

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	32	9	8	24
# contigs (>= 5000 bp)	8	0	0	7
# contigs (>= 10000 bp)	7	0	0	6
# contigs (>= 25000 bp)	3	0	0	3
# contigs (>= 50000 bp)	1	0	0	0
Total length (>= 1000 bp)	253181	24292	17421	183719
Total length (>= 5000 bp)	201665	0	0	150171
Total length (>= 10000 bp)	195467	0	0	142707
Total length (>= 25000 bp)	143181	0	0	101621
Total length (>= 50000 bp)	73506	0	0	0
# contigs	49	18	14	37
Largest contig	73506	4536	4790	45766
Total length	265598	30657	21410	192760
Reference length	3245471	3245471	3245471	3245471
GC (%)	44.19	45.85	44.35	44.87
Reference GC (%)	57.92	57.92	57.92	57.92
N50	28442	2538	1614	26316
N75	6198	1509	1111	7464
L50	3	5	4	3
L75	8	8	7	7
# misassemblies	4	0	0	3
# misassembled contigs	2	0	0	2
Misassembled contigs length	4341	0	0	13546
# local misassemblies	1	2	5	0
# structural variations	0	0	0	0
# unaligned contigs	0 + 25 part	0 + 5 part	0 + 5 part	0 + 23 part
Unaligned length	207712	10644	8932	144219
Genome fraction (%)	1.710	0.534	0.371	1.321
Duplication ratio	1.043	1.155	1.036	1.132
