

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	15	8	15	9
# contigs (>= 5000 bp)	5	5	1	5
# contigs (>= 10000 bp)	4	3	0	2
# contigs (>= 25000 bp)	4	1	0	2
# contigs (>= 50000 bp)	4	0	0	2
Total length (>= 1000 bp)	320415	89156	36017	170578
Total length (>= 5000 bp)	299088	79353	5607	160752
Total length (>= 10000 bp)	293689	68347	0	143151
Total length (>= 25000 bp)	293689	34367	0	143151
Total length (>= 50000 bp)	293689	0	0	143151
# contigs	22	11	31	13
Largest contig	111563	34367	5607	85969
Total length	325772	91111	46147	173487
Reference length	2517763	2517763	2517763	2517763
GC (%)	39.80	39.58	40.71	40.33
Reference GC (%)	33.79	33.79	33.79	33.79
N50	72102	21544	2021	57182
N75	50587	12436	1570	57182
L50	2	2	8	2
L75	4	3	14	2
# misassemblies	3	3	1	3
# misassembled contigs	1	1	1	1
Misassembled contigs length	50587	34367	1570	57182
# local misassemblies	3	2	3	3
# structural variations	0	0	0	0
# unaligned contigs	0 + 13 part	0 + 6 part	0 + 8 part	0 + 7 part
Unaligned length	257582	42581	8438	97509
Genome fraction (%)	1.990	1.628	1.494	2.084
Duplication ratio	1.361	1.184	1.002	1.448
# N's per 100 kbp	19.95	849.51	808.29	157.94
# mismatches per 100 kbp	2660.47	2880.70	2610.24	2478.13
# indels per 100 kbp	37.92	26.83	31.90	32.41
Largest alignment	14054	10443	3359	14252
NA50	-	-	1614	-
NGA50	-	-	-	-
NA75	-	-	559	-
LA50	-	-	11	-
LA75	-	-	25	-

