

# Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	250	264	1010	176
# contigs (>= 5000 bp)	138	129	45	107
# contigs (>= 10000 bp)	96	68	4	74
# contigs (>= 25000 bp)	48	15	0	41
# contigs (>= 50000 bp)	14	3	0	20
Total length (>= 1000 bp)	3618025	2204443	2080584	3242473
Total length (>= 5000 bp)	3364105	1867503	312980	3098584
Total length (>= 10000 bp)	3056608	1411000	48133	2851419
Total length (>= 25000 bp)	2311790	627590	0	2279533
Total length (>= 50000 bp)	1105297	181253	0	1547247
# contigs	320	315	2121	226
Largest contig	199153	64174	17296	144537
Total length	3667823	2241322	2855174	3278380
Reference length	5163189	5163189	5163189	5163189
GC (%)	42.45	42.52	42.04	42.03
Reference GC (%)	42.20	42.20	42.20	42.20
N50	33404	13593	1622	42745
NG50	18152	-	641	19088
N75	15060	7251	950	20783
L50	32	43	490	23
LG50	61	-	1638	55
L75	72	99	1073	49
# misassemblies	81	47	5	64
# misassembled contigs	52	39	4	35
Misassembled contigs length	1232196	539583	24446	1405008
# local misassemblies	10	130	76	14
# structural variations	3	1	1	3
# unaligned contigs	0 + 57 part	0 + 29 part	0 + 31 part	0 + 64 part
Unaligned length	817549	251792	38514	656525
Genome fraction (%)	52.172	35.540	54.116	46.982
Duplication ratio	1.058	1.084	1.008	1.081
# N's per 100 kbp	31.74	905.80	160.06	110.69
# mismatches per 100 kbp	518.35	482.56	435.95	539.82
# indels per 100 kbp	22.94	14.50	6.76	20.03
Largest alignment	68774	56627	16817	88018
NA50	13083	8598	1578	16459
NGA50	1932	-	613	-
NA75	-	2549	925	-
LA50	70	72	510	58
LGA50	206	-	1701	-
LA75	-	180	1111	-

