

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	24	6	8	15
# contigs (>= 5000 bp)	3	1	0	5
# contigs (>= 10000 bp)	1	0	0	1
# contigs (>= 25000 bp)	0	0	0	0
# contigs (>= 50000 bp)	0	0	0	0
Total length (>= 1000 bp)	72176	14817	12249	64121
Total length (>= 5000 bp)	25357	6935	0	38333
Total length (>= 10000 bp)	10542	0	0	10781
Total length (>= 25000 bp)	0	0	0	0
Total length (>= 50000 bp)	0	0	0	0
# contigs	37	14	27	25
Largest contig	10542	6935	3103	10781
Total length	81134	20275	24627	71127
Reference length	4241076	4241076	4241076	4241076
GC (%)	46.86	47.59	46.01	47.47
Reference GC (%)	59.11	59.11	59.11	59.11
N50	3419	1919	960	5029
N75	1849	855	633	2268
L50	7	3	9	5
L75	17	7	16	10
# misassemblies	0	0	0	1
# misassembled contigs	0	0	0	1
Misassembled contigs length	0	0	0	10781
# local misassemblies	1	0	20	1
# structural variations	0	0	0	0
# unaligned contigs	0 + 14 part	0 + 3 part	0 + 10 part	0 + 14 part
Unaligned length	30053	7778	4087	23693
Genome fraction (%)	1.173	0.270	0.449	1.050
Duplication ratio	1.027	1.093	1.078	1.065
# N's per 100 kbp	409.20	0.00	4754.94	850.59
# mismatches per 100 kbp	1799.36	1084.39	1117.93	1966.24
# indels per 100 kbp	50.26	0.00	47.24	26.93
Largest alignment	7442	2215	3004	8317
NA50	1066	627	600	1870
NGA50	-	-	-	-
NA75	-	-	246	-
LA50	16	9	10	10
LA75	-	-	24	-

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

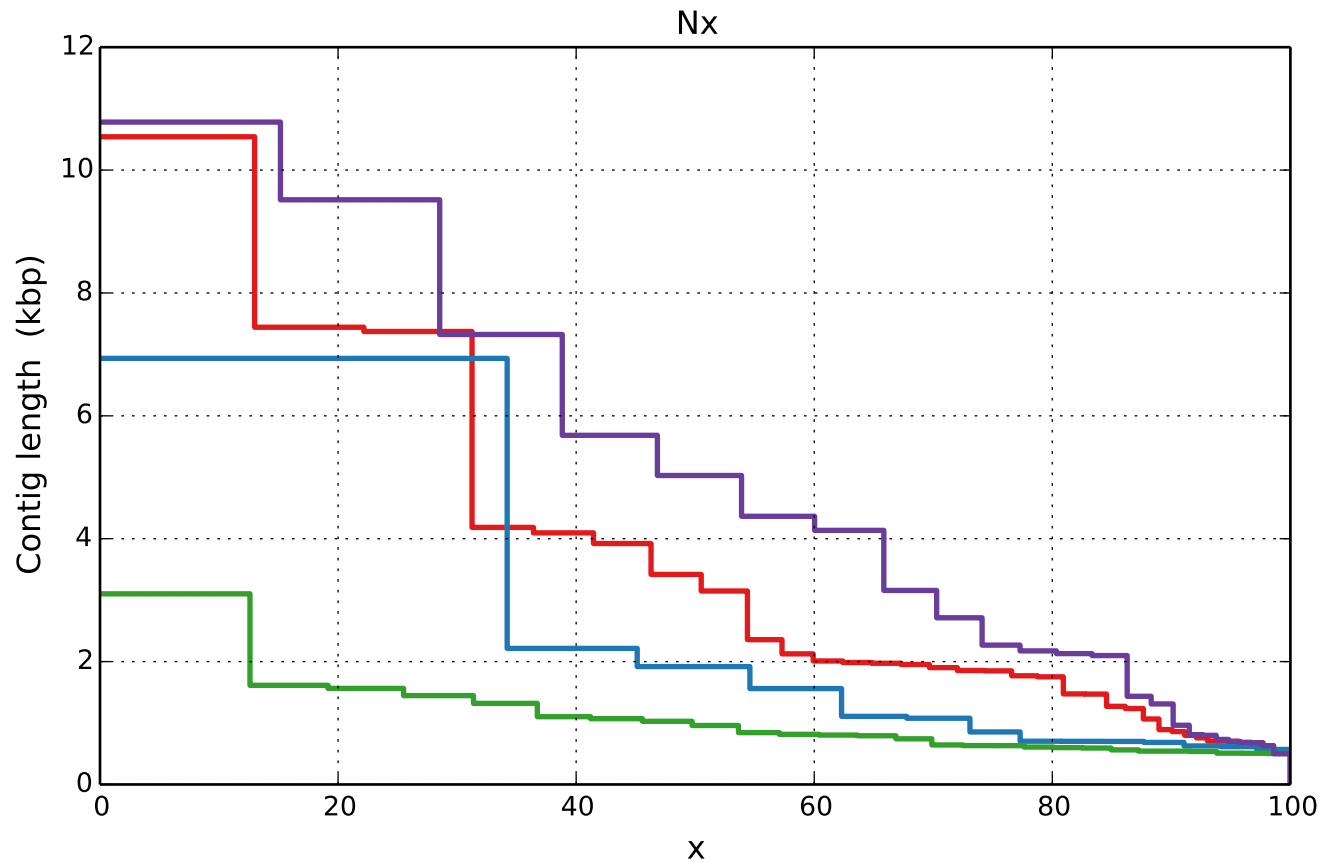
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	0	0	1
# relocations	0	0	0	1
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	1	0	0	4
# misassembled contigs	0	0	0	1
Misassembled contigs length	0	0	0	10781
# local misassemblies	1	0	20	1
# structural variations	0	0	0	0
# mismatches	895	124	213	876
# indels	25	0	9	12
# short indels	24	0	9	10
# long indels	1	0	0	2
Indels length	51	0	9	41

