

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	9	5	6	5
# contigs (>= 5000 bp)	3	0	0	2
# contigs (>= 10000 bp)	1	0	0	2
# contigs (>= 25000 bp)	0	0	0	1
# contigs (>= 50000 bp)	0	0	0	0
Total length (>= 1000 bp)	45827	10543	7871	63356
Total length (>= 5000 bp)	31582	0	0	57735
Total length (>= 10000 bp)	13115	0	0	57735
Total length (>= 25000 bp)	0	0	0	42610
Total length (>= 50000 bp)	0	0	0	0
# contigs	13	8	12	5
Largest contig	13115	3687	2005	42610
Total length	48468	13060	12244	63356
Reference length	1631609	1631609	1631609	1631609
GC (%)	46.13	47.78	49.80	46.02
Reference GC (%)	46.03	46.03	46.03	46.03
N50	8549	2018	1061	42610
N75	3759	1146	854	15125
L50	3	3	5	1
L75	5	5	8	2
# misassemblies	0	0	0	0
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	0	3	0
# structural variations	1	0	0	1
# unaligned contigs	0 + 5 part	0 + 1 part	0 + 0 part	0 + 2 part
Unaligned length	29657	1644	0	42647
Genome fraction (%)	1.100	0.699	0.710	1.079
Duplication ratio	1.048	1.002	1.057	1.176
# N's per 100 kbp	0.00	597.24	2678.86	97.86
# mismatches per 100 kbp	2496.80	728.20	621.71	2543.72
# indels per 100 kbp	195.06	35.09	0.00	136.27
Largest alignment	8518	3687	2005	12070
NA50	-	1265	1061	-
NGA50	-	-	-	-
NA75	-	893	797	-
LA50	-	3	5	-
LA75	-	6	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

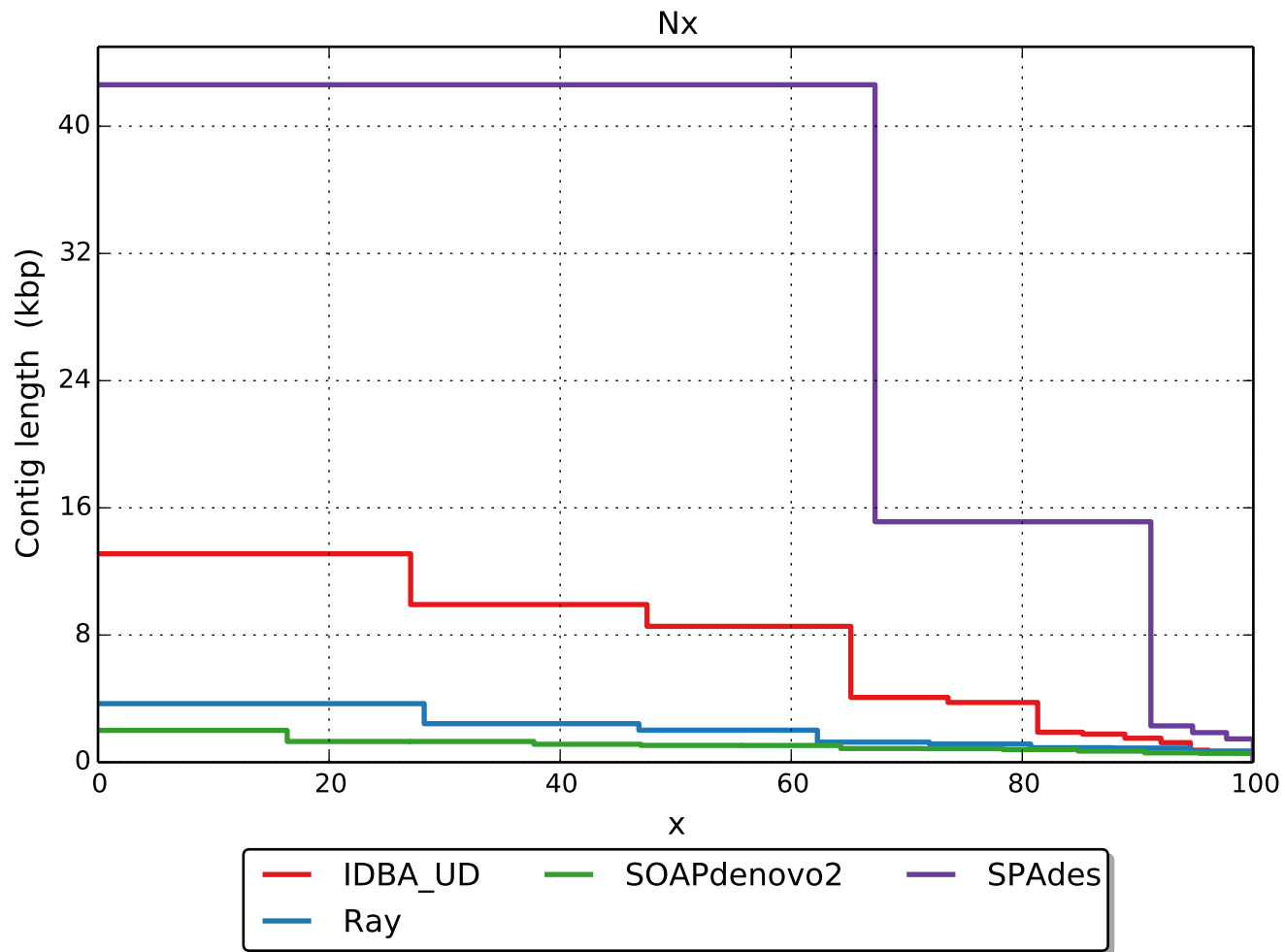
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	0	0	0
# relocations	0	0	0	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	0	0	0	1
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	0	3	0
# structural variations	1	0	0	1
# mismatches	448	83	72	448
# indels	35	4	0	24
# short indels	31	4	0	22
# long indels	4	0	0	2
Indels length	82	9	0	82

