

# Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	19	2	6	18
# contigs (>= 5000 bp)	8	1	0	0
# contigs (>= 10000 bp)	7	1	0	0
# contigs (>= 25000 bp)	5	0	0	0
# contigs (>= 50000 bp)	2	0	0	0
Total length (>= 1000 bp)	272397	15670	11972	29692
Total length (>= 5000 bp)	252973	14202	0	0
Total length (>= 10000 bp)	243263	14202	0	0
Total length (>= 25000 bp)	217410	0	0	0
Total length (>= 50000 bp)	131715	0	0	0
# contigs	32	2	19	37
Largest contig	80521	14202	4283	2545
Total length	281579	15670	20688	42308
Reference length	2550678	2550678	2550678	2550678
GC (%)	50.14	46.22	45.12	43.21
Reference GC (%)	53.27	53.27	53.27	53.27
N50	34804	14202	1198	1399
N75	25097	14202	655	917
L50	3	1	5	12
L75	5	1	11	21
# misassemblies	0	0	0	0
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	0	9	0
# structural variations	0	0	0	0
# unaligned contigs	0 + 19 part	0 + 1 part	0 + 8 part	0 + 25 part
Unaligned length	245925	471	3009	13567
Genome fraction (%)	1.366	0.595	0.610	1.117
Duplication ratio	1.023	1.001	1.137	1.009
# N's per 100 kbp	79.91	0.00	5524.94	1401.63
# mismatches per 100 kbp	1130.95	493.91	372.89	1797.56
# indels per 100 kbp	57.41	6.59	25.72	108.84
Largest alignment	14187	14187	4283	1938
NA50	-	14187	905	581
NGA50	-	-	-	-
NA75	-	14187	89	-
LA50	-	1	6	18
LA75	-	1	21	-

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

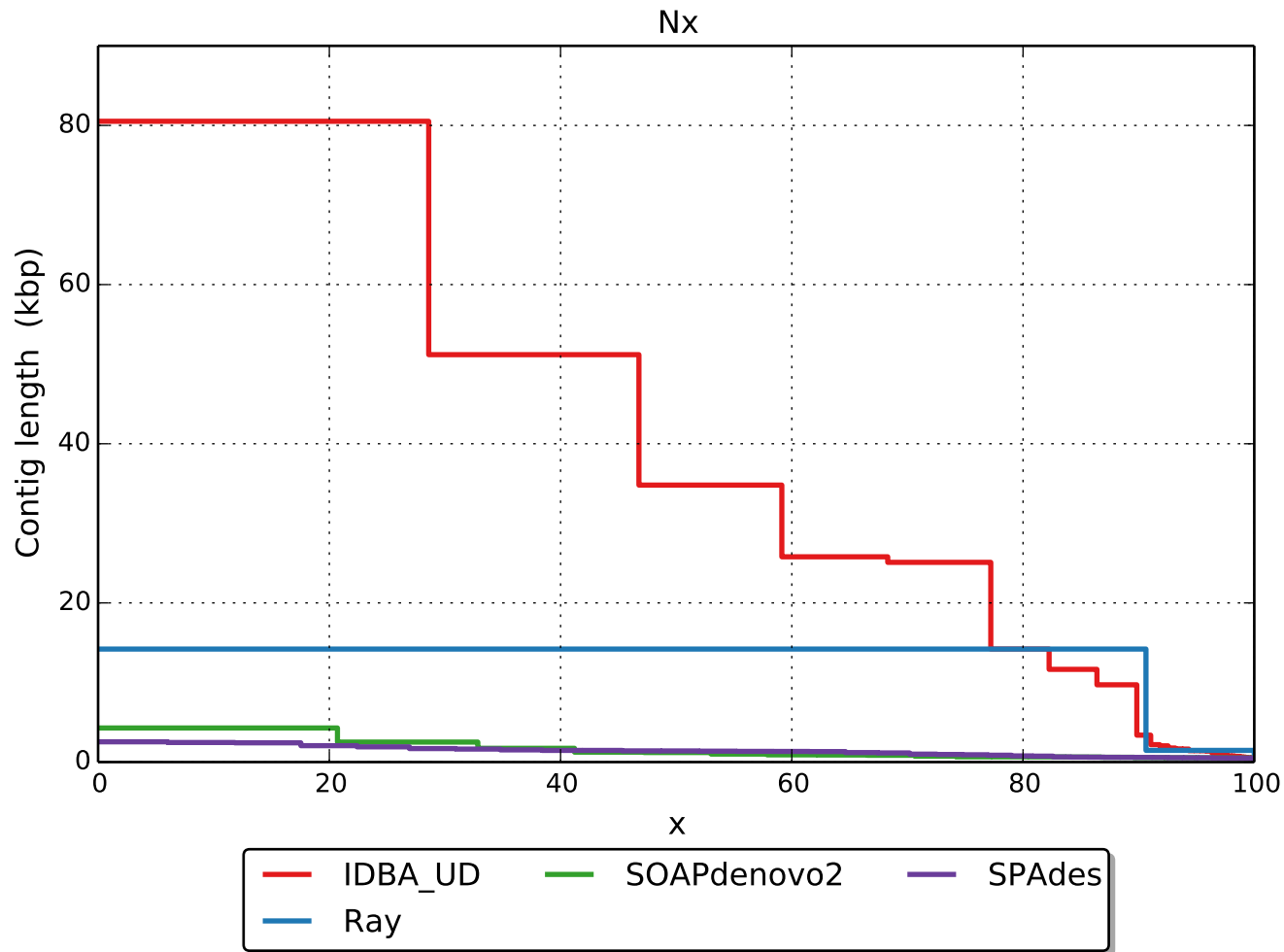
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	0	0	0
# relocations	0	0	0	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	3	0	1	4
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	0	9	0
# structural variations	0	0	0	0
# mismatches	394	75	58	512
# indels	20	1	4	31
# short indels	18	1	4	26
# long indels	2	0	0	5
Indels length	43	1	4	86

