

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	11	8	1	10
# contigs (>= 5000 bp)	2	1	0	4
# contigs (>= 10000 bp)	2	1	0	1
# contigs (>= 25000 bp)	1	1	0	1
# contigs (>= 50000 bp)	0	0	0	0
Total length (>= 1000 bp)	68461	45658	1089	67633
Total length (>= 5000 bp)	45529	33075	0	55041
Total length (>= 10000 bp)	45529	33075	0	33624
Total length (>= 25000 bp)	34820	33075	0	33624
Total length (>= 50000 bp)	0	0	0	0
# contigs	22	13	9	15
Largest contig	34820	33075	1089	33624
Total length	75522	49097	5850	71278
Reference length	29332	29332	29332	29332
GC (%)	41.01	42.33	36.04	41.76
Reference GC (%)	36.96	36.96	36.96	36.96
N50	10709	33075	624	9186
NG50	34820	33075	-	33624
N75	2686	2384	538	5578
NG75	34820	33075	-	33624
L50	2	1	4	2
LG50	1	1	-	1
L75	6	3	7	4
LG75	1	1	-	1
# misassemblies	0	1	0	0
# misassembled contigs	0	1	0	0
Misassembled contigs length	0	1168	0	0
# local misassemblies	0	1	10	0
# structural variations	0	0	0	0
# unaligned contigs	0 + 13 part	0 + 6 part	0 + 1 part	0 + 8 part
Unaligned length	52469	39210	446	54634
Genome fraction (%)	76.221	27.901	17.189	56.126
Duplication ratio	1.031	1.208	1.072	1.011
