

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	130	32	41	195
# contigs (>= 5000 bp)	23	6	2	26
# contigs (>= 10000 bp)	13	4	1	10
# contigs (>= 25000 bp)	8	1	0	3
# contigs (>= 50000 bp)	2	0	0	0
Total length (>= 1000 bp)	707820	143504	81108	634345
Total length (>= 5000 bp)	478089	89495	21035	322447
Total length (>= 10000 bp)	412985	77681	16010	221871
Total length (>= 25000 bp)	338732	27266	0	97486
Total length (>= 50000 bp)	144911	0	0	0
# contigs	378	48	167	530
Largest contig	73503	27266	16010	39677
Total length	881229	154274	167403	868144
Reference length	3341681	3341681	3341681	3341681
GC (%)	41.22	42.99	41.48	41.90
Reference GC (%)	40.93	40.93	40.93	40.93
N50	6582	10210	982	2464
N75	1427	2538	676	938
L50	17	4	44	60
L75	91	14	97	213
# misassemblies	7	1	3	3
# misassembled contigs	6	1	3	3
Misassembled contigs length	10871	5309	2774	3170
# local misassemblies	6	9	99	6
# structural variations	0	0	0	0
# unaligned contigs	0 + 155 part	0 + 14 part	0 + 48 part	0 + 299 part
Unaligned length	531834	88339	43857	450972
Genome fraction (%)	10.239	1.780	3.368	12.088
Duplication ratio	1.021	1.109	1.098	1.033
# N's per 100 kbp	141.51	1615.31	5921.04	1689.93
# mismatches per 100 kbp	1597.51	1861.29	1628.70	1805.18
# indels per 100 kbp	48.81	36.99	22.21	75.26
Largest alignment	16783	4204	2553	16672
NA50	-	-	565	-
NGA50	-	-	-	-
LA50	-	-	84	-

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

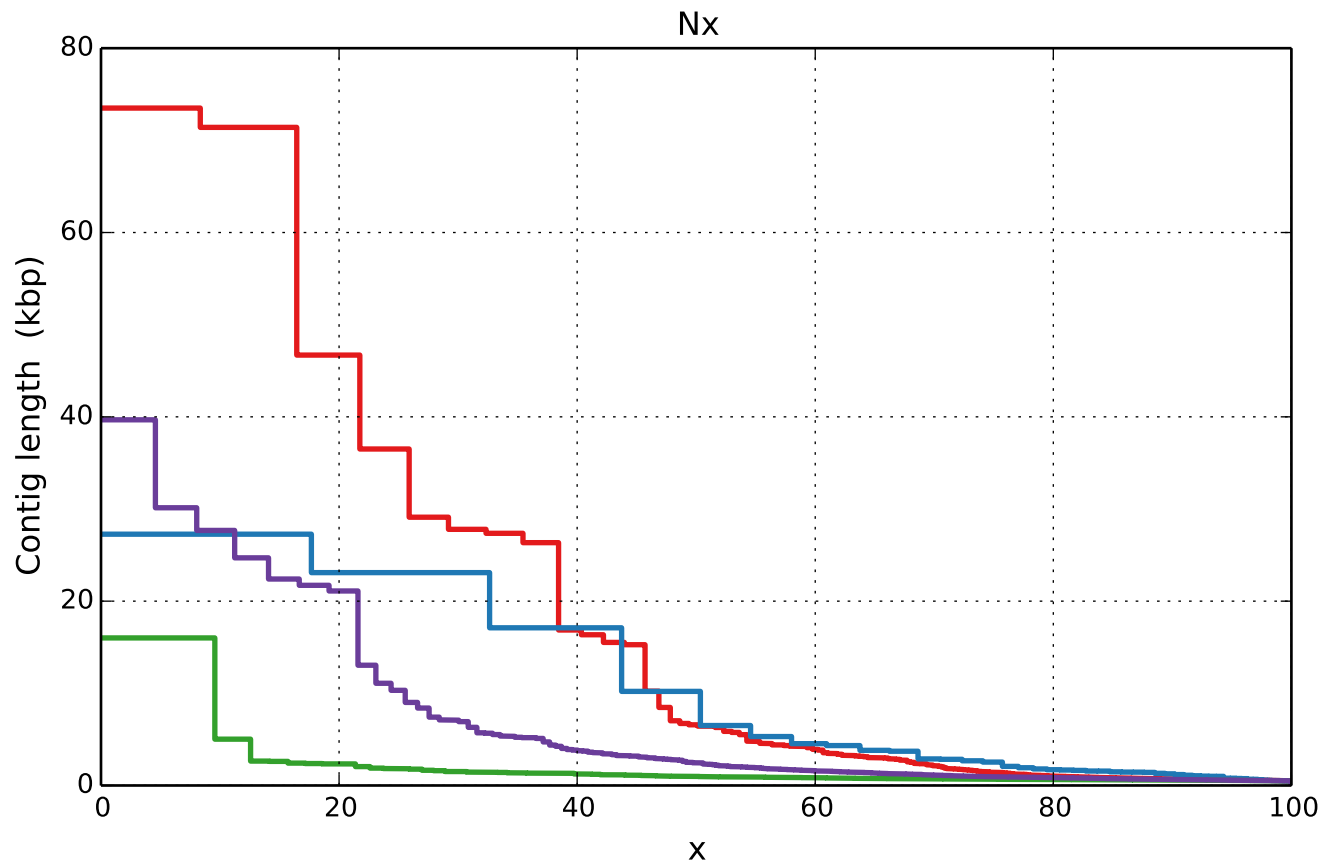
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	7	1	3	3
# relocations	7	1	3	3
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	25	11	5	49
# misassembled contigs	6	1	3	3
Misassembled contigs length	10871	5309	2774	3170
# local misassemblies	6	9	99	6
# structural variations	0	0	0	0
# mismatches	5466	1107	1833	7292
# indels	167	22	25	304
# short indels	141	19	22	236
# long indels	26	3	3	68
Indels length	481	61	112	1371

