

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	11	6	8	7
# contigs (>= 5000 bp)	7	0	0	3
# contigs (>= 10000 bp)	5	0	0	1
# contigs (>= 25000 bp)	3	0	0	1
# contigs (>= 50000 bp)	2	0	0	0
Total length (>= 1000 bp)	255551	12086	12443	54275
Total length (>= 5000 bp)	242489	0	0	46663
Total length (>= 10000 bp)	228831	0	0	32100
Total length (>= 25000 bp)	200533	0	0	32100
Total length (>= 50000 bp)	164253	0	0	0
# contigs	15	9	22	8
Largest contig	94894	3544	3110	32100
Total length	258741	14116	22918	54785
Reference length	6417332	6417332	6417332	6417332
GC (%)	46.66	43.34	49.62	45.22
Reference GC (%)	55.60	55.60	55.60	55.60
N50	69359	1614	1032	32100
N75	36280	1275	751	9295
L50	2	3	8	1
L75	3	5	14	2
# misassemblies	0	0	0	0
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	1	9	0
# structural variations	0	0	0	0
# unaligned contigs	0 + 13 part	0 + 5 part	0 + 5 part	0 + 7 part
Unaligned length	231226	6619	2549	41781
Genome fraction (%)	0.426	0.110	0.301	0.203
Duplication ratio	1.006	1.060	1.054	1.000
