

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	599	328	289	417
# contigs (>= 5000 bp)	38	159	14	76
# contigs (>= 10000 bp)	13	95	4	31
# contigs (>= 25000 bp)	2	15	0	5
# contigs (>= 50000 bp)	0	2	0	1
Total length (>= 1000 bp)	1428815	2753314	607356	1724643
Total length (>= 5000 bp)	382059	2339634	110721	1045833
Total length (>= 10000 bp)	217404	1873635	50668	718468
Total length (>= 25000 bp)	74297	631089	0	336414
Total length (>= 50000 bp)	0	196978	0	193324
# contigs	1288	500	904	832
Largest contig	40343	125129	14322	193324
Total length	1907799	2868917	1022604	2016966
Reference length	2426359	2426359	2426359	2426359
GC (%)	39.54	39.87	39.64	39.71
Reference GC (%)	39.52	39.52	39.52	39.52
N50	1869	14067	1245	5830
NG50	1324	16713	-	3327
N75	995	7143	742	1604
NG75	574	10675	-	812
L50	245	59	203	70
LG50	411	44	-	117
L75	602	128	477	248
LG75	1124	90	-	523
# misassemblies	19	44	6	26
# misassembled contigs	18	33	5	23
Misassembled contigs length	38165	459157	6873	178828
# local misassemblies	43	81	47	23
# structural variations	4	9	1	3
# unaligned contigs	0 + 203 part	0 + 104 part	0 + 261 part	0 + 168 part
Unaligned length	402691	800539	331636	599948
Genome fraction (%)	52.954	60.742	25.833	51.605
Duplication ratio	1.171	1.403	1.102	1.132
# N's per 100 kbp	0.63	421.59	3089.56	419.39
# mismatches per 100 kbp	2145.77	2931.37	1881.27	2606.78
# indels per 100 kbp	55.65	71.85	48.98	54.31
Largest alignment	18495	37162	6177	31312
NA50	1051	4356	570	1128
NGA50	715	6148	-	704
NA75	522	-	-	-
NGA75	-	921	-	-
LA50	475	143	517	299
LGA50	775	100	-	533
LA75	1132	-	-	-
LGA75	-	329	-	-

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	19	44	6	26
# relocations	12	34	5	14
# translocations	7	10	1	12
# inversions	0	0	0	0
# possibly misassembled contigs	61	87	54	74
# misassembled contigs	18	33	5	23
Misassembled contigs length	38165	459157	6873	178828
# local misassemblies	43	81	47	23
# structural variations	4	9	1	3
# mismatches	27570	43203	11792	32640
# indels	715	1059	307	680
# short indels	577	976	238	625
# long indels	138	83	69	55
Indels length	3914	2298	2885	2083