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

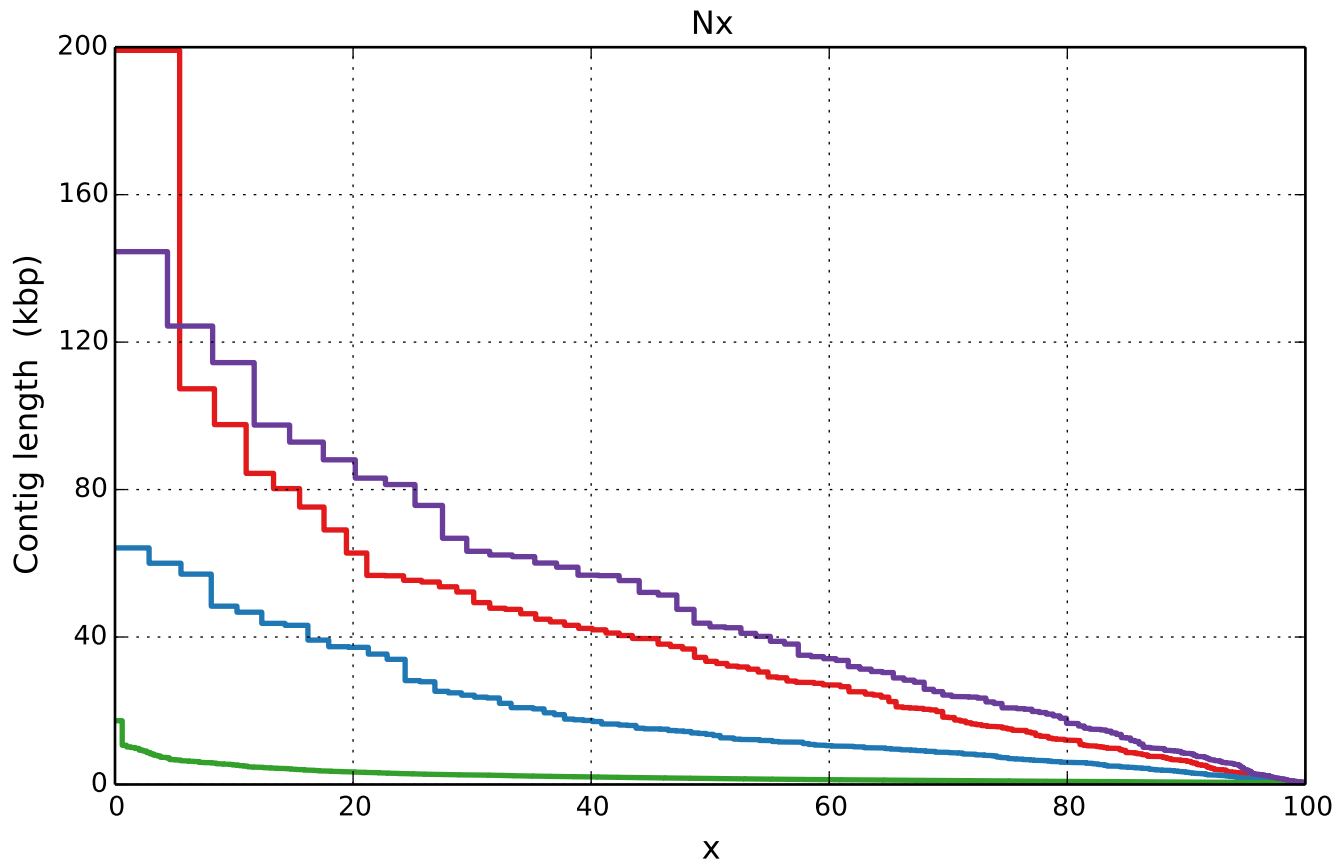
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	81	47	5	64
# relocations	78	47	5	56
# translocations	0	0	0	0
# inversions	3	0	0	8
# possibly misassembled contigs	50	40	7	48
# misassembled contigs	52	39	4	35
Misassembled contigs length	1232196	539583	24446	1405008
# local misassemblies	10	130	76	14
# structural variations	3	1	1	3
# mismatches	13963	8855	