

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	6	1	1	9
# contigs (>= 5000 bp)	1	0	0	1
# contigs (>= 10000 bp)	1	0	0	0
# contigs (>= 25000 bp)	1	0	0	0
# contigs (>= 50000 bp)	1	0	0	0
Total length (>= 1000 bp)	144540	3996	1211	23919
Total length (>= 5000 bp)	135115	0	0	9625
Total length (>= 10000 bp)	135115	0	0	0
Total length (>= 25000 bp)	135115	0	0	0
Total length (>= 50000 bp)	135115	0	0	0
# contigs	9	1	4	13
Largest contig	135115	3996	1211	9625
Total length	146201	3996	3590	26971
Reference length	3561737	3561737	3561737	3561737
GC (%)	43.33	38.68	44.52	41.71
Reference GC (%)	31.37	31.37	31.37	31.37
N50	135115	3996	884	2535
N75	135115	3996	769	1591
L50	1	1	2	3
L75	1	1	3	6
# misassemblies	0	0	0	0
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	1	0	1	1
# structural variations	0	0	0	0
# unaligned contigs	0 + 3 part	0 + 1 part	0 + 2 part	0 + 8 part
Unaligned length	133052	1238	1011	12329
Genome fraction (%)	0.365	0.077	0.056	0.405
Duplication ratio	1.010	1.000	1.288	1.015
# N's per 100 kbp	0.00	4129.13	10278.55	437.51
# mismatches per 100 kbp	3688.05	4131.93	3496.50	3651.61
# indels per 100 kbp	84.52	36.25	49.95	62.36
Largest alignment	4063	2758	884	4063
NA50	-	2758	360	601
NGA50	-	-	-	-
LA50	-	1	3	8

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

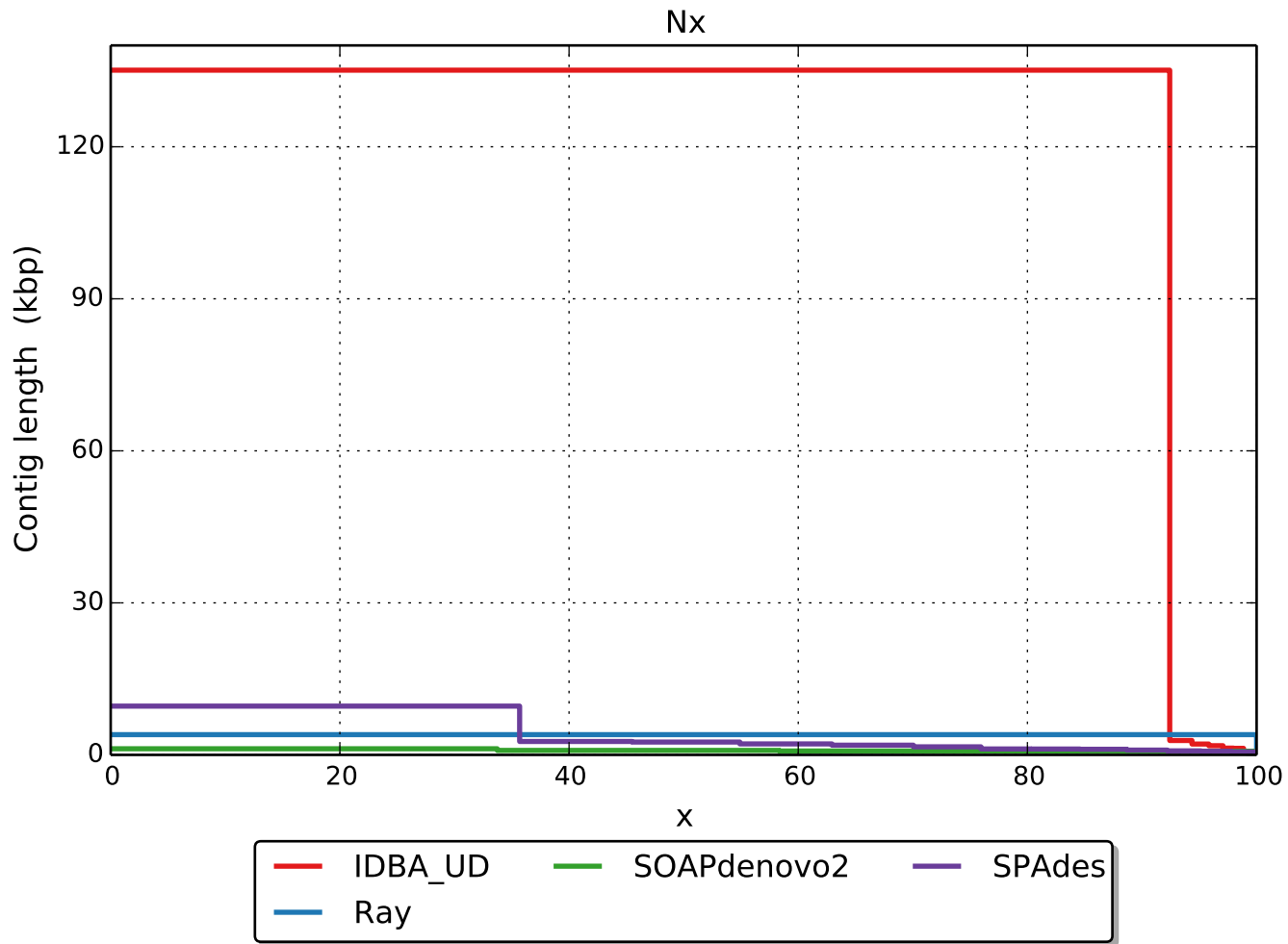
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	0	0	0
# relocations	0	0	0	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	2	1	1	2
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	1	0	1	1
# structural variations	0	0	0	0
# mismatches	480	114	70	527
# indels	11	1	1	9
# short indels	11	1	1	9
# long indels	0	0	0	0
Indels length	12	1	1	15