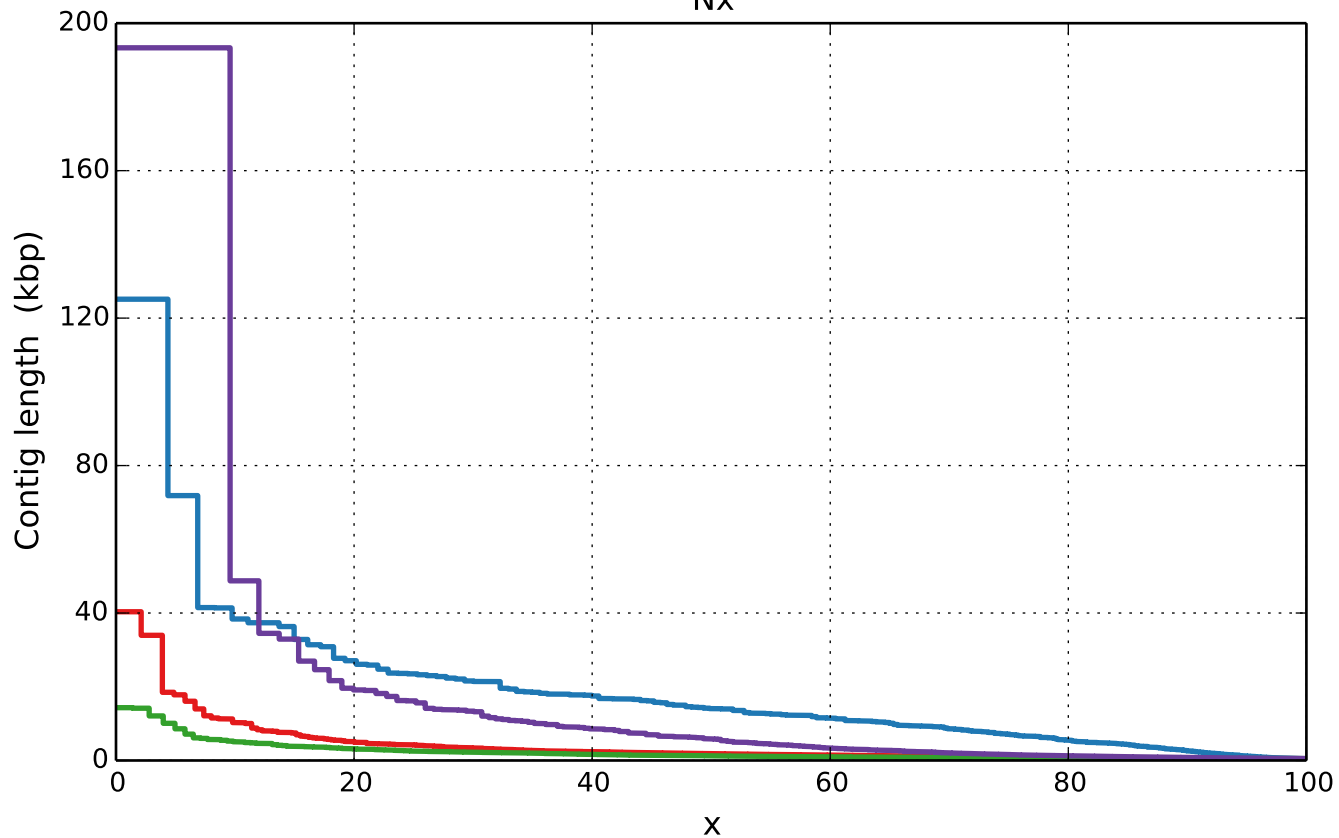
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	203	104	261	168
# with misassembly	19	21	29	19
# both parts are significant	54	54	43	60
Partially unaligned length	402691	800539	331636	599948
# N's	12	12095	31594	8459

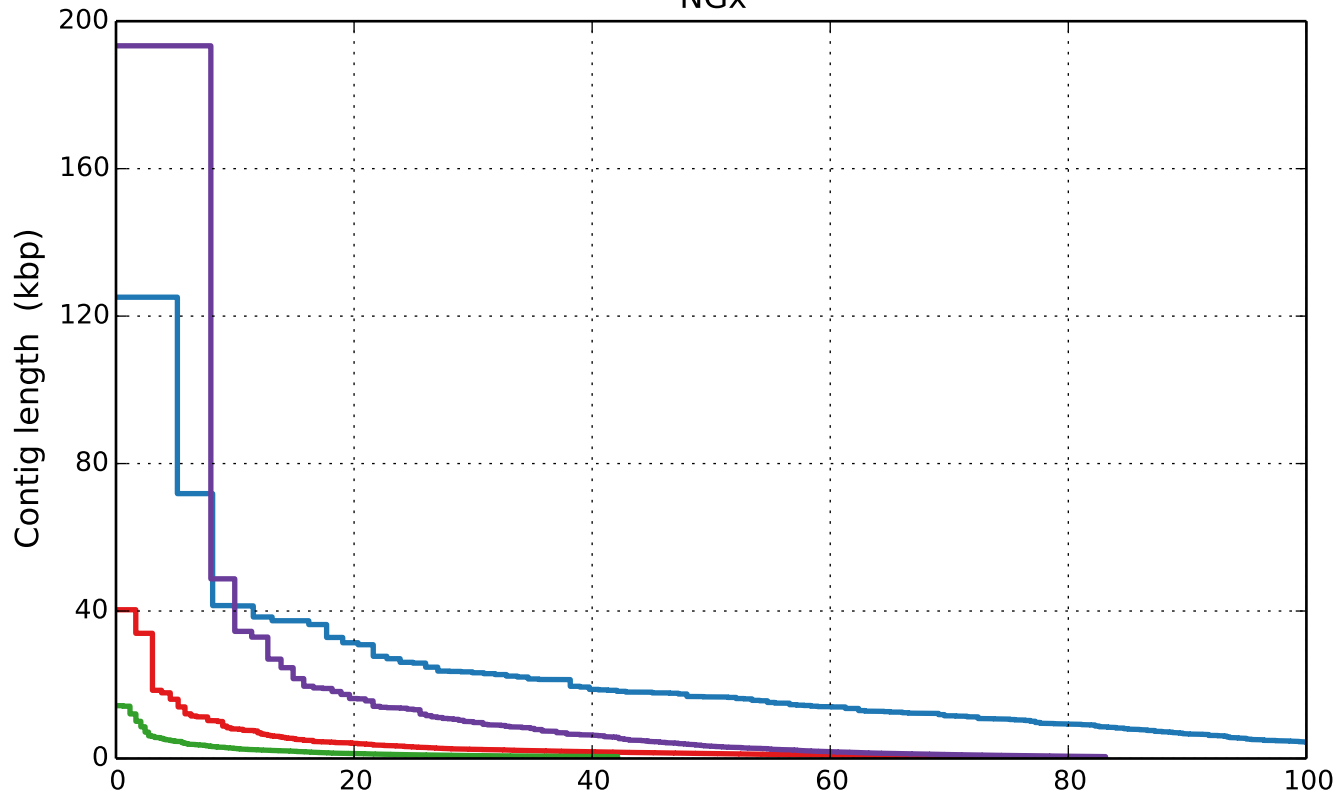
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

