

# Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	8	4	1	9
# contigs (>= 5000 bp)	5	2	0	3
# contigs (>= 10000 bp)	4	1	0	2
# contigs (>= 25000 bp)	3	0	0	2
# contigs (>= 50000 bp)	2	0	0	2
Total length (>= 1000 bp)	227716	31097	1695	172408
Total length (>= 5000 bp)	219399	28151	0	157308
Total length (>= 10000 bp)	213102	22545	0	151962
Total length (>= 25000 bp)	199978	0	0	151962
Total length (>= 50000 bp)	166554	0	0	151962
# contigs	11	5	3	12
Largest contig	94894	22545	1695	86580
Total length	229832	31689	2895	174553
Reference length	4548960	4548960	4548960	4548960
GC (%)	46.36	44.99	46.54	47.64
Reference GC (%)	49.55	49.55	49.55	49.55
N50	71660	22545	1695	65382
N75	33424	5606	679	65382
L50	2	1	1	2
L75	3	2	2	2
# misassemblies	0	0	0	0
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	0	2	0
# structural variations	0	0	0	0
# unaligned contigs	0 + 10 part	0 + 2 part	0 + 0 part	0 + 8 part
Unaligned length	218869	27911	0	167368
Genome fraction (%)	0.228	0.083	0.061	0.150
Duplication ratio	1.056	1.000	1.050	1.051
# N's per 100 kbp	11.75	0.00	4697.75	169.58
# mismatches per 100 kbp	751.16	1773.43	1668.48	1038.77
# indels per 100 kbp	0.00	0.00	0.00	87.78
Largest alignment	6297	1686	1693	1982
NA50	-	-	1693	-
NGA50	-	-	-	-
NA75	-	-	679	-
LA50	-	-	1	-
LA75	-	-	2	-

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

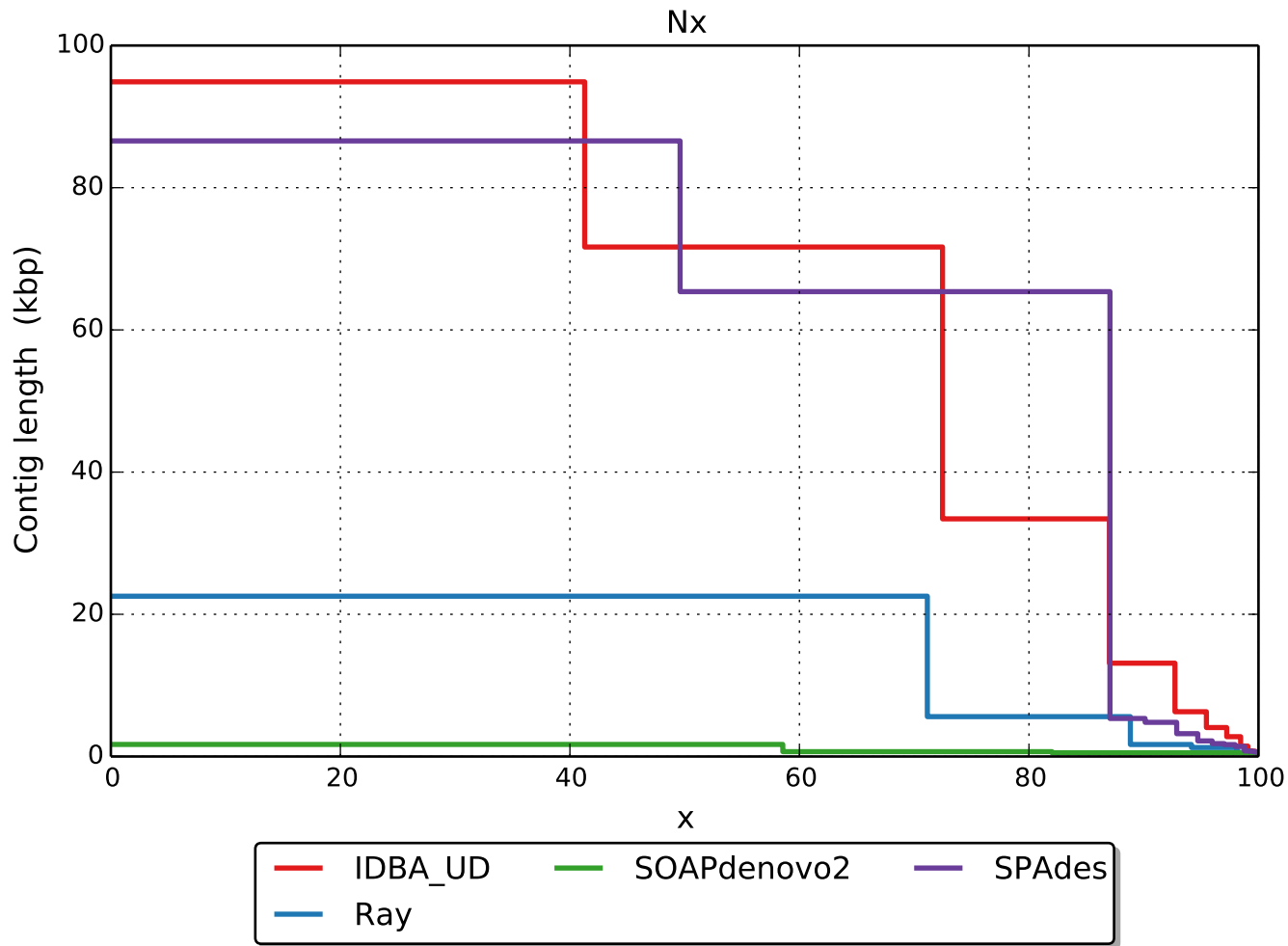
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	0	0	0
# relocations	0	0	0	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	1	0	0	1
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	0	2	0
# structural variations	0	0	0	0
# mismatches	78	67	46	71
# indels	0	0	0	6
# short indels	0	0	0	5
# long indels	0	0	0	1
Indels length	0	0	0	12