# N's per 100 kbp	186.70	1433.90	6752.14	171.16
# mismatches per 100 kbp	1212.15	1832.84	515.67	1093.36
# indels per 100 kbp	134.19	61.09	59.50	91.11
Largest alignment	3695	2326	1044	2624
NA50	-	-	538	-
NGA50	1793	-	-	667
NA75	-	-	372	-
NGA75	262	-	-	-
LA50	-	-	5	-
LGA50	6	-	-	12
LA75	-	-	8	-
LGA75	17	-	-	-

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

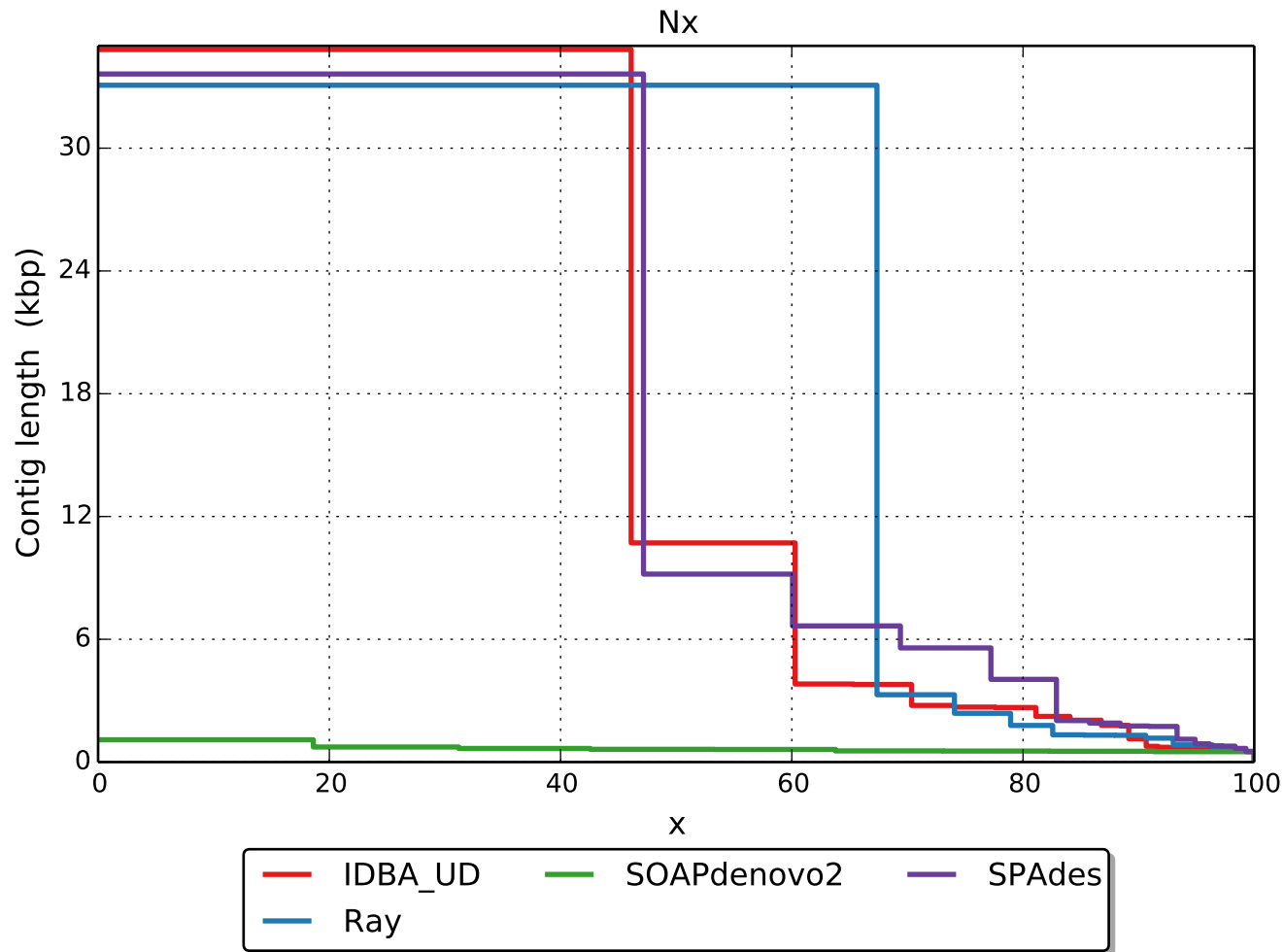
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	1	0	0
# relocations	0	1	0	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	3	1	0	6
# misassembled contigs	0	1	0	0
Misassembled contigs length	0	1168	0	0
# local misassemblies	0	1	10	0
# structural variations	0	0	0	0
# mismatches	271	150	26	180
# indels	