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).

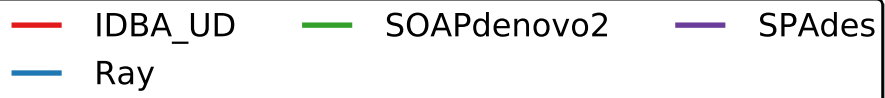
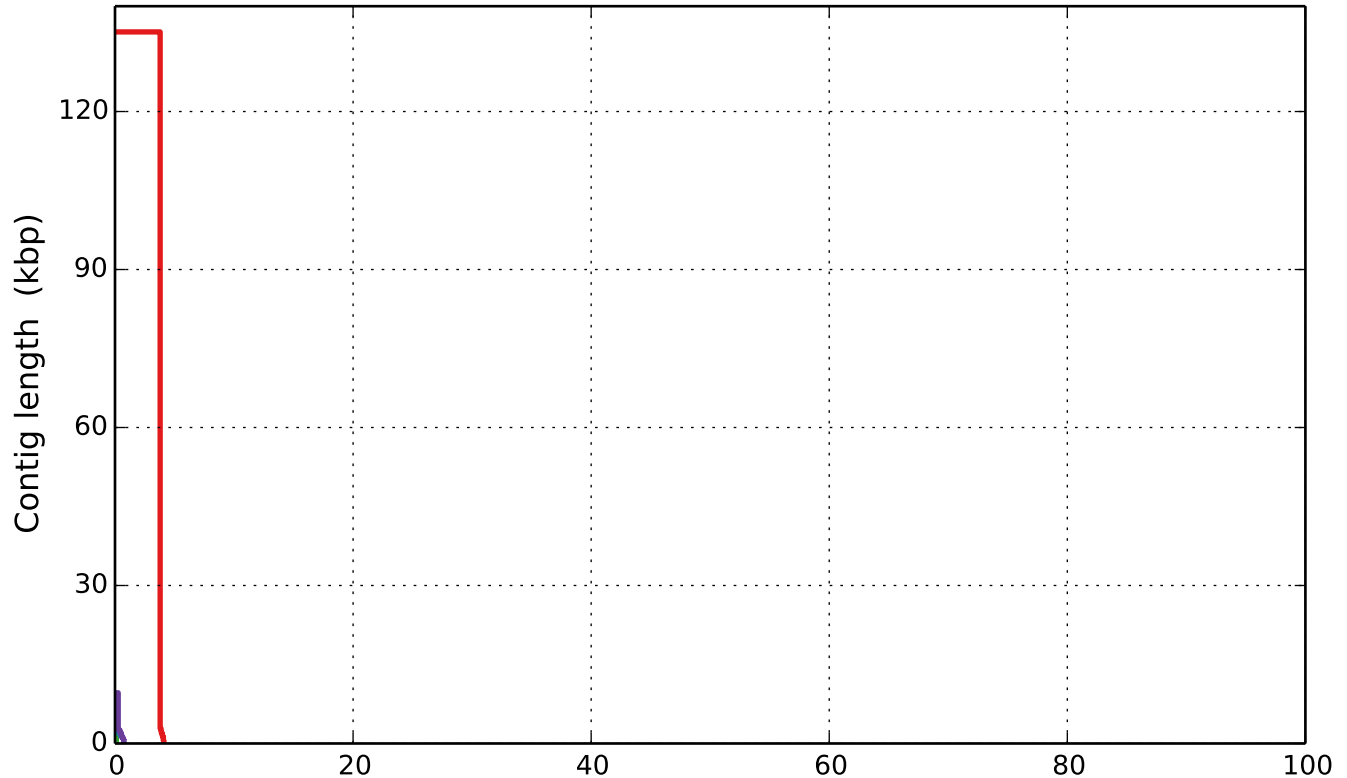
Unaligned report

