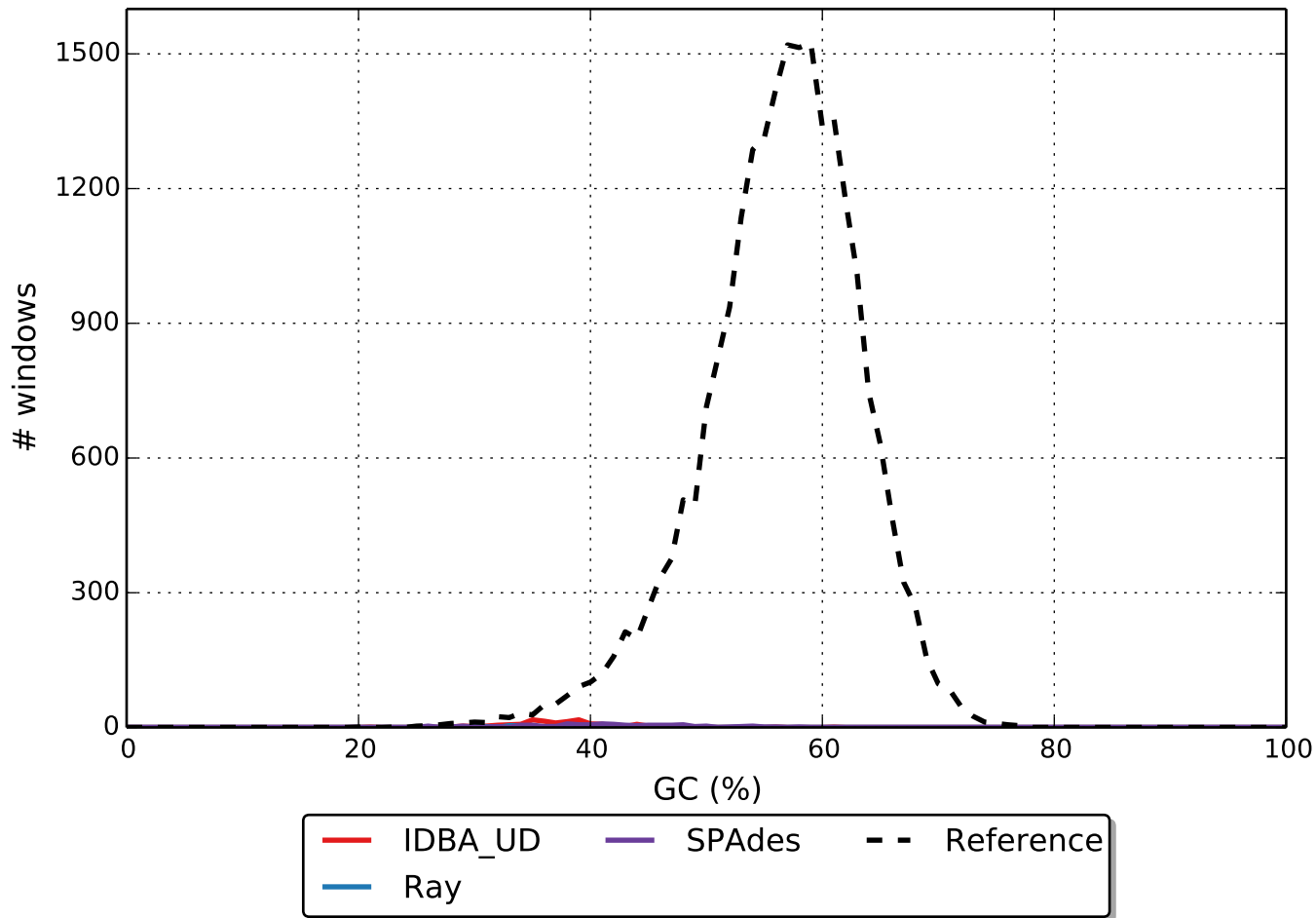
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

