

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	421	108	210	438
# contigs (>= 5000 bp)	149	15	1	140
# contigs (>= 10000 bp)	57	4	0	39
# contigs (>= 25000 bp)	9	0	0	4
# contigs (>= 50000 bp)	2	0	0	0
Total length (>= 1000 bp)	2386643	320499	321886	2129879
Total length (>= 5000 bp)	1685427	126913	5401	1360168
Total length (>= 10000 bp)	1040379	55765	0	681962
Total length (>= 25000 bp)	362634	0	0	144046
Total length (>= 50000 bp)	124125	0	0	0
# contigs	527	259	731	537
Largest contig	71408	23096	5401	47342
Total length	2466476	421246	686041	2203180
Reference length	3214418	3214418	3214418	3214418
GC (%)	54.25	48.97	53.66	53.85
Reference GC (%)	55.65	55.65	55.65	55.65
N50	8489	2618	963	6267
NG50	5527	-	-	3766
N75	4139	1061	698	3564
NG75	863	-	-	-
L50	78	39	232	95
LG50	135	-	-	197
L75	185	104	442	210
LG75	448	-	-	-
# misassemblies	49	11	4	44
# misassembled contigs	43	9	4	35
Misassembled contigs length	286221	28312	5028	239154
# local misassemblies	65	29	226	36
# structural variations	11	1	4	6
# unaligned contigs	0 + 323 part	0 + 106 part	0 + 458 part	0 + 383 part
Unaligned length	1219306	159924	269466	1031470
Genome fraction (%)	34.996	7.496	11.830	33.160
Duplication ratio	1.109	1.085	1.095	1.099
# N's per 100 kbp	183.74	2938.66	8048.06	325.76
# mismatches per 100 kbp	3261.79	2363.56	2529.26	3345.95
# indels per 100 kbp	86.58	67.65	55.75	77.59
Largest alignment	25026	8313	3584	14312
NA50	-	550	234	-
NGA50	-	-	-	-
LA50	-	176	555	-