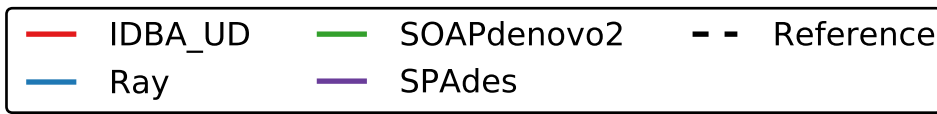
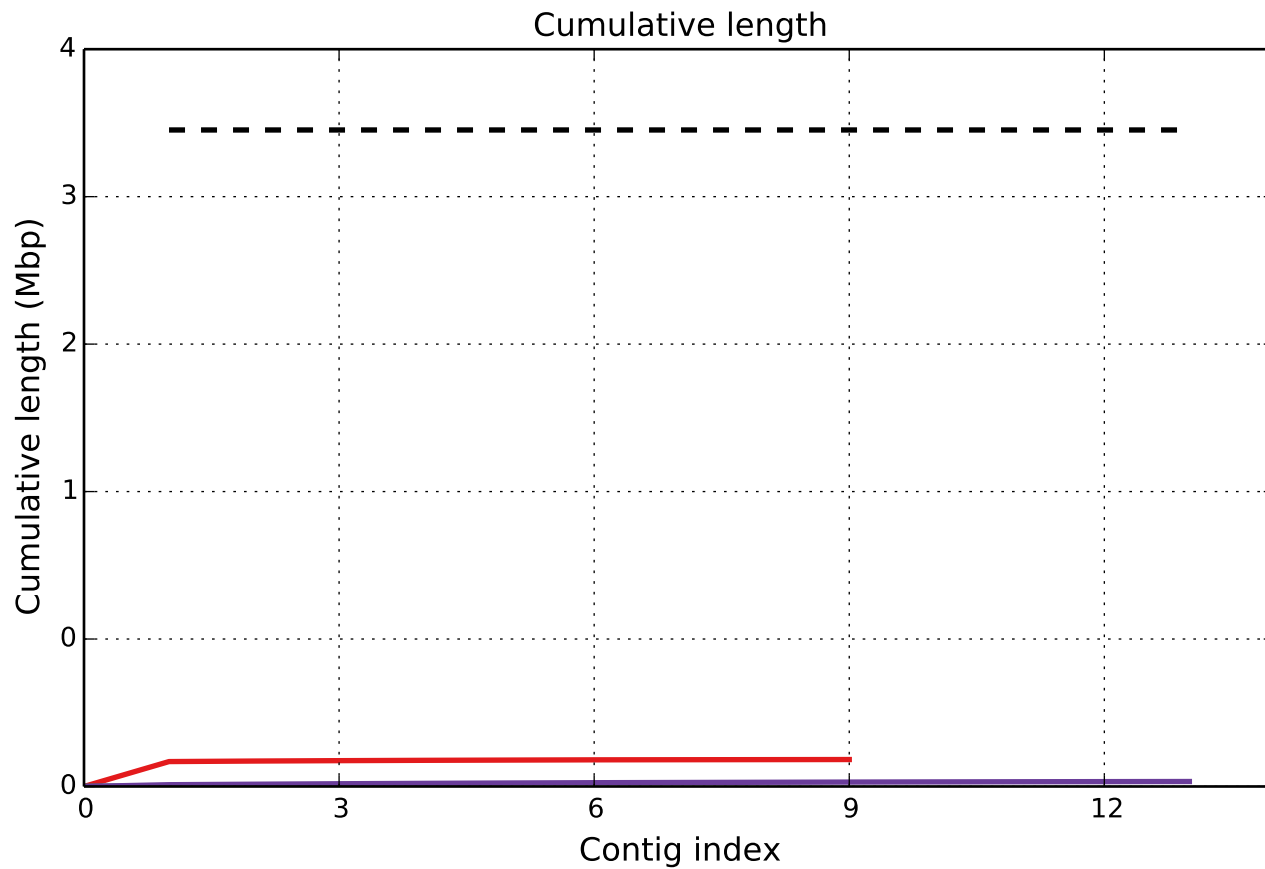
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	3	1	2	8
# with misassembly	0	0	0	0
# both parts are significant	2	1	0	2
Partially unaligned length	133052	1238	1011	12329
# N's	0	165	369	118