12181	13095
# indels	618	266	189	486
# short indels	528	239	175	411
# long indels	90	27	14	75
Indels length	2008	660	419	1497

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

## Unaligned report

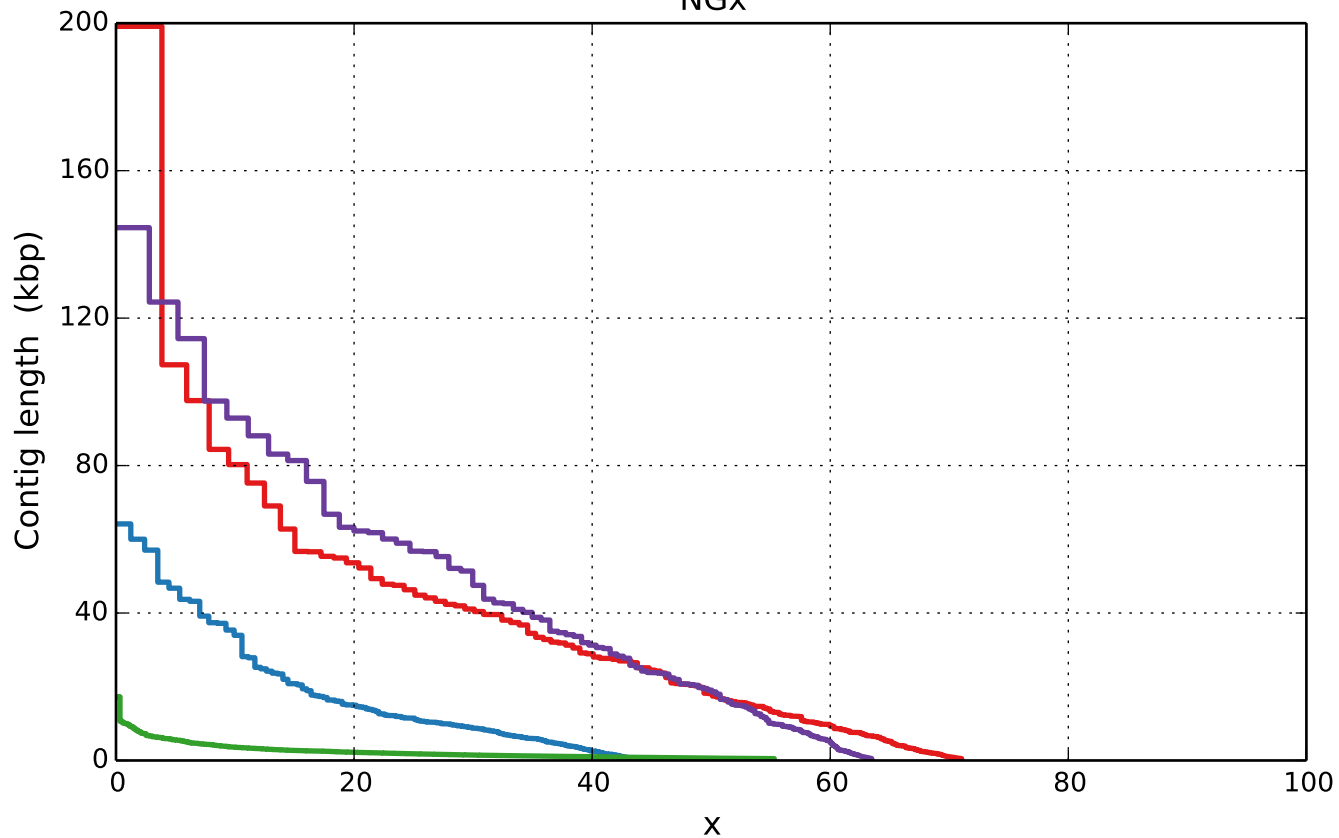
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	57	29	31	64
# with misassembly	10	3	2	8
# both parts are significant	20	14	6	29
Partially unaligned length	817549	251792	38514	656525
# N's	1164	20302	4570	3629

