

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	57	265	117	77
# contigs (>= 5000 bp)	35	23	47	51
# contigs (>= 10000 bp)	31	4	20	32
# contigs (>= 25000 bp)	14	1	2	9
# contigs (>= 50000 bp)	8	0	0	2
Total length (>= 1000 bp)	1104053	667703	684272	982291
Total length (>= 5000 bp)	1057924	184975	512444	914782
Total length (>= 10000 bp)	1030530	57877	321646	764654
Total length (>= 25000 bp)	731508	26575	57328	372174
Total length (>= 50000 bp)	534925	0	0	153129
# contigs	85	459	141	100
Largest contig	95558	26575	30789	92179
Total length	1123700	809327	701601	998568
Reference length	1778912	1778912	1778912	1778912
GC (%)	39.62	39.90	39.36	39.32
Reference GC (%)	39.79	39.79	39.79	39.79
N50	42175	2409	8628	20312
NG50	17439	-	-	6964
N75	21283	1191	4625	10776
L50	9	87	24	15
LG50	22	-	-	47
L75	19	210	50	31
# misassemblies	30	8	8	19
# misassembled contigs	15	7	8	12
Misassembled contigs length	611159	39382	51509	246851
# local misassemblies	18	29	10	6
# structural variations	2	0	0	0
# unaligned contigs	0 + 39 part	0 + 66 part	0 + 57 part	0 + 41 part
Unaligned length	270111	106908	265950	305423
Genome fraction (%)	37.088	36.463	22.809	36.174
Duplication ratio	1.294	1.083	1.074	1.077
# N's per 100 kbp	0.00	1166.15	1688.00	12.92
# mismatches per 100 kbp	4114.39	3626.36	3525.36	3976.53
# indels per 100 kbp	85.79	48.72	76.65	80.81
Largest alignment	61441	9609	15009	28053
NA50	3778	1481	1368	4720
NGA50	-	-	-	-
NA75	-	723	-	-
LA50	46	141	85	48
LA75	-	337	-	-

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

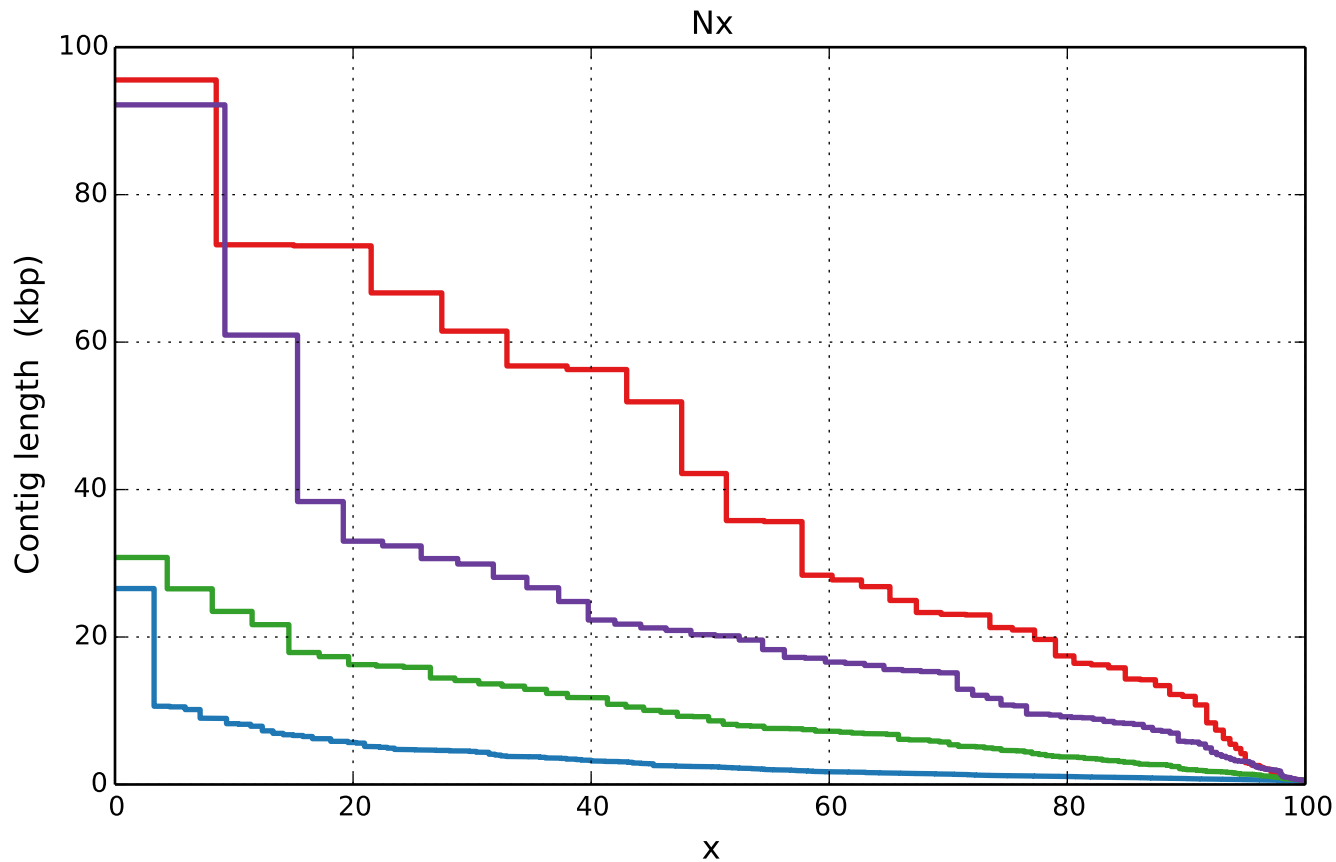
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	30	8	8	19
# relocations	8	4	0	7
# translocations	22	4	8	12
# inversions	0	0	0	0
# possibly misassembled contigs	35	31	42	36
# misassembled contigs	15	7	8	12
Misassembled contigs length	611159	39382	51509	246851
# local misassemblies	18	29	10	6
# structural variations	2	0	0	0
# mismatches	27145	23522	14304	25589
# indels	566	316	311	520
# short indels	538	306	227	480
# long indels	28	10	84	40
Indels length	1022	501	2069	1107