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

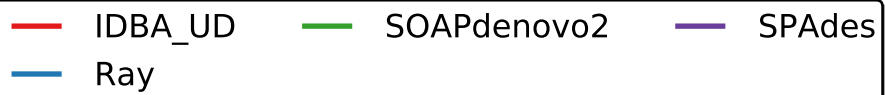
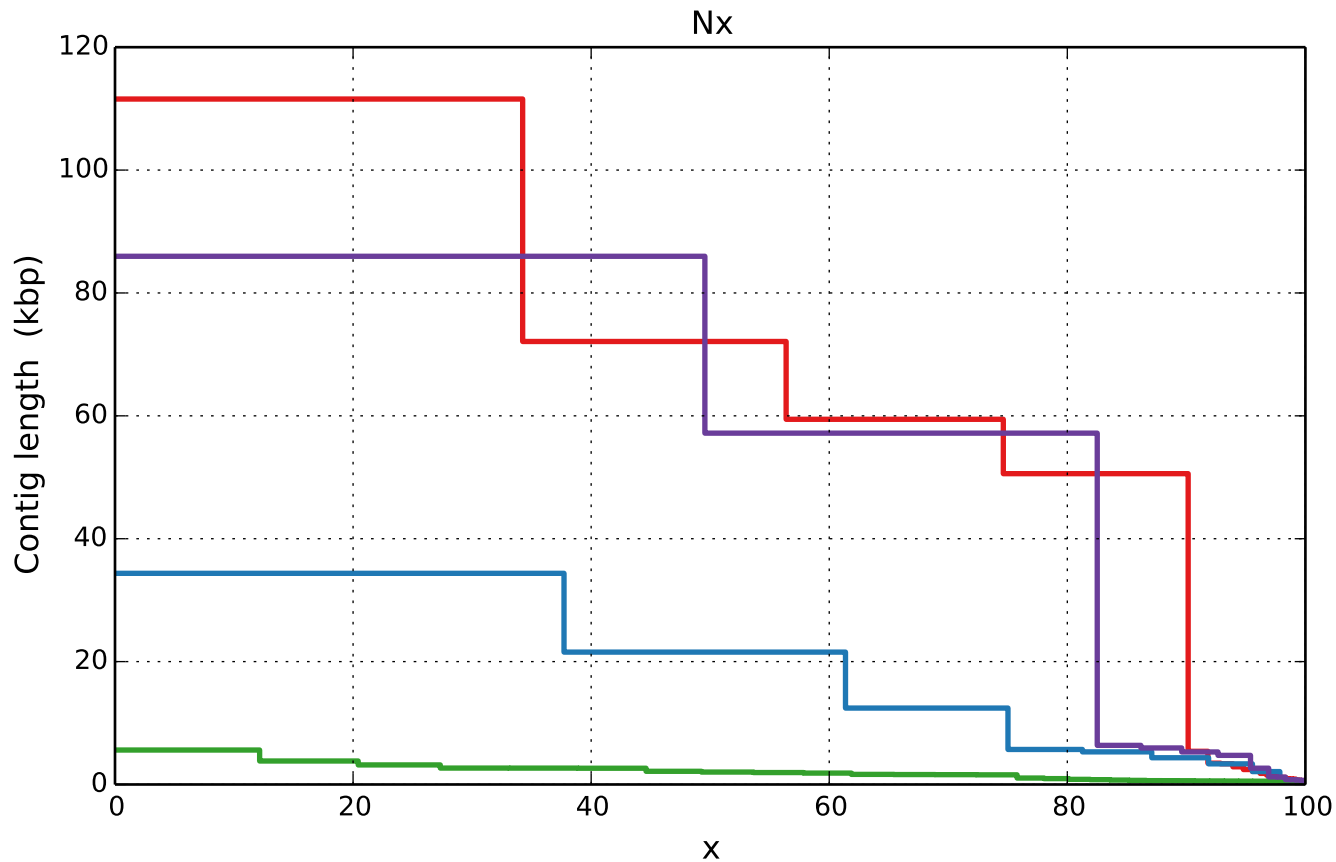
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	3	3	1	3
# relocations	3	3	1	3
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	7	6	3	4
# misassembled contigs	1	1	1	1
Misassembled contigs length	50587	34367	1570	57182
# local misassemblies	3	2	3	3
# structural variations	0	0	0	0
# mismatches	1333	1181	982	1300
# indels	19	11	12	17
# short indels	16	8	10	13
# long indels	3	3	2	4
Indels length	48	38	28	66

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).

