

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	177	123	214	150
# contigs (>= 5000 bp)	103	86	93	106
# contigs (>= 10000 bp)	64	66	49	73
# contigs (>= 25000 bp)	25	28	18	30
# contigs (>= 50000 bp)	7	12	7	6
Total length (>= 1000 bp)	2288190	2484110	1948869	2385954
Total length (>= 5000 bp)	2121921	2401356	1690795	2286874
Total length (>= 10000 bp)	1841935	2250672	1391214	2042696
Total length (>= 25000 bp)	1175538	1599649	907428	1346361
Total length (>= 50000 bp)	507359	1007527	538000	534356
# contigs	232	148	315	198
Largest contig	128273	128291	162453	128587
Total length	2327345	2502442	2021002	2420957
Reference length	2574015	2574015	2574015	2574015
GC (%)	28.04	27.99	27.88	27.94
Reference GC (%)	27.76	27.76	27.76	27.76
N50	26520	40495	19527	29418
NG50	23125	38494	13452	25226
N75	12312	19477	7380	14832
NG75	8439	18482	1196	11808
L50	25	18	23	25
LG50	30	19	40	28
L75	56	41	64	55
LG75	74	44	198	63
# misassemblies	199	243	129	191
# misassembled contigs	67	66	52	63
Misassembled contigs length	1494028	1944569	1121650	1453907
# local misassemblies	161	195	151	149
# structural variations	42	45	31	41
# unaligned contigs	0 + 92 part	0 + 38 part	0 + 127 part	0 + 81 part
Unaligned length	327450	281128	316272	433818
Genome fraction (%)	63.775	65.342	55.492	64.445
Duplication ratio	1.218	1.321	1.193	1.198
# N's per 100 kbp	0.00	111.85	919.74	140.15
# mismatches per 100 kbp	2657.73	2694.90	2608.69	2697.87
# indels per 100 kbp	97.04	95.90	92.90	95.43
Largest alignment	44224	44224	44294	33519
NA50	5720	5897	4742	5641
NGA50	4330	5641	1251	4626
LA50	93	92	93	102
LGA50	118	98	205	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).

