

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	46	34	48	41
# contigs (>= 5000 bp)	28	25	38	27
# contigs (>= 10000 bp)	20	24	32	25
# contigs (>= 25000 bp)	14	17	22	18
# contigs (>= 50000 bp)	10	13	14	15
Total length (>= 1000 bp)	2252667	2463898	2194820	2243874
Total length (>= 5000 bp)	2218178	2440578	2180426	2218485
Total length (>= 10000 bp)	2164465	2433390	2139811	2203680
Total length (>= 25000 bp)	2060962	2319542	1956580	2100480
Total length (>= 50000 bp)	1929589	2175123	1687093	2008426
# contigs	72	36	70	54
Largest contig	442644	442828	509581	386771
Total length	2271018	2465497	2209979	2253226
Reference length	2292986	2292986	2292986	2292986
GC (%)	48.92	48.98	49.12	49.14
Reference GC (%)	49.01	49.01	49.01	49.01
N50	169548	151751	113192	142442
NG50	169548	185849	113192	142442
N75	114011	107687	55295	83957
NG75	114011	117080	39771	83957
L50	4	5	6	6
LG50	4	4	6	6
L75	8	9	14	11
LG75	8	8	15	11
# misassemblies	24	46	19	29
# misassembled contigs	15	21	14	16
Misassembled contigs length	1829271	2127664	1394888	1620603
# local misassemblies	23	35	26	24
# structural variations	15	15	15	15
# unaligned contigs	0 + 27 part	0 + 5 part	0 + 6 part	0 + 9 part
Unaligned length	40559	24133	3918	10806
Genome fraction (%)	93.660	93.339	92.842	93.339
Duplication ratio	1.039	1.141	1.036	1.048
# N's per 100 kbp	0.00	128.09	136.20	42.52
# mismatches per 100 kbp	1264.29	1270.79	1254.86	1263.91
# indels per 100 kbp	37.16	37.47	38.00	36.40
Largest alignment	281176	281272	248978	281176
NA50	82588	72264	60608	71056
NGA50	82588	79282	58291	67401
NA75	33679	30732	29056	32621
NGA75	32584	36825	27866	31818
LA50	8	10	11	10
LGA50	8	8	12	11
LA75	16	21	24	20
LGA75	17	17	26	21

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	24	46	19	29
# relocations	5	12	6	7
# translocations	19	34	13	22
# inversions	0	0	0	0
# possibly misassembled contigs	17	19	15	18
# misassembled contigs	15	21	14	16
Misassembled contigs length	1829271	2127664	1394888	1620603
# local misassemblies	23	35	26	24
# structural variations	15	15	15	15
# mismatches	27152	27198	26714	27051
# indels	798	802	809	779
# short indels	748	757	733	740
# long indels	50	45	76	39
Indels length	1714	1468	2126	1374