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).

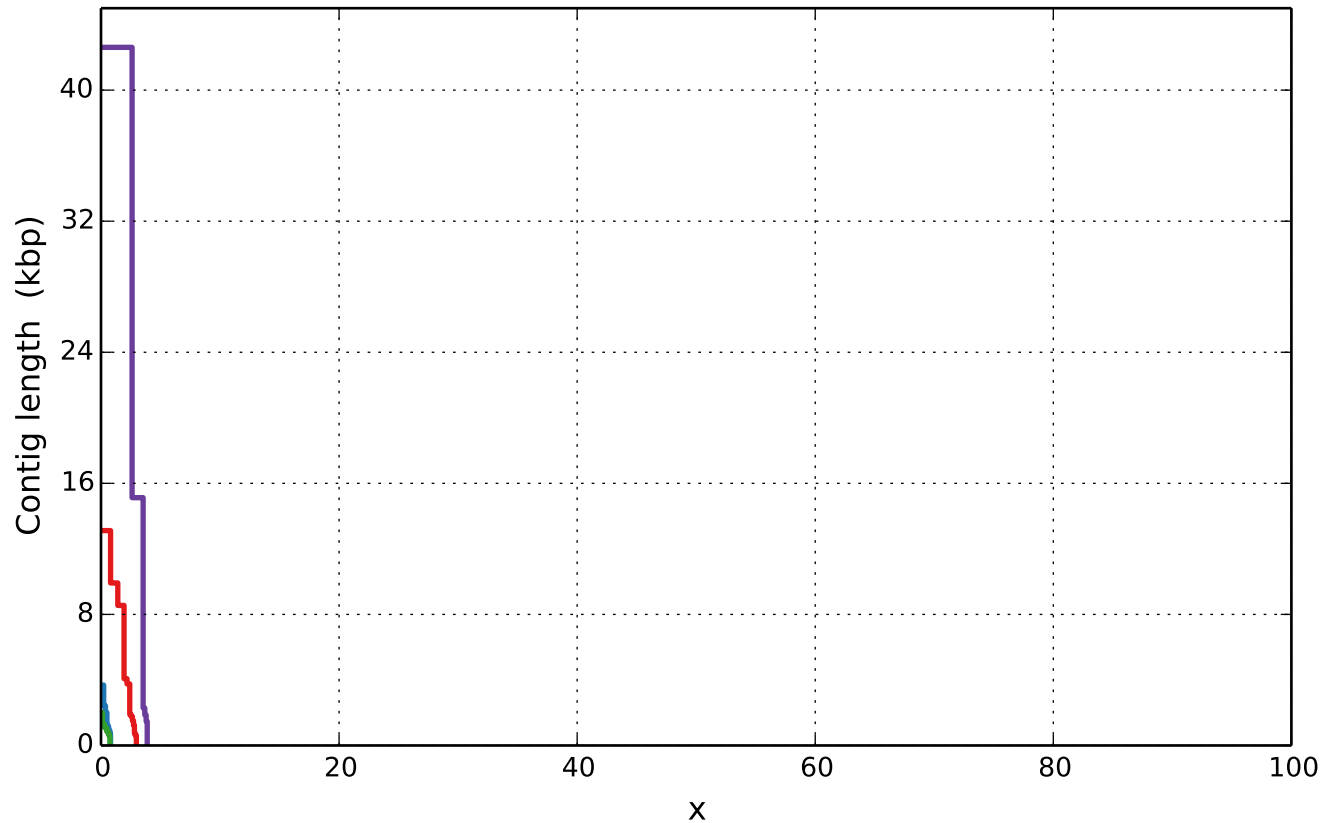
Unaligned report

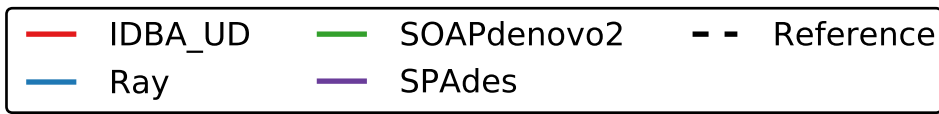
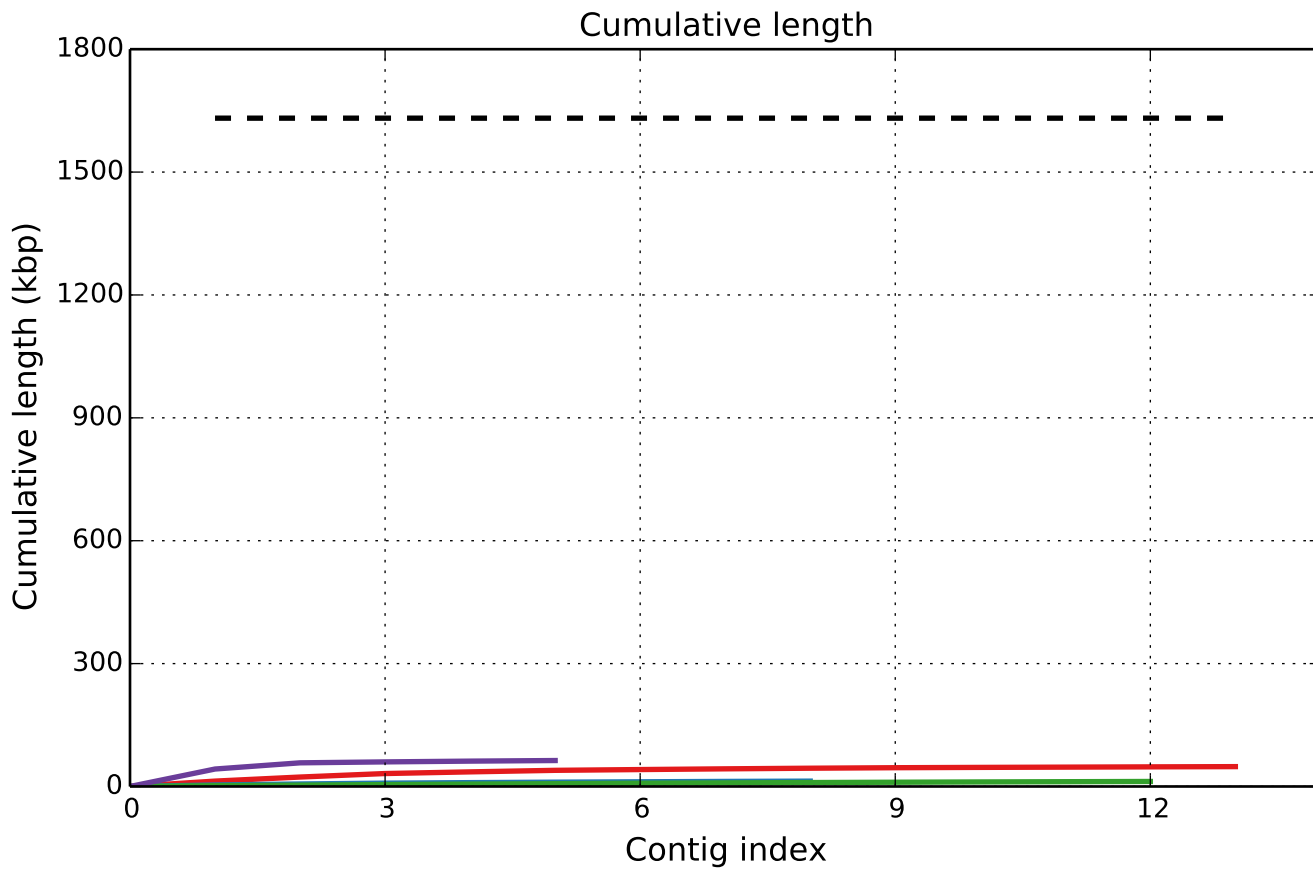
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	5	1	0	2
# with misassembly	0	0	0	0
# both parts are significant	0	0	0	0
Partially unaligned length	29657	1644	0	42647
# N's	0	78	328	62