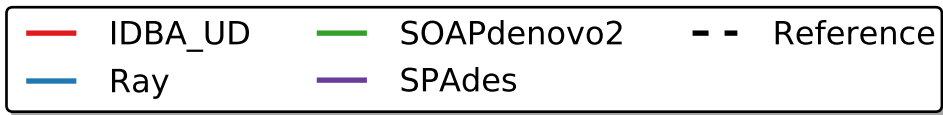
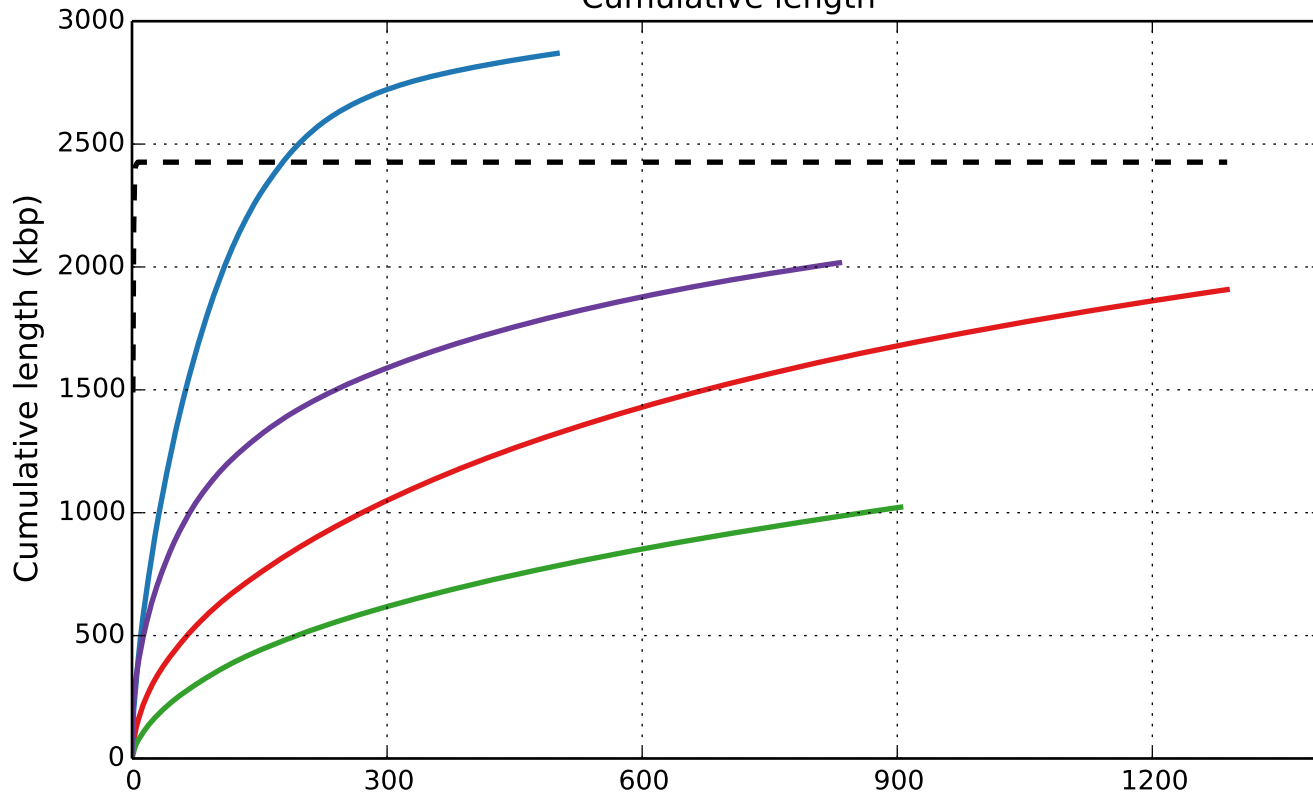