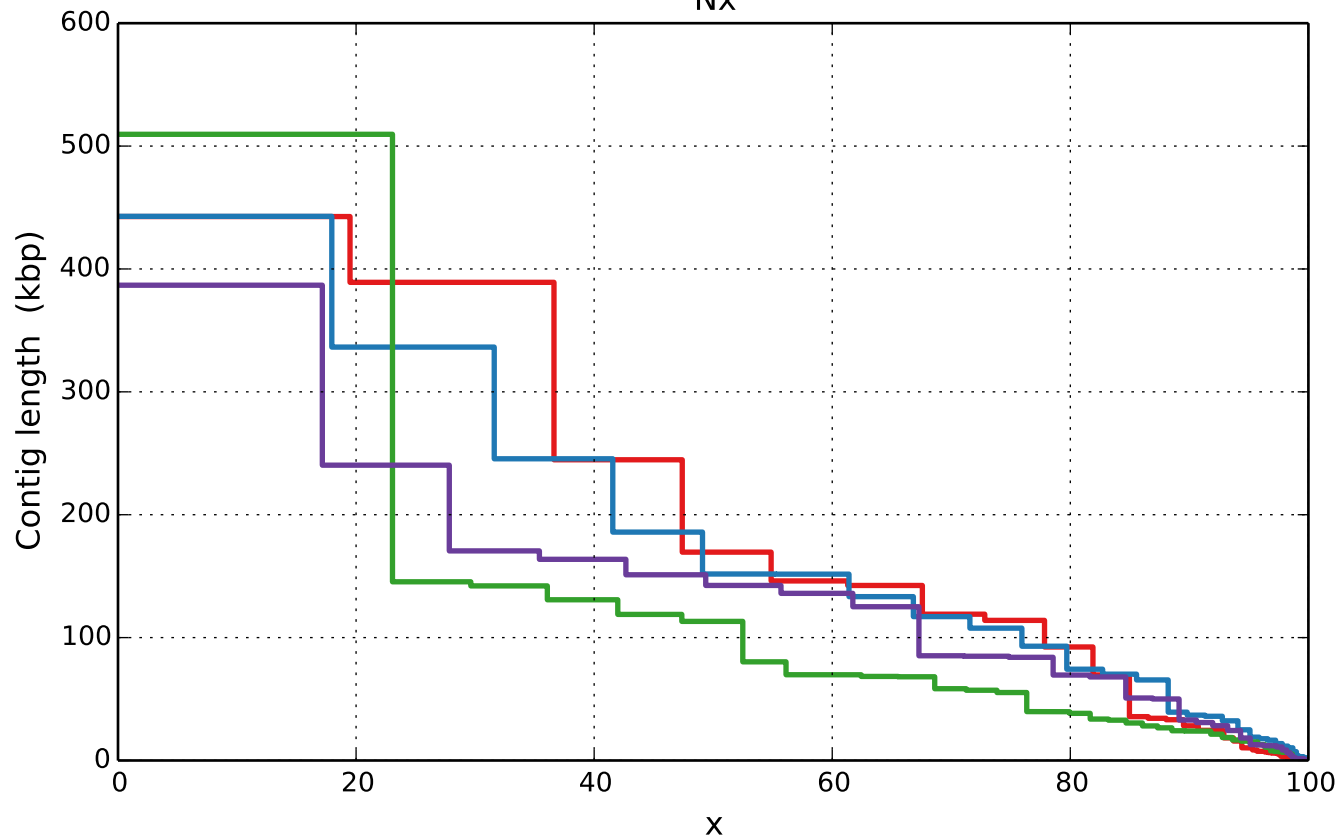
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	27	5	6	9
# with misassembly	1	0	0	1
# both parts are significant	5	1	2	3