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).

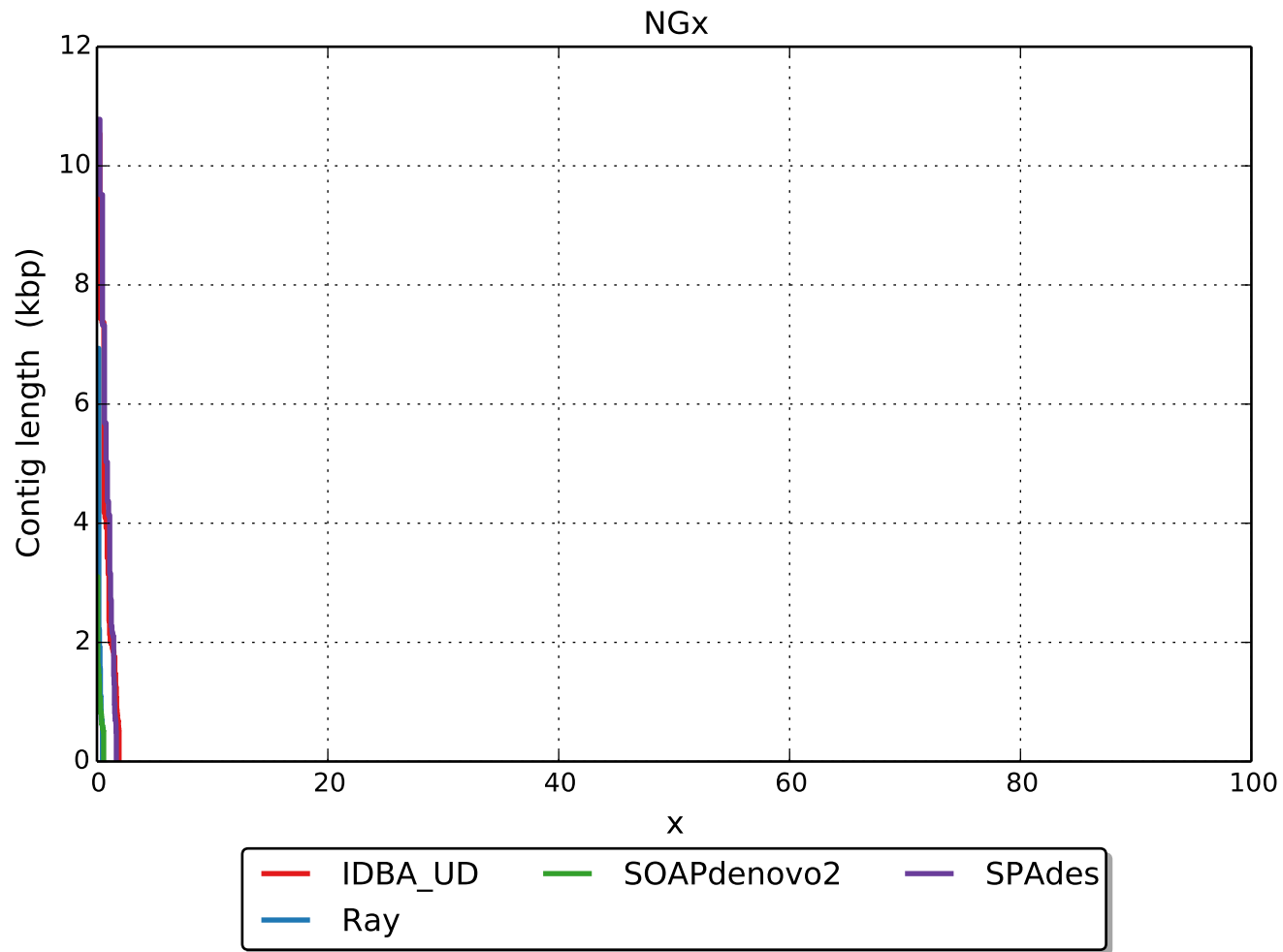
Unaligned report

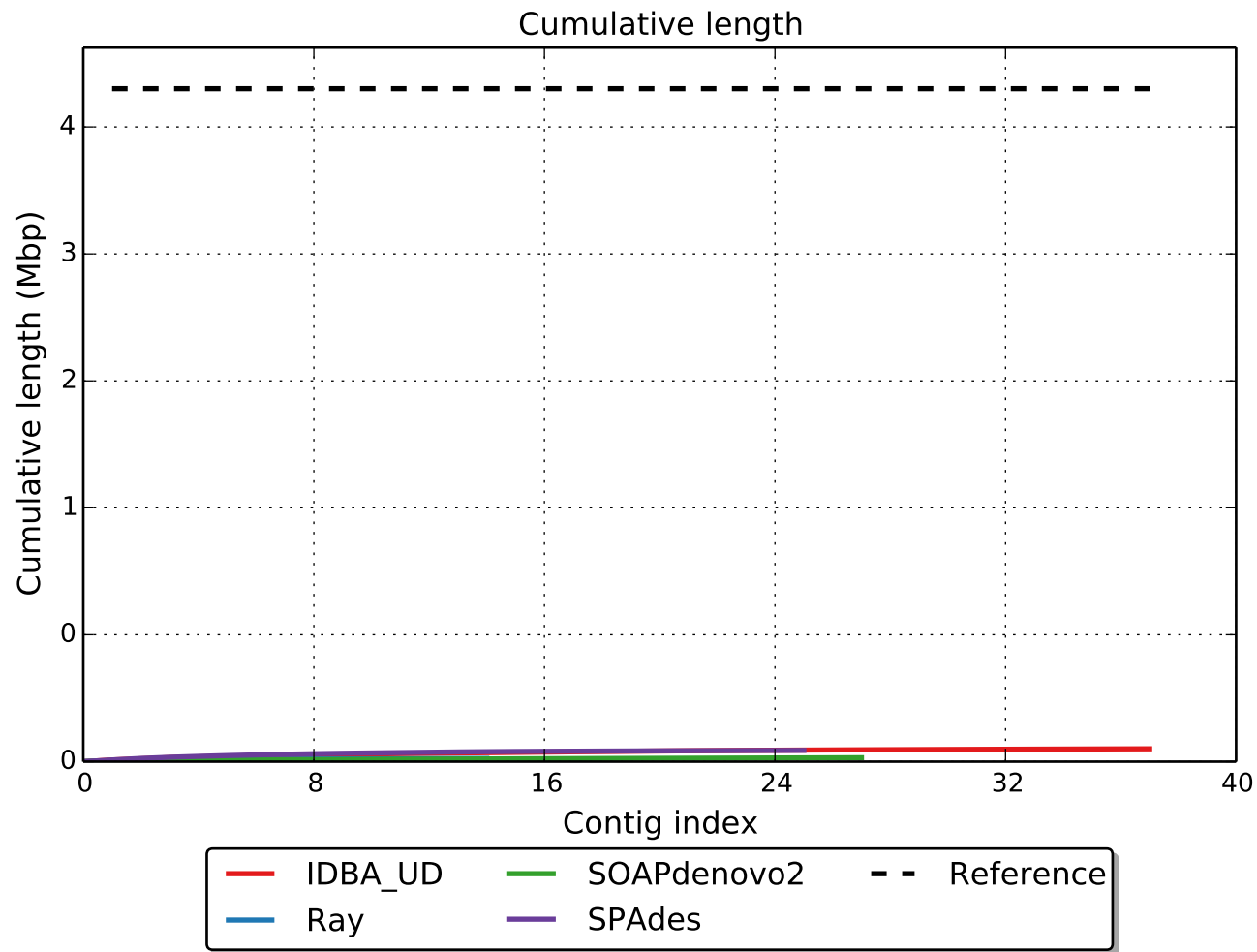
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	14	3	10	14
# with misassembly	1	0	0	0
# both parts are significant	1	0	0	3
Partially unaligned length	30053	7778	4087	23693
# N's	332	0	1171	605