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).

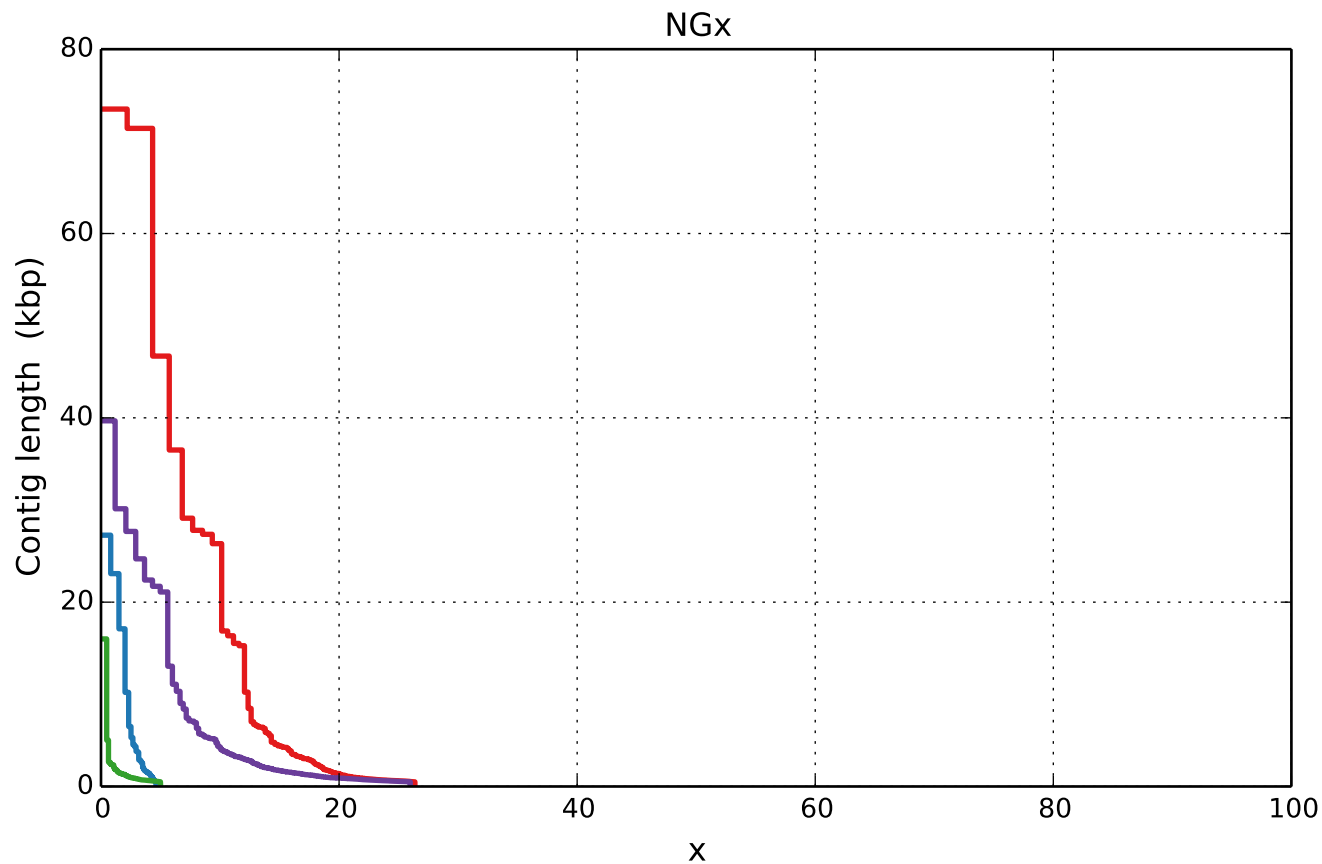
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	155	14	48	299
# with misassembly	4	2	10	5
# both parts are significant	24	8	3	44
Partially unaligned length	531834	88339	43857	450972
# N's	1247	2492	9912	14671