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).

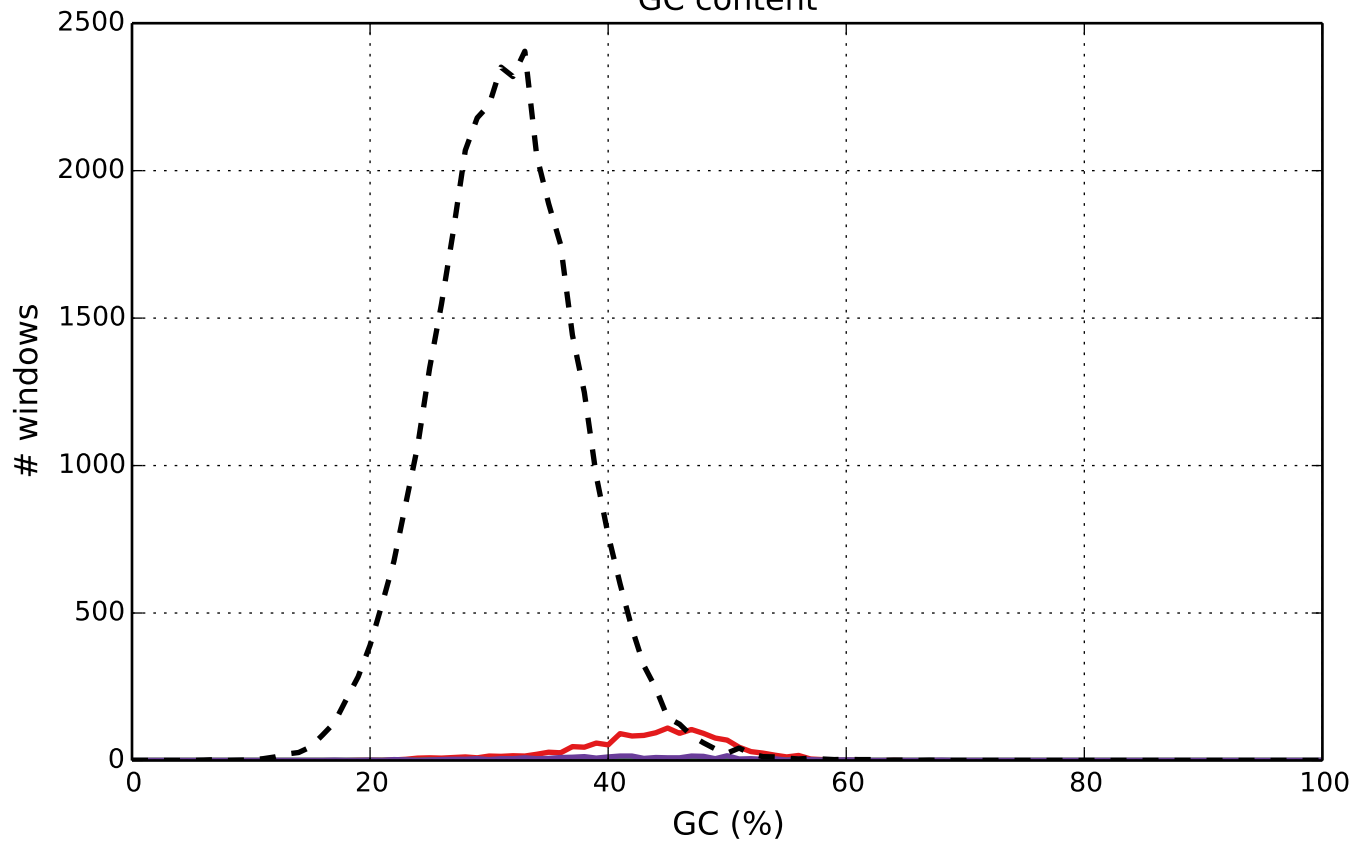


NGx

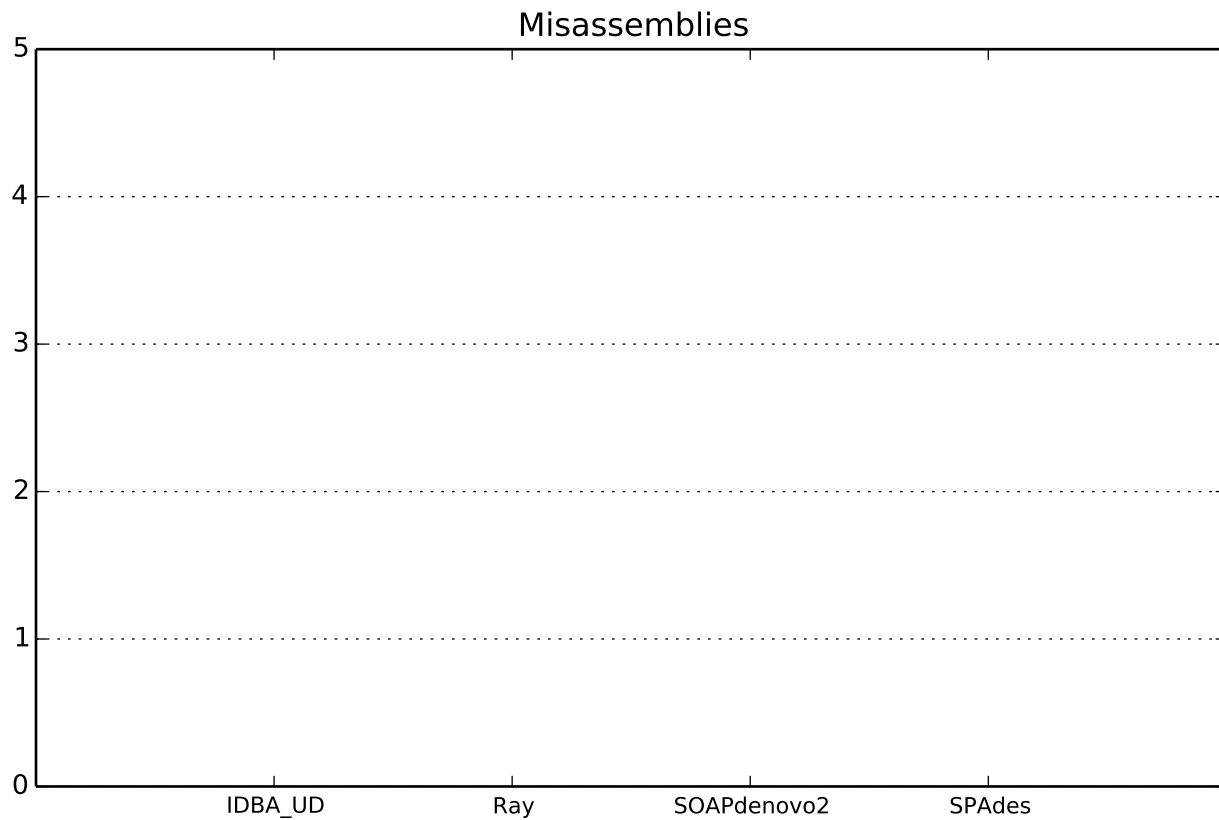