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).

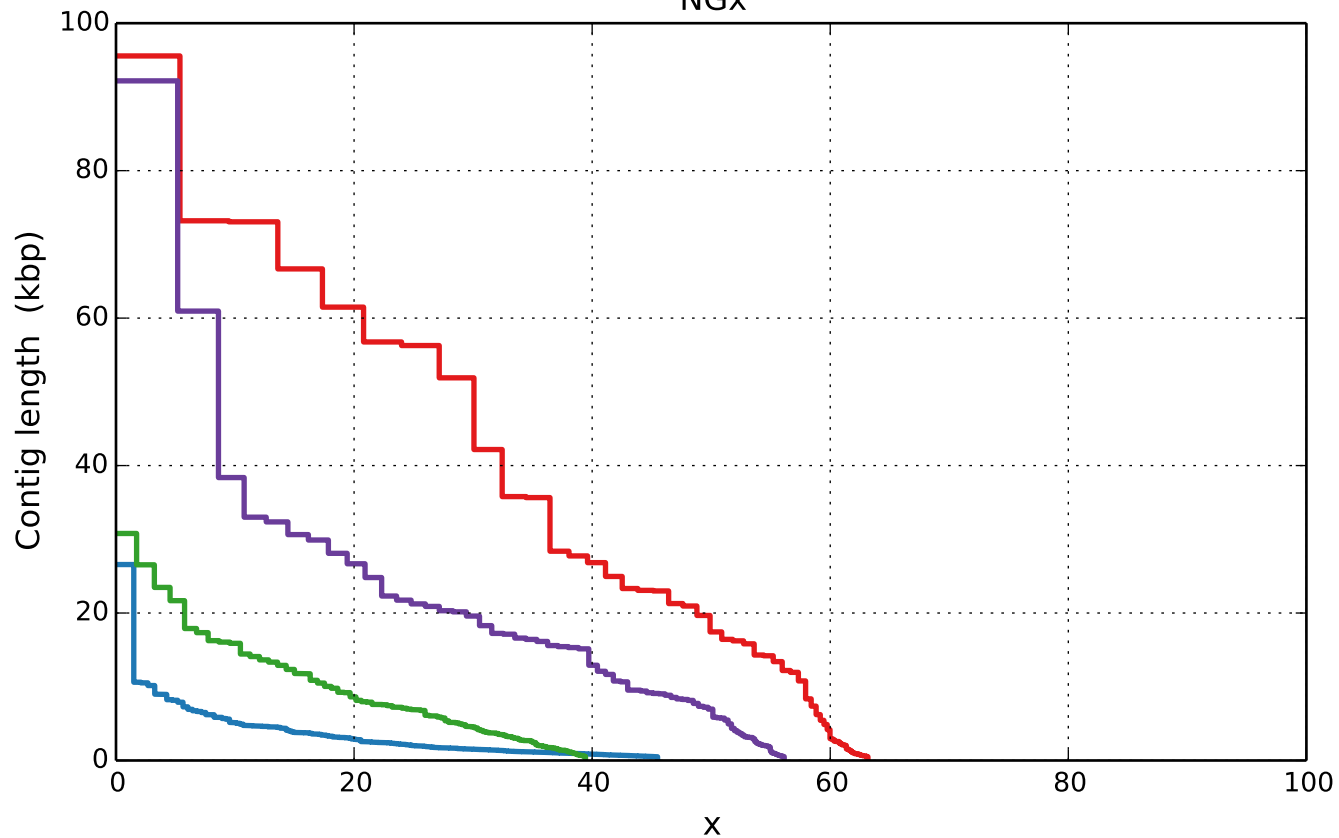
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	39	66	57	41
# with misassembly	10	6	12	8
# both parts are significant	18	24	31	23
Partially unaligned length	270111	106908	265950	305423
# N's	0	9438	11843	129