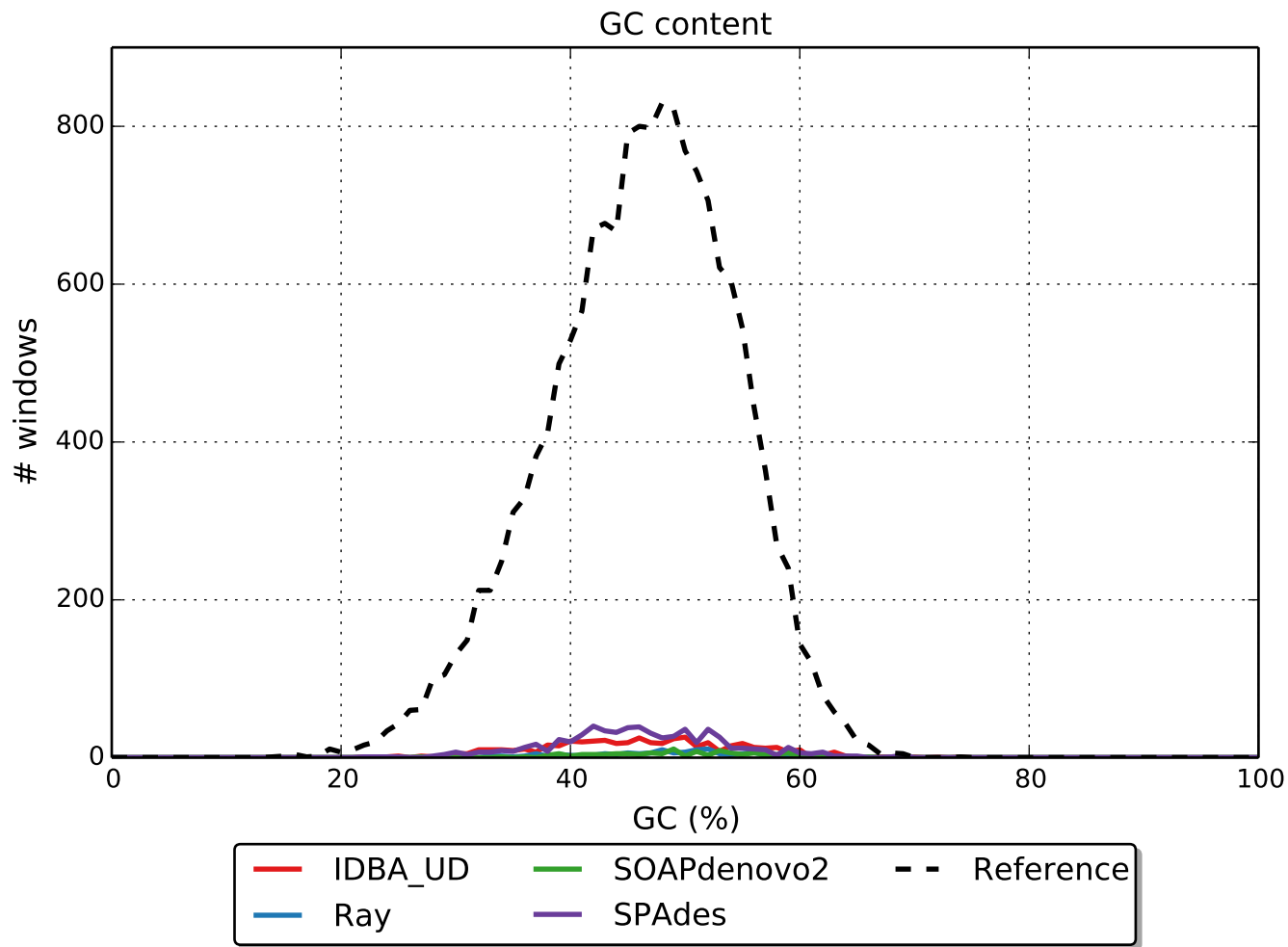
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