IDBA_UD SOAPdenovo2 SPAdes Ray

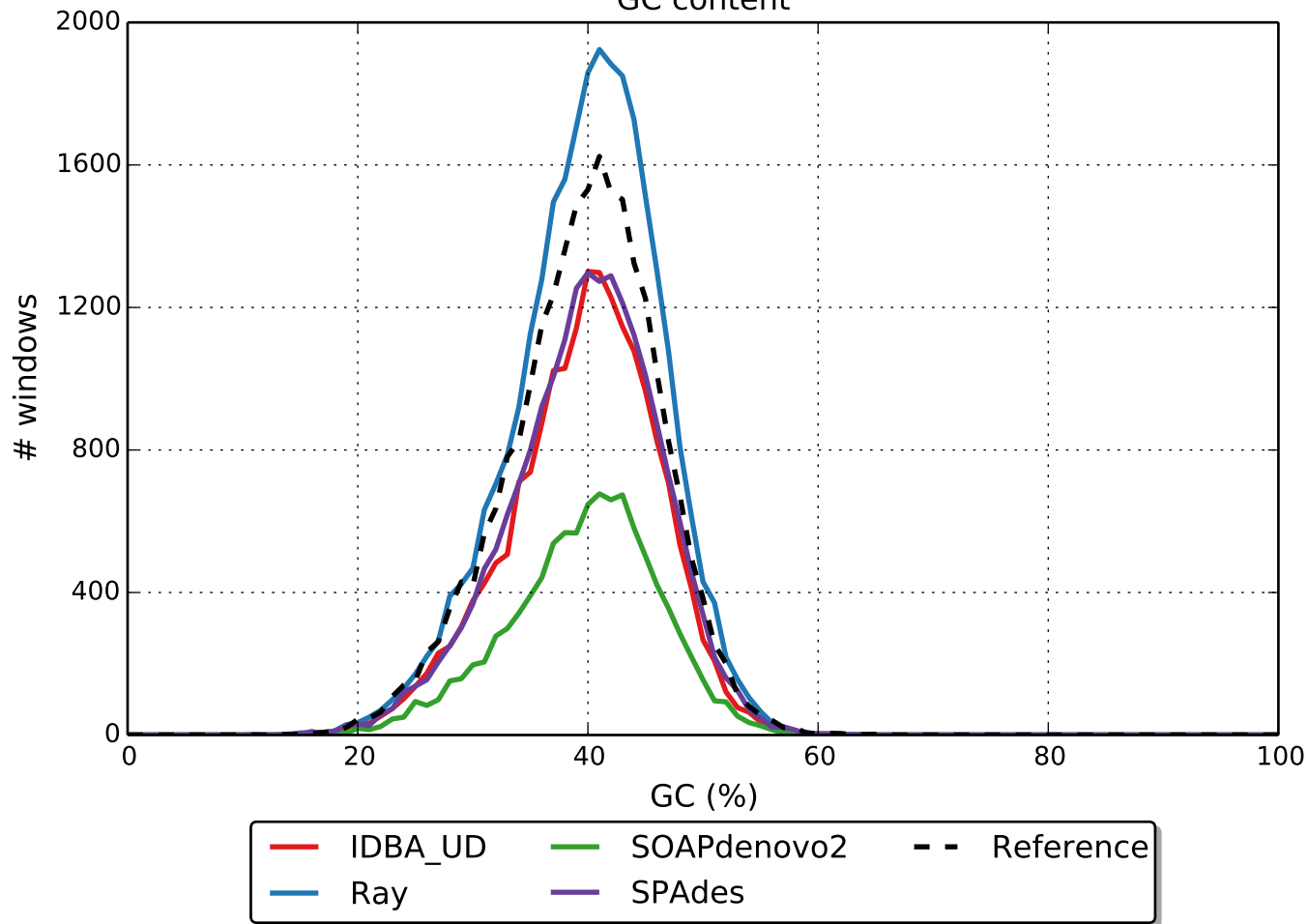
NGx