# N's per 100 kbp	199.93	2345.30	3362.91	326.83
# mismatches per 100 kbp	2185.86	2031.28	1693.51	2064.19
# indels per 100 kbp	104.52	11.54	33.21	81.63
Largest alignment	4273	3753	2895	4410
NA50	-	615	609	-
NGA50	-	-	-	-
LA50	-	12	8	-

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

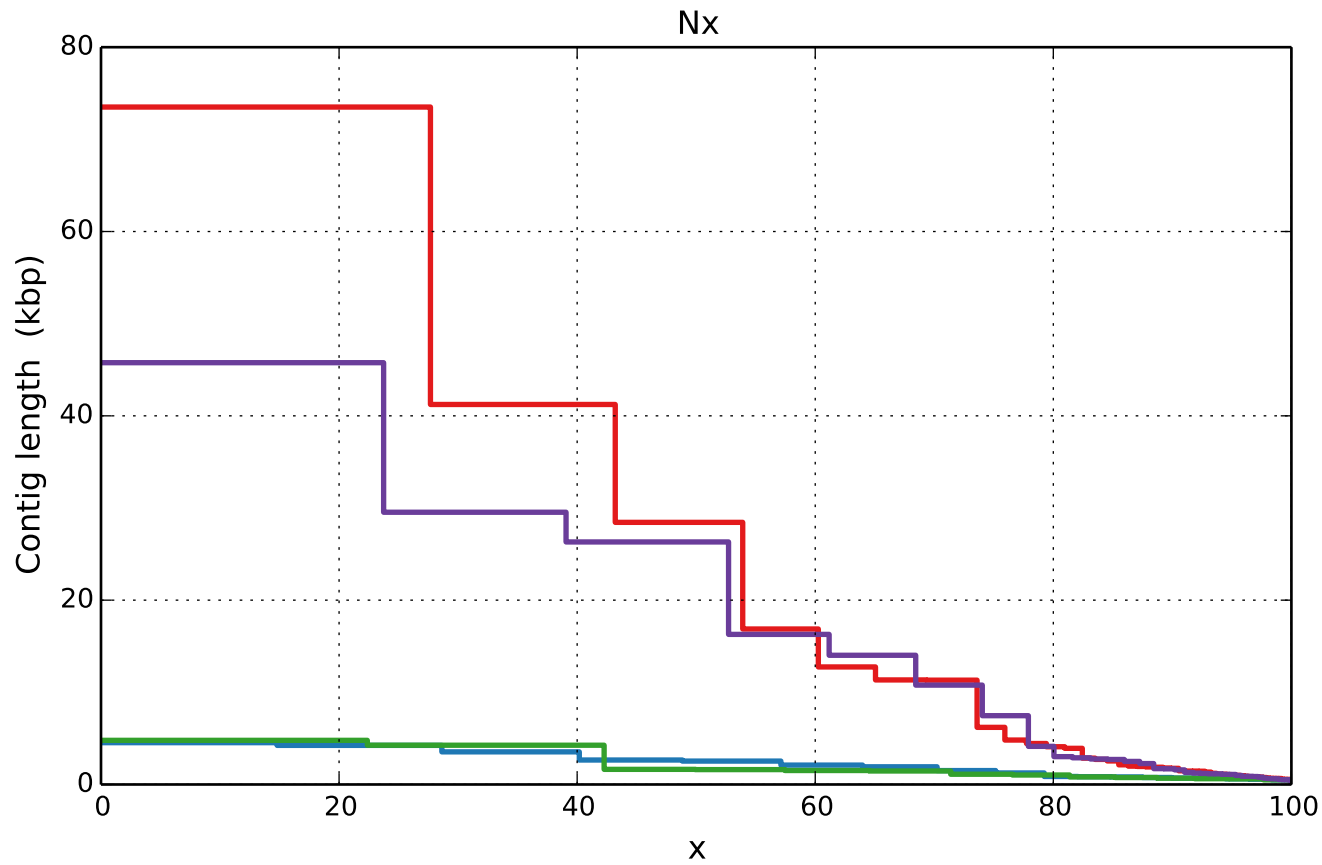
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	4	0	0	3