Partially unaligned length	40559	24133	3918	10806
# N's	0	3158	3010	958

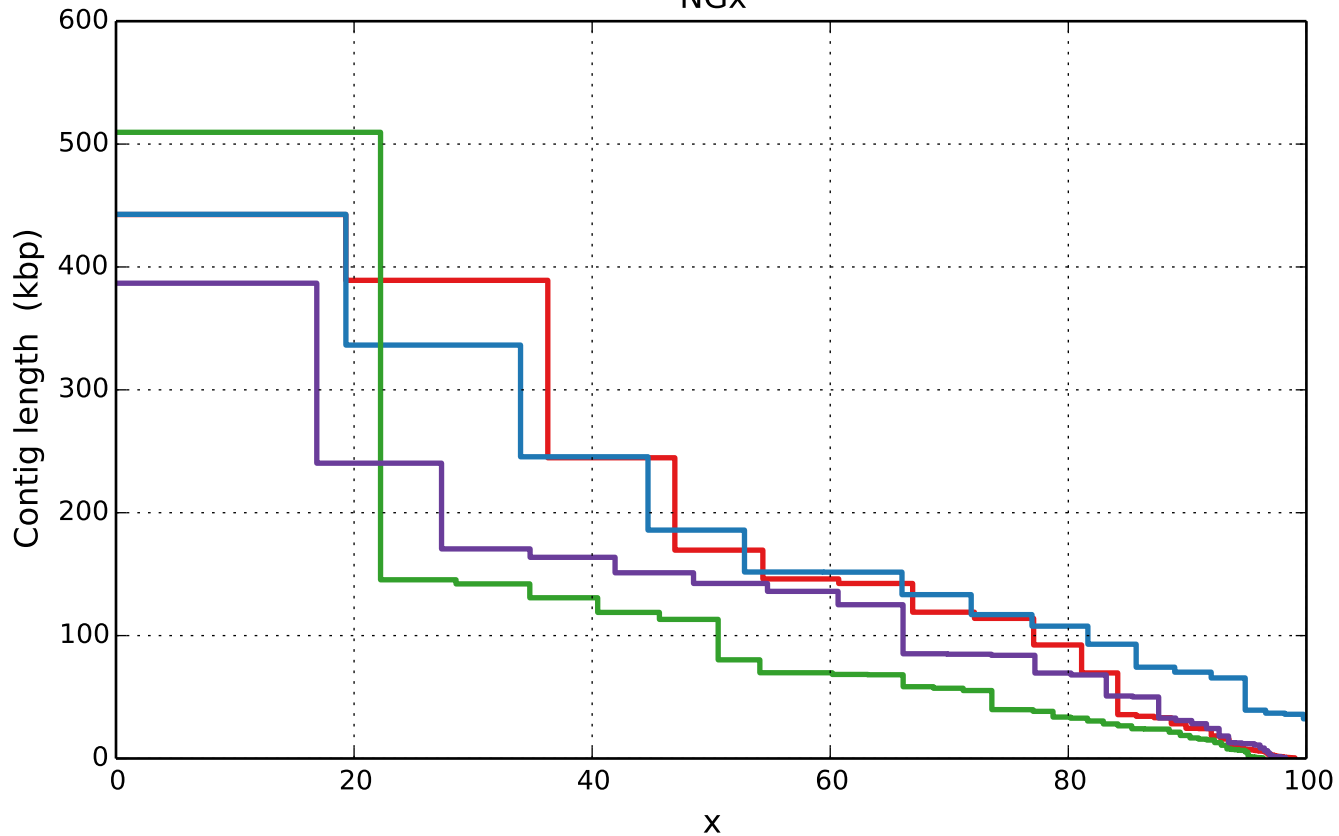
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