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

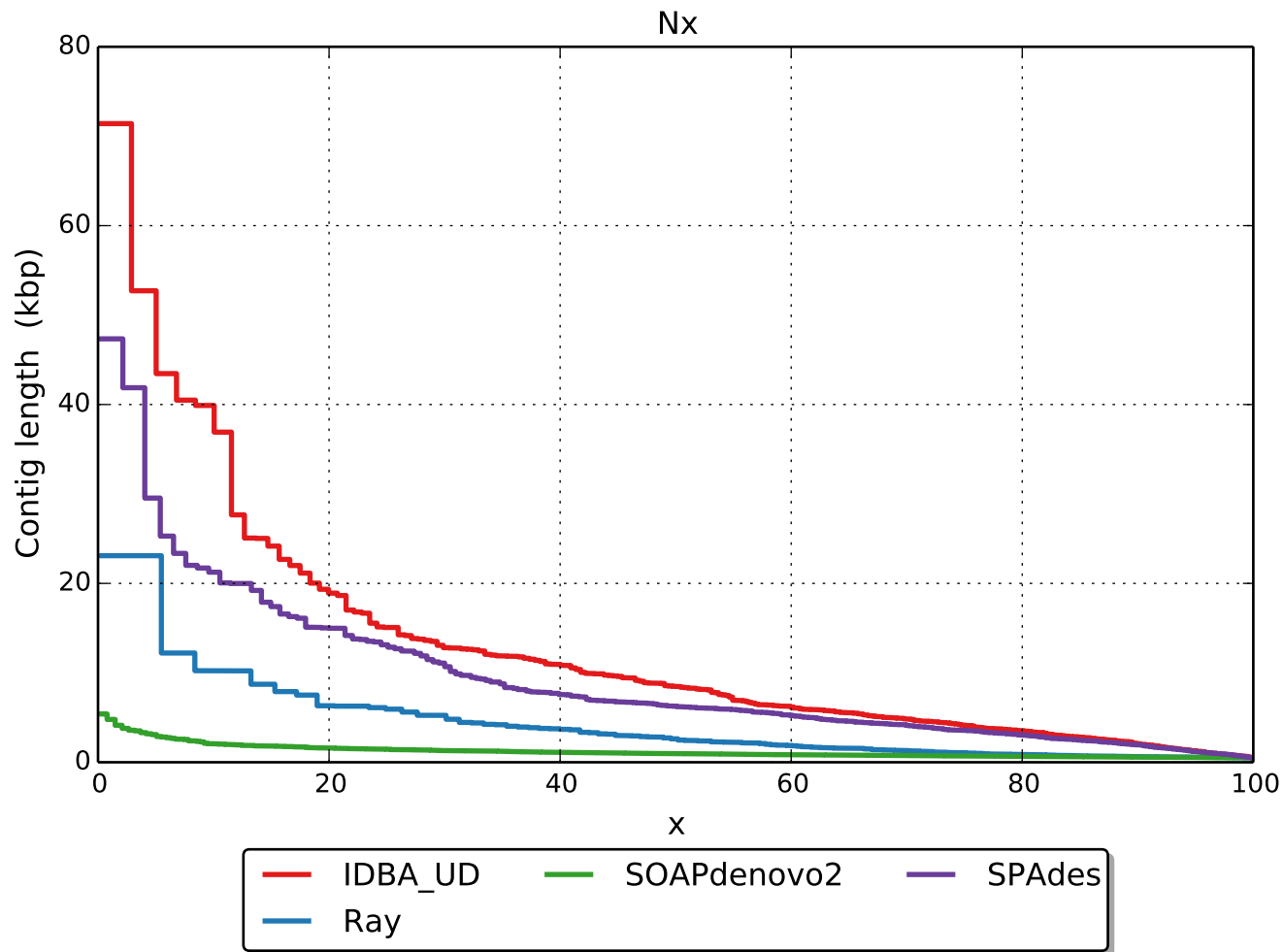
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	49	11	4	44
# relocations	49	11	4	44
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	203	41	56	214
# misassembled contigs	43	9	4	35
Misassembled contigs length	286221	28312	5028	239154