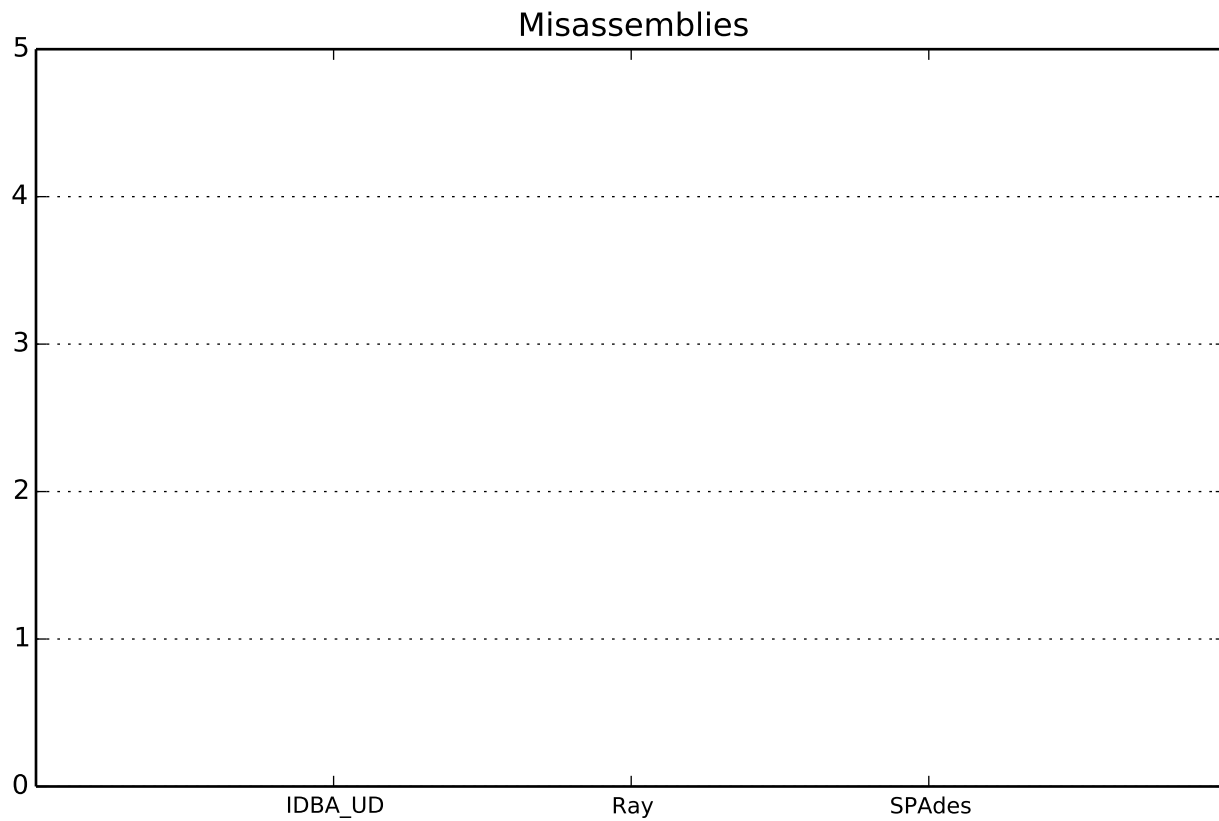




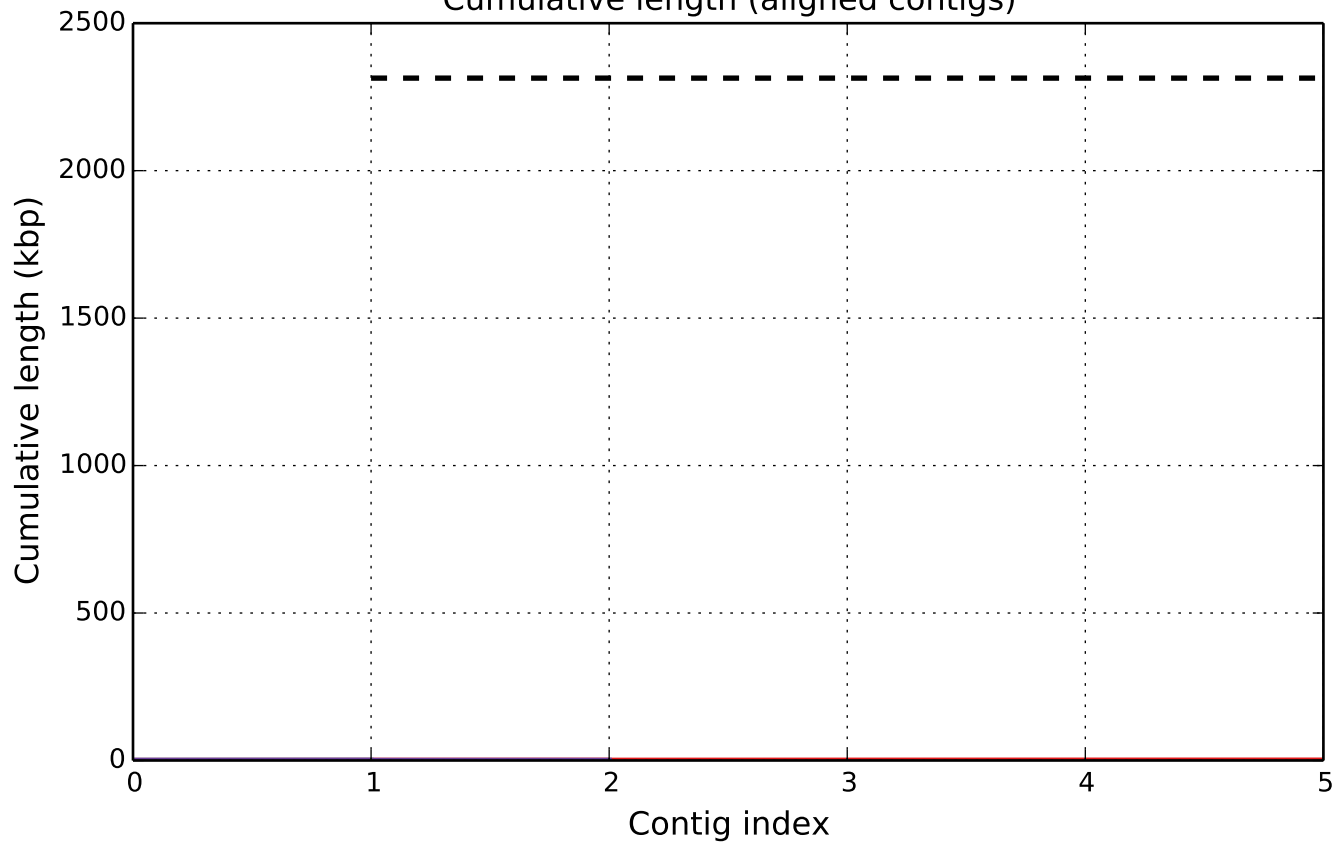


GC content