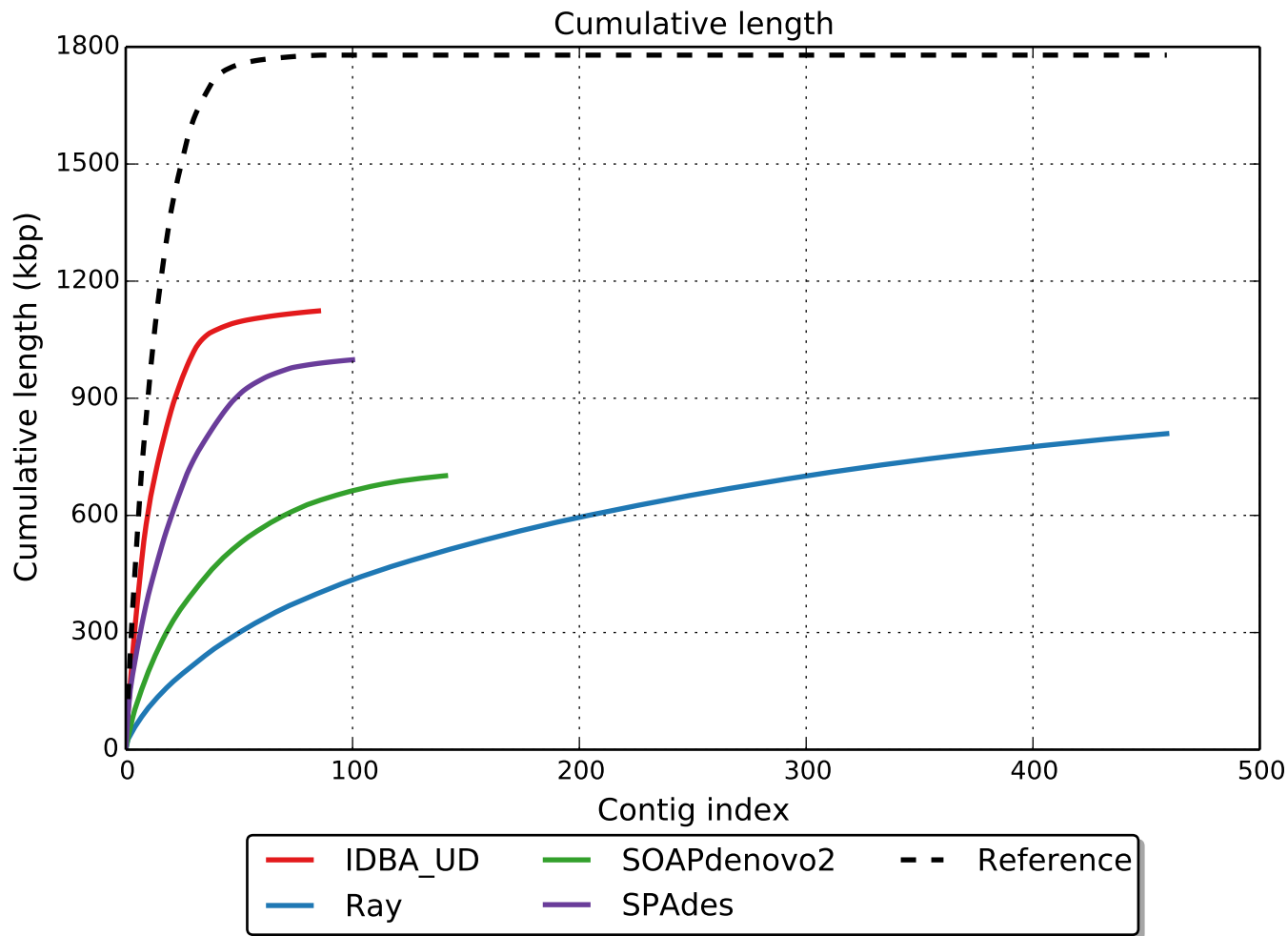
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