# local misassemblies	65	29	226	36
# structural variations	11	1	4	6
# mismatches	36693	5695	9618	35665
# indels	974	163	212	827
# short indels	897	160	206	787
# long indels	77	3	6	40
Indels length	2319	230	334	1554

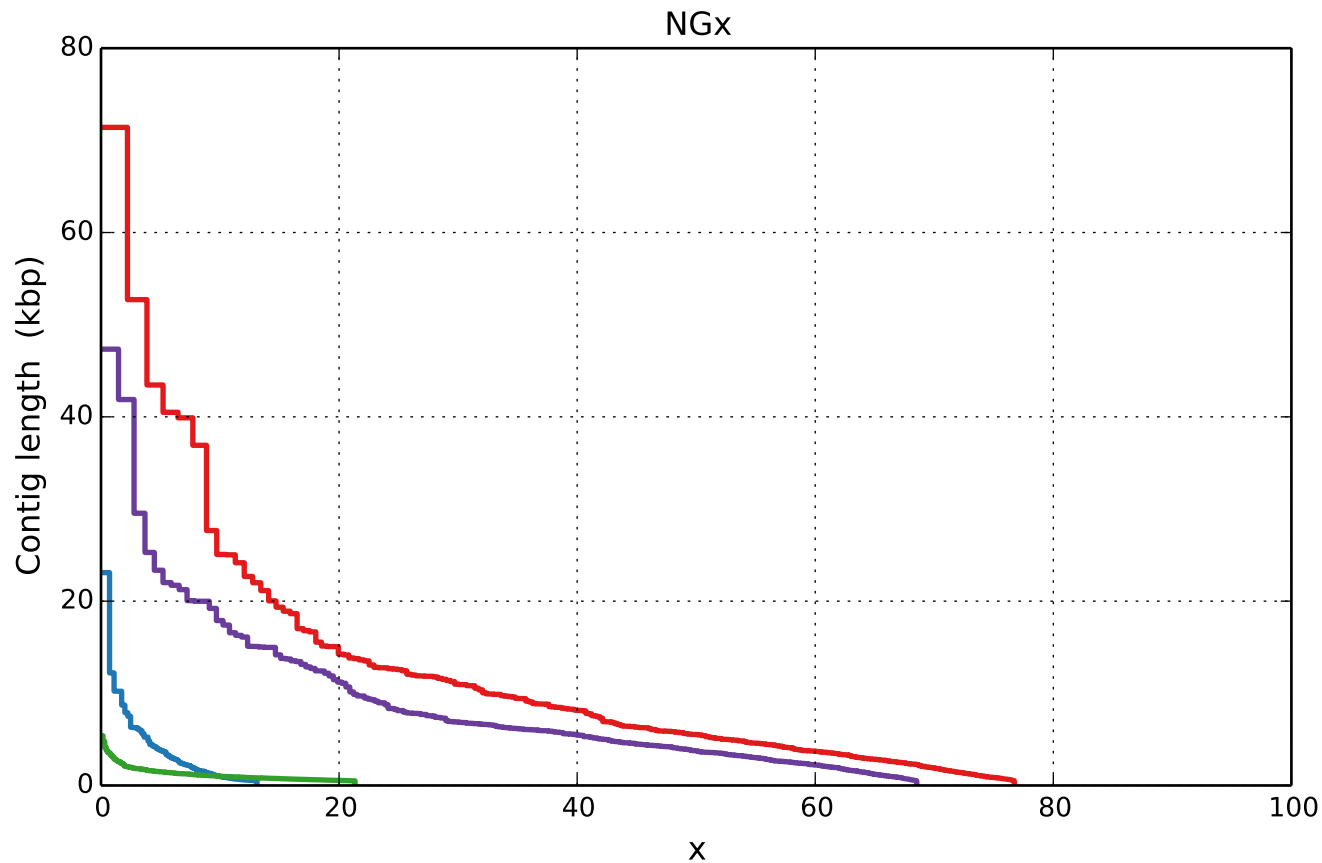
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