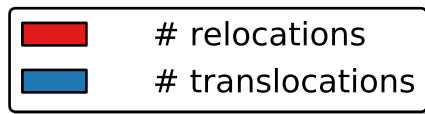
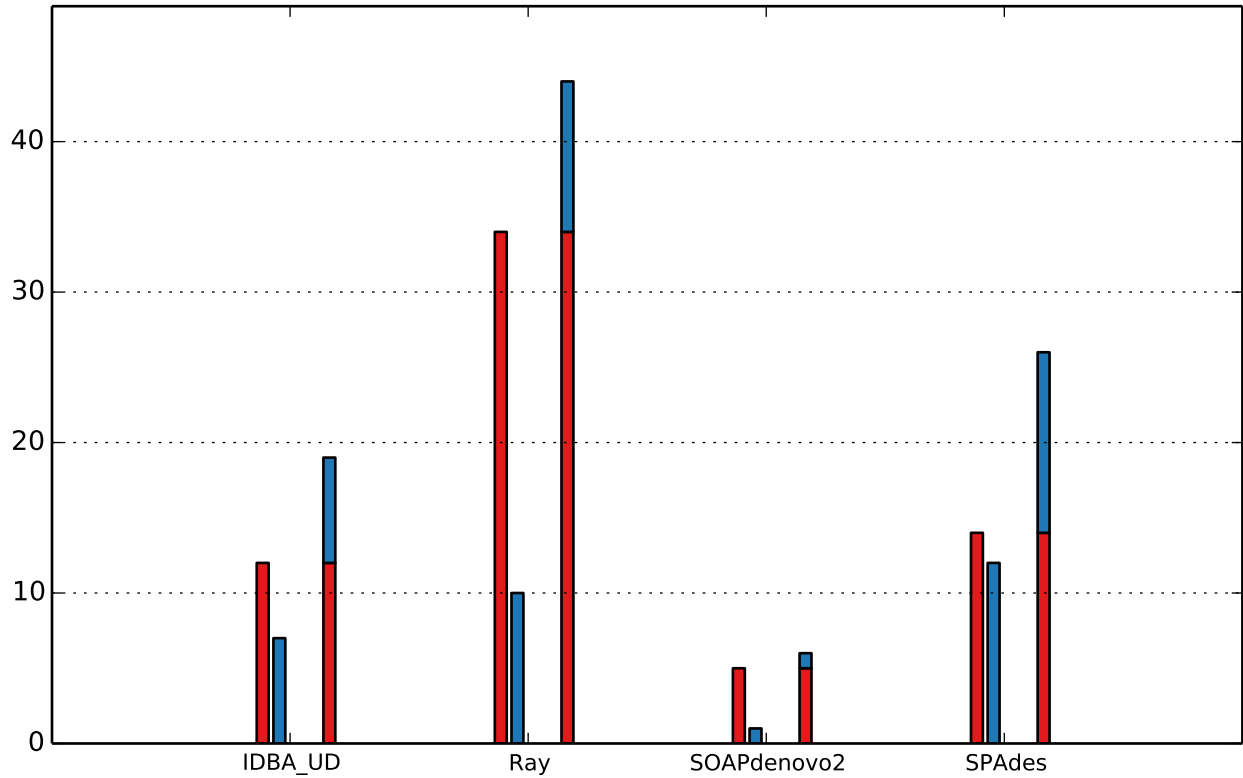
Cumulative length