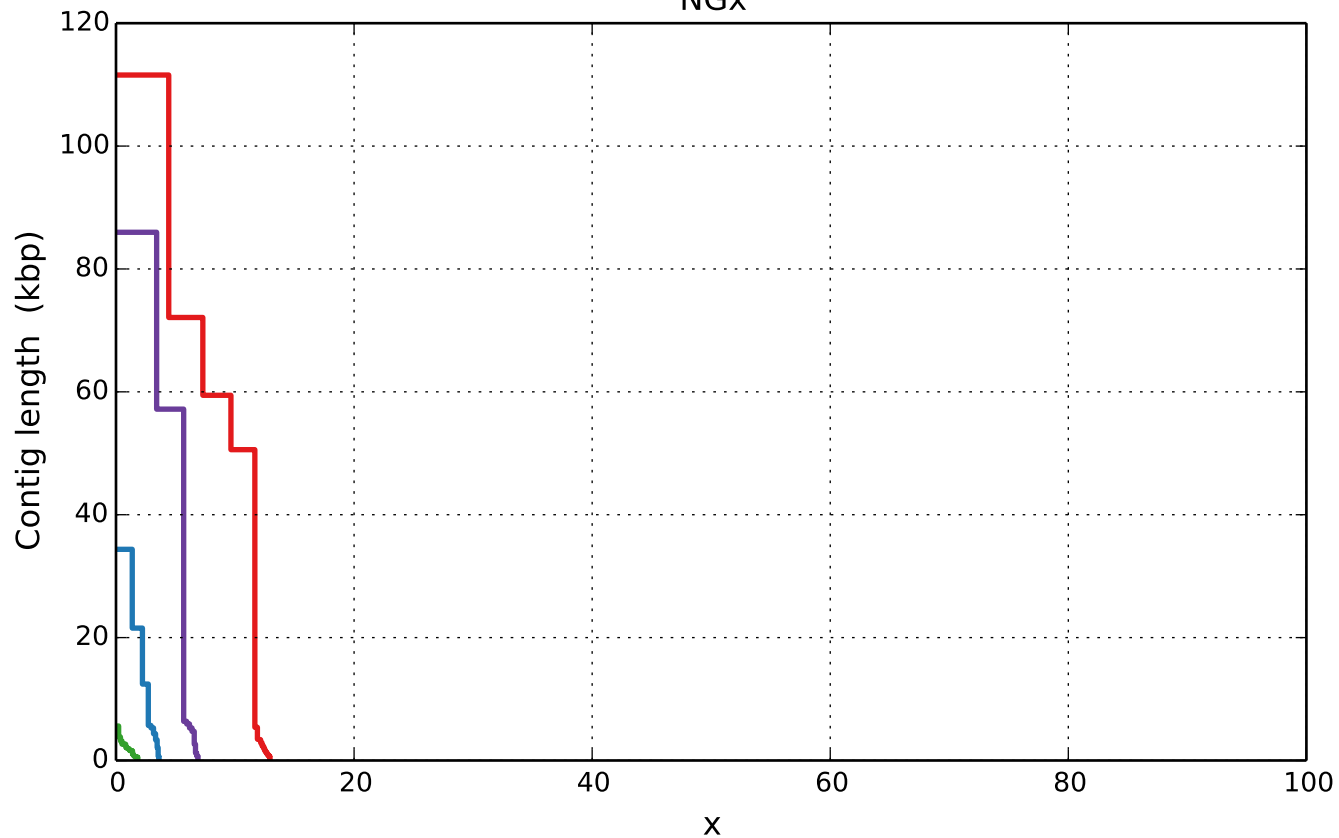
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	13	6	8	7
# with misassembly	0	1	1	1
# both parts are significant	5	5	3	3
Partially unaligned length	257582	42581	8438	97509