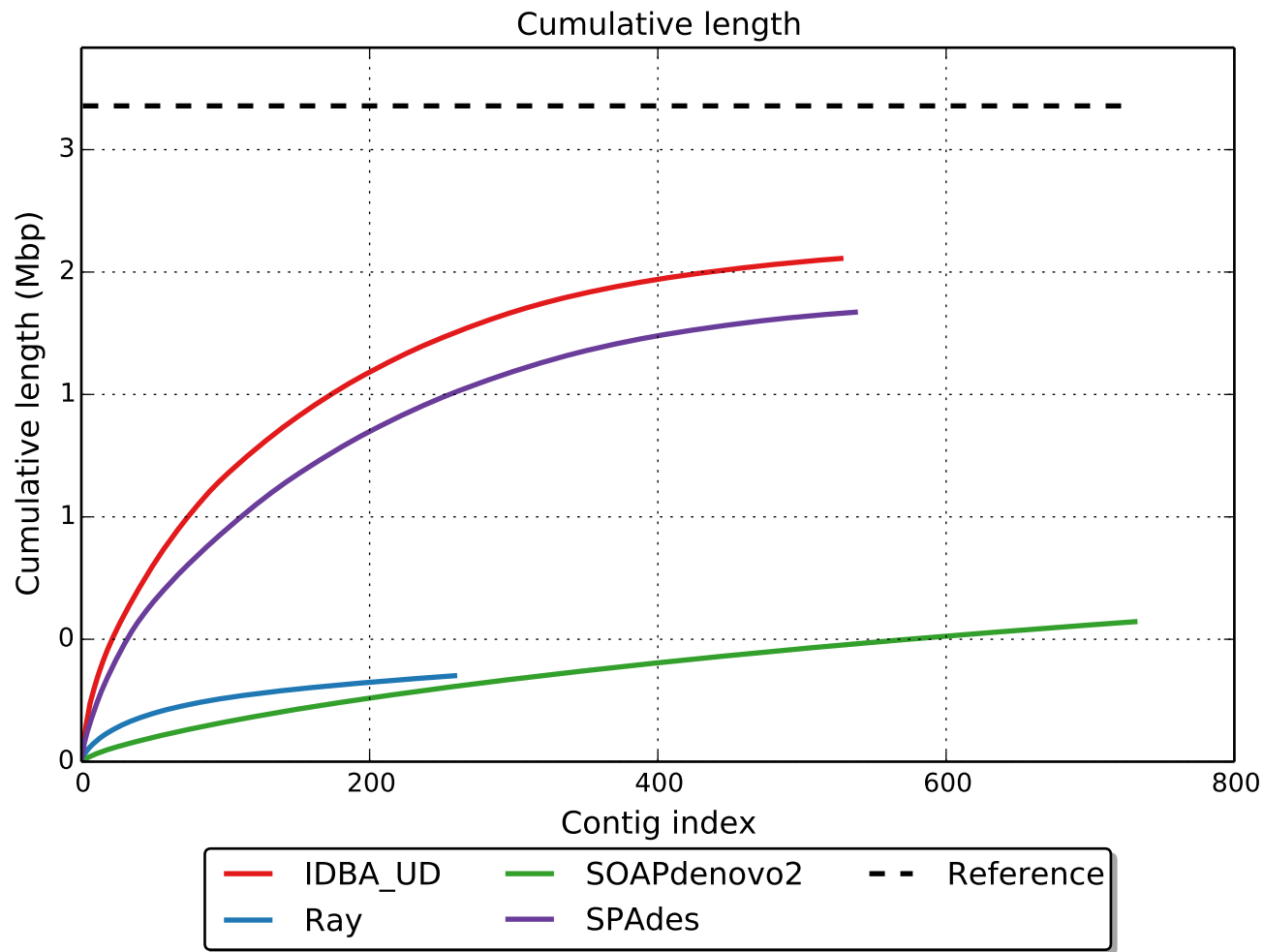
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	323	106	458	383
# with misassembly	40	6	51	25
# both parts are significant	152	31	46	176
Partially unaligned length	1219306	159924	269466	1031470
# N's	4532	12379	55213	7177