# N's per 100 kbp	81.55	3804.19	3071.82	292.05
# mismatches per 100 kbp	3737.16	1683.17	2468.18	2461.35
# indels per 100 kbp	76.79	28.29	25.87	76.92
Largest alignment	8256	1952	3090	4835
NA50	-	596	906	-
NGA50	-	-	-	-
NA75	-	-	545	-
LA50	-	8	8	-
LA75	-	-	16	-

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

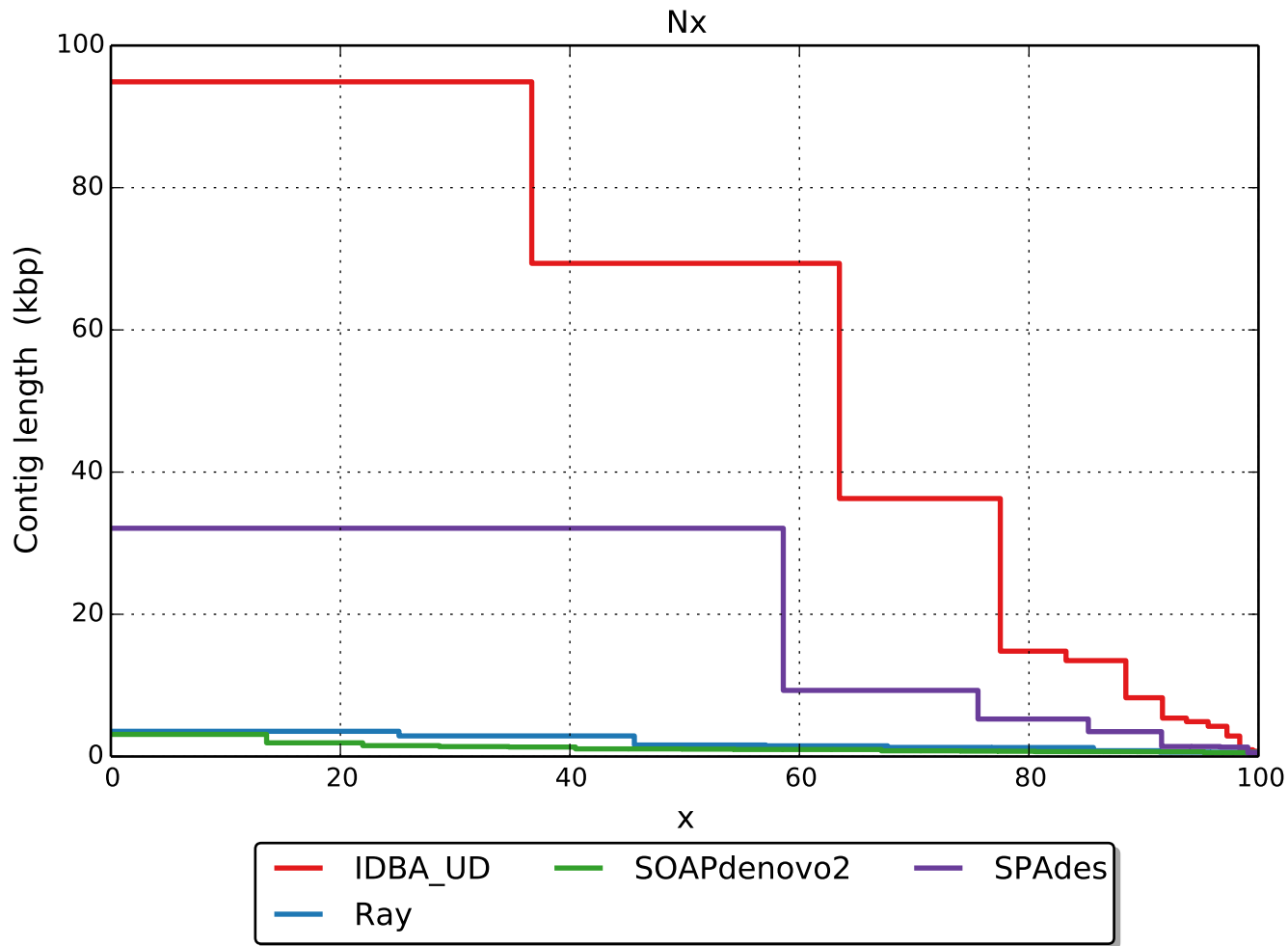