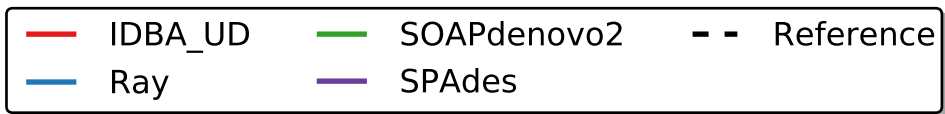
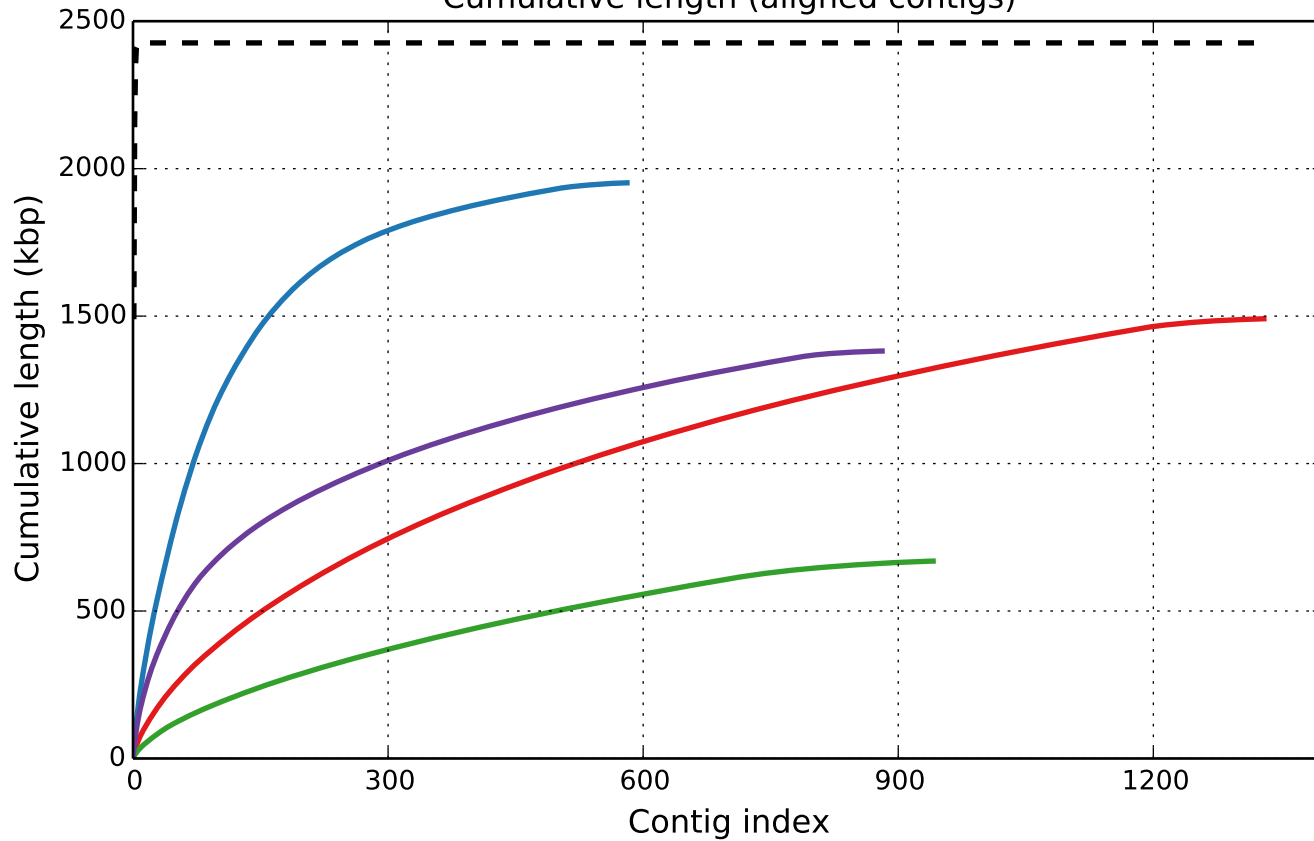
GC content