Misassemblies report

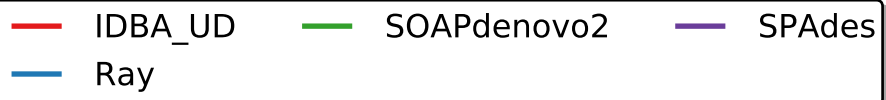
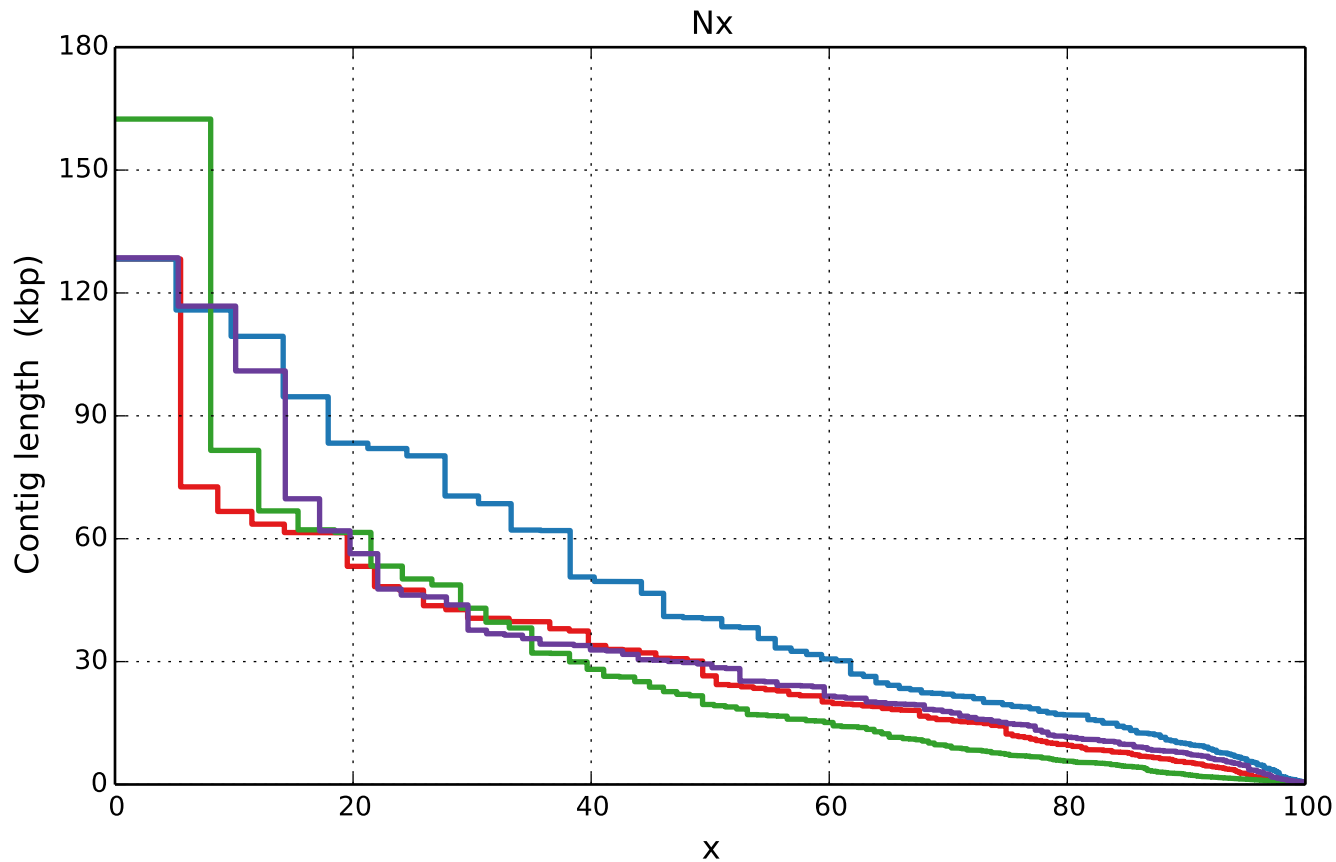
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	199	243	129	191
# relocations	52	64	36	46
# translocations	139	179	87	140
# inversions	8	0	6	5
# possibly misassembled contigs	109	95	98	104
# misassembled contigs	67	66	52	63
Misassembled contigs length	1494028	1944569	1121650	1453907
# local misassemblies	161	195	151	149
# structural variations	42	45	31	41
# mismatches	43629	45326	37262	44753
# indels	1593	1613	1327	1583
# short indels	1431	1464	1127	1436
# long indels	162	149	200	147
Indels length	4676	4130	5595	4299

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).