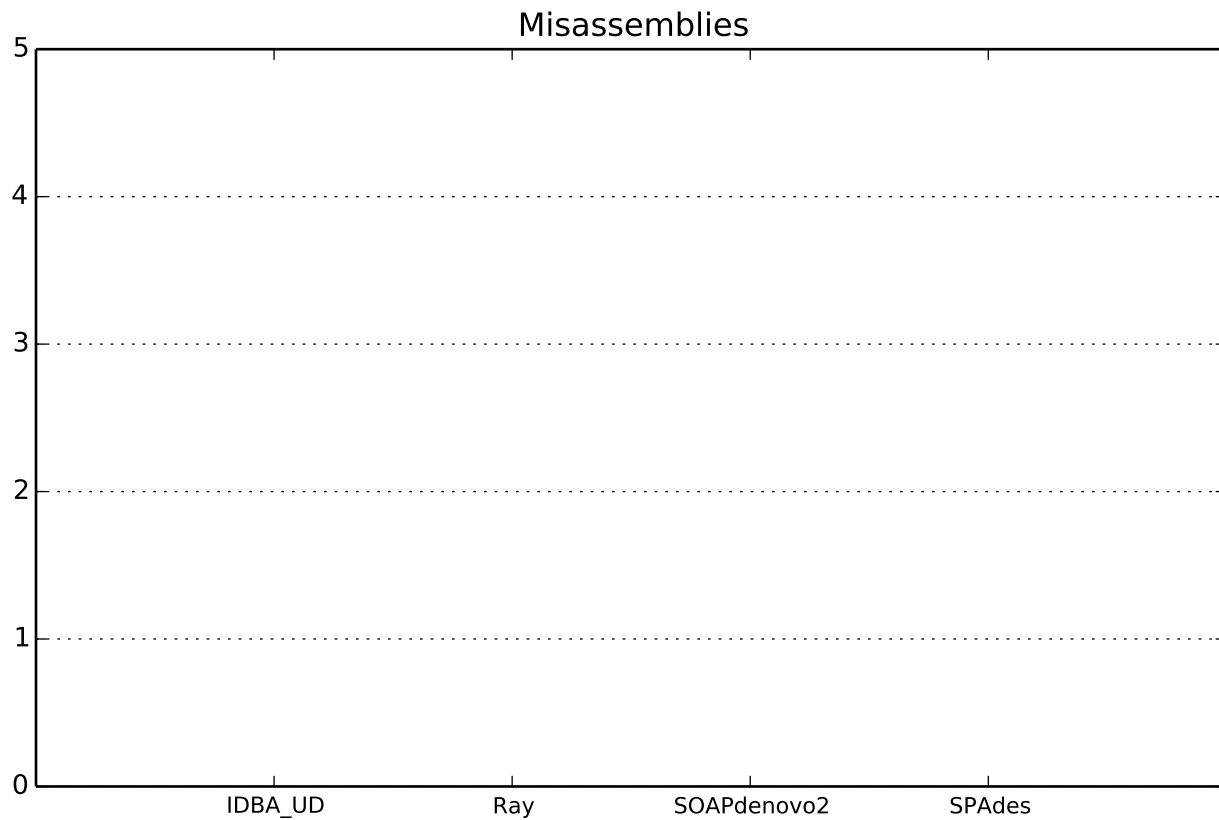


NGx