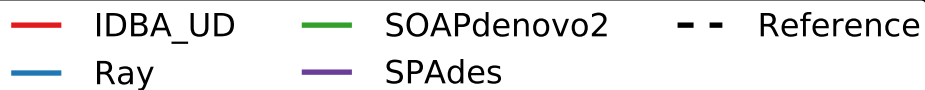
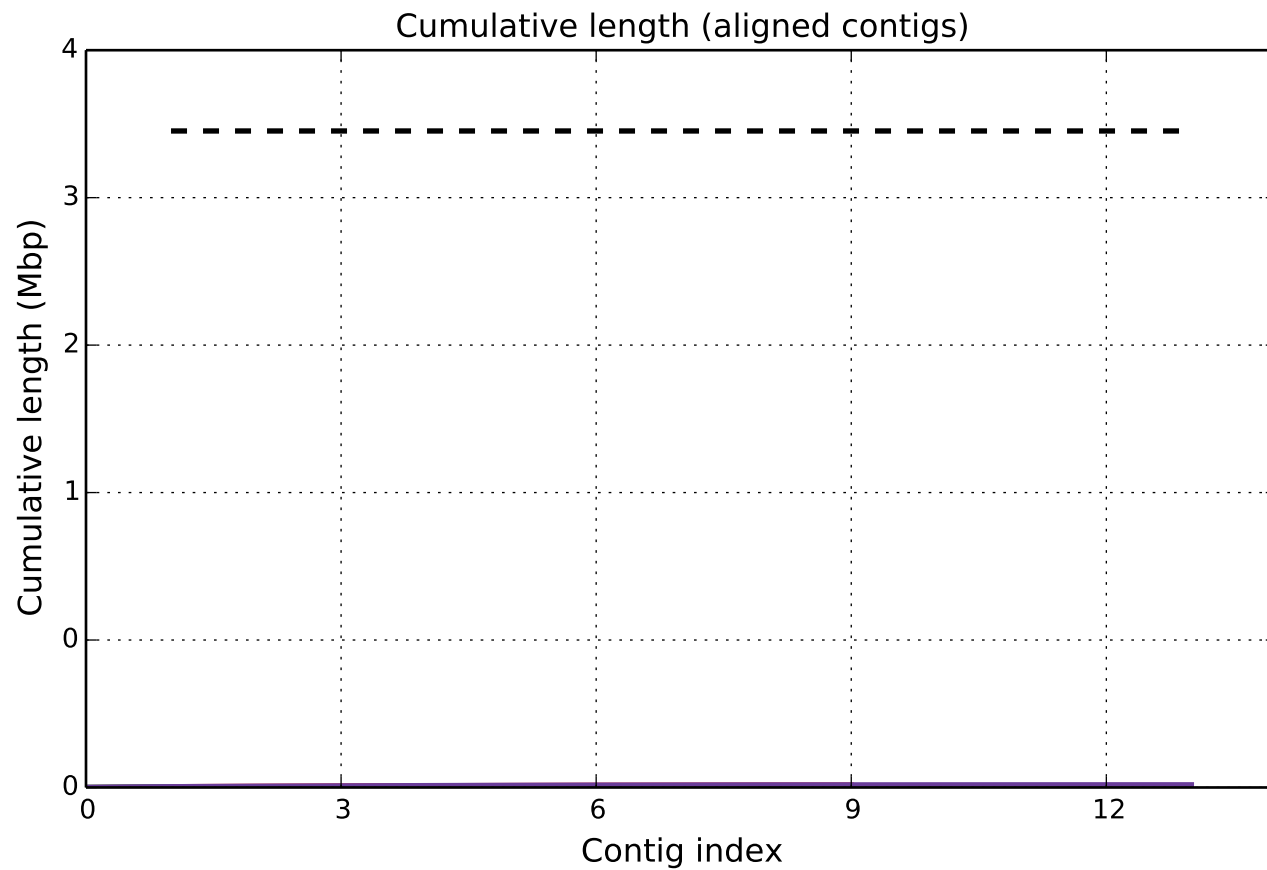