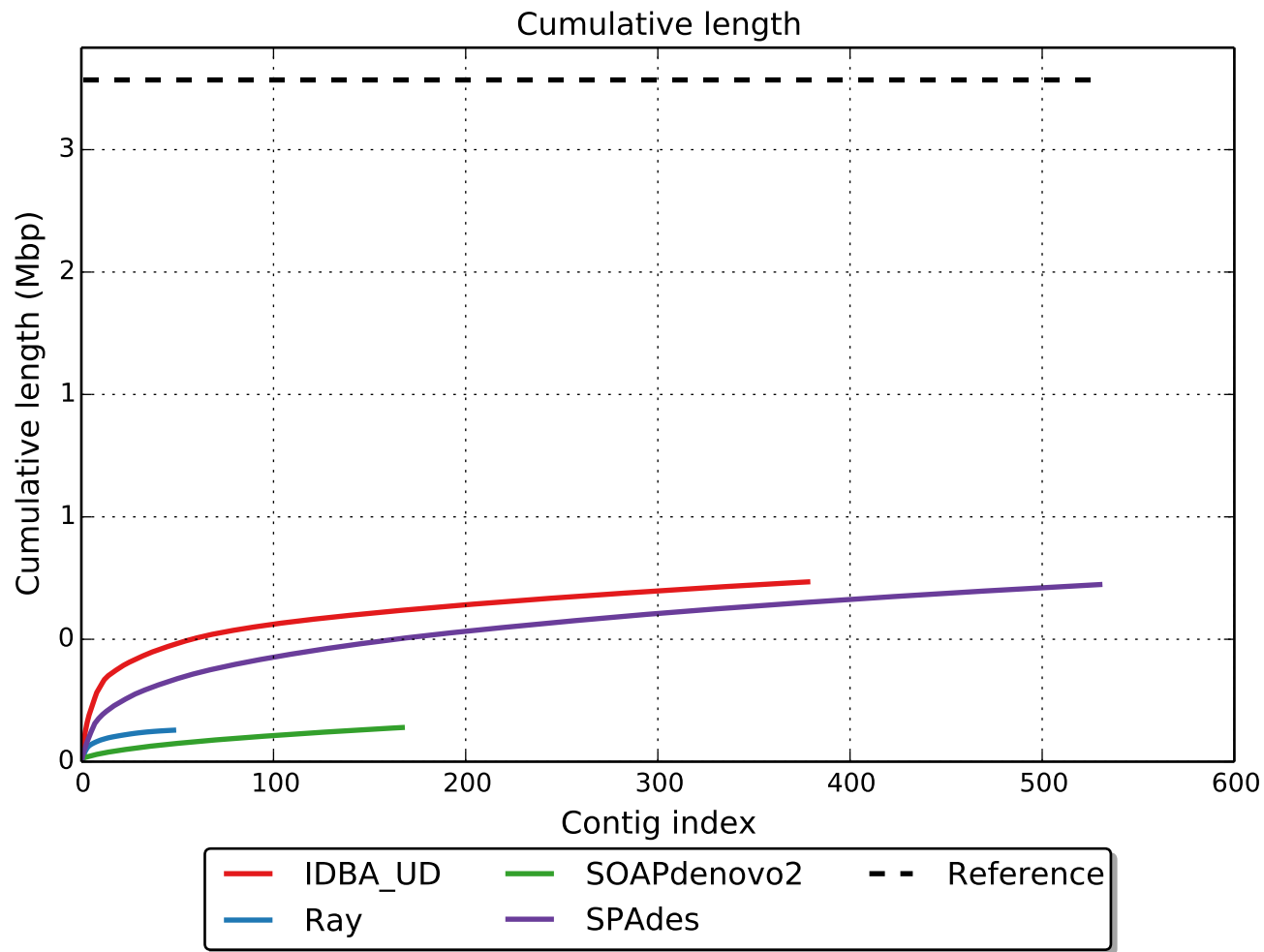
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