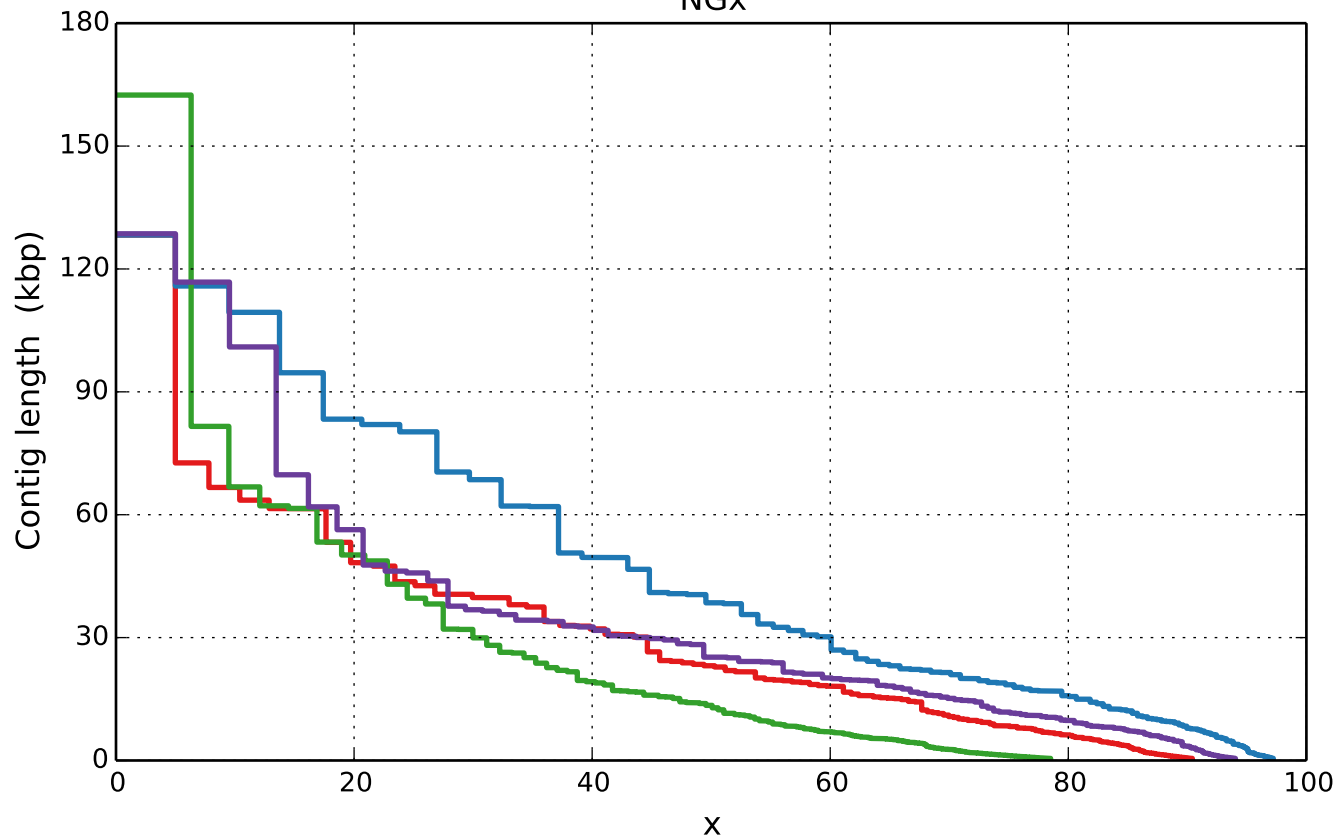
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	92	38	127	81
# with misassembly	21	16	20	18
# both parts are significant	33	28	45	38
Partially unaligned