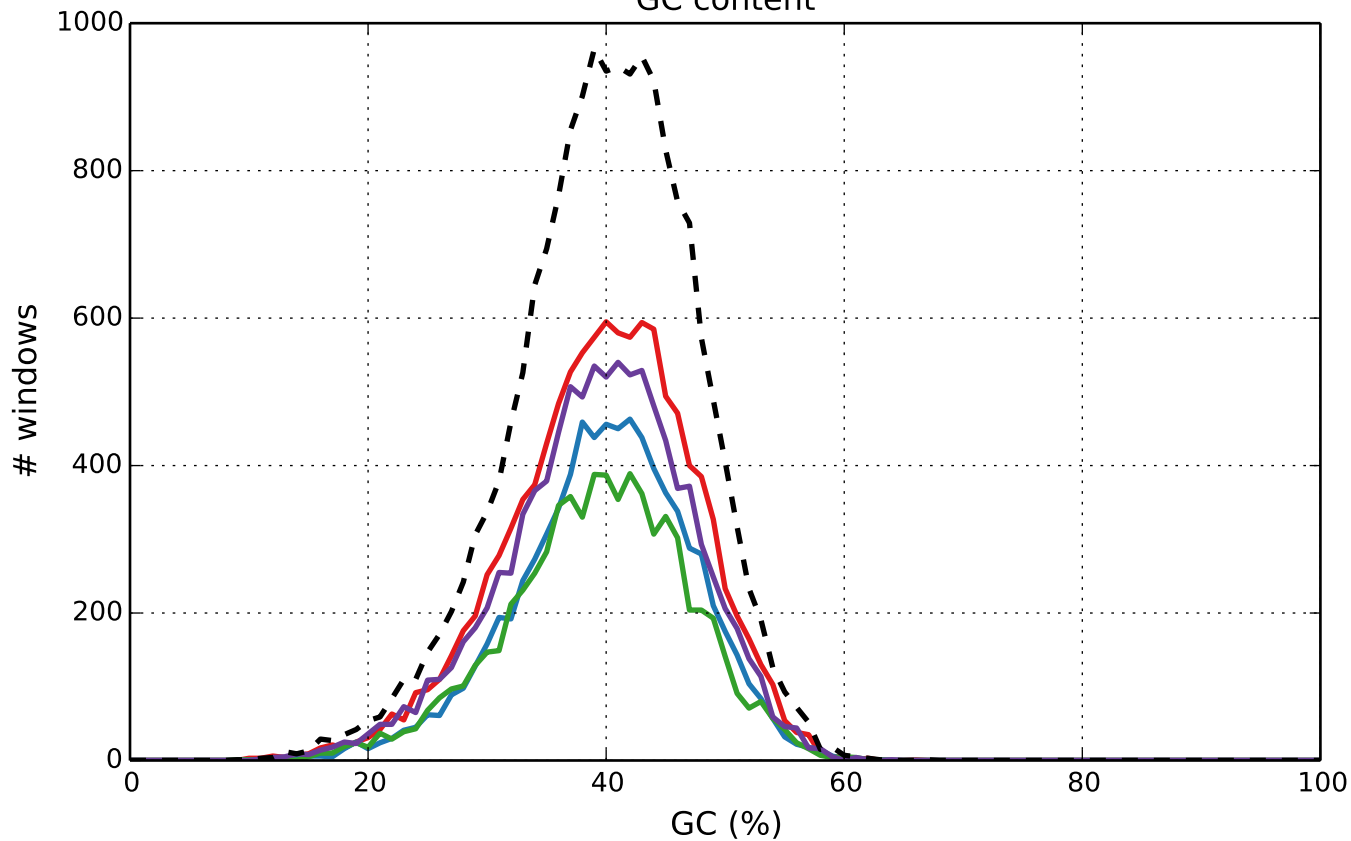
NGx



— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray

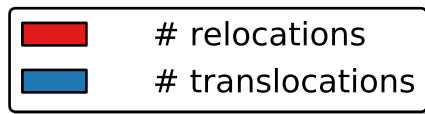
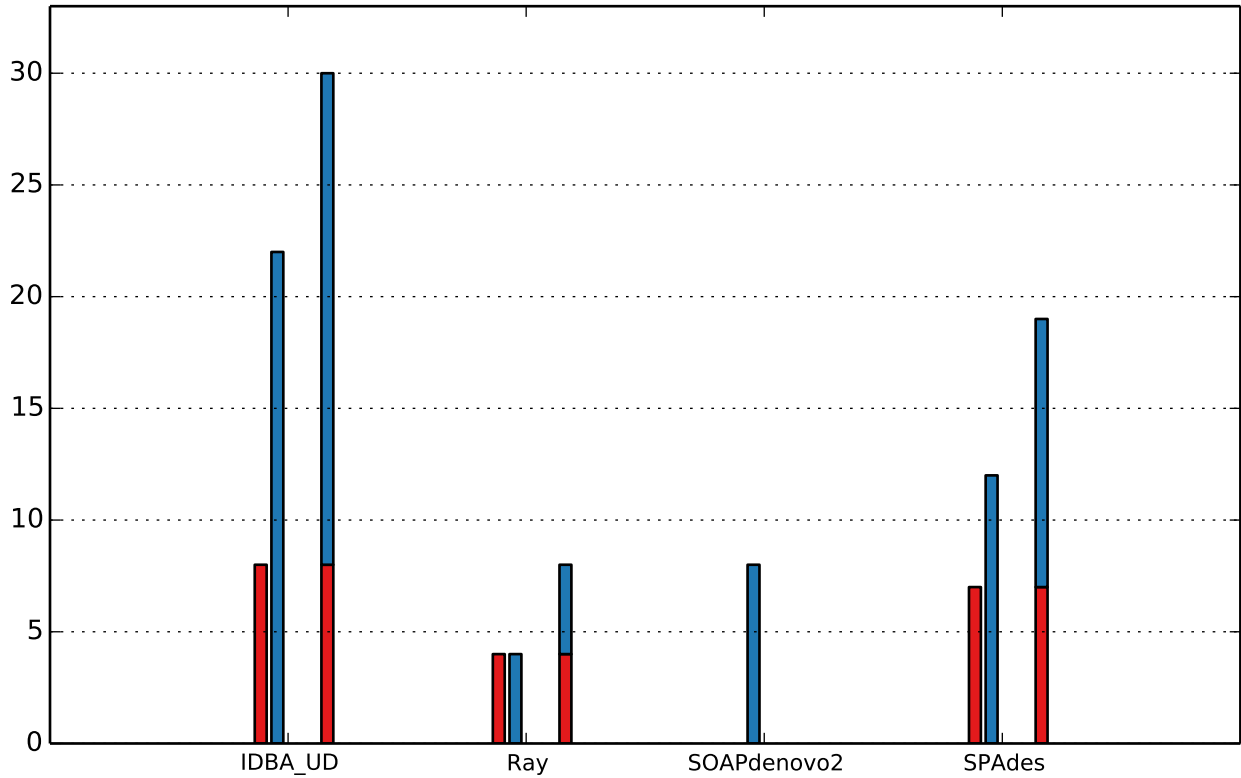