# N's	65	774	373	274

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).

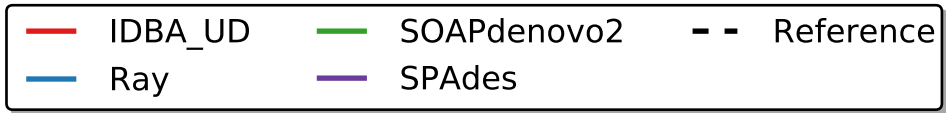
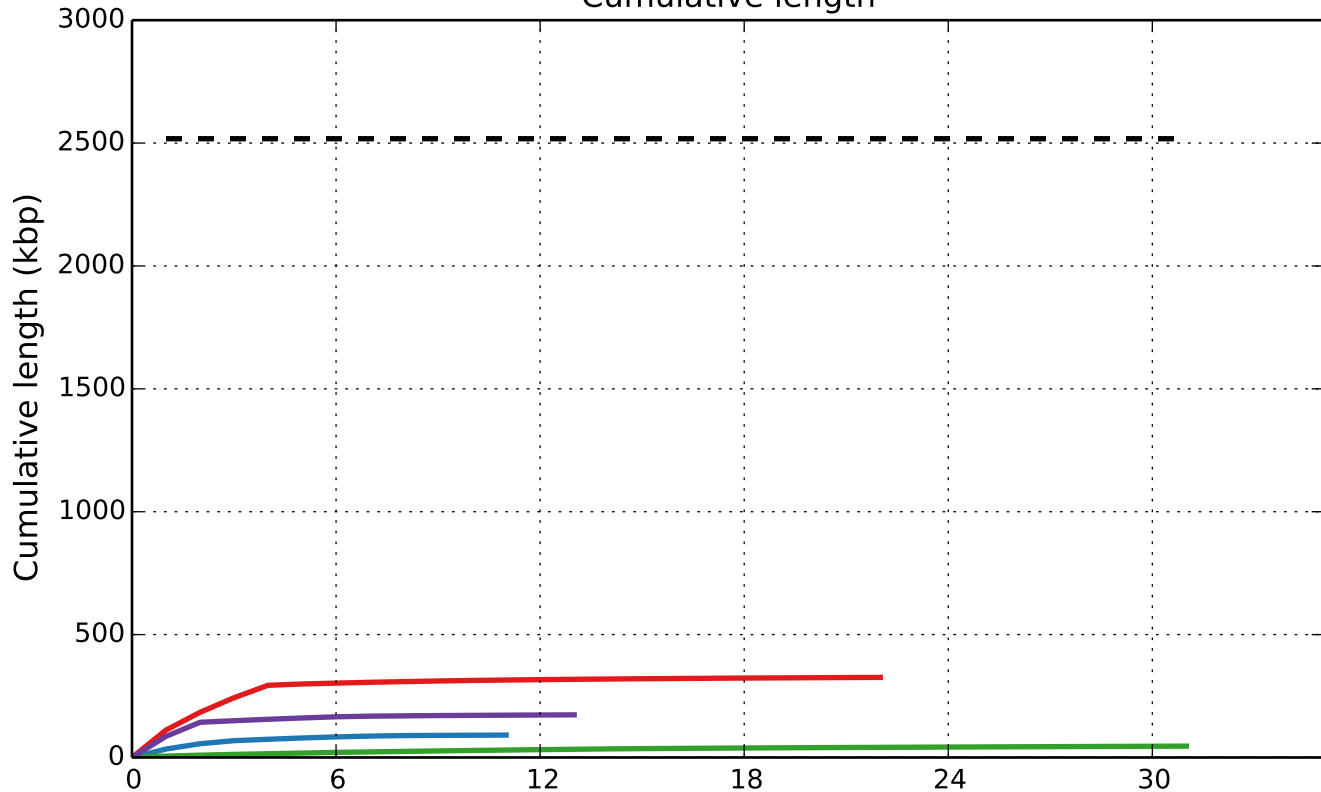