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

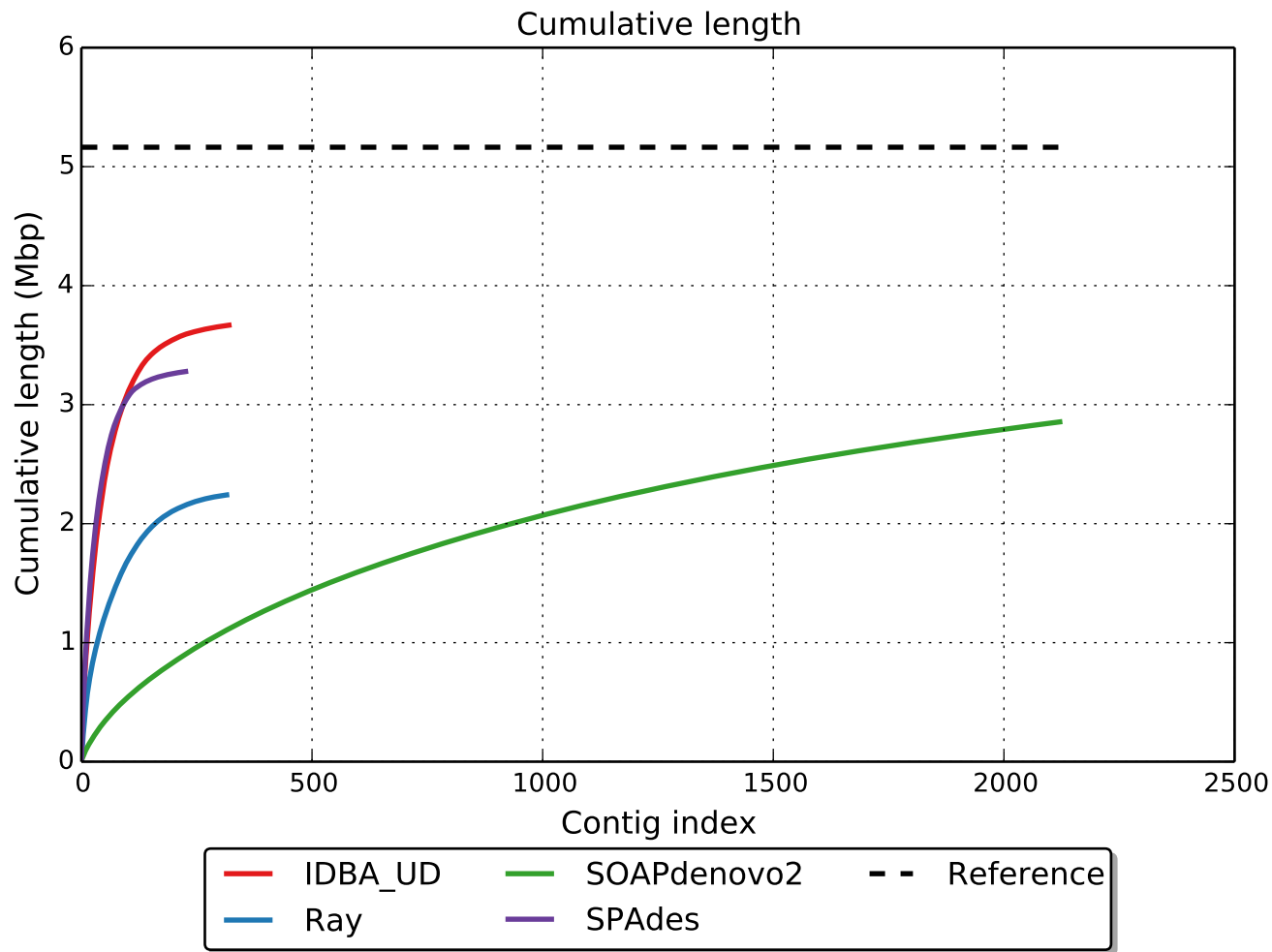


— IDBA\_UD    — SOAPdenovo2    — SPAdes  