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

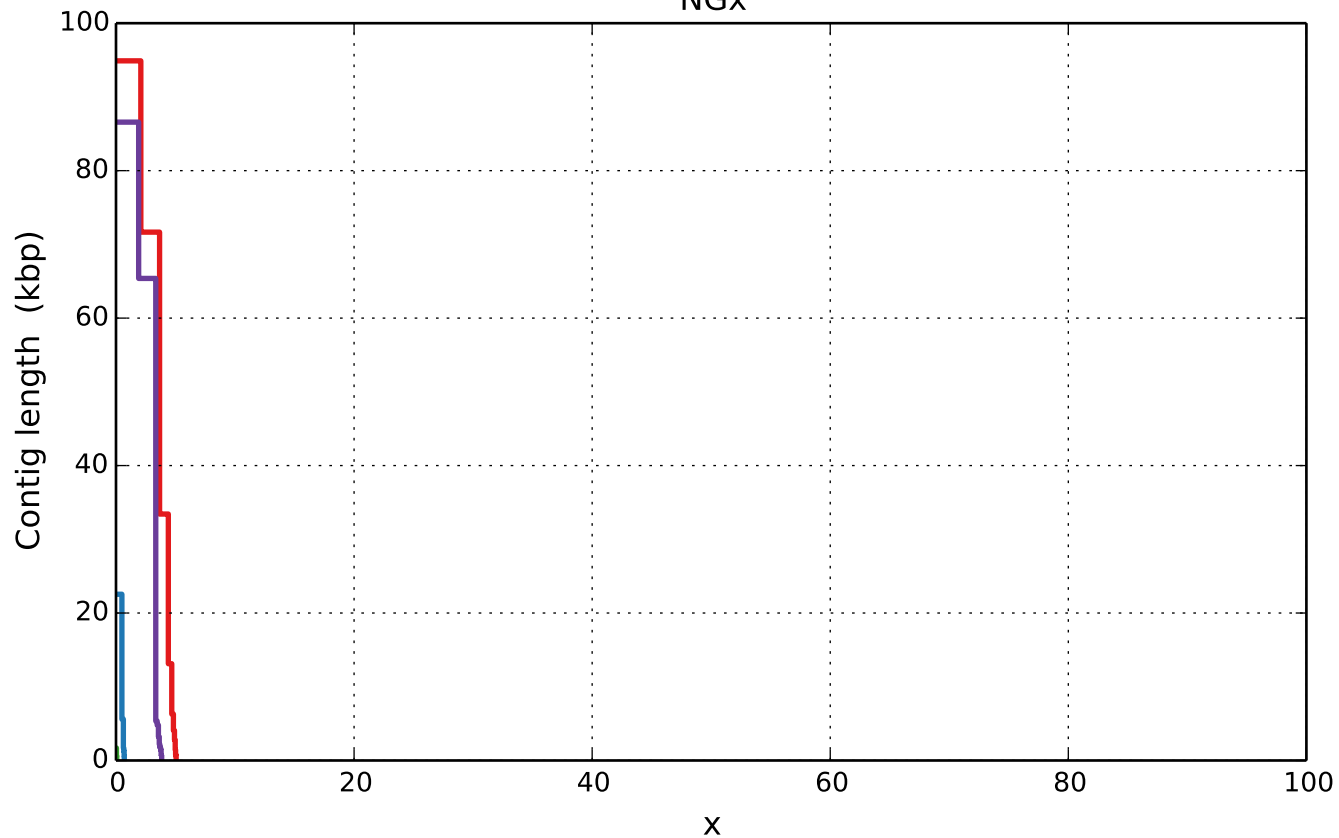
## Unaligned report

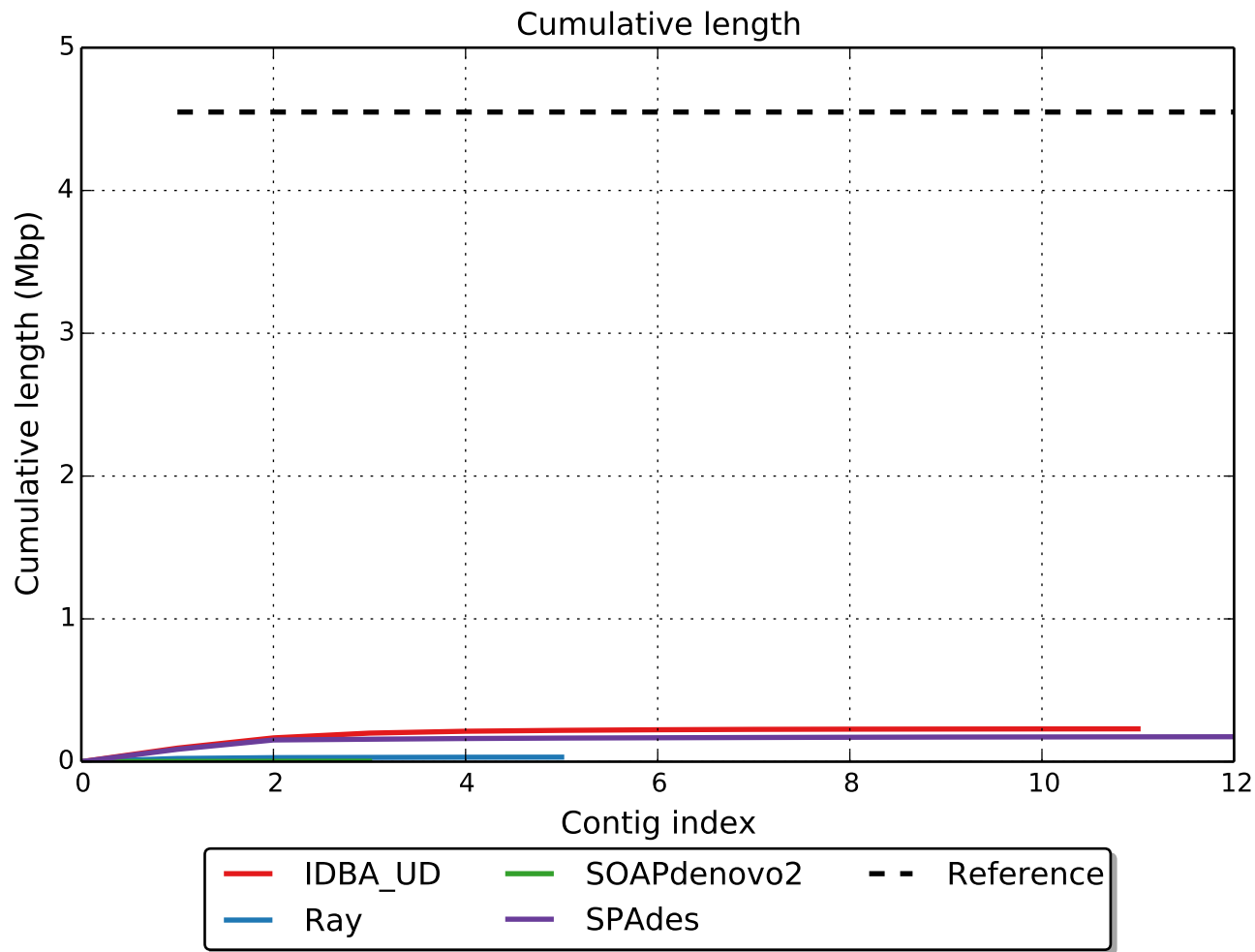
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	10	2	0	8
# with misassembly	4	1	0	1
# both parts are significant	1	0	0	1
Partially unaligned length	218869	27911	0	167368
# N's	27	0	136	296