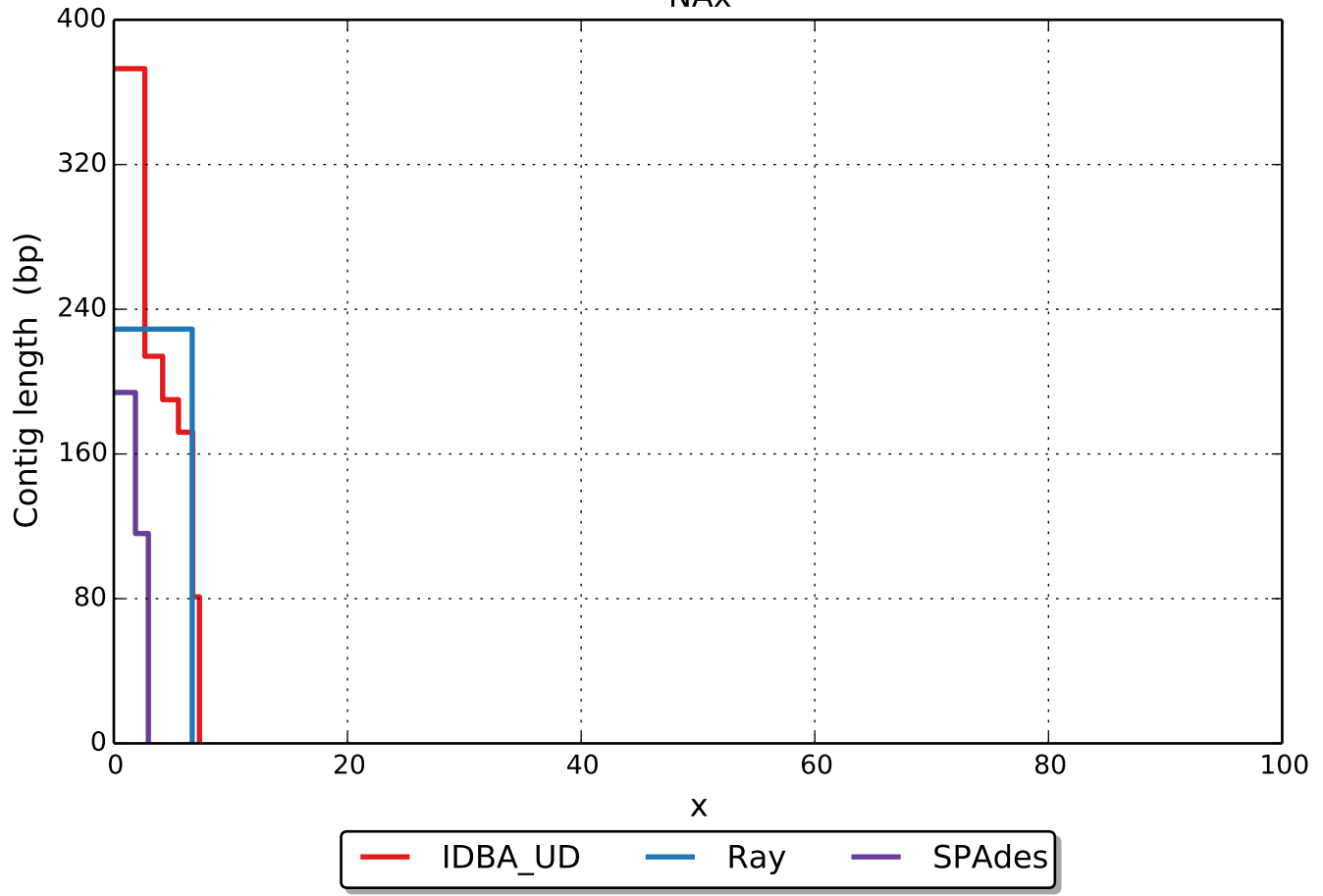




Cumulative length (aligned contigs)



NAx



NGAx