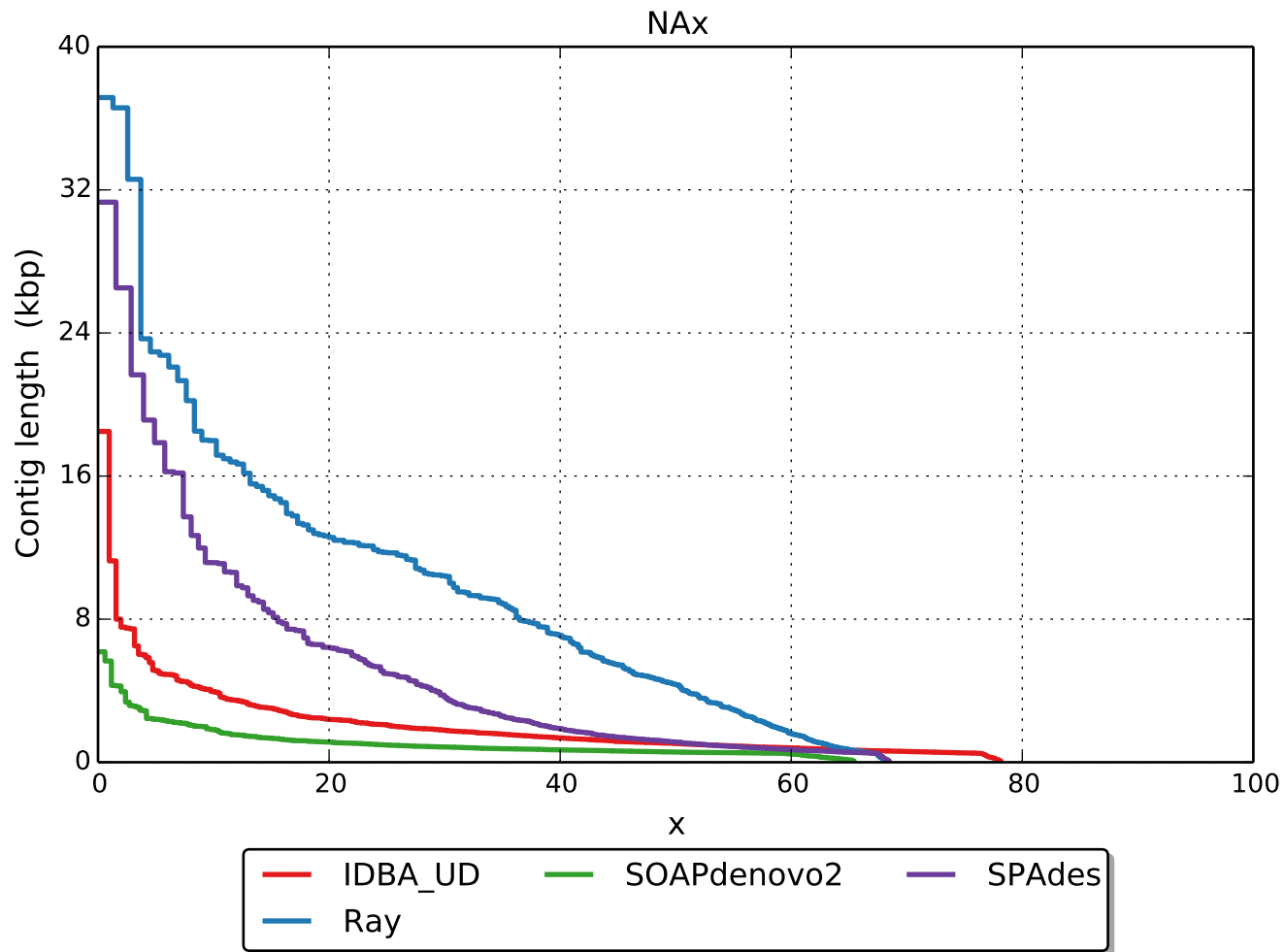


Misassemblies



Cumulative length (aligned contigs)





NGAx