GC content

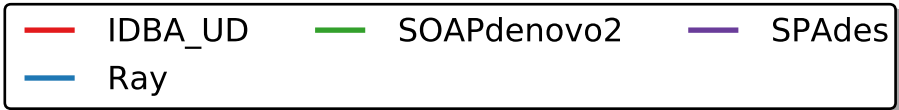
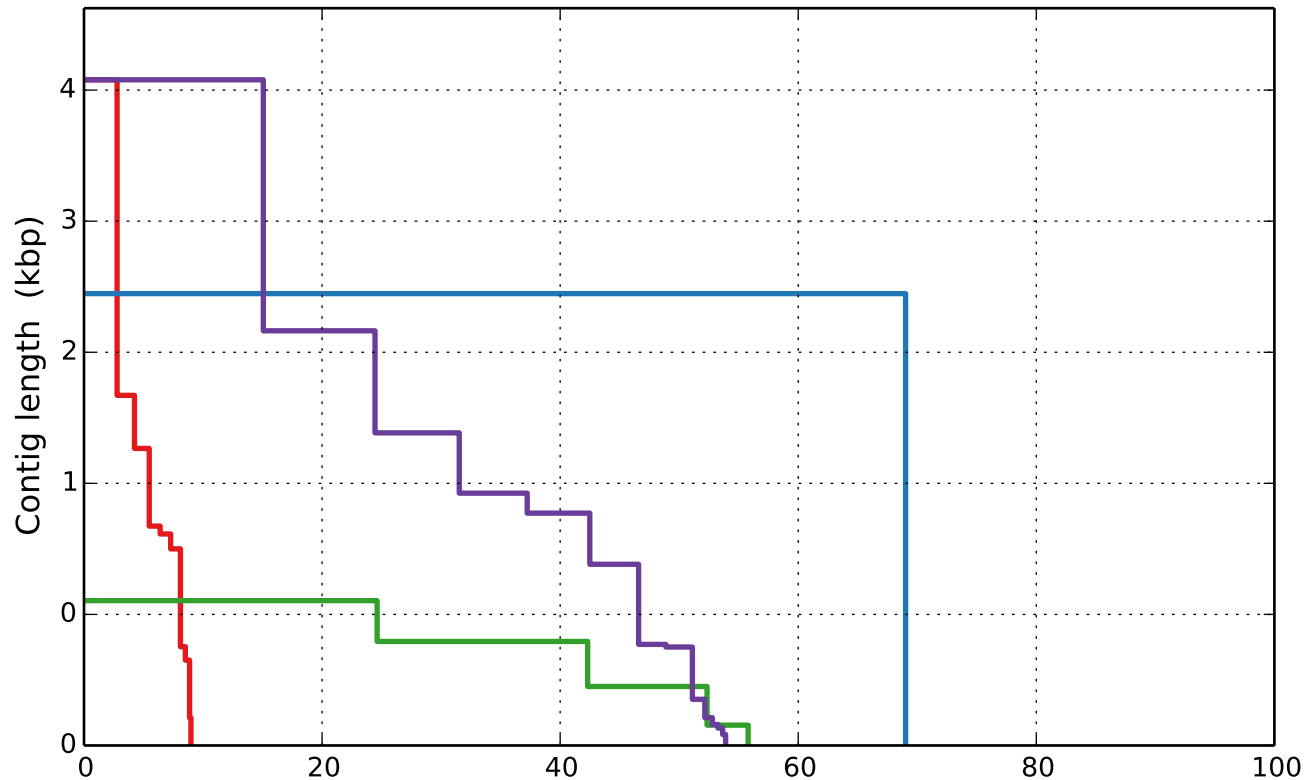