# relocations	3	0	0	3
# translocations	0	0	0	0
# inversions	1	0	0	0
# possibly misassembled contigs	10	4	1	5
# misassembled contigs	2	0	0	2
Misassembled contigs length	4341	0	0	13546
# local misassemblies	1	2	5	0
# structural variations	0	0	0	0
# mismatches	1213	352	204	885
# indels	58	2	4	35
# short indels	55	2	4	31
# long indels	3	0	0	4
Indels length	135	2	5	96

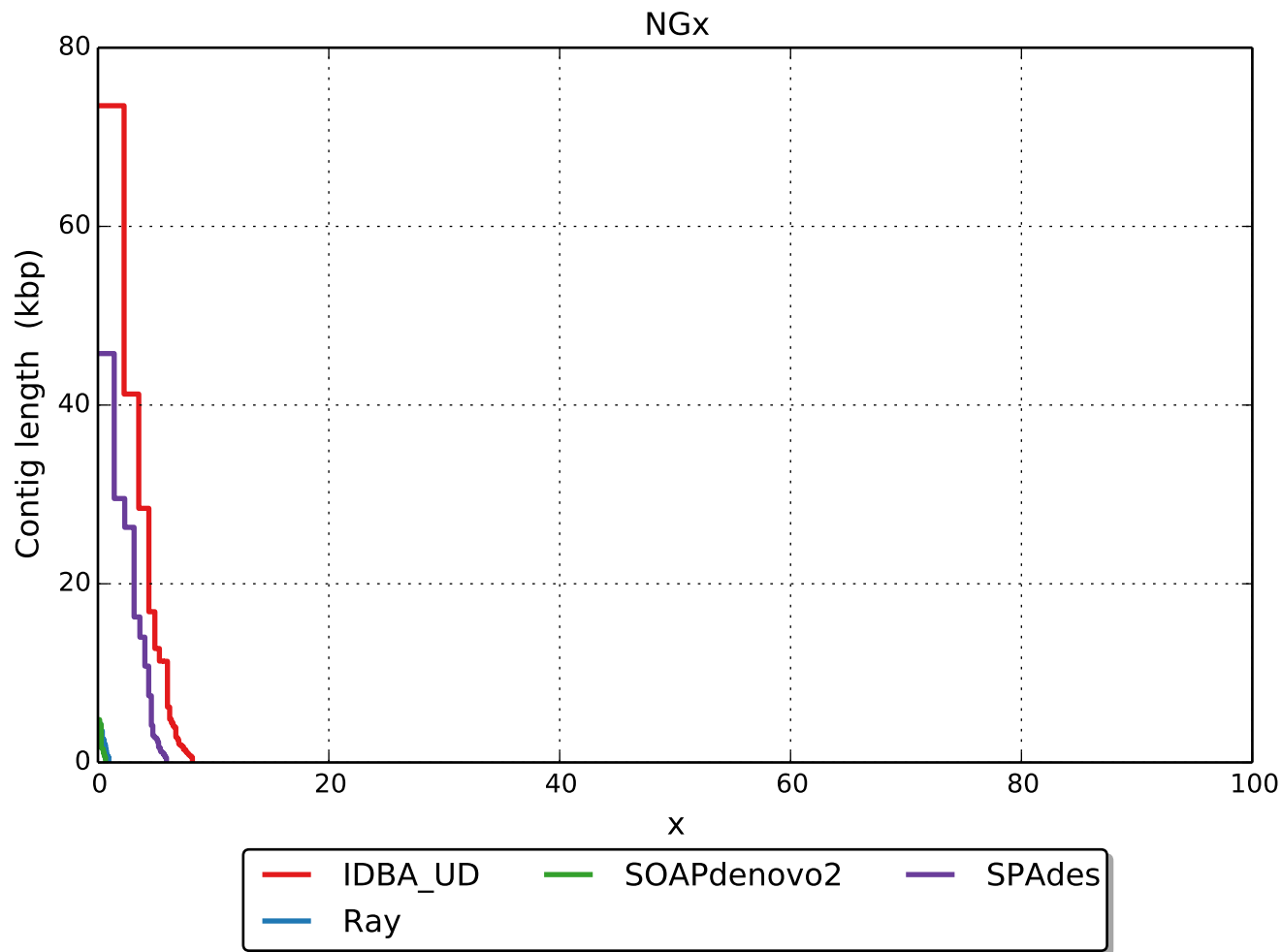
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

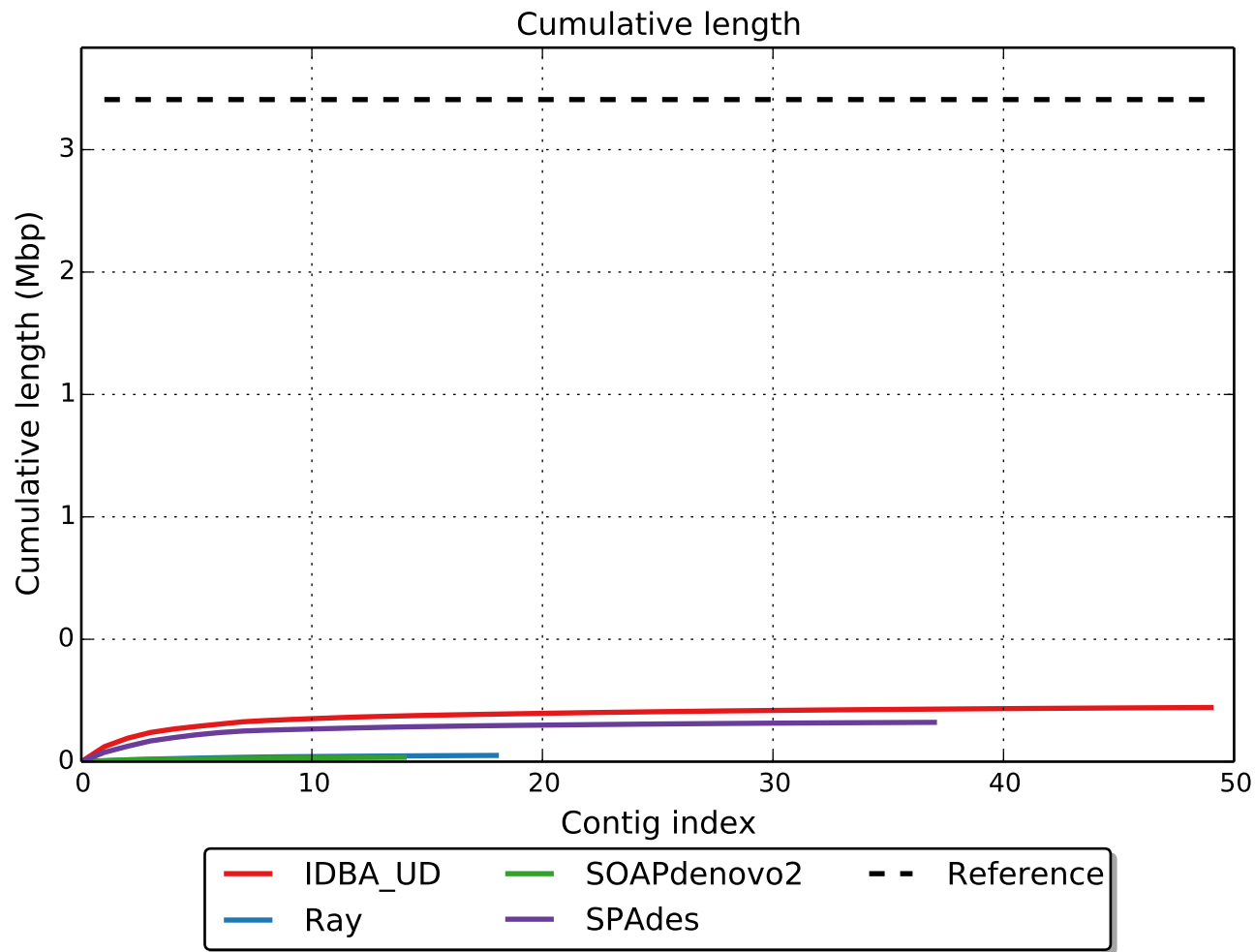
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	25	5	5	23
# with misassembly	4	0	0	2
# both parts are significant	9	2	1	4
Partially unaligned length	207712	10644	8932	144219