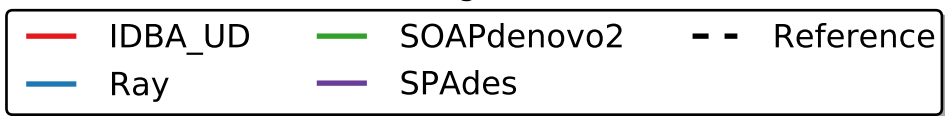
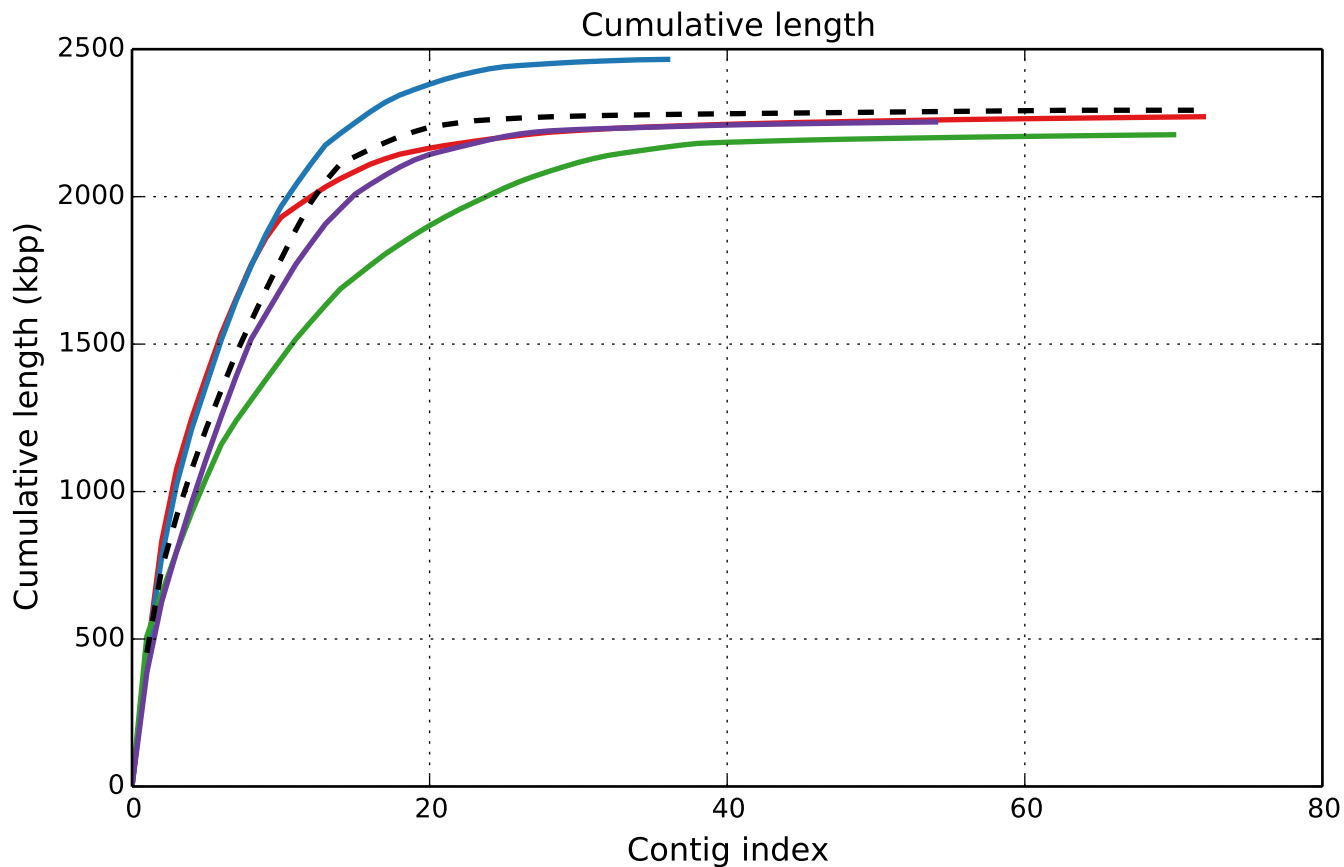


— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray

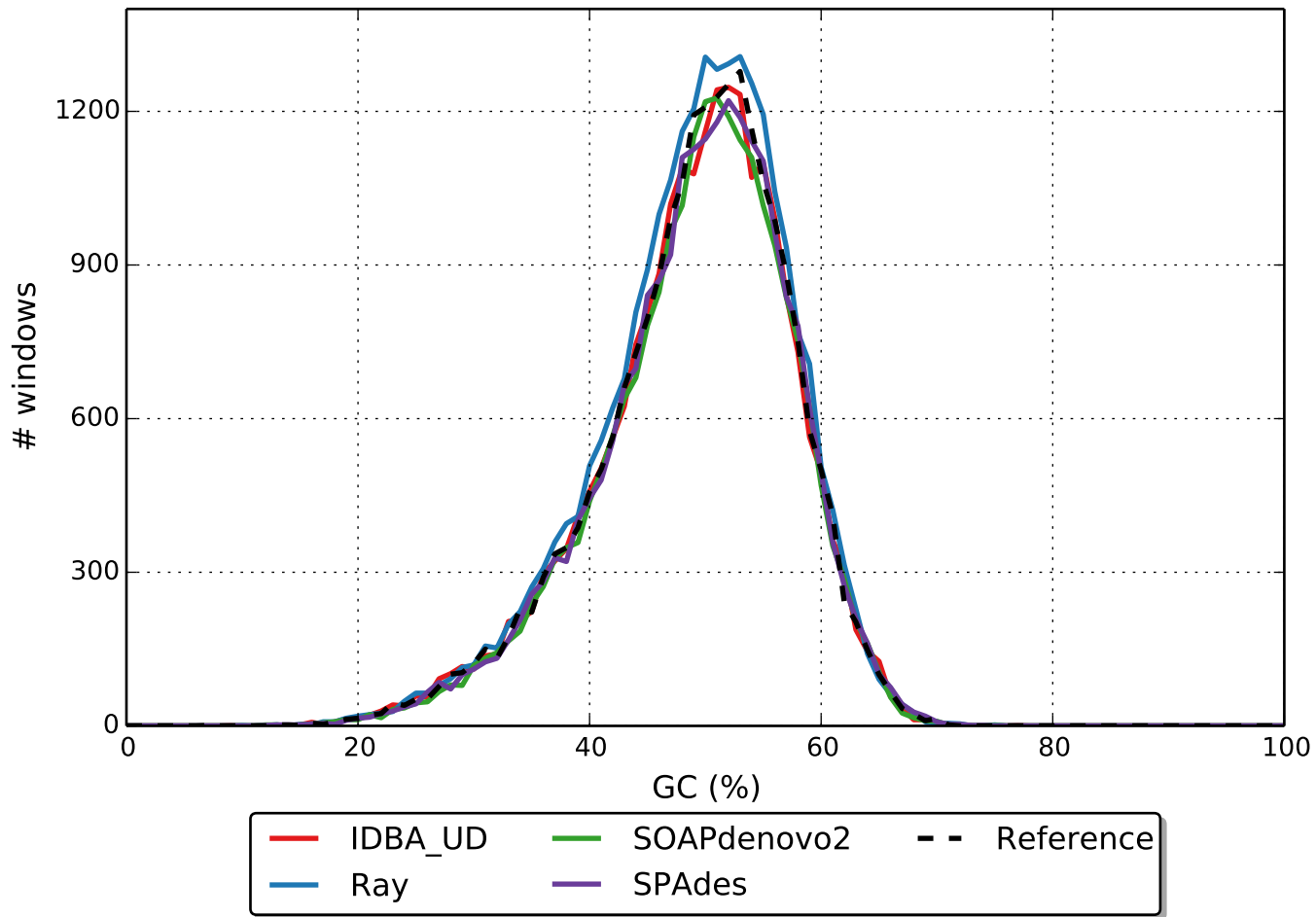
NGx



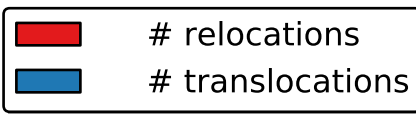
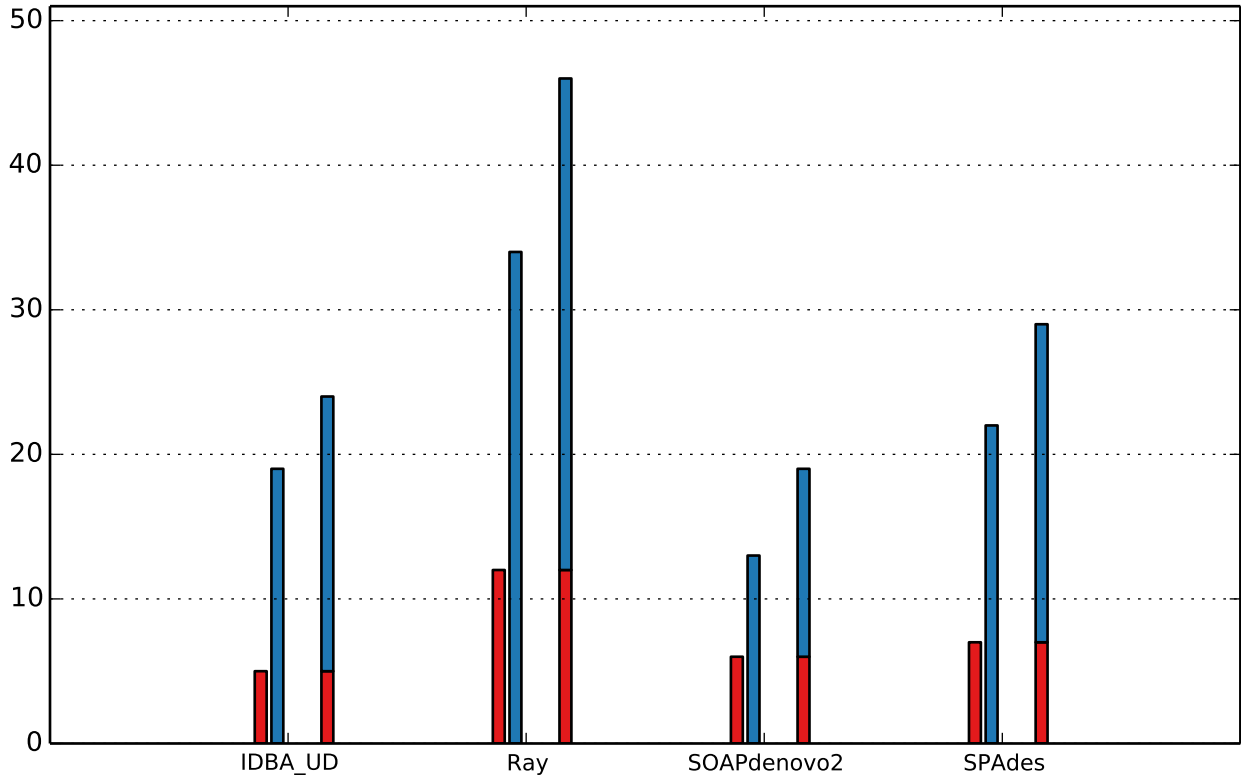
IDBA_UD SOAPdenovo2 SPAdes
Ray