— IDBA_UD — SOAPdenovo2 - - Reference
— Ray — SPAdes

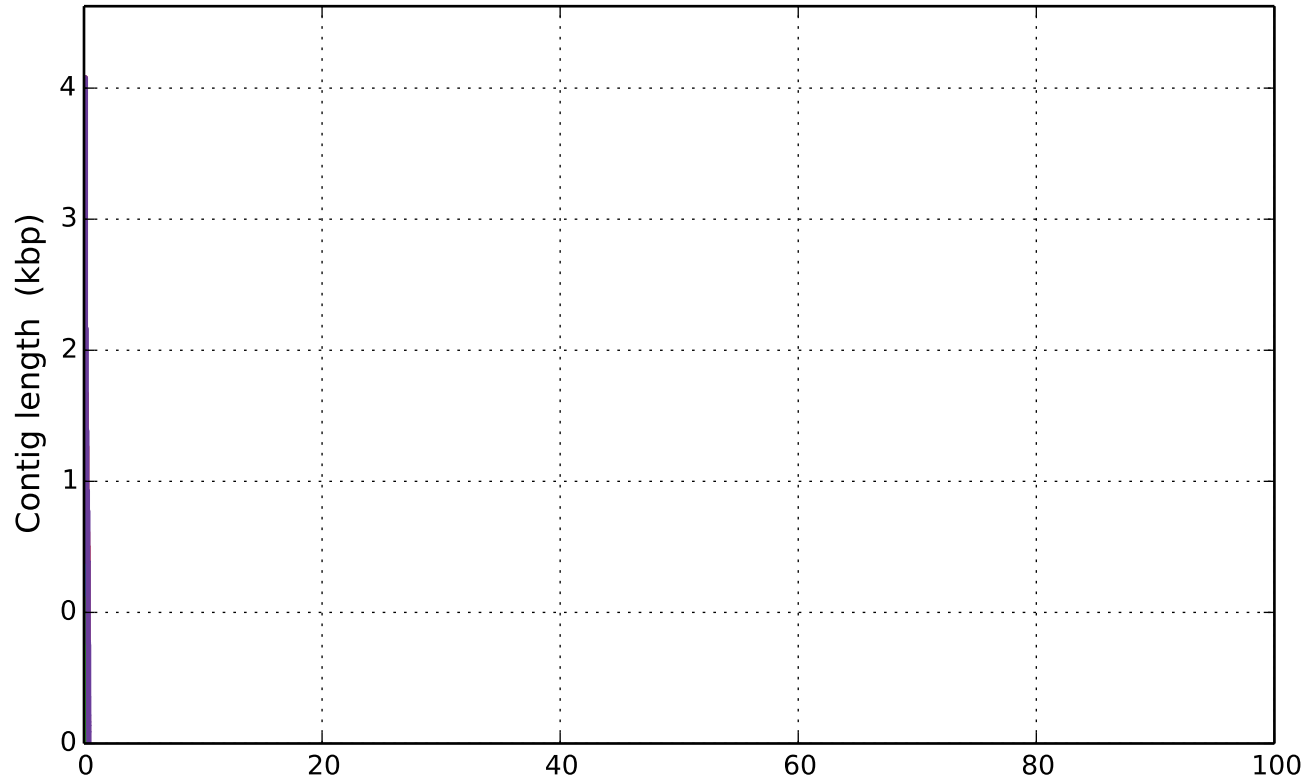




NAx



NGAx



IDBA_UD

SOAPdenovo2

SPAdes

Ray