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	0	0	0
# relocations	0	0	0	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	3	4	0	2
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	1	9	0
# structural variations	0	0	0	0
# mismatches	1022	119	477	320
# indels	21	2	5	10
# short indels	19	2	5	9
# long indels	2	0	0	1
Indels length	40	2	5	19

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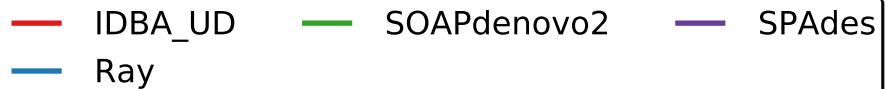
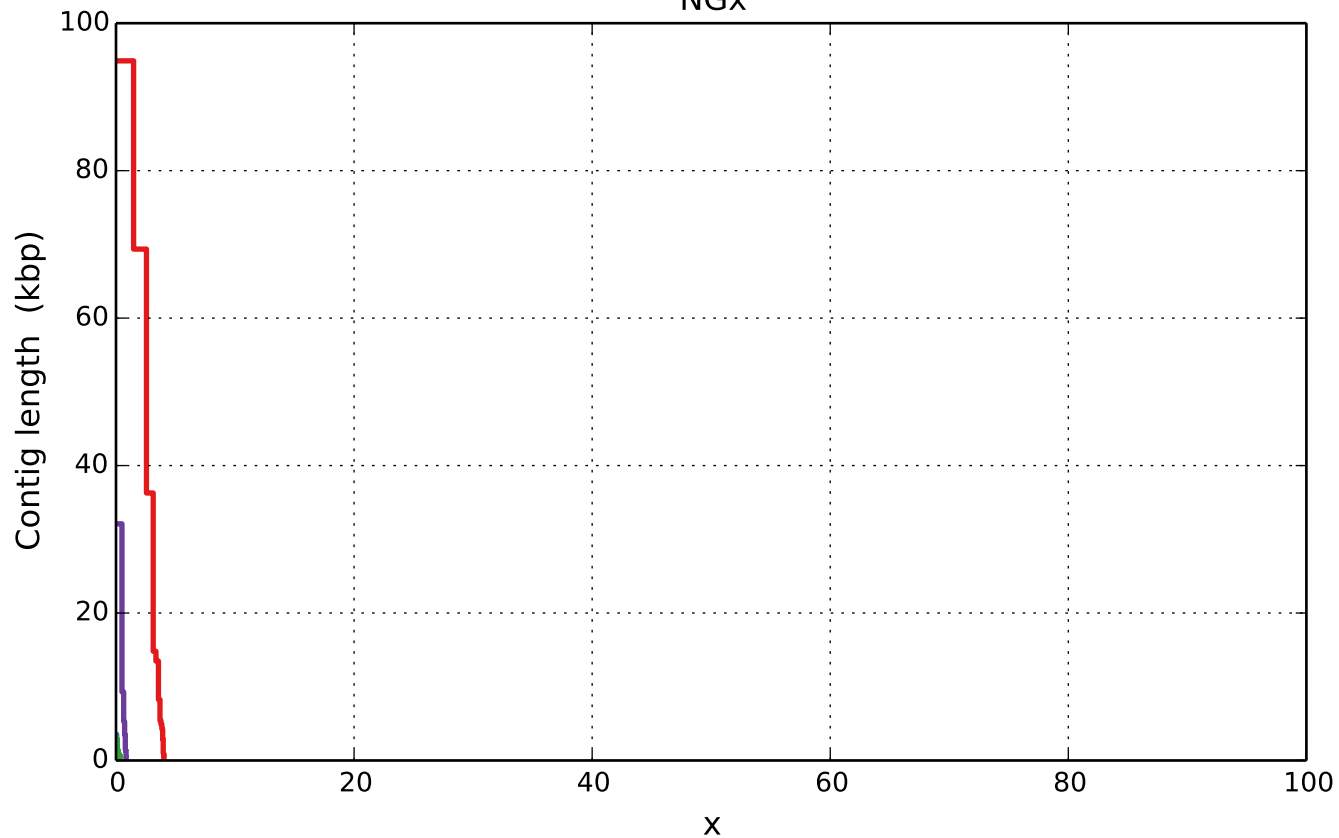
Unaligned report

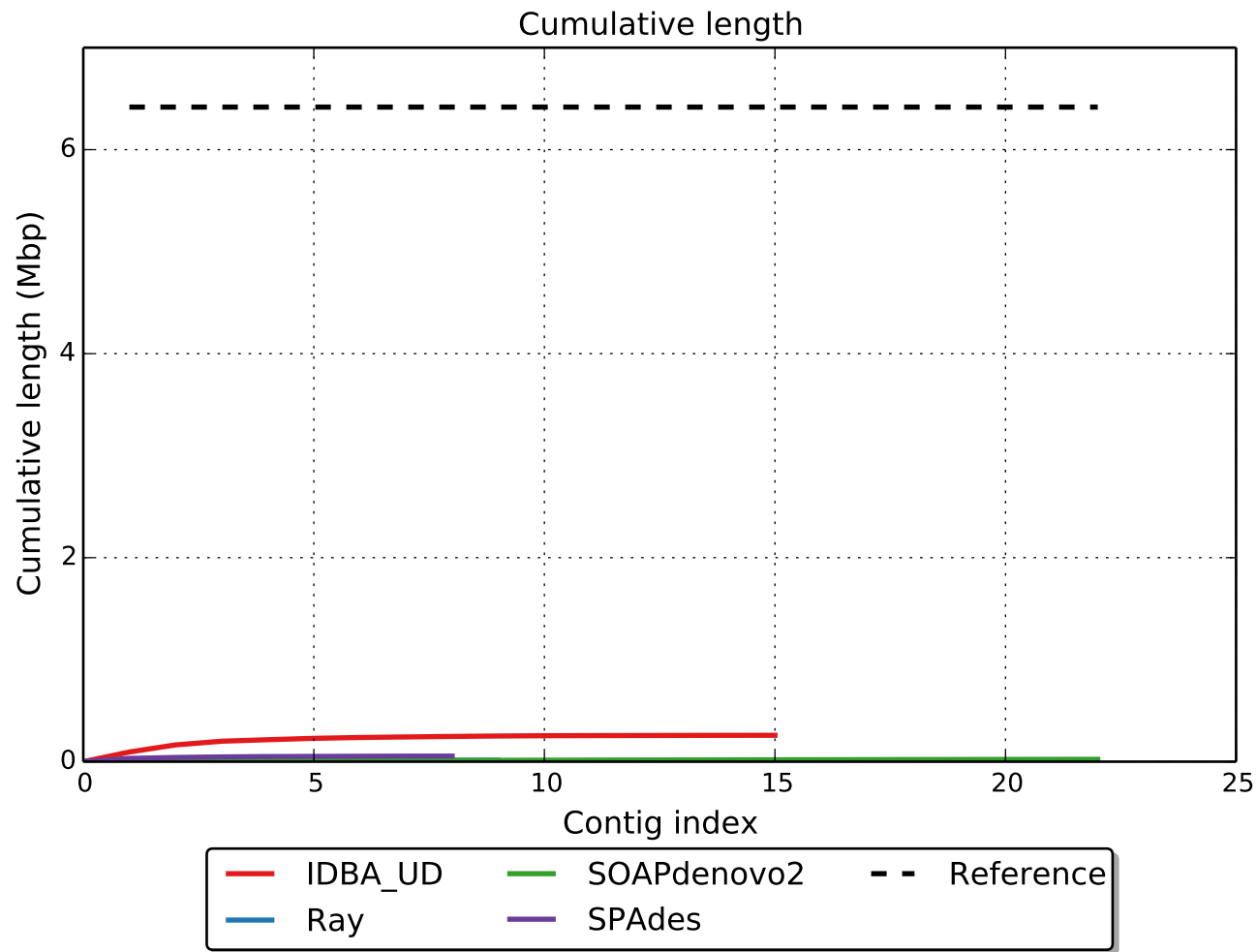
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	13	5	5	7
# with misassembly	0	0	0	0
# both parts are significant	3	4	0	2
Partially unaligned length	231226	6619	2549	41781