length	327450	281128	316272	433818
# N's	0	2799	18588	3393

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).

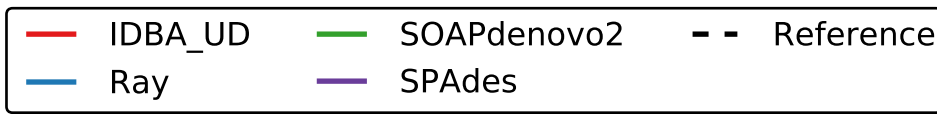
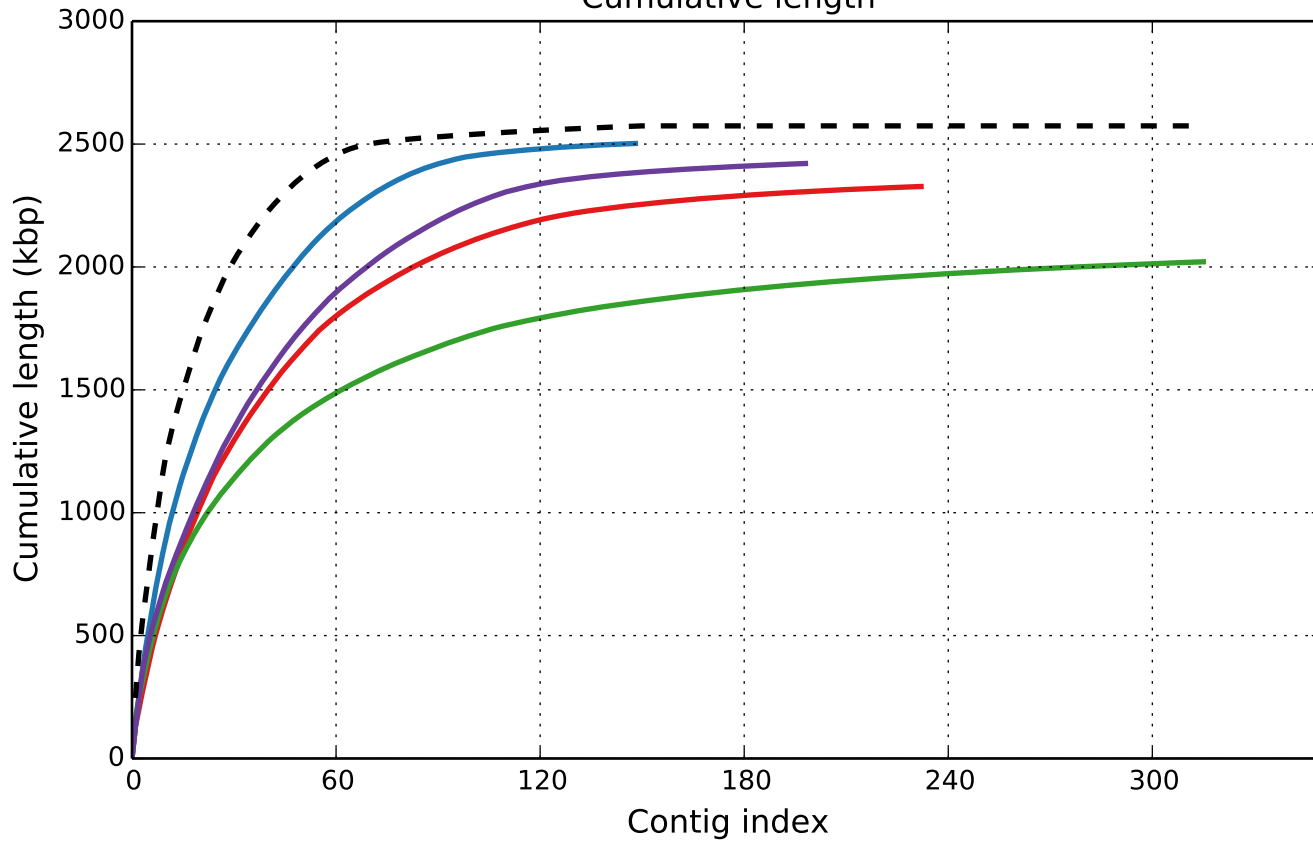