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

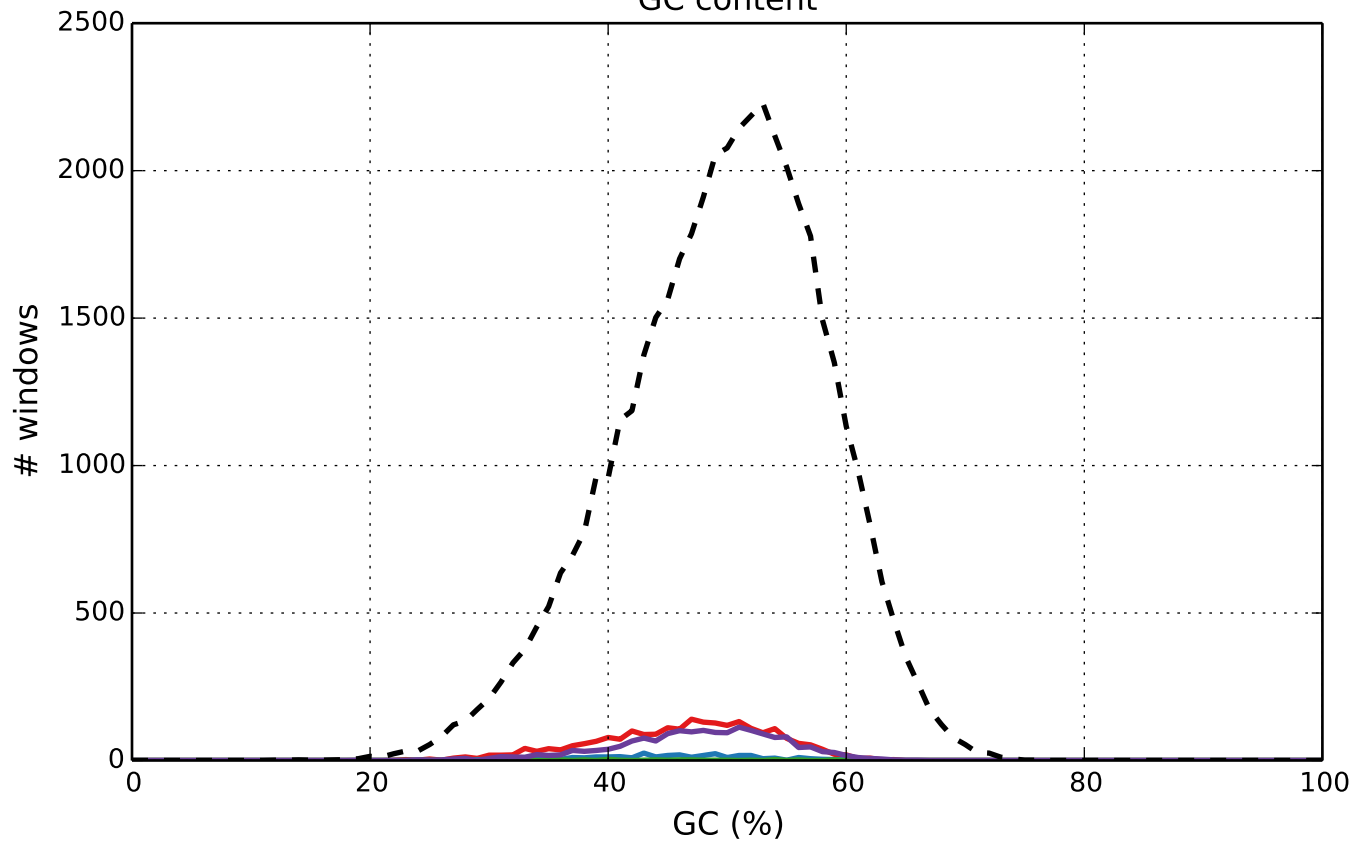