# N's	211	537	704	160

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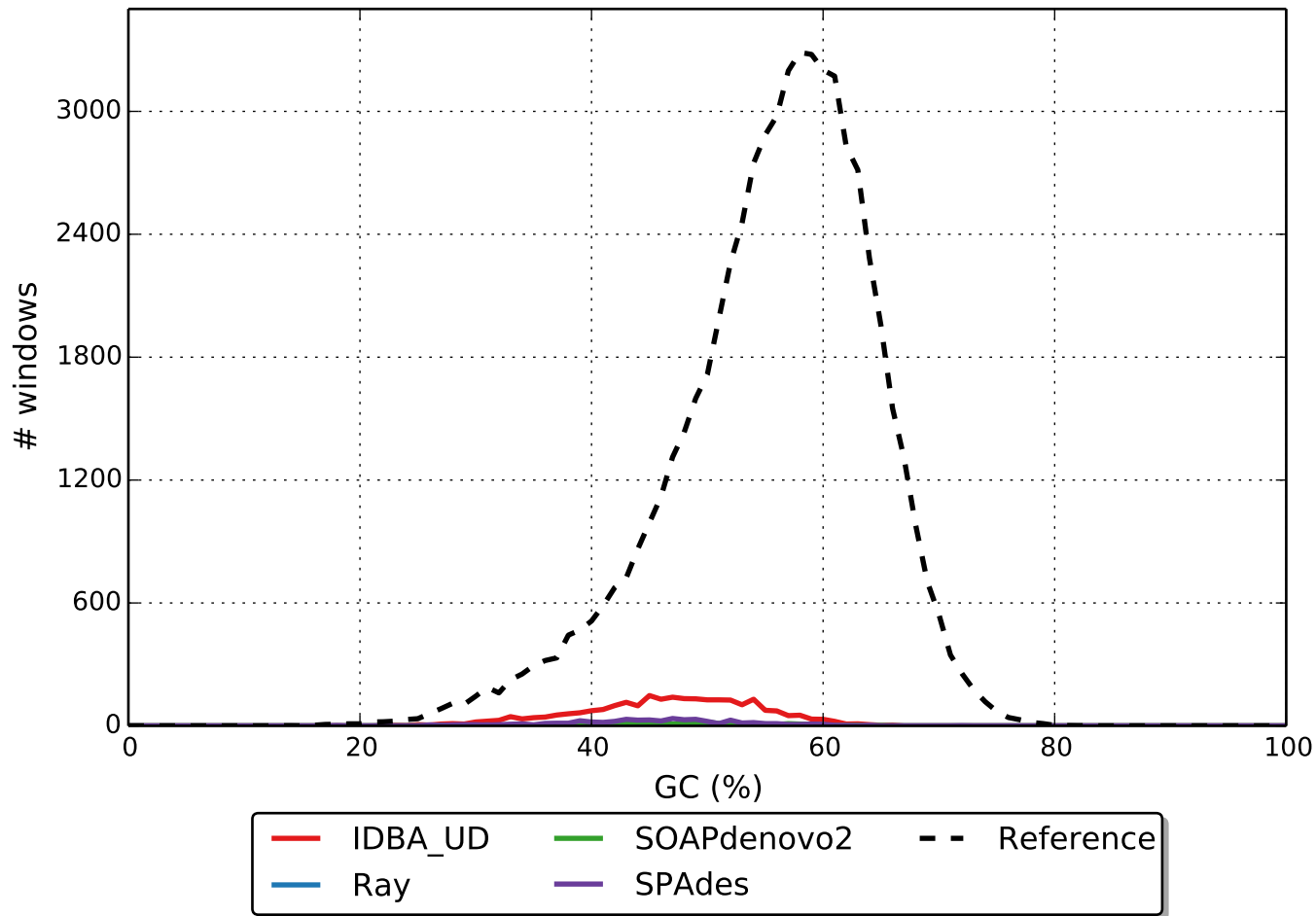


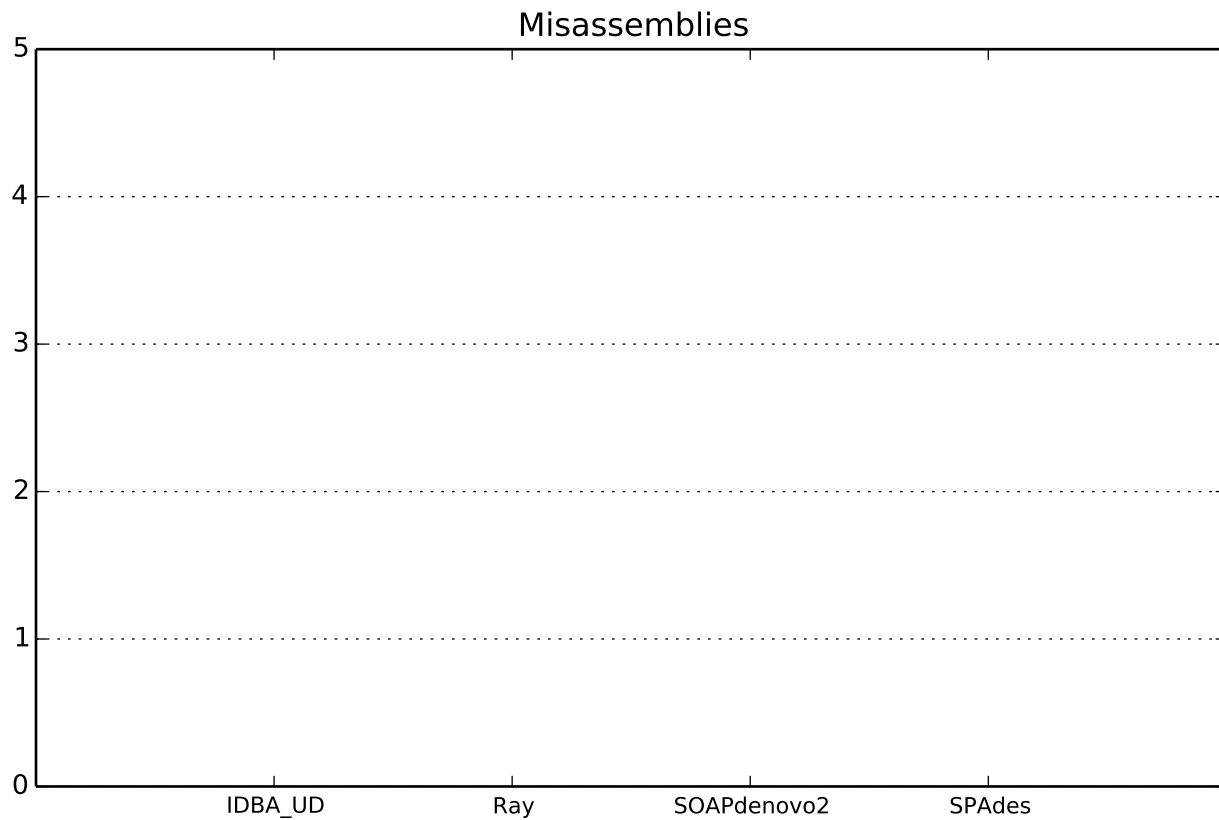
NGx

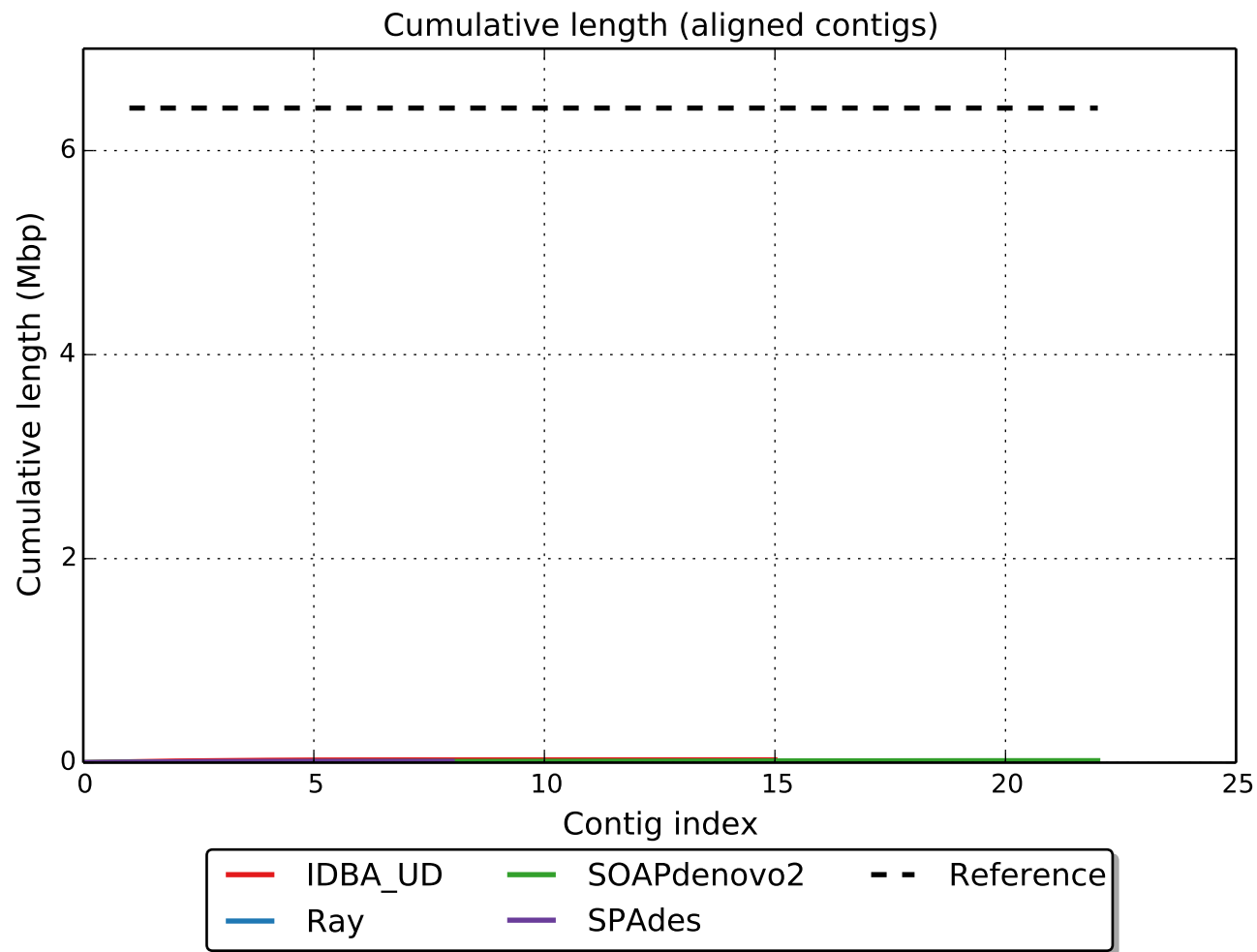




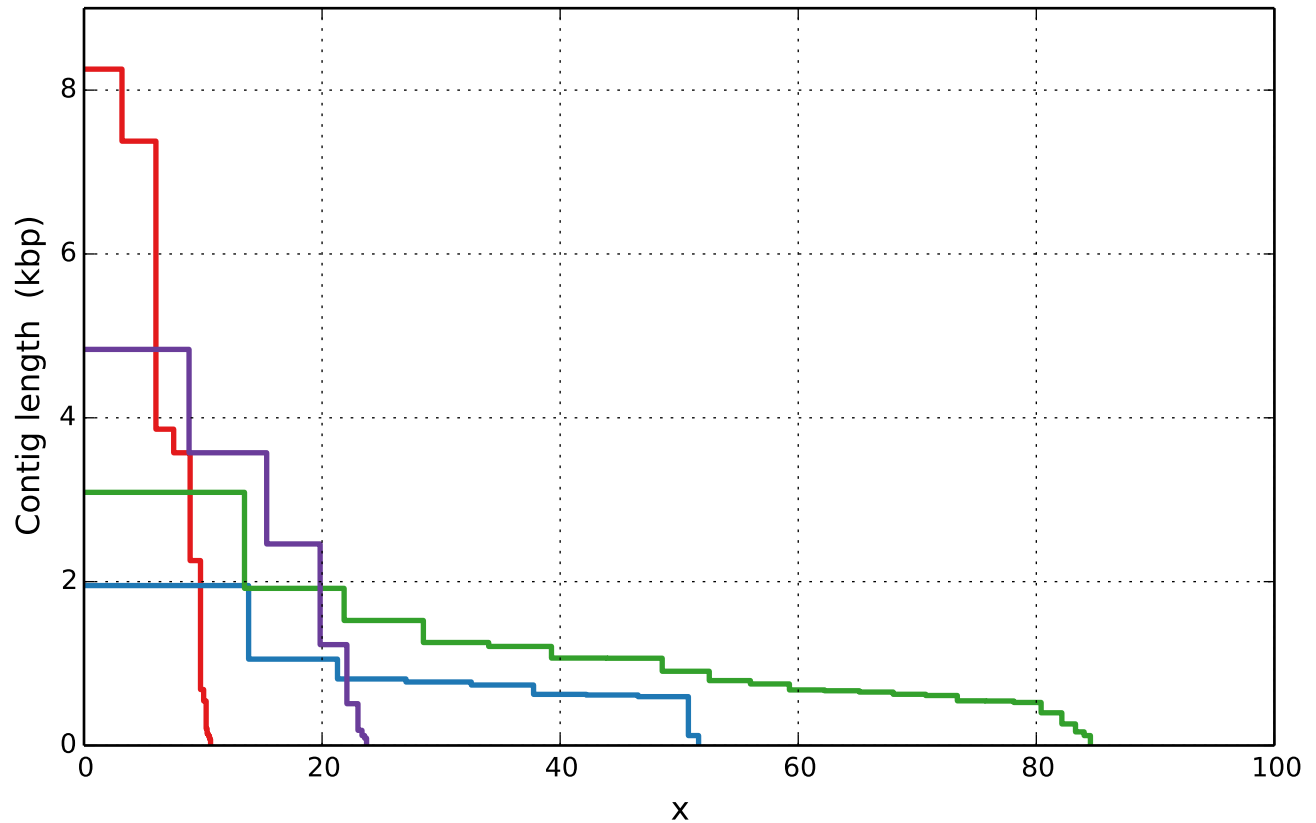
GC content







NAx



— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray