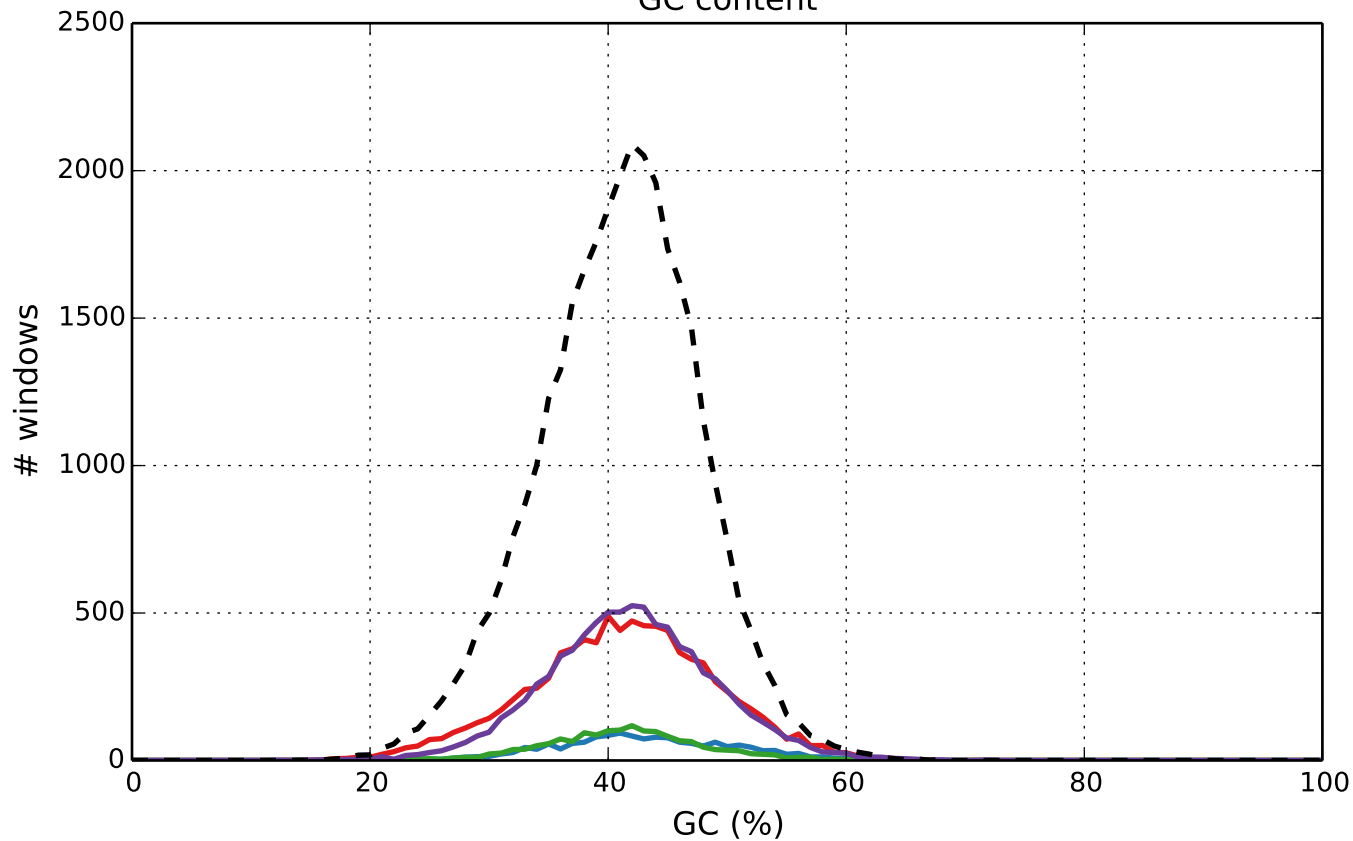
— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray