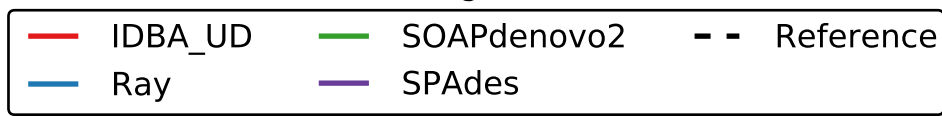
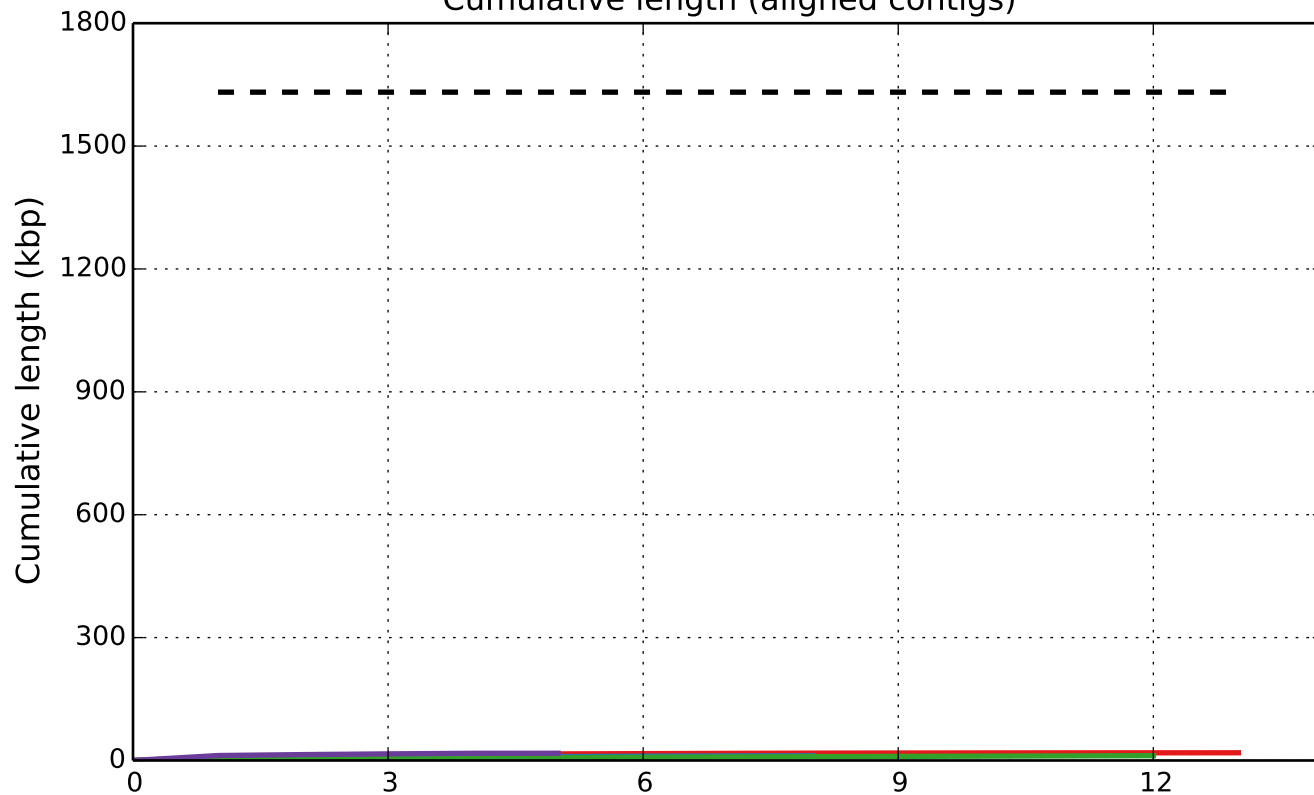