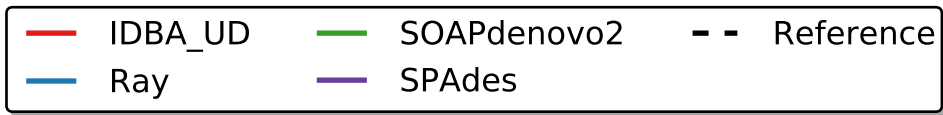
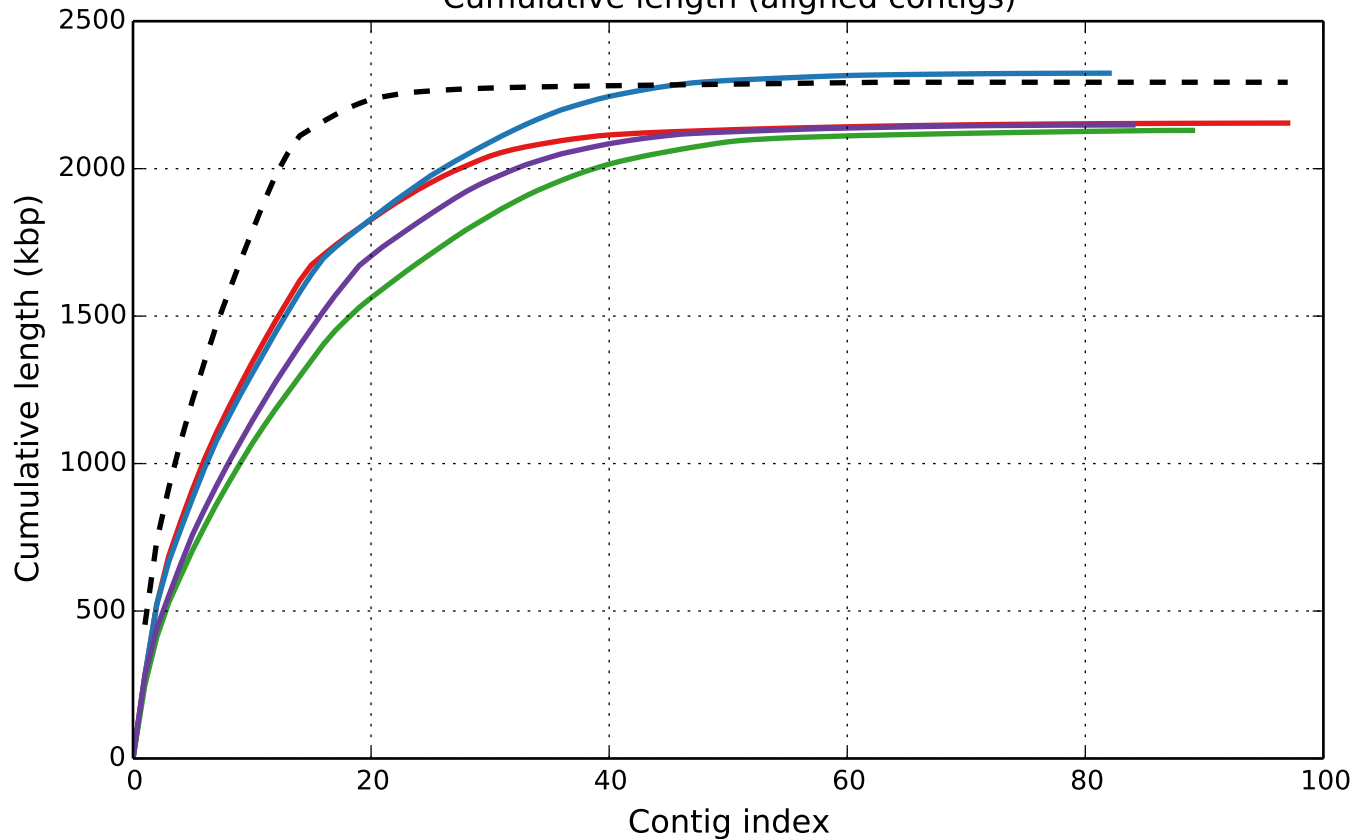
GC content