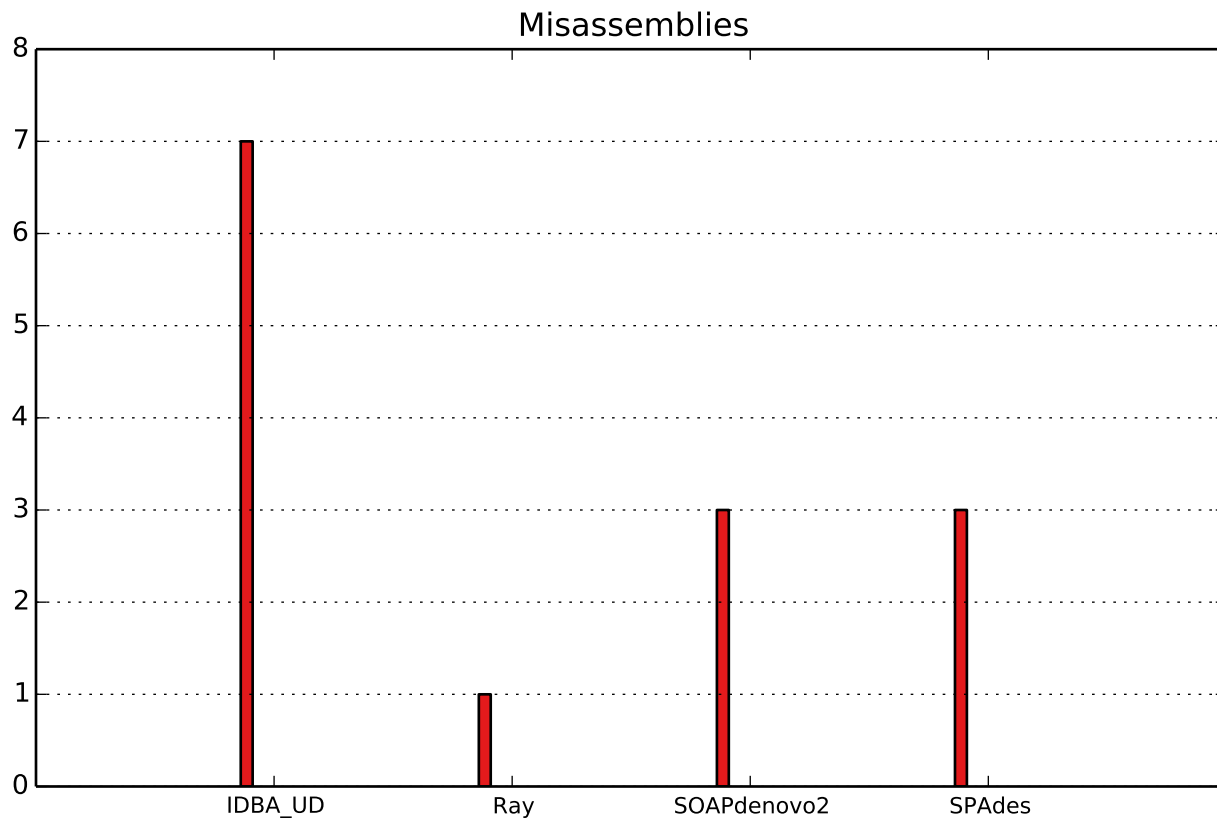
— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray