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).

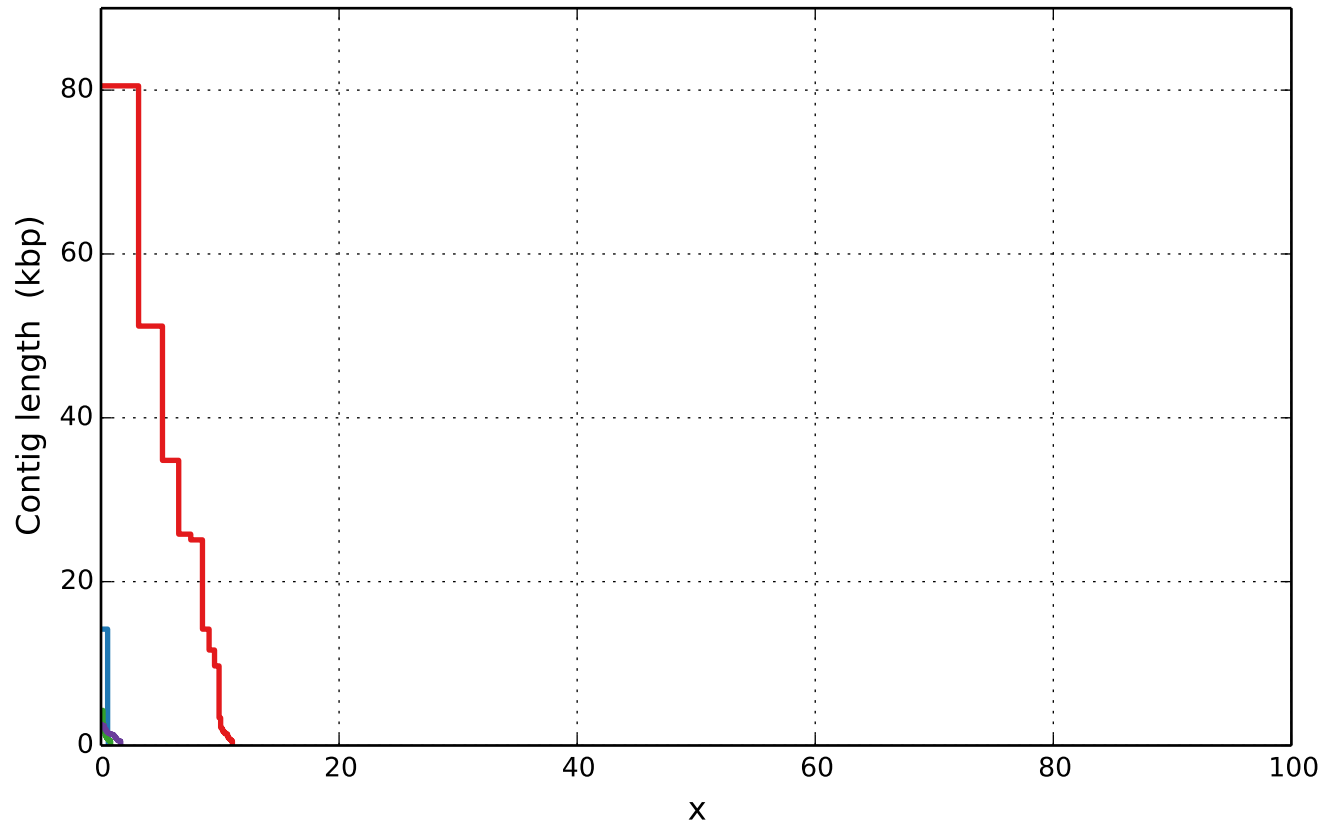
## Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	19	1	8	25
# with misassembly	0	0	3	1
# both parts are significant	3	0	0	4
Partially unaligned length	245925	471	3009	13567
# N's	225	0	1143	593