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).

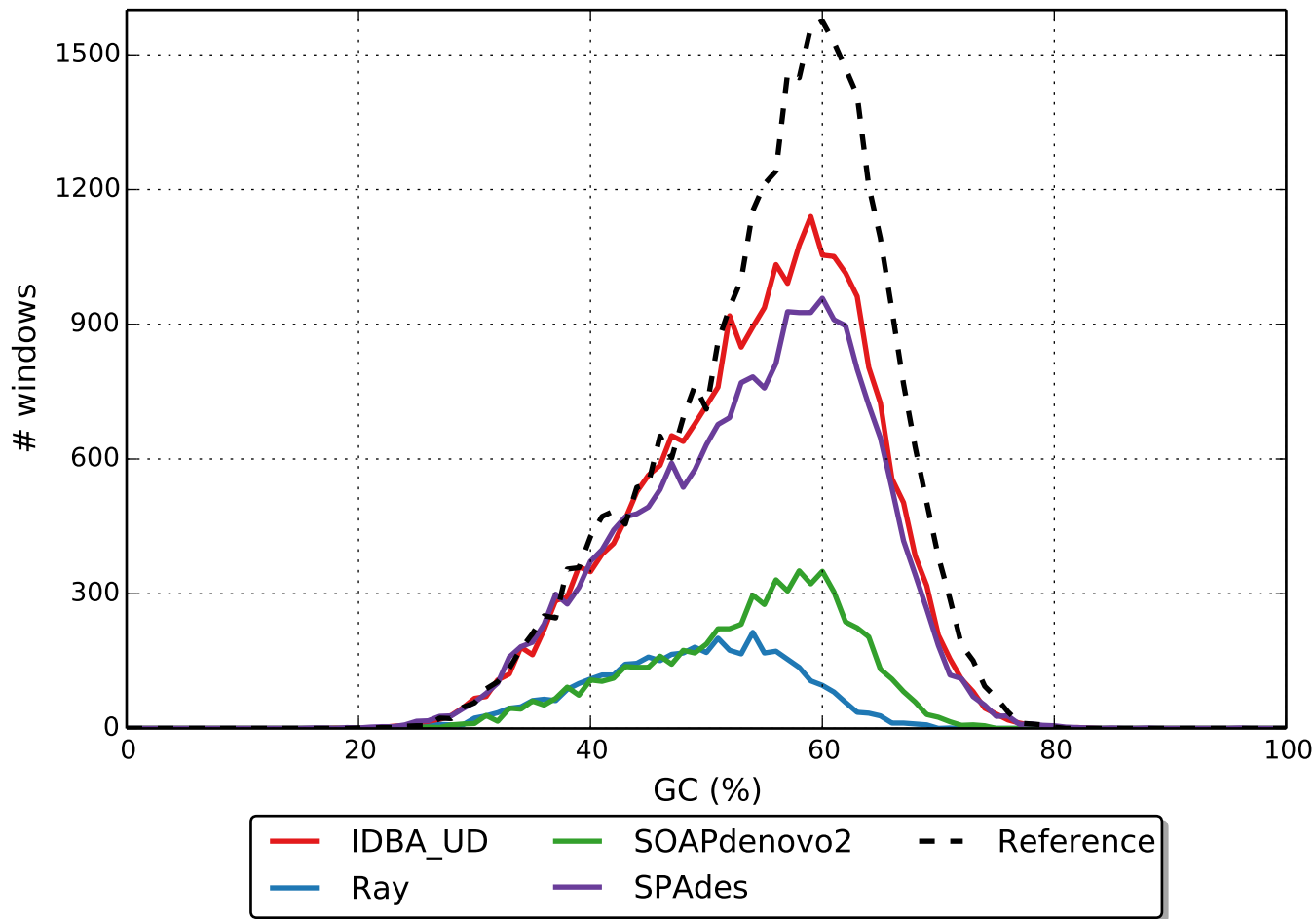




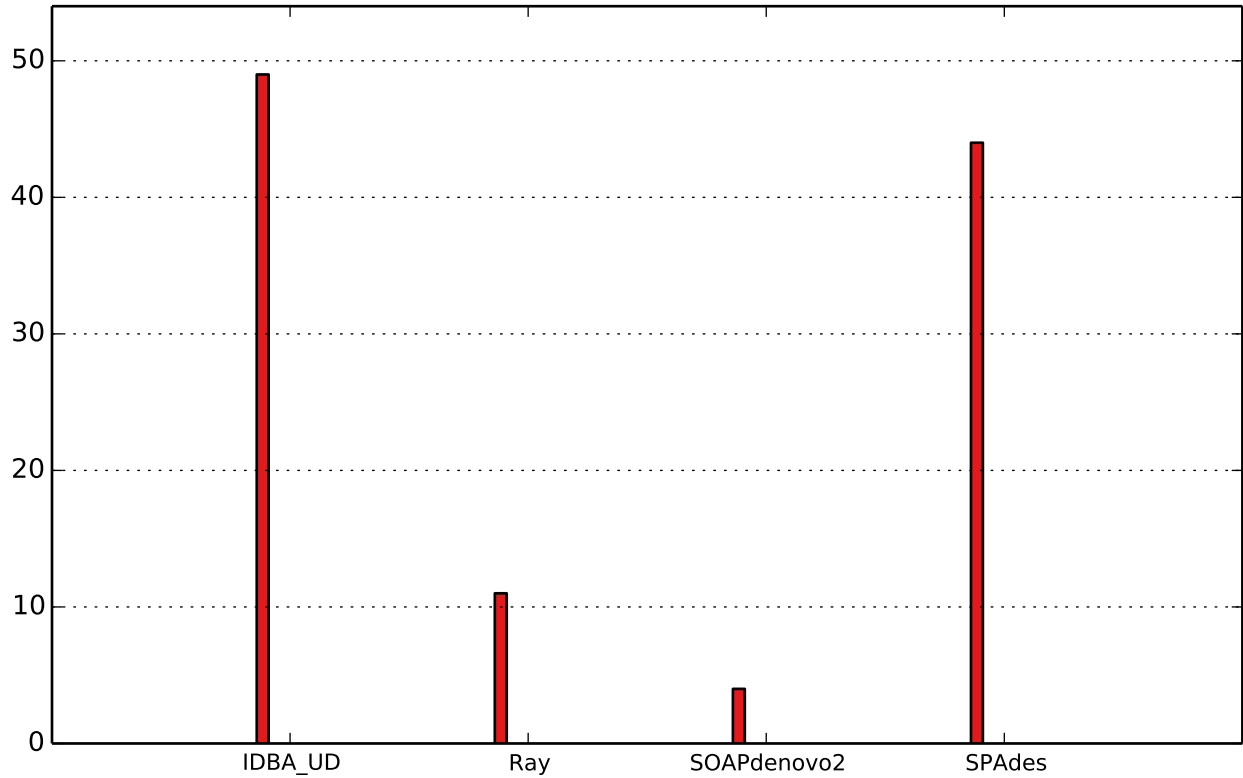
— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray