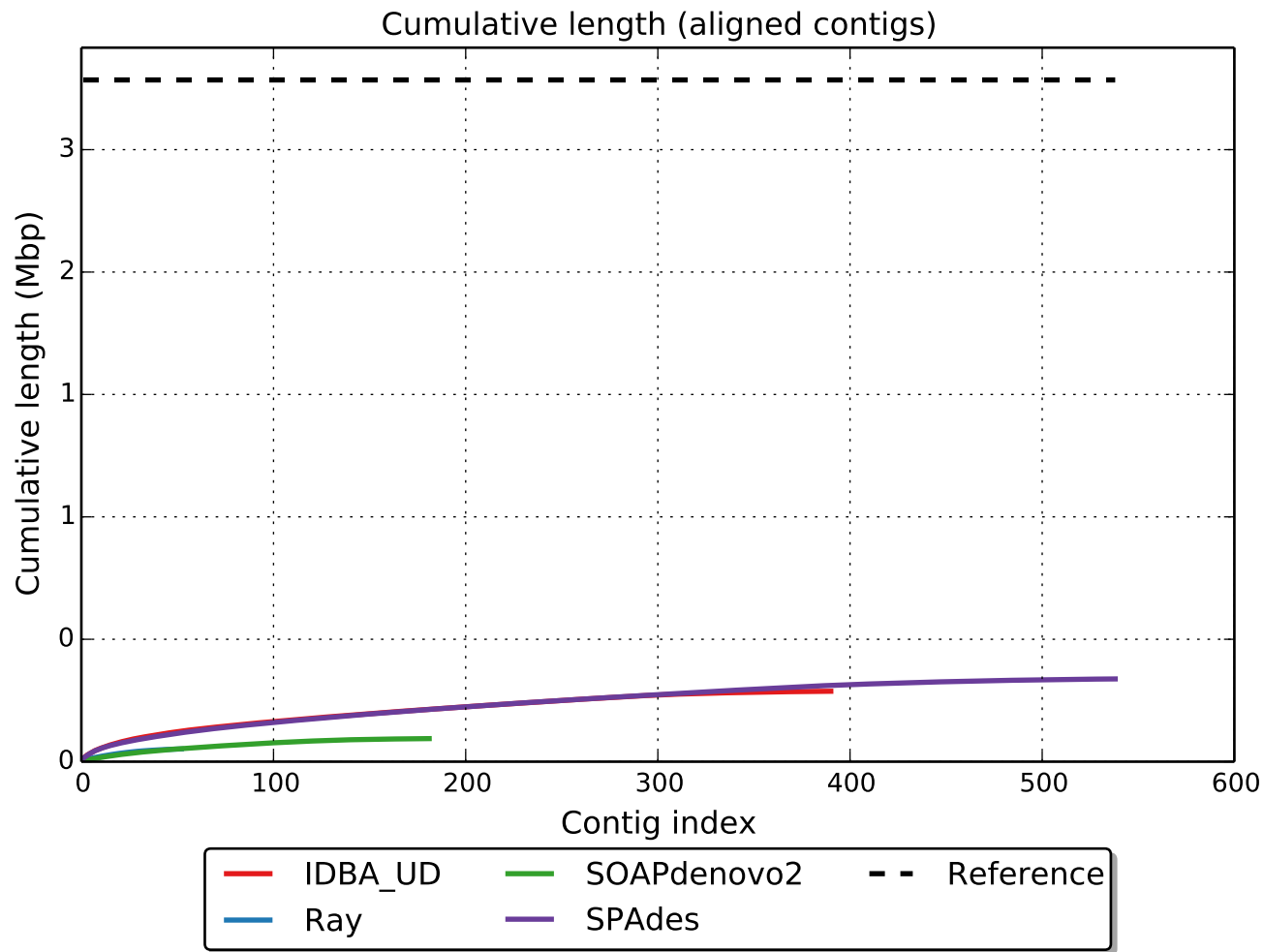
GC content

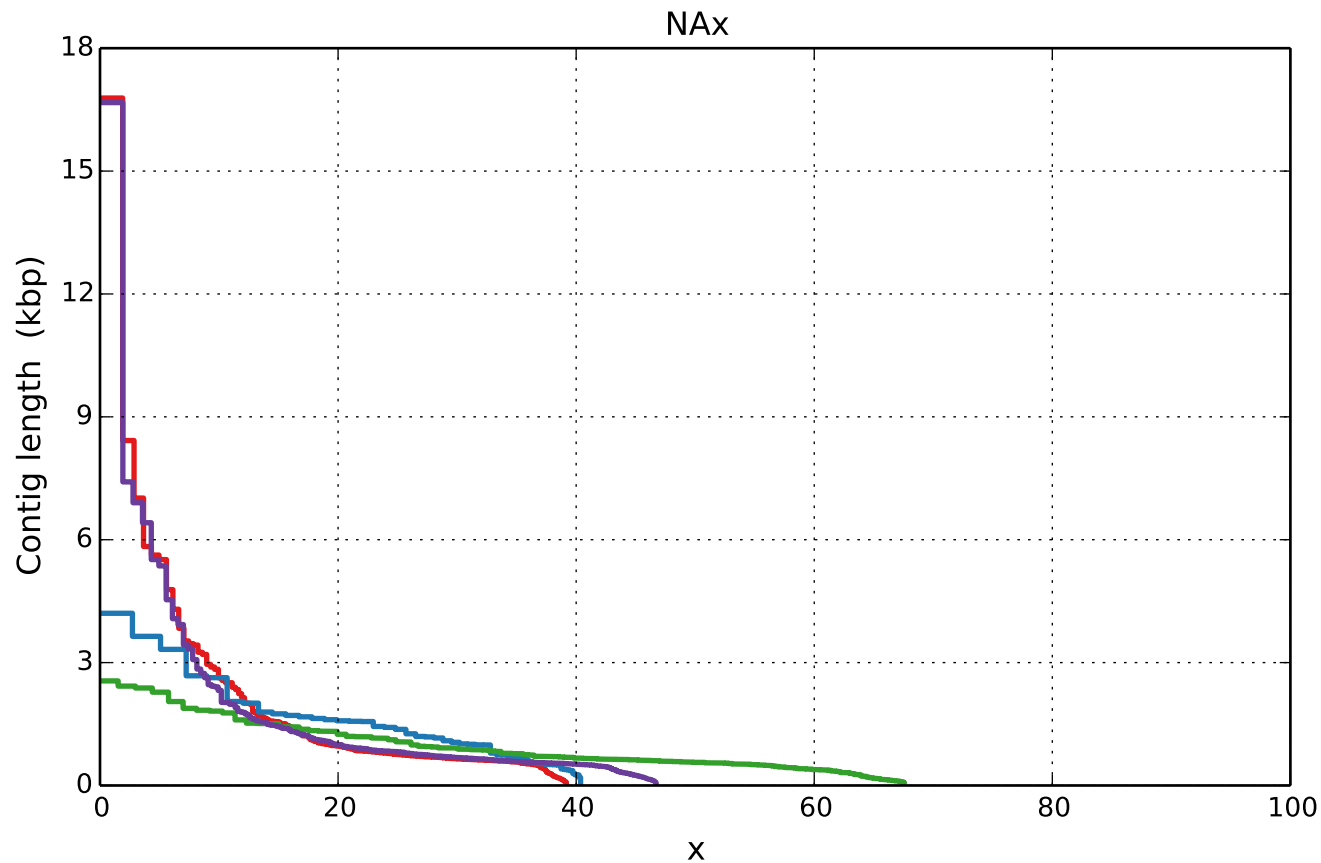


— IDBA_UD — SOAPdenovo2 - - Reference
— Ray — SPAdes



 # relocations





IDBA_UD SOAPdenovo2 SPAdes
Ray