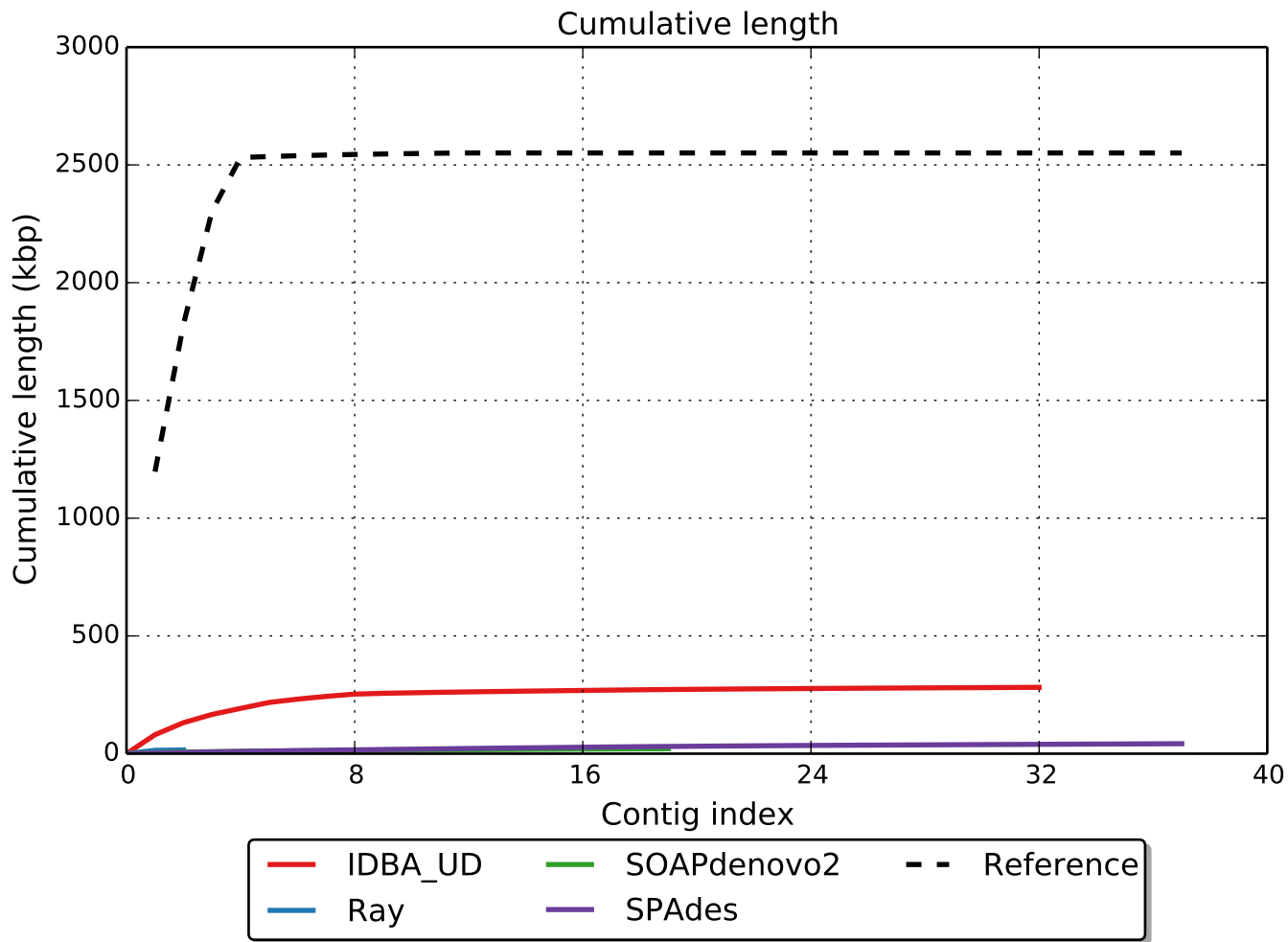
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