NGx

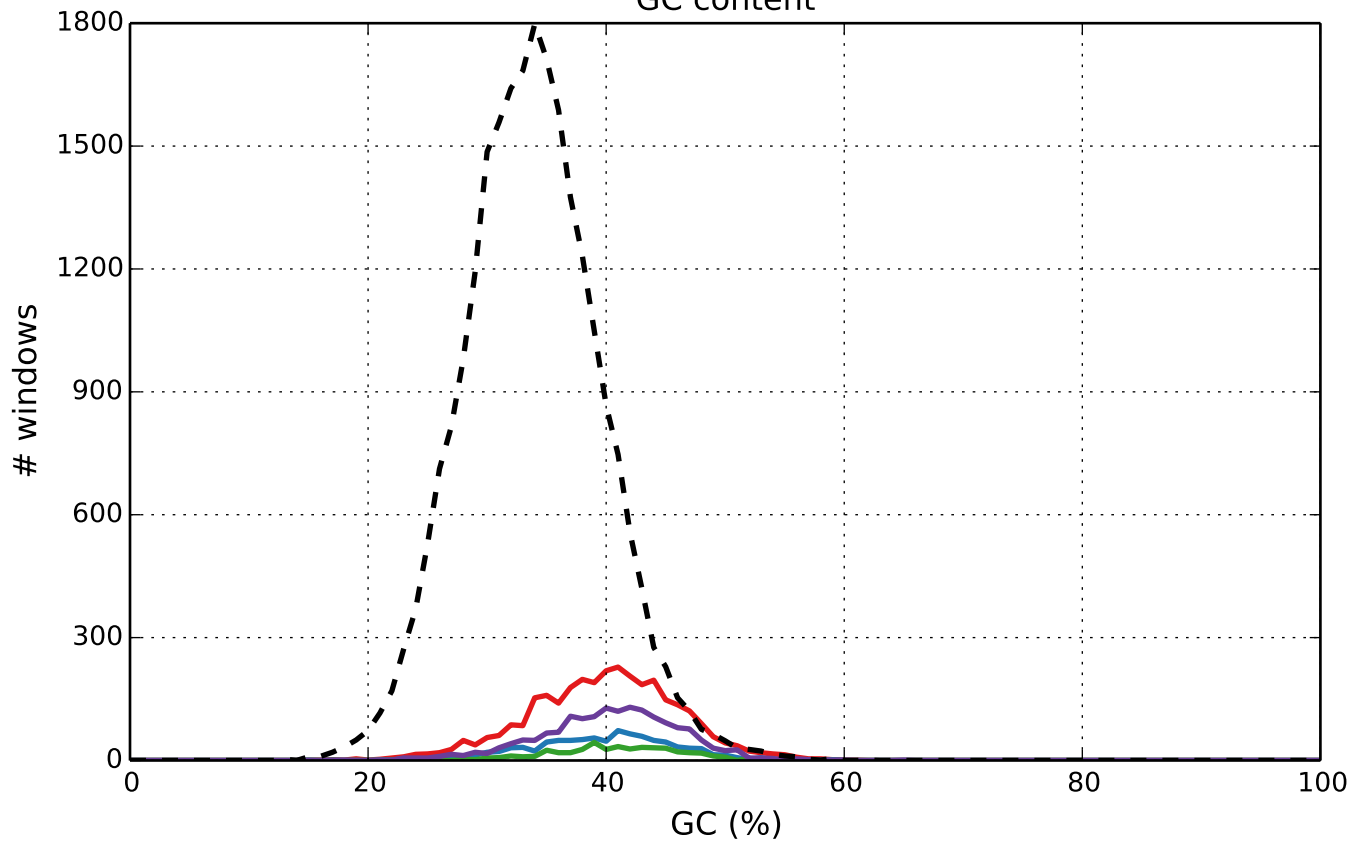


— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray

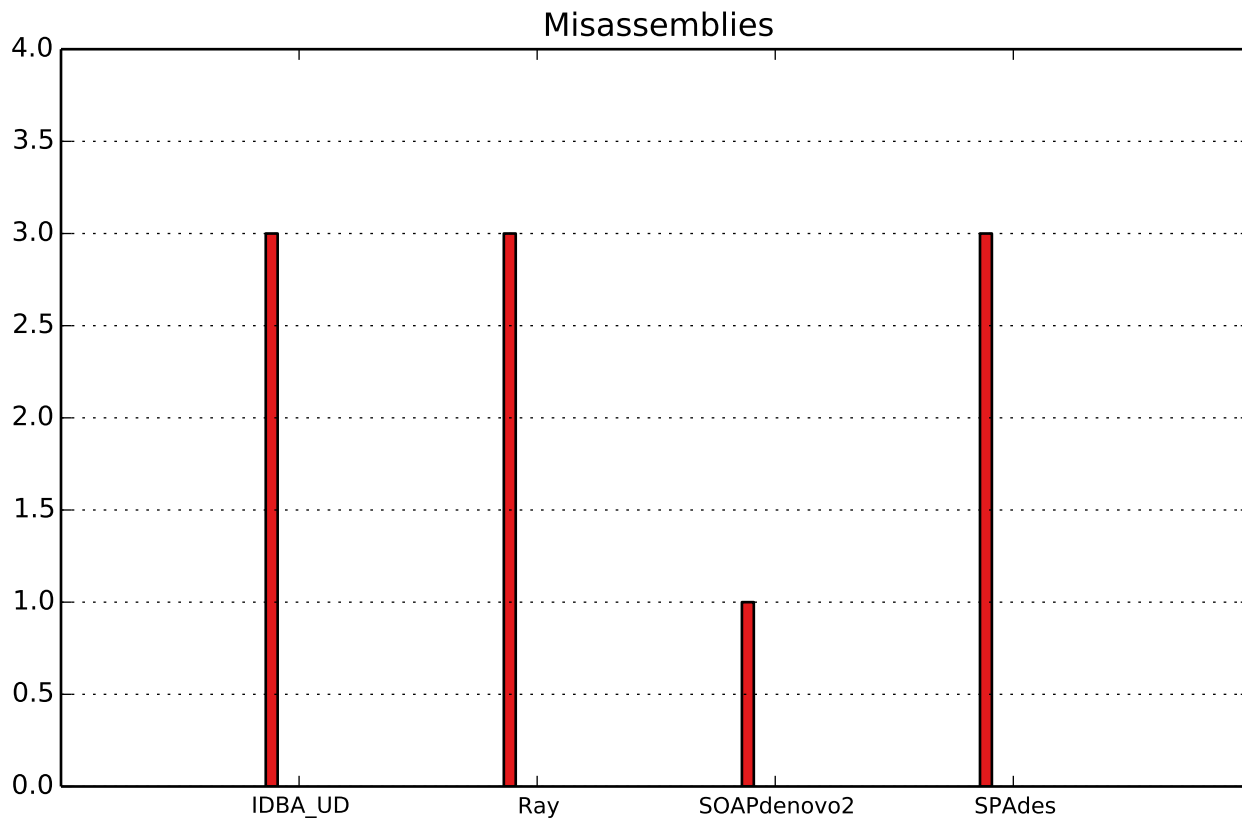
Cumulative length



GC content

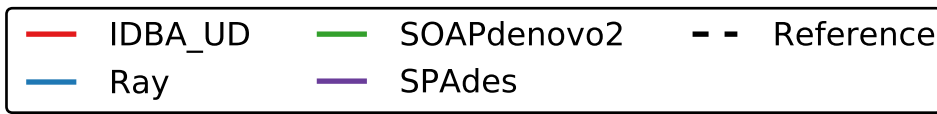
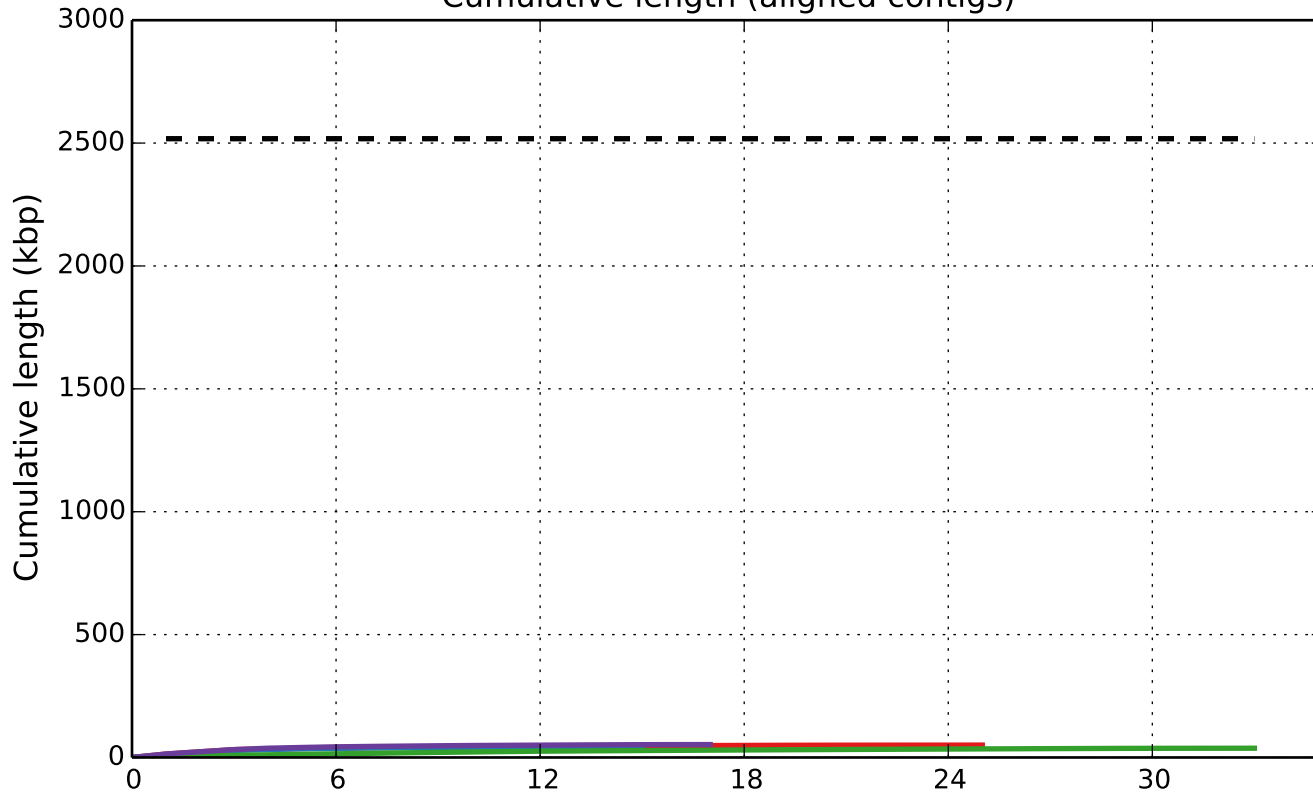


— IDBA_UD — SOAPdenovo2 - - Reference
— Ray — SPAdes

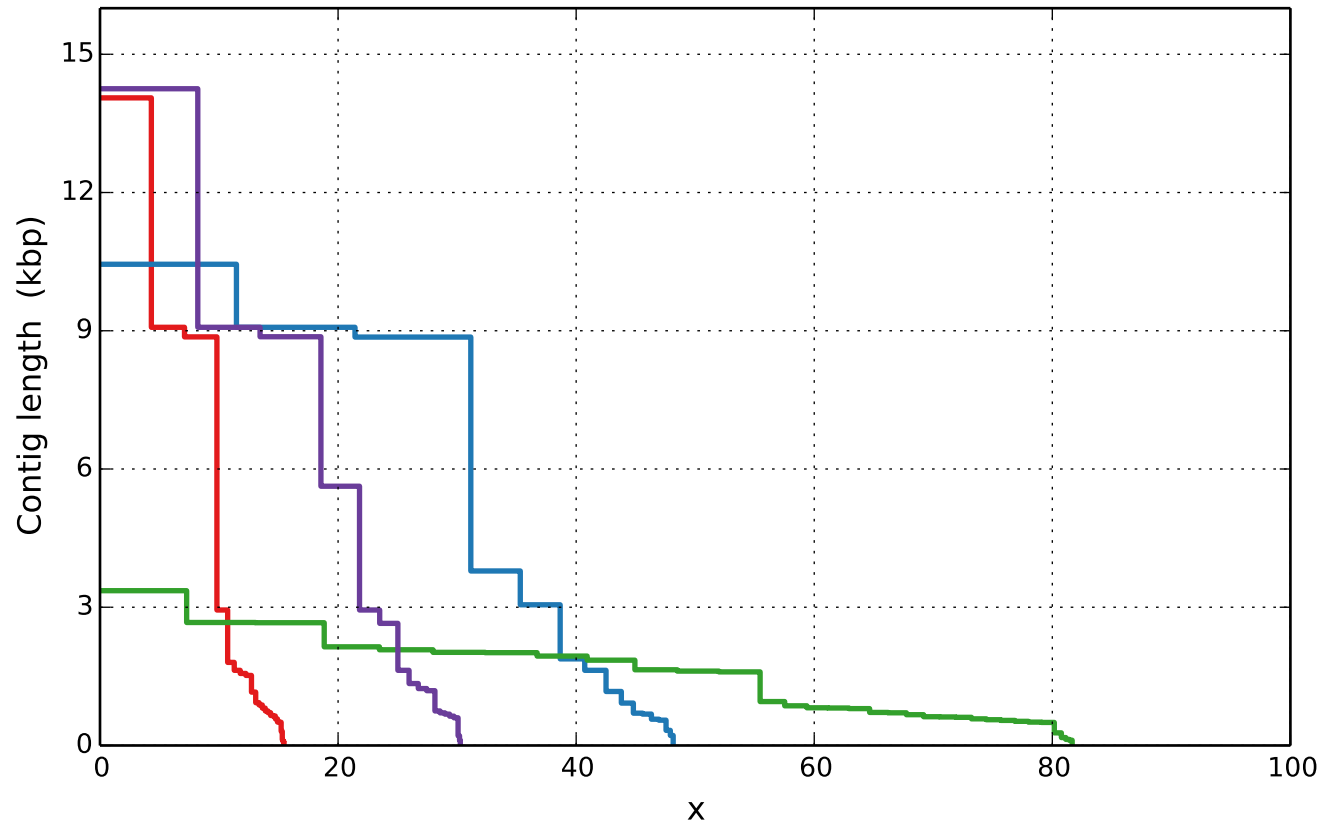


 # relocations

Cumulative length (aligned contigs)



NAx



— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray

NGAx