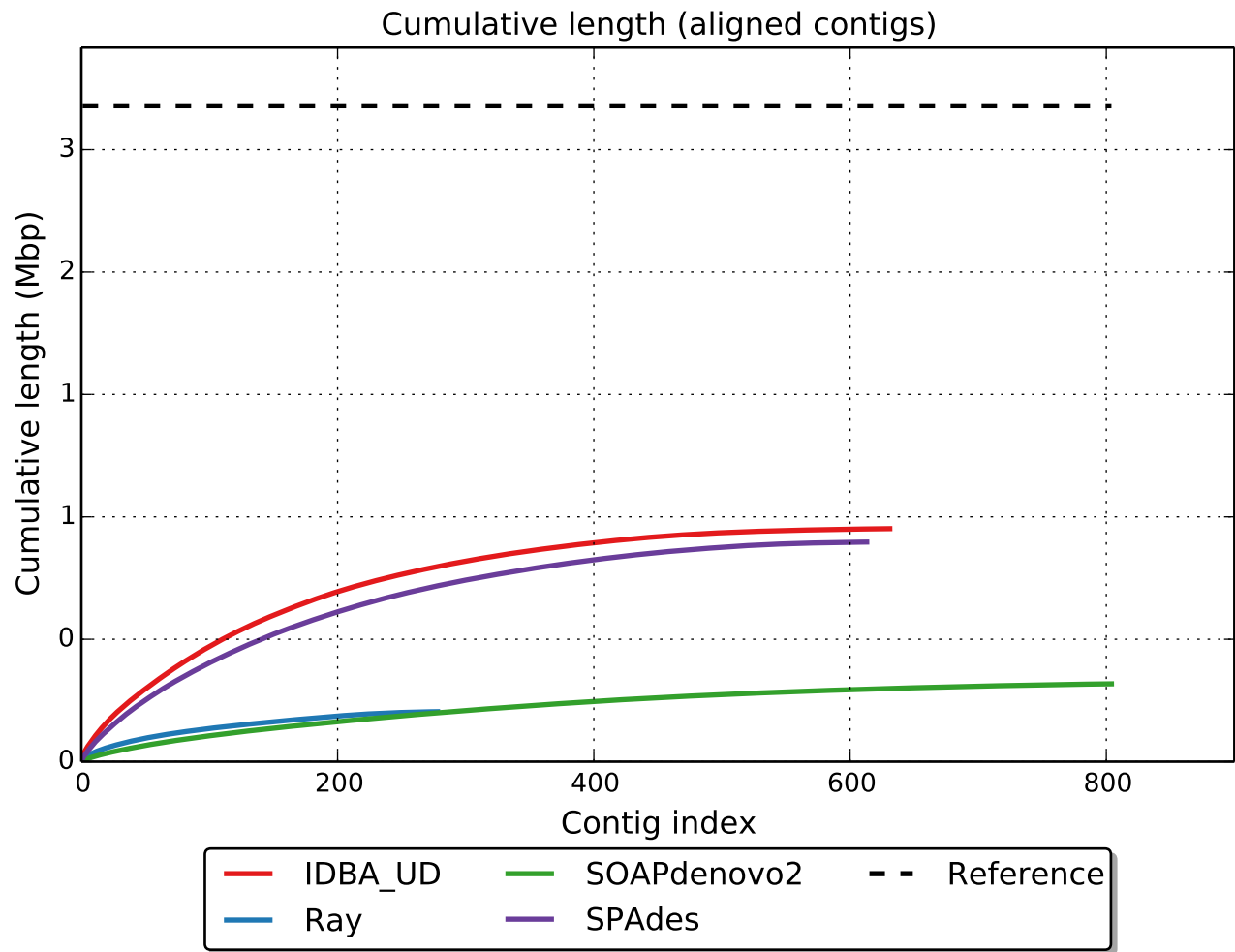
GC content

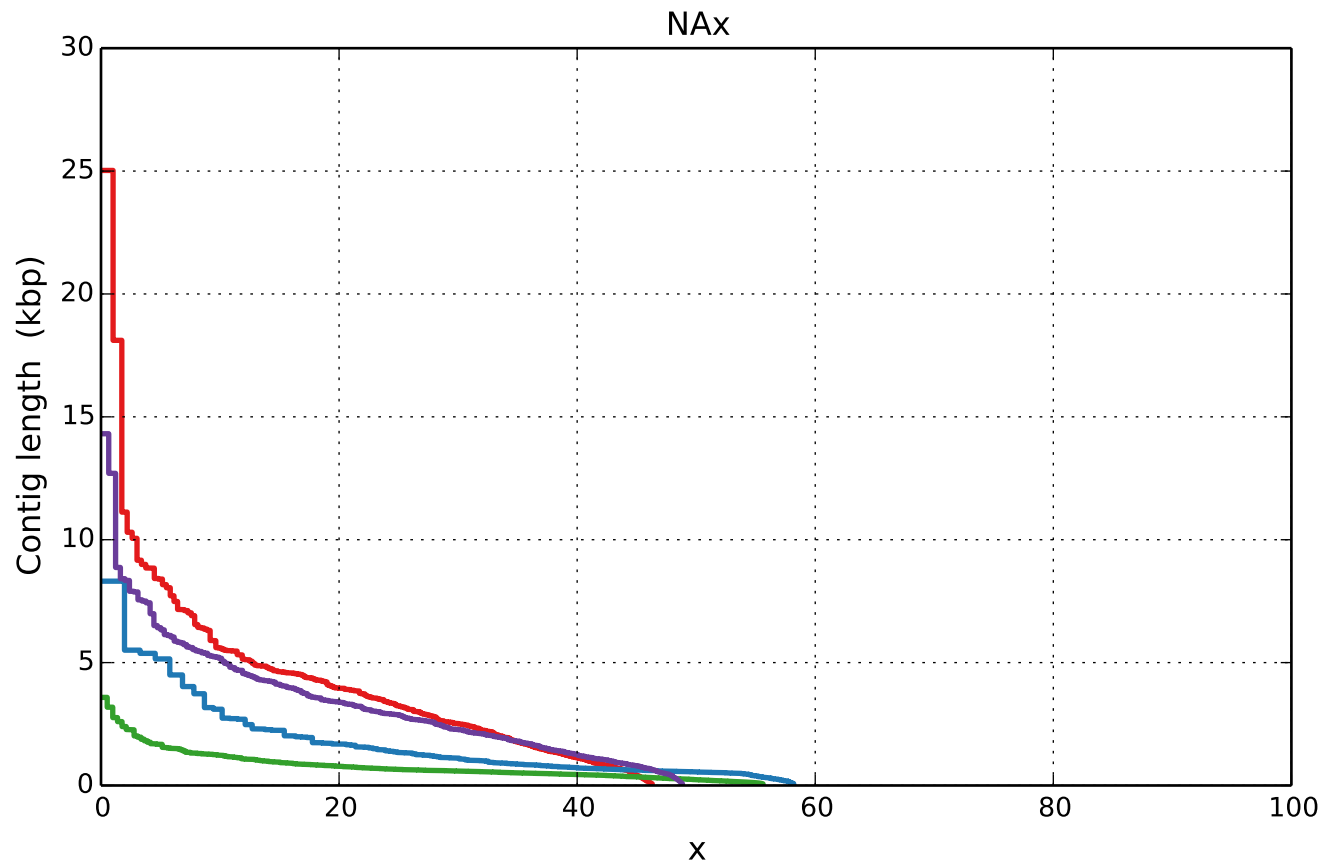


Misassemblies



 # relocations





IDBA_UD SOAPdenovo2 SPAdes
Ray

NGAx