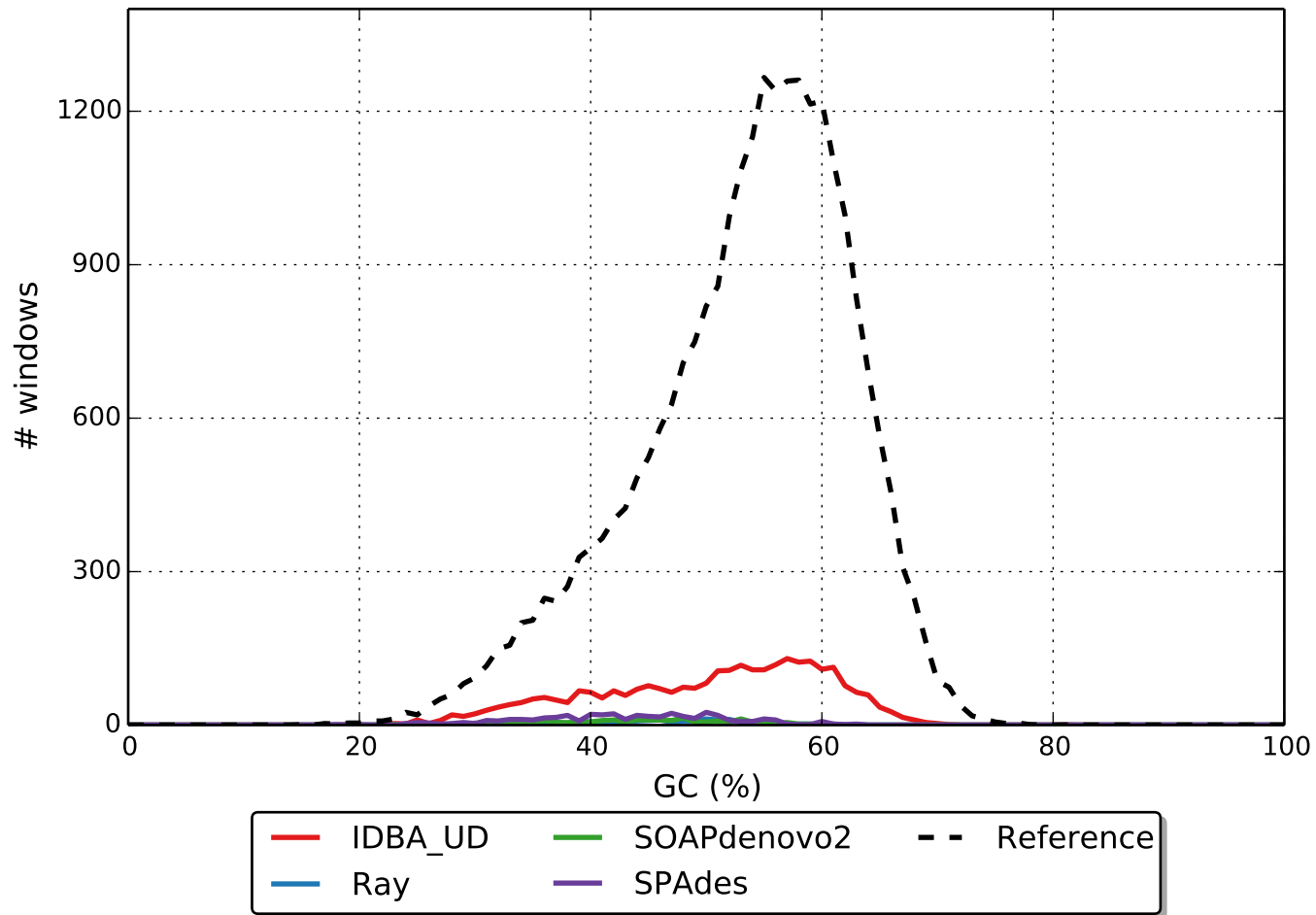
NGx

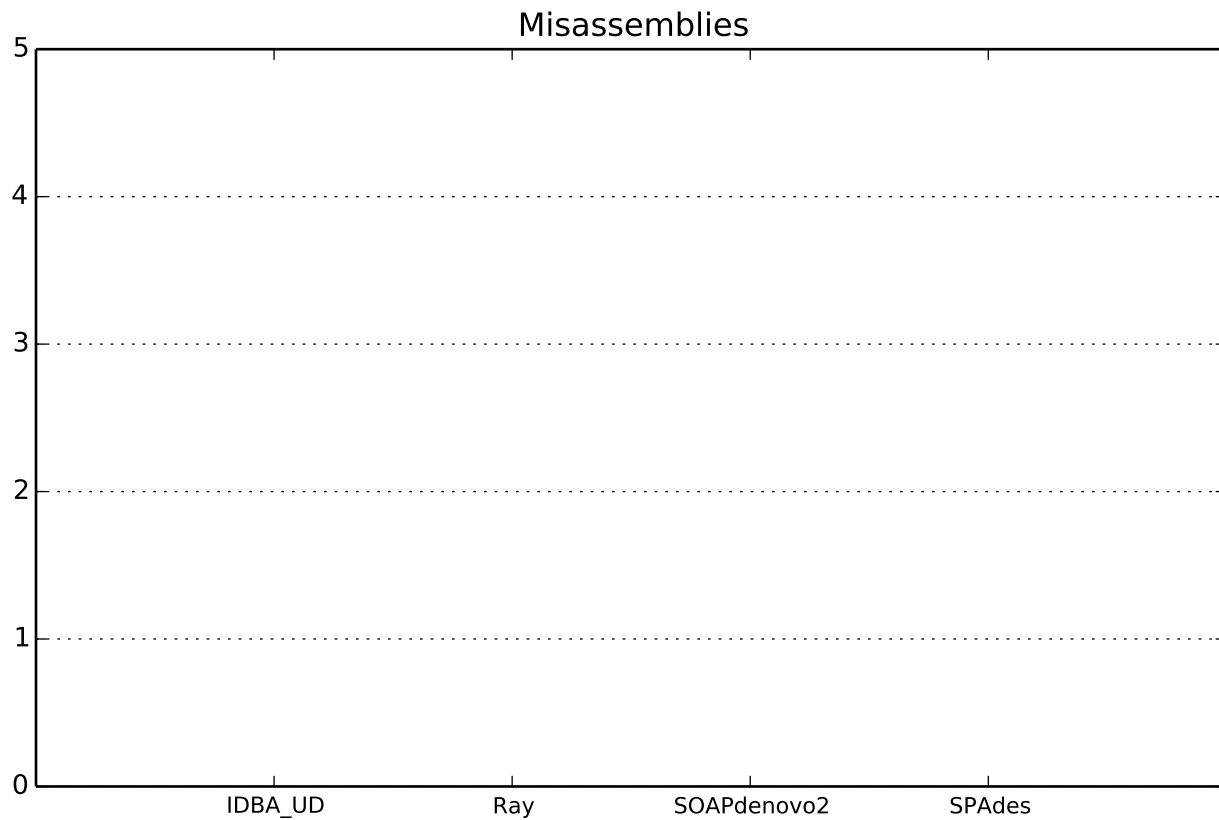