# N's	531	719	720	630

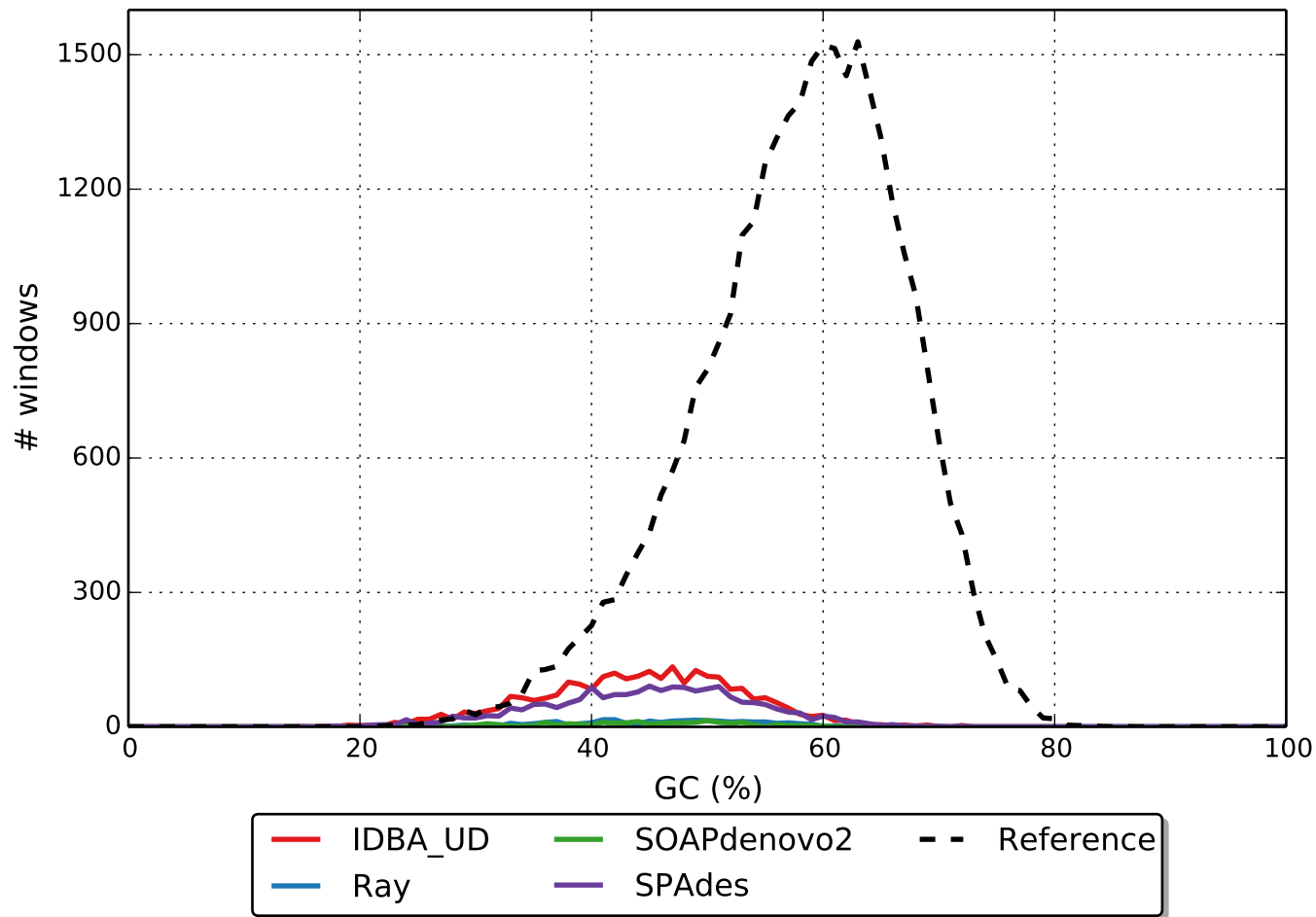
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

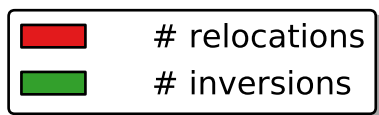
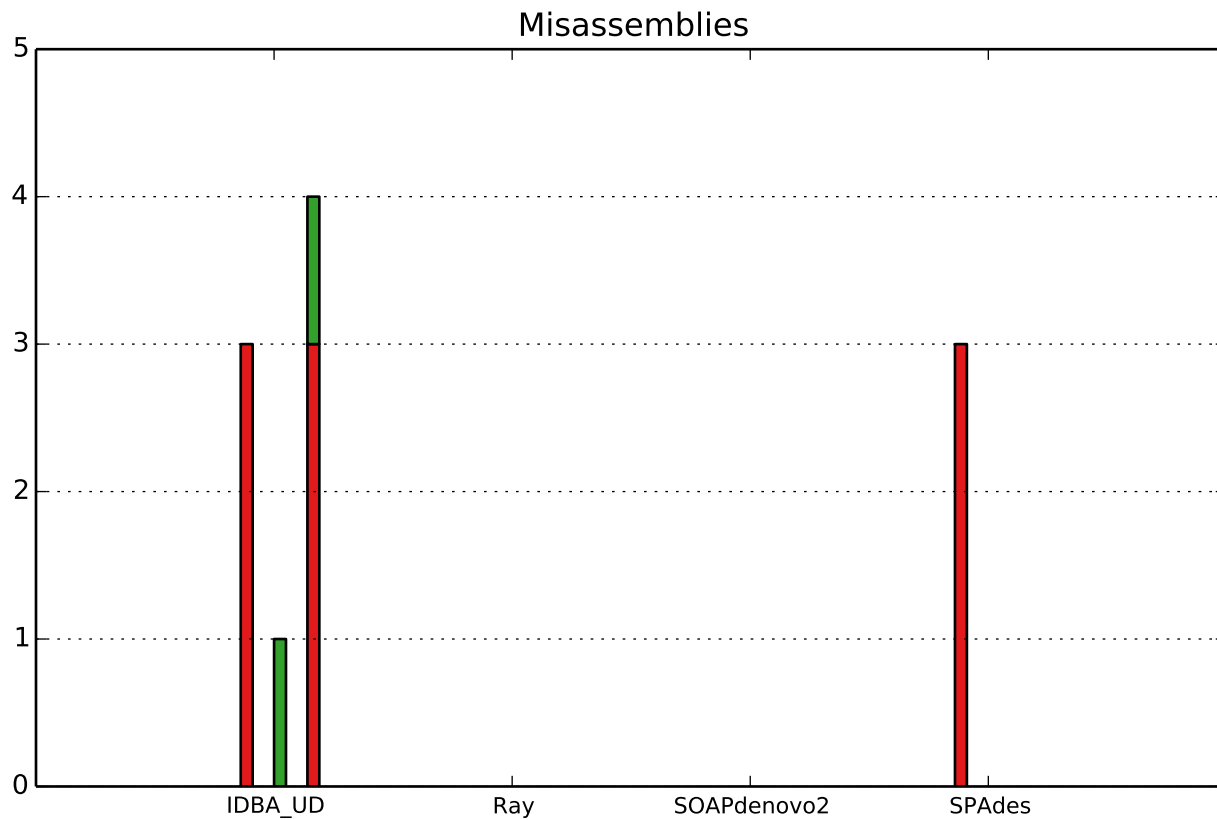


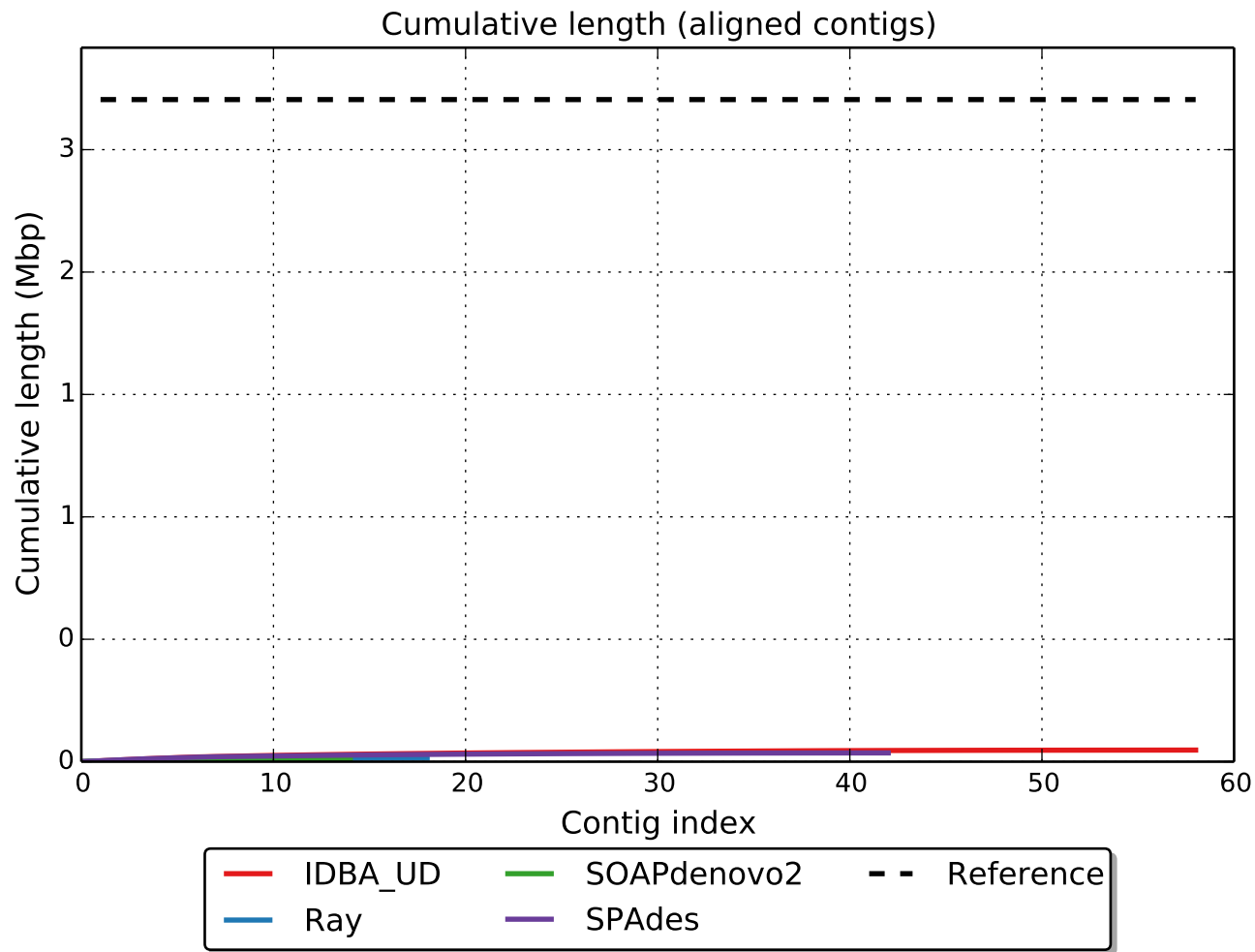




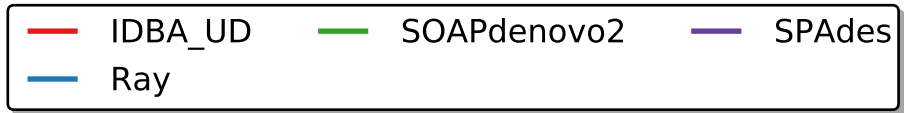
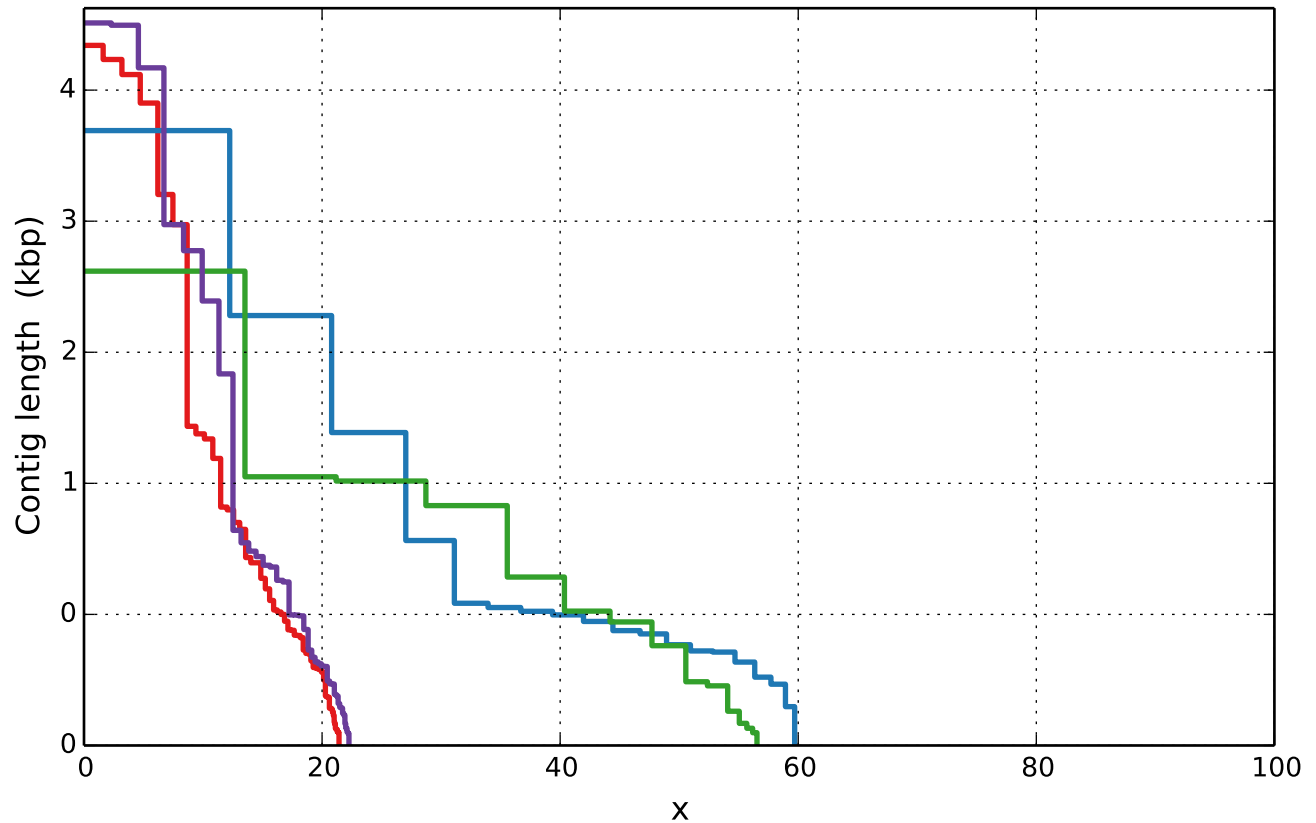
GC content







NAx



NGAx