— Ray

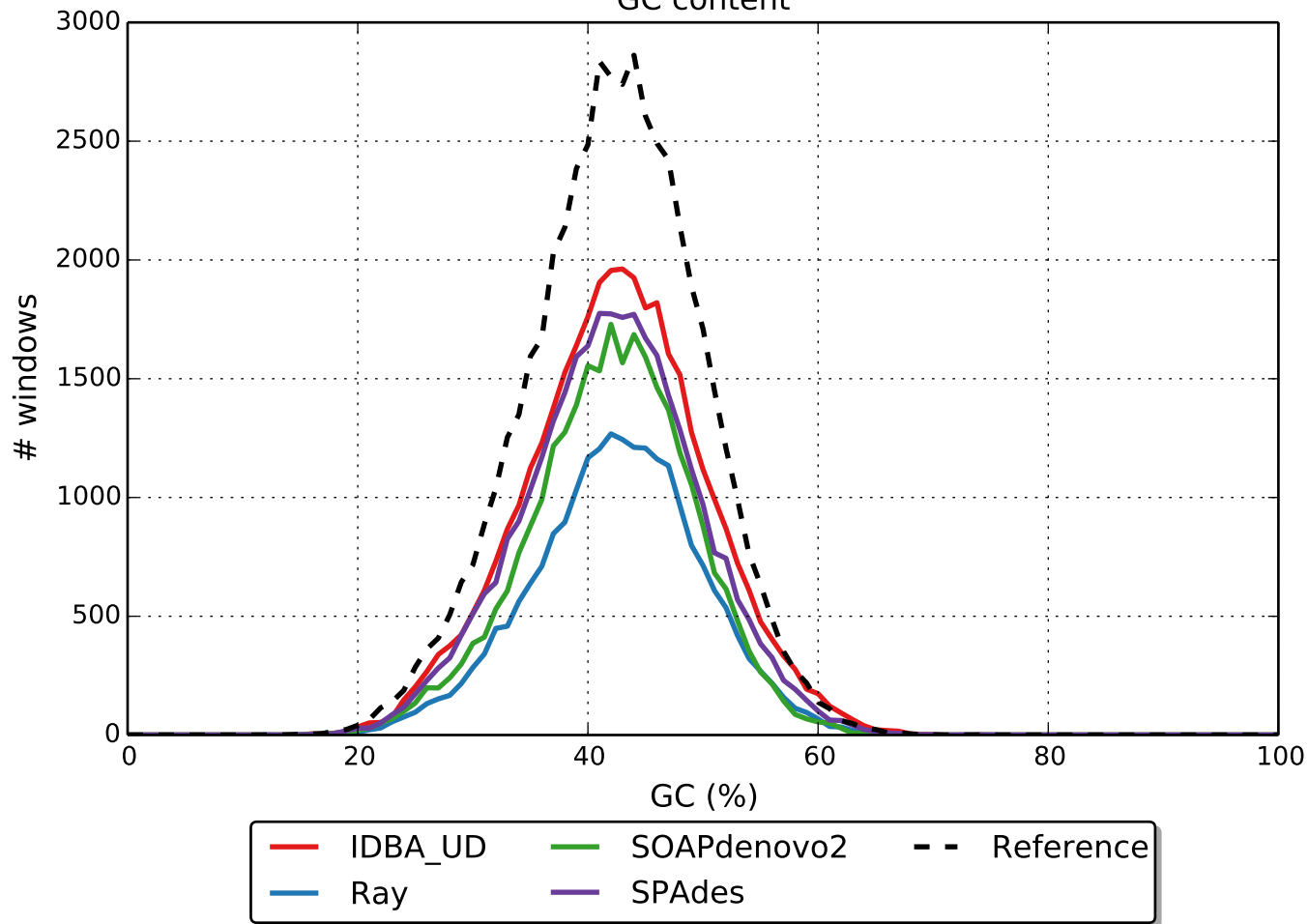
NGx



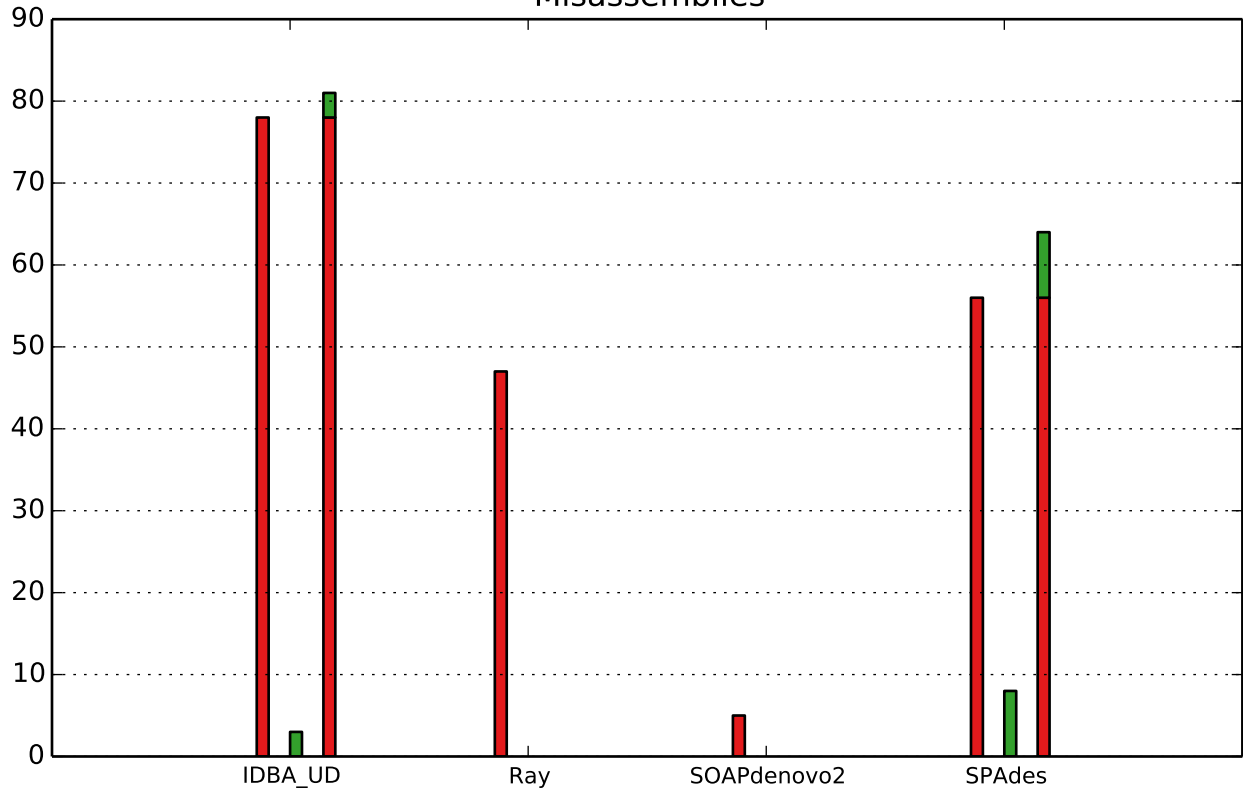
— IDBA\_UD    — SOAPdenovo2    — SPAdes  
— Ray



GC content



# Misassemblies

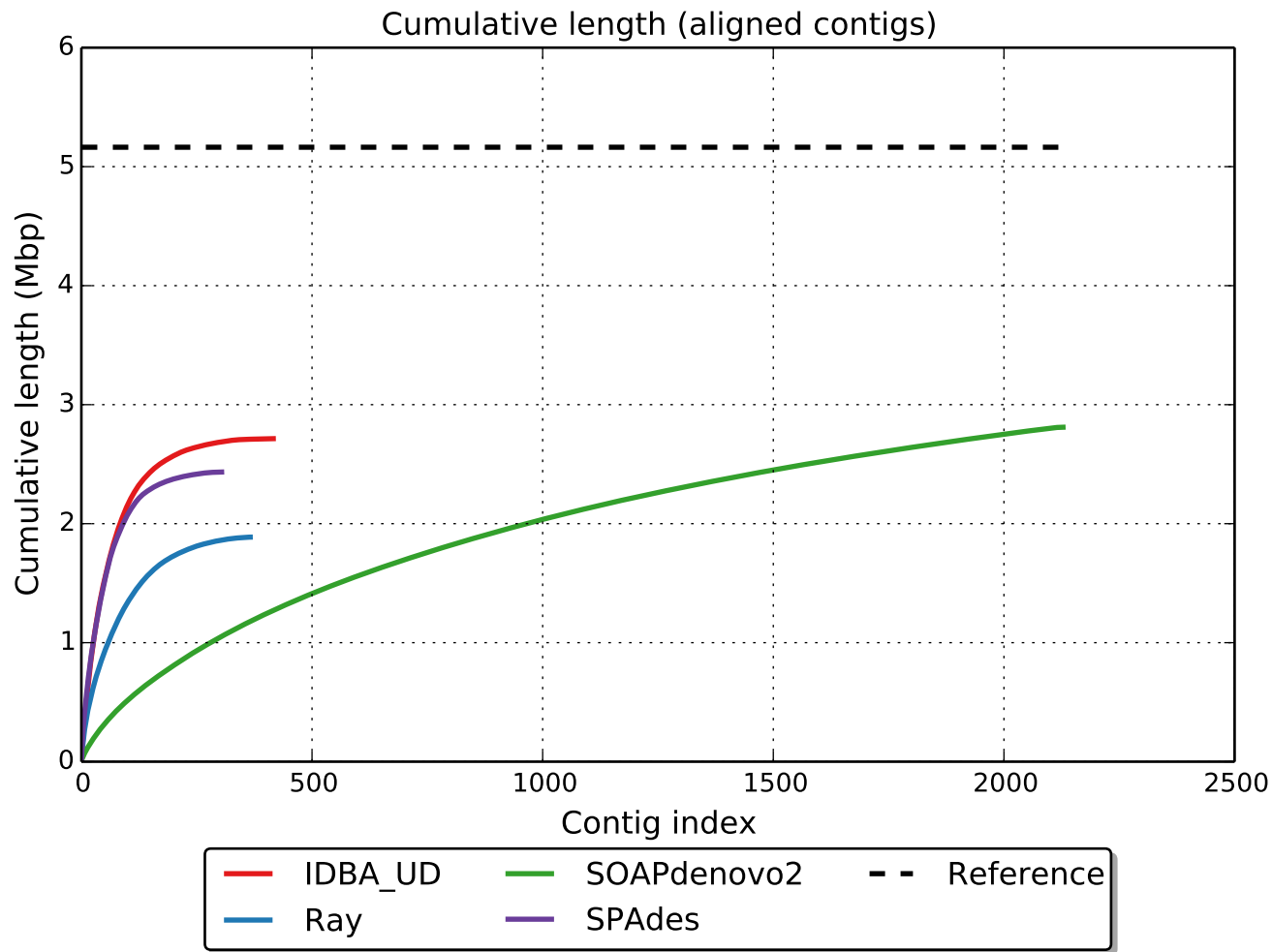