— IDBA\_UD    — SOAPdenovo2    — SPAdes  
— Ray



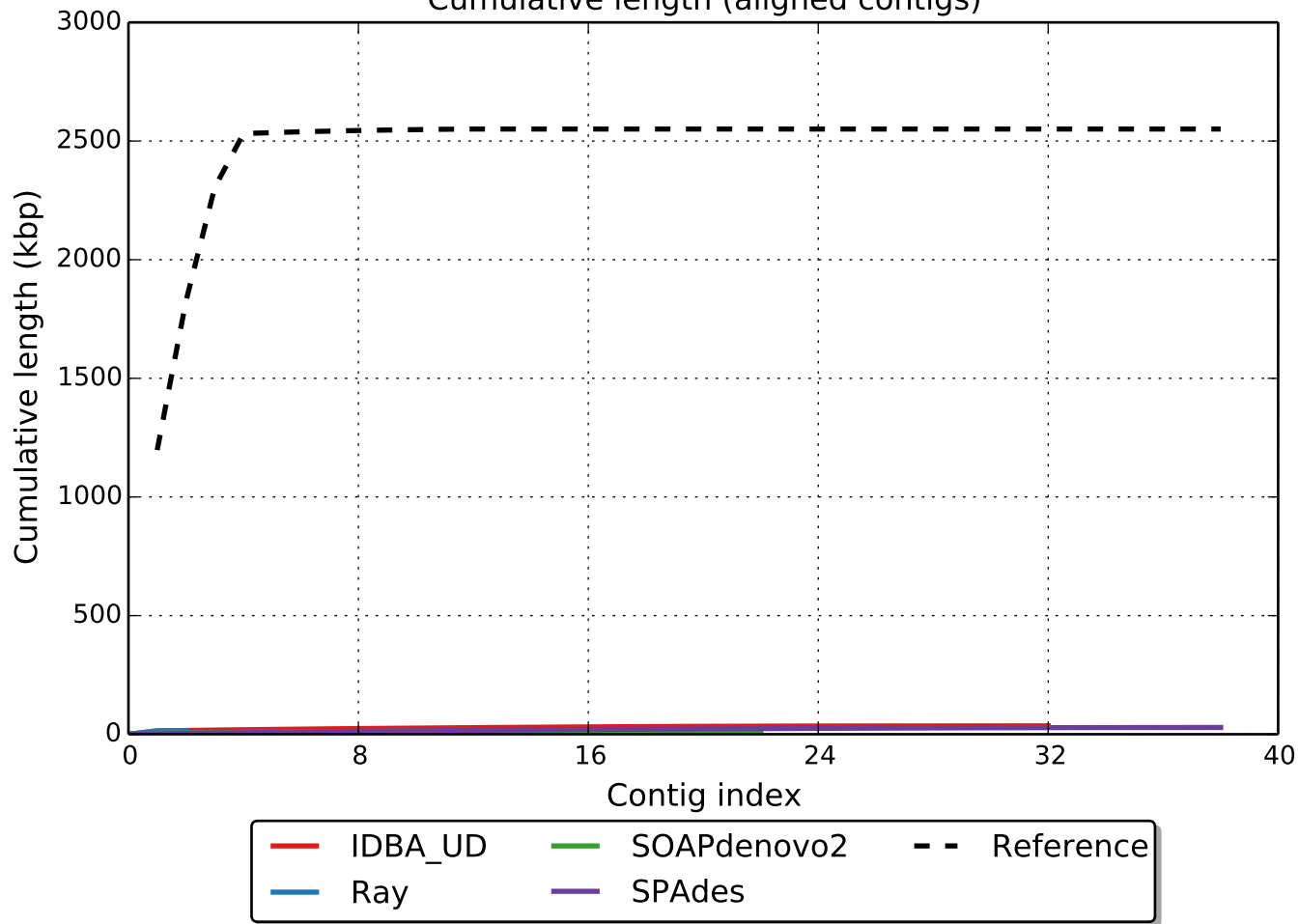