NGx

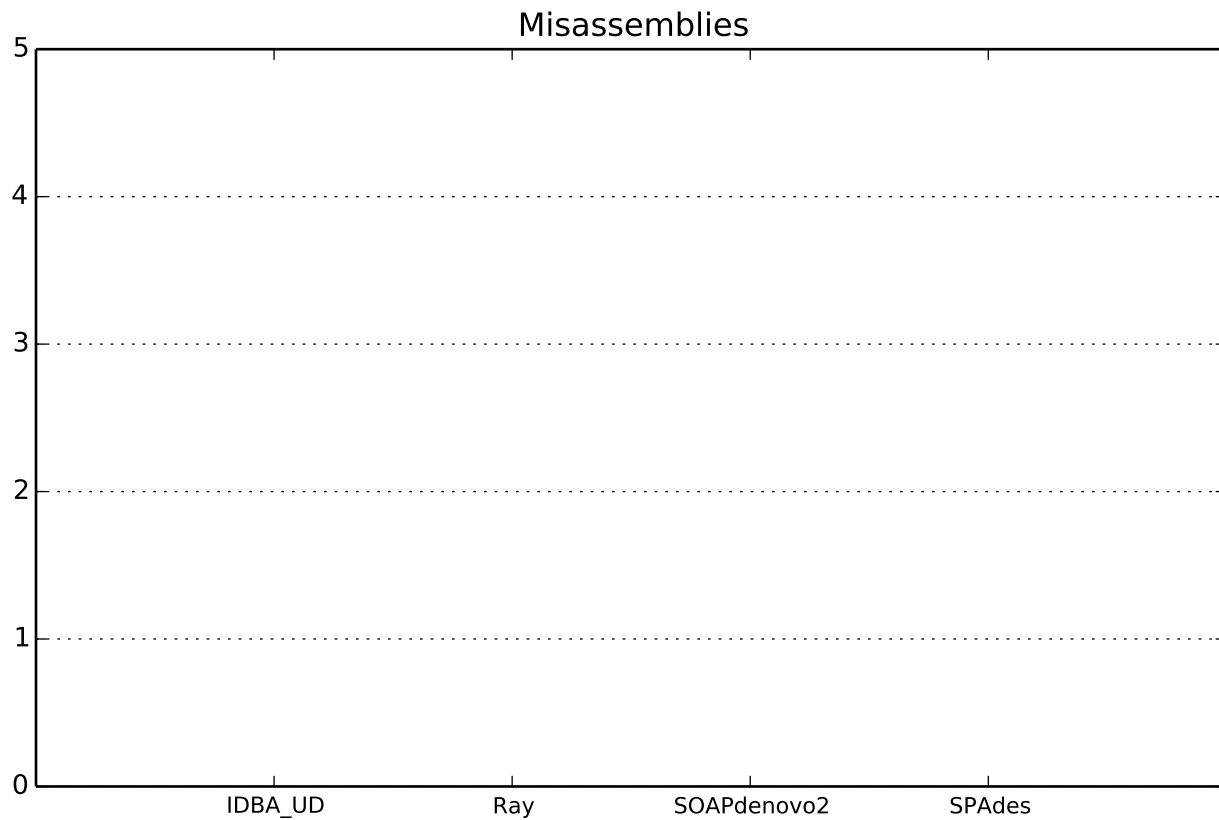