# relocations

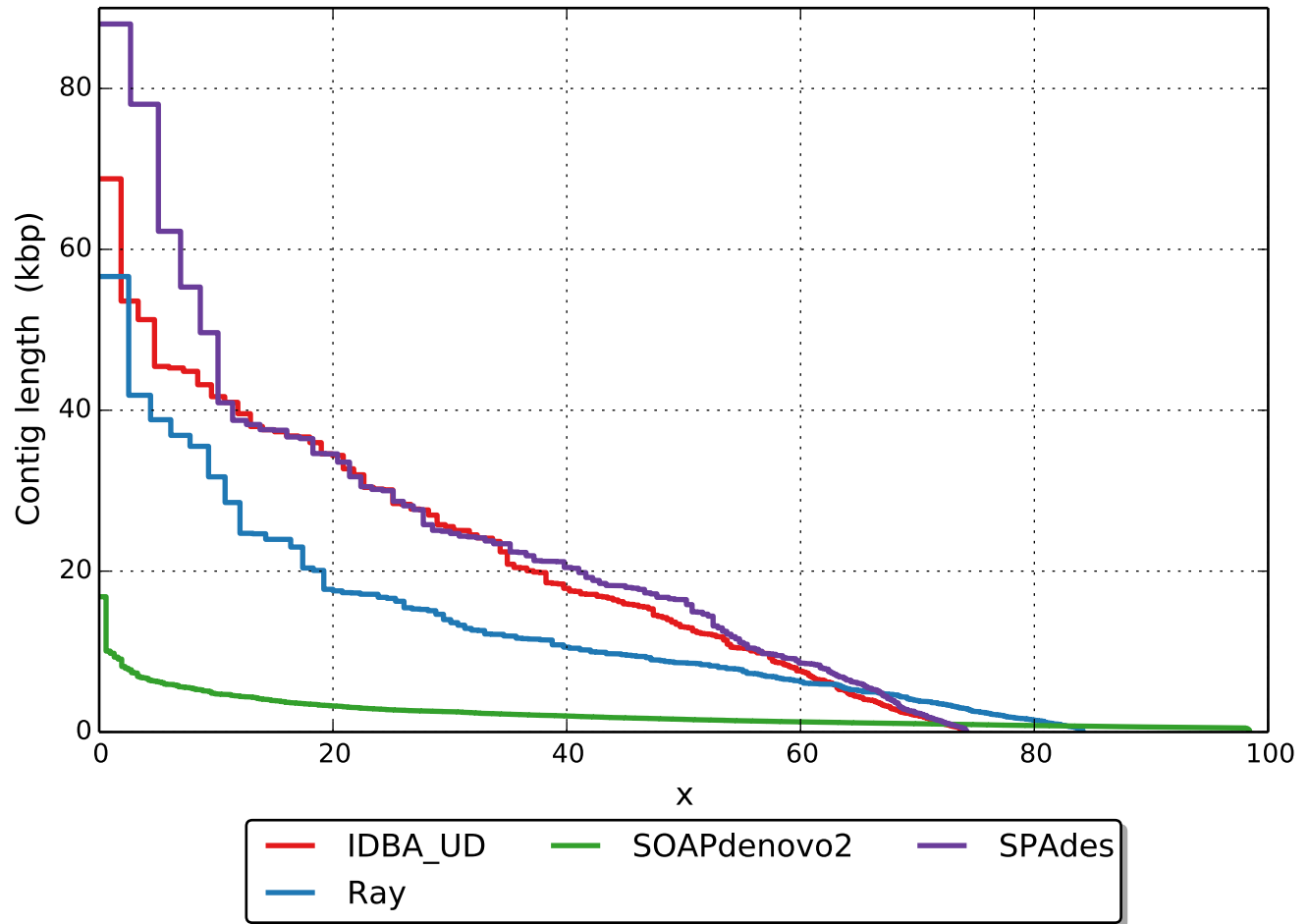


# inversions





NAx



# NGAx