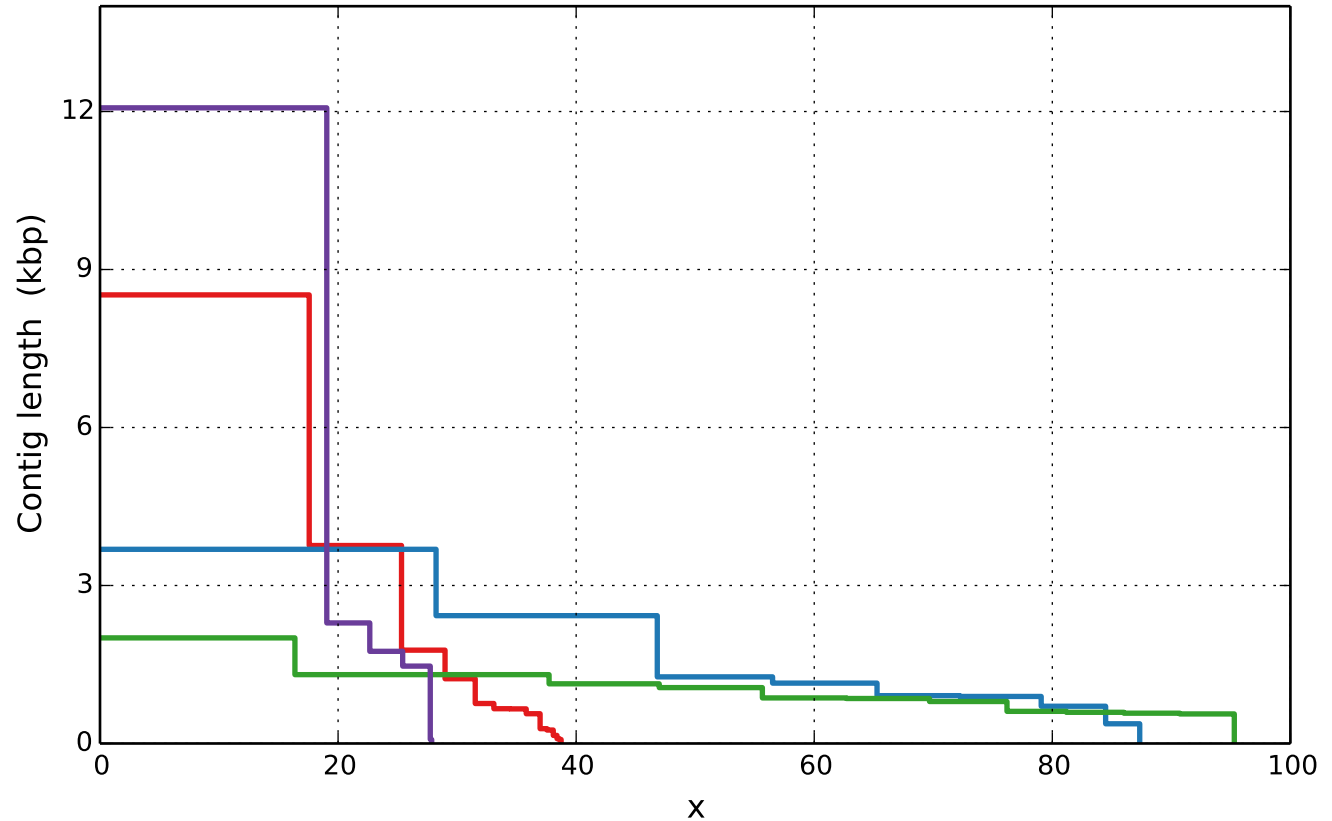




Cumulative length (aligned contigs)



NAx



— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray