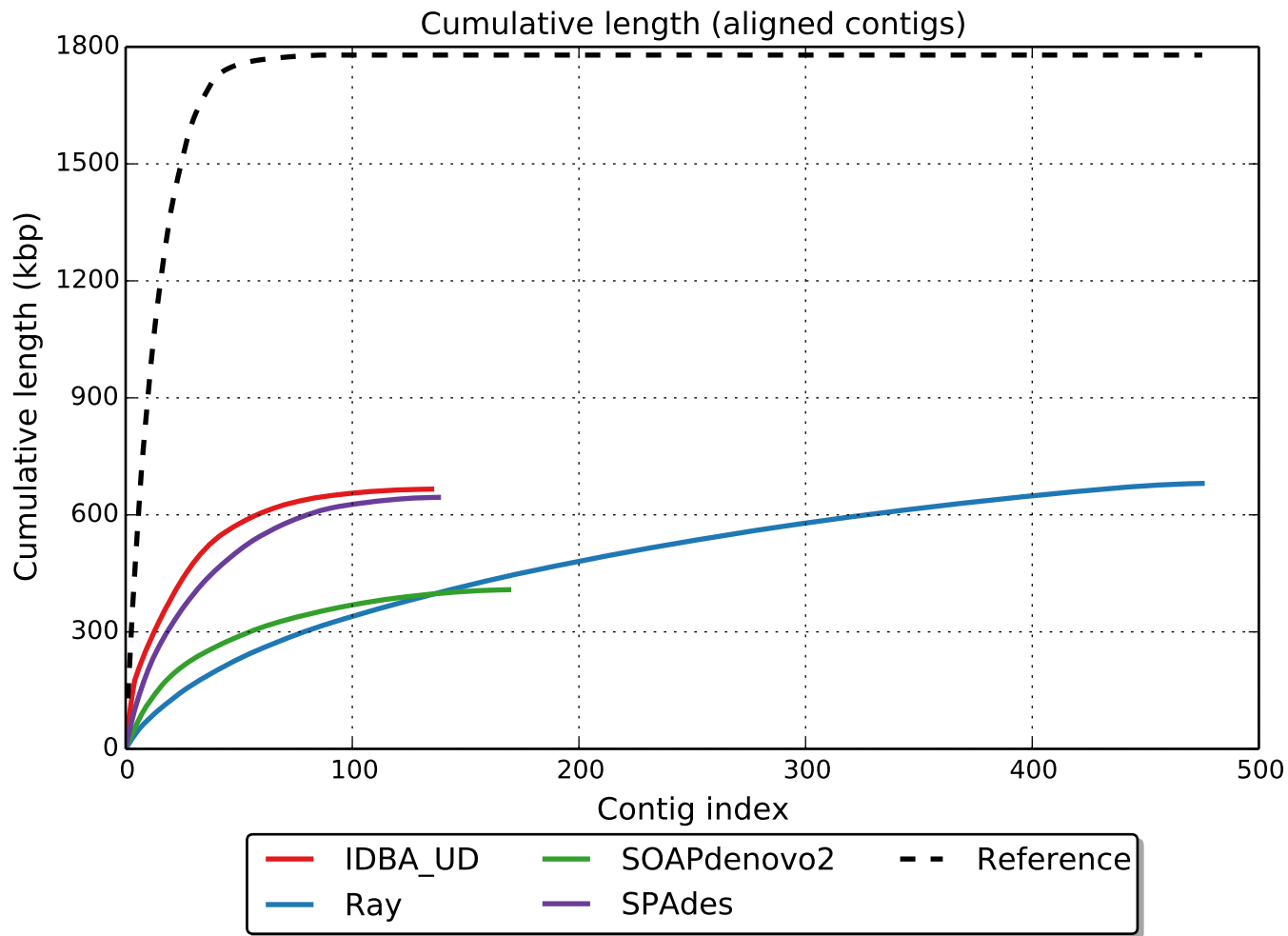
GC content



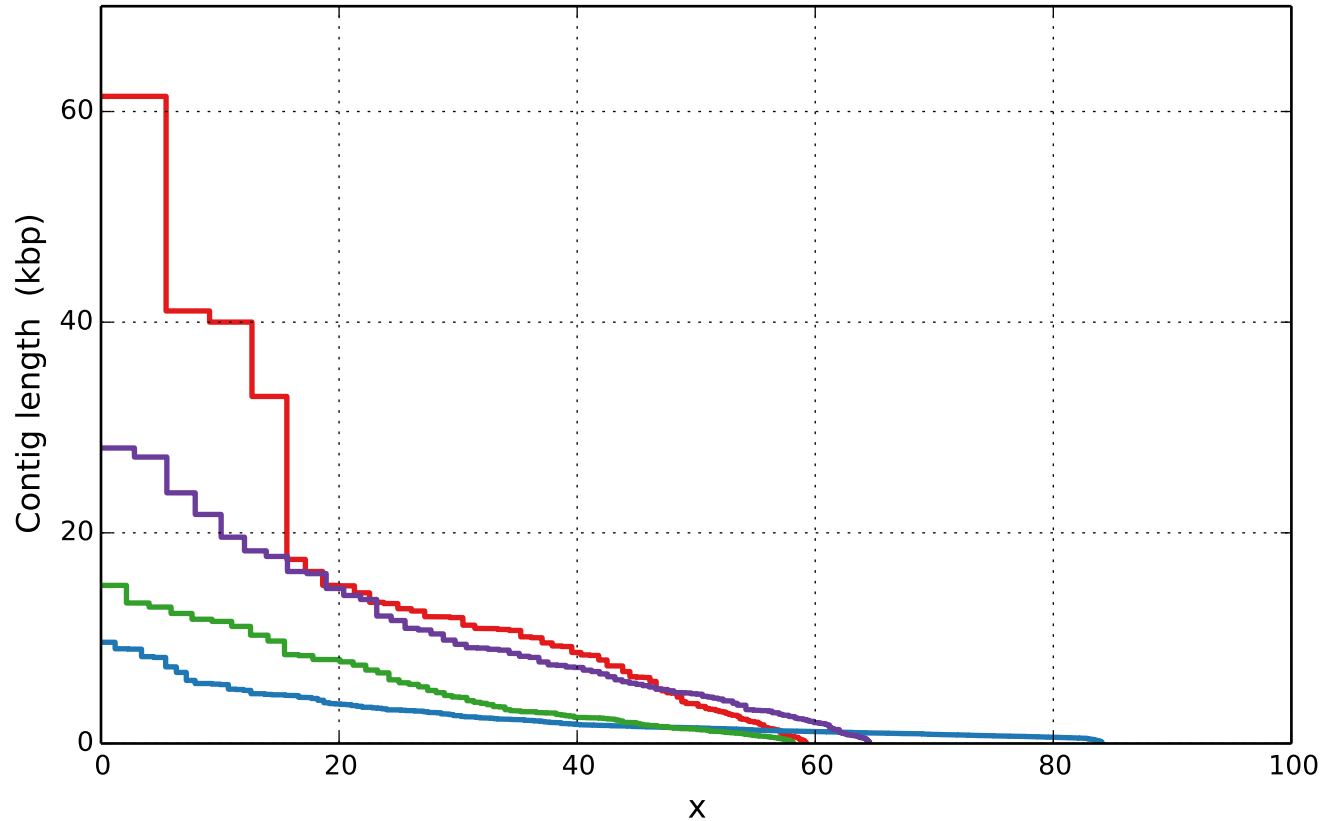
— IDBA_UD — SOAPdenovo2 - - Reference
— Ray — SPAdes

Misassemblies





NAx



— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray

NGAx