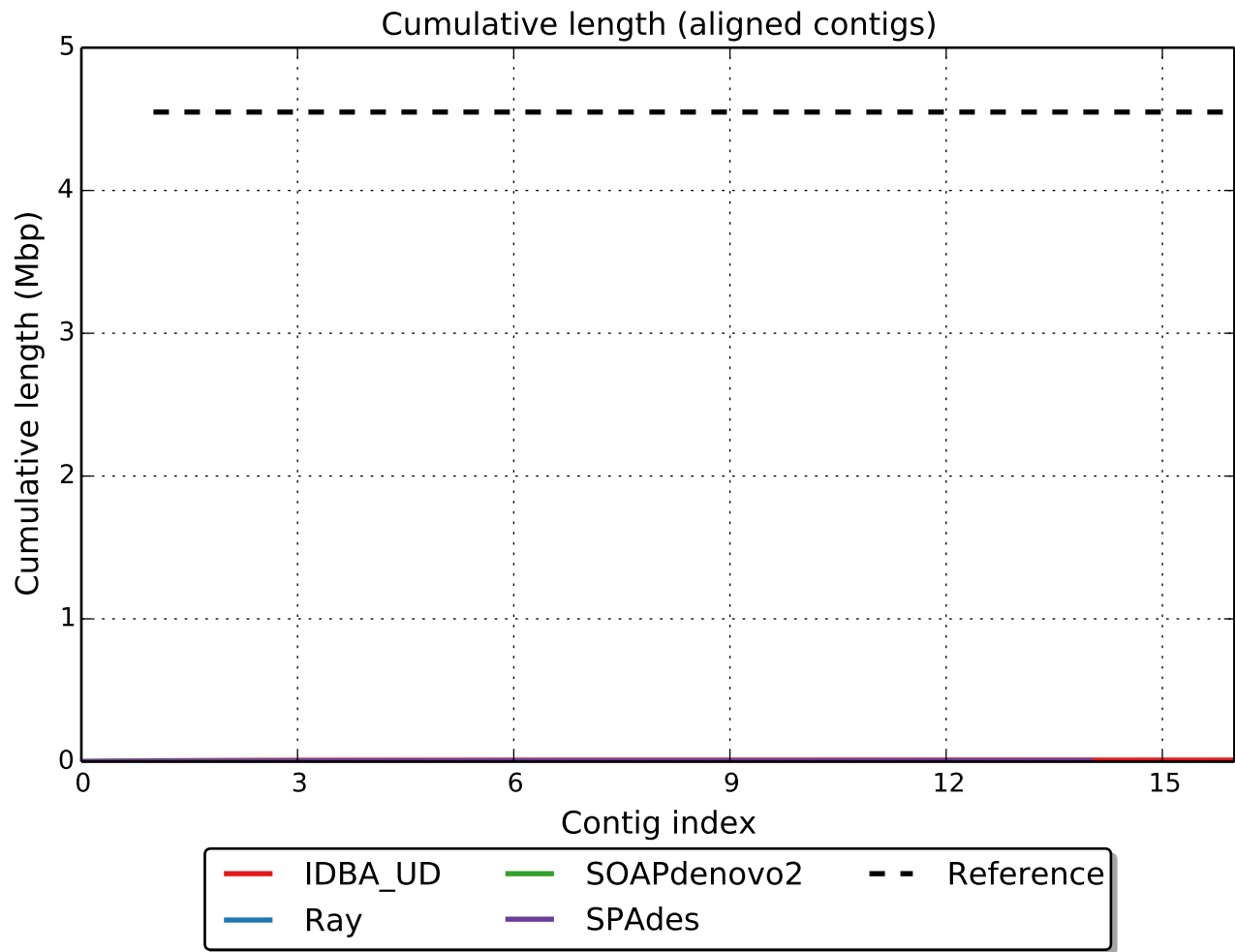
GC content



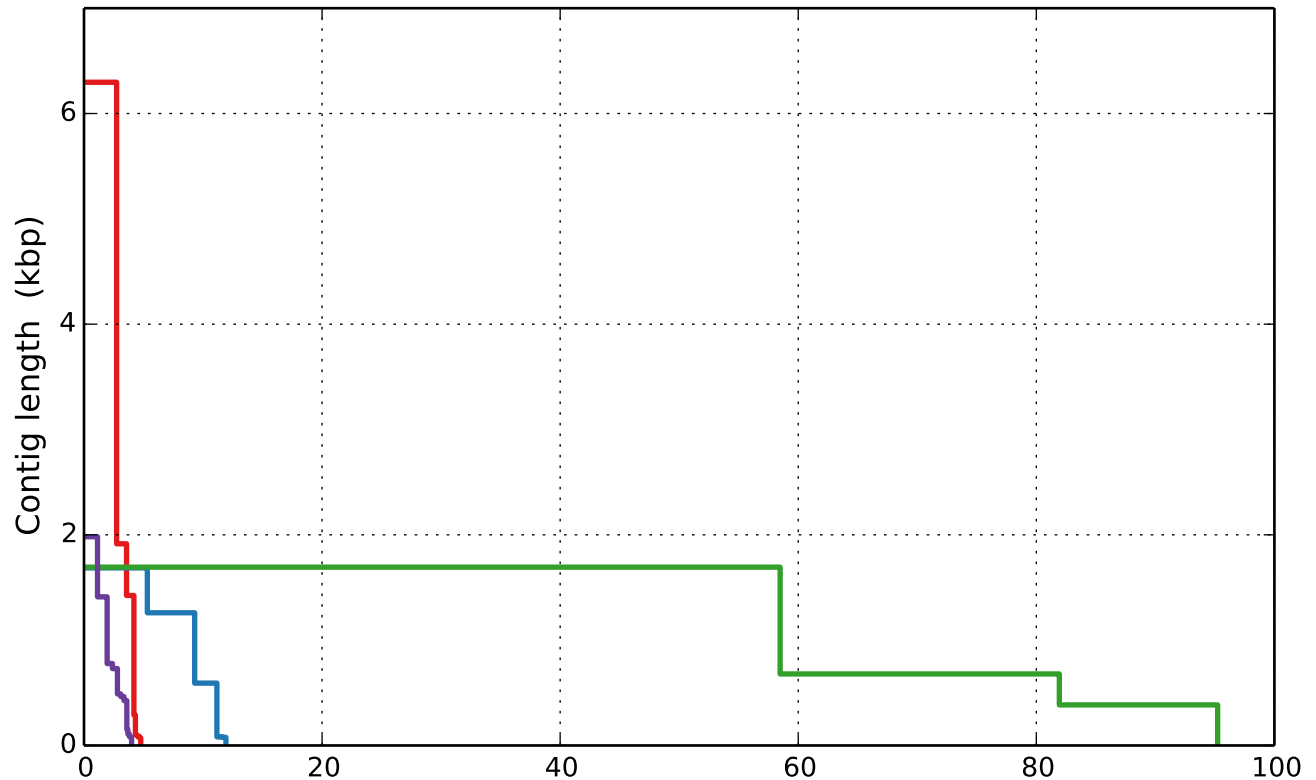
— IDBA\_UD    — SOAPdenovo2    - - Reference  
— Ray    — SPAdes







NAx



NGAx