GC content



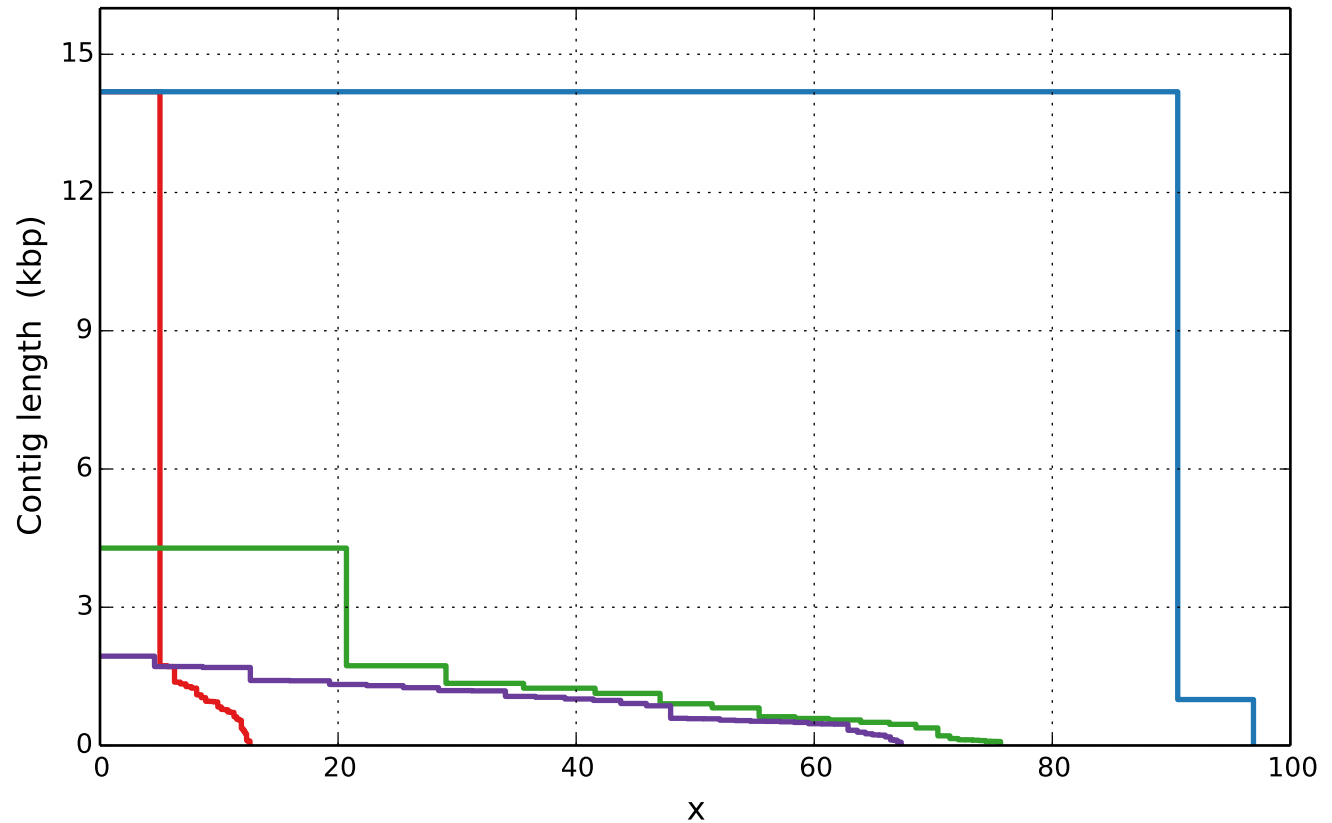




Cumulative length (aligned contigs)



NAx



— IDBA\_UD    — SOAPdenovo2    — SPAdes  
— Ray