NGx

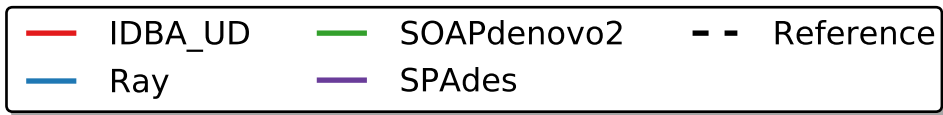
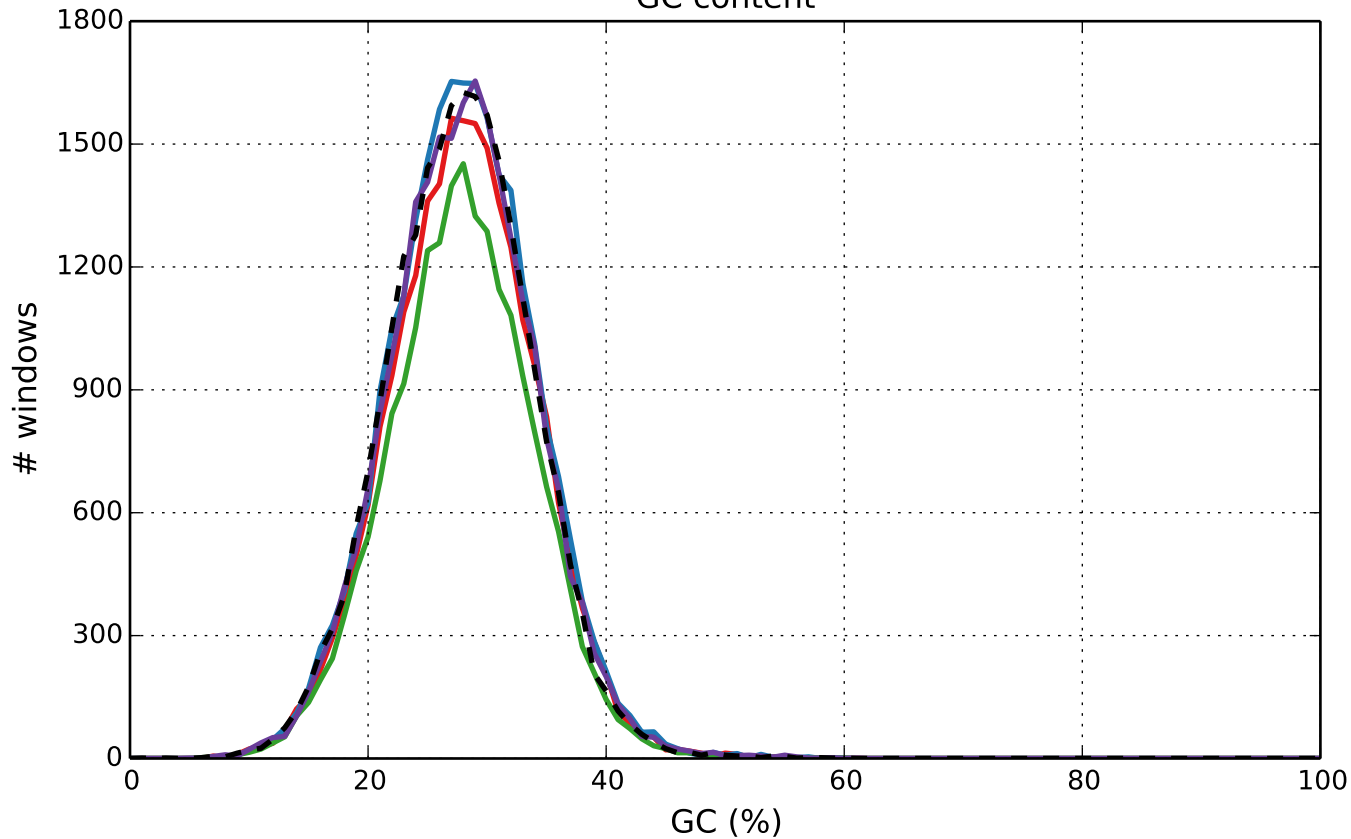


— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray

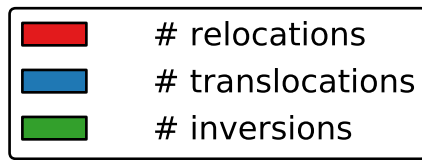
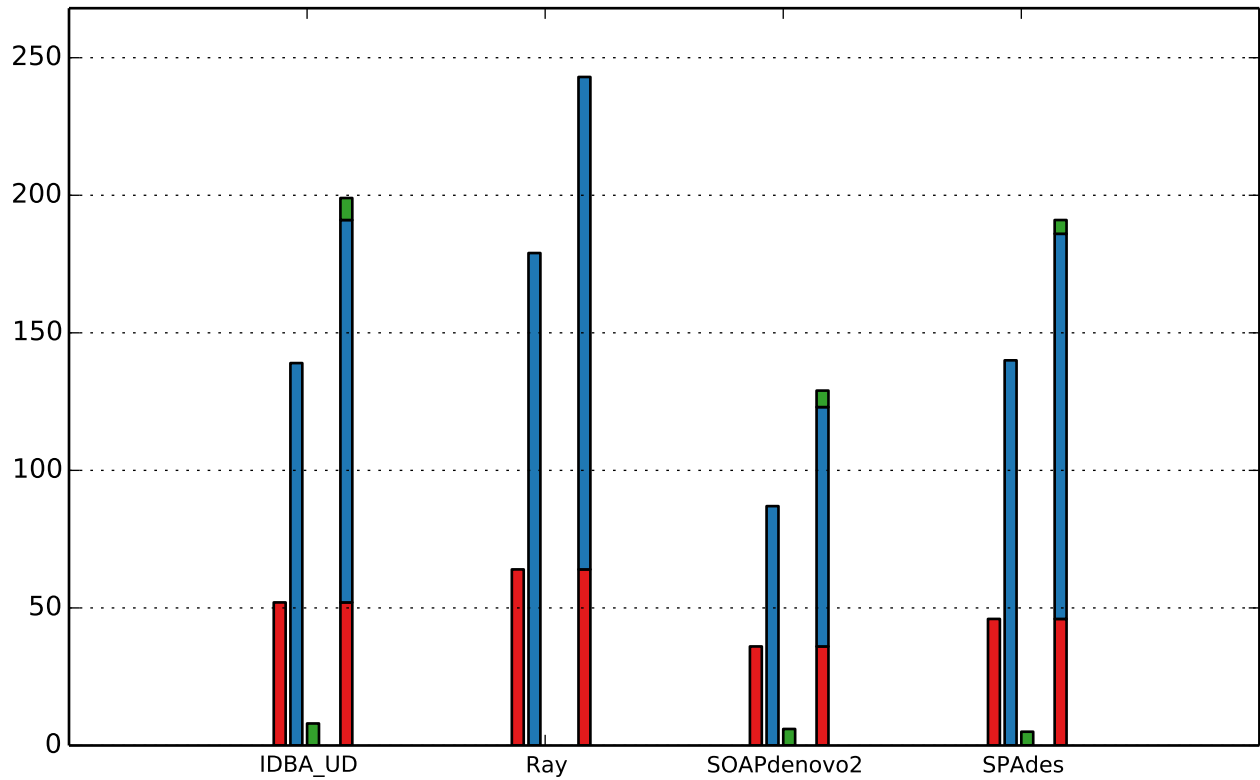
Cumulative length