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).

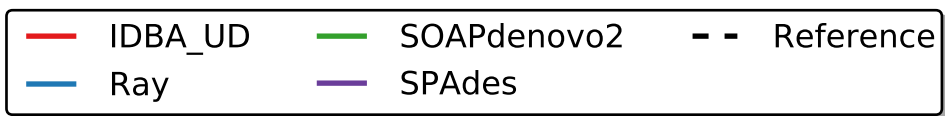
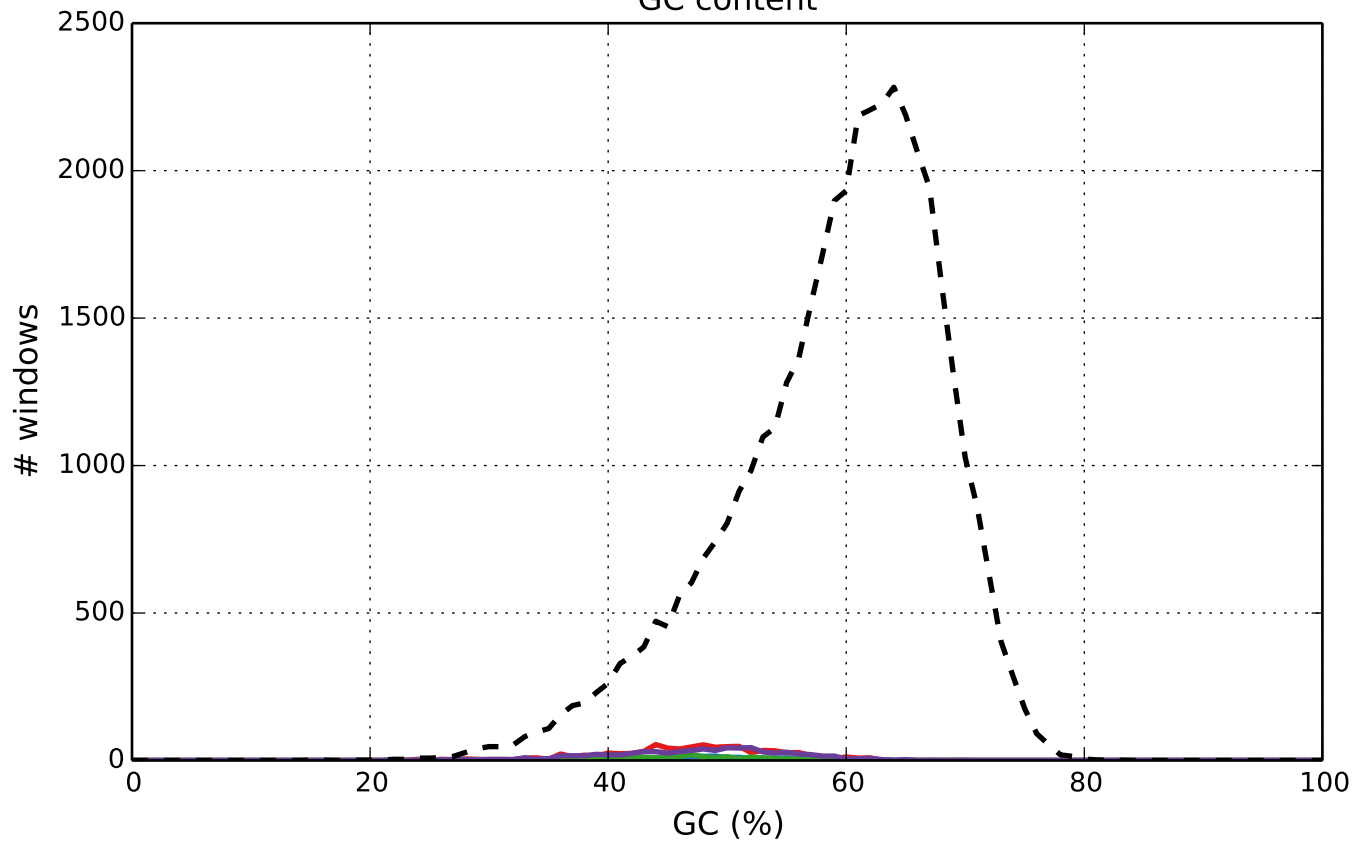