30	5	3	15
# short indels	29	5	3	15
# long indels	1	0	0	0
Indels length	39	5	3	21

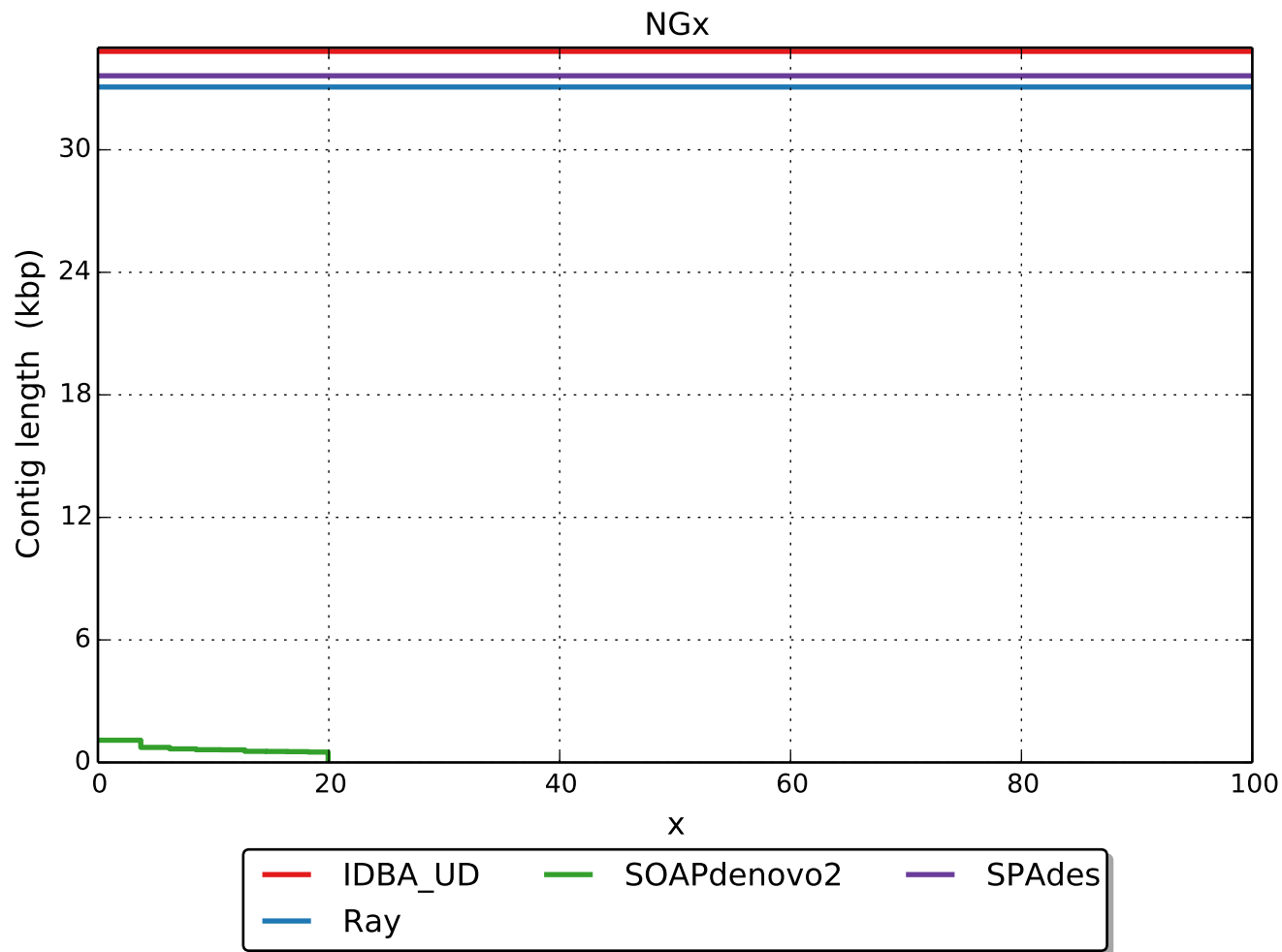
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

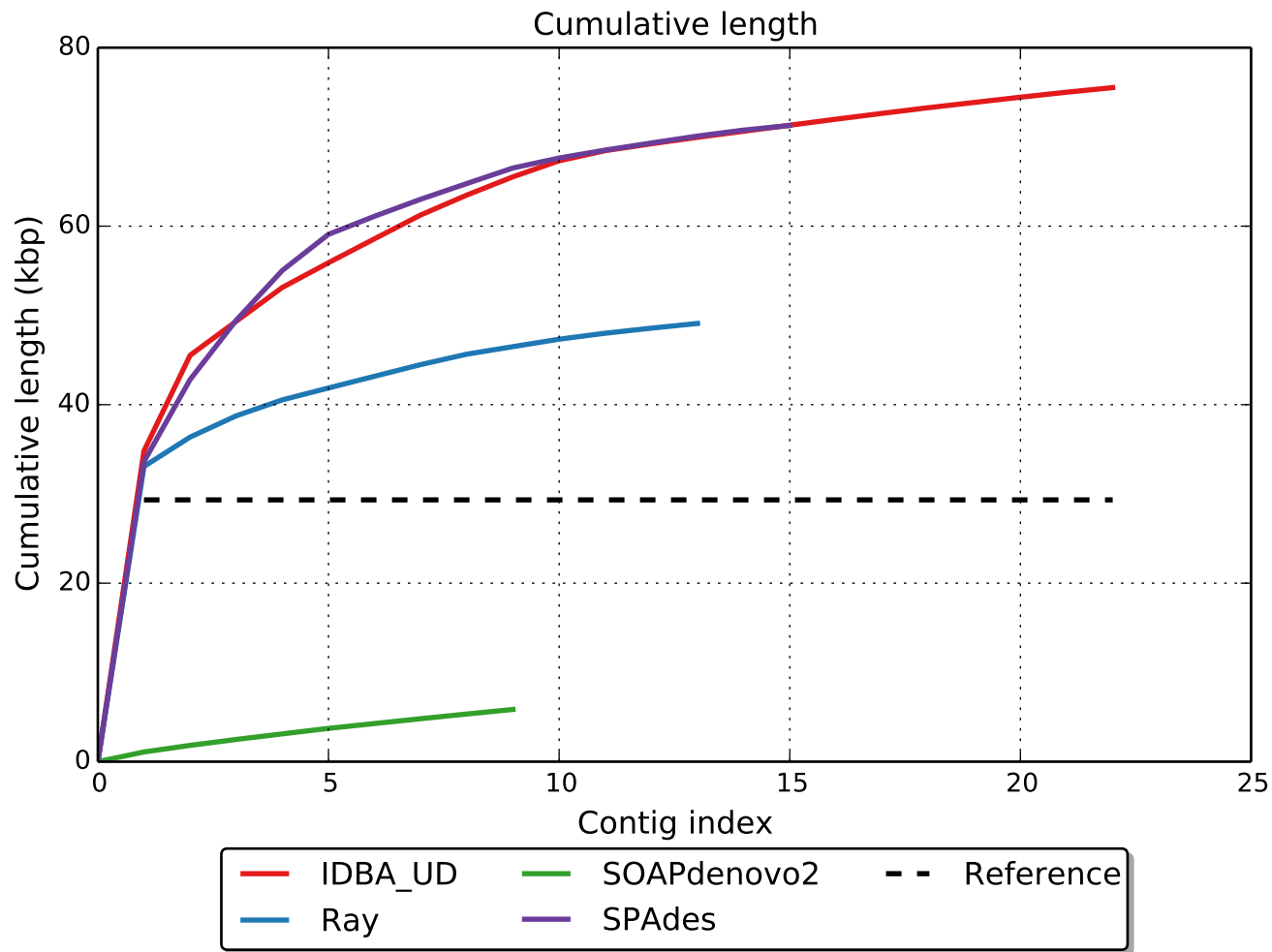
Unaligned report

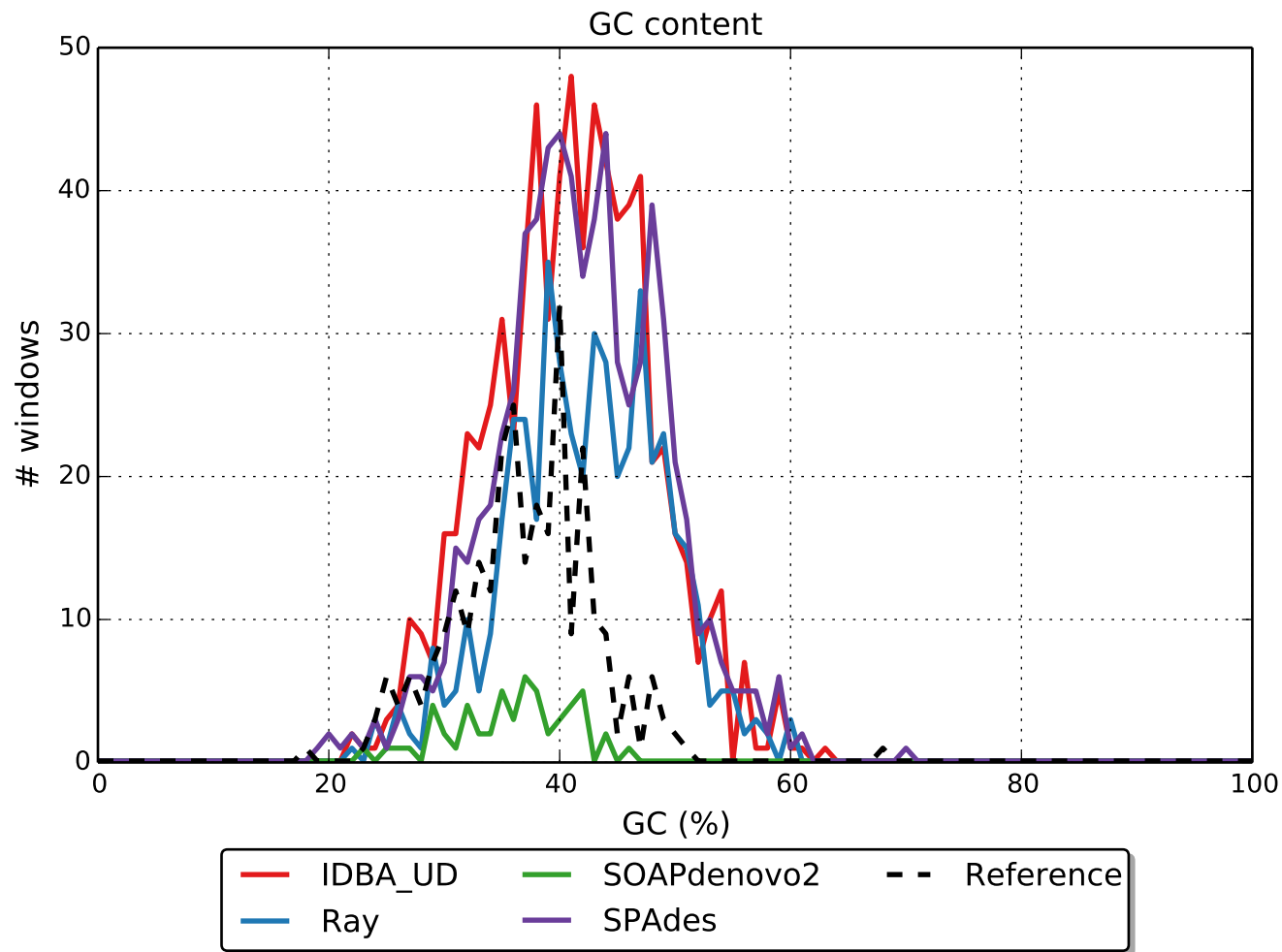
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	13	6	1	8
# with misassembly	1	0	1	2
# both parts are significant	3	1	0	6
Partially unaligned length	52469	39210	446	54634
# N's	141	704	395	122

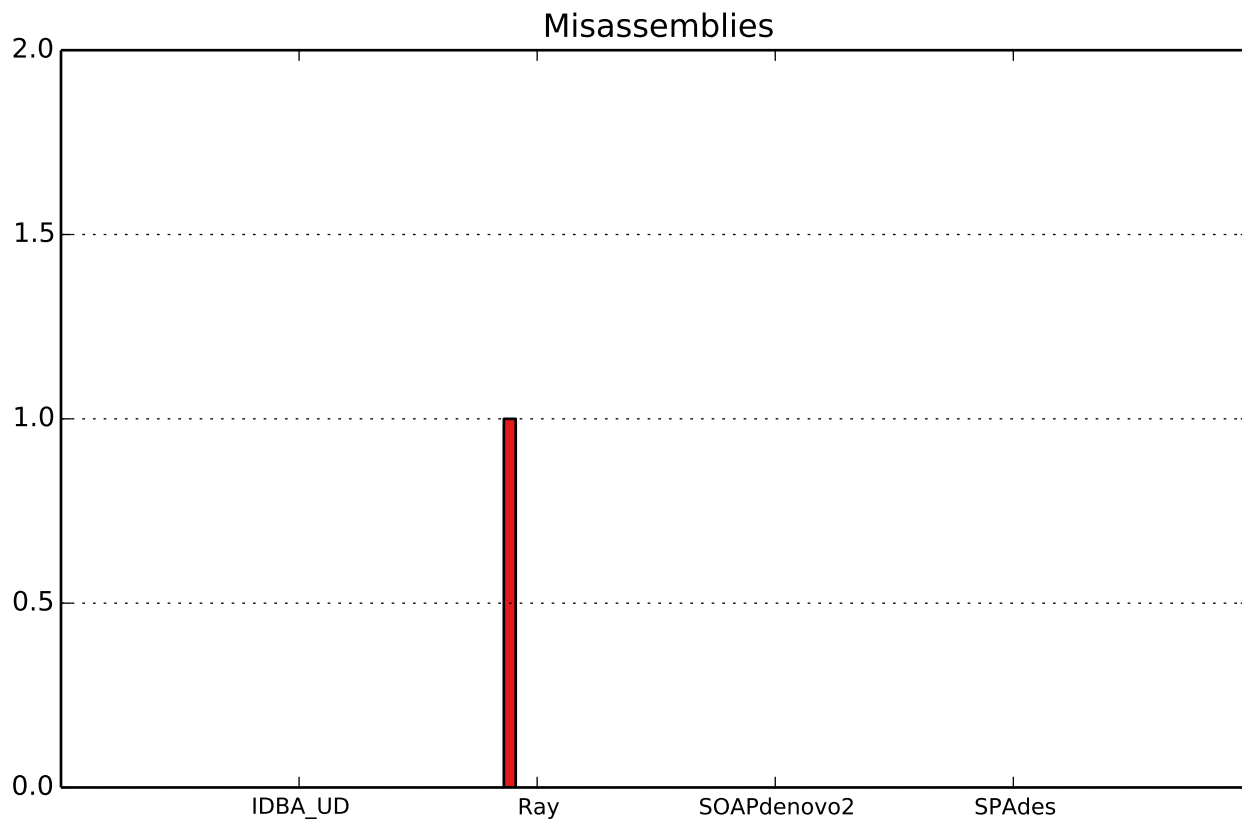
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



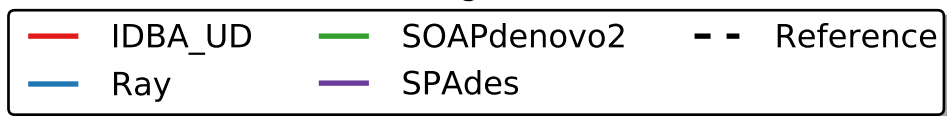
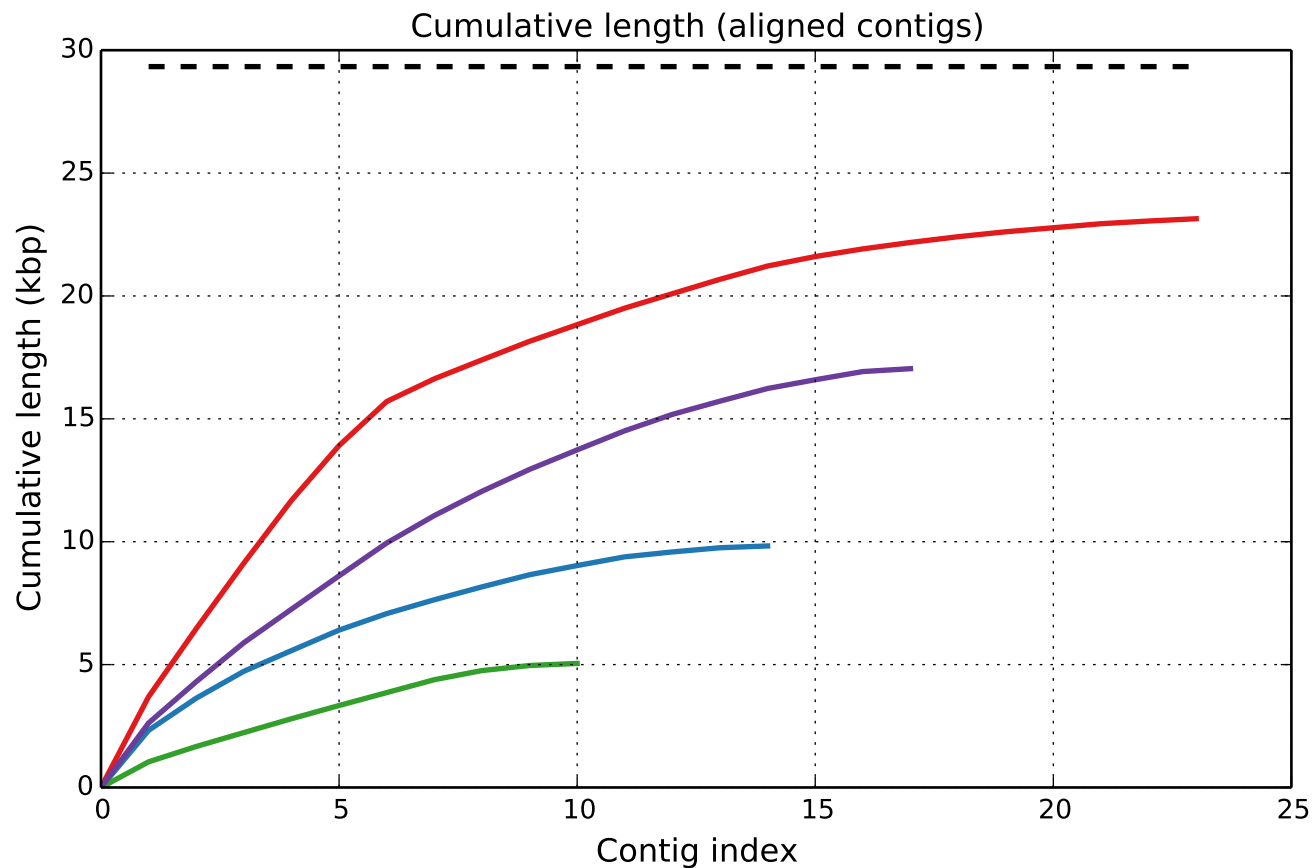


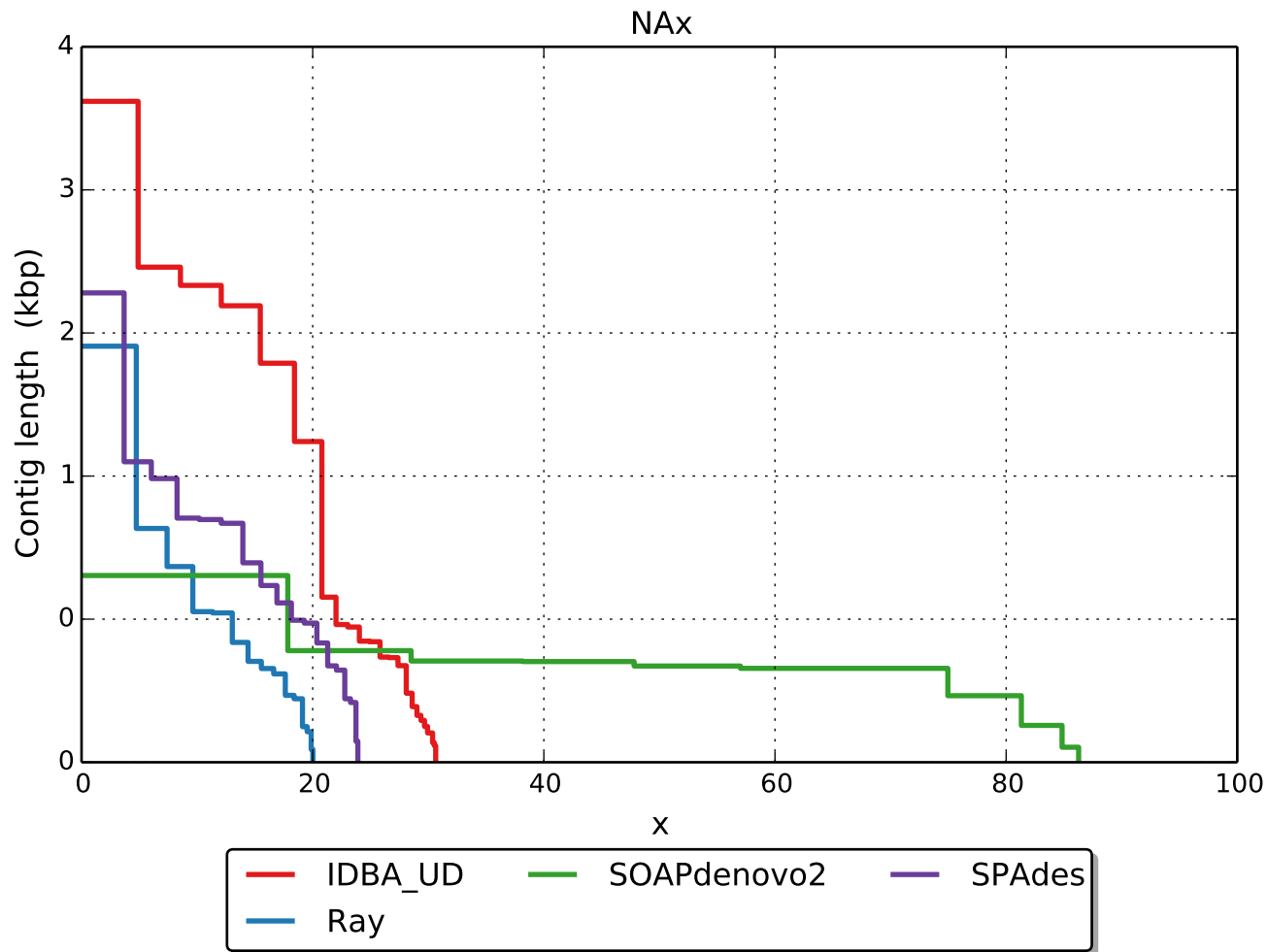






 # relocations





NGAx