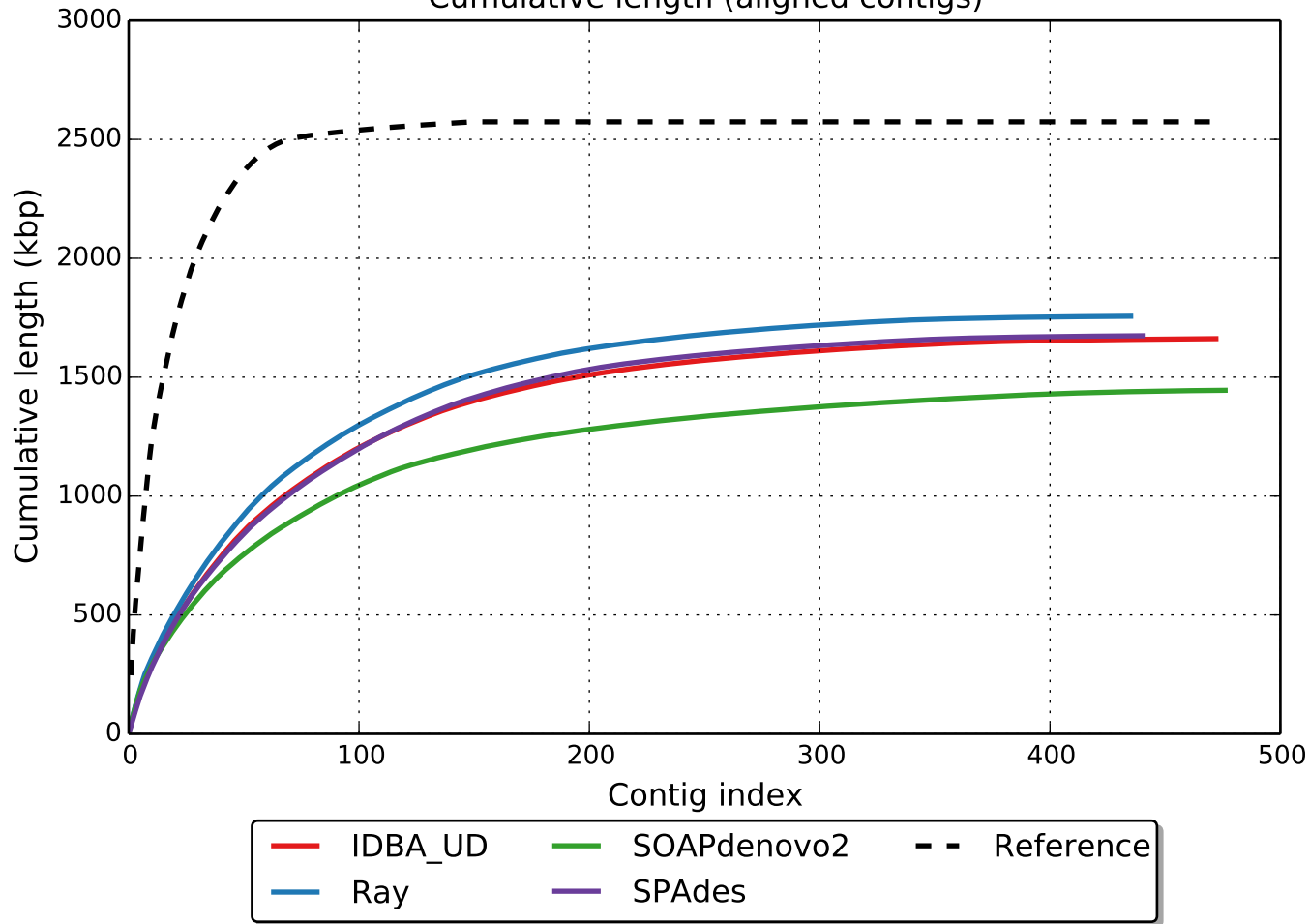
GC content



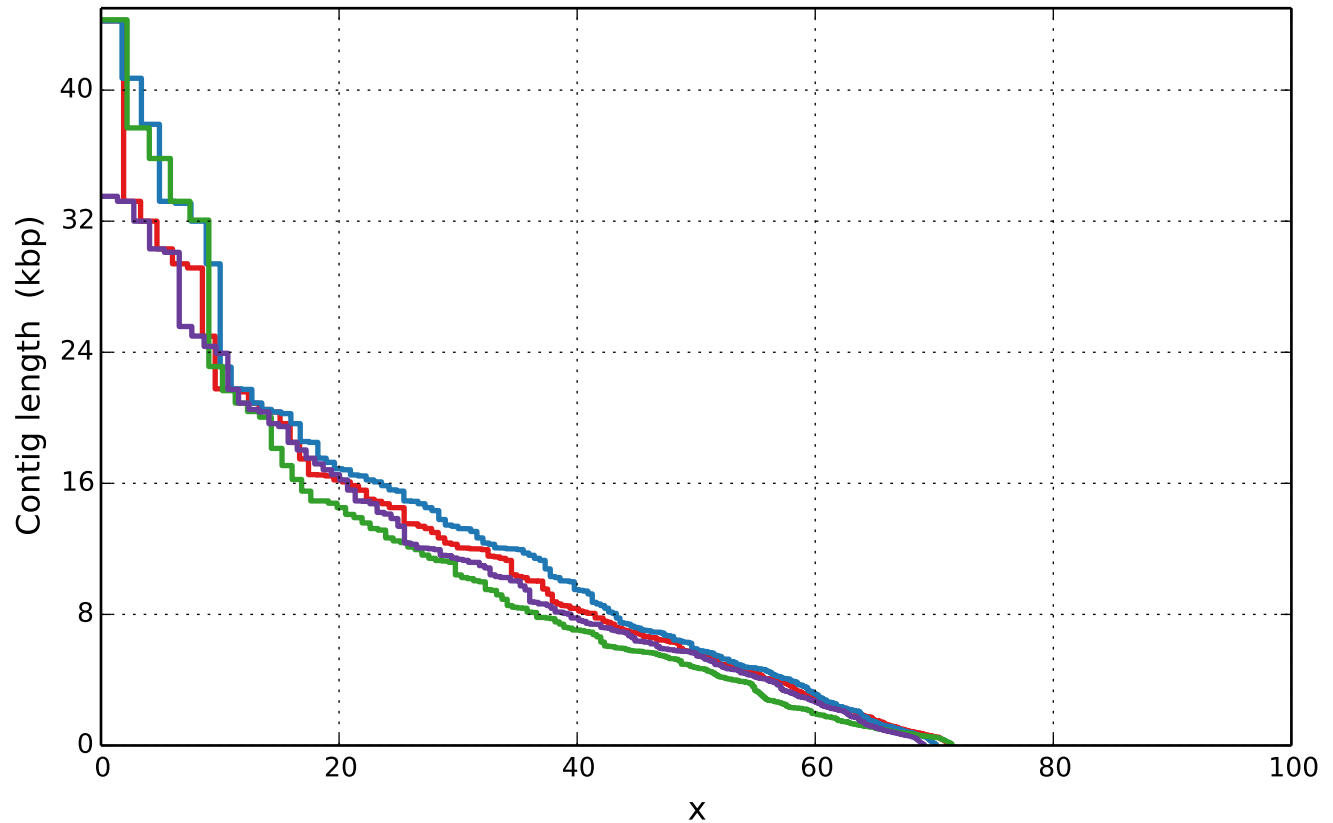
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