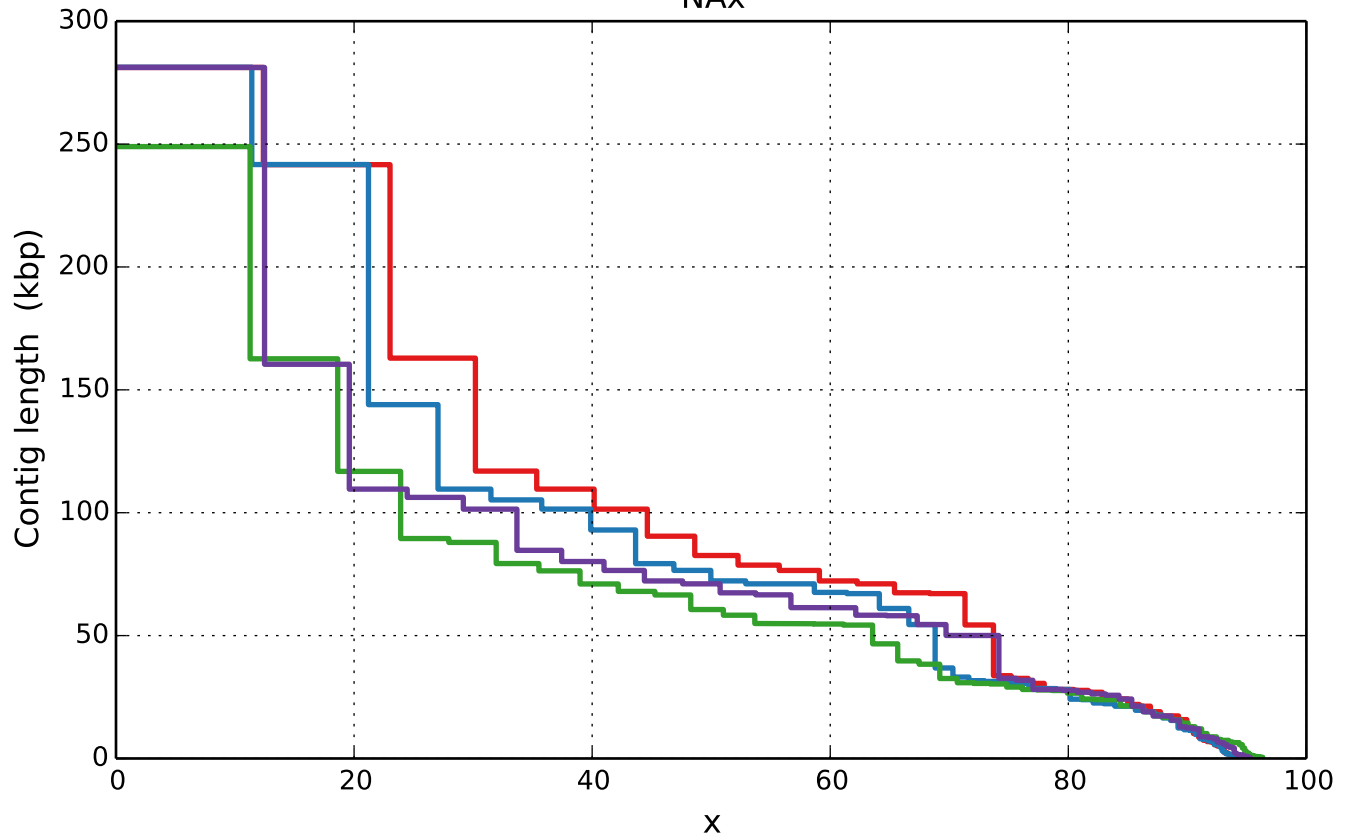
Misassemblies



Cumulative length (aligned contigs)



NAx



— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray

NGAx