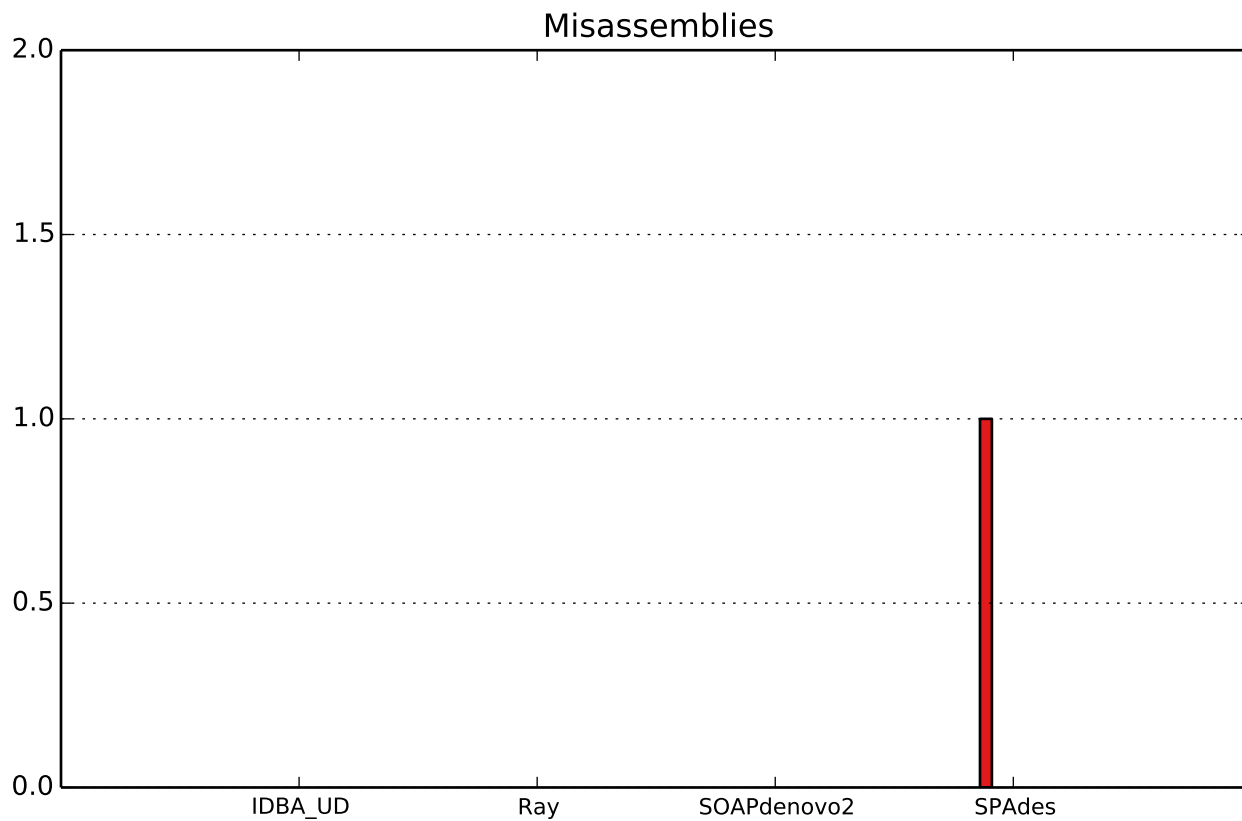
— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray



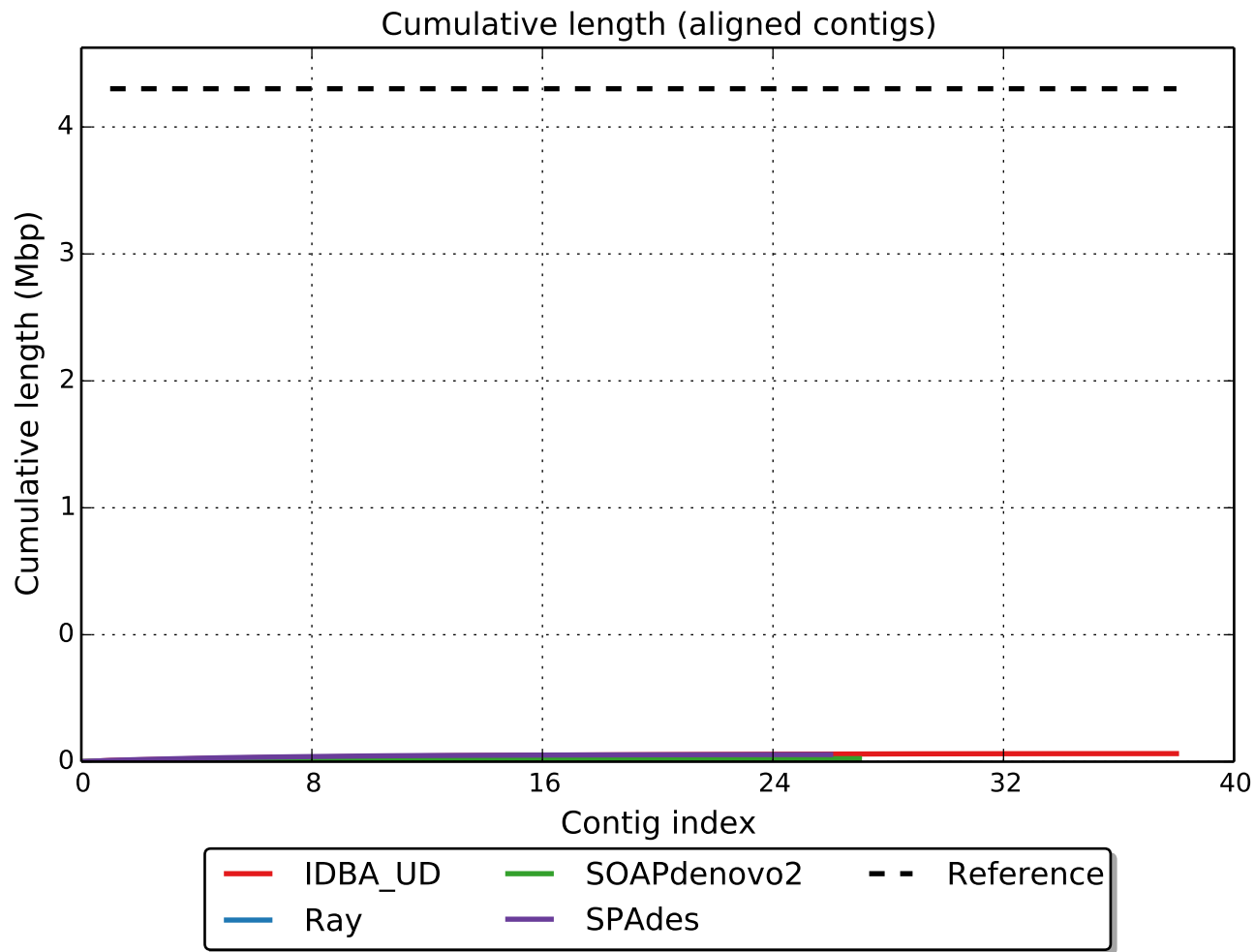


GC content





 # relocations



NAx

